Full wwPDB X-ray Structure Validation Report ⓘ

Mar 30, 2026 – 01:06 PM UTC

PDB ID	:	4WSD / pdb_00004wsd
Title	:	Complex of 70S ribosome with tRNA-Phe and mRNA with C-A mismatch in the second position in the A-site and with antibiotic paromomycin.
Authors	:	Rozov, A.; Demeshkina, N.; Yusupov, M.; Yusupova, G.
Deposited on	:	2014-10-27
Resolution	:	2.95 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references ⓘ) were used in the production of this report:

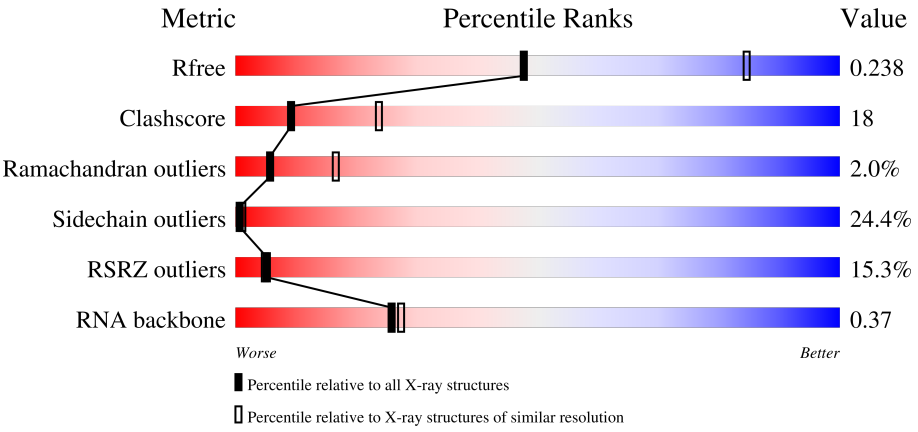
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.95 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1130 (2.98-2.94)
Clashscore	190562	1157 (2.98-2.94)
Ramachandran outliers	187476	1101 (2.98-2.94)
Sidechain outliers	187428	1101 (2.98-2.94)
RSRZ outliers	180081	1130 (2.98-2.94)
RNA backbone	3983	1046 (3.16-2.76)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	13	1522	9% 43% 42% 13%
1	1G	1522	14% 38% 46% 14%
2	12	256	34% 37% 39% 16% 7%
2	1E	256	23% 38% 44% 11% 7%

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Mol	Chain	Length	Quality of chain
3	22	239	40% 37% 40% 10% 14%
3	2E	239	8% 48% 30% 8% 14%
4	32	209	24% 49% 39% 10%
4	3E	209	11% 47% 41% 11%
5	42	162	35% 42% 39% 12% 7%
5	4E	162	12% 52% 30% 12% 7%
6	52	101	8% 54% 35% 11%
6	5E	101	9% 51% 42% 7%
7	62	156	28% 51% 38% 9%
7	6E	156	17% 55% 33% 11%
8	72	138	23% 60% 28% 9%
8	7E	138	15% 46% 41% 14%
9	82	128	34% 43% 44% 9%
9	8E	128	16% 42% 45% 12%
10	1A	105	23% 38% 45% 10% 6%
10	1I	105	32% 38% 42% 13% 6%
11	2A	129	21% 50% 28% 12% 10%
11	2I	129	12% 54% 29% 6% 10%
12	3A	132	29% 50% 30% 12% 5%
12	3I	132	20% 48% 34% 12% 5%
13	4A	126	35% 38% 41% 13% 7%
13	4I	126	12% 43% 37% 13% 6%
14	5A	61	34% 49% 38% 8% 5%
14	5I	61	8% 49% 36% 11%
15	6A	89	16% 49% 42% 8%

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Mol	Chain	Length	Quality of chain
15	6I	89	12% 56% 33% 10%
16	7A	88	8% 44% 44% 7% 5%
16	7I	88	25% 33% 51% 10% 5%
17	8A	105	21% 58% 32% 5% 5%
17	8I	105	18% 51% 34% 9% 5%
18	9A	88	9% 49% 28% 18%
18	9I	88	9% 43% 33% 6% 18%
19	AA	93	30% 29% 38% 17% 16%
19	AI	93	17% 41% 27% 15% 13%
20	BA	106	35% 46% 38% 8% 7%
20	BI	106	45% 39% 41% 12% 7%
21	1B	27	30% 37% 48% 7% 7%
21	1F	27	7% 59% 26% 7% 7%
22	1K	76	25% 26% 45% 26%
23	2K	77	5% 47% 32% 21%
23	2L	77	13% 42% 43% 13%
24	3K	76	25% 21% 37% 38%
25	4K	30	20% 17% 7% 57%
25	4L	30	3% 10% 13% 13% 63%
26	14	2917	7% 43% 44% 13%
26	1H	2917	6% 43% 42% 14%
27	16	122	2% 46% 40% 14%
27	1J	122	16% 31% 47% 22%
28	11	276	4% 50% 35% 13%
28	19	276	11% 50% 34% 12%

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Mol	Chain	Length	Quality of chain
29	21	206	14% 40% 37% 20%
29	29	206	22% 41% 38% 16% 5%
30	31	210	11% 45% 40% 10%
30	39	210	16% 35% 45% 15% 5%
31	41	182	14% 47% 40% 13%
31	49	182	22% 42% 48% 9%
32	51	180	18% 40% 36% 17%
32	59	180	39% 34% 43% 16% 6%
33	61	148	22% 41% 36% 17%
33	69	148	45% 43% 36% 15% 5%
34	15	140	23% 49% 34% 14%
34	58	140	14% 48% 38% 10%
35	25	122	7% 48% 39% 11%
35	68	122	10% 52% 39% 8%
36	35	150	21% 40% 35% 17% 8%
36	78	150	7% 39% 33% 25%
37	45	141	21% 37% 44% 17%
37	88	141	6% 42% 30% 23%
38	55	118	13% 40% 45% 13%
38	98	118	15% 36% 47% 14%
39	65	112	21% 29% 52% 17%
39	A8	112	10% 30% 46% 21%
40	75	146	12% 34% 45% 14% 6%
40	B8	146	20% 35% 38% 18% 6%
41	85	118	19% 55% 32% 10%

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Mol	Chain	Length	Quality of chain
41	C8	118	16% 37% 48% 13%
42	95	101	33% 37% 43% 17%
42	D8	101	26% 46% 44% 9%
43	A5	113	4% 50% 34% 17%
43	E8	113	12% 51% 35% 12%
44	B5	96	7% 43% 45% 9%
44	F8	96	6% 50% 33% 14%
45	C5	110	38% 38% 32% 24% 5%
45	G8	110	17% 29% 41% 19% 5% 5%
46	D5	206	24% 30% 44% 11% 13%
46	H8	206	15% 31% 40% 11% 15%
47	E5	85	13% 45% 33% 13% 9%
47	I8	85	14% 46% 34% 13% 6%
48	F5	98	28% 46% 36% 13%
48	J8	98	14% 48% 34% 16%
49	G5	72	15% 44% 31% 11% 7% 7%
49	K8	72	17% 22% 42% 25% 7%
50	H5	60	22% 50% 42% 7%
50	L8	60	12% 43% 33% 17% 5%
51	I5	71	24% 23% 48% 13% 15%
51	M8	71	27% 39% 27% 25% 7%
52	J5	60	23% 47% 37% 12%
52	N8	60	22% 53% 22% 18%
53	K5	54	52% 28% 33% 19% 17%
53	O8	54	24% 20% 30% 30% 17%

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Mol	Chain	Length	Quality of chain
54	L5	49	4% 47% 45% 6%
54	P8	49	4% 47% 39% 6% 8%
55	M5	65	18% 34% 32% 18% 8% 8%
55	Q8	65	34% 11% 31% 25% 26% 8%
56	1L	76	30% 28% 38% 33%
57	3L	76	34% 16% 50% 28% 7%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
56	PSU	1L	32	-	-	-	X
58	MG	13	1627	-	-	-	X
58	MG	13	1662	-	-	-	X
58	MG	13	1701	-	-	-	X
58	MG	13	1704	-	-	-	X
58	MG	13	1710	-	-	-	X
58	MG	13	1713	-	-	-	X
58	MG	14	3019	-	-	-	X
58	MG	14	3023	-	-	-	X
58	MG	14	3028	-	-	-	X
58	MG	14	3050	-	-	-	X
58	MG	14	3051	-	-	-	X
58	MG	14	3089	-	-	-	X
58	MG	14	3130	-	-	-	X
58	MG	14	3140	-	-	-	X
58	MG	14	3160	-	-	-	X
58	MG	14	3178	-	-	-	X
58	MG	14	3239	-	-	-	X
58	MG	14	3287	-	-	-	X
58	MG	1G	1601	-	-	-	X
58	MG	1G	1616	-	-	-	X
58	MG	1G	1619	-	-	-	X
58	MG	1G	1665	-	-	-	X
58	MG	1G	1677	-	-	-	X
58	MG	1H	3016	-	-	-	X
58	MG	1H	3020	-	-	-	X
58	MG	1H	3051	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
58	MG	1H	3054	-	-	-	X
58	MG	1H	3098	-	-	-	X
58	MG	1H	3162	-	-	-	X
58	MG	1H	3325	-	-	-	X
58	MG	1J	202	-	-	-	X
58	MG	1J	204	-	-	-	X
58	MG	25	201	-	-	-	X

2 Entry composition (i)

There are 61 unique types of molecules in this entry. The entry contains 300252 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	13	1498	Total	C	N	O	P	0	0	0
			32207	14334	5973	10402	1498			
1	1G	1498	Total	C	N	O	P	0	0	0
			32204	14334	5973	10400	1497			

- Molecule 2 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	1E	237	Total	C	N	O	S	0	0	0
			1924	1228	344	347	5			
2	12	237	Total	C	N	O	S	0	0	0
			1924	1228	344	347	5			

- Molecule 3 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	2E	205	Total	C	N	O	S	0	0	0
			1605	1011	313	280	1			
3	22	206	Total	C	N	O	S	0	0	0
			1612	1016	314	281	1			

- Molecule 4 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	3E	208	Total	C	N	O	S	0	0	0
			1702	1066	339	290	7			
4	32	208	Total	C	N	O	S	0	0	0
			1702	1066	339	290	7			

- Molecule 5 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	4E	151	Total	C	N	O	S	0	0	0
			1155	729	218	204	4			
5	42	151	Total	C	N	O	S	0	0	0
			1155	729	218	204	4			

- Molecule 6 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	5E	101	Total	C	N	O	S	0	0	0
			842	531	155	153	3			
6	52	101	Total	C	N	O	S	0	0	0
			842	531	155	153	3			

- Molecule 7 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	6E	155	Total	C	N	O	S	0	0	0
			1256	781	252	217	6			
7	62	152	Total	C	N	O	S	0	0	0
			1243	774	249	214	6			

- Molecule 8 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	7E	138	Total	C	N	O	S	0	0	0
			1115	705	215	192	3			
8	72	138	Total	C	N	O	S	0	0	0
			1115	705	215	192	3			

- Molecule 9 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
9	8E	127	Total	C	N	O	0	0	0
			1009	639	197	173			
9	82	124	Total	C	N	O	0	0	0
			983	624	190	169			

- Molecule 10 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	1I	99	Total	C	N	O	S	0	0	0
			801	504	157	139	1			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	1A	99	Total	C	N	O	S	0	0	0
			801	504	157	139	1			

- Molecule 11 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	2I	116	Total	C	N	O	S	0	0	0
			864	537	164	160	3			
11	2A	116	Total	C	N	O	S	0	0	0
			864	537	164	160	3			

- Molecule 12 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	3I	125	Total	C	N	O	S	0	0	0
			975	614	196	164	1			
12	3A	125	Total	C	N	O	S	0	0	0
			975	614	196	164	1			

- Molecule 13 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	4I	118	Total	C	N	O	S	0	0	0
			938	580	193	163	2			
13	4A	117	Total	C	N	O	S	0	0	0
			933	577	192	162	2			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
4I	119	ALA	GLY	conflict	UNP P80377
4A	119	ALA	GLY	conflict	UNP P80377

- Molecule 14 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	5I	60	Total	C	N	O	S	0	0	0
			491	312	104	71	4			
14	5A	58	Total	C	N	O	S	0	0	0
			475	303	99	69	4			

- Molecule 15 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
15	6I	88	Total	C	N	O	S	0	0	0
			733	459	147	125	2			
15	6A	88	Total	C	N	O	S	0	0	0
			733	459	147	125	2			

- Molecule 16 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
16	7I	84	Total	C	N	O	S	0	0	0
			705	446	140	118	1			
16	7A	84	Total	C	N	O	S	0	0	0
			705	446	140	118	1			

- Molecule 17 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
17	8I	100	Total	C	N	O	S	0	0	0
			834	534	155	143	2			
17	8A	100	Total	C	N	O	S	0	0	0
			834	534	155	143	2			

- Molecule 18 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
18	9I	72	Total	C	N	O	0	0	0
			590	376	117	97			
18	9A	72	Total	C	N	O	0	0	0
			590	376	117	97			

- Molecule 19 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	AI	81	Total	C	N	O	S	0	0	0
			647	413	119	113	2			
19	AA	78	Total	C	N	O	S	0	0	0
			624	398	115	109	2			

- Molecule 20 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	BI	99	Total	C	N	O	S	0	0	0
			762	470	162	128	2			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	BA	99	Total	C	N	O	S	0	0	0
			762	470	162	128	2			

- Molecule 21 is a protein called 30S ribosomal protein Thx.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
21	1F	25	Total	C	N	O	0	0	0
			217	134	52	31			
21	1B	25	Total	C	N	O	0	0	0
			217	134	52	31			

- Molecule 22 is a RNA chain called tRNA-Phe.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
22	1K	76	Total	C	N	O	P	S	0	0	0
			1627	730	290	530	75	2			

- Molecule 23 is a RNA chain called tRNA-fMet.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
23	2K	77	Total	C	N	O	P	S	0	0	0
			1646	735	298	535	77	1			
23	2L	77	Total	C	N	O	P	S	0	0	0
			1646	735	298	535	77	1			

- Molecule 24 is a RNA chain called tRNA-Phe.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
24	3K	75	Total	C	N	O	P	S	0	0	0
			1603	719	285	524	74	1			

- Molecule 25 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
25	4K	13	Total	C	N	O	P	0	0	0
			279	126	55	85	13			
25	4L	11	Total	C	N	O	P	0	0	0
			235	106	45	73	11			

- Molecule 26 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	1H	2912	Total	C	N	O	P	0	0	0
			62707	27911	11722	20163	2911			
26	14	2909	Total	C	N	O	P	0	0	0
			62647	27884	11716	20139	2908			

- Molecule 27 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
27	16	122	Total	C	N	O	P	0	0	0
			2617	1166	486	844	121			
27	1J	122	Total	C	N	O	P	0	0	0
			2617	1166	486	844	121			

- Molecule 28 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
28	11	272	Total	C	N	O	S	0	0	0
			2115	1335	420	357	3			
28	19	273	Total	C	N	O	S	0	0	0
			2120	1338	421	358	3			

- Molecule 29 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
29	21	205	Total	C	N	O	S	0	0	0
			1568	991	300	271	6			
29	29	205	Total	C	N	O	S	0	0	0
			1568	991	300	271	6			

- Molecule 30 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
30	31	202	Total	C	N	O	S	0	0	0
			1585	1011	297	275	2			
30	39	208	Total	C	N	O	S	0	0	0
			1627	1037	304	283	3			

- Molecule 31 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
31	41	181	Total	C	N	O	S	0	0	0
			1473	942	268	259	4			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
31	49	181	Total	C	N	O	S	0	0	0
			1473	942	268	259	4			

- Molecule 32 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
32	51	174	Total	C	N	O	S	0	0	0
			1336	848	251	236	1			
32	59	170	Total	C	N	O	S	0	0	0
			1307	829	245	232	1			

- Molecule 33 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
33	61	146	Total	C	N	O	S	0	0	0
			1136	726	201	208	1			
33	69	146	Total	C	N	O	S	0	0	0
			1136	726	201	208	1			

- Molecule 34 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
34	58	138	Total	C	N	O	S	0	0	0
			1104	712	206	182	4			
34	15	138	Total	C	N	O	S	0	0	0
			1104	712	206	182	4			

- Molecule 35 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
35	68	122	Total	C	N	O	S	0	0	0
			932	588	171	169	4			
35	25	122	Total	C	N	O	S	0	0	0
			932	588	171	169	4			

- Molecule 36 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
36	78	150	Total	C	N	O	S	0	0	0
			1144	712	232	197	3			
36	35	150	Total	C	N	O	S	0	0	0
			1144	712	232	197	3			

- Molecule 37 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
37	88	138	Total	C	N	O	S	0	0	0
			1086	693	208	179	6			
37	45	141	Total	C	N	O	S	0	0	0
			1121	715	212	187	7			

- Molecule 38 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
38	98	118	Total	C	N	O	S	0	0	0
			967	604	203	159	1			
38	55	117	Total	C	N	O		0	0	0
			959	599	202	158				

- Molecule 39 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
39	A8	111	Total	C	N	O	0	0	0
			881	556	176	149			
39	65	111	Total	C	N	O	0	0	0
			881	556	176	149			

- Molecule 40 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
40	B8	137	Total	C	N	O	S	0	0	0
			1141	710	234	196	1			
40	75	137	Total	C	N	O	S	0	0	0
			1141	710	234	196	1			

- Molecule 41 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
41	C8	117	Total	C	N	O	S	0	0	0
			963	610	202	150	1			
41	85	117	Total	C	N	O	S	0	0	0
			963	610	202	150	1			

- Molecule 42 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
42	D8	101	Total	C	N	O	S	0	0	0
			778	501	142	134	1			
42	95	101	Total	C	N	O	S	0	0	0
			778	501	142	134	1			

- Molecule 43 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
43	E8	113	Total	C	N	O	S	0	0	0
			899	566	177	154	2			
43	A5	113	Total	C	N	O	S	0	0	0
			899	566	177	154	2			

- Molecule 44 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
44	F8	94	Total	C	N	O	S	0	0	0
			742	482	134	125	1			
44	B5	94	Total	C	N	O		0	0	0
			735	477	133	125				

- Molecule 45 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
45	G8	104	Total	C	N	O	S	0	0	0
			791	510	149	127	5			
45	C5	104	Total	C	N	O	S	0	0	0
			794	510	152	127	5			

- Molecule 46 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
46	H8	175	Total	C	N	O	S	0	0	0
			1397	892	251	251	3			
46	D5	179	Total	C	N	O	S	0	0	0
			1428	911	255	259	3			

- Molecule 47 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
47	I8	80	Total	C	N	O	S	0	0	0
			626	388	132	105	1			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
47	E5	77	Total	C	N	O	S	0	0	0
			612	379	129	103	1			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
I8	6	ALA	GLY	conflict	UNP P60493
I8	8	ALA	GLY	conflict	UNP P60493
E5	6	ALA	GLY	conflict	UNP P60493
E5	8	ALA	GLY	conflict	UNP P60493

- Molecule 48 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
48	J8	97	Total	C	N	O	S	0	0	0
			762	481	150	130	1			
48	F5	94	Total	C	N	O	S	0	0	0
			737	463	146	127	1			

- Molecule 49 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
49	K8	67	Total	C	N	O	S	0	0	0
			563	349	114	99	1			
49	G5	67	Total	C	N	O	S	0	0	0
			563	349	114	99	1			

- Molecule 50 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
50	L8	57	Total	C	N	O	0	0	0
			452	288	88	76			
50	H5	59	Total	C	N	O	0	0	0
			468	298	90	80			

- Molecule 51 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
51	M8	66	Total	C	N	O	S	0	0	0
			533	335	96	97	5			
51	I5	60	Total	C	N	O	S	0	0	0
			481	305	84	87	5			

- Molecule 52 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
52	N8	58	Total	C	N	O	S	0	0	0
			453	285	89	74	5			
52	J5	59	Total	C	N	O	S	0	0	0
			458	288	90	75	5			

- Molecule 53 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
53	O8	45	Total	C	N	O	S	0	0	0
			389	241	79	65	4			
53	K5	45	Total	C	N	O	S	0	0	0
			389	241	79	65	4			

- Molecule 54 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
54	P8	45	Total	C	N	O	S	0	0	0
			391	240	97	52	2			
54	L5	46	Total	C	N	O	S	0	0	0
			398	245	98	53	2			

- Molecule 55 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
55	Q8	60	Total	C	N	O	S	0	0	0
			480	306	98	74	2			
55	M5	60	Total	C	N	O	S	0	0	0
			477	303	98	74	2			

- Molecule 56 is a RNA chain called tRNA-Phe.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
56	1L	76	Total	C	N	O	P	S	0	0	0
			1627	730	290	531	75	1			

- Molecule 57 is a RNA chain called tRNA-Phe.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
57	3L	76	Total	C	N	O	P	S	0	0	0
			1624	725	290	532	76	1			

- Molecule 58 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
58	13	148	Total Mg 148 148	0	0
58	3E	2	Total Mg 2 2	0	0
58	5E	1	Total Mg 1 1	0	0
58	2I	1	Total Mg 1 1	0	0
58	5I	2	Total Mg 2 2	0	0
58	1K	2	Total Mg 2 2	0	0
58	2K	5	Total Mg 5 5	0	0
58	3K	1	Total Mg 1 1	0	0
58	4K	1	Total Mg 1 1	0	0
58	1H	520	Total Mg 520 520	0	0
58	16	13	Total Mg 13 13	0	0
58	11	4	Total Mg 4 4	0	0
58	21	2	Total Mg 2 2	0	0
58	41	2	Total Mg 2 2	0	0
58	78	1	Total Mg 1 1	0	0
58	88	2	Total Mg 2 2	0	0
58	98	2	Total Mg 2 2	0	0
58	G8	1	Total Mg 1 1	0	0
58	I8	1	Total Mg 1 1	0	0
58	L8	1	Total Mg 1 1	0	0
58	P8	1	Total Mg 1 1	0	0

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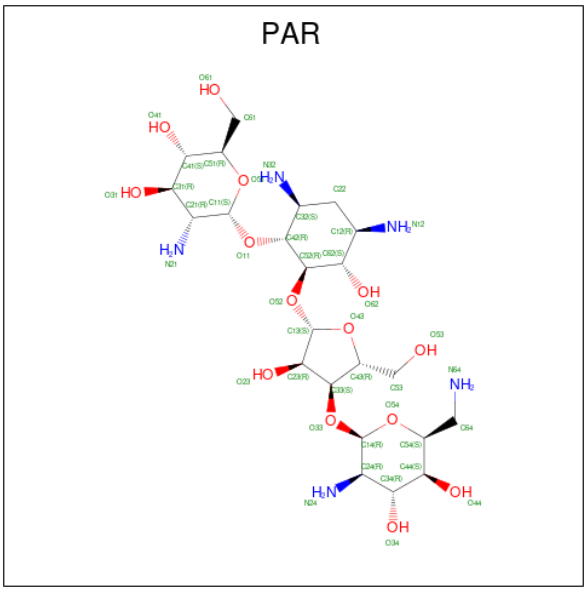
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
58	1G	96	Total Mg 96 96	0	0
58	2A	2	Total Mg 2 2	0	0
58	7A	1	Total Mg 1 1	0	0
58	2L	3	Total Mg 3 3	0	0
58	3L	2	Total Mg 2 2	0	0
58	14	407	Total Mg 407 407	0	0
58	1J	5	Total Mg 5 5	0	0
58	29	4	Total Mg 4 4	0	0
58	49	1	Total Mg 1 1	0	0
58	25	1	Total Mg 1 1	0	0
58	55	1	Total Mg 1 1	0	0
58	C5	1	Total Mg 1 1	0	0
58	J5	1	Total Mg 1 1	0	0

- Molecule 59 is PAROMOMYCIN (CCD ID: PAR) (formula: $C_{23}H_{45}N_5O_{14}$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
59	13	1	Total C N O 42 23 5 14	0	0
59	1G	1	Total C N O 42 23 5 14	0	0

- Molecule 60 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
60	3E	1	Total Zn 1 1	0	0
60	5I	1	Total Zn 1 1	0	0
60	G8	1	Total Zn 1 1	0	0
60	32	1	Total Zn 1 1	0	0
60	5A	1	Total Zn 1 1	0	0
60	C5	1	Total Zn 1 1	0	0

- Molecule 61 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
61	13	197	Total O 197 197	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
61	3E	3	Total O 3 3	0	0
61	8E	2	Total O 2 2	0	0
61	1I	2	Total O 2 2	0	0
61	3I	1	Total O 1 1	0	0
61	5I	2	Total O 2 2	0	0
61	6I	1	Total O 1 1	0	0
61	7I	1	Total O 1 1	0	0
61	1K	5	Total O 5 5	0	0
61	2K	6	Total O 6 6	0	0
61	3K	1	Total O 1 1	0	0
61	4K	2	Total O 2 2	0	0
61	1H	999	Total O 999 999	0	0
61	16	21	Total O 21 21	0	0
61	11	13	Total O 13 13	0	0
61	21	4	Total O 4 4	0	0
61	31	4	Total O 4 4	0	0
61	58	2	Total O 2 2	0	0
61	78	5	Total O 5 5	0	0
61	B8	1	Total O 1 1	0	0
61	C8	3	Total O 3 3	0	0
61	D8	1	Total O 1 1	0	0

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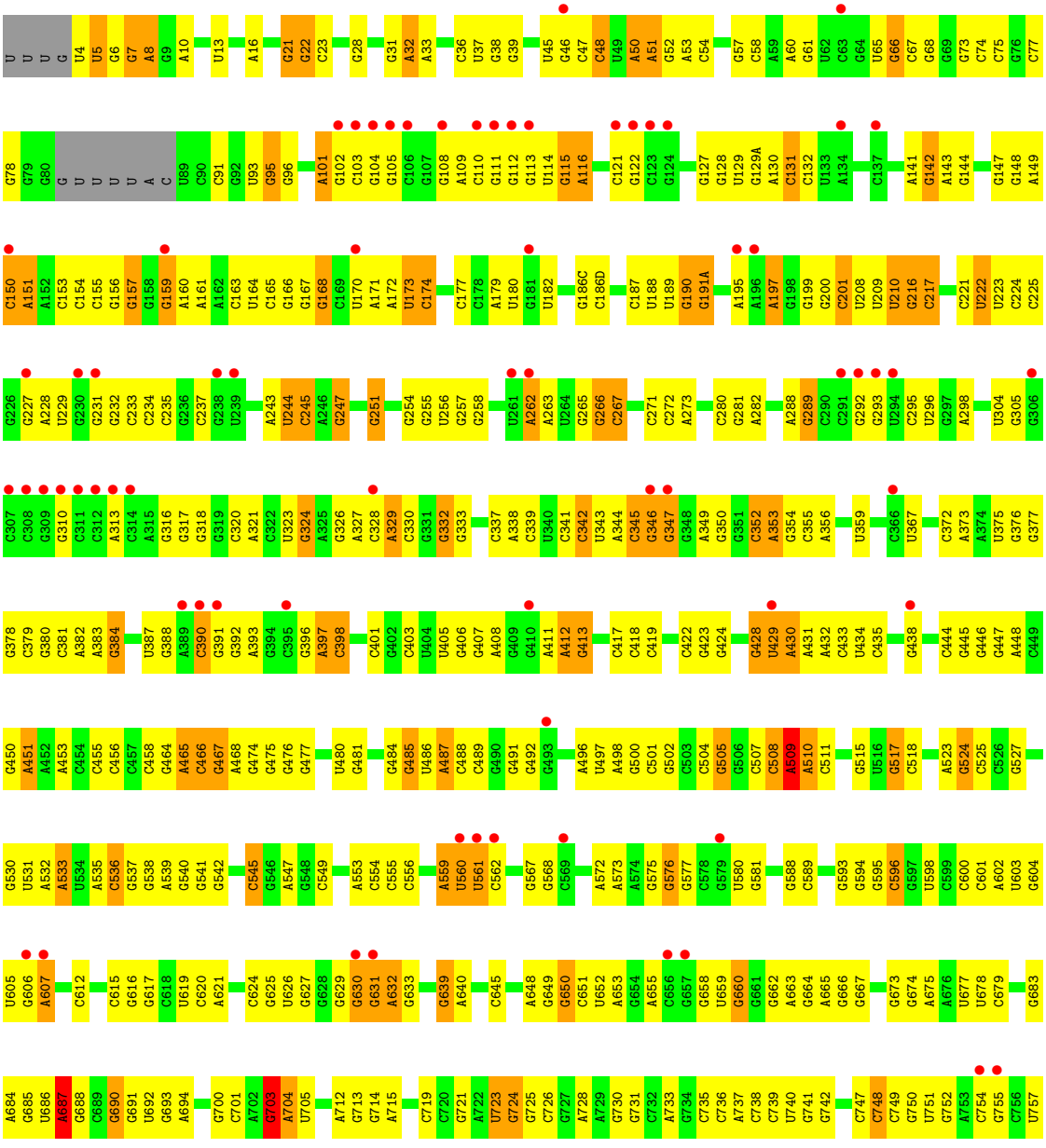
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
61	G8	4	Total O 4 4	0	0
61	I8	7	Total O 7 7	0	0
61	L8	1	Total O 1 1	0	0
61	P8	1	Total O 1 1	0	0
61	Q8	2	Total O 2 2	0	0
61	1G	82	Total O 82 82	0	0
61	7A	1	Total O 1 1	0	0
61	BA	1	Total O 1 1	0	0
61	3L	6	Total O 6 6	0	0
61	14	598	Total O 598 598	0	0
61	19	13	Total O 13 13	0	0
61	39	7	Total O 7 7	0	0
61	35	1	Total O 1 1	0	0
61	85	1	Total O 1 1	0	0
61	A5	1	Total O 1 1	0	0
61	G5	1	Total O 1 1	0	0
61	L5	1	Total O 1 1	0	0

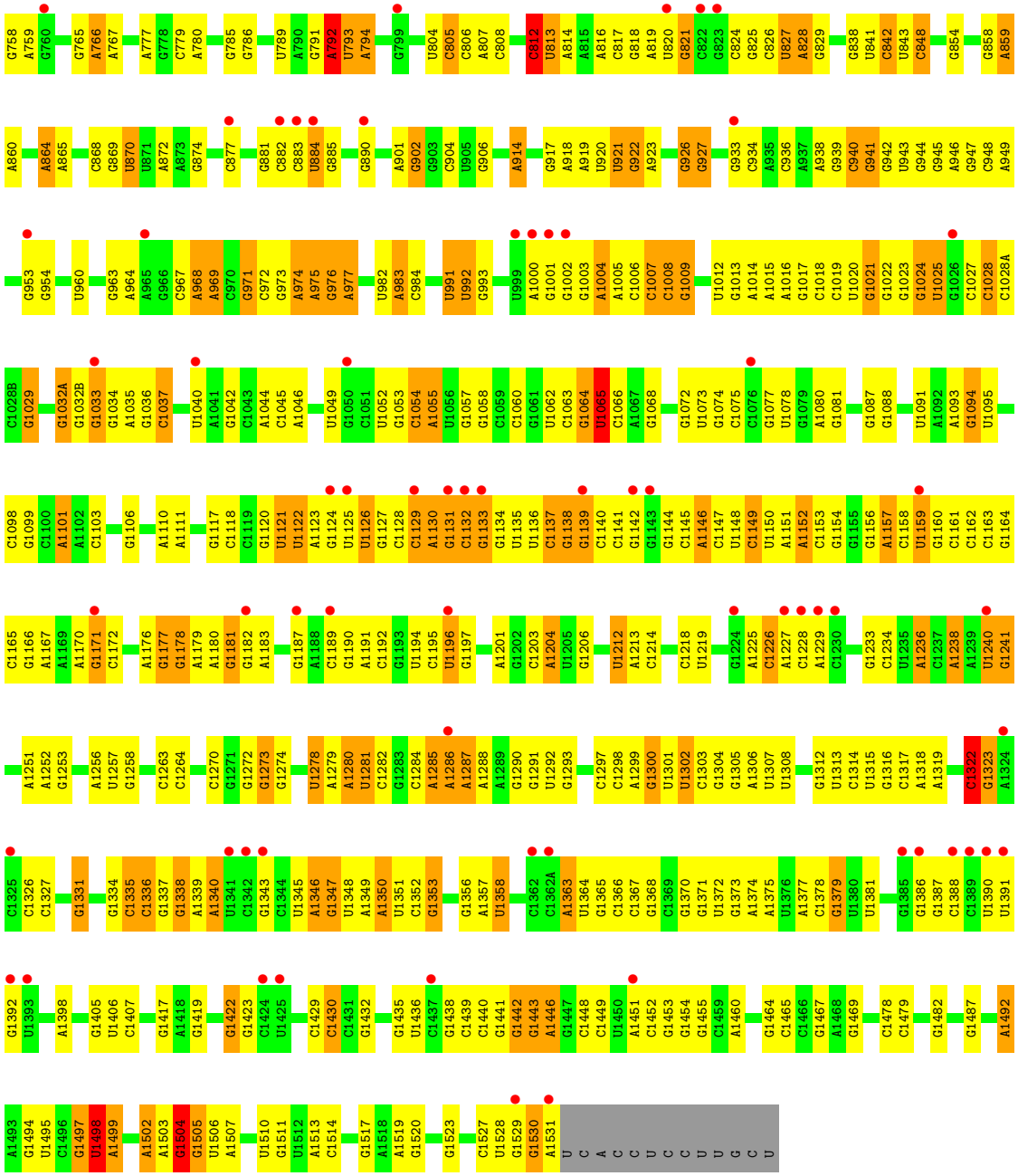
3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: 16S ribosomal RNA

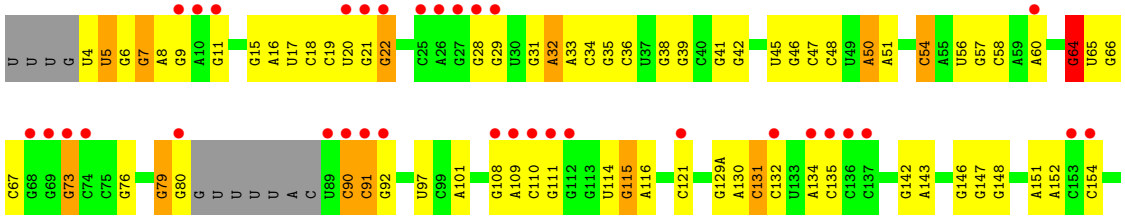
Chain 13:

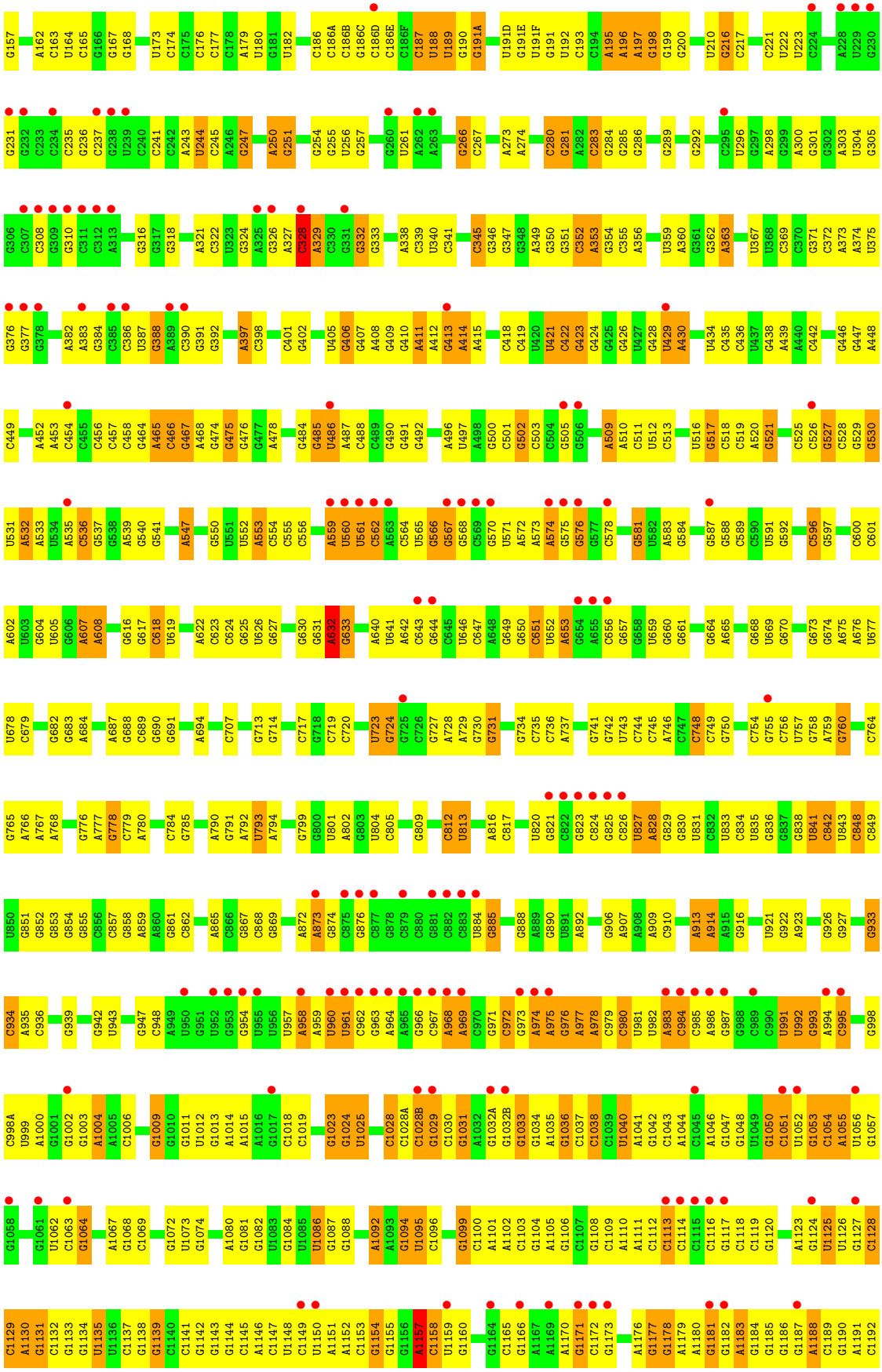


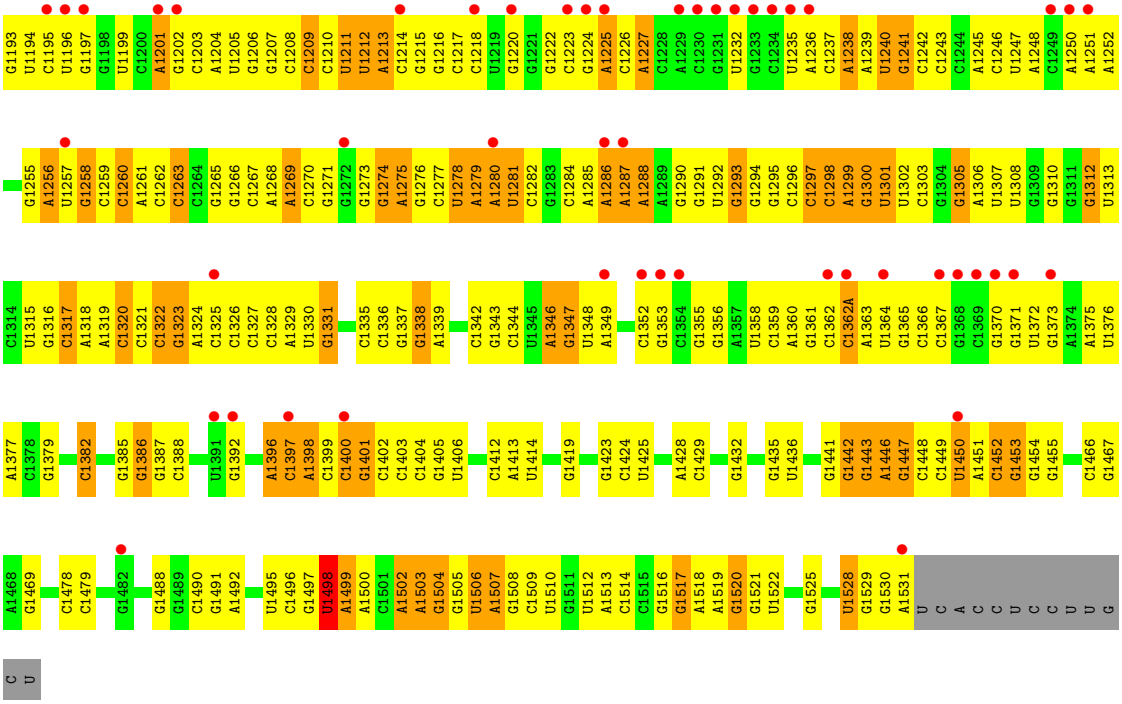


• Molecule 1: 16S ribosomal RNA

Chain 1G:

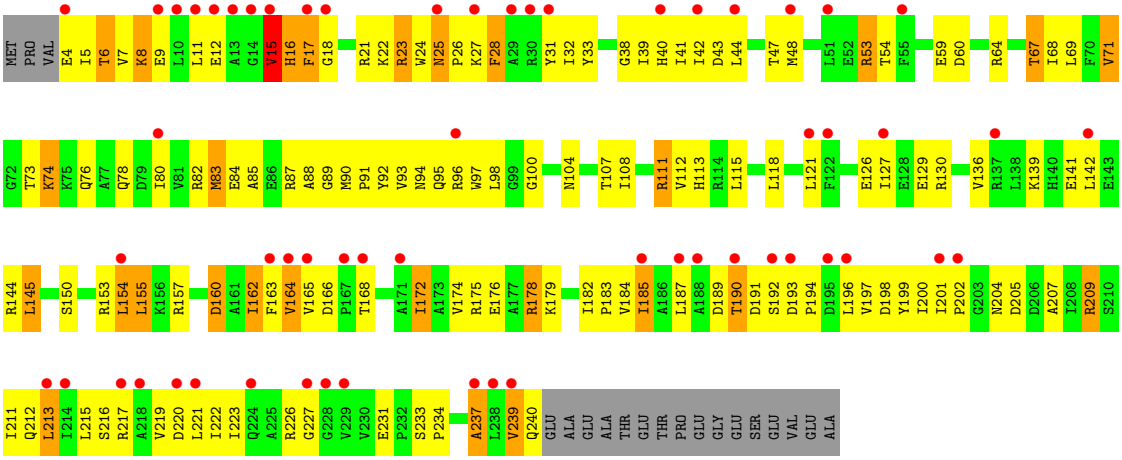






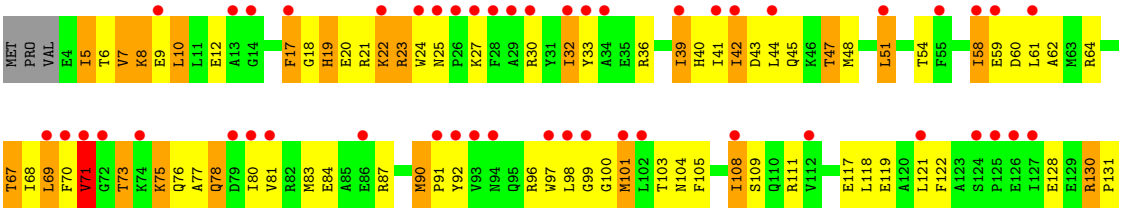
• Molecule 2: 30S ribosomal protein S2

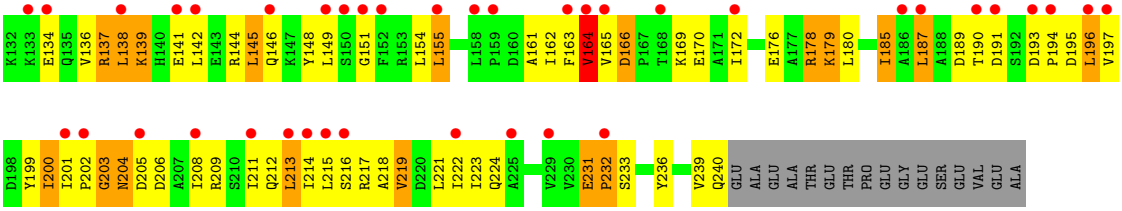
Chain 1E:

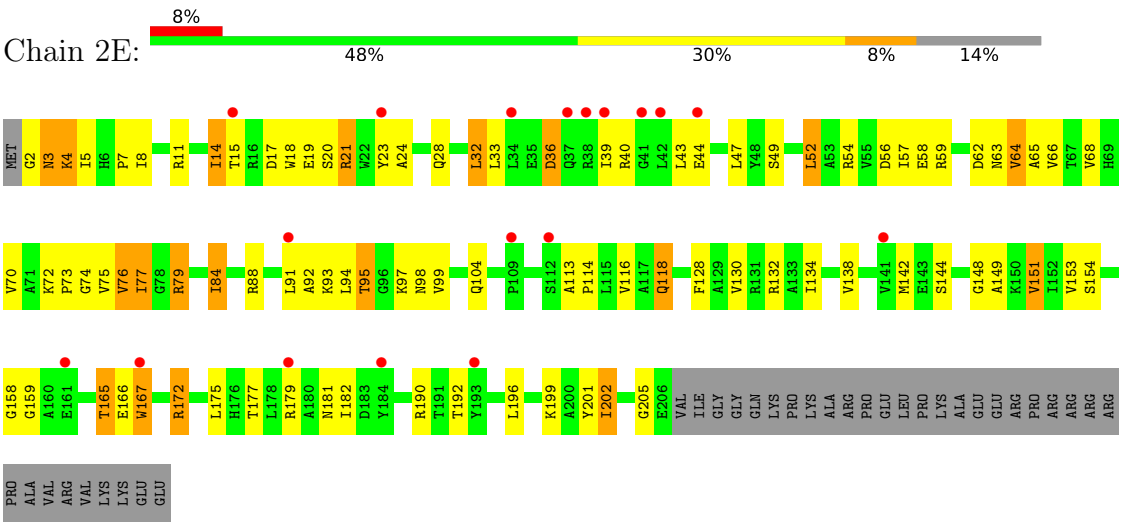


• Molecule 2: 30S ribosomal protein S2

Chain 12:





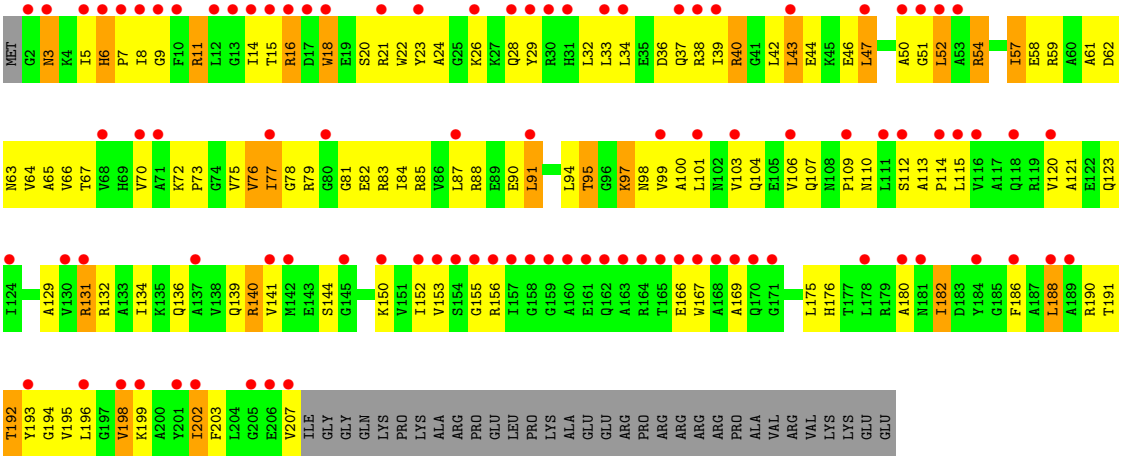


• Molecule 3: 30S ribosomal protein S3

Chain 2E:

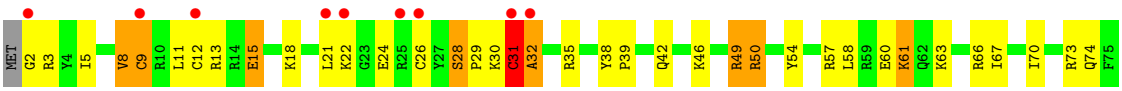
• Molecule 3: 30S ribosomal protein S3

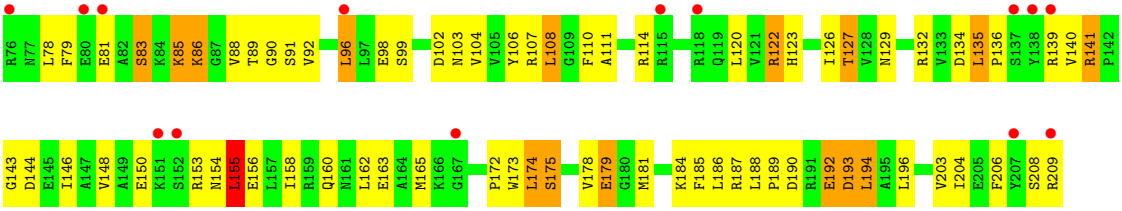
Chain 22:



• Molecule 4: 30S ribosomal protein S4

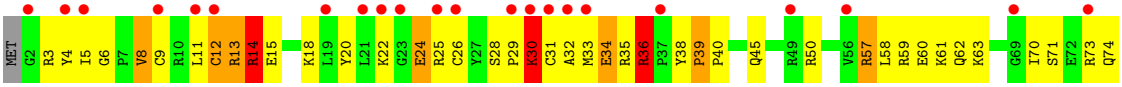
Chain 3E:

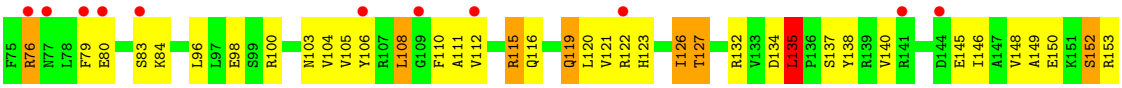


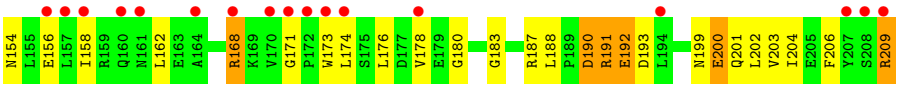


• Molecule 4: 30S ribosomal protein S4

Chain 32:

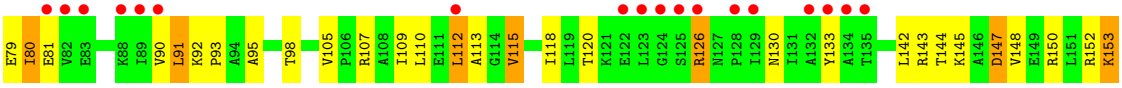


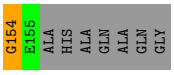




• Molecule 5: 30S ribosomal protein S5

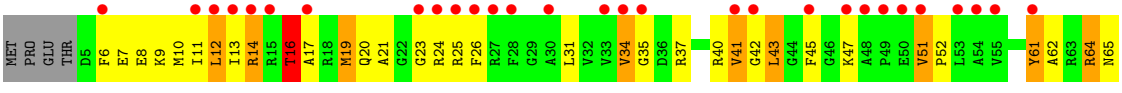
Chain 4E:

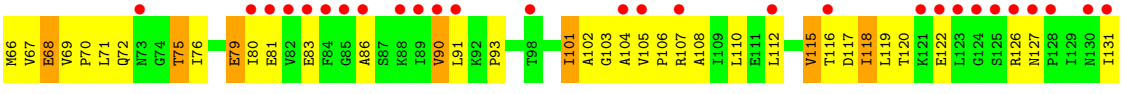


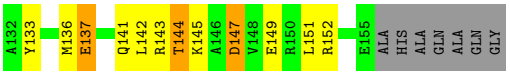


• Molecule 5: 30S ribosomal protein S5

Chain 42:

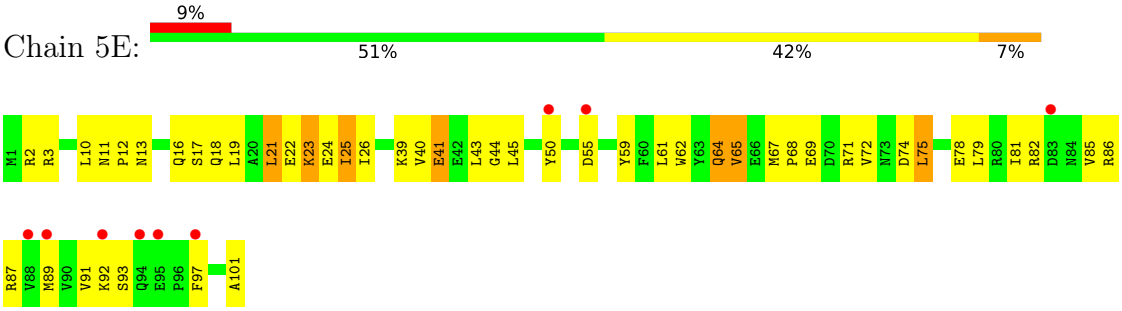






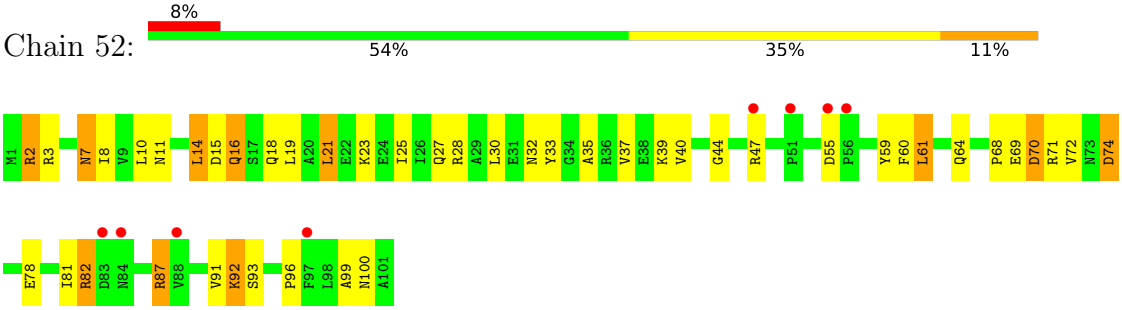
• Molecule 6: 30S ribosomal protein S6

Chain 5E:



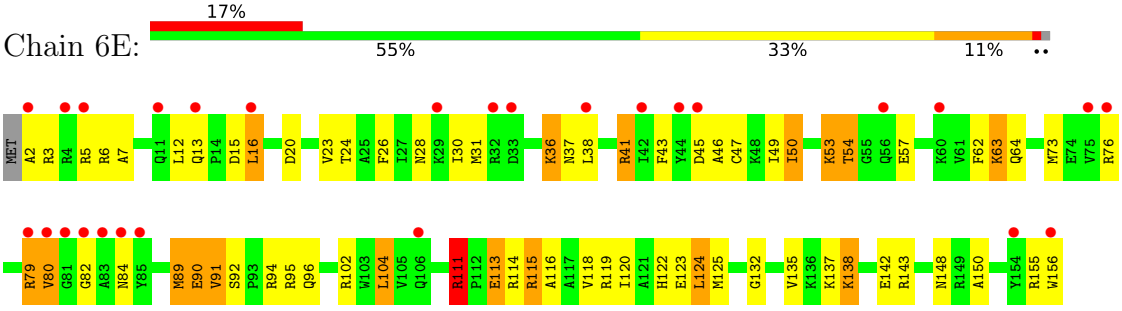
• Molecule 6: 30S ribosomal protein S6

Chain 52:



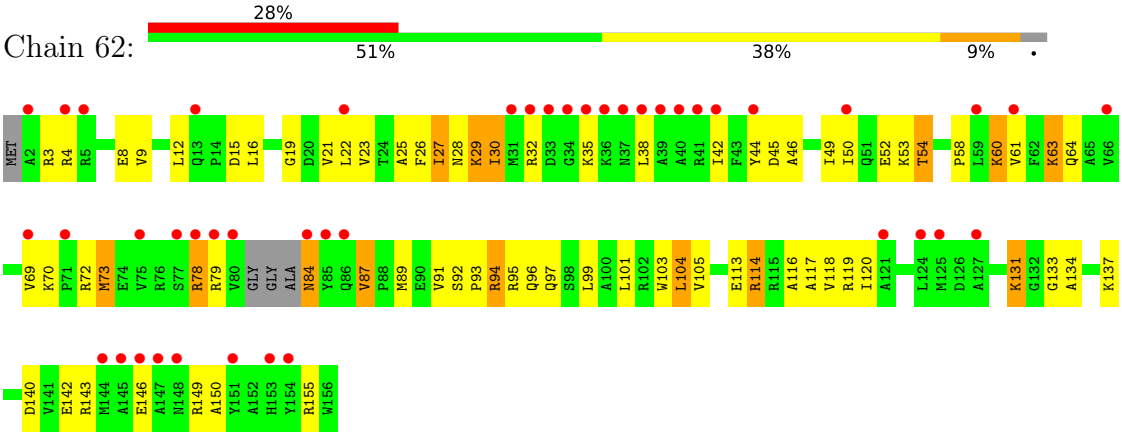
• Molecule 7: 30S ribosomal protein S7

Chain 6E:



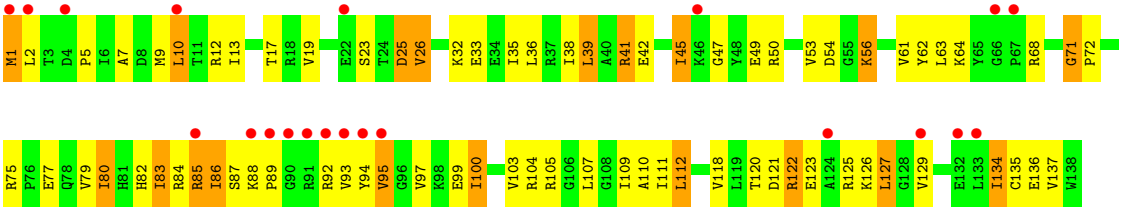
• Molecule 7: 30S ribosomal protein S7

Chain 62:



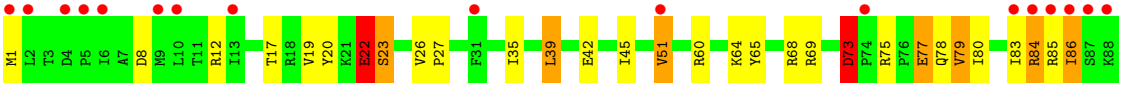
• Molecule 8: 30S ribosomal protein S8

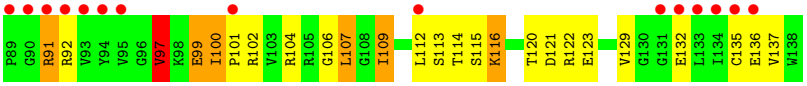
Chain 7E:



• Molecule 8: 30S ribosomal protein S8

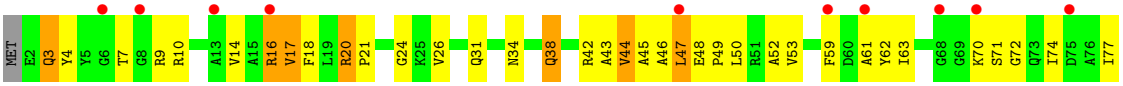
Chain 72:





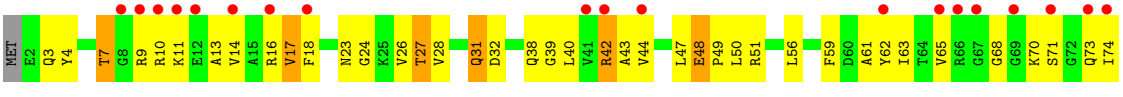
• Molecule 9: 30S ribosomal protein S9

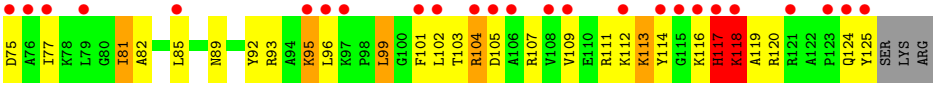
Chain 8E:



• Molecule 9: 30S ribosomal protein S9

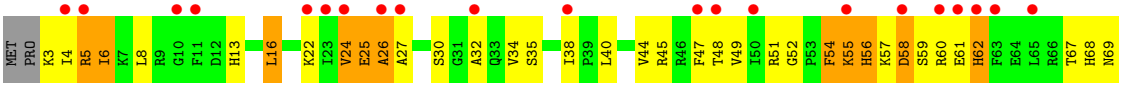
Chain 82:

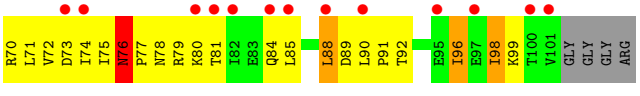




• Molecule 10: 30S ribosomal protein S10

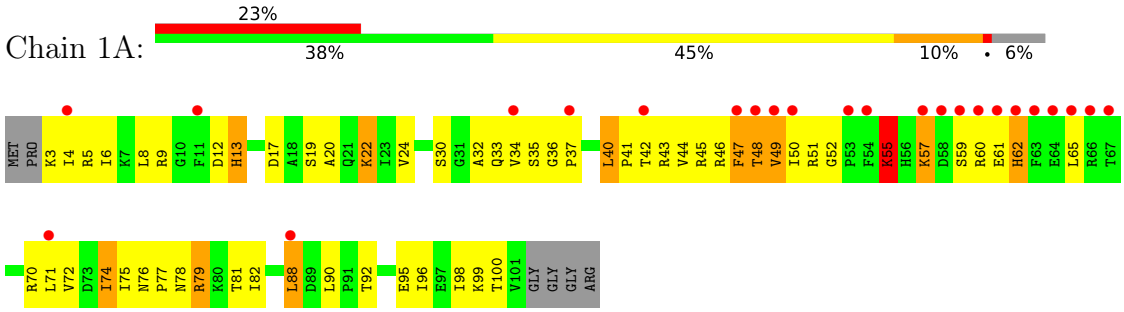
Chain 1I:





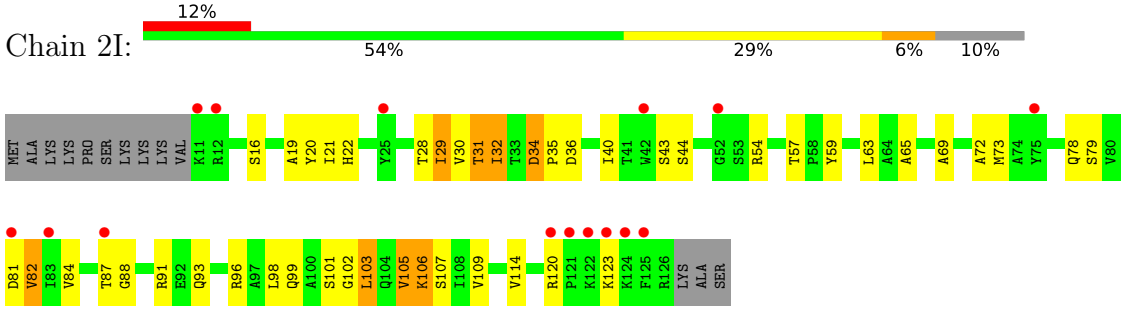
• Molecule 10: 30S ribosomal protein S10

Chain 1A:



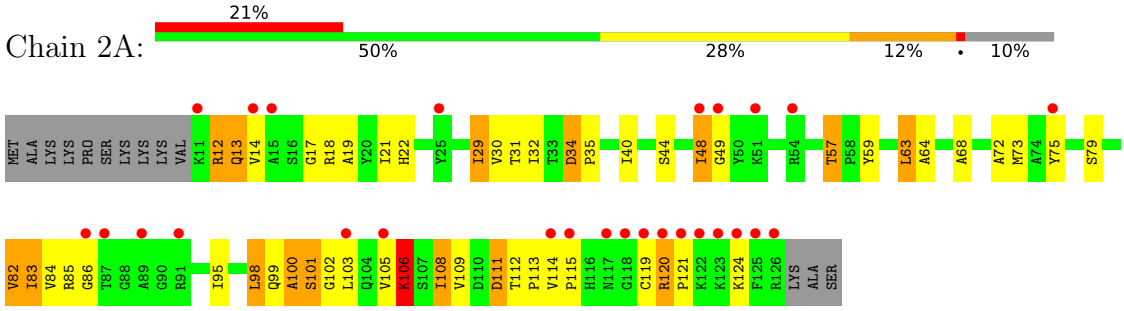
• Molecule 11: 30S ribosomal protein S11

Chain 2I:



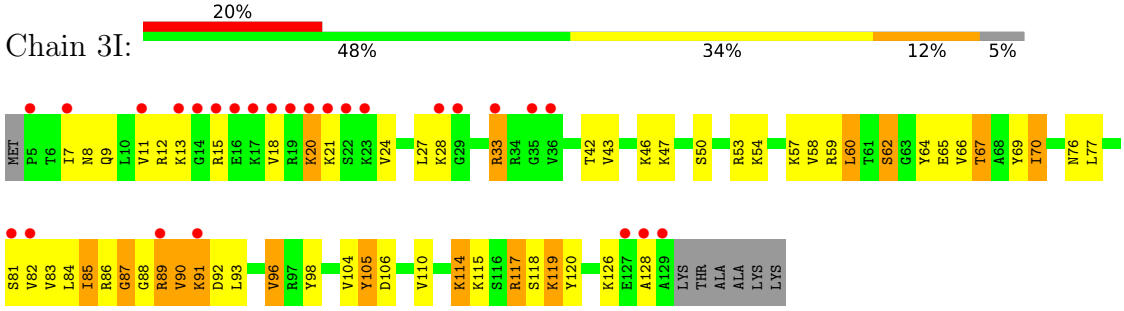
• Molecule 11: 30S ribosomal protein S11

Chain 2A:



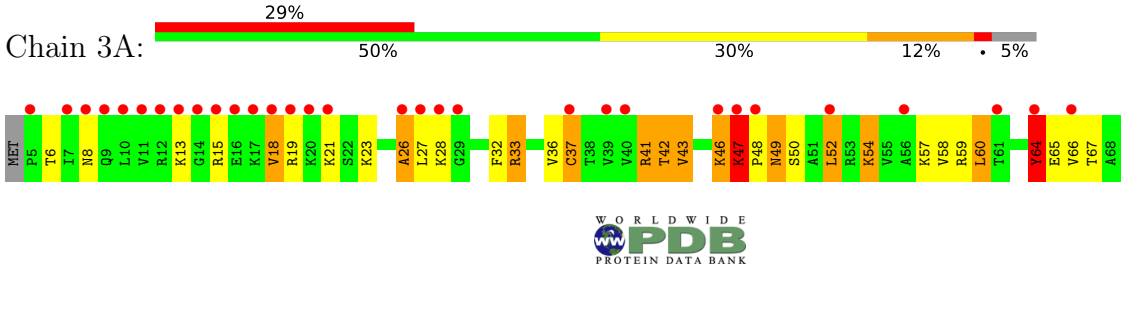
• Molecule 12: 30S ribosomal protein S12

Chain 3I:



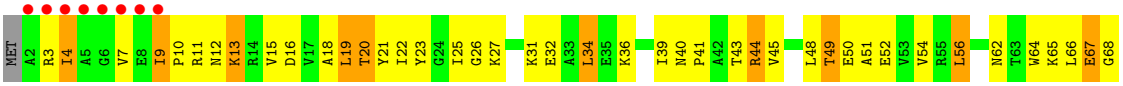
• Molecule 12: 30S ribosomal protein S12

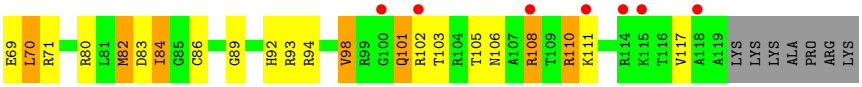
Chain 3A:



• Molecule 13: 30S ribosomal protein S13

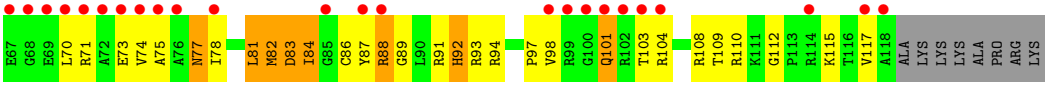
Chain 4I:





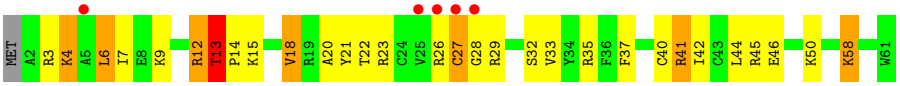
• Molecule 13: 30S ribosomal protein S13

Chain 4A:



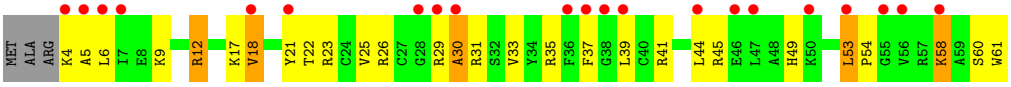
• Molecule 14: 30S ribosomal protein S14 type Z

Chain 5I:



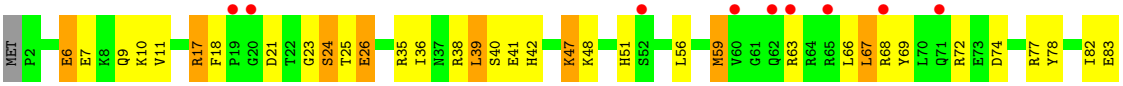
• Molecule 14: 30S ribosomal protein S14 type Z

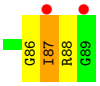
Chain 5A:



• Molecule 15: 30S ribosomal protein S15

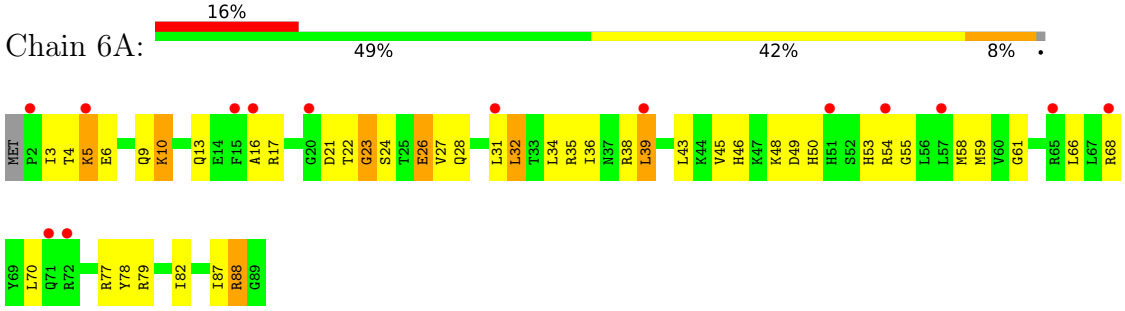
Chain 6I:





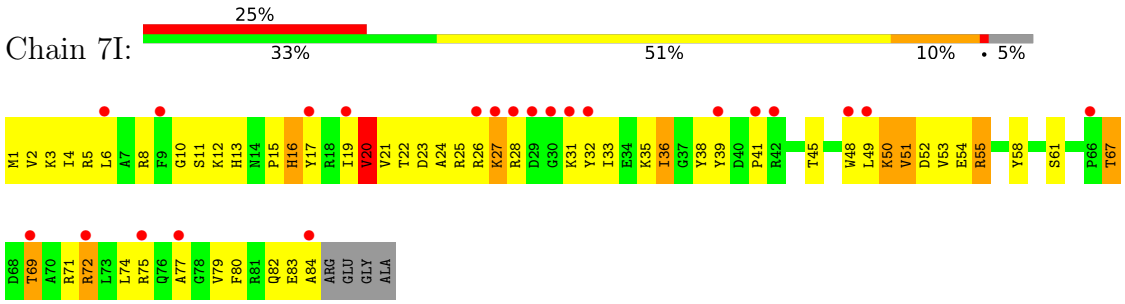
• Molecule 15: 30S ribosomal protein S15

Chain 6A:



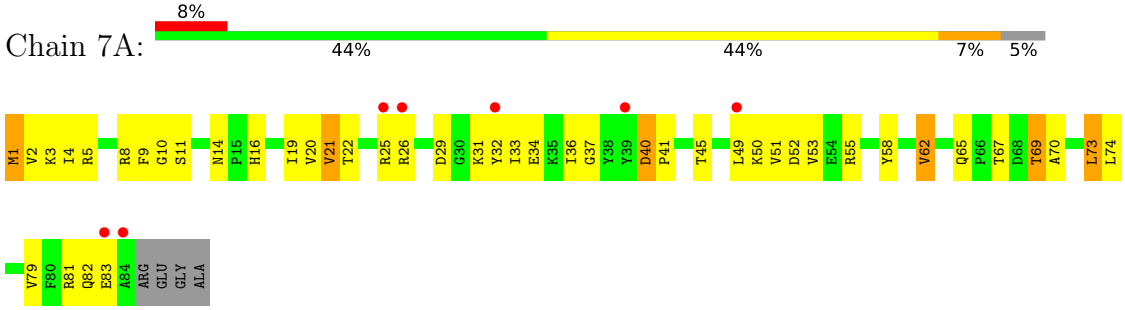
• Molecule 16: 30S ribosomal protein S16

Chain 7I:



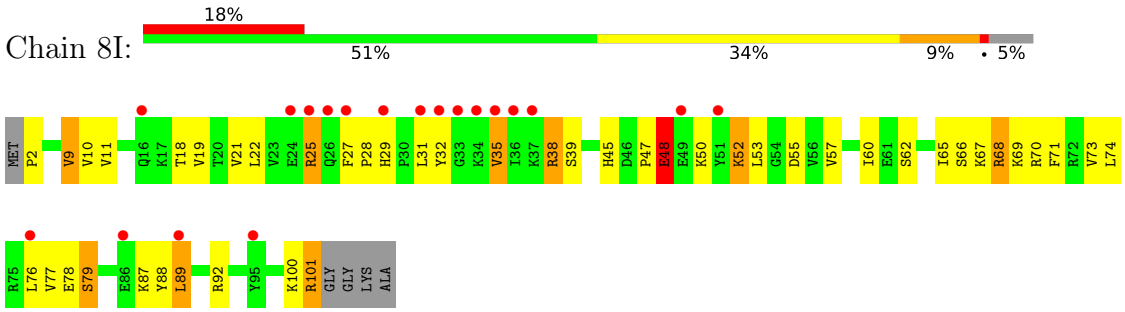
• Molecule 16: 30S ribosomal protein S16

Chain 7A:



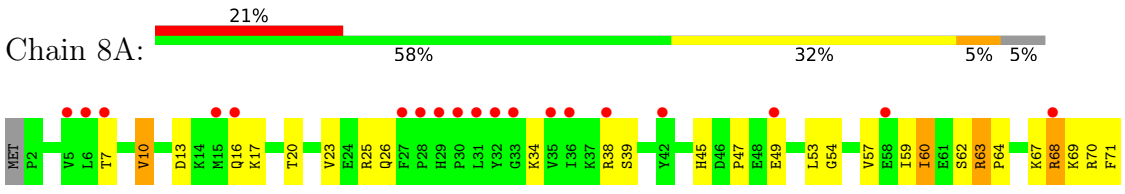
• Molecule 17: 30S ribosomal protein S17

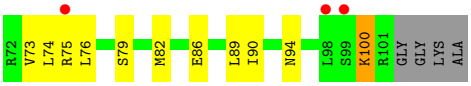
Chain 8I:



• Molecule 17: 30S ribosomal protein S17

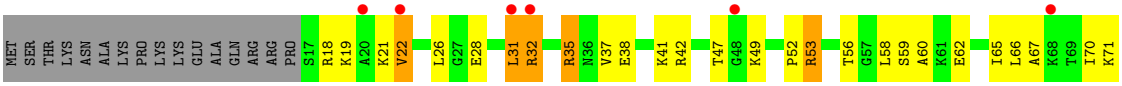
Chain 8A:

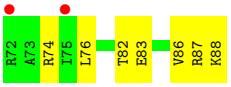




• Molecule 18: 30S ribosomal protein S18

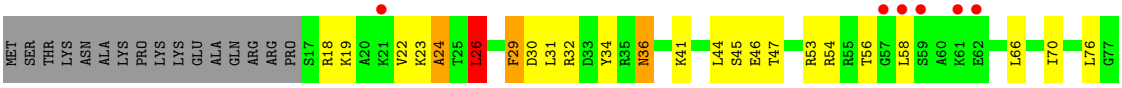
Chain 9I:

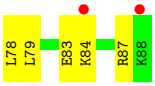




• Molecule 18: 30S ribosomal protein S18

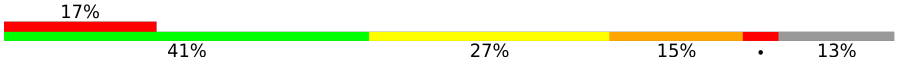
Chain 9A:

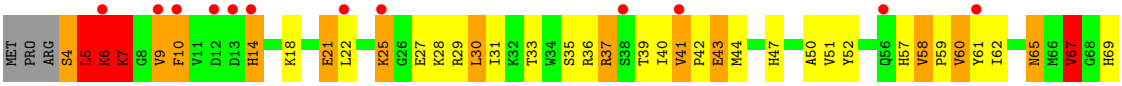


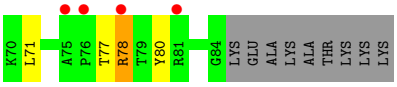


• Molecule 19: 30S ribosomal protein S19

Chain AI:

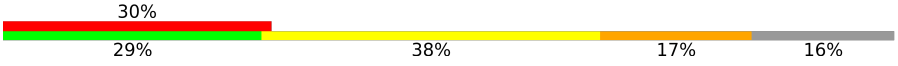


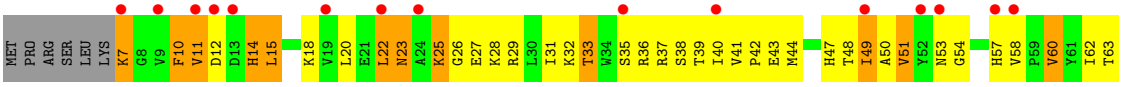


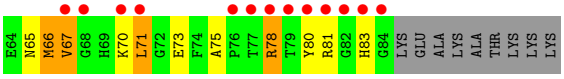


• Molecule 19: 30S ribosomal protein S19

Chain AA:

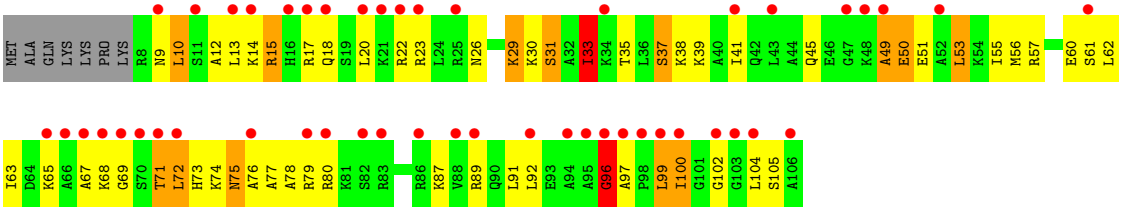




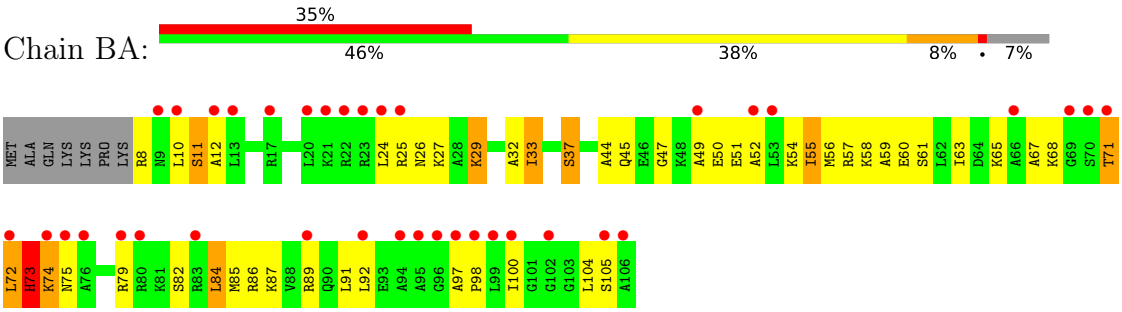


• Molecule 20: 30S ribosomal protein S20

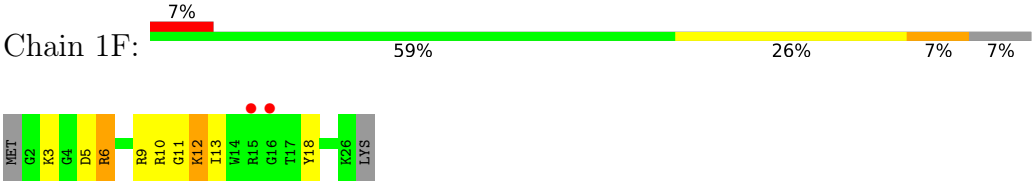
Chain BI:



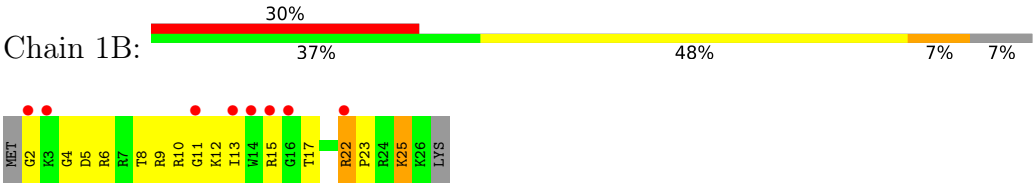
• Molecule 20: 30S ribosomal protein S20



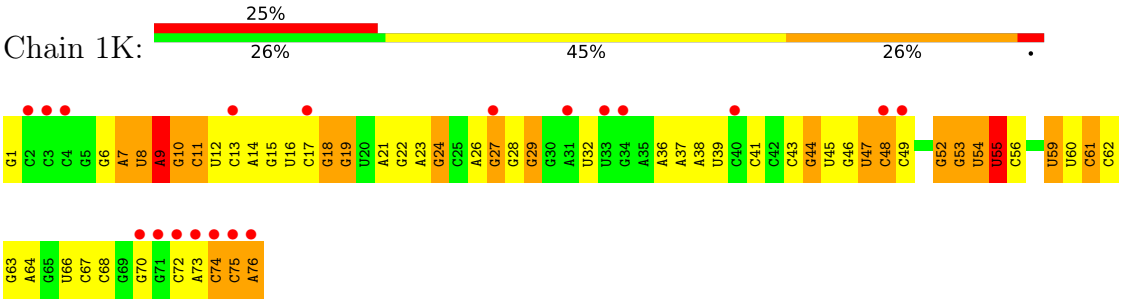
• Molecule 21: 30S ribosomal protein Thx



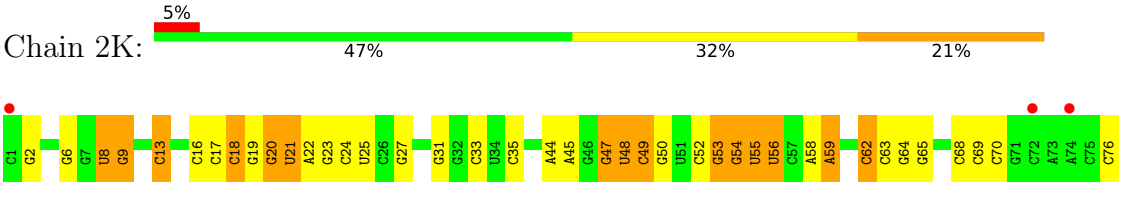
• Molecule 21: 30S ribosomal protein Thx



• Molecule 22: tRNA-Phe

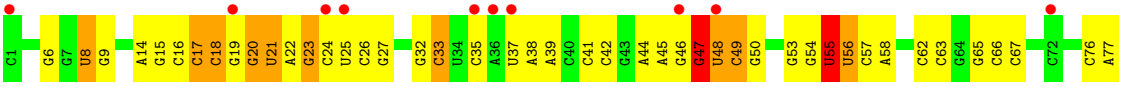


• Molecule 23: tRNA-fMet



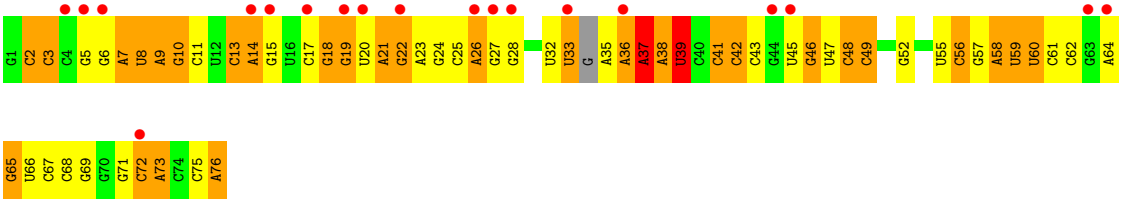
• Molecule 23: tRNA-fMet

Chain 2L:



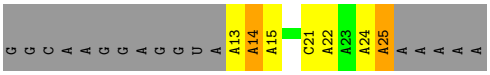
• Molecule 24: tRNA-Phe

Chain 3K:



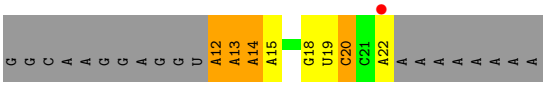
• Molecule 25: mRNA

Chain 4K:



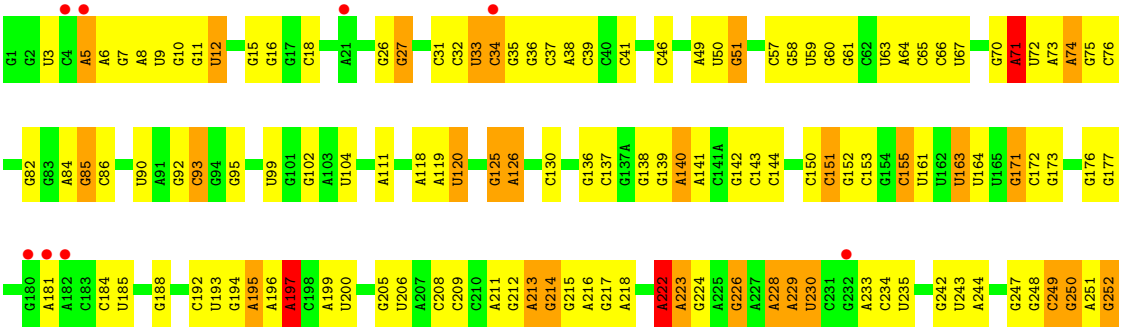
• Molecule 25: mRNA

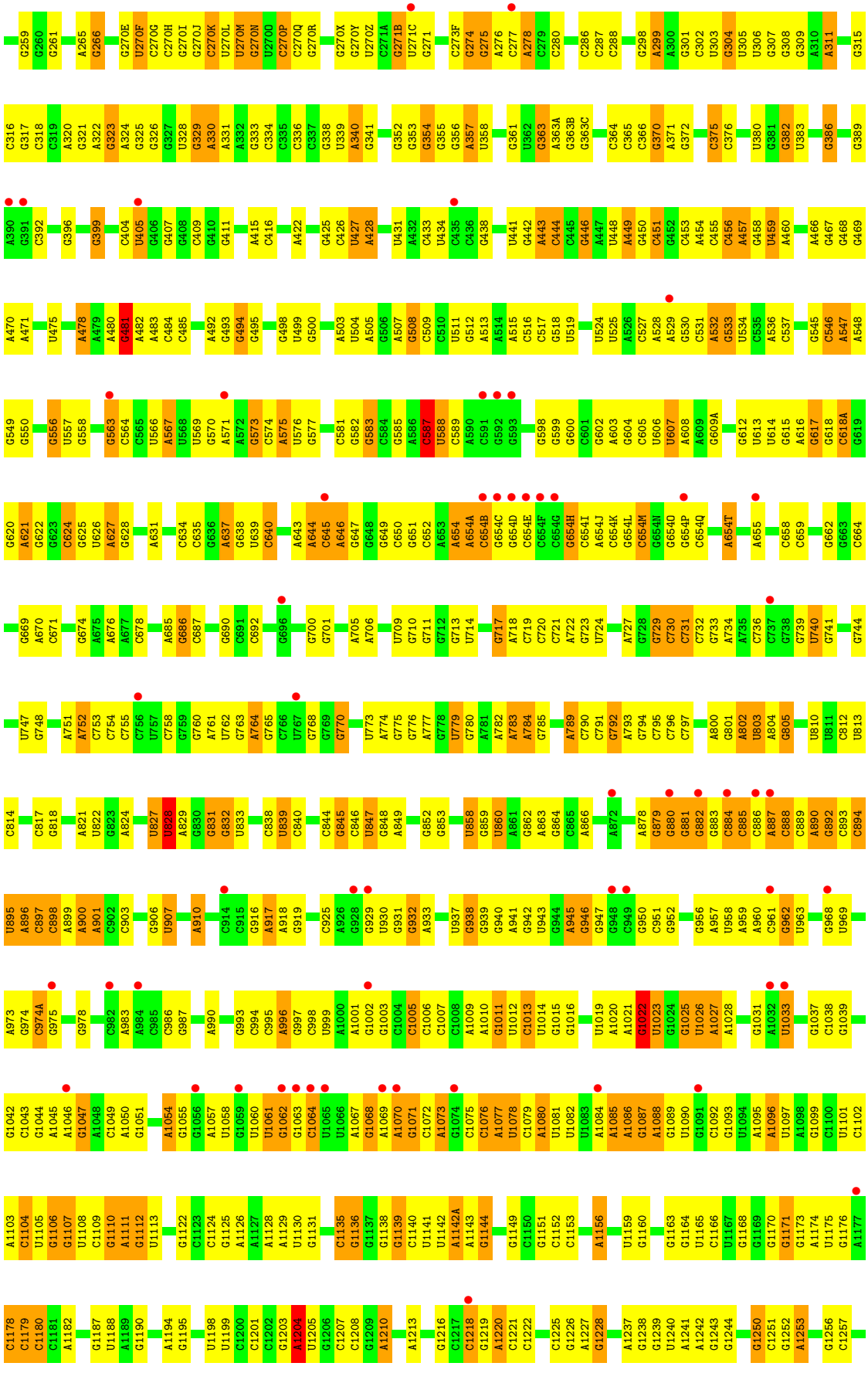
Chain 4L:

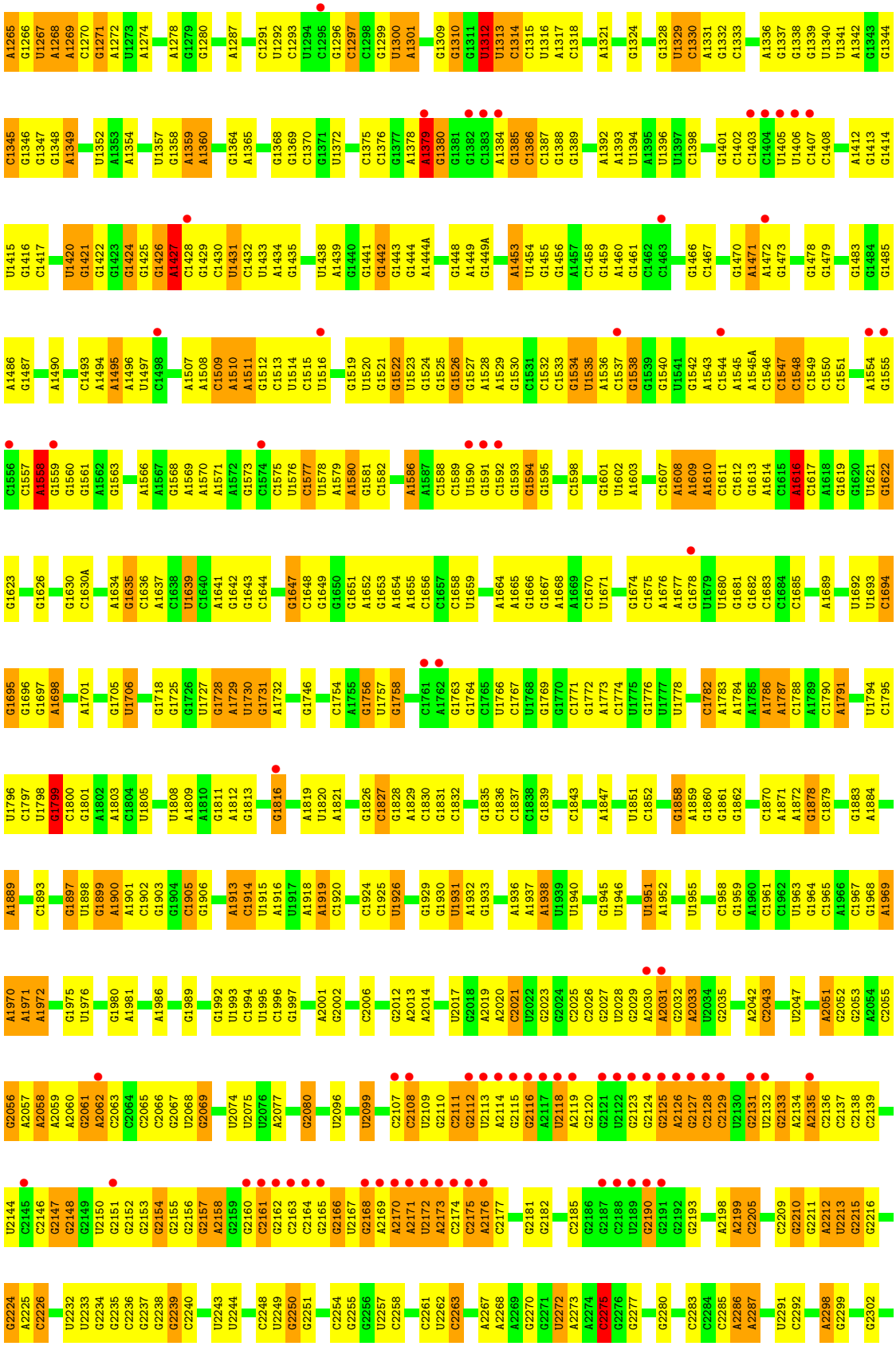


• Molecule 26: 23S ribosomal RNA

Chain 1H:






A1265 G1266 U1267 A1268 A1269 C1270 G1271 A1272 U1273 A1274 A1278 G1279 G1280 A1287 C1291 U1292 C1293 U1294 C1295 G1296 C1297 C1298 G1299 U1300 A1301 G1309 G1310 G1311 U1312 U1313 C1314 C1315 U1316 A1317 C1318 A1321 G1324 G1328 U1329 C1330 A1331 G1332 C1333 A1336 G1337 G1338 G1339 U1340 U1341 A1342 G1343 G1344
C1345 G1346 G1347 G1348 A1349 U1352 A1353 A1354 U1357 G1358 A1359 A1360 G1364 A1365 G1368 G1369 C1370 G1371 U1372 C1375 C1376 G1377 A1378 A1379 G1380 G1381 G1382 C1383 A1384 G1385 C1386 C1387 G1388 G1389 A1392 A1393 U1394 A1395 U1396 U1397 C1398 G1401 C1402 C1403 C1404 U1405 U1406 C1407 C1408 A1412 G1413 G1414
U1415 G1416 C1417 U1420 G1421 G1422 G1423 G1424 G1425 G1426 A1427 C1428 G1429 C1430 U1431 C1432 U1433 A1434 G1435 U1438 A1439 G1440 G1441 G1442 G1443 G1444 A1444A G1448 A1449 G1449A A1453 U1454 G1455 G1456 A1457 C1458 G1459 A1460 G1461 C1462 C1463 G1466 C1467 G1470 A1471 A1472 G1473 G1478 G1479 G1483 G1484 G1485
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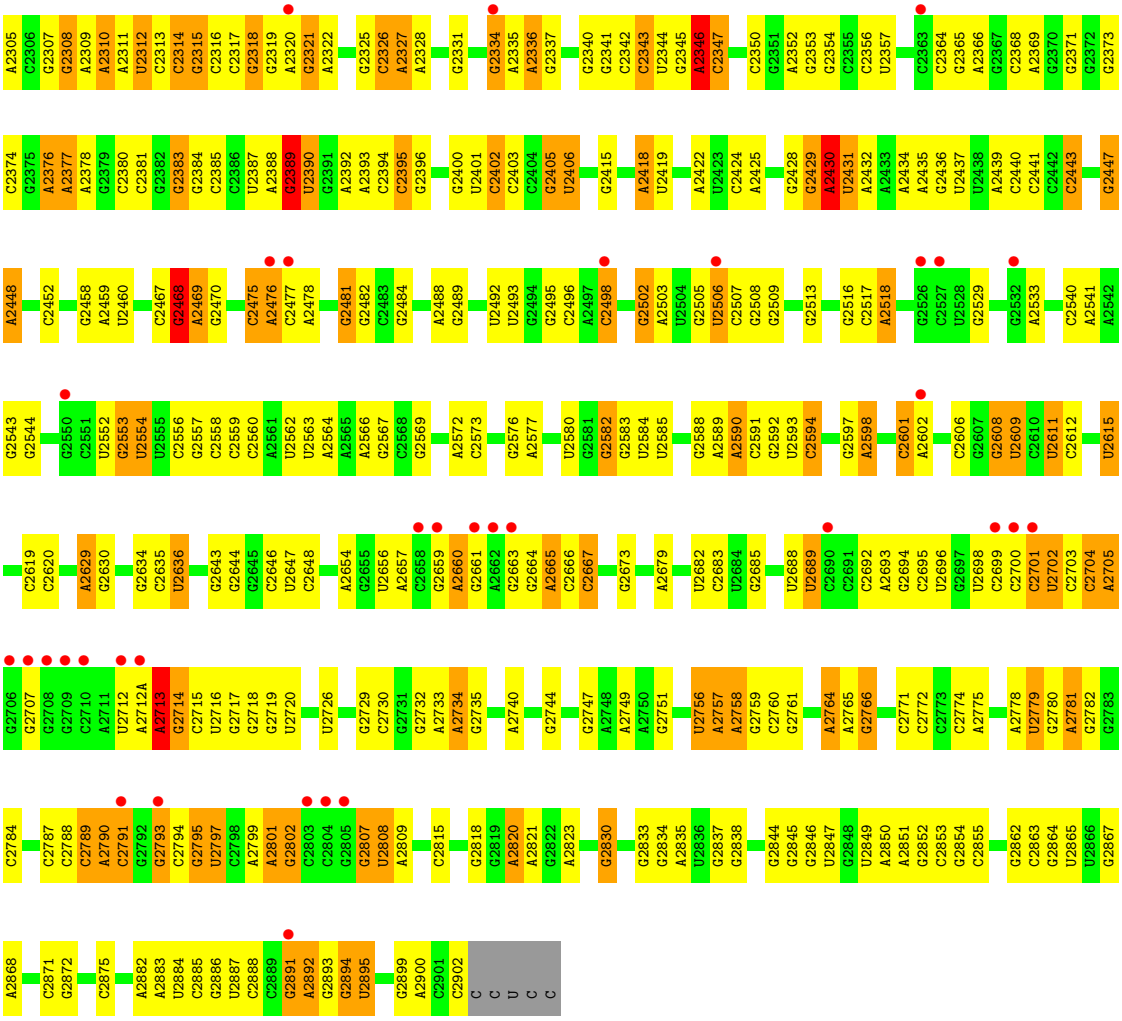

• Molecule 26: 23S ribosomal RNA

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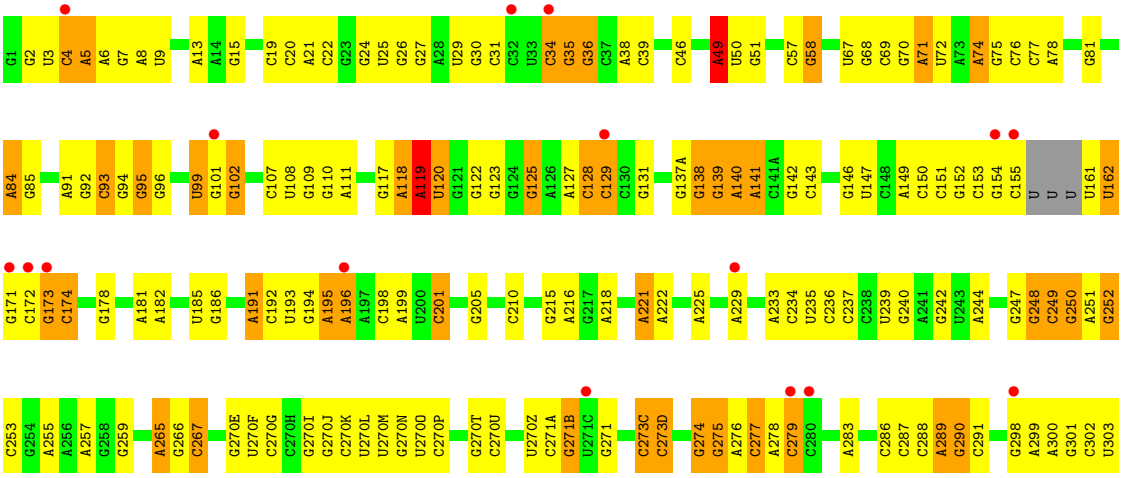

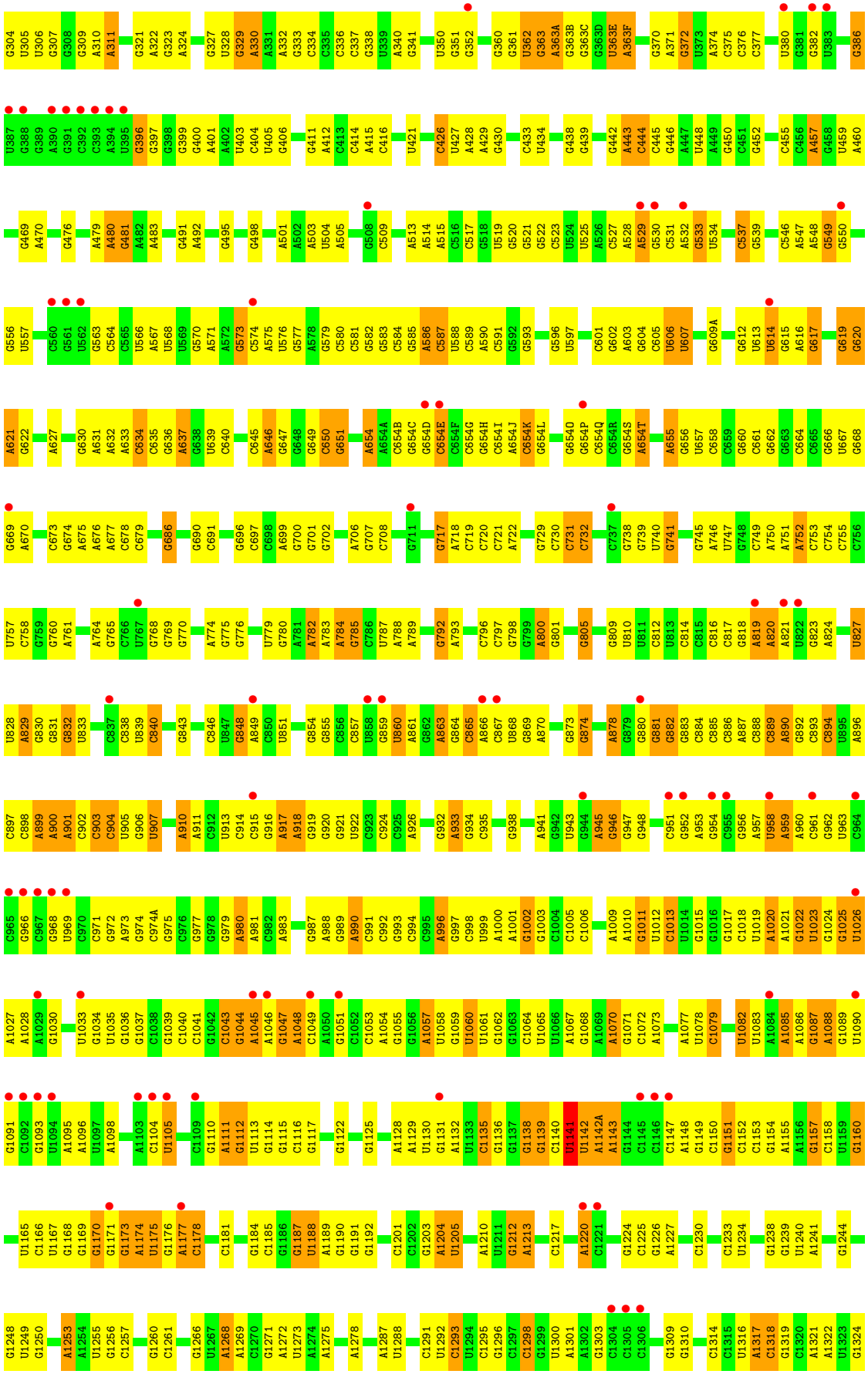

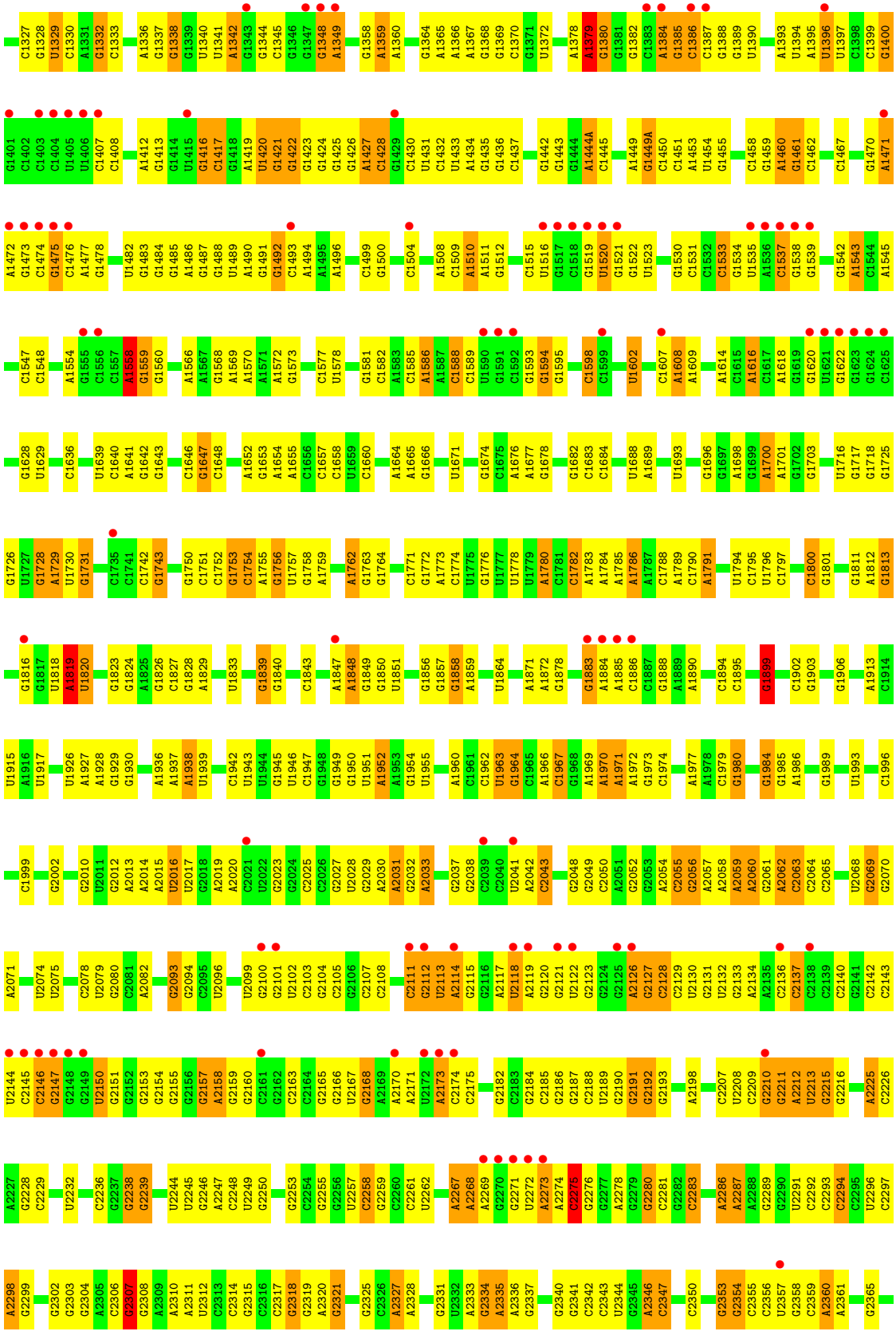
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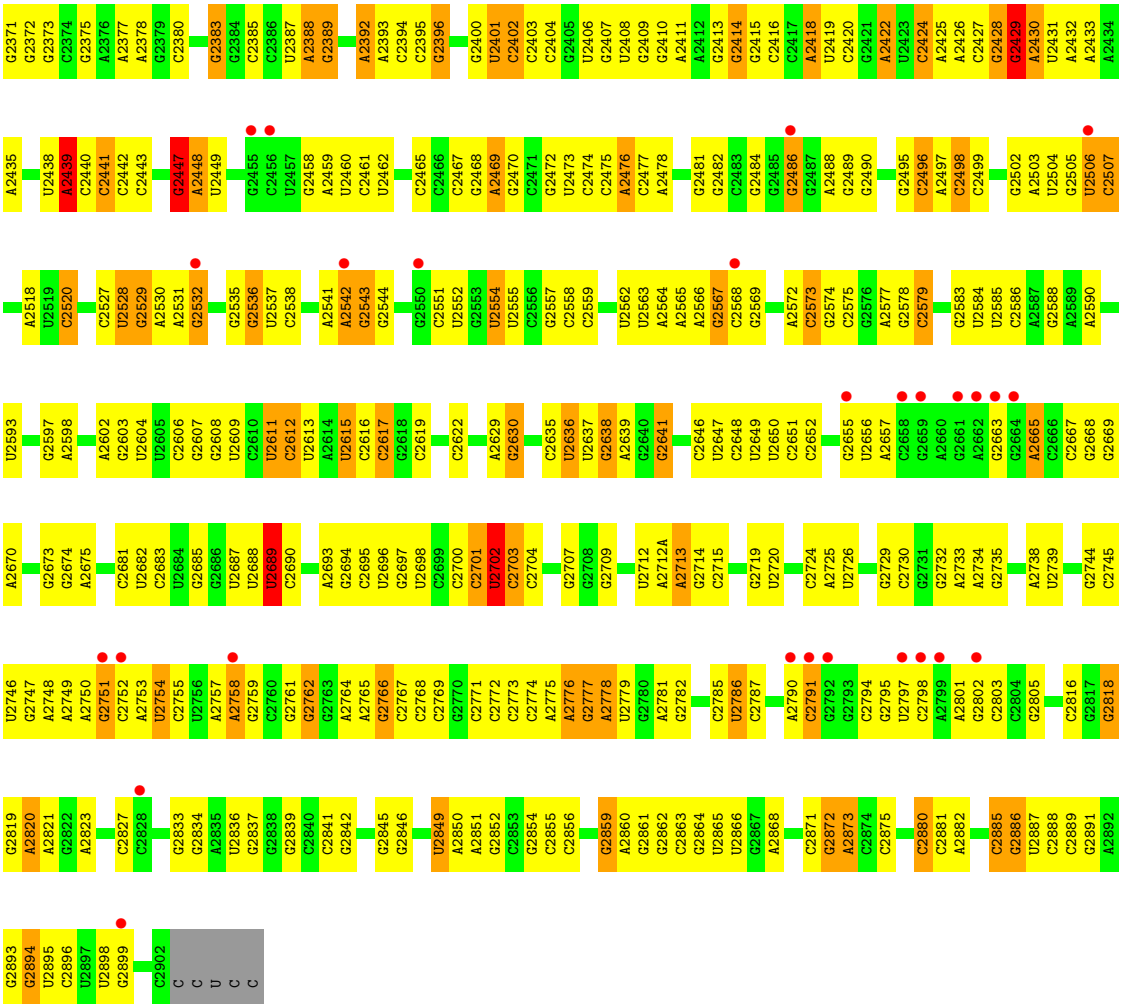

• Molecule 27: 5S ribosomal RNA

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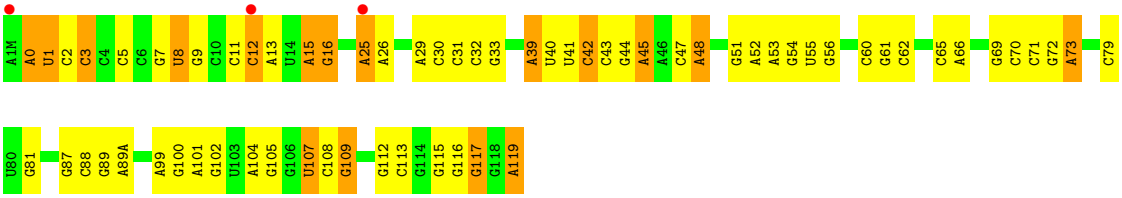
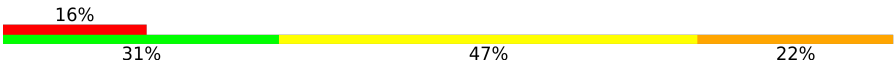
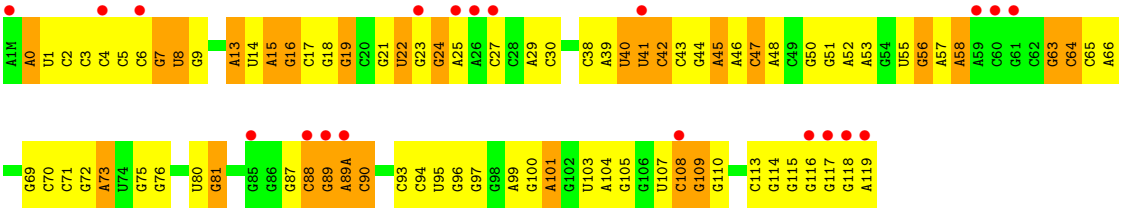


• Molecule 27: 5S ribosomal RNA

Chain 1J:





• Molecule 28: 50S ribosomal protein L2

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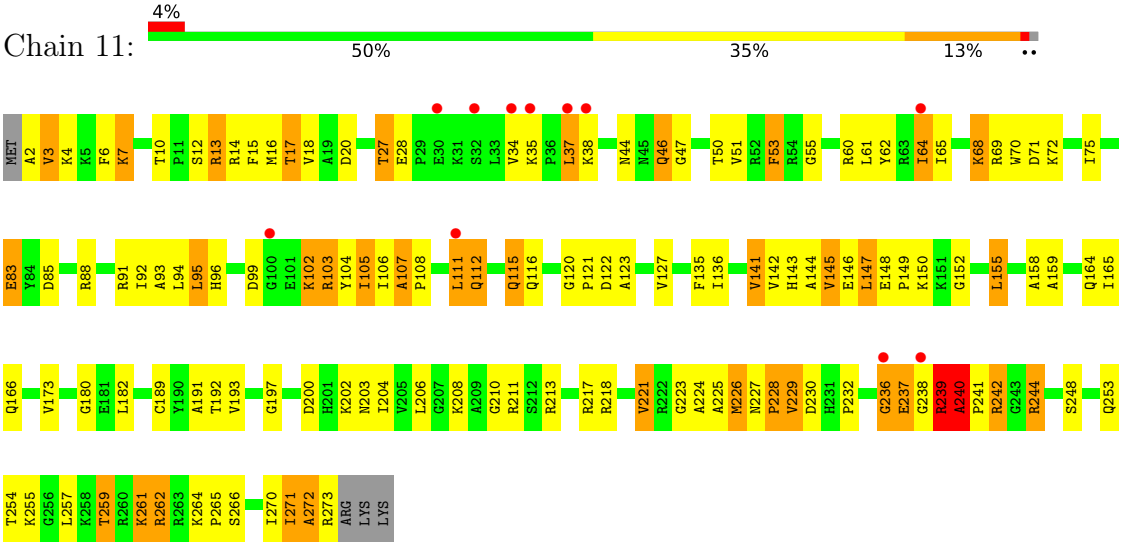

• Molecule 28: 50S ribosomal protein L2

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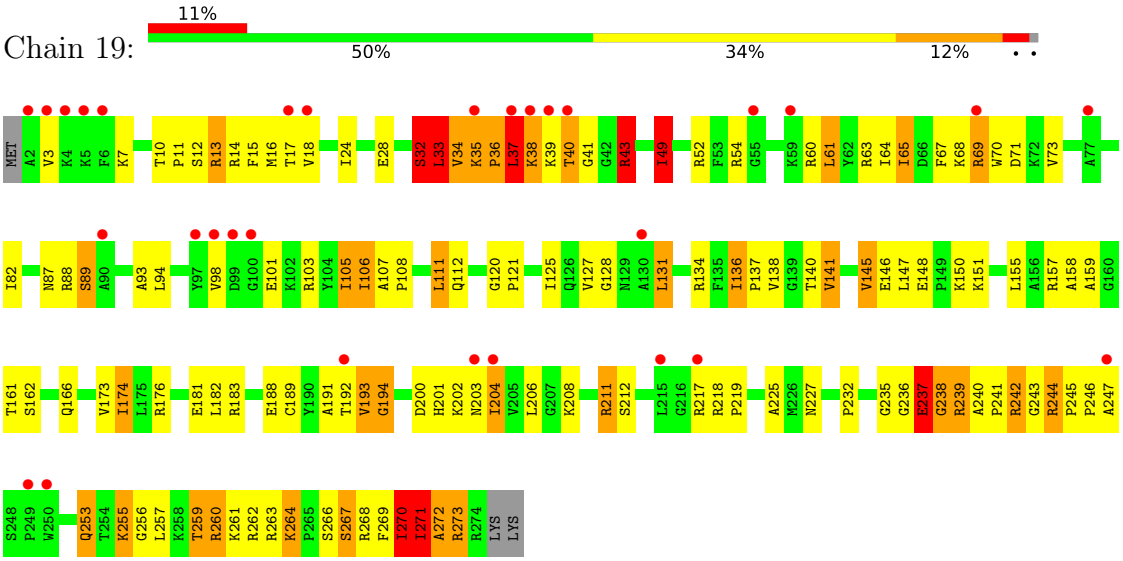

• Molecule 29: 50S ribosomal protein L3

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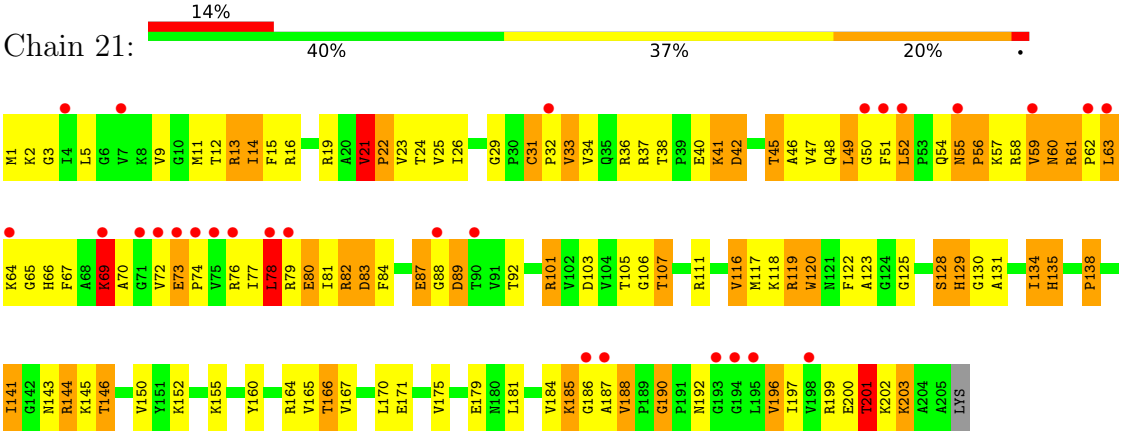

• Molecule 29: 50S ribosomal protein L3

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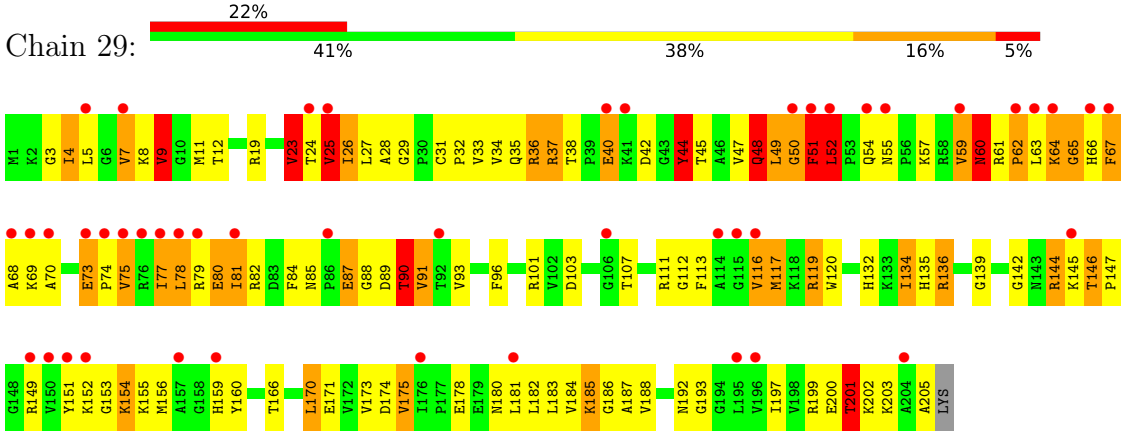

• Molecule 30: 50S ribosomal protein L4

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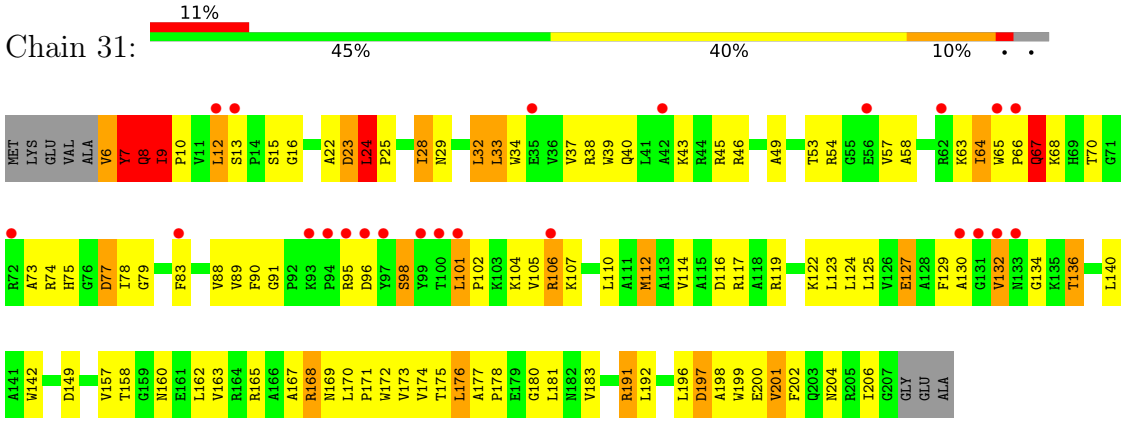

• Molecule 30: 50S ribosomal protein L4

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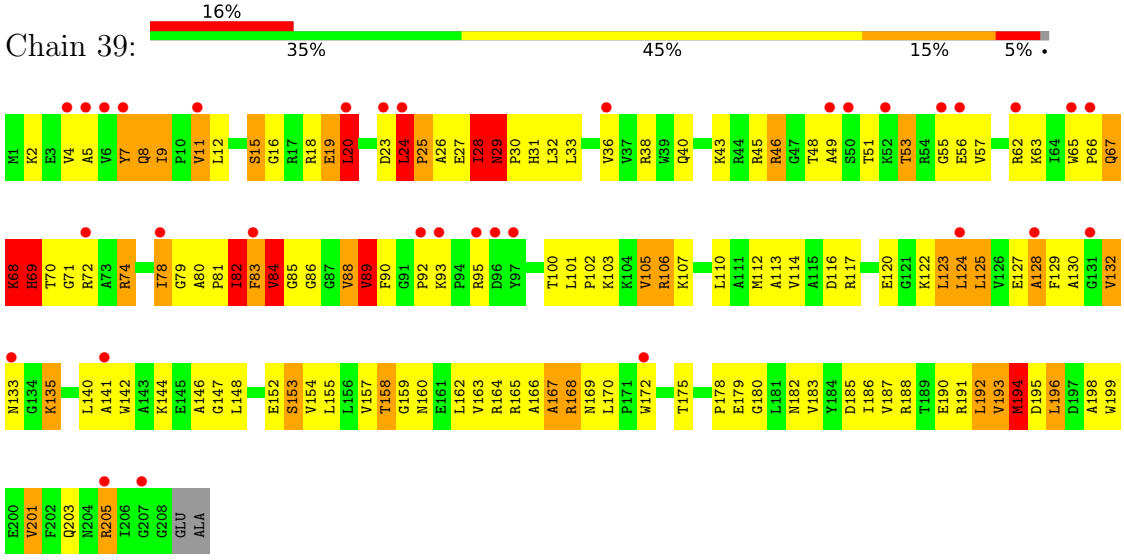

• Molecule 31: 50S ribosomal protein L5

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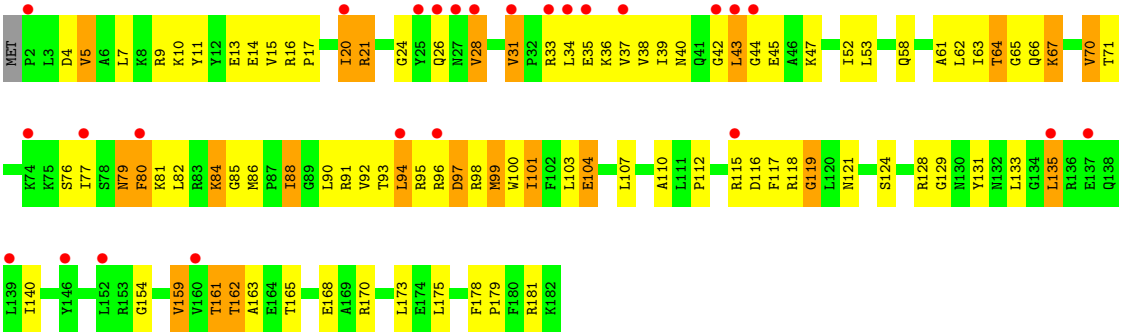

• Molecule 31: 50S ribosomal protein L5

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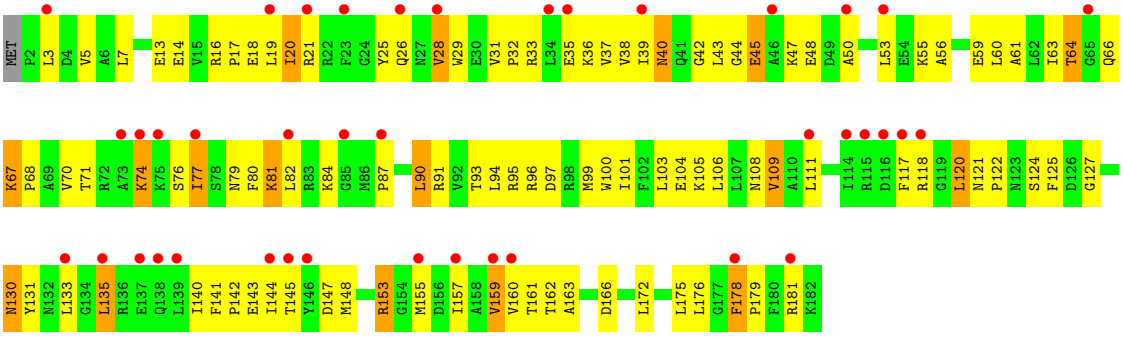

• Molecule 32: 50S ribosomal protein L6

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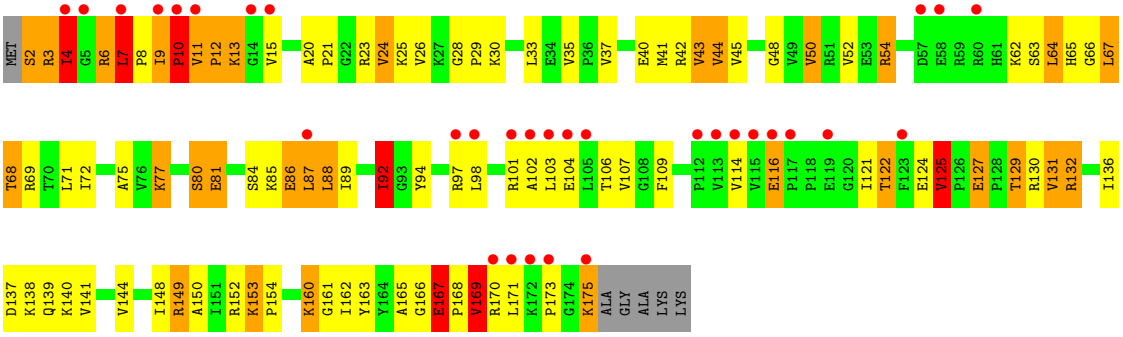

• Molecule 32: 50S ribosomal protein L6

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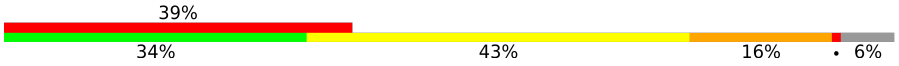

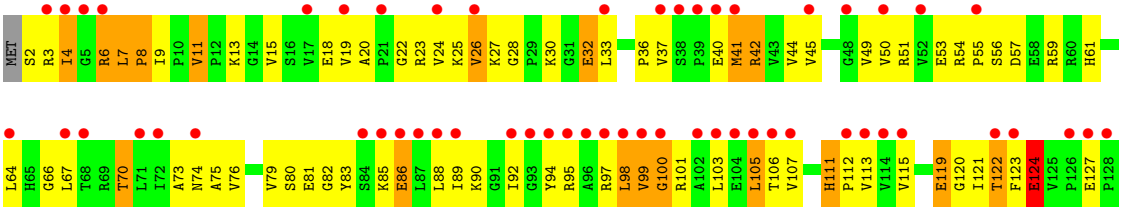

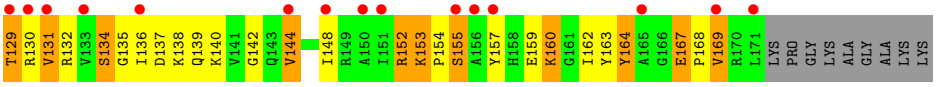

• Molecule 33: 50S ribosomal protein L9

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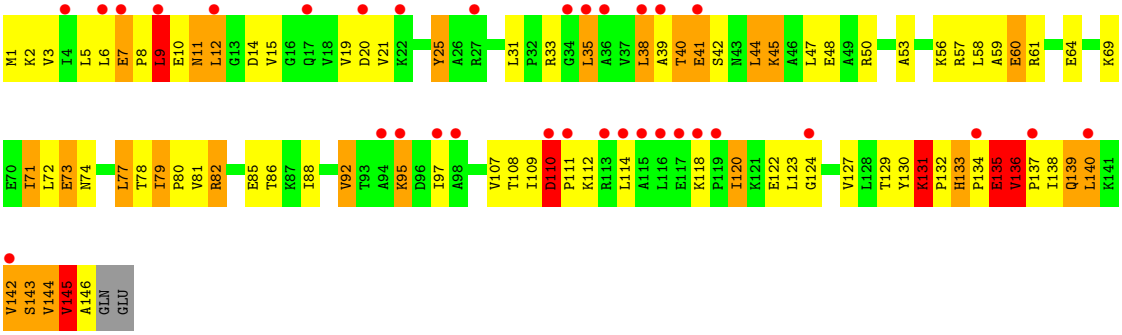

• Molecule 33: 50S ribosomal protein L9

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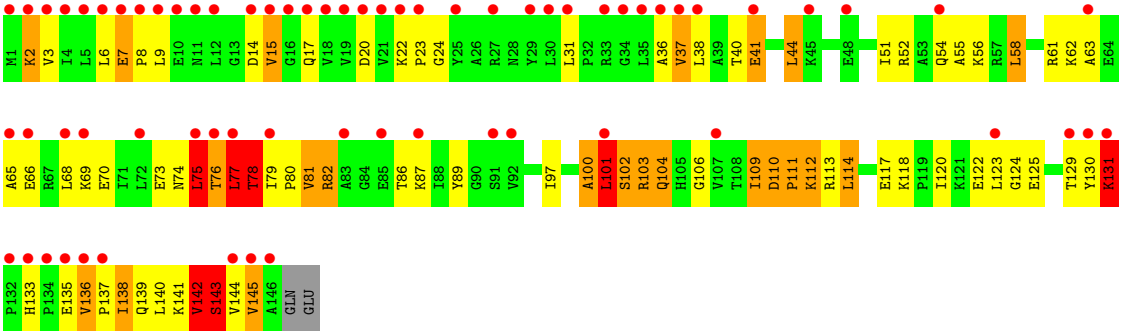

• Molecule 34: 50S ribosomal protein L13

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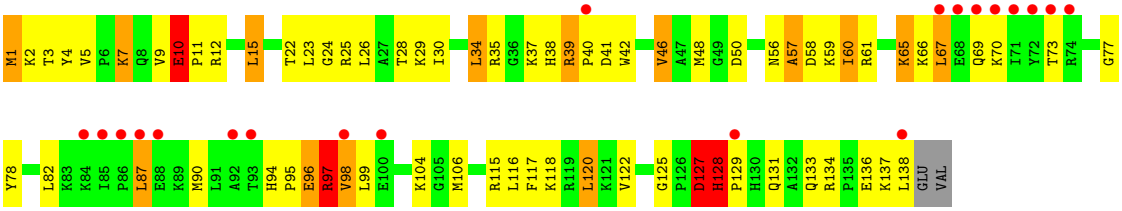

• Molecule 34: 50S ribosomal protein L13

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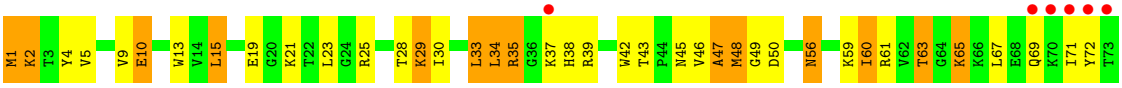
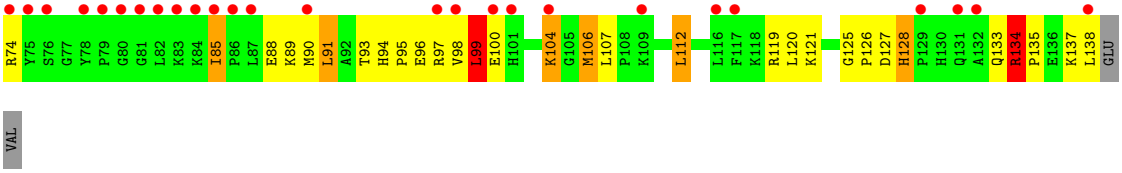
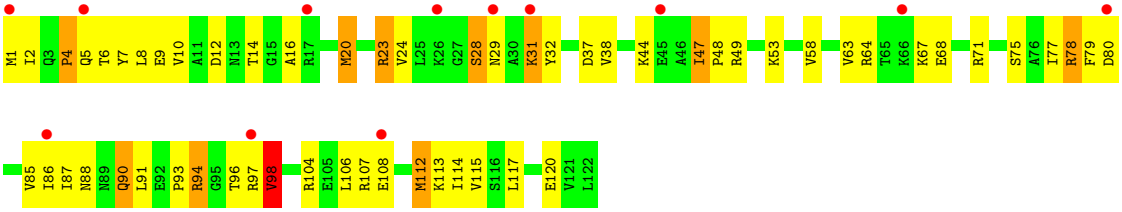
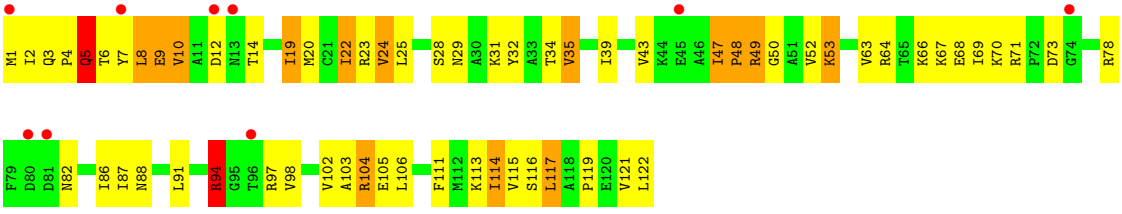




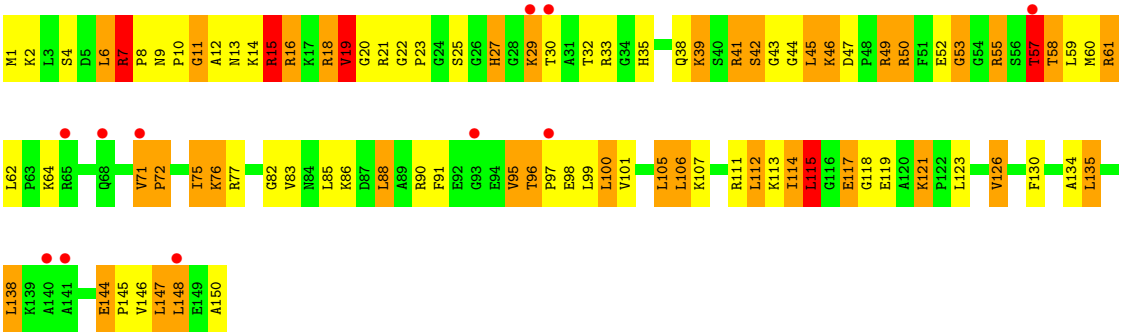
• Molecule 35: 50S ribosomal protein L14



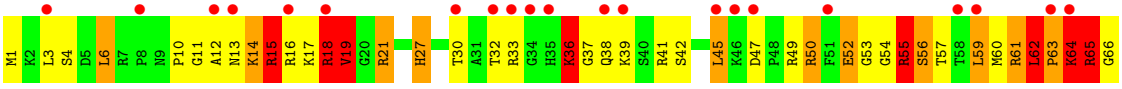
• Molecule 35: 50S ribosomal protein L14

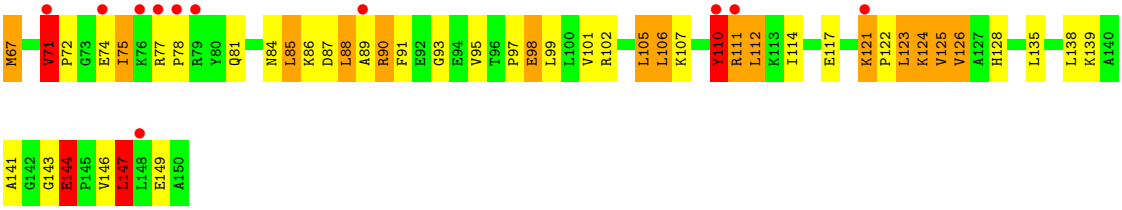


• Molecule 36: 50S ribosomal protein L15



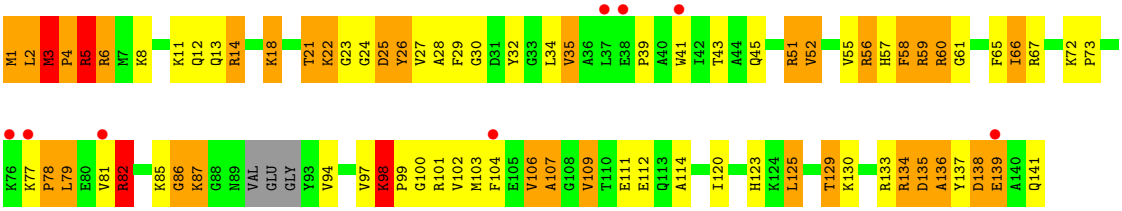
• Molecule 36: 50S ribosomal protein L15





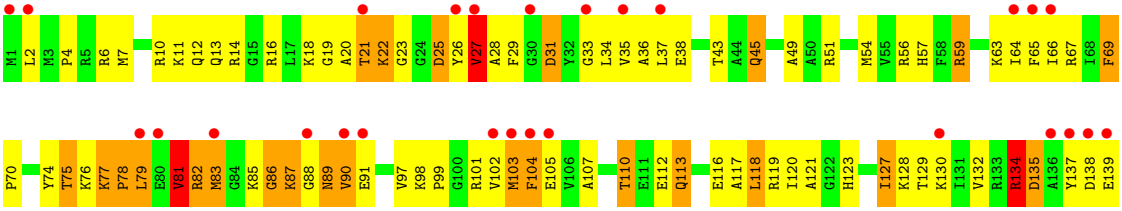
• Molecule 37: 50S ribosomal protein L16

Chain 88:



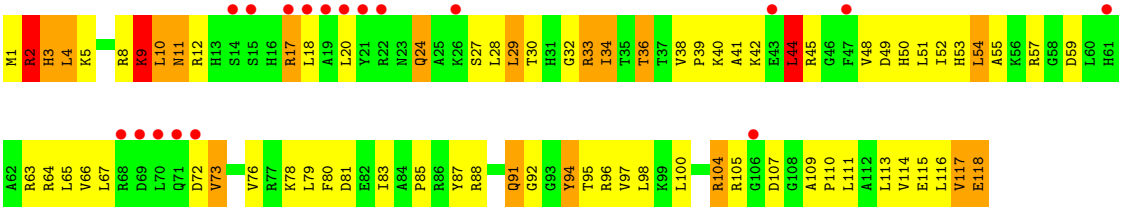
• Molecule 37: 50S ribosomal protein L16

Chain 45:



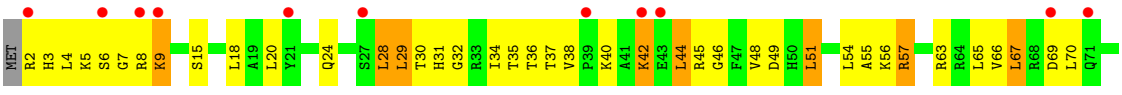
• Molecule 38: 50S ribosomal protein L17

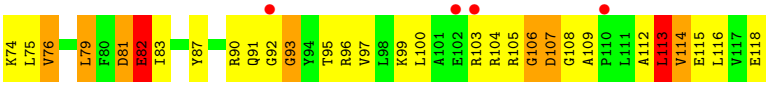
Chain 98:



• Molecule 38: 50S ribosomal protein L17

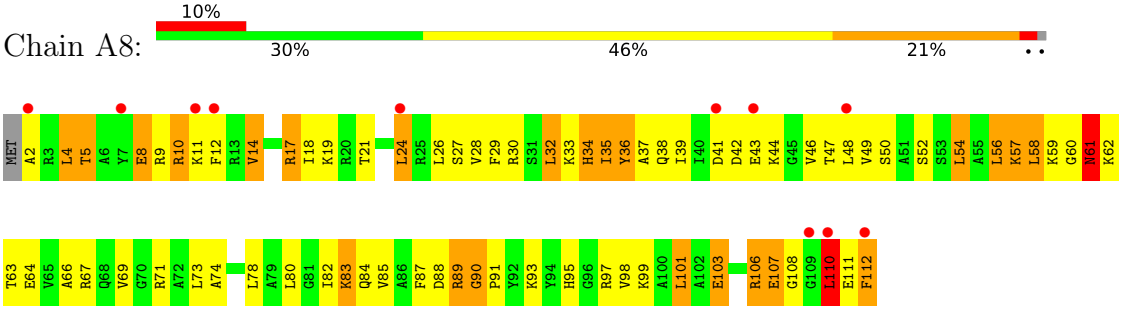
Chain 55:





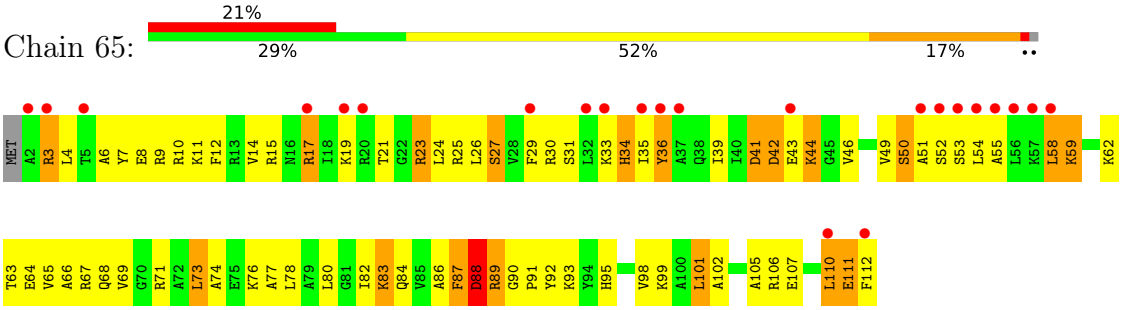
• Molecule 39: 50S ribosomal protein L18

Chain A8:



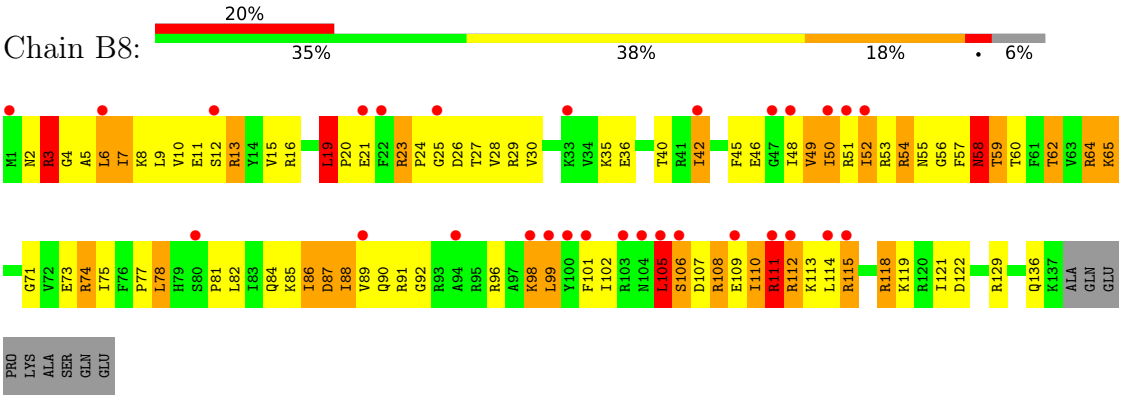
• Molecule 39: 50S ribosomal protein L18

Chain 65:



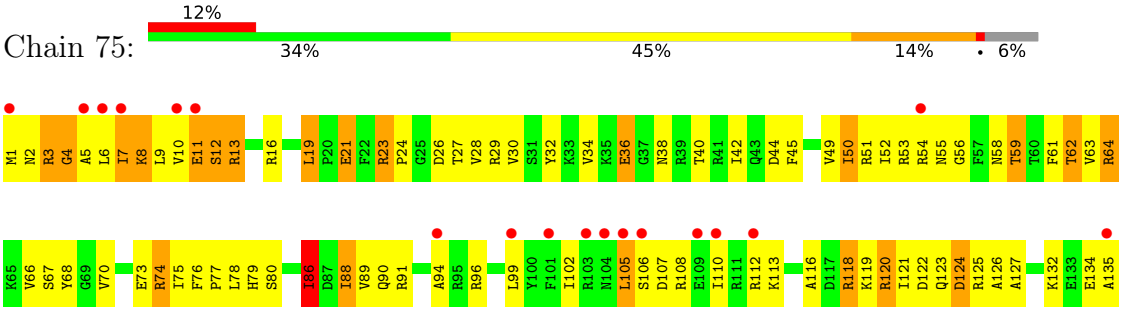
• Molecule 40: 50S ribosomal protein L19

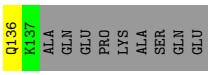
Chain B8:



• Molecule 40: 50S ribosomal protein L19

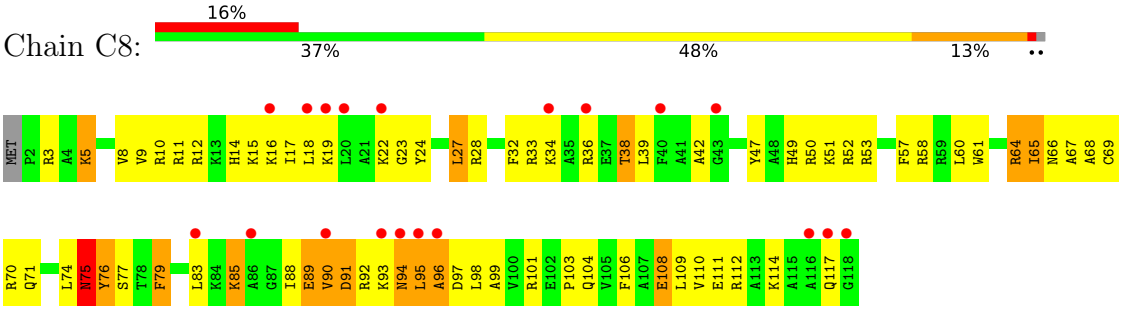
Chain 75:





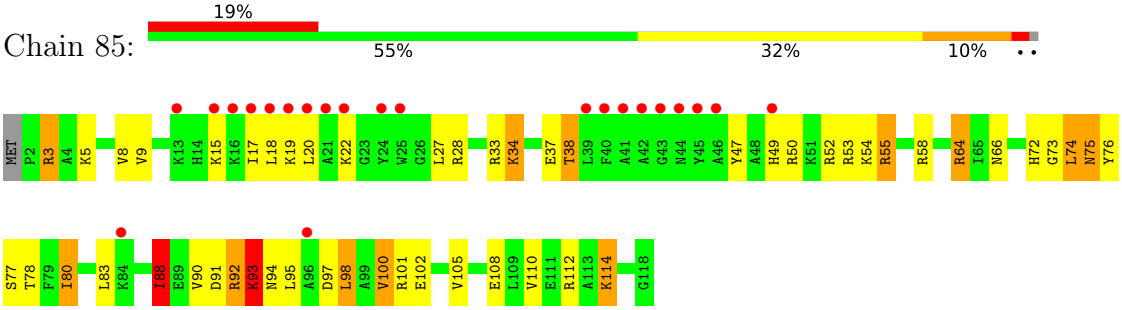
• Molecule 41: 50S ribosomal protein L20

Chain C8:



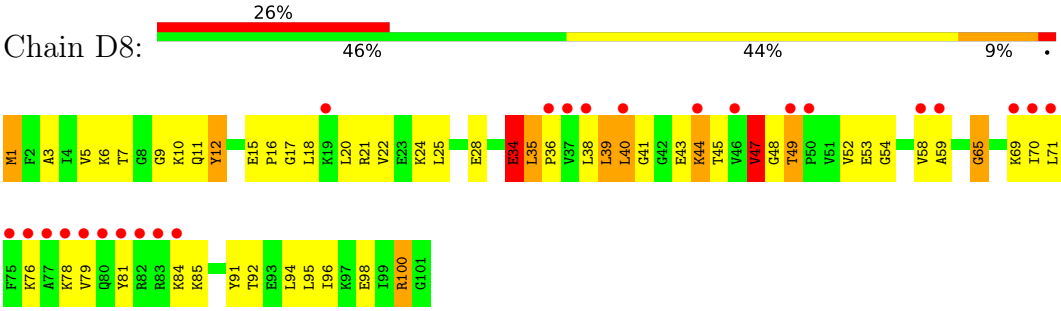
• Molecule 41: 50S ribosomal protein L20

Chain 85:



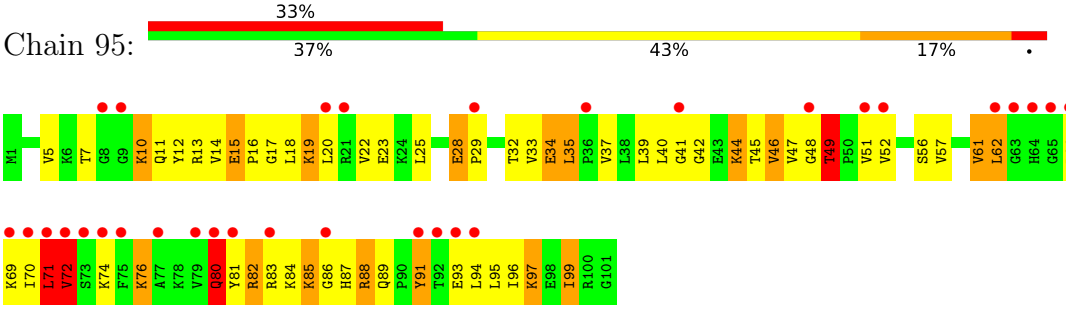
• Molecule 42: 50S ribosomal protein L21

Chain D8:



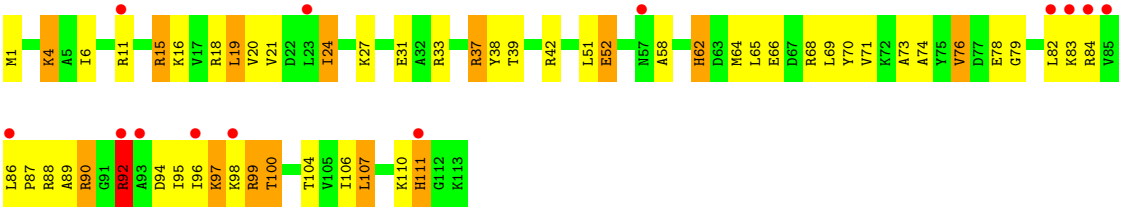
• Molecule 42: 50S ribosomal protein L21

Chain 95:



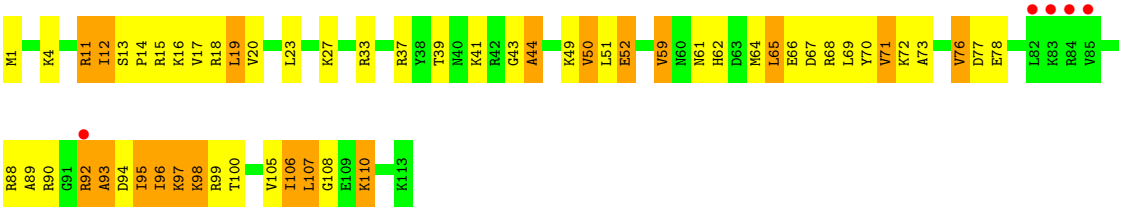
• Molecule 43: 50S ribosomal protein L22

Chain E8:



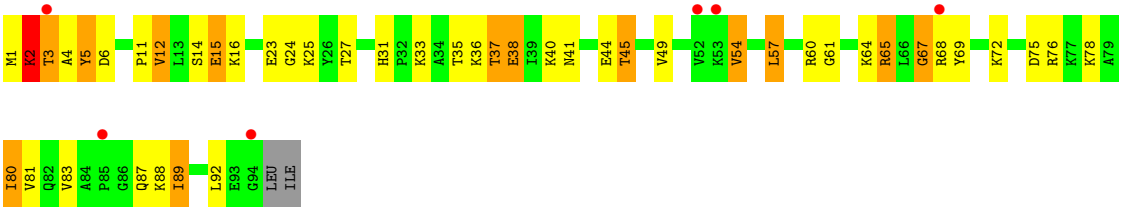
• Molecule 43: 50S ribosomal protein L22

Chain A5:



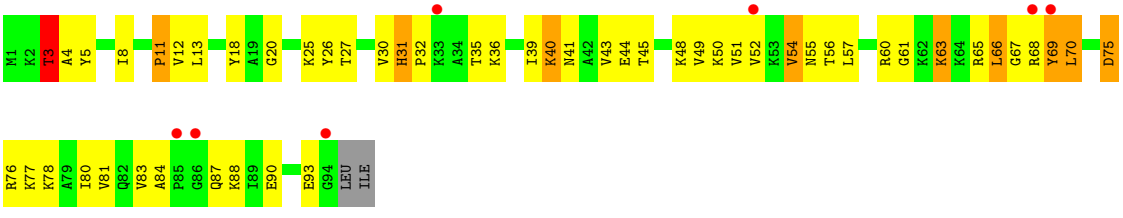
• Molecule 44: 50S ribosomal protein L23

Chain F8:



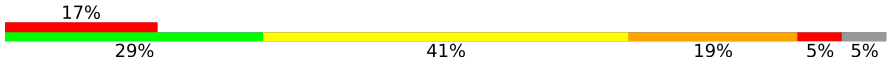
• Molecule 44: 50S ribosomal protein L23

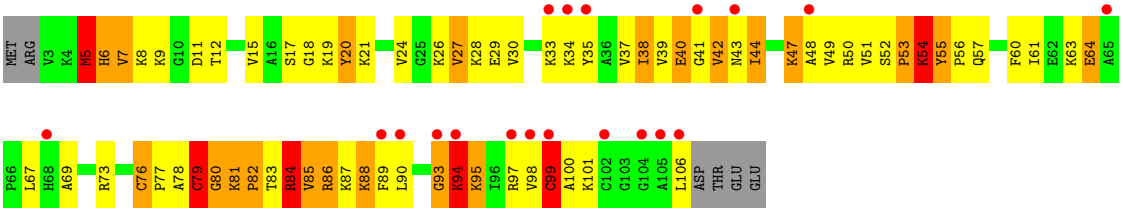
Chain B5:



• Molecule 45: 50S ribosomal protein L24

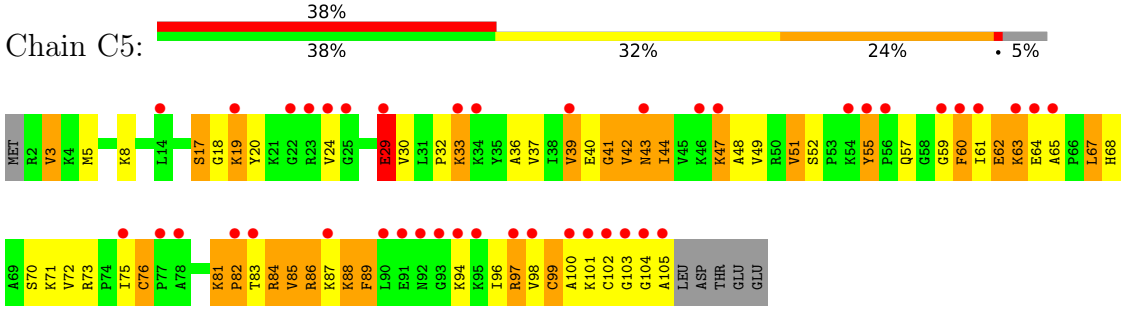
Chain G8:





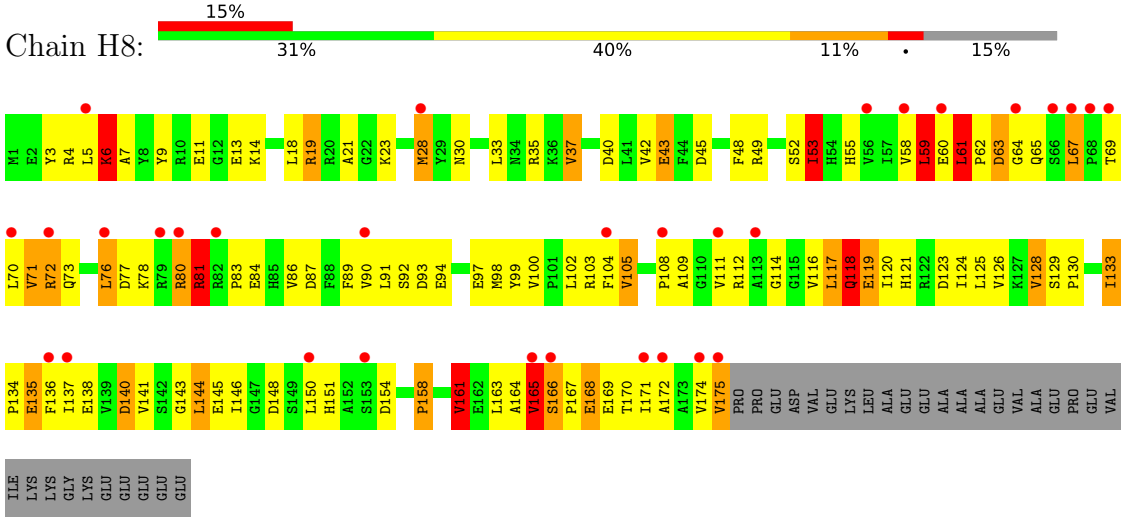
• Molecule 45: 50S ribosomal protein L24

Chain C5:



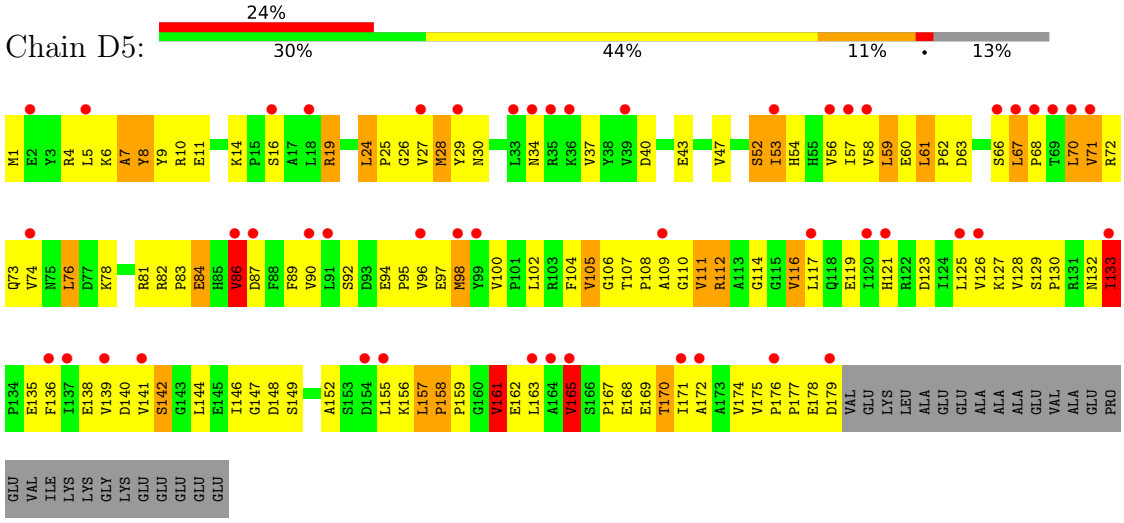
• Molecule 46: 50S ribosomal protein L25

Chain H8:



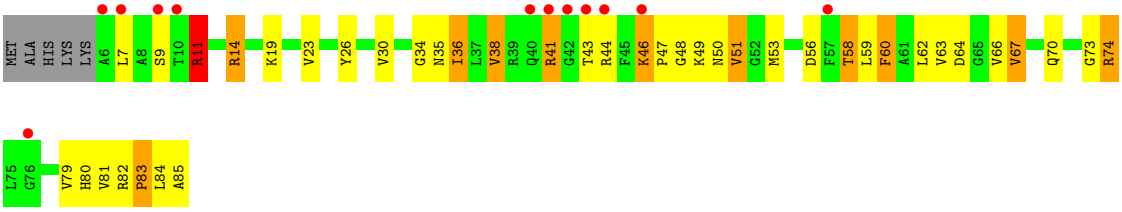
• Molecule 46: 50S ribosomal protein L25

Chain D5:



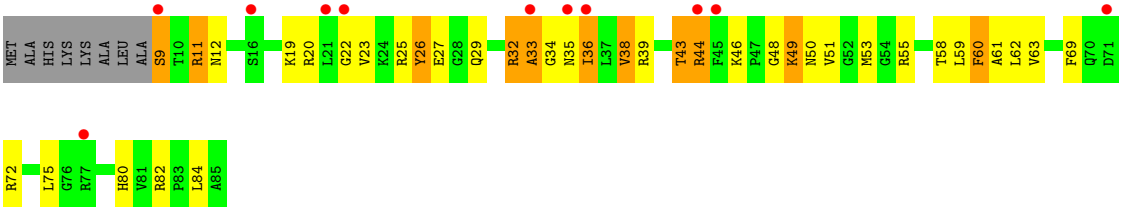
• Molecule 47: 50S ribosomal protein L27

Chain I8:



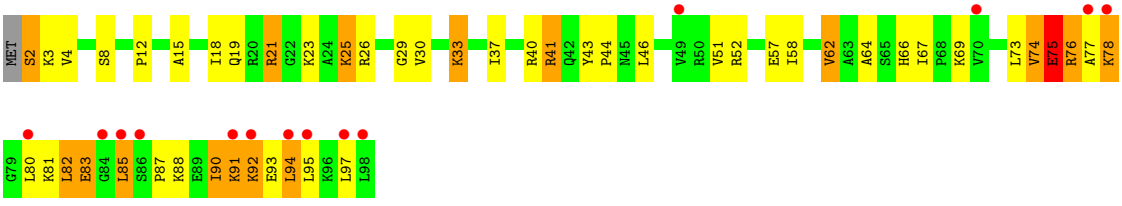
• Molecule 47: 50S ribosomal protein L27

Chain E5:



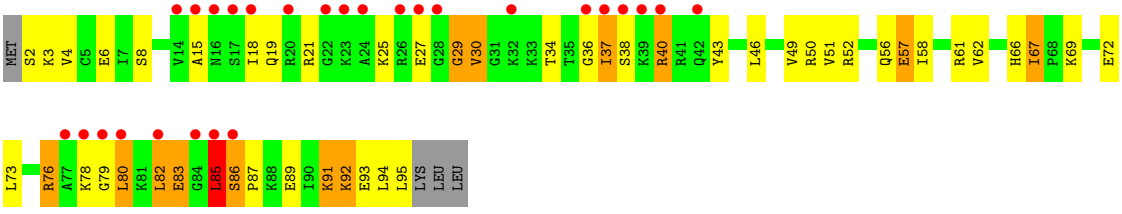
• Molecule 48: 50S ribosomal protein L28

Chain J8:



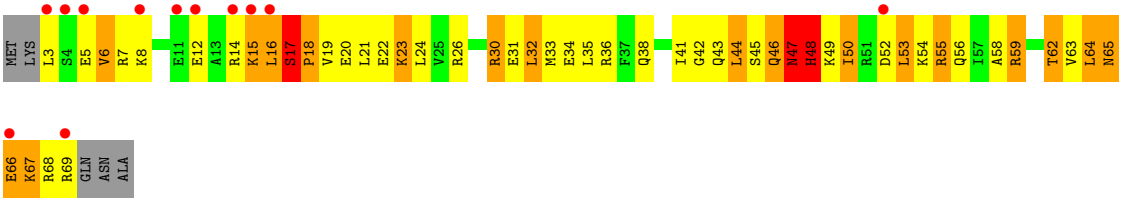
• Molecule 48: 50S ribosomal protein L28

Chain F5:



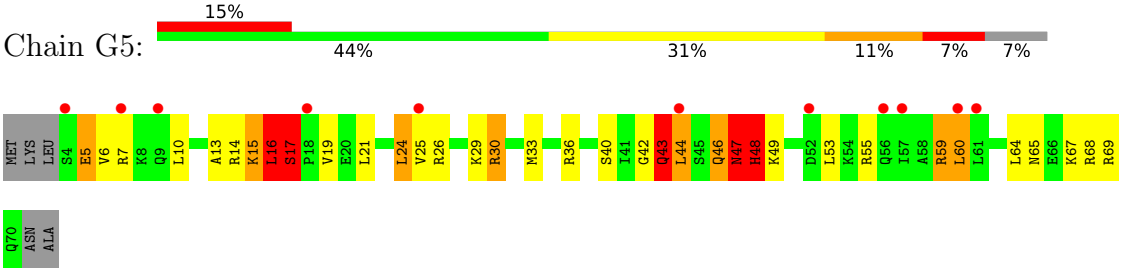
• Molecule 49: 50S ribosomal protein L29

Chain K8:



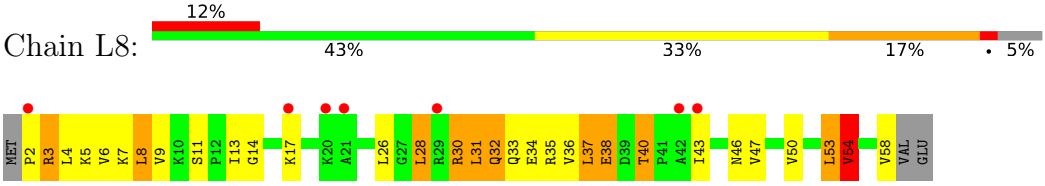
• Molecule 49: 50S ribosomal protein L29

Chain G5:



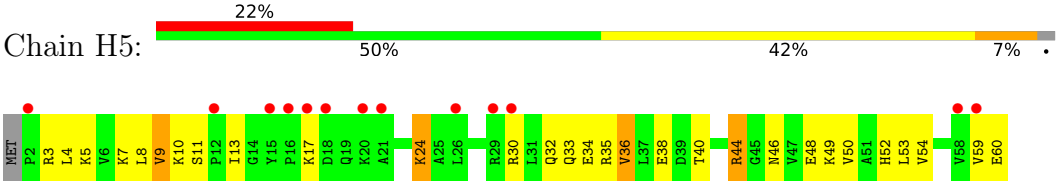
• Molecule 50: 50S ribosomal protein L30

Chain L8:



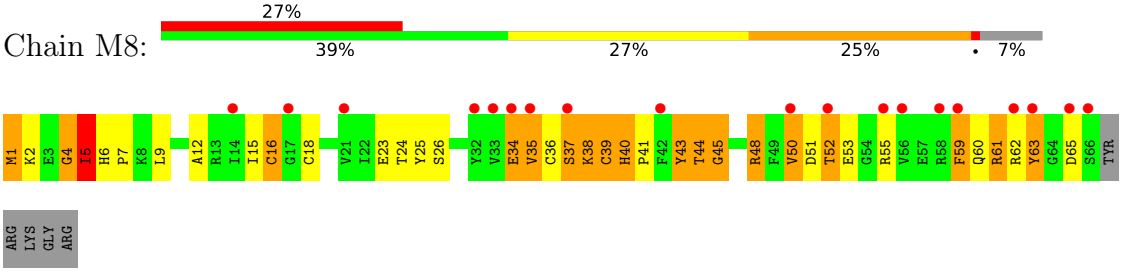
• Molecule 50: 50S ribosomal protein L30

Chain H5:



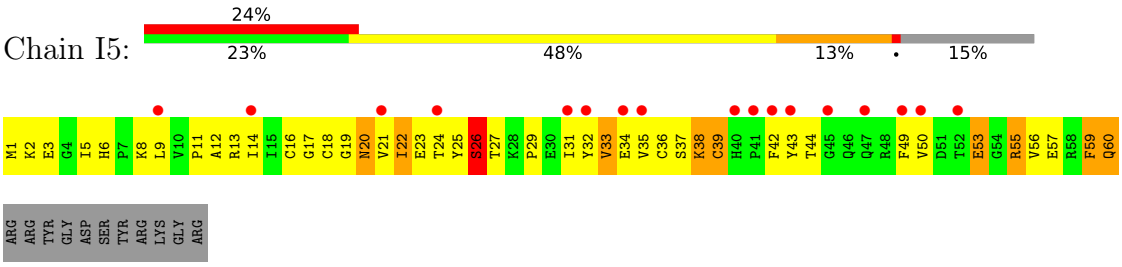
• Molecule 51: 50S ribosomal protein L31

Chain M8:



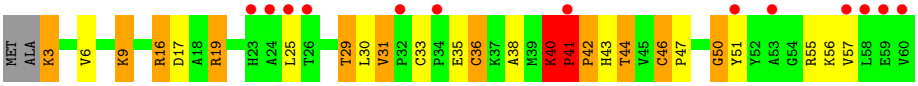
• Molecule 51: 50S ribosomal protein L31

Chain I5:

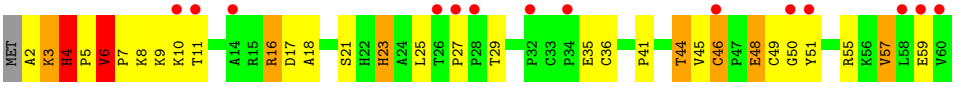


• Molecule 52: 50S ribosomal protein L32

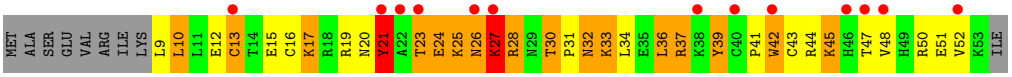
Chain N8:



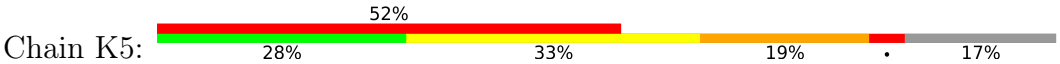
• Molecule 52: 50S ribosomal protein L32



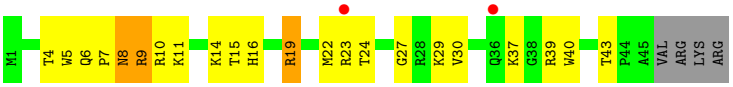
• Molecule 53: 50S ribosomal protein L33



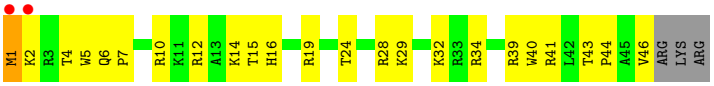
• Molecule 53: 50S ribosomal protein L33



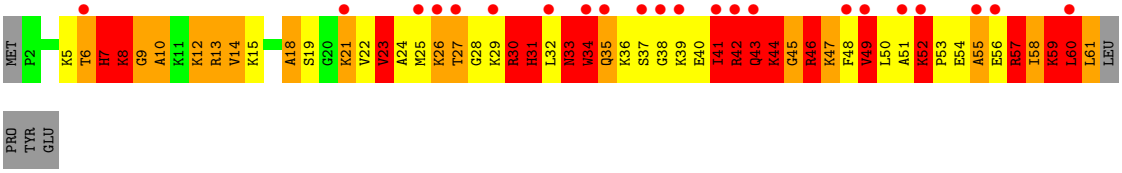
• Molecule 54: 50S ribosomal protein L34



• Molecule 54: 50S ribosomal protein L34

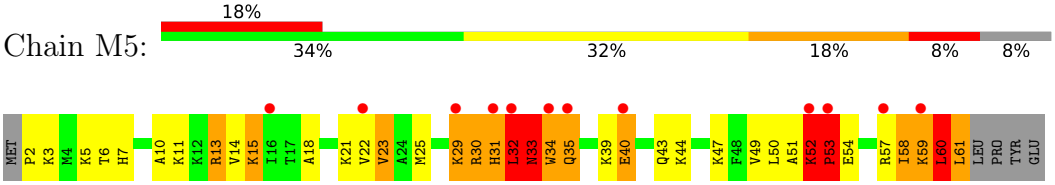


• Molecule 55: 50S ribosomal protein L35



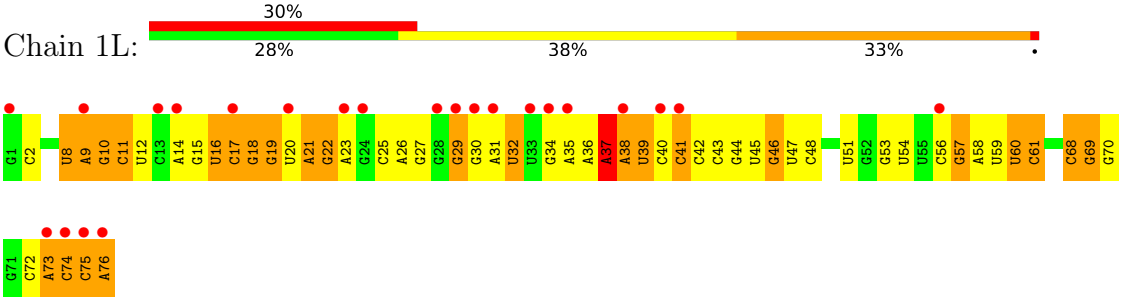
• Molecule 55: 50S ribosomal protein L35

Chain M5:



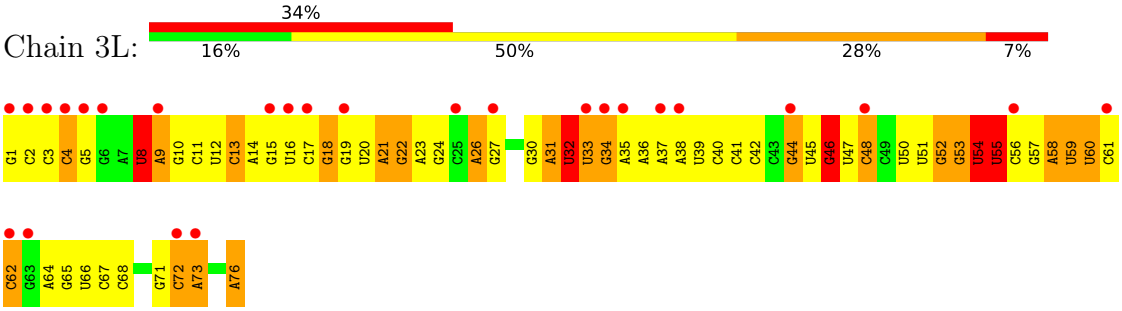
• Molecule 56: tRNA-Phe

Chain 1L:



• Molecule 57: tRNA-Phe

Chain 3L:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	209.40Å 449.20Å 621.20Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	255.47 – 2.95 255.47 – 2.95	Depositor EDS
% Data completeness (in resolution range)	99.9 (255.47-2.95) 94.1 (255.47-2.95)	Depositor EDS
R_{merge}	0.30	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	0.89 (at 2.96Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.193 , 0.235 0.195 , 0.238	Depositor DCC
R_{free} test set	1999 reflections (0.16%)	wwPDB-VP
Wilson B-factor (Å^2)	78.0	Xtriage
Anisotropy	0.287	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 122.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.45$, $< L^2 > = 0.27$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	300252	wwPDB-VP
Average B, all atoms (Å^2)	104.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.47% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: OMC, 4SU, ZN, MIA, 5MU, MG, PSU, 7MG, PAR

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|$ >5	RMSZ	#$\|Z\|$ >5
1	13	0.50	0/36052	0.77	20/56266 (0.0%)
1	1G	0.42	0/36049	0.69	12/56262 (0.0%)
2	12	0.54	0/1959	1.09	19/2642 (0.7%)
2	1E	0.60	0/1959	1.05	6/2642 (0.2%)
3	22	0.56	0/1636	1.06	8/2205 (0.4%)
3	2E	0.77	0/1629	1.07	4/2195 (0.2%)
4	32	0.69	0/1732	1.19	18/2318 (0.8%)
4	3E	0.84	1/1732 (0.1%)	1.21	16/2318 (0.7%)
5	42	0.66	0/1171	1.17	8/1576 (0.5%)
5	4E	0.83	0/1171	1.20	9/1576 (0.6%)
6	52	0.75	0/855	1.13	3/1154 (0.3%)
6	5E	0.76	0/855	1.07	2/1154 (0.2%)
7	62	0.61	0/1261	1.02	2/1689 (0.1%)
7	6E	0.69	0/1275	1.08	5/1709 (0.3%)
8	72	0.57	0/1135	0.98	1/1527 (0.1%)
8	7E	0.74	0/1135	1.24	10/1527 (0.7%)
9	82	0.58	0/1002	1.06	3/1346 (0.2%)
9	8E	0.67	0/1028	1.10	6/1379 (0.4%)
10	1A	0.54	0/814	1.01	3/1095 (0.3%)
10	1I	0.82	2/814 (0.2%)	1.18	9/1095 (0.8%)
11	2A	0.69	0/879	1.18	6/1187 (0.5%)
11	2I	0.80	0/879	1.22	4/1187 (0.3%)
12	3A	0.79	0/991	1.16	5/1327 (0.4%)
12	3I	1.07	3/991 (0.3%)	1.44	10/1327 (0.8%)
13	4A	0.52	0/943	1.06	9/1265 (0.7%)
13	4I	0.74	0/948	1.07	3/1272 (0.2%)
14	5A	0.57	0/484	0.99	1/643 (0.2%)
14	5I	0.88	2/500 (0.4%)	1.22	3/664 (0.5%)
15	6A	0.69	0/744	0.97	2/992 (0.2%)
15	6I	0.81	1/744 (0.1%)	1.11	1/992 (0.1%)
16	7A	0.73	0/721	1.14	3/970 (0.3%)
16	7I	0.74	0/721	1.11	4/970 (0.4%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
17	8A	0.67	0/847	1.03	3/1131 (0.3%)
17	8I	0.74	0/847	1.18	4/1131 (0.4%)
18	9A	0.69	0/595	1.06	3/790 (0.4%)
18	9I	0.77	0/595	1.22	4/790 (0.5%)
19	AA	0.58	0/638	1.03	3/860 (0.3%)
19	AI	0.78	0/661	1.27	6/890 (0.7%)
20	BA	0.70	0/764	1.21	8/1007 (0.8%)
20	BI	0.64	0/764	1.10	4/1007 (0.4%)
21	1B	0.64	0/221	1.01	2/288 (0.7%)
21	1F	0.66	0/221	1.10	0/288
22	1K	0.36	0/1673	0.60	2/2606 (0.1%)
23	2K	0.57	1/1721 (0.1%)	0.80	0/2682
23	2L	0.45	0/1721	0.71	0/2682
24	3K	0.37	0/1712	0.63	0/2663
25	4K	0.59	0/313	0.68	0/485
25	4L	0.57	0/262	0.82	0/403
26	14	0.56	0/70167	0.81	44/109541 (0.0%)
26	1H	0.67	1/70233 (0.0%)	0.91	68/109643 (0.1%)
27	16	0.56	0/2928	0.87	0/4568
27	1J	0.46	0/2928	0.73	0/4568
28	11	1.23	8/2165 (0.4%)	1.58	43/2919 (1.5%)
28	19	1.05	2/2170 (0.1%)	1.51	41/2926 (1.4%)
29	21	0.98	2/1601 (0.1%)	1.61	35/2160 (1.6%)
29	29	0.97	1/1601 (0.1%)	1.51	21/2160 (1.0%)
30	31	1.09	0/1620	1.39	16/2194 (0.7%)
30	39	0.89	2/1662 (0.1%)	1.46	28/2249 (1.2%)
31	41	0.80	0/1498	1.19	4/2016 (0.2%)
31	49	0.54	0/1498	1.08	8/2016 (0.4%)
32	51	0.90	1/1362 (0.1%)	1.48	20/1841 (1.1%)
32	59	0.65	0/1332	1.26	15/1802 (0.8%)
33	61	0.76	0/1151	1.25	15/1558 (1.0%)
33	69	0.73	0/1151	1.35	23/1558 (1.5%)
34	15	0.72	0/1131	1.19	10/1525 (0.7%)
34	58	0.85	0/1131	1.30	9/1525 (0.6%)
35	25	0.85	0/942	1.23	2/1269 (0.2%)
35	68	0.99	0/942	1.30	7/1269 (0.6%)
36	35	1.02	2/1161 (0.2%)	1.59	21/1544 (1.4%)
36	78	1.11	3/1161 (0.3%)	1.53	17/1544 (1.1%)
37	45	0.96	2/1142 (0.2%)	1.36	12/1527 (0.8%)
37	88	1.23	5/1106 (0.5%)	1.79	29/1478 (2.0%)
38	55	0.99	0/973	1.32	5/1302 (0.4%)
38	98	0.94	0/981	1.30	8/1312 (0.6%)
39	65	0.78	1/891 (0.1%)	1.30	5/1187 (0.4%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
39	A8	0.93	1/891 (0.1%)	1.31	6/1187 (0.5%)
40	75	0.83	1/1155 (0.1%)	1.19	5/1542 (0.3%)
40	B8	0.99	1/1155 (0.1%)	1.39	10/1542 (0.6%)
41	85	0.81	0/981	1.17	8/1306 (0.6%)
41	C8	1.04	1/981 (0.1%)	1.35	10/1306 (0.8%)
42	95	0.93	3/789 (0.4%)	1.39	7/1057 (0.7%)
42	D8	0.92	0/789	1.45	11/1057 (1.0%)
43	A5	1.04	1/910 (0.1%)	1.23	2/1220 (0.2%)
43	E8	0.98	0/910	1.32	4/1220 (0.3%)
44	B5	1.05	0/749	1.28	7/1007 (0.7%)
44	F8	1.13	0/756	1.39	7/1014 (0.7%)
45	C5	0.92	0/807	1.37	7/1076 (0.7%)
45	G8	1.04	0/804	1.56	20/1073 (1.9%)
46	D5	0.61	0/1460	1.19	15/1982 (0.8%)
46	H8	0.74	2/1427 (0.1%)	1.31	13/1935 (0.7%)
47	E5	0.93	0/620	1.35	11/827 (1.3%)
47	I8	1.10	1/634 (0.2%)	1.41	8/847 (0.9%)
48	F5	0.96	0/744	1.35	7/989 (0.7%)
48	J8	1.07	1/769 (0.1%)	1.33	5/1022 (0.5%)
49	G5	0.76	0/565	1.29	6/748 (0.8%)
49	K8	1.06	0/565	1.50	7/748 (0.9%)
50	H5	0.74	0/473	1.31	2/635 (0.3%)
50	L8	0.91	0/457	1.50	7/613 (1.1%)
51	I5	0.71	0/492	1.21	2/663 (0.3%)
51	M8	0.78	0/545	1.27	4/733 (0.5%)
52	J5	1.02	2/472 (0.4%)	1.51	7/639 (1.1%)
52	N8	0.96	1/467 (0.2%)	1.86	8/632 (1.3%)
53	K5	0.96	0/396	1.41	7/529 (1.3%)
53	O8	1.05	0/396	1.50	9/529 (1.7%)
54	L5	1.03	0/406	1.36	3/536 (0.6%)
54	P8	1.27	1/399 (0.3%)	1.45	2/526 (0.4%)
55	M5	1.29	4/483 (0.8%)	1.73	14/634 (2.2%)
55	Q8	1.79	10/486 (2.1%)	2.49	28/638 (4.4%)
56	1L	0.28	0/1717	0.47	0/2674
57	3L	0.40	1/1698 (0.1%)	0.60	0/2646
All	All	0.66	71/322340 (0.0%)	0.96	1029/482707 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	1E	0	2
4	32	0	2
9	82	0	1
10	1A	0	1
11	2A	0	1
12	3I	0	1
13	4I	0	2
14	5A	0	1
19	AI	0	2
20	BA	0	2
20	BI	0	1
28	11	0	2
28	19	0	5
29	21	0	4
29	29	0	5
30	31	0	3
30	39	0	7
31	41	0	2
31	49	0	1
32	59	0	1
33	61	0	4
33	69	0	3
36	35	0	3
36	78	0	3
37	45	0	6
37	88	0	4
38	55	0	2
38	98	0	2
39	65	0	1
40	75	0	2
40	B8	0	2
41	85	0	2
41	C8	0	1
42	95	0	2
42	D8	0	1
43	A5	0	2
44	B5	0	1
45	C5	0	1
45	G8	0	3
46	D5	0	1
46	H8	0	3
47	I8	0	2
48	F5	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
48	J8	0	2
49	G5	0	4
49	K8	0	2
51	I5	0	1
51	M8	0	2
52	N8	0	1
53	K5	0	4
53	O8	0	2
55	M5	0	3
55	Q8	0	8
All	All	0	127

All (71) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
37	45	82	ARG	CA-C	9.98	1.65	1.52
55	Q8	49	VAL	CA-CB	9.75	1.67	1.54
37	88	79	LEU	N-CA	9.00	1.57	1.46
37	88	82	ARG	N-CA	8.42	1.57	1.46
36	35	61	ARG	CA-C	7.86	1.61	1.52
28	11	224	ALA	CA-CB	-7.74	1.41	1.53
55	Q8	25	MET	CA-C	7.57	1.62	1.52
30	39	84	VAL	CA-CB	7.43	1.64	1.54
37	88	82	ARG	CA-C	7.05	1.62	1.52
42	95	72	VAL	CA-CB	7.04	1.64	1.54
29	29	135	HIS	CA-C	-7.00	1.46	1.52
55	M5	34	TRP	N-CA	6.76	1.54	1.46
57	3L	8	4SU	O3'-P	6.75	1.63	1.56
55	M5	52	LYS	CA-C	6.75	1.61	1.52
55	Q8	6	THR	CA-CB	6.71	1.64	1.53
39	A8	110	LEU	CA-C	6.70	1.59	1.53
28	11	271	ILE	CA-C	6.62	1.61	1.53
47	I8	79	VAL	CA-CB	6.45	1.62	1.54
28	11	272	ALA	CA-C	6.38	1.59	1.53
37	88	78	PRO	CA-C	6.27	1.63	1.52
42	95	80	GLN	CA-C	6.22	1.60	1.52
55	Q8	44	LYS	CA-C	-6.16	1.44	1.52
10	1I	55	LYS	CA-C	-6.06	1.46	1.53
36	35	19	VAL	CA-C	6.01	1.60	1.52
55	Q8	26	LYS	CA-C	6.00	1.60	1.52
39	65	88	ASP	CA-C	-5.98	1.50	1.53
28	11	225	ALA	CA-CB	-5.95	1.43	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
36	78	15	ARG	CA-C	5.89	1.60	1.52
26	1H	783	A	C5-C6	-5.88	1.29	1.41
52	J5	27	PRO	CA-C	5.88	1.55	1.51
32	51	9	ILE	CA-CB	5.87	1.61	1.54
15	6I	87	ILE	CA-C	5.72	1.60	1.52
37	45	82	ARG	N-CA	5.71	1.52	1.46
37	88	109	VAL	CA-CB	5.68	1.61	1.55
52	N8	19	ARG	CA-C	-5.64	1.45	1.52
28	19	271	ILE	CA-C	5.62	1.59	1.52
55	Q8	18	ALA	CA-CB	-5.61	1.45	1.53
42	95	82	ARG	CA-C	5.60	1.59	1.52
40	B8	105	LEU	CA-C	-5.59	1.49	1.52
55	Q8	31	HIS	CA-C	5.57	1.58	1.52
12	3I	104	VAL	CA-CB	-5.52	1.47	1.54
12	3I	86	ARG	CA-C	-5.51	1.45	1.52
46	H8	165	VAL	CA-CB	5.50	1.61	1.54
40	75	86	ILE	CA-CB	-5.48	1.49	1.55
14	5I	13	THR	CA-CB	5.48	1.62	1.53
43	A5	44	ALA	CA-CB	-5.42	1.44	1.53
28	19	272	ALA	CA-C	5.42	1.59	1.52
41	C8	65	ILE	CA-CB	-5.41	1.48	1.54
14	5I	27	CYS	CB-SG	-5.39	1.63	1.81
30	39	28	ILE	CA-CB	5.38	1.61	1.54
55	Q8	24	ALA	CA-C	5.38	1.60	1.53
10	1I	56	HIS	CA-C	-5.37	1.47	1.53
28	11	51	VAL	CA-CB	-5.36	1.47	1.54
52	J5	6	VAL	C-O	-5.26	1.20	1.24
12	3I	88	GLY	CA-C	5.24	1.56	1.52
46	H8	53	ILE	CA-CB	5.21	1.61	1.54
55	Q8	59	LYS	CA-CB	-5.21	1.45	1.53
55	M5	53	PRO	CA-C	5.19	1.57	1.52
54	P8	30	VAL	CA-CB	-5.18	1.48	1.54
55	M5	61	LEU	CA-CB	5.16	1.63	1.53
23	2K	8	4SU	O3'-P	5.11	1.61	1.56
36	78	19	VAL	C-O	5.11	1.30	1.24
55	Q8	25	MET	N-CA	5.10	1.52	1.46
28	11	144	ALA	CA-CB	-5.09	1.44	1.53
36	78	27	HIS	CA-CB	-5.08	1.45	1.53
28	11	102	LYS	CA-C	5.06	1.58	1.52
4	3E	9	CYS	CB-SG	5.06	1.98	1.81
28	11	240	ALA	C-O	-5.01	1.17	1.24
29	21	123	ALA	CA-CB	-5.01	1.45	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
29	21	129	HIS	C-N	-5.01	1.27	1.34
48	J8	33	LYS	CA-C	5.00	1.58	1.52

All (1029) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
55	Q8	45	GLY	N-CA-C	-22.03	82.66	111.52
52	N8	40	LYS	CA-C-N	-17.57	102.28	120.38
52	N8	40	LYS	C-N-CA	-17.57	102.28	120.38
37	88	86	GLY	N-CA-C	-17.00	94.70	112.04
28	19	272	ALA	N-CA-C	15.37	131.50	108.14
33	69	118	LYS	CA-C-N	-14.50	106.16	120.52
33	69	118	LYS	C-N-CA	-14.50	106.16	120.52
52	N8	41	PRO	CA-C-N	14.26	137.66	119.84
52	N8	41	PRO	C-N-CA	14.26	137.66	119.84
28	19	235	GLY	N-CA-C	14.02	126.33	112.04
28	11	271	ILE	N-CA-C	13.39	126.08	111.88
55	Q8	28	GLY	N-CA-C	13.25	129.29	113.79
45	C5	39	VAL	N-CA-C	12.95	124.47	112.17
50	L8	11	SER	CA-C-N	12.88	133.26	119.87
50	L8	11	SER	C-N-CA	12.88	133.26	119.87
29	29	88	GLY	N-CA-C	12.80	132.69	110.80
32	51	167	GLU	CA-C-N	-12.65	104.03	119.84
32	51	167	GLU	C-N-CA	-12.65	104.03	119.84
30	39	80	ALA	CA-C-N	-12.57	104.12	119.84
30	39	80	ALA	C-N-CA	-12.57	104.12	119.84
55	Q8	25	MET	N-CA-C	12.54	137.51	110.80
42	D8	35	LEU	CA-C-N	12.36	131.93	119.82
42	D8	35	LEU	C-N-CA	12.36	131.93	119.82
52	J5	4	HIS	CA-C-N	-12.32	106.97	119.90
52	J5	4	HIS	C-N-CA	-12.32	106.97	119.90
11	2I	102	GLY	N-CA-C	-12.32	93.95	110.58
42	95	80	GLN	N-CA-C	12.29	125.21	107.88
37	45	82	ARG	N-CA-C	12.29	131.33	113.02
28	11	272	ALA	N-CA-C	12.24	122.57	108.49
28	11	75	ILE	CA-C-N	-11.91	108.24	120.98
28	11	75	ILE	C-N-CA	-11.91	108.24	120.98
42	95	49	THR	CA-C-N	-11.77	105.13	119.84
42	95	49	THR	C-N-CA	-11.77	105.13	119.84
37	88	106	VAL	N-CA-C	11.69	123.42	110.21
37	88	3	MET	CA-C-N	-11.59	108.95	120.31
37	88	3	MET	C-N-CA	-11.59	108.95	120.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
29	29	73	GLU	CA-C-N	11.46	132.18	119.92
29	29	73	GLU	C-N-CA	11.46	132.18	119.92
50	H5	11	SER	CA-C-N	11.33	131.65	119.87
50	H5	11	SER	C-N-CA	11.33	131.65	119.87
32	59	153	LYS	CA-C-N	-11.30	105.72	119.84
32	59	153	LYS	C-N-CA	-11.30	105.72	119.84
37	88	78	PRO	N-CA-C	11.25	127.87	114.03
36	35	62	LEU	N-CA-C	11.11	134.36	109.81
37	88	82	ARG	N-CA-C	11.02	134.27	110.80
46	H8	161	VAL	N-CA-C	10.96	121.07	107.70
49	K8	17	SER	CA-C-N	10.87	133.43	119.84
49	K8	17	SER	C-N-CA	10.87	133.43	119.84
31	41	44	GLY	N-CA-C	-10.65	101.46	114.66
29	29	80	GLU	N-CA-C	10.45	126.34	113.17
55	M5	33	ASN	N-CA-C	10.34	125.68	107.80
36	78	15	ARG	N-CA-C	10.28	123.60	110.24
32	51	125	VAL	CA-C-N	10.26	132.66	119.84
32	51	125	VAL	C-N-CA	10.26	132.66	119.84
29	21	21	VAL	CA-C-N	10.18	132.56	119.84
29	21	21	VAL	C-N-CA	10.18	132.56	119.84
42	95	42	GLY	N-CA-C	10.12	124.88	112.64
18	9I	19	LYS	N-CA-C	10.04	122.87	108.00
7	62	133	GLY	N-CA-C	-10.01	102.25	114.66
37	88	77	LYS	CA-C-N	9.97	130.24	119.87
37	88	77	LYS	C-N-CA	9.97	130.24	119.87
26	1H	271(B)	G	P-O3'-C3'	9.81	131.47	119.70
30	39	68	LYS	CA-C-N	-9.74	107.94	123.23
30	39	68	LYS	C-N-CA	-9.74	107.94	123.23
29	29	52	LEU	CA-C-N	9.68	129.31	119.24
29	29	52	LEU	C-N-CA	9.68	129.31	119.24
36	35	71	VAL	CA-C-N	-9.66	109.80	119.56
36	35	71	VAL	C-N-CA	-9.66	109.80	119.56
37	88	24	GLY	N-CA-C	-9.63	95.46	112.22
54	L5	6	GLN	CA-C-N	9.63	130.24	119.93
54	L5	6	GLN	C-N-CA	9.63	130.24	119.93
32	59	167	GLU	CA-C-N	9.56	131.79	119.84
32	59	167	GLU	C-N-CA	9.56	131.79	119.84
39	A8	110	LEU	N-CA-C	9.55	119.47	108.49
29	21	52	LEU	CA-C-N	9.54	131.77	119.84
29	21	52	LEU	C-N-CA	9.54	131.77	119.84
36	35	65	ARG	N-CA-C	-9.54	91.20	107.99
42	D8	49	THR	CA-C-N	-9.48	109.11	118.97

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
42	D8	49	THR	C-N-CA	-9.48	109.11	118.97
29	21	65	GLY	N-CA-C	-9.44	99.37	115.80
52	N8	50	GLY	N-CA-C	9.37	123.98	112.64
48	F5	29	GLY	N-CA-C	9.36	123.06	110.43
36	35	19	VAL	N-CA-C	9.33	121.00	107.75
37	88	106	VAL	CB-CA-C	-9.32	101.01	111.45
14	5I	27	CYS	N-CA-C	9.32	121.13	110.97
29	29	67	PHE	N-CA-C	-9.28	101.72	113.23
55	Q8	52	LYS	C-N-CD	-9.18	100.41	120.60
41	C8	95	LEU	N-CA-C	9.12	122.20	111.71
40	B8	4	GLY	N-CA-C	-9.05	101.79	112.83
39	A8	90	GLY	CA-C-N	-9.03	108.56	119.84
39	A8	90	GLY	C-N-CA	-9.03	108.56	119.84
1	13	1498	U	C2'-C3'-O3'	9.00	123.01	109.50
36	78	25	SER	N-CA-C	-8.96	102.34	113.28
30	39	83	PHE	N-CA-C	8.90	124.39	113.17
46	D5	67	LEU	CA-C-N	8.90	130.97	119.84
46	D5	67	LEU	C-N-CA	8.90	130.97	119.84
5	42	23	GLY	N-CA-C	8.84	121.61	110.29
55	M5	53	PRO	CA-C-N	8.78	133.20	120.38
55	M5	53	PRO	C-N-CA	8.78	133.20	120.38
29	21	31	CYS	CA-C-N	8.77	130.80	119.84
29	21	31	CYS	C-N-CA	8.77	130.80	119.84
32	51	86	GLU	N-CA-C	8.75	124.61	111.04
45	G8	7	VAL	N-CA-C	8.74	120.08	110.21
55	Q8	52	LYS	CA-C-N	8.72	147.93	127.00
55	Q8	52	LYS	C-N-CA	8.72	147.93	127.00
45	G8	81	LYS	N-CA-C	-8.66	90.68	109.81
49	G5	44	LEU	N-CA-C	-8.51	102.44	113.17
29	21	188	VAL	N-CA-C	8.51	117.29	108.95
29	21	119	ARG	N-CA-C	-8.49	100.28	111.24
16	7A	40	ASP	CA-C-N	8.47	128.68	119.87
16	7A	40	ASP	C-N-CA	8.47	128.68	119.87
11	2A	34	ASP	CA-C-N	-8.40	111.07	119.56
11	2A	34	ASP	C-N-CA	-8.40	111.07	119.56
50	L8	53	LEU	N-CA-C	-8.39	92.94	110.80
12	3I	70	ILE	CA-C-N	8.36	128.50	120.31
12	3I	70	ILE	C-N-CA	8.36	128.50	120.31
32	51	54	ARG	CA-C-N	8.36	128.33	119.05
32	51	54	ARG	C-N-CA	8.36	128.33	119.05
28	11	152	GLY	N-CA-C	8.34	119.87	111.95
32	51	4	ILE	N-CA-C	8.28	120.98	109.55

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
26	14	752	A	C2'-C3'-O3'	8.28	121.92	109.50
36	78	71	VAL	CA-C-N	-8.25	111.23	119.56
36	78	71	VAL	C-N-CA	-8.25	111.23	119.56
26	1H	1379	A	N9-C1'-C2'	8.21	126.31	114.00
5	4E	67	VAL	N-CA-C	8.20	119.18	108.35
6	52	55	ASP	CA-C-N	8.19	127.83	119.56
6	52	55	ASP	C-N-CA	8.19	127.83	119.56
53	K5	23	THR	N-CA-C	8.13	121.52	109.24
36	35	144	GLU	CA-C-N	8.13	128.57	120.52
36	35	144	GLU	C-N-CA	8.13	128.57	120.52
46	D5	14	LYS	CA-C-N	8.12	127.84	119.56
46	D5	14	LYS	C-N-CA	8.12	127.84	119.56
36	35	62	LEU	CA-C-N	8.11	129.98	119.84
36	35	62	LEU	C-N-CA	8.11	129.98	119.84
46	H8	161	VAL	CB-CA-C	-8.10	104.12	111.74
36	35	107	LYS	N-CA-C	8.05	122.49	111.54
28	11	264	LYS	CA-C-N	8.04	128.80	119.47
28	11	264	LYS	C-N-CA	8.04	128.80	119.47
44	F8	3	THR	CA-C-N	8.04	136.17	121.70
44	F8	3	THR	C-N-CA	8.04	136.17	121.70
4	3E	12	CYS	N-CA-C	-8.01	101.50	111.11
46	H8	14	LYS	CA-C-N	8.01	128.45	119.32
46	H8	14	LYS	C-N-CA	8.01	128.45	119.32
28	19	13	ARG	N-CA-C	-7.98	102.99	112.89
43	E8	92	ARG	N-CA-C	7.97	123.53	112.45
40	B8	113	LYS	N-CA-C	-7.96	102.10	112.68
38	98	3	HIS	CA-C-N	-7.95	109.45	122.65
38	98	3	HIS	C-N-CA	-7.95	109.45	122.65
26	14	1786	A	N9-C1'-C2'	7.93	125.90	114.00
32	51	11	VAL	CA-C-N	7.92	129.74	119.84
32	51	11	VAL	C-N-CA	7.92	129.74	119.84
18	9I	21	LYS	N-CA-C	7.92	123.12	113.38
37	88	65	PHE	N-CA-C	7.91	123.23	113.50
29	21	55	ASN	CA-C-N	-7.91	109.96	119.84
29	21	55	ASN	C-N-CA	-7.91	109.96	119.84
4	32	3	ARG	CB-CA-C	-7.91	107.46	116.63
33	69	143	SER	CB-CA-C	-7.89	107.47	116.54
5	4E	69	VAL	CA-C-N	7.88	129.69	119.84
5	4E	69	VAL	C-N-CA	7.88	129.69	119.84
28	11	180	GLY	N-CA-C	-7.77	104.31	115.27
33	69	120	ILE	N-CA-C	7.75	117.82	110.53
46	H8	67	LEU	CA-C-N	7.75	129.53	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
46	H8	67	LEU	C-N-CA	7.75	129.53	119.84
37	88	57	HIS	CA-C-N	-7.74	111.86	122.86
37	88	57	HIS	C-N-CA	-7.74	111.86	122.86
46	D5	157	LEU	CA-C-N	7.74	128.35	120.38
46	D5	157	LEU	C-N-CA	7.74	128.35	120.38
53	O8	28	ARG	N-CA-C	7.73	121.50	109.52
4	32	180	GLY	N-CA-C	-7.71	105.09	114.66
2	12	25	ASN	CA-C-N	7.68	127.35	119.82
2	12	25	ASN	C-N-CA	7.68	127.35	119.82
33	69	78	THR	N-CA-C	7.67	120.61	111.02
3	22	194	GLY	N-CA-C	7.67	121.52	111.70
45	G8	79	CYS	N-CA-C	7.67	127.13	110.80
2	12	17	PHE	N-CA-C	7.66	121.96	109.85
33	61	136	VAL	CA-C-N	7.65	128.25	120.14
33	61	136	VAL	C-N-CA	7.65	128.25	120.14
28	19	35	LYS	CA-C-N	-7.64	112.83	120.31
28	19	35	LYS	C-N-CA	-7.64	112.83	120.31
37	88	125	LEU	CA-C-N	7.63	127.30	119.82
37	88	125	LEU	C-N-CA	7.63	127.30	119.82
13	4A	112	GLY	CA-C-N	7.62	128.07	119.92
13	4A	112	GLY	C-N-CA	7.62	128.07	119.92
10	1I	58	ASP	N-CA-C	-7.54	99.94	110.35
29	21	58	ARG	N-CA-C	-7.53	103.21	113.30
55	M5	52	LYS	CA-C-N	-7.53	111.02	120.51
55	M5	52	LYS	C-N-CA	-7.53	111.02	120.51
55	Q8	30	ARG	N-CA-C	7.53	119.80	107.23
29	29	87	GLU	CA-C-N	-7.51	112.22	121.38
29	29	87	GLU	C-N-CA	-7.51	112.22	121.38
30	39	9	ILE	CA-C-N	-7.50	111.17	118.97
30	39	9	ILE	C-N-CA	-7.50	111.17	118.97
55	Q8	8	LYS	CA-C-N	-7.46	114.72	123.08
55	Q8	8	LYS	C-N-CA	-7.46	114.72	123.08
29	21	188	VAL	CA-C-N	7.45	127.49	119.89
29	21	188	VAL	C-N-CA	7.45	127.49	119.89
38	55	113	LEU	CA-C-N	-7.44	113.39	123.14
38	55	113	LEU	C-N-CA	-7.44	113.39	123.14
30	31	7	TYR	N-CA-C	7.44	120.84	111.69
47	E5	46	LYS	CA-C-N	7.44	129.14	119.84
47	E5	46	LYS	C-N-CA	7.44	129.14	119.84
34	15	47	ALA	N-CA-C	7.43	119.60	110.91
31	41	119	GLY	N-CA-C	7.42	119.00	111.95
26	1H	271(B)	G	C2'-C3'-O3'	7.42	120.63	109.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
55	Q8	23	VAL	N-CA-C	7.40	118.25	107.75
40	75	13	ARG	N-CA-C	-7.39	104.29	113.38
16	7I	20	VAL	N-CA-C	7.35	119.33	108.45
34	58	57	ALA	N-CA-C	-7.33	101.40	110.41
36	35	50	ARG	N-CA-C	7.31	122.48	112.90
35	68	29	ASN	N-CA-C	7.26	121.45	112.59
33	61	135	GLU	N-CA-C	7.25	117.54	108.19
47	I8	46	LYS	CA-C-N	-7.24	112.52	119.76
47	I8	46	LYS	C-N-CA	-7.24	112.52	119.76
5	4E	154	GLY	N-CA-C	-7.22	105.09	111.95
29	21	186	GLY	CA-C-N	-7.20	110.66	122.54
29	21	186	GLY	C-N-CA	-7.20	110.66	122.54
50	L8	54	VAL	N-CA-C	7.20	124.31	109.34
55	Q8	31	HIS	N-CA-C	7.19	120.00	107.49
30	31	24	LEU	CA-C-N	7.16	128.79	119.84
30	31	24	LEU	C-N-CA	7.16	128.79	119.84
26	14	2439	A	P-O3'-C3'	7.15	130.92	120.20
26	14	752	A	P-O3'-C3'	7.15	130.92	120.20
2	12	231	GLU	CA-C-N	7.14	127.56	119.92
2	12	231	GLU	C-N-CA	7.14	127.56	119.92
34	58	39	ARG	CA-C-N	-7.13	110.93	119.84
34	58	39	ARG	C-N-CA	-7.13	110.93	119.84
45	G8	81	LYS	CA-C-N	7.13	144.10	127.00
45	G8	81	LYS	C-N-CA	7.13	144.10	127.00
45	G8	99	CYS	N-CA-C	7.13	119.95	111.33
45	G8	17	SER	N-CA-C	7.12	119.00	108.60
3	22	78	GLY	N-CA-C	-7.12	101.41	112.45
5	42	14	ARG	N-CA-C	7.12	120.08	108.26
8	7E	100	ILE	CA-C-N	7.12	127.04	119.85
8	7E	100	ILE	C-N-CA	7.12	127.04	119.85
44	F8	67	GLY	N-CA-C	-7.12	96.31	113.18
32	59	100	GLY	N-CA-C	7.11	122.63	112.81
29	21	129	HIS	CA-C-N	-7.10	111.39	120.34
29	21	129	HIS	C-N-CA	-7.10	111.39	120.34
45	G8	73	ARG	CA-C-N	7.10	127.14	119.90
45	G8	73	ARG	C-N-CA	7.10	127.14	119.90
3	22	6	HIS	CA-C-N	7.10	127.25	119.87
3	22	6	HIS	C-N-CA	7.10	127.25	119.87
53	O8	23	THR	N-CA-C	7.09	121.12	109.06
51	I5	55	ARG	N-CA-C	7.08	117.32	108.19
26	1H	1799	G	C2'-C3'-O3'	7.08	120.11	109.50
36	35	111	ARG	N-CA-C	7.07	121.84	109.96

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
35	25	29	ASN	N-CA-C	7.07	120.77	112.72
38	98	9	LYS	N-CA-C	-7.06	98.22	109.59
29	29	23	VAL	N-CA-C	7.05	124.00	109.34
42	95	82	ARG	N-CA-C	7.04	121.14	108.48
44	B5	25	LYS	N-CA-C	7.03	120.23	108.20
19	AI	67	VAL	N-CA-C	7.03	123.96	109.34
34	15	39	ARG	CA-C-N	-7.03	111.05	119.84
34	15	39	ARG	C-N-CA	-7.03	111.05	119.84
55	Q8	10	ALA	N-CA-C	-7.03	103.23	111.03
26	1H	752	A	C2'-C3'-O3'	7.02	120.03	109.50
34	58	46	VAL	N-CA-C	7.01	118.01	112.12
26	1H	587	C	C4'-C3'-O3'	7.01	119.92	109.40
2	12	8	LYS	CB-CA-C	-6.98	108.53	116.63
4	3E	28	SER	CA-C-N	-6.98	113.47	120.31
4	3E	28	SER	C-N-CA	-6.98	113.47	120.31
31	49	121	ASN	CA-C-N	6.98	126.61	119.56
31	49	121	ASN	C-N-CA	6.98	126.61	119.56
16	7I	16	HIS	N-CA-C	-6.96	98.74	109.52
29	29	51	PHE	N-CA-C	6.95	125.60	110.80
34	58	7	LYS	N-CA-C	-6.94	99.96	109.95
44	B5	31	HIS	CA-C-N	6.94	126.54	119.19
44	B5	31	HIS	C-N-CA	6.94	126.54	119.19
28	19	238	GLY	N-CA-C	-6.93	101.28	113.76
5	42	12	LEU	N-CA-C	6.91	120.22	107.99
55	M5	60	LEU	CB-CA-C	-6.90	107.85	117.23
26	14	2225	A	C4'-C3'-O3'	6.90	119.75	109.40
53	O8	42	TRP	N-CA-C	-6.89	104.86	113.20
49	K8	17	SER	N-CA-C	6.88	120.46	108.82
26	14	2702	U	C4'-C3'-O3'	-6.88	102.69	113.00
45	G8	5	MET	CB-CA-C	-6.88	106.81	115.89
55	Q8	41	ILE	N-CA-C	-6.86	106.04	112.83
48	J8	2	SER	CA-C-N	-6.85	112.63	122.77
48	J8	2	SER	C-N-CA	-6.85	112.63	122.77
50	L8	40	THR	CA-C-N	-6.85	111.93	119.19
50	L8	40	THR	C-N-CA	-6.85	111.93	119.19
30	31	91	GLY	CA-C-N	6.83	126.59	119.76
30	31	91	GLY	C-N-CA	6.83	126.59	119.76
55	Q8	45	GLY	CA-C-O	-6.81	115.41	122.01
5	4E	95	ALA	CA-C-N	-6.80	112.94	120.14
5	4E	95	ALA	C-N-CA	-6.80	112.94	120.14
33	61	118	LYS	CA-C-N	6.77	126.80	119.90
33	61	118	LYS	C-N-CA	6.77	126.80	119.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	12	90	MET	CA-C-N	6.77	126.79	119.89
2	12	90	MET	C-N-CA	6.77	126.79	119.89
37	45	31	ASP	N-CA-C	6.75	120.00	111.69
36	78	71	VAL	N-CA-C	6.75	123.46	108.88
26	1H	1297	C	OP2-P-O3'	-6.74	87.77	108.00
4	3E	12	CYS	CA-CB-SG	6.74	129.90	114.40
37	88	98	LYS	CA-C-N	-6.74	113.03	119.76
37	88	98	LYS	C-N-CA	-6.74	113.03	119.76
44	B5	40	LYS	CA-C-N	-6.73	112.06	122.16
44	B5	40	LYS	C-N-CA	-6.73	112.06	122.16
17	8I	79	SER	N-CA-C	6.72	119.76	110.35
55	M5	29	LYS	N-CA-C	-6.72	104.96	113.02
30	39	29	ASN	CA-C-N	6.71	125.94	118.97
30	39	29	ASN	C-N-CA	6.71	125.94	118.97
1	1G	1498	U	C2'-C3'-O3'	6.68	119.53	109.50
37	45	69	PHE	CA-C-N	6.68	128.20	119.84
37	45	69	PHE	C-N-CA	6.68	128.20	119.84
32	59	90	LYS	N-CA-C	6.67	119.16	108.41
52	N8	46	CYS	N-CA-C	6.67	117.27	109.60
28	19	49	ILE	N-CA-CB	6.66	118.22	110.82
1	13	812	C	C2'-C3'-O3'	6.66	119.49	109.50
19	AI	25	LYS	N-CA-C	-6.66	96.61	110.80
29	21	134	ILE	N-CA-C	6.66	118.50	112.17
33	69	102	SER	N-CA-C	-6.66	96.61	110.80
26	1H	2468	G	O4'-C1'-N9	6.65	118.17	108.20
22	1K	9	A	C2'-C3'-O3'	6.64	119.46	109.50
26	1H	783	A	OP1-P-O3'	-6.64	88.09	108.00
36	78	9	ASN	CA-C-N	6.63	128.13	119.84
36	78	9	ASN	C-N-CA	6.63	128.13	119.84
32	51	81	GLU	N-CA-C	6.61	120.37	111.24
7	6E	132	GLY	N-CA-C	6.61	120.53	111.54
2	1E	16	HIS	N-CA-C	6.59	121.48	113.17
55	M5	32	LEU	CA-C-N	-6.59	112.88	122.44
55	M5	32	LEU	C-N-CA	-6.59	112.88	122.44
29	29	49	LEU	N-CA-C	6.59	119.57	110.35
29	29	48	GLN	N-CA-C	6.58	119.94	112.97
40	B8	111	ARG	N-CA-C	-6.58	101.41	110.35
26	14	2447	G	P-O3'-C3'	6.57	130.05	120.20
26	1H	2430	A	O5'-P-OP1	6.56	127.69	108.00
55	Q8	60	LEU	N-CA-C	6.56	120.22	111.30
12	3A	105	TYR	CB-CA-C	-6.56	108.31	117.23
26	14	1819	A	C4'-C3'-O3'	6.55	119.23	109.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
45	C5	82	PRO	N-CA-C	6.55	121.50	111.34
53	K5	40	CYS	N-CA-C	6.54	117.90	109.65
29	21	190	GLY	CA-C-N	6.54	126.50	120.03
29	21	190	GLY	C-N-CA	6.54	126.50	120.03
30	39	78	ILE	CA-C-N	-6.52	112.57	122.28
30	39	78	ILE	C-N-CA	-6.52	112.57	122.28
30	39	24	LEU	CA-C-N	-6.51	111.70	119.84
30	39	24	LEU	C-N-CA	-6.51	111.70	119.84
20	BI	96	GLY	N-CA-C	6.50	123.31	110.77
35	68	4	PRO	CA-C-O	-6.50	114.24	121.32
18	9I	19	LYS	CB-CA-C	-6.49	107.25	116.34
29	29	135	HIS	N-CA-C	-6.46	103.28	112.13
32	59	95	ARG	N-CA-C	6.45	117.96	108.86
51	M8	4	GLY	N-CA-C	-6.45	101.24	110.46
29	21	73	GLU	CA-C-N	6.44	127.89	119.84
29	21	73	GLU	C-N-CA	6.44	127.89	119.84
37	45	104	PHE	N-CA-C	6.43	124.50	110.80
33	61	143	SER	N-CA-C	6.42	124.48	110.80
26	1H	1022	G	C2'-C3'-O3'	6.42	119.13	109.50
14	5A	39	LEU	N-CA-C	6.42	116.75	108.34
45	C5	103	GLY	N-CA-C	6.41	128.37	113.18
28	11	115	GLN	N-CA-C	6.40	119.52	110.50
38	55	93	GLY	N-CA-C	6.40	120.95	110.97
32	51	11	VAL	N-CA-C	6.40	116.24	109.01
26	14	2702	U	N1-C1'-C2'	6.40	121.59	112.00
42	D8	39	LEU	N-CA-C	6.39	121.22	113.17
55	Q8	24	ALA	CA-C-O	-6.38	115.31	122.01
26	14	2689	U	P-O3'-C3'	6.38	129.78	120.20
53	O8	13	CYS	N-CA-C	6.37	119.36	108.02
53	O8	21	TYR	N-CA-C	6.37	124.36	110.80
33	69	135	GLU	N-CA-C	6.36	119.47	110.50
1	13	792	A	N9-C1'-C2'	6.35	123.52	114.00
47	I8	84	LEU	N-CA-C	-6.34	97.28	110.80
37	45	98	LYS	CA-C-N	-6.34	113.24	119.90
37	45	98	LYS	C-N-CA	-6.34	113.24	119.90
30	39	95	ARG	N-CA-C	6.34	117.48	108.74
17	8I	48	GLU	CA-C-N	-6.33	113.10	122.41
17	8I	48	GLU	C-N-CA	-6.33	113.10	122.41
4	32	201	GLN	N-CA-C	-6.33	105.56	113.28
20	BA	74	LYS	CB-CA-C	-6.32	109.27	116.54
4	32	135	LEU	CA-C-N	6.32	126.80	119.47
4	32	135	LEU	C-N-CA	6.32	126.80	119.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
30	39	69	HIS	N-CA-C	6.32	120.17	107.41
32	59	115	VAL	N-CA-C	6.32	116.97	107.75
12	3I	117	ARG	N-CA-C	6.31	120.54	112.34
38	55	82	GLU	N-CA-C	6.31	124.24	110.80
30	31	58	ALA	N-CA-C	6.30	118.95	111.71
33	61	41	GLU	N-CA-C	-6.29	105.09	112.89
9	82	17	VAL	N-CA-C	6.28	116.91	107.80
28	19	107	ALA	CA-C-N	-6.28	114.16	120.31
28	19	107	ALA	C-N-CA	-6.28	114.16	120.31
5	4E	105	VAL	CA-C-N	-6.27	113.23	119.56
5	4E	105	VAL	C-N-CA	-6.27	113.23	119.56
4	32	171	GLY	CA-C-N	6.27	125.95	119.56
4	32	171	GLY	C-N-CA	6.27	125.95	119.56
51	M8	51	ASP	N-CA-C	6.26	119.07	110.24
46	H8	133	ILE	CA-C-N	6.26	127.66	119.84
46	H8	133	ILE	C-N-CA	6.26	127.66	119.84
26	1H	2346	A	O4'-C1'-N9	6.26	117.59	108.20
39	A8	5	THR	N-CA-C	6.25	118.62	110.43
28	11	83	GLU	N-CA-C	6.24	118.44	109.14
4	32	30	LYS	CA-C-N	-6.24	112.00	122.92
4	32	30	LYS	C-N-CA	-6.24	112.00	122.92
26	1H	2713	A	OP1-P-O3'	-6.24	89.27	108.00
28	19	68	LYS	CA-C-N	-6.24	110.45	122.06
28	19	68	LYS	C-N-CA	-6.24	110.45	122.06
28	11	55	GLY	CA-C-O	-6.24	117.81	122.37
30	39	71	GLY	N-CA-C	-6.24	106.02	115.00
44	B5	11	PRO	CA-C-N	-6.24	113.99	122.91
44	B5	11	PRO	C-N-CA	-6.24	113.99	122.91
53	O8	48	VAL	N-CA-C	6.23	117.79	111.00
40	B8	114	LEU	N-CA-C	6.22	119.89	112.93
4	3E	32	ALA	N-CA-C	-6.21	97.58	110.80
10	1A	52	GLY	CA-C-N	6.21	125.94	119.05
10	1A	52	GLY	C-N-CA	6.21	125.94	119.05
2	12	23	ARG	N-CA-C	-6.20	97.07	107.80
26	14	1141	U	P-O3'-C3'	6.19	129.49	120.20
55	M5	39	LYS	N-CA-C	-6.18	101.13	110.28
35	68	98	VAL	N-CA-C	6.18	118.08	109.55
19	AA	75	ALA	CA-C-N	6.18	125.94	119.76
19	AA	75	ALA	C-N-CA	6.18	125.94	119.76
12	3I	60	LEU	N-CA-C	6.17	119.62	110.48
34	15	134	ARG	CA-C-N	6.17	127.55	119.84
34	15	134	ARG	C-N-CA	6.17	127.55	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
45	G8	60	PHE	N-CA-C	6.17	118.99	108.02
12	3I	18	VAL	N-CA-C	6.16	119.69	111.44
45	G8	93	GLY	CA-C-O	-6.16	117.98	122.23
28	19	194	GLY	N-CA-C	-6.15	101.66	110.46
37	88	29	PHE	N-CA-C	6.15	121.54	113.30
33	69	110	ASP	CA-C-N	6.15	127.52	119.84
33	69	110	ASP	C-N-CA	6.15	127.52	119.84
1	13	792	A	O4'-C1'-N9	6.14	117.42	108.20
26	1H	222	A	P-O3'-C3'	6.14	129.41	120.20
30	39	170	LEU	CA-C-N	6.14	125.36	118.97
30	39	170	LEU	C-N-CA	6.14	125.36	118.97
34	58	69	GLN	N-CA-C	6.14	118.77	111.71
54	P8	6	GLN	CA-C-N	6.13	126.49	119.93
54	P8	6	GLN	C-N-CA	6.13	126.49	119.93
28	11	262	ARG	N-CA-C	6.13	117.65	110.97
26	14	49	A	P-O3'-C3'	6.12	129.38	120.20
49	G5	42	GLY	N-CA-C	-6.12	103.99	112.18
3	2E	159	GLY	N-CA-C	-6.11	106.72	115.64
41	C8	94	ASN	N-CA-C	-6.09	105.49	113.17
12	3A	43	VAL	N-CA-C	6.09	117.13	108.42
42	D8	28	GLU	CA-C-N	-6.08	113.71	119.85
42	D8	28	GLU	C-N-CA	-6.08	113.71	119.85
1	1G	812	C	C2'-C3'-O3'	6.08	118.62	109.50
45	G8	95	LYS	N-CA-C	-6.07	97.87	110.80
30	39	16	GLY	N-CA-C	-6.07	106.14	114.64
28	11	230	ASP	N-CA-C	6.05	118.78	111.40
30	31	197	ASP	N-CA-C	-6.05	97.91	110.80
53	O8	45	LYS	N-CA-C	6.05	118.35	108.55
13	4I	62	ASN	N-CA-C	6.05	119.13	111.69
50	L8	54	VAL	CB-CA-C	-6.04	101.38	111.29
39	A8	34	HIS	N-CA-C	6.04	118.65	109.95
2	12	19	HIS	N-CA-C	6.03	116.05	108.45
29	21	120	TRP	N-CA-C	6.01	120.32	112.92
2	1E	15	VAL	N-CA-C	6.00	118.66	112.90
44	F8	5	TYR	N-CA-C	-6.00	105.72	113.16
28	19	98	VAL	N-CA-C	-6.00	104.17	112.50
19	AI	6	LYS	N-CA-C	5.99	123.56	110.80
22	1K	9	A	P-O3'-C3'	5.98	129.17	120.20
32	59	28	GLY	CA-C-N	5.98	125.46	119.24
32	59	28	GLY	C-N-CA	5.98	125.46	119.24
12	3I	105	TYR	CB-CA-C	-5.96	109.72	116.63
28	11	237	GLU	CA-C-N	-5.96	114.68	120.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
28	11	237	GLU	C-N-CA	-5.96	114.68	120.34
37	45	49	ALA	N-CA-C	-5.96	104.70	111.14
37	88	136	ALA	N-CA-C	-5.96	104.86	111.71
54	L5	10	ARG	N-CA-C	-5.96	104.70	111.14
1	13	687	A	C2'-C3'-O3'	5.96	118.43	109.50
20	BI	9	ASN	N-CA-C	5.96	117.90	108.79
43	A5	77	ASP	N-CA-C	-5.95	100.91	110.14
29	29	32	PRO	CA-C-O	-5.95	114.25	121.03
26	1H	1899	G	N3-C4-N9	-5.94	108.17	126.00
26	1H	2430	A	O5'-P-OP2	-5.94	90.18	108.00
37	45	83	MET	N-CA-C	5.94	118.79	107.75
28	11	203	ASN	CA-C-N	-5.93	112.09	120.75
28	11	203	ASN	C-N-CA	-5.93	112.09	120.75
7	6E	111	ARG	CA-C-N	5.93	125.63	119.64
7	6E	111	ARG	C-N-CA	5.93	125.63	119.64
26	14	2447	G	C4'-C3'-O3'	5.93	118.29	109.40
2	1E	23	ARG	N-CA-C	-5.92	105.92	113.02
29	21	141	ILE	N-CA-C	5.92	118.58	112.90
13	4I	82	MET	N-CA-C	-5.92	103.13	110.41
4	3E	29	PRO	CA-C-O	-5.91	114.79	122.12
28	11	91	ARG	CA-C-N	-5.91	114.46	122.91
28	11	91	ARG	C-N-CA	-5.91	114.46	122.91
33	61	131	LYS	CA-C-N	5.91	141.18	127.00
33	61	131	LYS	C-N-CA	5.91	141.18	127.00
26	14	2701	C	O3'-P-O5'	5.91	112.86	104.00
26	1H	945	A	C4-N9-C1'	5.90	144.00	126.30
46	D5	7	ALA	CB-CA-C	-5.90	108.77	115.79
28	11	107	ALA	CA-C-N	5.90	125.81	119.85
28	11	107	ALA	C-N-CA	5.90	125.81	119.85
40	B8	19	LEU	CA-C-N	5.89	126.08	120.31
40	B8	19	LEU	C-N-CA	5.89	126.08	120.31
33	61	110	ASP	CA-C-N	5.89	141.13	127.00
33	61	110	ASP	C-N-CA	5.89	141.13	127.00
35	68	58	VAL	N-CA-C	5.89	115.71	108.53
47	E5	11	ARG	CA-C-N	-5.89	114.47	122.95
47	E5	11	ARG	C-N-CA	-5.89	114.47	122.95
55	M5	34	TRP	N-CA-C	5.88	123.33	110.80
48	F5	36	GLY	N-CA-C	5.88	127.11	113.18
11	2A	57	THR	CA-C-N	5.88	125.26	118.85
11	2A	57	THR	C-N-CA	5.88	125.26	118.85
28	11	136	ILE	CA-C-N	-5.88	113.89	119.76
28	11	136	ILE	C-N-CA	-5.88	113.89	119.76

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
11	2A	120	ARG	CA-C-N	5.88	126.34	120.52
11	2A	120	ARG	C-N-CA	5.88	126.34	120.52
53	O8	21	TYR	CA-CB-CG	5.87	124.46	113.90
47	E5	60	PHE	N-CA-C	5.87	118.03	108.76
37	88	28	ALA	N-CA-C	5.87	120.58	112.90
48	F5	37	ILE	N-CA-C	5.86	116.98	109.30
6	52	60	PHE	N-CA-C	5.86	117.96	108.41
35	25	94	ARG	N-CA-C	-5.86	105.98	113.01
51	M8	63	TYR	N-CA-C	5.85	117.53	111.03
1	13	509	A	C2'-C3'-O3'	5.85	122.47	113.70
32	59	124	GLU	N-CA-C	5.85	119.00	109.06
47	I8	48	GLY	N-CA-C	5.85	119.97	112.13
36	35	55	ARG	N-CA-C	-5.85	100.67	109.79
31	49	155	MET	N-CA-C	5.85	117.03	108.14
4	32	12	CYS	N-CA-C	-5.84	104.26	111.33
28	19	244	ARG	CA-C-N	-5.84	114.36	120.38
28	19	244	ARG	C-N-CA	-5.84	114.36	120.38
28	19	137	PRO	CA-C-O	-5.84	114.98	121.23
44	F8	11	PRO	CA-C-N	-5.84	114.84	122.37
44	F8	11	PRO	C-N-CA	-5.84	114.84	122.37
53	K5	27	LYS	CA-C-N	-5.84	115.25	122.84
53	K5	27	LYS	C-N-CA	-5.84	115.25	122.84
46	H8	118	GLN	N-CA-C	5.84	117.74	110.91
20	BI	49	ALA	CB-CA-C	-5.84	109.29	117.23
51	I5	20	ASN	N-CA-C	5.83	115.72	108.19
1	1G	1346	A	P-O3'-C3'	5.83	128.94	120.20
26	14	829	A	OP1-P-OP2	5.83	137.08	119.60
20	BA	12	ALA	N-CA-C	-5.82	105.50	113.30
18	9I	22	VAL	N-CA-C	5.82	121.45	109.34
32	51	85	LYS	CA-C-N	5.82	129.62	120.89
32	51	85	LYS	C-N-CA	5.82	129.62	120.89
36	78	35	HIS	N-CA-C	5.82	123.19	110.80
2	1E	25	ASN	CA-C-N	5.81	125.49	119.56
2	1E	25	ASN	C-N-CA	5.81	125.49	119.56
40	B8	25	GLY	CA-C-N	-5.81	114.22	122.94
40	B8	25	GLY	C-N-CA	-5.81	114.22	122.94
46	D5	86	VAL	N-CA-C	5.81	116.02	108.35
26	14	1332	G	C4-N9-C1'	5.81	143.92	126.50
8	7E	75	ARG	CA-C-N	5.80	126.13	119.92
8	7E	75	ARG	C-N-CA	5.80	126.13	119.92
17	8A	63	ARG	CA-C-N	5.80	126.14	119.93
17	8A	63	ARG	C-N-CA	5.80	126.14	119.93

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
7	62	87	VAL	N-CA-C	5.80	114.21	107.89
43	E8	62	HIS	N-CA-C	-5.79	100.26	109.59
26	1H	1598	C	OP1-P-O3'	5.79	125.37	108.00
26	14	2689	U	C2'-C3'-O3'	5.79	118.18	109.50
26	1H	1786	A	N9-C1'-C2'	5.78	122.67	114.00
3	22	57	ILE	N-CA-C	5.77	116.38	107.78
4	3E	9	CYS	N-CA-C	-5.77	105.50	112.54
1	1G	812	C	P-O3'-C3'	5.77	128.86	120.20
48	J8	62	VAL	CB-CA-C	-5.77	101.62	110.50
12	3I	20	LYS	N-CA-C	5.76	118.19	110.35
51	M8	45	GLY	N-CA-C	-5.76	99.53	113.18
28	11	223	GLY	N-CA-C	-5.75	105.82	112.73
10	1I	44	VAL	N-CA-C	5.75	115.88	107.37
30	39	147	GLY	N-CA-C	-5.75	106.72	115.00
34	15	127	ASP	CB-CA-C	-5.75	108.95	115.79
28	19	227	ASN	CA-C-N	-5.75	112.66	119.84
28	19	227	ASN	C-N-CA	-5.75	112.66	119.84
52	N8	38	ALA	N-CA-C	5.74	117.31	110.19
1	13	812	C	P-O3'-C3'	5.74	128.80	120.20
26	1H	2389	G	O3'-P-O5'	-5.74	95.40	104.00
26	1H	740	U	OP1-P-O3'	-5.73	90.81	108.00
36	35	147	LEU	CA-CB-CG	5.73	136.35	116.30
6	5E	41	GLU	N-CA-C	5.73	119.25	112.72
30	31	9	ILE	N-CA-C	5.72	114.13	107.89
30	31	95	ARG	N-CA-C	5.72	117.49	108.96
30	39	15	SER	CB-CA-C	-5.72	109.96	116.54
9	8E	91	ASP	N-CA-C	-5.72	106.35	113.38
26	14	1602	U	O5'-P-OP2	5.72	125.16	108.00
47	E5	35	ASN	CA-C-N	-5.71	113.36	122.50
47	E5	35	ASN	C-N-CA	-5.71	113.36	122.50
41	85	74	LEU	N-CA-C	5.71	117.66	110.24
28	19	131	LEU	CA-C-N	-5.71	113.88	119.76
28	19	131	LEU	C-N-CA	-5.71	113.88	119.76
26	1H	195	A	O3'-P-O5'	5.70	112.56	104.00
28	11	254	THR	N-CA-C	5.70	119.93	112.92
45	C5	86	ARG	N-CA-C	5.70	118.25	110.55
12	3A	23	LYS	N-CA-C	-5.70	106.17	113.01
33	69	143	SER	N-CA-C	5.70	116.97	108.31
28	11	239	ARG	CA-CB-CG	-5.70	102.71	114.10
32	51	89	ILE	N-CA-C	5.70	116.41	108.89
2	12	130	ARG	CA-C-N	5.68	125.70	119.90
2	12	130	ARG	C-N-CA	5.68	125.70	119.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
28	11	248	SER	CA-C-N	-5.68	113.82	119.56
28	11	248	SER	C-N-CA	-5.68	113.82	119.56
2	12	164	VAL	N-CA-C	5.68	116.93	108.46
26	1H	195	A	P-O3'-C3'	5.68	128.72	120.20
26	1H	2390	U	O5'-P-OP1	-5.68	90.96	108.00
26	1H	1398	C	O5'-P-OP2	5.68	125.03	108.00
38	98	9	LYS	CA-C-N	-5.68	114.02	123.33
38	98	9	LYS	C-N-CA	-5.68	114.02	123.33
37	88	25	ASP	N-CA-C	5.67	122.87	110.80
30	31	8	GLN	N-CA-C	5.67	119.08	107.69
4	32	39	PRO	CA-C-N	5.67	126.46	120.11
4	32	39	PRO	C-N-CA	5.67	126.46	120.11
33	69	77	LEU	CB-CA-C	-5.67	108.41	116.34
48	F5	29	GLY	CA-C-N	5.66	132.16	121.97
48	F5	29	GLY	C-N-CA	5.66	132.16	121.97
29	21	52	LEU	N-CA-C	5.66	122.31	109.81
36	78	55	ARG	CA-C-O	-5.66	116.07	122.01
52	N8	41	PRO	C-N-CD	-5.65	101.83	125.00
26	14	1342	A	N9-C1'-C2'	5.65	122.47	114.00
11	2I	81	ASP	N-CA-C	5.64	120.28	113.17
55	M5	52	LYS	N-CA-C	5.64	122.28	109.81
55	Q8	6	THR	CB-CA-C	-5.63	99.21	110.42
45	C5	41	GLY	N-CA-C	-5.63	99.84	113.18
1	13	1504	G	C4'-C3'-O3'	5.63	117.84	109.40
29	29	50	GLY	N-CA-C	5.63	126.52	113.18
39	65	88	ASP	O-C-N	5.63	125.69	121.47
33	61	131	LYS	C-N-CD	-5.63	108.22	120.60
55	Q8	13	ARG	N-CA-C	5.63	120.84	113.30
55	Q8	34	TRP	N-CA-C	5.62	122.77	110.80
26	1H	226	G	O4'-C1'-N9	5.62	116.63	108.20
9	8E	112	LYS	N-CA-C	-5.61	98.84	110.80
33	69	77	LEU	N-CA-C	5.61	116.30	108.00
29	21	61	ARG	CA-C-N	-5.60	113.34	120.23
29	21	61	ARG	C-N-CA	-5.60	113.34	120.23
1	13	690	G	O4'-C1'-N9	5.60	116.90	108.50
28	19	36	PRO	CA-C-N	-5.60	114.89	123.07
28	19	36	PRO	C-N-CA	-5.60	114.89	123.07
1	13	703	G	C4'-C3'-O3'	5.60	117.80	109.40
34	58	24	GLY	N-CA-C	-5.60	105.87	113.37
1	13	1492	A	O5'-P-OP2	-5.59	91.22	108.00
36	35	38	GLN	N-CA-C	5.59	118.10	111.33
46	H8	94	GLU	N-CA-C	-5.59	100.90	108.11

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
32	59	42	ARG	N-CA-C	5.59	116.96	108.07
1	1G	64	G	C4'-C3'-O3'	5.59	117.78	109.40
1	13	1504	G	P-O3'-C3'	5.58	128.57	120.20
46	D5	52	SER	N-CA-C	5.58	118.94	111.24
29	21	135	HIS	N-CA-C	5.58	117.80	111.11
40	75	135	ALA	CB-CA-C	-5.57	110.17	116.63
40	B8	3	ARG	N-CA-C	-5.57	103.73	111.30
26	14	741	G	O5'-P-OP1	-5.57	91.30	108.00
52	J5	46	CYS	CA-C-N	5.57	125.18	119.56
52	J5	46	CYS	C-N-CA	5.57	125.18	119.56
26	14	1819	A	P-O3'-C3'	5.56	128.54	120.20
55	Q8	33	ASN	CA-C-N	5.56	132.16	121.54
55	Q8	33	ASN	C-N-CA	5.56	132.16	121.54
12	3I	119	LYS	N-CA-C	-5.56	103.19	110.53
26	1H	2275	C	OP1-P-O3'	5.56	124.67	108.00
37	88	5	ARG	N-CA-C	-5.56	101.25	109.86
4	32	6	GLY	CA-C-N	5.55	126.78	119.84
4	32	6	GLY	C-N-CA	5.55	126.78	119.84
49	K8	16	LEU	CA-C-N	-5.55	111.41	122.90
49	K8	16	LEU	C-N-CA	-5.55	111.41	122.90
26	1H	2275	C	C5'-C4'-O4'	-5.55	100.77	109.10
26	1H	740	U	O5'-P-OP2	-5.55	91.35	108.00
43	E8	37	ARG	N-CA-C	-5.55	105.31	111.36
35	68	96	THR	N-CA-C	-5.54	101.81	110.17
29	29	44	TYR	CA-CB-CG	5.54	123.87	113.90
29	21	201	THR	N-CA-C	5.54	117.68	110.43
34	15	10	GLU	CA-C-N	5.54	125.51	120.03
34	15	10	GLU	C-N-CA	5.54	125.51	120.03
18	9A	24	ALA	N-CA-C	-5.54	106.30	113.16
26	1H	945	A	C6-C5-N7	-5.53	115.70	132.30
26	1H	1312	U	C2'-C3'-O3'	5.53	117.80	109.50
32	51	7	LEU	N-CA-C	5.53	119.31	110.73
40	B8	13	ARG	N-CA-C	-5.53	106.38	113.02
46	D5	149	SER	N-CA-C	5.53	116.63	107.73
30	31	157	VAL	N-CA-C	5.53	115.55	107.37
26	14	195	A	P-O3'-C3'	5.53	128.49	120.20
26	14	1255	U	N1-C1'-C2'	5.52	120.29	112.00
28	11	46	GLN	CA-C-N	-5.52	110.59	121.41
28	11	46	GLN	C-N-CA	-5.52	110.59	121.41
53	K5	49	HIS	N-CA-C	5.52	122.56	110.80
28	11	46	GLN	N-CA-C	-5.52	101.15	109.60
3	2E	205	GLY	N-CA-C	5.52	122.20	111.66

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
37	88	58	PHE	N-CA-C	5.52	117.84	108.02
4	32	34	GLU	N-CA-C	-5.52	106.13	112.86
9	82	48	GLU	CA-C-N	-5.52	113.93	119.56
9	82	48	GLU	C-N-CA	-5.52	113.93	119.56
28	11	68	LYS	CA-C-N	-5.52	113.44	122.54
28	11	68	LYS	C-N-CA	-5.52	113.44	122.54
32	51	87	LEU	N-CA-C	5.51	122.54	110.80
26	14	1899	G	N1-C2-N2	-5.51	99.66	116.20
16	7I	75	ARG	N-CA-C	-5.51	105.19	111.14
26	14	2689	U	OP1-P-O3'	-5.50	91.49	108.00
15	6I	87	ILE	N-CA-C	5.50	120.78	109.34
26	1H	71	A	O5'-C5'-C4'	-5.50	103.45	111.70
45	G8	81	LYS	C-N-CD	-5.50	108.50	120.60
26	14	1379	A	N9-C1'-C2'	5.50	122.25	114.00
4	3E	174	LEU	N-CA-C	5.50	118.18	109.50
42	95	41	GLY	CA-C-N	5.50	126.20	119.99
42	95	41	GLY	C-N-CA	5.50	126.20	119.99
30	31	67	GLN	N-CA-C	5.49	122.50	110.80
12	3A	64	TYR	N-CA-C	5.49	118.10	111.40
1	13	5	U	P-O3'-C3'	5.49	128.43	120.20
26	1H	197	A	OP1-P-O3'	-5.48	91.55	108.00
8	72	97	VAL	N-CA-C	5.48	115.68	110.42
13	4A	83	ASP	N-CA-C	-5.48	103.67	110.41
30	39	82	ILE	N-CA-C	-5.48	106.49	112.80
6	5E	65	VAL	N-CA-C	5.48	120.74	109.34
40	75	3	ARG	N-CA-C	-5.47	102.78	110.50
26	1H	1694	C	C4'-C3'-O3'	5.47	117.60	109.40
46	D5	112	ARG	CB-CA-C	-5.47	109.80	117.23
26	1H	624	C	O5'-P-OP2	5.46	124.38	108.00
45	G8	80	GLY	N-CA-C	5.46	126.13	113.18
26	1H	2434	A	OP1-P-O3'	-5.46	91.63	108.00
26	1H	1204	A	O4'-C1'-N9	5.45	116.38	108.20
1	13	687	A	P-O3'-C3'	5.45	128.37	120.20
28	19	272	ALA	CA-C-N	5.45	131.95	121.54
28	19	272	ALA	C-N-CA	5.45	131.95	121.54
26	14	1999	C	OP2-P-O3'	5.45	124.34	108.00
52	J5	59	GLU	N-CA-C	5.45	118.45	109.85
36	78	15	ARG	CA-C-N	5.44	131.50	121.70
36	78	15	ARG	C-N-CA	5.44	131.50	121.70
45	G8	20	TYR	N-CA-C	-5.44	106.83	112.93
15	6A	23	GLY	N-CA-C	5.44	126.08	113.18
49	G5	43	GLN	N-CA-C	5.44	117.92	110.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	42	17	ALA	N-CA-C	5.44	117.89	110.55
28	11	53	PHE	N-CA-C	5.43	119.20	112.24
4	32	36	ARG	CA-C-N	-5.43	116.17	121.65
4	32	36	ARG	C-N-CA	-5.43	116.17	121.65
33	69	131	LYS	CA-C-N	5.43	140.03	127.00
33	69	131	LYS	C-N-CA	5.43	140.03	127.00
55	M5	34	TRP	CA-C-N	5.43	131.91	121.54
55	M5	34	TRP	C-N-CA	5.43	131.91	121.54
41	C8	95	LEU	CA-C-N	5.43	131.47	121.70
41	C8	95	LEU	C-N-CA	5.43	131.47	121.70
14	5I	27	CYS	CB-CA-C	-5.42	102.61	110.96
28	19	270	ILE	N-CA-C	5.42	117.01	109.80
20	BA	27	LYS	N-CA-C	-5.42	105.54	111.82
36	35	52	GLU	N-CA-C	-5.42	101.20	109.65
8	7E	2	LEU	N-CA-C	5.42	117.25	110.91
26	1H	774	A	C8-N9-C1'	5.41	143.93	127.70
29	29	132	HIS	N-CA-C	5.41	122.33	110.80
26	14	2225	A	P-O3'-C3'	5.40	128.30	120.20
28	19	40	THR	N-CA-C	5.40	117.47	109.69
39	65	58	LEU	N-CA-C	5.40	115.41	108.34
47	E5	22	GLY	N-CA-C	5.40	119.48	111.76
3	2E	158	GLY	N-CA-C	-5.39	108.20	115.21
26	1H	752	A	C4'-C3'-O3'	5.39	117.49	109.40
1	13	690	G	C4-N9-C1'	5.39	142.67	126.50
26	1H	1799	G	P-O3'-C3'	5.39	128.29	120.20
55	Q8	12	LYS	CA-C-N	-5.39	114.14	122.49
55	Q8	12	LYS	C-N-CA	-5.39	114.14	122.49
2	12	45	GLN	N-CA-C	5.39	116.96	111.14
41	85	88	ILE	N-CA-C	5.39	115.54	107.51
26	1H	1426	G	N9-C1'-C2'	5.38	120.08	112.00
53	O8	24	GLU	N-CA-C	5.38	116.83	109.18
28	19	54	ARG	N-CA-C	5.38	117.18	108.41
28	19	145	VAL	N-CA-C	5.38	116.96	109.80
44	F8	25	LYS	N-CA-C	5.38	117.40	108.20
26	14	1332	G	N9-C1'-C2'	-5.38	105.94	114.00
1	13	1502	A	N9-C1'-C2'	5.38	122.06	114.00
45	G8	99	CYS	CA-C-N	5.38	131.38	121.70
45	G8	99	CYS	C-N-CA	5.38	131.38	121.70
46	D5	133	ILE	CA-C-N	5.37	125.68	119.93
46	D5	133	ILE	C-N-CA	5.37	125.68	119.93
31	49	178	PHE	CA-C-N	5.37	125.54	119.90
31	49	178	PHE	C-N-CA	5.37	125.54	119.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
10	1I	55	LYS	CA-C-N	-5.36	114.43	122.47
10	1I	55	LYS	C-N-CA	-5.36	114.43	122.47
34	15	99	LEU	N-CA-C	-5.36	105.47	112.23
10	1I	76	ASN	CA-C-N	5.36	125.12	119.76
10	1I	76	ASN	C-N-CA	5.36	125.12	119.76
40	75	38	ASN	N-CA-C	-5.36	106.42	113.17
47	E5	82	ARG	CA-C-N	5.36	125.00	119.05
47	E5	82	ARG	C-N-CA	5.36	125.00	119.05
4	3E	38	TYR	CA-C-N	5.35	123.56	119.66
4	3E	38	TYR	C-N-CA	5.35	123.56	119.66
30	31	16	GLY	N-CA-C	5.35	120.19	112.81
13	4A	40	ASN	CA-C-N	5.34	124.85	119.19
13	4A	40	ASN	C-N-CA	5.34	124.85	119.19
33	69	31	LEU	CA-C-N	-5.34	113.53	119.19
33	69	31	LEU	C-N-CA	-5.34	113.53	119.19
3	22	180	ALA	N-CA-C	5.33	117.51	111.11
28	19	237	GLU	N-CA-C	5.33	122.17	110.80
55	Q8	42	ARG	CA-C-N	5.33	131.29	121.70
55	Q8	42	ARG	C-N-CA	5.33	131.29	121.70
26	14	2225	A	N9-C1'-C2'	-5.33	106.01	114.00
3	22	82	GLU	CB-CA-C	-5.33	109.99	117.23
31	49	44	GLY	N-CA-C	-5.33	106.52	115.62
36	35	18	ARG	N-CA-C	5.33	117.56	109.63
39	A8	110	LEU	CA-CB-CG	5.32	134.94	116.30
26	14	2429	G	OP1-P-O3'	-5.32	92.03	108.00
20	BA	10	LEU	CA-C-N	-5.32	113.83	122.34
20	BA	10	LEU	C-N-CA	-5.32	113.83	122.34
26	1H	2712	U	P-O3'-C3'	5.32	126.08	119.70
33	69	131	LYS	C-N-CD	-5.31	108.91	120.60
33	61	144	VAL	N-CA-C	5.31	116.02	108.42
36	78	96	THR	CA-C-N	-5.31	114.75	121.91
36	78	96	THR	C-N-CA	-5.31	114.75	121.91
48	J8	44	PRO	CA-C-N	-5.31	113.85	122.34
48	J8	44	PRO	C-N-CA	-5.31	113.85	122.34
26	1H	2598	A	O5'-P-OP2	5.30	123.92	108.00
29	29	36	ARG	N-CA-C	5.30	119.85	113.17
26	14	2275	C	C4'-C3'-O3'	5.30	117.35	109.40
32	59	129	THR	N-CA-C	5.30	116.50	108.07
29	21	80	GLU	N-CA-C	-5.30	101.70	109.81
31	41	79	ASN	N-CA-C	5.30	117.75	111.33
46	H8	61	LEU	CA-C-N	5.29	126.45	119.84
46	H8	61	LEU	C-N-CA	5.29	126.45	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
8	7E	56	LYS	CA-C-N	5.29	126.45	119.84
8	7E	56	LYS	C-N-CA	5.29	126.45	119.84
28	11	226	MET	N-CA-C	5.29	118.55	110.36
41	C8	91	ASP	N-CA-C	5.28	122.05	110.80
41	85	9	VAL	N-CA-C	5.28	115.49	110.42
32	59	75	ALA	N-CA-C	-5.28	106.34	112.89
45	C5	42	VAL	N-CA-C	5.28	116.22	109.30
5	4E	154	GLY	CA-C-O	-5.28	118.79	122.22
26	1H	1698	A	N9-C1'-C2'	5.28	121.92	114.00
36	78	19	VAL	CB-CA-C	-5.28	102.63	111.29
26	1H	2390	U	P-O5'-C5'	-5.28	112.99	120.90
36	35	64	LYS	N-CA-C	-5.27	104.86	111.92
39	65	42	ASP	N-CA-C	-5.27	103.73	110.53
26	1H	1616	A	O4'-C1'-N9	5.27	116.11	108.20
30	39	128	ALA	N-CA-C	5.27	122.02	110.80
37	88	139	GLU	CB-CA-C	-5.26	108.97	116.34
28	19	264	LYS	CA-C-N	-5.26	114.25	119.56
28	19	264	LYS	C-N-CA	-5.26	114.25	119.56
28	19	98	VAL	CA-C-N	5.26	129.01	120.60
28	19	98	VAL	C-N-CA	5.26	129.01	120.60
47	I8	11	ARG	N-CA-C	-5.24	106.88	113.28
49	G5	5	GLU	N-CA-C	-5.24	105.24	111.69
26	14	119	A	OP2-P-O3'	-5.24	92.29	108.00
20	BA	74	LYS	N-CA-C	5.23	116.27	108.31
37	88	4	PRO	CA-C-O	-5.23	115.63	122.12
37	88	26	TYR	N-CA-C	5.23	119.63	112.88
26	1H	1427	A	C4'-C3'-O3'	5.23	117.24	109.40
1	1G	632	A	P-O3'-C3'	5.23	128.04	120.20
26	1H	1694	C	P-O3'-C3'	5.23	128.04	120.20
12	3I	64	TYR	N-CA-C	5.22	119.14	111.04
29	21	125	GLY	CA-C-N	5.22	125.23	119.90
29	21	125	GLY	C-N-CA	5.22	125.23	119.90
30	31	67	GLN	CB-CA-C	-5.22	100.03	110.42
4	3E	39	PRO	CA-C-N	5.22	125.20	120.03
4	3E	39	PRO	C-N-CA	5.22	125.20	120.03
28	11	236	GLY	N-CA-C	5.22	123.60	115.72
28	19	259	THR	N-CA-C	5.22	119.80	113.38
10	1I	26	ALA	N-CA-C	-5.21	106.90	113.20
4	3E	39	PRO	O-C-N	5.21	123.70	121.31
36	78	58	THR	N-CA-C	-5.21	106.88	114.12
19	AI	60	VAL	CA-C-N	5.21	128.49	121.05
19	AI	60	VAL	C-N-CA	5.21	128.49	121.05

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	1G	345	C	C2'-C3'-O3'	5.21	117.31	109.50
29	29	60	ASN	N-CA-C	5.21	121.89	110.80
32	51	92	ILE	N-CA-C	5.20	120.16	109.34
40	75	118	ARG	N-CA-C	-5.20	105.05	111.40
12	3I	15	ARG	N-CA-C	5.20	120.48	113.72
36	78	72	PRO	N-CA-C	-5.20	107.36	113.86
7	6E	57	GLU	CA-C-N	5.20	126.34	119.84
7	6E	57	GLU	C-N-CA	5.20	126.34	119.84
26	1H	1573	G	OP1-P-O3'	-5.20	92.40	108.00
37	45	81	VAL	N-CA-C	5.20	120.15	109.34
31	49	45	GLU	N-CA-C	-5.20	106.20	112.54
4	3E	42	GLN	N-CA-C	5.20	117.62	111.33
26	1H	828	U	N1-C1'-C2'	5.20	119.79	112.00
26	1H	2326	C	C3'-C2'-O2'	-5.19	102.91	110.70
12	3A	128	ALA	CB-CA-C	-5.19	110.17	117.23
32	51	13	LYS	N-CA-C	5.19	121.85	110.80
15	6A	5	LYS	N-CA-C	-5.19	106.78	113.01
26	14	1984	G	O5'-P-OP2	-5.19	92.43	108.00
16	7A	83	GLU	CB-CA-C	-5.19	110.18	117.23
32	59	122	THR	N-CA-C	5.19	115.90	108.74
33	61	110	ASP	C-N-CD	-5.18	109.19	120.60
28	11	244	ARG	CA-C-N	-5.18	115.04	120.38
28	11	244	ARG	C-N-CA	-5.18	115.04	120.38
5	42	16	THR	N-CA-C	5.18	116.77	107.80
45	C5	101	LYS	N-CA-C	5.18	121.84	110.80
1	1G	913	A	C2'-C3'-O3'	5.18	117.27	109.50
46	D5	61	LEU	CA-C-N	5.18	126.32	119.84
46	D5	61	LEU	C-N-CA	5.18	126.32	119.84
26	14	191	A	OP1-P-O3'	-5.18	92.46	108.00
13	4I	84	ILE	N-CA-C	-5.18	105.30	112.50
26	1H	481	G	C4'-C3'-O3'	5.17	117.16	109.40
26	1H	1694	C	OP1-P-O3'	-5.17	92.48	108.00
36	35	42	SER	CA-C-N	-5.17	114.19	119.94
36	35	42	SER	C-N-CA	-5.17	114.19	119.94
48	F5	40	ARG	CA-C-N	-5.17	115.69	122.99
48	F5	40	ARG	C-N-CA	-5.17	115.69	122.99
37	88	107	ALA	N-CA-C	5.17	116.93	109.07
53	K5	25	LYS	N-CA-C	5.17	117.67	109.24
35	68	37	ASP	CA-C-N	-5.17	116.42	122.93
35	68	37	ASP	C-N-CA	-5.17	116.42	122.93
26	1H	1899	G	C8-N9-C1'	5.17	142.50	127.00
28	11	120	GLY	CA-C-N	5.17	126.30	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
28	11	120	GLY	C-N-CA	5.17	126.30	119.84
19	AA	14	HIS	N-CA-C	5.17	116.77	111.03
26	14	2258	C	OP1-P-O3'	5.17	123.50	108.00
16	7I	48	TRP	N-CA-C	5.17	119.21	113.01
49	K8	18	PRO	N-CA-C	5.17	123.11	112.47
26	1H	1694	C	N1-C1'-C2'	-5.16	106.25	114.00
30	39	132	VAL	N-CA-C	-5.16	98.60	109.34
33	69	7	GLU	CA-C-N	-5.16	114.67	120.14
33	69	7	GLU	C-N-CA	-5.16	114.67	120.14
52	J5	23	HIS	N-CA-C	5.16	118.84	112.54
42	D8	65	GLY	N-CA-C	5.16	119.64	112.57
28	19	272	ALA	N-CA-CB	-5.16	102.91	111.57
9	8E	17	VAL	N-CA-C	5.16	115.48	107.28
28	11	145	VAL	N-CA-C	5.15	116.22	109.21
39	65	34	HIS	N-CA-C	5.15	118.09	110.46
4	3E	13	ARG	N-CA-C	5.15	116.58	110.97
47	I8	41	ARG	CA-C-N	-5.15	116.16	122.75
47	I8	41	ARG	C-N-CA	-5.15	116.16	122.75
33	69	142	VAL	N-CA-C	5.15	116.00	108.53
34	15	2	LYS	N-CA-C	-5.15	99.88	108.07
38	98	104	ARG	CA-C-N	-5.15	114.58	122.87
38	98	104	ARG	C-N-CA	-5.15	114.58	122.87
26	1H	802	A	O5'-P-OP2	-5.14	92.57	108.00
55	Q8	14	VAL	N-CA-C	5.14	115.59	108.23
28	19	256	GLY	N-CA-C	5.14	120.81	114.69
1	13	792	A	C3'-C2'-C1'	-5.14	96.36	101.50
32	51	85	LYS	N-CA-C	5.14	121.75	110.80
2	12	166	ASP	CA-C-N	5.14	124.94	119.28
2	12	166	ASP	C-N-CA	5.14	124.94	119.28
41	85	3	ARG	CA-C-N	-5.14	115.53	123.14
41	85	3	ARG	C-N-CA	-5.14	115.53	123.14
41	85	73	GLY	N-CA-C	5.14	116.98	110.20
33	61	9	LEU	N-CA-C	5.13	119.50	112.88
55	Q8	7	HIS	N-CA-C	5.13	118.80	111.92
10	1I	54	PHE	CA-C-N	-5.13	113.82	121.72
10	1I	54	PHE	C-N-CA	-5.13	113.82	121.72
17	8I	78	GLU	N-CA-C	5.13	118.84	112.59
26	1H	1392	A	OP2-P-O3'	5.13	123.38	108.00
33	69	75	LEU	N-CA-C	5.13	116.08	108.60
28	19	15	PHE	N-CA-C	5.12	119.80	113.50
31	49	143	GLU	N-CA-C	-5.12	106.72	113.17
13	4A	9	ILE	CA-C-N	-5.12	115.32	120.85

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
13	4A	9	ILE	C-N-CA	-5.12	115.32	120.85
14	5I	13	THR	N-CA-C	5.12	121.12	109.81
26	14	1332	G	C8-N9-C1'	-5.12	111.64	127.00
37	45	118	LEU	N-CA-C	-5.12	107.09	113.38
42	D8	34	GLU	N-CA-C	-5.11	100.97	109.46
41	85	98	LEU	N-CA-C	-5.11	103.39	110.35
5	42	105	VAL	CA-C-N	-5.11	114.40	119.56
5	42	105	VAL	C-N-CA	-5.11	114.40	119.56
26	1H	2272	U	O5'-P-OP1	5.11	123.33	108.00
18	9A	26	LEU	N-CA-C	5.11	115.79	108.74
41	C8	9	VAL	N-CA-C	5.11	115.72	110.36
9	8E	97	LYS	CA-C-N	-5.11	113.66	119.28
9	8E	97	LYS	C-N-CA	-5.11	113.66	119.28
26	1H	1905	C	O3'-P-O5'	-5.11	96.34	104.00
29	21	69	LYS	N-CA-C	-5.11	107.07	113.15
26	14	2689	U	OP2-P-O3'	5.11	123.32	108.00
30	39	93	LYS	CA-C-N	-5.11	114.50	119.76
30	39	93	LYS	C-N-CA	-5.11	114.50	119.76
1	13	1492	A	N9-C1'-C2'	5.11	119.66	112.00
49	G5	17	SER	N-CA-C	5.11	121.09	109.81
20	BA	71	THR	CA-C-N	-5.10	111.79	121.54
20	BA	71	THR	C-N-CA	-5.10	111.79	121.54
17	8A	57	VAL	N-CA-C	5.10	117.37	108.90
26	1H	1558	A	P-O3'-C3'	5.10	127.85	120.20
43	A5	110	LYS	N-CA-C	5.10	116.84	111.28
36	78	53	GLY	N-CA-C	-5.10	108.20	115.64
29	29	145	LYS	N-CA-C	5.09	117.57	111.71
2	1E	211	ILE	N-CA-C	5.09	115.31	110.42
53	K5	17	LYS	N-CA-C	-5.09	99.96	110.80
26	1H	839	U	O5'-P-OP2	-5.08	92.74	108.00
41	C8	27	LEU	CA-CB-CG	5.08	134.09	116.30
1	1G	1498	U	P-O3'-C3'	5.08	127.82	120.20
1	1G	1297	C	P-O3'-C3'	5.08	127.82	120.20
45	G8	94	LYS	CA-C-N	5.08	131.23	121.54
45	G8	94	LYS	C-N-CA	5.08	131.23	121.54
28	19	243	GLY	N-CA-C	-5.08	108.11	115.27
37	45	78	PRO	N-CA-C	5.08	122.92	112.47
26	1H	803	U	OP1-P-O3'	-5.07	92.78	108.00
29	21	47	VAL	N-CA-C	5.07	115.76	107.24
38	98	73	VAL	N-CA-C	5.07	115.29	110.42
10	1A	49	VAL	N-CA-C	5.07	117.03	108.81
11	2I	34	ASP	CA-C-N	-5.07	114.44	119.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
11	2I	34	ASP	C-N-CA	-5.07	114.44	119.56
28	19	247	ALA	N-CA-C	5.07	117.86	109.85
30	39	194	MET	N-CA-C	5.07	116.77	108.76
26	1H	2443	C	C3'-C2'-O2'	-5.07	103.10	110.70
41	85	100	VAL	N-CA-C	-5.07	100.95	108.45
33	69	100	ALA	CA-C-N	-5.06	115.28	122.77
33	69	100	ALA	C-N-CA	-5.06	115.28	122.77
31	41	40	ASN	N-CA-C	5.06	116.66	108.26
55	Q8	31	HIS	N-CA-CB	-5.06	102.98	110.37
26	1H	1782	C	O5'-P-OP1	-5.06	92.82	108.00
37	88	14	ARG	N-CA-C	5.06	116.48	111.07
3	22	110	ASN	N-CA-C	-5.06	105.86	112.23
26	14	2307	G	O4'-C1'-N9	5.05	116.08	108.50
42	D8	71	LEU	CA-C-N	-5.05	116.31	122.93
42	D8	71	LEU	C-N-CA	-5.05	116.31	122.93
26	1H	60	G	OP1-P-O3'	-5.05	92.85	108.00
5	42	147	ASP	N-CA-C	-5.05	105.46	110.97
41	C8	76	TYR	N-CA-C	-5.05	105.48	111.69
1	1G	1157	A	C2'-C3'-O3'	5.05	117.07	109.50
26	14	141	A	OP2-P-O3'	5.05	116.31	105.20
47	I8	14	ARG	N-CA-C	5.05	117.31	110.35
2	12	203	GLY	N-CA-C	5.05	117.65	110.74
49	G5	16	LEU	N-CA-C	-5.05	99.88	108.26
20	BI	33	ILE	CB-CA-C	-5.04	105.43	111.88
26	1H	1310	G	O5'-P-OP2	5.04	123.12	108.00
13	4A	93	ARG	CA-C-N	-5.04	115.84	122.85
13	4A	93	ARG	C-N-CA	-5.04	115.84	122.85
4	32	154	ASN	N-CA-C	5.04	117.43	111.33
28	19	236	GLY	CA-C-O	5.04	127.46	120.25
39	65	46	VAL	N-CA-C	5.04	115.17	108.27
19	AI	5	LEU	N-CA-C	5.04	121.53	110.80
41	C8	70	ARG	N-CA-C	-5.04	107.13	113.28
36	35	56	SER	N-CA-C	5.04	119.52	113.17
9	8E	3	GLN	N-CA-C	5.04	115.84	107.73
28	11	191	ALA	CA-C-N	-5.04	114.98	122.74
28	11	191	ALA	C-N-CA	-5.04	114.98	122.74
41	C8	75	ASN	N-CA-C	5.04	116.44	110.19
49	K8	16	LEU	N-CA-C	-5.04	100.31	108.52
47	E5	26	TYR	N-CA-C	5.03	117.32	109.52
34	58	10	GLU	CA-C-N	5.03	125.27	119.83
34	58	10	GLU	C-N-CA	5.03	125.27	119.83
4	3E	179	GLU	N-CA-C	-5.03	106.99	113.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
30	39	159	GLY	N-CA-C	-5.03	107.26	115.46
8	7E	71	GLY	CA-C-N	-5.03	115.05	120.03
8	7E	71	GLY	C-N-CA	-5.03	115.05	120.03
26	14	2638	G	N9-C1'-C2'	5.03	119.54	112.00
26	1H	974(A)	C	C4'-C3'-O3'	5.03	116.94	109.40
52	J5	51	TYR	N-CA-C	5.02	116.31	109.18
1	13	1065	U	C2'-C3'-O3'	5.02	117.03	109.50
21	1B	22	ARG	CA-C-N	5.01	124.78	119.76
21	1B	22	ARG	C-N-CA	5.01	124.78	119.76
26	14	1558	A	C2'-C3'-O3'	5.01	117.02	109.50
38	55	7	GLY	N-CA-C	-5.01	106.26	112.33
3	2E	118	GLN	N-CA-C	5.01	116.74	111.28
30	31	9	ILE	CA-C-N	5.01	126.10	119.84
30	31	9	ILE	C-N-CA	5.01	126.10	119.84
46	H8	6	LYS	N-CA-C	-5.01	100.13	110.80
1	1G	328	C	C2'-C3'-O3'	5.01	117.02	109.50
26	14	752	A	C4'-C3'-O3'	5.01	116.92	109.40
28	19	43	ARG	CG-CD-NE	5.01	123.02	112.00
26	1H	1899	G	O3'-P-O5'	-5.01	96.48	104.00
37	88	135	ASP	N-CA-C	5.01	115.14	108.38
2	12	232	PRO	N-CA-C	5.01	119.10	111.34
8	7E	84	ARG	N-CA-C	5.01	117.60	109.24
2	12	76	GLN	N-CA-C	-5.01	105.53	111.69
26	14	677	A	O5'-C5'-C4'	-5.01	103.99	111.50
1	13	1322	C	C2'-C3'-O3'	5.00	117.00	109.50
43	E8	90	ARG	NE-CZ-NH1	-5.00	116.50	121.50
18	9A	83	GLU	N-CA-C	-5.00	101.95	109.85

There are no chirality outliers.

All (127) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
28	11	141	VAL	Peptide
28	11	197	GLY	Peptide
28	19	237	GLU	Peptide
28	19	270	ILE	Peptide
28	19	271	ILE	Peptide
28	19	32	SER	Peptide
28	19	37	LEU	Peptide
10	1A	55	LYS	Peptide
2	1E	15	VAL	Peptide
2	1E	237	ALA	Peptide

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Mol	Chain	Res	Type	Group
29	21	56	PRO	Peptide
29	21	78	LEU	Peptide
29	21	87	GLU	Peptide
29	21	89	ASP	Peptide
29	29	139	GLY	Peptide
29	29	201	THR	Peptide
29	29	44	TYR	Peptide
29	29	61	ARG	Peptide
29	29	65	GLY	Peptide
11	2A	49	GLY	Peptide
30	31	23	ASP	Peptide
30	31	6	VAL	Peptide
30	31	73	ALA	Peptide
4	32	152	SER	Peptide
4	32	30	LYS	Peptide
36	35	110	TYR	Peptide
36	35	36	LYS	Peptide
36	35	64	LYS	Peptide
30	39	127	GLU	Peptide
30	39	166	ALA	Peptide
30	39	20	LEU	Peptide
30	39	24	LEU	Peptide
30	39	26	ALA	Peptide
30	39	69	HIS	Mainchain
30	39	89	VAL	Peptide
12	3I	87	GLY	Peptide
31	41	85	GLY	Peptide
31	41	95	ARG	Peptide
37	45	134	ARG	Peptide
37	45	135	ASP	Peptide
37	45	25	ASP	Peptide
37	45	27	VAL	Peptide
37	45	86	GLY	Peptide
37	45	87	LYS	Peptide
31	49	13	GLU	Peptide
13	4I	105	THR	Peptide
13	4I	4	ILE	Peptide
38	55	106	GLY	Peptide,Mainchain
32	59	155	SER	Peptide
14	5A	30	ALA	Peptide
33	61	11	ASN	Peptide
33	61	114	LEU	Peptide

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Mol	Chain	Res	Type	Group
33	61	134	PRO	Peptide
33	61	82	ARG	Peptide
39	65	59	LYS	Peptide
33	69	101	LEU	Peptide
33	69	112	LYS	Peptide
33	69	143	SER	Peptide
40	75	12	SER	Peptide
40	75	4	GLY	Peptide
36	78	11	GLY	Peptide
36	78	115	LEU	Peptide
36	78	14	LYS	Peptide
9	82	117	HIS	Peptide
41	85	72	HIS	Peptide
41	85	98	LEU	Peptide
37	88	1	MET	Peptide
37	88	23	GLY	Peptide
37	88	58	PHE	Peptide
37	88	78	PRO	Peptide
42	95	44	LYS	Peptide
42	95	80	GLN	Peptide
38	98	1	MET	Peptide
38	98	44	LEU	Peptide
43	A5	43	GLY	Peptide
43	A5	93	ALA	Peptide
19	AI	6	LYS	Peptide
19	AI	7	LYS	Peptide
44	B5	61	GLY	Peptide
40	B8	54	ARG	Peptide
40	B8	58	ASN	Peptide
20	BA	11	SER	Peptide
20	BA	72	LEU	Peptide
20	BI	96	GLY	Peptide
45	C5	81	LYS	Peptide
41	C8	96	ALA	Peptide
46	D5	142	SER	Peptide
42	D8	47	VAL	Peptide
48	F5	85	LEU	Peptide
49	G5	15	LYS	Peptide
49	G5	17	SER	Peptide
49	G5	43	GLN	Peptide
49	G5	69	ARG	Peptide
45	G8	5	MET	Peptide

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Mol	Chain	Res	Type	Group
45	G8	53	PRO	Peptide
45	G8	94	LYS	Peptide
46	H8	158	PRO	Peptide
46	H8	59	LEU	Peptide
46	H8	63	ASP	Peptide
51	I5	26	SER	Peptide
47	I8	83	PRO	Peptide
47	I8	9	SER	Peptide
48	J8	75	GLU	Peptide
48	J8	85	LEU	Peptide
53	K5	15	GLU	Peptide
53	K5	16	CYS	Peptide
53	K5	43	CYS	Peptide
53	K5	44	ARG	Peptide
49	K8	17	SER	Peptide
49	K8	46	GLN	Peptide
55	M5	30	ARG	Peptide
55	M5	33	ASN	Peptide
55	M5	40	GLU	Peptide
51	M8	38	LYS	Peptide
51	M8	40	HIS	Peptide
52	N8	41	PRO	Peptide
53	O8	15	GLU	Peptide
53	O8	27	LYS	Peptide
55	Q8	18	ALA	Peptide
55	Q8	27	THR	Peptide
55	Q8	44	LYS	Peptide
55	Q8	46	ARG	Peptide
55	Q8	49	VAL	Peptide
55	Q8	57	ARG	Peptide
55	Q8	7	HIS	Peptide
55	Q8	9	GLY	Peptide

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	13	32207	0	16256	721	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1G	32204	0	16255	827	0
2	12	1924	0	1975	99	0
2	1E	1924	0	1975	106	0
3	22	1612	0	1677	90	0
3	2E	1605	0	1668	54	0
4	32	1702	0	1763	89	0
4	3E	1702	0	1762	65	0
5	42	1155	0	1213	59	0
5	4E	1155	0	1213	54	0
6	52	842	0	857	31	0
6	5E	842	0	857	26	0
7	62	1243	0	1284	59	0
7	6E	1256	0	1296	48	0
8	72	1115	0	1177	42	0
8	7E	1115	0	1177	58	0
9	82	983	0	1006	63	0
9	8E	1009	0	1037	62	0
10	1A	801	0	849	44	0
10	1I	801	0	849	51	0
11	2A	864	0	881	32	0
11	2I	864	0	881	28	0
12	3A	975	0	1062	48	0
12	3I	975	0	1062	49	0
13	4A	933	0	992	68	0
13	4I	938	0	997	56	0
14	5A	475	0	511	30	0
14	5I	491	0	529	24	0
15	6A	733	0	771	35	0
15	6I	733	0	771	30	0
16	7A	705	0	725	30	0
16	7I	705	0	725	55	0
17	8A	834	0	904	22	0
17	8I	834	0	904	36	0
18	9A	590	0	662	20	0
18	9I	590	0	662	28	0
19	AA	624	0	636	47	0
19	AI	647	0	665	52	0
20	BA	762	0	861	33	0
20	BI	762	0	861	48	0
21	1B	217	0	234	19	0
21	1F	217	0	234	9	0
22	1K	1627	0	836	35	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
23	2K	1646	0	845	27	0
23	2L	1646	0	845	33	0
24	3K	1603	0	824	55	0
25	4K	279	0	142	4	0
25	4L	235	0	121	14	0
26	14	62647	0	31578	1353	0
26	1H	62707	0	31600	1535	1
27	16	2617	0	1328	54	0
27	1J	2617	0	1328	107	0
28	11	2115	0	2195	88	0
28	19	2120	0	2197	93	0
29	21	1568	0	1634	91	0
29	29	1568	0	1634	97	0
30	31	1585	0	1632	96	0
30	39	1627	0	1680	110	0
31	41	1473	0	1535	82	0
31	49	1473	0	1535	65	0
32	51	1336	0	1418	72	0
32	59	1307	0	1382	64	0
33	61	1136	0	1223	54	0
33	69	1136	0	1223	57	0
34	15	1104	0	1180	55	0
34	58	1104	0	1180	56	0
35	25	932	0	996	51	0
35	68	932	0	996	37	0
36	35	1144	0	1228	108	0
36	78	1144	0	1228	100	0
37	45	1121	0	1179	78	0
37	88	1086	0	1129	67	0
38	55	959	0	1021	46	0
38	98	967	0	1033	55	0
39	65	881	0	943	71	0
39	A8	881	0	943	61	0
40	75	1141	0	1202	66	0
40	B8	1141	0	1202	69	0
41	85	963	0	1022	51	0
41	C8	963	0	1022	88	0
42	95	778	0	852	72	0
42	D8	778	0	852	35	0
43	A5	899	0	964	32	0
43	E8	899	0	964	35	0
44	B5	735	0	785	32	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	F8	742	0	803	44	0
45	C5	794	0	883	61	0
45	G8	791	0	882	61	0
46	D5	1428	0	1454	75	0
46	H8	1397	0	1430	86	0
47	E5	612	0	633	32	0
47	I8	626	0	642	27	0
48	F5	737	0	813	34	0
48	J8	762	0	848	39	0
49	G5	563	0	612	21	1
49	K8	563	0	612	39	0
50	H5	468	0	518	13	0
50	L8	452	0	503	22	0
51	I5	481	0	479	49	0
51	M8	533	0	526	48	0
52	J5	458	0	480	32	0
52	N8	453	0	475	28	0
53	K5	389	0	404	21	0
53	O8	389	0	404	29	0
54	L5	398	0	441	17	0
54	P8	391	0	432	18	0
55	M5	477	0	540	49	0
55	Q8	480	0	549	98	0
56	1L	1627	0	836	39	0
57	3L	1624	0	827	68	0
58	11	4	0	0	0	0
58	13	148	0	0	0	0
58	14	407	0	0	0	0
58	16	13	0	0	0	0
58	1G	96	0	0	0	0
58	1H	520	0	0	0	0
58	1J	5	0	0	0	0
58	1K	2	0	0	0	0
58	21	2	0	0	0	0
58	25	1	0	0	0	0
58	29	4	0	0	0	0
58	2A	2	0	0	0	0
58	2I	1	0	0	0	0
58	2K	5	0	0	0	0
58	2L	3	0	0	0	0
58	3E	2	0	0	0	0
58	3K	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
58	3L	2	0	0	0	0
58	41	2	0	0	0	0
58	49	1	0	0	0	0
58	4K	1	0	0	0	0
58	55	1	0	0	0	0
58	5E	1	0	0	0	0
58	5I	2	0	0	0	0
58	78	1	0	0	0	0
58	7A	1	0	0	0	0
58	88	2	0	0	0	0
58	98	2	0	0	0	0
58	C5	1	0	0	0	0
58	G8	1	0	0	0	0
58	I8	1	0	0	0	0
58	J5	1	0	0	0	0
58	L8	1	0	0	0	0
58	P8	1	0	0	0	0
59	13	42	0	45	1	0
59	1G	42	0	45	2	0
60	32	1	0	0	0	0
60	3E	1	0	0	0	0
60	5A	1	0	0	0	0
60	5I	1	0	0	0	0
60	C5	1	0	0	0	0
60	G8	1	0	0	0	0
61	11	13	0	0	3	0
61	13	197	0	0	29	0
61	14	598	0	0	153	0
61	16	21	0	0	4	0
61	19	13	0	0	3	0
61	1G	82	0	0	18	0
61	1H	999	0	0	280	0
61	1I	2	0	0	1	0
61	1K	5	0	0	0	0
61	21	4	0	0	0	0
61	2K	6	0	0	0	0
61	31	4	0	0	0	0
61	35	1	0	0	0	0
61	39	7	0	0	1	0
61	3E	3	0	0	0	0
61	3I	1	0	0	0	0
61	3K	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
61	3L	6	0	0	1	0
61	4K	2	0	0	0	0
61	58	2	0	0	0	0
61	5I	2	0	0	1	0
61	6I	1	0	0	0	0
61	78	5	0	0	1	0
61	7A	1	0	0	0	0
61	7I	1	0	0	0	0
61	85	1	0	0	0	0
61	8E	2	0	0	0	0
61	A5	1	0	0	0	0
61	B8	1	0	0	0	0
61	BA	1	0	0	0	0
61	C8	3	0	0	0	0
61	D8	1	0	0	0	0
61	G5	1	0	0	0	0
61	G8	4	0	0	1	0
61	I8	7	0	0	0	0
61	L5	1	0	0	0	0
61	L8	1	0	0	1	0
61	P8	1	0	0	0	0
61	Q8	2	0	0	0	0
All	All	300252	0	200448	8805	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 18.

All (8805) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:14:2701:C:H3'	26:14:2702:U:H5"	1.27	1.15
26:1H:2592:G:OP1	61:1H:4524:HOH:O	1.68	1.10
40:B8:50:ILE:HD11	40:B8:102:ILE:HD11	1.32	1.10
26:1H:1614:A:OP1	61:1H:3947:HOH:O	1.70	1.09
26:1H:945:A:OP1	61:1H:4167:HOH:O	1.70	1.09
26:1H:1315:C:OP2	61:1H:3970:HOH:O	1.72	1.08
26:1H:2006:C:OP1	61:1H:4447:HOH:O	1.72	1.08
26:1H:2615:U:OP1	61:1H:3611:HOH:O	1.73	1.07
41:C8:61:TRP:HB3	41:C8:95:LEU:HD21	1.28	1.07
26:14:1783:A:OP2	61:14:4021:HOH:O	1.72	1.07
26:1H:567:A:OP1	61:1H:3601:HOH:O	1.72	1.07

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1H:810:U:OP1	61:1H:3712:HOH:O	1.72	1.06
1:1G:963:G:H21	10:1A:55:LYS:HE3	1.16	1.05
41:C8:96:ALA:HB3	41:C8:98:LEU:H	1.12	1.04
26:1H:730:C:OP2	61:1H:3685:HOH:O	1.73	1.04
26:14:1774:C:OP1	61:14:3560:HOH:O	1.75	1.04
26:1H:1013:C:OP2	61:1H:3774:HOH:O	1.75	1.03
26:1H:2685:G:N7	61:1H:4134:HOH:O	1.90	1.03
26:1H:1997:G:OP2	61:1H:4031:HOH:O	1.77	1.03
26:1H:71:A:H2	44:F8:31:HIS:HE1	1.06	1.01
26:1H:450:G:OP2	61:1H:3918:HOH:O	1.77	1.01
36:35:62:LEU:HD12	55:M5:25:MET:HB2	1.41	1.01
26:14:1614:A:OP1	61:14:3507:HOH:O	1.77	1.01
26:1H:1774:C:OP1	61:1H:3800:HOH:O	1.77	1.01
30:31:29:ASN:H	30:31:112:MET:HE1	1.25	1.01
26:1H:2431:U:OP2	61:1H:3934:HOH:O	1.80	1.00
26:1H:763:G:OP1	61:1H:3681:HOH:O	1.79	1.00
26:14:662:G:H5'	36:35:15:ARG:HA	1.41	1.00
26:14:785:G:OP2	61:14:4038:HOH:O	1.80	0.99
26:14:1327:C:OP2	61:14:3655:HOH:O	1.79	0.99
26:1H:1647:G:OP2	61:1H:3955:HOH:O	1.79	0.99
26:1H:1665:A:OP2	61:1H:4466:HOH:O	1.79	0.99
26:1H:1138:G:H21	34:58:106:MET:HE3	1.27	0.99
26:1H:2248:C:OP2	61:1H:3722:HOH:O	1.81	0.98
2:12:185:ILE:HG22	2:12:199:TYR:HB2	1.46	0.98
36:35:65:ARG:HB2	36:35:65:ARG:HH11	1.30	0.97
27:1J:80:U:H2'	27:1J:81:G:H21	1.27	0.97
26:1H:1968:G:OP1	61:1H:4520:HOH:O	1.80	0.97
8:7E:41:ARG:NH2	8:7E:123:GLU:OE1	1.97	0.97
26:14:958:U:OP2	37:45:14:ARG:NH1	1.96	0.97
26:1H:1332:G:OP1	61:1H:3973:HOH:O	1.81	0.96
34:15:47:ALA:HB2	34:15:112:LEU:HD21	1.47	0.96
26:1H:1771:C:HO2'	26:1H:1786:A:H8	1.06	0.96
26:14:1771:C:HO2'	26:14:1786:A:H8	1.00	0.96
39:A8:78:LEU:HD12	39:A8:108:GLY:HA2	1.47	0.96
26:14:1533:C:H42	26:14:1538:G:H1	1.11	0.96
26:14:1616:A:O2'	61:14:3642:HOH:O	1.83	0.96
26:14:1899:G:H21	26:14:1902:C:N4	1.64	0.96
26:1H:2588:G:OP2	61:1H:4453:HOH:O	1.82	0.96
2:12:42:ILE:HD11	2:12:202:PRO:HB2	1.48	0.95
57:3L:1:G:H1	57:3L:72:C:H42	1.05	0.95
26:1H:1639:U:OP1	61:1H:3671:HOH:O	1.82	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:Q8:27:THR:HG22	55:Q8:29:LYS:HB3	1.48	0.95
1:13:1502:A:H2	1:13:1505:G:H1	1.12	0.95
26:1H:1689:A:H62	26:1H:1698:A:H2	1.14	0.94
26:1H:2576:G:OP1	61:1H:3809:HOH:O	1.85	0.94
26:14:2593:U:O4	61:14:3600:HOH:O	1.83	0.94
26:14:2598:A:OP1	61:14:3584:HOH:O	1.85	0.94
26:1H:1613:G:N7	61:1H:4579:HOH:O	1.99	0.94
49:K8:47:ASN:HB2	49:K8:50:ILE:HD11	1.50	0.94
26:14:1890:A:OP2	61:14:3967:HOH:O	1.85	0.94
26:14:2588:G:OP2	61:14:3593:HOH:O	1.85	0.94
26:1H:1187:G:OP2	61:1H:3899:HOH:O	1.83	0.94
1:1G:1248:A:N3	9:82:70:LYS:NZ	2.16	0.94
1:1G:1508:G:OP1	61:1G:1760:HOH:O	1.86	0.94
1:1G:588:G:H1	1:1G:651:C:H42	1.14	0.93
26:14:2414:G:H21	36:35:67:MET:HE1	1.31	0.93
26:1H:574:C:OP2	61:1H:4043:HOH:O	1.87	0.93
26:1H:1496:A:H8	26:1H:1577:C:HO2'	1.02	0.93
1:1G:961:U:O2	1:1G:1201:A:N6	2.02	0.93
26:1H:607:U:H3	26:1H:621:A:H2	1.14	0.92
26:1H:2588:G:OP1	61:1H:3943:HOH:O	1.85	0.92
26:1H:155:C:H42	26:1H:171:G:H1	1.13	0.92
26:1H:1658:C:OP1	61:1H:3700:HOH:O	1.86	0.92
26:1H:2419:U:H5'	53:O8:23:THR:HG21	1.51	0.92
26:1H:2781:A:H5"	26:1H:2782:G:H5'	1.50	0.92
26:14:586:A:OP2	61:14:4026:HOH:O	1.87	0.92
26:14:1839:G:OP2	61:14:4001:HOH:O	1.85	0.92
55:M5:34:TRP:CG	55:M5:35:GLN:H	1.82	0.92
26:1H:1265:A:OP2	61:1H:3611:HOH:O	1.87	0.92
26:1H:1728:G:H8	26:1H:1732:A:H62	1.18	0.92
26:1H:585:G:OP2	61:1H:3853:HOH:O	1.88	0.91
26:1H:2597:G:O3'	61:1H:3647:HOH:O	1.88	0.91
26:1H:1623:G:O6	61:1H:3965:HOH:O	1.89	0.91
26:1H:566:U:OP1	36:78:29:LYS:NZ	2.02	0.91
26:1H:805:G:OP1	61:1H:4480:HOH:O	1.88	0.91
41:C8:94:ASN:C	41:C8:96:ALA:HB2	1.95	0.91
26:14:1664:A:OP2	61:14:3613:HOH:O	1.88	0.91
42:95:85:LYS:HG3	42:95:87:HIS:H	1.35	0.91
26:1H:1828:G:OP2	61:1H:4459:HOH:O	1.87	0.91
61:1H:3700:HOH:O	29:21:135:HIS:NE2	2.02	0.91
26:14:2134:A:O2'	26:14:2159:G:N2	2.04	0.91
41:85:90:VAL:HG22	42:95:39:LEU:HB3	1.51	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:13:1110:A:OP2	61:13:1921:HOH:O	1.86	0.91
2:1E:87:ARG:NH2	2:1E:220:ASP:OD1	2.04	0.91
26:1H:741:G:OP1	61:1H:3997:HOH:O	1.87	0.90
26:1H:571:A:OP2	61:1H:3894:HOH:O	1.87	0.90
1:13:1178:G:H5"	9:8E:93:ARG:HH22	1.35	0.90
11:2A:29:ILE:HG22	11:2A:44:SER:HB2	1.53	0.90
24:3K:22:G:N7	24:3K:46:G:N2	2.19	0.90
1:1G:1157:A:H61	1:1G:1178:G:H21	1.14	0.90
30:39:25:PRO:HB2	30:39:27:GLU:H	1.37	0.90
24:3K:5:G:N2	24:3K:68:C:N3	2.20	0.90
26:1H:1153:C:OP2	61:1H:4023:HOH:O	1.88	0.90
26:1H:2354:G:N7	61:1H:4565:HOH:O	2.03	0.90
4:32:26:CYS:HA	4:32:31:CYS:HB3	1.52	0.90
26:14:2588:G:OP1	61:14:3591:HOH:O	1.90	0.89
26:1H:2074:U:OP1	61:1H:3680:HOH:O	1.90	0.89
1:13:664:G:H22	1:13:741:G:H1	1.13	0.89
26:14:2499:C:OP1	61:14:3703:HOH:O	1.89	0.89
26:1H:1417:C:OP2	61:1H:4059:HOH:O	1.89	0.89
26:14:574:C:OP2	61:14:3659:HOH:O	1.91	0.89
26:1H:120:U:OP2	61:1H:4182:HOH:O	1.89	0.89
26:14:397:G:N7	61:14:3977:HOH:O	2.06	0.89
26:1H:2582:G:OP2	61:1H:3822:HOH:O	1.90	0.88
26:1H:1601:G:N7	61:1H:4048:HOH:O	2.07	0.88
26:1H:1828:G:OP1	61:1H:4514:HOH:O	1.90	0.88
10:1I:77:PRO:HB2	10:1I:79:ARG:HH12	1.35	0.88
57:3L:5:G:N2	57:3L:68:C:N3	2.20	0.88
26:1H:946:G:OP2	61:1H:4162:HOH:O	1.91	0.88
26:1H:1386:C:H2'	26:1H:1387:C:H6	1.38	0.88
26:14:1496:A:H8	26:14:1577:C:HO2'	0.93	0.88
26:14:2597:G:O3'	61:14:3585:HOH:O	1.92	0.88
2:1E:111:ARG:HG2	2:1E:111:ARG:HH11	1.37	0.88
26:1H:576:U:OP1	61:1H:4548:HOH:O	1.91	0.88
17:8I:67:LYS:HA	17:8I:70:ARG:HH12	1.38	0.87
26:1H:49:A:N7	26:1H:120:U:H5	1.72	0.87
26:1H:2468:G:H5"	37:88:120:ILE:HD12	1.56	0.87
40:B8:57:PHE:O	40:B8:58:ASN:ND2	2.08	0.87
26:1H:1783:A:OP1	61:1H:4506:HOH:O	1.91	0.87
33:69:81:VAL:HG23	33:69:143:SER:HB2	1.57	0.87
29:21:57:LYS:HG3	29:21:59:VAL:HG12	1.57	0.87
55:Q8:57:ARG:HB3	55:Q8:59:LYS:HE2	1.57	0.87
26:1H:733:G:OP2	61:1H:4112:HOH:O	1.92	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1H:987:G:OP2	61:1H:4019:HOH:O	1.91	0.87
26:14:676:A:H8	26:14:2069:G:H21	1.22	0.87
26:14:1828:G:OP1	61:14:3570:HOH:O	1.92	0.87
45:C5:97:ARG:NH1	45:C5:104:GLY:O	2.08	0.87
26:1H:780:G:H21	26:1H:783:A:H62	1.18	0.87
26:14:567:A:OP1	61:14:3679:HOH:O	1.91	0.87
26:1H:1664:A:OP2	61:1H:4129:HOH:O	1.93	0.86
40:75:1:MET:HB3	40:75:5:ALA:HB3	1.56	0.86
26:1H:1525:G:H2'	26:1H:1526:G:H8	1.38	0.86
30:31:9:ILE:HD13	30:31:123:LEU:HG	1.57	0.86
47:E5:49:LYS:HG3	47:E5:80:HIS:HB3	1.57	0.86
1:13:1029:G:H1'	1:13:1032(A):G:H22	1.38	0.86
19:AI:41:VAL:HG21	19:AI:67:VAL:HG12	1.57	0.86
33:61:7:GLU:HA	33:61:15:VAL:HG22	1.55	0.86
13:4A:13:LYS:HA	13:4A:44:ARG:HH11	1.38	0.86
26:14:2074:U:OP1	61:14:3503:HOH:O	1.92	0.86
26:1H:2406:U:OP1	61:1H:3729:HOH:O	1.94	0.86
26:1H:2608:G:N7	61:1H:3823:HOH:O	2.08	0.86
26:1H:2432:A:OP2	61:1H:3931:HOH:O	1.92	0.86
33:69:75:LEU:HD22	33:69:76:THR:H	1.39	0.86
26:1H:973:A:OP2	61:1H:3890:HOH:O	1.94	0.86
27:16:100:G:OP2	61:16:317:HOH:O	1.91	0.86
1:13:785:G:N7	61:13:1934:HOH:O	2.09	0.86
26:1H:270(X):G:O6	61:1H:4468:HOH:O	1.92	0.86
26:14:833:U:O2	36:35:55:ARG:NH1	2.09	0.86
41:85:92:ARG:HD3	41:85:94:ASN:HB3	1.57	0.86
26:14:1782:C:OP1	61:14:4021:HOH:O	1.94	0.86
26:1H:1009:A:OP2	34:58:37:LYS:NZ	2.09	0.85
35:68:88:ASN:HD21	35:68:90:GLN:HB2	1.39	0.85
26:1H:734:A:OP2	61:1H:4491:HOH:O	1.93	0.85
10:1I:61:GLU:OE2	14:5I:45:ARG:NH1	2.10	0.85
34:58:56:ASN:N	34:58:125:GLY:O	2.08	0.85
26:14:2062:A:OP1	61:14:3788:HOH:O	1.94	0.85
36:35:39:LYS:HD2	36:35:45:LEU:HD21	1.56	0.85
26:1H:1728:G:H3'	26:1H:1729:A:H5"	1.59	0.85
26:14:2836:U:H2'	26:14:2837:G:C8	2.11	0.85
1:13:877:C:OP1	8:7E:88:LYS:NZ	2.08	0.85
26:1H:2017:U:OP2	61:1H:4475:HOH:O	1.94	0.85
26:1H:2838:G:N7	61:1H:4288:HOH:O	2.09	0.85
55:Q8:53:PRO:HB3	55:Q8:56:GLU:HG3	1.57	0.85
26:14:571:A:OP2	61:14:3695:HOH:O	1.94	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:14:2293:C:H5"	39:65:89:ARG:HH12	1.40	0.85
38:55:100:LEU:HD21	38:55:113:LEU:HD13	1.59	0.85
52:N8:50:GLY:H	52:N8:56:LYS:HG3	1.41	0.85
24:3K:76:A:H8	26:1H:2394:C:H42	1.19	0.85
15:6A:82:ILE:HD11	15:6A:88:ARG:HB2	1.58	0.85
26:1H:1313:U:OP1	61:1H:3982:HOH:O	1.95	0.84
26:1H:1332:G:H5'	26:1H:1332:G:C8	2.12	0.84
37:88:51:ARG:HH12	37:88:52:VAL:HG23	1.42	0.84
26:14:1647:G:OP2	61:14:3639:HOH:O	1.93	0.84
5:4E:8:GLU:OE1	5:4E:63:ARG:NH2	2.09	0.84
1:13:505:G:N7	61:13:1850:HOH:O	2.11	0.84
26:1H:71:A:H2	44:F8:31:HIS:CE1	1.94	0.84
26:1H:2656:U:H3	26:1H:2665:A:H2	1.25	0.84
26:14:273(D):C:N4	26:14:363(B):G:O6	2.10	0.84
26:1H:1784:A:OP2	61:1H:4505:HOH:O	1.93	0.84
55:Q8:34:TRP:CH2	55:Q8:39:LYS:HB2	2.12	0.84
1:1G:998:G:N2	1:1G:1043:C:N3	2.25	0.84
26:14:123:G:N7	61:14:4047:HOH:O	2.10	0.84
30:39:188:ARG:HA	36:35:3:LEU:HD11	1.60	0.84
26:1H:450:G:O6	61:1H:3920:HOH:O	1.96	0.84
45:C5:87:LYS:HG2	45:C5:88:LYS:H	1.43	0.84
26:1H:2126:A:N6	26:1H:2163:C:O2	2.10	0.84
26:14:1757:U:H3	26:14:1762:A:H2	1.23	0.84
1:1G:589:C:H42	1:1G:650:G:H1	1.23	0.84
59:1G:1697:PAR:O44	59:1G:1697:PAR:N64	2.10	0.84
26:14:800:A:OP1	61:14:3727:HOH:O	1.96	0.84
26:14:1048:A:N6	26:14:1112:G:O2'	2.09	0.84
12:3A:47:LYS:HG2	12:3A:48:PRO:HD2	1.58	0.83
5:4E:63:ARG:HA	5:4E:66:MET:HE2	1.57	0.83
26:14:399:G:OP2	61:14:3828:HOH:O	1.96	0.83
26:1H:533:G:O6	61:1H:4555:HOH:O	1.94	0.83
1:1G:576:G:N2	1:1G:759:A:OP1	2.11	0.83
26:14:593:G:H4'	55:M5:60:LEU:HD22	1.57	0.83
27:1J:15:A:H5'	27:1J:16:G:H8	1.41	0.83
27:1J:18:G:N2	27:1J:65:C:N3	2.27	0.83
29:21:29:GLY:H	29:21:51:PHE:HE1	1.24	0.83
36:35:19:VAL:HG13	36:35:21:ARG:H	1.43	0.83
16:7I:53:VAL:HG13	16:7I:79:VAL:HG22	1.60	0.83
26:1H:1798:U:H5'	28:11:259:THR:HG22	1.59	0.83
26:1H:2033:A:OP1	61:1H:4101:HOH:O	1.94	0.83
30:39:40:GLN:HE22	30:39:182:ASN:HB2	1.43	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:14:2777:G:H5”	26:14:2778:A:H5’	1.59	0.83
26:14:2782:G:OP2	61:14:3879:HOH:O	1.97	0.83
26:1H:1267:U:O3’	61:1H:4450:HOH:O	1.96	0.83
26:1H:2518:A:OP2	61:1H:4105:HOH:O	1.95	0.83
56:1L:74:C:N4	26:14:2554:U:O2	2.11	0.83
26:14:2304:G:N2	26:14:2312:U:O4	2.11	0.82
1:1G:1502:A:H2	1:1G:1505:G:H1	1.27	0.82
9:82:51:ARG:HG2	9:82:56:LEU:HD13	1.60	0.82
57:3L:5:G:H1	57:3L:68:C:H42	1.24	0.82
26:1H:885:C:O2	26:1H:890:A:N6	2.11	0.82
14:5A:21:TYR:OH	14:5A:23:ARG:NH2	2.11	0.82
26:14:152:G:H1	26:14:174:C:H42	1.25	0.82
26:14:801:G:OP2	61:14:3840:HOH:O	1.97	0.82
27:1J:14:U:O2’	27:1J:107:U:O2’	1.96	0.82
23:2K:47:7MG:H81	23:2K:48:U:H5	1.43	0.82
45:G8:82:PRO:HG3	45:G8:97:ARG:HG3	1.61	0.82
46:H8:72:ARG:NH2	46:H8:97:GLU:O	2.12	0.82
1:1G:589:C:N3	1:1G:650:G:N2	2.26	0.82
1:1G:963:G:N2	10:1A:55:LYS:HE3	1.94	0.82
1:13:446:G:H1	1:13:488:C:H42	1.24	0.82
41:C8:96:ALA:HB3	41:C8:98:LEU:N	1.93	0.82
26:1H:882:G:N2	26:1H:895:U:O4	2.13	0.82
26:1H:2533:A:OP2	61:1H:4383:HOH:O	1.96	0.82
26:14:1187:G:OP2	61:14:3684:HOH:O	1.98	0.82
28:11:85:ASP:OD2	28:11:88:ARG:NH1	2.12	0.81
26:1H:576:U:O4	61:1H:4039:HOH:O	1.98	0.81
46:H8:62:PRO:C	46:H8:64:GLY:HA2	2.05	0.81
48:J8:92:LYS:HA	48:J8:95:LEU:HB2	1.62	0.81
1:1G:1014:A:H2’	1:1G:1015:A:C8	2.15	0.81
21:1B:8:THR:HG22	21:1B:11:GLY:H	1.44	0.81
57:3L:18:G:H22	57:3L:55:PSU:H1’	1.45	0.81
26:1H:731:C:H5”	61:1H:3840:HOH:O	1.80	0.81
42:D8:1:MET:HG2	42:D8:43:GLU:HB3	1.62	0.81
47:I8:53:MET:HG3	47:I8:59:LEU:HD23	1.61	0.81
26:14:1342:A:H2	26:14:1602:U:H3	1.25	0.81
51:I5:22:ILE:HG12	51:I5:23:GLU:H	1.45	0.81
26:14:800:A:OP1	61:14:3730:HOH:O	1.98	0.81
12:3A:41:ARG:HD2	12:3A:42:THR:H	1.45	0.81
26:14:635:C:O2’	26:14:639:U:OP1	1.98	0.81
32:59:137:ASP:HB3	32:59:140:LYS:HB2	1.61	0.81
26:1H:624:C:OP1	61:1H:4329:HOH:O	1.98	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:21:116:VAL:HG11	29:21:138:PRO:HB3	1.61	0.81
1:1G:1256:A:OP2	3:22:26:LYS:NZ	2.13	0.81
26:1H:67:U:H3	26:1H:74:A:H2	1.29	0.81
26:1H:620:G:H4'	26:1H:621:A:H5"	1.63	0.81
26:14:907:U:O2'	37:45:101:ARG:NH2	2.11	0.81
32:59:119:GLU:O	32:59:140:LYS:NZ	2.14	0.81
15:6I:17:ARG:HD3	15:6I:26:GLU:HG3	1.63	0.81
38:98:51:LEU:HD22	38:98:66:VAL:HG13	1.63	0.81
26:14:2873:A:H8	38:55:6:SER:H	1.24	0.81
27:1J:38:C:H42	27:1J:44:G:H1	1.29	0.81
1:13:1178:G:OP2	9:8E:93:ARG:NH2	2.13	0.81
26:1H:2069:G:O3'	61:1H:4177:HOH:O	1.99	0.81
26:1H:2249:U:O4	61:1H:3722:HOH:O	1.98	0.81
28:19:238:GLY:O	61:19:311:HOH:O	1.98	0.81
31:49:40:ASN:HB2	31:49:91:ARG:HG3	1.62	0.80
1:13:1240:U:OP2	7:6E:116:ALA:N	2.13	0.80
26:1H:2849:U:O4	40:B8:23:ARG:NH2	2.15	0.80
26:14:566:U:O3'	61:14:3679:HOH:O	1.98	0.80
26:1H:446:G:OP2	61:1H:3695:HOH:O	1.98	0.80
26:1H:654(E):C:N3	26:1H:654(P):G:N2	2.28	0.80
1:1G:1154:G:H2'	1:1G:1155:G:H8	1.45	0.80
1:13:1008:C:N4	1:13:1021:G:O6	2.13	0.80
26:1H:880:G:H1	26:1H:897:C:H42	1.29	0.80
26:1H:2308:G:H1	26:1H:2311:A:H2	1.29	0.80
2:12:163:PHE:HD2	2:12:185:ILE:HG13	1.46	0.80
26:14:1141:U:OP2	34:15:63:THR:OG1	1.99	0.80
1:1G:1506:U:O2'	61:1G:1763:HOH:O	1.98	0.80
43:A5:92:ARG:NH1	43:A5:94:ASP:OD1	2.14	0.80
26:14:2357:U:OP1	47:E5:20:ARG:NH1	2.13	0.80
5:4E:143:ARG:NE	8:7E:77:GLU:OE1	2.13	0.80
15:6A:87:ILE:HG22	15:6A:88:ARG:H	1.46	0.80
26:14:71:A:H2	44:B5:31:HIS:HE2	1.26	0.80
1:13:509:A:OP2	61:13:1950:HOH:O	1.99	0.80
1:13:1305:G:N2	1:13:1331:G:H2'	1.96	0.80
26:1H:999:U:OP2	61:1H:4022:HOH:O	1.99	0.80
26:1H:2589:A:OP1	61:1H:4575:HOH:O	1.99	0.80
2:12:12:GLU:HB3	2:12:213:LEU:HD22	1.64	0.80
9:82:112:LYS:HA	9:82:119:ALA:HB2	1.62	0.80
30:39:133:ASN:HA	30:39:162:LEU:HD23	1.64	0.80
1:13:972:C:OP1	61:13:1822:HOH:O	1.98	0.79
26:1H:862:G:OP2	61:1H:4015:HOH:O	2.00	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:6A:17:ARG:HD3	15:6A:26:GLU:HG3	1.64	0.79
27:1J:15:A:H3'	27:1J:16:G:H5'	1.64	0.79
26:1H:674:G:H1'	30:31:74:ARG:HD3	1.63	0.79
4:32:14:ARG:HH11	4:32:14:ARG:HG3	1.47	0.79
44:B5:65:ARG:HB2	44:B5:70:LEU:HB3	1.64	0.79
45:C5:19:LYS:HG3	45:C5:20:TYR:H	1.47	0.79
1:13:1353:G:OP1	21:1F:10:ARG:NH2	2.15	0.79
26:1H:1678:G:N2	26:1H:1989:G:H22	1.81	0.79
56:1L:74:C:H1'	56:1L:75:C:H5'	1.64	0.79
23:2L:8:4SU:O2	23:2L:14:A:N6	2.15	0.79
26:14:2392:A:H2	26:14:2424:C:H42	1.29	0.79
26:1H:422:A:OP2	61:1H:4488:HOH:O	2.01	0.79
40:B8:56:GLY:O	40:B8:59:THR:HG22	1.82	0.79
11:2A:85:ARG:HE	11:2A:111:ASP:HB3	1.47	0.79
29:29:111:ARG:HA	38:55:2:ARG:HH12	1.47	0.79
1:13:1129:C:H4'	1:13:1130:A:H5'	1.65	0.79
30:31:66:PRO:O	30:31:67:GLN:HB3	1.82	0.79
1:1G:768:A:OP2	61:1G:1703:HOH:O	2.00	0.79
26:14:2137:C:N3	26:14:2155:G:N1	2.30	0.79
8:7E:87:SER:HB2	8:7E:93:VAL:HB	1.63	0.79
16:7I:5:ARG:HE	16:7I:22:THR:HG21	1.48	0.79
26:1H:370:G:OP2	61:1H:4486:HOH:O	1.99	0.79
26:1H:1064:C:N4	26:1H:1070:A:OP1	2.16	0.79
36:78:47:ASP:OD2	36:78:50:ARG:NH2	2.15	0.79
36:78:138:LEU:HD12	36:78:144:GLU:HG3	1.63	0.79
55:Q8:47:LYS:HA	55:Q8:47:LYS:NZ	1.97	0.79
26:14:898:C:H3'	26:14:899:A:H5"	1.64	0.79
40:B8:6:LEU:HA	40:B8:9:LEU:HB2	1.63	0.79
1:1G:406:G:H21	4:32:119:GLN:HE22	1.30	0.79
14:5A:45:ARG:O	14:5A:49:HIS:ND1	2.15	0.79
1:13:975:A:H4'	1:13:976:G:H5"	1.64	0.79
26:1H:259:G:H21	26:1H:621:A:H8	1.28	0.79
1:1G:438:G:H4'	4:32:123:HIS:HD2	1.47	0.79
26:1H:2864:G:N7	61:1H:4191:HOH:O	2.14	0.79
26:14:400:G:O6	61:14:3831:HOH:O	2.00	0.79
26:1H:2318:G:H22	39:A8:2:ALA:N	1.81	0.79
35:25:24:VAL:HA	35:25:39:ILE:HG22	1.63	0.79
44:B5:36:LYS:HG2	44:B5:54:VAL:HB	1.65	0.79
1:13:963:G:H21	10:1I:55:LYS:NZ	1.81	0.78
26:1H:2830:G:N7	61:1H:4297:HOH:O	2.16	0.78
26:1H:879:G:O6	26:1H:898:C:N4	2.15	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:K8:18:PRO:HA	49:K8:21:LEU:HB2	1.64	0.78
26:1H:1153:C:OP2	61:1H:4024:HOH:O	2.00	0.78
26:1H:1332:G:N2	26:1H:1609:A:O2'	2.17	0.78
30:39:4:VAL:HA	30:39:19:GLU:HB3	1.65	0.78
26:1H:1010:A:OP2	61:1H:4208:HOH:O	2.02	0.78
26:14:1330:C:OP1	61:14:3757:HOH:O	2.00	0.78
26:14:1168:G:O6	26:14:1181:C:N4	2.16	0.78
34:15:33:LEU:HD12	34:15:38:HIS:HD2	1.48	0.78
26:1H:71:A:C2	44:F8:31:HIS:HE1	1.97	0.78
30:31:29:ASN:N	30:31:112:MET:HE1	1.98	0.78
39:A8:48:LEU:HD23	39:A8:82:ILE:HD11	1.66	0.78
26:14:1249:U:OP1	61:14:4027:HOH:O	2.01	0.78
26:14:1780:A:OP1	61:14:4022:HOH:O	2.01	0.78
30:39:66:PRO:O	30:39:67:GLN:HB3	1.82	0.78
26:1H:1143:A:OP2	61:1H:3778:HOH:O	2.02	0.78
29:21:13:ARG:HG2	29:21:13:ARG:HH11	1.49	0.78
45:G8:87:LYS:H	45:G8:94:LYS:HG2	1.47	0.78
26:14:309:G:H4'	45:C5:18:GLY:HA3	1.66	0.78
26:1H:1653:G:H3'	38:98:2:ARG:HG3	1.66	0.78
26:14:2689:U:OP2	26:14:2719:G:N2	2.16	0.78
27:1J:18:G:H1	27:1J:65:C:H42	1.29	0.78
19:AI:40:ILE:HG23	19:AI:41:VAL:HG13	1.64	0.78
26:1H:33:U:H4'	26:1H:34:C:OP1	1.83	0.78
26:1H:818:G:OP2	61:1H:4501:HOH:O	2.01	0.78
3:22:91:LEU:HB2	3:22:99:VAL:HG11	1.64	0.78
26:14:450:G:OP2	61:14:3734:HOH:O	2.00	0.78
35:25:7:TYR:HE1	35:25:20:MET:HE3	1.47	0.78
26:1H:751:A:P	61:1H:3948:HOH:O	2.42	0.78
1:13:396:G:O2'	1:13:398:C:OP1	2.00	0.77
1:13:1122:U:O4	1:13:1123:A:N6	2.17	0.77
12:3A:60:LEU:HB2	12:3A:64:TYR:HB2	1.65	0.77
26:14:2028:U:O4	61:14:4058:HOH:O	1.98	0.77
26:1H:800:A:OP1	61:1H:3642:HOH:O	2.00	0.77
29:21:128:SER:OG	29:21:129:HIS:N	2.12	0.77
55:Q8:39:LYS:O	55:Q8:40:GLU:HB3	1.82	0.77
2:1E:15:VAL:HG21	2:1E:209:ARG:HB3	1.66	0.77
24:3K:72:C:H3'	24:3K:73:A:H5"	1.65	0.77
1:13:187:C:O2	1:13:191(A):G:N1	2.18	0.77
4:3E:30:LYS:HB2	4:3E:35:ARG:HE	1.49	0.77
26:1H:302:C:H2'	26:1H:303:U:H6	1.48	0.77
9:82:10:ARG:HD2	9:82:105:ASP:HB3	1.66	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1H:860:U:H5	26:1H:917:A:C2	2.02	0.77
1:1G:1298:C:OP2	7:62:114:ARG:NH2	2.18	0.77
1:1G:1305:G:H22	1:1G:1331:G:H2'	1.49	0.77
29:21:105:THR:HG22	29:21:106:GLY:H	1.49	0.77
31:41:64:THR:HG22	31:41:66:GLN:H	1.50	0.77
26:14:2327:A:H2'	26:14:2328:A:C8	2.19	0.77
36:35:14:LYS:O	36:35:16:ARG:N	2.17	0.77
42:95:85:LYS:HD2	42:95:86:GLY:H	1.48	0.77
1:13:413:G:O2'	1:13:428:G:N2	2.16	0.77
10:1I:61:GLU:OE1	14:5I:58:LYS:NZ	2.17	0.77
26:14:1970:A:OP2	61:14:3573:HOH:O	2.02	0.77
38:98:33:ARG:HG3	38:98:115:GLU:HB3	1.67	0.77
1:1G:286:G:N7	61:1G:1742:HOH:O	2.18	0.77
26:14:517:C:OP1	52:J5:16:ARG:NH2	2.18	0.77
26:14:2272:U:O4	61:14:3909:HOH:O	2.03	0.77
31:49:109:VAL:HG11	31:49:142:PRO:HG3	1.67	0.77
41:85:28:ARG:NH1	41:85:38:THR:OG1	2.17	0.77
26:1H:2096:U:H3	26:1H:2193:G:H1	1.33	0.77
37:88:5:ARG:H	37:88:5:ARG:HD3	1.50	0.77
2:12:105:PHE:HA	2:12:108:ILE:HB	1.65	0.77
26:14:1962:C:O2'	26:14:1964:G:OP2	2.01	0.77
11:2I:99:GLN:HA	11:2I:105:VAL:HG11	1.67	0.77
26:1H:1664:A:OP1	61:1H:4464:HOH:O	2.01	0.77
26:1H:2447:G:OP2	61:1H:3865:HOH:O	2.02	0.77
26:1H:2789:C:O2	26:1H:2894:G:N2	2.14	0.77
9:82:28:VAL:HG22	9:82:63:ILE:HB	1.65	0.77
26:14:910:A:H62	37:45:12:GLN:HA	1.48	0.77
40:75:50:ILE:HD11	40:75:102:ILE:HD11	1.66	0.77
53:K5:27:LYS:HZ3	53:K5:28:ARG:HH12	1.32	0.77
11:2I:79:SER:OG	11:2I:106:LYS:NZ	2.17	0.76
26:1H:409:C:OP1	61:1H:3749:HOH:O	2.03	0.76
26:1H:625:G:N7	36:78:107:LYS:NZ	2.33	0.76
15:6A:16:ALA:HB1	15:6A:21:ASP:HB3	1.65	0.76
26:1H:217:G:OP2	61:1H:3763:HOH:O	2.02	0.76
26:1H:607:U:OP1	30:31:102:PRO:HA	1.85	0.76
26:1H:1332:G:H5"	61:1H:3971:HOH:O	1.84	0.76
1:1G:411:A:H62	1:1G:413:G:H21	1.32	0.76
19:AA:39:THR:OG1	19:AA:70:LYS:NZ	2.17	0.76
26:14:1359:A:H62	26:14:1372:U:H3	1.32	0.76
29:29:12:THR:HG22	40:75:58:ASN:HD21	1.49	0.76
1:13:510:A:OP2	4:3E:49:ARG:NH2	2.18	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:62:113:GLU:HB2	7:62:119:ARG:HG2	1.66	0.76
26:14:2210:G:O5'	26:14:2211:G:N2	2.19	0.76
40:75:16:ARG:HH21	40:75:19:LEU:HD21	1.51	0.76
12:3I:126:LYS:HG3	12:3I:128:ALA:H	1.49	0.76
36:78:19:VAL:HG11	36:78:27:HIS:HB2	1.65	0.76
1:1G:1435:G:H2'	1:1G:1436:U:C6	2.21	0.76
10:1A:48:THR:HA	10:1A:62:HIS:HB3	1.65	0.76
44:B5:41:ASN:HA	44:B5:44:GLU:HB2	1.68	0.76
27:16:12:C:O2	47:I8:74:ARG:NH1	2.19	0.76
3:22:70:VAL:HG12	3:22:72:LYS:H	1.49	0.76
1:13:1004:A:O5'	1:13:1025:U:N3	2.17	0.76
48:J8:83:GLU:HG2	48:J8:85:LEU:H	1.48	0.76
1:1G:1002:G:H2'	1:1G:1003:G:H8	1.49	0.76
26:14:1729:A:H2'	26:14:1731:G:N2	2.01	0.76
28:19:37:LEU:HB2	28:19:38:LYS:HG2	1.66	0.76
32:59:89:ILE:HG21	32:59:130:ARG:HA	1.68	0.76
48:F5:91:LYS:HZ3	48:F5:91:LYS:HA	1.48	0.76
26:1H:2502:G:OP2	61:1H:3625:HOH:O	2.02	0.76
28:11:221:VAL:HG22	28:11:226:MET:HE3	1.67	0.76
26:14:363:G:H2'	26:14:363(A):A:H8	1.49	0.76
2:12:87:ARG:HE	2:12:233:SER:HB3	1.49	0.76
26:14:372:G:OP2	48:F5:69:LYS:NZ	2.18	0.76
30:39:46:ARG:HG2	30:39:46:ARG:HH11	1.51	0.76
38:55:103:ARG:NH1	38:55:108:GLY:O	2.19	0.76
1:13:353:A:H8	1:13:353:A:H5'	1.50	0.76
39:A8:74:ALA:HB1	39:A8:108:GLY:HA3	1.67	0.76
1:1G:1503:A:N3	25:4L:13:A:N6	2.34	0.76
26:14:761:A:N7	61:14:4077:HOH:O	2.17	0.76
30:39:123:LEU:O	30:39:125:LEU:N	2.16	0.76
35:25:2:ILE:HD12	35:25:6:THR:HG21	1.66	0.76
1:13:398:C:OP2	61:13:1982:HOH:O	2.03	0.75
26:1H:226:G:H21	26:1H:228:A:H2	1.33	0.75
26:1H:311:A:OP2	61:1H:4542:HOH:O	2.04	0.75
26:1H:1828:G:OP1	61:1H:4516:HOH:O	2.05	0.75
33:61:110:ASP:HB2	33:61:112:LYS:H	1.51	0.75
1:1G:1126:U:H4'	1:1G:1127:G:C8	2.21	0.75
26:14:274:G:H2'	26:14:275:G:H4'	1.66	0.75
31:49:161:THR:HG22	31:49:163:ALA:H	1.51	0.75
33:69:73:GLU:HG3	33:69:136:VAL:HG23	1.68	0.75
13:4I:10:PRO:HB2	13:4I:18:ALA:HB1	1.69	0.75
18:9I:38:GLU:OE1	18:9I:41:LYS:NZ	2.15	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:BI:69:GLY:O	20:BI:73:HIS:NE2	2.19	0.75
26:1H:450:G:O6	61:1H:3922:HOH:O	2.03	0.75
1:1G:587:G:N2	1:1G:754:C:OP2	2.18	0.75
1:1G:631:G:H3'	1:1G:632:A:H8	1.51	0.75
28:19:246:PRO:HD2	28:19:255:LYS:HE2	1.69	0.75
23:2K:54:G:H2'	23:2K:55:5MU:H6	1.51	0.75
24:3K:6:G:N2	24:3K:67:C:O2	2.18	0.75
26:1H:330:A:HO2'	26:1H:331:A:H8	1.32	0.75
26:1H:732:C:OP2	61:1H:4116:HOH:O	2.03	0.75
26:14:780:G:H21	26:14:783:A:H62	1.34	0.75
26:14:2210:G:H3'	26:14:2211:G:C2	2.21	0.75
40:75:64:ARG:HB2	40:75:73:GLU:HG2	1.66	0.75
53:K5:28:ARG:O	53:K5:32:ASN:ND2	2.19	0.75
26:1H:574:C:OP1	61:1H:3803:HOH:O	2.04	0.75
26:14:2701:C:H3'	26:14:2702:U:C5'	2.14	0.75
35:25:10:VAL:HG12	35:25:19:ILE:HG12	1.67	0.75
1:1G:490:G:OP2	4:32:132:ARG:NH2	2.19	0.75
26:14:1043:C:N3	26:14:1112:G:N2	2.32	0.75
14:5I:6:LEU:HD13	14:5I:23:ARG:HH22	1.50	0.75
49:K8:30:ARG:HG3	49:K8:30:ARG:HH11	1.51	0.75
26:14:990:A:H5'	26:14:990:A:H8	1.52	0.75
27:16:102:G:N7	61:16:302:HOH:O	2.18	0.75
1:1G:979:C:H3'	1:1G:980:C:H5"	1.69	0.75
26:1H:2017:U:P	61:1H:4475:HOH:O	2.44	0.75
26:14:662:G:OP1	36:35:15:ARG:NH2	2.20	0.75
26:14:900:A:H3'	26:14:901:A:H8	1.52	0.75
26:1H:751:A:OP1	61:1H:3949:HOH:O	2.05	0.75
26:1H:2164:C:OP2	26:1H:2166:G:N2	2.20	0.75
26:14:1823:G:N7	61:14:3852:HOH:O	2.20	0.75
1:13:1007:C:H42	1:13:1022:G:H1	1.32	0.74
32:51:169:VAL:O	32:51:170:ARG:NE	2.20	0.74
1:13:201:C:H42	1:13:216:G:H1	1.33	0.74
20:BI:53:LEU:HD12	20:BI:56:MET:HE2	1.69	0.74
23:2K:62:C:H2'	23:2K:63:C:H6	1.52	0.74
26:14:252:G:OP2	36:35:50:ARG:NH2	2.19	0.74
26:14:446:G:OP2	61:14:3824:HOH:O	2.04	0.74
28:19:93:ALA:HB3	28:19:105:ILE:HG22	1.70	0.74
37:45:31:ASP:H	37:45:107:ALA:HB2	1.52	0.74
26:1H:76:C:O2'	49:K8:62:THR:HG21	1.87	0.74
26:1H:1007:C:OP2	61:1H:4205:HOH:O	2.05	0.74
26:1H:1386:C:H2'	26:1H:1387:C:C6	2.21	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:C8:8:VAL:HG23	41:C8:11:ARG:HH21	1.52	0.74
55:Q8:46:ARG:HH11	55:Q8:46:ARG:HG2	1.52	0.74
1:13:376:G:H1	1:13:387:U:H3	1.35	0.74
26:1H:441:U:O2	30:31:46:ARG:NH2	2.20	0.74
26:1H:839:U:N3	26:1H:939:G:O6	2.18	0.74
26:14:2025:C:N4	61:14:3715:HOH:O	2.19	0.74
3:2E:21:ARG:NH2	3:2E:56:ASP:OD2	2.21	0.74
26:1H:142:G:H1'	44:F8:37:THR:HG21	1.70	0.74
26:1H:598:G:H5'	36:78:11:GLY:HA3	1.69	0.74
26:1H:1253:A:N7	61:1H:3712:HOH:O	2.20	0.74
26:1H:1478:G:H2'	26:1H:1479:G:H8	1.53	0.74
26:1H:1525:G:H2'	26:1H:1526:G:C8	2.22	0.74
26:1H:1778:U:H2'	26:1H:1784:A:N6	2.02	0.74
26:1H:2495:G:OP1	61:1H:4388:HOH:O	2.05	0.74
1:1G:976:G:N2	1:1G:1362(A):C:OP2	2.15	0.74
9:82:111:ARG:HB3	9:82:113:LYS:HE2	1.69	0.74
20:BA:89:ARG:NH1	20:BA:105:SER:O	2.19	0.74
26:14:617:G:OP1	30:39:40:GLN:NE2	2.19	0.74
29:29:81:ILE:HG22	29:29:82:ARG:H	1.52	0.74
30:39:103:LYS:HA	30:39:106:ARG:HG3	1.68	0.74
26:1H:376:C:OP2	61:1H:3750:HOH:O	2.04	0.74
26:1H:2850:A:OP1	61:1H:4190:HOH:O	2.05	0.74
39:A8:56:LEU:HB3	39:A8:58:LEU:HD21	1.68	0.74
1:1G:960:U:H3	1:1G:1225:A:H1'	1.53	0.74
26:1H:2583:G:OP1	61:1H:4423:HOH:O	2.05	0.74
46:H8:108:PRO:HB2	46:H8:112:ARG:HA	1.70	0.74
33:69:124:GLY:H	33:69:142:VAL:HG12	1.52	0.74
1:13:1009:G:N1	1:13:1020:U:O2	2.19	0.74
26:1H:229:A:H4'	26:1H:230:U:H5'	1.70	0.74
26:1H:993:G:OP1	41:C8:50:ARG:NH2	2.20	0.74
26:14:1582:C:HO2'	26:14:1586:A:H8	1.35	0.74
1:13:1423:G:OP1	35:68:49:ARG:NH2	2.21	0.74
1:13:1497:G:H2'	1:13:1498:U:H5'	1.69	0.74
18:9I:38:GLU:HA	18:9I:41:LYS:HZ2	1.53	0.74
20:BI:33:ILE:O	20:BI:37:SER:OG	2.06	0.74
26:1H:2503:A:OP1	61:1H:4545:HOH:O	2.04	0.74
41:C8:50:ARG:HH12	42:D8:72:VAL:HG12	1.51	0.74
26:14:1537:C:H2'	26:14:1538:G:C8	2.23	0.74
26:14:2685:G:O6	61:14:3617:HOH:O	2.06	0.74
36:35:55:ARG:HG2	36:35:56:SER:H	1.51	0.74
1:13:1177:G:OP1	1:13:1177:G:H4'	1.86	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:13:1292:U:OP2	7:6E:41:ARG:NH2	2.21	0.74
3:22:182:ILE:HG22	3:22:203:PHE:HA	1.68	0.74
26:14:1665:A:N7	61:14:3608:HOH:O	2.19	0.74
26:14:2056:G:H1	52:J5:4:HIS:HB3	1.52	0.74
1:13:601:C:H2'	1:13:602:A:H8	1.53	0.73
1:13:1305:G:H21	1:13:1331:G:H2'	1.52	0.73
26:1H:2518:A:OP2	61:1H:4107:HOH:O	2.06	0.73
30:39:102:PRO:HB2	30:39:105:VAL:HG23	1.70	0.73
34:15:56:ASN:HA	34:15:125:GLY:H	1.53	0.73
35:25:115:VAL:HG13	35:25:121:VAL:HG21	1.70	0.73
42:95:85:LYS:HG3	42:95:87:HIS:N	2.03	0.73
26:1H:1899:G:H22	26:1H:1902:C:H5	1.33	0.73
26:1H:2062:A:OP2	61:1H:3859:HOH:O	2.05	0.73
33:61:3:VAL:HG12	33:61:38:LEU:HA	1.69	0.73
57:3L:71:G:HO2'	26:14:1851:U:HO2'	1.20	0.73
26:14:1942:C:OP2	26:14:1943:U:O2'	2.05	0.73
26:14:2415:G:H4'	36:35:67:MET:H	1.52	0.73
26:14:2738:A:OP2	61:14:3914:HOH:O	2.06	0.73
26:1H:731:C:OP2	61:1H:3685:HOH:O	2.06	0.73
1:1G:826:C:O2	1:1G:874:G:N2	2.18	0.73
26:14:259:G:H21	26:14:621:A:H8	1.35	0.73
47:E5:53:MET:HG3	47:E5:59:LEU:CD2	2.19	0.73
1:13:827:U:H5	1:13:872:A:N1	1.86	0.73
26:1H:1616:A:O2'	61:1H:3951:HOH:O	2.07	0.73
26:1H:2312:U:H5'	31:41:88:ILE:HD12	1.70	0.73
33:61:92:VAL:HG13	33:61:120:ILE:HG23	1.69	0.73
26:14:654(B):C:O2	26:14:654(S):G:N2	2.20	0.73
27:1J:80:U:H2'	27:1J:81:G:N2	2.01	0.73
35:25:68:GLU:HA	35:25:78:ARG:HB3	1.70	0.73
1:13:1124:G:O2'	1:13:1145:C:N4	2.21	0.73
1:13:1422:G:H5"	35:68:48:PRO:HB3	1.70	0.73
24:3K:37:MIA:H8	24:3K:37:MIA:O5'	1.87	0.73
26:1H:1486:A:H2'	26:1H:1487:G:H8	1.54	0.73
30:31:6:VAL:N	30:31:24:LEU:O	2.22	0.73
37:45:88:GLY:O	37:45:89:ASN:ND2	2.21	0.73
26:1H:654(A):A:H2	26:1H:654(T):A:N1	1.87	0.73
26:1H:1588:C:H2'	26:1H:1589:C:H6	1.52	0.73
26:1H:2392:A:H2	26:1H:2424:C:H42	1.35	0.73
31:41:67:LYS:HE2	51:M8:6:HIS:CE1	2.23	0.73
36:78:114:ILE:HD11	36:78:130:PHE:HD2	1.53	0.73
1:1G:474:G:H2'	1:1G:475:G:C8	2.23	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:62:116:ALA:HA	7:62:119:ARG:HE	1.52	0.73
26:14:567:A:P	61:14:3679:HOH:O	2.47	0.73
26:14:881:G:O6	26:14:882:G:N2	2.22	0.73
26:14:2037:G:N7	61:14:3712:HOH:O	2.21	0.73
26:14:2681:C:H5	26:14:2725:A:H62	1.33	0.73
30:39:25:PRO:HB3	30:39:28:ILE:HG23	1.68	0.73
3:2E:40:ARG:O	3:2E:44:GLU:HG2	1.87	0.73
5:4E:126:ARG:HG3	5:4E:126:ARG:HH11	1.53	0.73
39:A8:27:SER:HA	39:A8:88:ASP:HB3	1.69	0.73
45:G8:38:ILE:HD11	45:G8:64:GLU:HG3	1.71	0.73
1:1G:957:U:O2'	1:1G:959:A:N7	2.21	0.73
15:6A:54:ARG:NH1	15:6A:58:MET:SD	2.62	0.73
1:13:1322:C:O2'	1:13:1323:G:O5'	2.07	0.73
31:41:21:ARG:HG2	31:41:21:ARG:HH11	1.54	0.73
32:51:4:ILE:HG21	32:51:6:ARG:NH1	2.02	0.73
5:42:11:ILE:HD12	5:42:31:LEU:HD12	1.70	0.73
21:1B:10:ARG:HA	21:1B:13:ILE:HD12	1.69	0.73
26:14:1327:C:OP2	61:14:3653:HOH:O	2.05	0.73
26:14:1678:G:H22	26:14:1989:G:H22	1.37	0.73
3:22:6:HIS:HB3	14:5A:49:HIS:CD2	2.24	0.73
26:14:1443:G:H1	26:14:1548:C:H42	1.33	0.73
27:1J:3:C:N3	27:1J:117:G:N2	2.37	0.73
1:13:991:U:O2'	1:13:992:U:O5'	2.06	0.73
26:1H:1006:C:OP2	61:1H:4209:HOH:O	2.07	0.73
26:1H:1171:G:N2	26:1H:1178:C:N3	2.35	0.73
29:21:82:ARG:O	29:21:84:PHE:N	2.22	0.73
2:12:70:PHE:HB2	2:12:92:TYR:HB2	1.69	0.73
26:14:1657:C:OP2	29:29:136:ARG:HG3	1.89	0.73
26:14:739:G:OP1	61:14:3751:HOH:O	2.06	0.72
26:1H:733:G:N7	61:1H:4113:HOH:O	2.23	0.72
38:98:55:ALA:HA	38:98:80:PHE:CE1	2.23	0.72
26:14:452:G:OP2	61:14:3733:HOH:O	2.06	0.72
26:1H:958:U:OP2	37:88:14:ARG:NH1	2.22	0.72
26:1H:1165:U:H2'	26:1H:1166:C:C6	2.24	0.72
34:58:73:THR:HB	34:58:82:LEU:HD11	1.68	0.72
1:1G:521:G:O6	1:1G:528:C:N4	2.19	0.72
57:3L:21:A:N6	57:3L:46:7MG:HN21	1.87	0.72
26:14:2504:U:OP2	61:14:3667:HOH:O	2.07	0.72
26:14:2819:G:O6	26:14:2827:C:N4	2.18	0.72
44:B5:65:ARG:HG3	44:B5:67:GLY:H	1.54	0.72
5:4E:8:GLU:HG2	5:4E:34:VAL:HG22	1.71	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1H:1900:A:H5'	26:1H:1900:A:H8	1.55	0.72
26:14:570:G:OP1	61:14:3697:HOH:O	2.07	0.72
55:M5:30:ARG:O	55:M5:32:LEU:N	2.22	0.72
1:13:504:C:OP1	61:13:1854:HOH:O	2.08	0.72
2:1E:185:ILE:HG23	2:1E:199:TYR:HB2	1.70	0.72
26:1H:2255:G:OP2	61:1H:4171:HOH:O	2.07	0.72
26:1H:2392:A:H8	36:78:61:ARG:HG2	1.55	0.72
55:Q8:39:LYS:HD2	55:Q8:40:GLU:H	1.55	0.72
1:1G:1302:U:OP1	13:4A:13:LYS:NZ	2.22	0.72
26:14:570:G:O6	61:14:3703:HOH:O	2.07	0.72
26:14:674:G:O2'	30:39:74:ARG:HG3	1.89	0.72
46:D5:10:ARG:NH2	46:D5:26:GLY:O	2.22	0.72
7:6E:15:ASP:HB3	7:6E:20:ASP:H	1.52	0.72
23:2K:47:7MG:H81	23:2K:48:U:C5	2.22	0.72
26:1H:780:G:H21	26:1H:783:A:N6	1.86	0.72
2:12:91:PRO:HG3	2:12:154:LEU:HB2	1.71	0.72
26:14:2273:A:H2'	26:14:2274:A:C8	2.25	0.72
27:1J:44:G:H1'	27:1J:47:C:H42	1.54	0.72
17:8I:18:THR:OG1	17:8I:69:LYS:NZ	2.17	0.72
31:41:161:THR:HG23	31:41:163:ALA:H	1.54	0.72
46:H8:19:ARG:NH1	46:H8:84:GLU:O	2.22	0.72
55:Q8:53:PRO:HA	55:Q8:54:GLU:C	2.14	0.72
28:19:69:ARG:NE	28:19:105:ILE:HD11	2.05	0.72
46:D5:8:TYR:HD1	46:D5:62:PRO:HG3	1.54	0.72
26:1H:250:G:P	36:78:60:MET:HE1	2.30	0.72
26:1H:800:A:P	61:1H:3642:HOH:O	2.47	0.72
26:1H:1534:G:H2'	26:1H:1535:U:H4'	1.71	0.72
26:1H:1970:A:OP2	61:1H:4003:HOH:O	2.08	0.72
57:3L:9:A:O2'	57:3L:10:G:N7	2.19	0.72
26:14:588:U:H2'	26:14:589:C:C6	2.24	0.72
1:13:1062:U:H2'	1:13:1063:C:C6	2.25	0.72
45:G8:30:VAL:HG22	45:G8:37:VAL:HG12	1.72	0.72
2:12:18:GLY:O	2:12:204:ASN:ND2	2.23	0.72
26:14:2448:A:O5'	61:14:3698:HOH:O	2.07	0.72
1:13:1132:C:N4	1:13:1142:G:O6	2.18	0.72
26:1H:305:U:O4	61:1H:4540:HOH:O	2.07	0.72
26:1H:587:C:OP2	36:78:21:ARG:NH2	2.22	0.72
26:14:1013:C:H42	26:14:1149:G:H1	1.38	0.72
40:75:4:GLY:O	40:75:7:ILE:N	2.22	0.72
49:G5:47:ASN:O	49:G5:49:LYS:N	2.23	0.72
55:M5:40:GLU:HA	55:M5:43:GLN:HB2	1.72	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1H:1784:A:OP1	61:1H:3995:HOH:O	2.07	0.71
26:1H:2134:A:OP2	26:1H:2157:G:N2	2.23	0.71
31:41:112:PRO:HB3	51:M8:37:SER:H	1.54	0.71
26:14:193:U:OP2	61:14:3723:HOH:O	2.07	0.71
26:14:1689:A:H62	26:14:1698:A:H2	1.35	0.71
28:19:242:ARG:O	61:19:309:HOH:O	2.08	0.71
30:39:113:ALA:HB1	30:39:186:ILE:HG21	1.70	0.71
45:C5:76:CYS:SG	45:C5:97:ARG:HG3	2.29	0.71
26:1H:761:A:OP1	61:1H:3685:HOH:O	2.07	0.71
1:1G:324:G:N7	61:1G:1748:HOH:O	2.23	0.71
23:2L:24:C:H2'	23:2L:25:U:H6	1.54	0.71
53:K5:28:ARG:HG3	53:K5:31:PRO:HD2	1.71	0.71
34:58:96:GLU:O	34:58:98:VAL:HG12	1.90	0.71
40:B8:26:ASP:HB2	40:B8:91:ARG:HA	1.71	0.71
5:42:102:ALA:HB1	5:42:106:PRO:HG2	1.71	0.71
28:19:40:THR:OG1	28:19:41:GLY:N	2.22	0.71
38:55:67:LEU:HD12	38:55:76:VAL:HG11	1.72	0.71
42:95:69:LYS:HB3	42:95:86:GLY:HA3	1.72	0.71
48:F5:85:LEU:HA	48:F5:87:PRO:HD2	1.72	0.71
1:13:541:G:N7	61:13:1931:HOH:O	2.22	0.71
26:1H:910:A:N7	37:88:13:GLN:HG3	2.04	0.71
26:1H:2588:G:P	61:1H:4453:HOH:O	2.47	0.71
26:1H:2701:C:H3'	26:1H:2702:U:H5"	1.72	0.71
44:F8:5:TYR:O	49:K8:36:ARG:NH2	2.21	0.71
26:14:1041:C:H42	26:14:1114:G:H22	1.39	0.71
26:14:2211:G:O2'	26:14:2212:A:OP1	2.08	0.71
43:A5:65:LEU:HD13	43:A5:68:ARG:HD2	1.70	0.71
15:6I:17:ARG:HH11	15:6I:17:ARG:HG3	1.54	0.71
55:Q8:59:LYS:HZ2	55:Q8:59:LYS:HB3	1.54	0.71
1:1G:1002:G:H2'	1:1G:1003:G:C8	2.25	0.71
26:14:2849:U:O4	40:75:23:ARG:NH2	2.20	0.71
46:D5:5:LEU:HD12	46:D5:47:VAL:HG21	1.72	0.71
26:1H:275:G:N2	26:1H:276:A:N1	2.37	0.71
26:1H:739:G:OP1	61:1H:4509:HOH:O	2.07	0.71
26:1H:943:U:OP2	61:1H:4444:HOH:O	2.08	0.71
26:1H:2849:U:O2'	61:1H:4193:HOH:O	2.09	0.71
30:31:6:VAL:HG11	30:31:119:ARG:HA	1.71	0.71
50:L8:13:ILE:O	61:L8:201:HOH:O	2.08	0.71
15:6A:26:GLU:OE2	15:6A:77:ARG:NH1	2.24	0.71
1:13:262:A:H2'	1:13:263:A:C8	2.25	0.71
17:8I:76:LEU:HD21	17:8I:79:SER:HB3	1.71	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1H:1951:U:O4	61:1H:4035:HOH:O	2.08	0.71
1:1G:1226:C:N4	13:4A:104:ARG:HD2	2.06	0.71
23:2L:41:C:H2'	23:2L:42:C:H6	1.55	0.71
26:14:2748:A:H2'	26:14:2749:A:H8	1.54	0.71
29:29:55:ASN:O	29:29:57:LYS:N	2.23	0.71
1:13:1345:U:OP1	61:13:1941:HOH:O	2.08	0.71
26:1H:1333:C:OP2	61:1H:3980:HOH:O	2.08	0.71
26:1H:1359:A:H2	26:1H:1372:U:O4	1.74	0.71
26:1H:2033:A:H8	61:1H:4101:HOH:O	1.73	0.71
26:1H:2270:G:OP2	61:1H:4280:HOH:O	2.09	0.71
30:31:29:ASN:H	30:31:112:MET:CE	2.02	0.71
47:I8:50:ASN:ND2	47:I8:81:VAL:O	2.22	0.71
26:14:1980:G:H4'	61:14:3532:HOH:O	1.91	0.71
34:15:42:TRP:O	41:85:64:ARG:NH2	2.19	0.71
45:C5:73:ARG:NH2	45:C5:81:LYS:O	2.24	0.71
26:1H:999:U:OP2	61:1H:4025:HOH:O	2.09	0.71
26:1H:1164:G:H2'	26:1H:1165:U:C6	2.25	0.71
26:1H:2334:G:O6	47:I8:74:ARG:NH2	2.23	0.71
44:F8:67:GLY:O	44:F8:69:TYR:N	2.24	0.71
45:G8:76:CYS:O	45:G8:78:ALA:N	2.21	0.71
1:1G:1300:G:O2'	1:1G:1301:U:O5'	2.08	0.71
5:42:51:VAL:HG23	5:42:52:PRO:HD3	1.73	0.71
13:4A:54:VAL:HA	13:4A:57:ARG:HB3	1.71	0.71
1:13:677:U:H3	1:13:713:G:H22	1.39	0.71
26:1H:453:C:OP1	61:1H:3925:HOH:O	2.08	0.71
26:1H:910:A:C5	37:88:13:GLN:HG3	2.26	0.71
26:1H:1287:A:N7	38:98:107:ASP:HB2	2.06	0.71
55:Q8:7:HIS:ND1	55:Q8:7:HIS:O	2.23	0.71
26:14:2378:A:H4'	39:65:23:ARG:HH11	1.56	0.71
12:3I:58:VAL:O	12:3I:65:GLU:HA	1.90	0.70
26:1H:1426:G:OP2	26:1H:1427:A:O2'	2.08	0.70
26:1H:1622:G:OP2	61:1H:4330:HOH:O	2.09	0.70
26:1H:2576:G:OP1	61:1H:3814:HOH:O	2.09	0.70
46:H8:45:ASP:OD2	46:H8:49:ARG:NH1	2.24	0.70
41:85:92:ARG:HD2	41:85:95:LEU:HD12	1.70	0.70
51:I5:14:ILE:HG12	51:I5:33:VAL:HG11	1.72	0.70
26:1H:804:A:OP2	61:1H:4481:HOH:O	2.08	0.70
1:13:1034:G:N2	1:13:1035:A:N7	2.40	0.70
1:13:1334:G:OP2	61:13:1952:HOH:O	2.09	0.70
3:2E:15:THR:HG21	3:2E:181:ASN:HA	1.73	0.70
10:1I:48:THR:HA	10:1I:62:HIS:HB3	1.73	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1H:740:U:OP2	61:1H:4503:HOH:O	2.08	0.70
26:1H:2452:C:OP1	61:1H:4400:HOH:O	2.08	0.70
4:32:31:CYS:C	4:32:33:MET:H	1.96	0.70
34:15:43:THR:H	34:15:48:MET:HE1	1.56	0.70
1:13:786:G:N7	61:13:1932:HOH:O	2.23	0.70
26:1H:392:C:OP1	61:1H:3753:HOH:O	2.07	0.70
45:G8:9:LYS:HA	45:G8:27:VAL:HG22	1.73	0.70
26:14:2287:A:N6	26:14:2344:U:H3	1.90	0.70
26:1H:330:A:H2	26:1H:1210:A:HO2'	1.39	0.70
26:1H:1253:A:C8	61:1H:3712:HOH:O	2.43	0.70
26:1H:1676:A:OP2	61:1H:3706:HOH:O	2.08	0.70
1:1G:1324:A:H4'	1:1G:1362:C:H4'	1.73	0.70
57:3L:53:G:O2'	57:3L:54:5MU:OP2	2.09	0.70
26:14:120:U:OP2	61:14:4046:HOH:O	2.09	0.70
26:14:1019:U:H2'	26:14:1020:A:C8	2.27	0.70
45:G8:100:ALA:HB1	45:G8:101:LYS:HB2	1.71	0.70
4:32:119:GLN:O	4:32:123:HIS:ND1	2.24	0.70
39:65:27:SER:HA	39:65:88:ASP:HB2	1.73	0.70
47:E5:53:MET:HG3	47:E5:59:LEU:HD23	1.72	0.70
13:4I:3:ARG:HB3	13:4I:9:ILE:HG12	1.73	0.70
15:6I:26:GLU:OE2	15:6I:77:ARG:NH1	2.23	0.70
26:1H:31:C:OP1	61:1H:3788:HOH:O	2.08	0.70
26:1H:1776:G:OP2	61:1H:3650:HOH:O	2.09	0.70
26:1H:2844:G:O6	61:1H:4140:HOH:O	2.09	0.70
34:58:96:GLU:O	34:58:98:VAL:N	2.23	0.70
13:4A:91:ARG:HB2	13:4A:98:VAL:HG12	1.73	0.70
27:1J:48:A:H4'	39:65:95:HIS:HD2	1.54	0.70
26:1H:2636:U:OP1	29:21:79:ARG:HA	1.91	0.70
8:72:17:THR:O	8:72:78:GLN:NE2	2.24	0.70
26:14:4:C:H42	26:14:2899:G:H1	1.39	0.70
26:14:602:G:HO2'	26:14:604:G:HO2'	1.36	0.70
32:59:41:MET:N	32:59:41:MET:SD	2.65	0.70
41:85:92:ARG:HH22	42:95:10:LYS:HA	1.57	0.70
1:13:1263:C:H2'	1:13:1264:C:H6	1.57	0.70
46:H8:77:ASP:OD2	46:H8:80:ARG:NH1	2.24	0.70
51:M8:12:ALA:HB3	51:M8:24:THR:HB	1.73	0.70
4:32:4:TYR:HE2	4:32:11:LEU:HD11	1.55	0.70
12:3A:52:LEU:O	12:3A:54:LYS:NZ	2.25	0.70
26:14:249:C:OP1	61:14:3516:HOH:O	2.10	0.70
26:14:1776:G:OP2	61:14:3531:HOH:O	2.08	0.70
42:95:37:VAL:HG21	42:95:57:VAL:HG12	1.74	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:D5:4:ARG:NH1	46:D5:60:GLU:OE2	2.24	0.70
39:A8:34:HIS:HB2	39:A8:36:TYR:HE1	1.56	0.70
1:1G:474:G:H2'	1:1G:475:G:H8	1.57	0.70
2:12:58:ILE:O	2:12:62:ALA:N	2.22	0.70
3:22:57:ILE:HG12	3:22:66:VAL:HG22	1.74	0.70
36:35:47:ASP:OD2	36:35:50:ARG:NH1	2.24	0.70
1:13:1023:G:H3'	1:13:1024:G:H5"	1.74	0.69
1:13:1348:U:N3	1:13:1374:A:H2	1.90	0.69
26:1H:298:G:N7	61:1H:4199:HOH:O	2.24	0.69
26:1H:376:C:OP1	61:1H:3754:HOH:O	2.10	0.69
26:1H:2287:A:H62	26:1H:2344:U:H3	1.40	0.69
26:14:1005:C:O2'	34:15:28:THR:HG21	1.92	0.69
2:1E:8:LYS:HG2	2:1E:9:GLU:H	1.57	0.69
27:16:42:C:O2'	31:41:67:LYS:HE3	1.92	0.69
55:Q8:53:PRO:HA	55:Q8:55:ALA:N	2.07	0.69
2:12:75:LYS:HA	2:12:78:GLN:HB2	1.71	0.69
26:14:2107:C:N3	26:14:2182:G:N2	2.39	0.69
26:14:2503:A:OP1	61:14:3665:HOH:O	2.09	0.69
7:6E:62:PHE:HA	7:6E:124:LEU:HD21	1.73	0.69
26:1H:270(N):G:OP2	33:61:57:ARG:NH2	2.25	0.69
26:1H:963:U:OP1	61:1H:3872:HOH:O	2.08	0.69
26:1H:1803:A:O2'	28:11:259:THR:HG21	1.92	0.69
29:21:77:ILE:O	29:21:79:ARG:N	2.24	0.69
31:41:97:ASP:O	31:41:100:TRP:N	2.26	0.69
44:F8:3:THR:HA	44:F8:6:ASP:OD2	1.92	0.69
1:1G:6:G:O2'	1:1G:7:G:H5'	1.92	0.69
1:1G:353:A:H5'	1:1G:353:A:H8	1.57	0.69
13:4A:82:MET:SD	13:4A:83:ASP:N	2.64	0.69
26:14:1416:G:O2'	26:14:1417:C:O5'	2.09	0.69
29:29:3:GLY:HA3	29:29:81:ILE:HD12	1.75	0.69
30:39:53:THR:HG23	30:39:55:GLY:H	1.57	0.69
27:16:8:U:N3	27:16:112:G:O6	2.15	0.69
40:B8:111:ARG:HD3	40:B8:111:ARG:H	1.56	0.69
45:G8:76:CYS:HB2	45:G8:82:PRO:HD3	1.74	0.69
55:Q8:37:SER:HA	55:Q8:39:LYS:O	1.93	0.69
26:14:654(D):G:H22	26:14:654(Q):C:H42	1.38	0.69
48:F5:87:PRO:O	48:F5:91:LYS:N	2.22	0.69
1:13:538:G:H5"	12:3I:114:LYS:HB2	1.73	0.69
11:2I:57:THR:HG22	11:2I:59:TYR:H	1.57	0.69
55:Q8:34:TRP:C	55:Q8:34:TRP:CD1	2.69	0.69
1:1G:458:C:N3	1:1G:474:G:N2	2.39	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:14:2057:A:OP2	61:14:4031:HOH:O	2.10	0.69
42:95:67:GLY:O	42:95:88:ARG:HD2	1.92	0.69
7:6E:155:ARG:O	7:6E:155:ARG:NH2	2.26	0.69
26:1H:839:U:OP2	61:1H:3905:HOH:O	2.08	0.69
26:1H:1021:A:H62	26:1H:1141:U:H3	1.40	0.69
26:1H:1062:G:H2'	26:1H:1063:G:C8	2.28	0.69
39:A8:83:LYS:HE2	39:A8:84:GLN:HG2	1.73	0.69
1:1G:1014:A:H4'	19:AA:14:HIS:CE1	2.27	0.69
26:14:607:U:H3	26:14:621:A:H2	1.38	0.69
47:E5:36:ILE:HD11	47:E5:39:ARG:HG2	1.74	0.69
26:1H:2212:A:H1'	26:1H:2215:G:C5	2.26	0.69
30:31:8:GLN:H	30:31:8:GLN:CD	1.99	0.69
5:42:101:ILE:HD11	5:42:119:LEU:HD23	1.74	0.69
26:14:2296:U:OP2	39:65:9:ARG:NH1	2.20	0.69
52:J5:49:CYS:SG	52:J5:50:GLY:N	2.65	0.69
4:3E:26:CYS:HA	4:3E:31:CYS:HB2	1.73	0.69
5:4E:153:LYS:HD3	5:4E:154:GLY:H	1.57	0.69
26:1H:10:G:O2'	26:1H:2801:A:N3	2.26	0.69
26:1H:860:U:C5	26:1H:917:A:H2	2.11	0.69
26:1H:1619:G:N7	61:1H:3960:HOH:O	2.25	0.69
39:A8:93:LYS:HG2	39:A8:95:HIS:HB2	1.74	0.69
43:E8:1:MET:HE3	43:E8:62:HIS:HB3	1.75	0.69
1:1G:673:G:H2'	1:1G:674:G:C8	2.28	0.69
1:1G:1004:A:OP1	1:1G:1024:G:N1	2.24	0.69
1:1G:1095:U:OP1	1:1G:1108:G:N1	2.26	0.69
26:14:1141:U:O2'	26:14:1142:U:OP2	2.11	0.69
26:14:1298:C:OP2	61:14:3522:HOH:O	2.11	0.69
26:14:2420:C:N4	55:M5:31:HIS:O	2.26	0.69
26:14:2448:A:OP1	61:14:3703:HOH:O	2.11	0.69
26:14:2652:C:H42	26:14:2668:G:H1	1.39	0.69
37:45:20:ALA:HA	37:45:99:PRO:HG2	1.74	0.69
1:13:1502:A:H2	1:13:1505:G:N1	1.90	0.69
26:1H:249:C:OP1	61:1H:3656:HOH:O	2.09	0.69
26:1H:1226:G:OP1	42:D8:69:LYS:NZ	2.16	0.69
26:1H:2027:G:N7	61:1H:4099:HOH:O	2.24	0.69
41:C8:69:CYS:HG	41:C8:79:PHE:HD2	1.40	0.69
49:K8:42:GLY:O	49:K8:44:LEU:N	2.25	0.69
1:1G:973:G:O3'	14:5A:41:ARG:NH2	2.26	0.69
1:1G:1048:G:H1	1:1G:1209:C:H42	1.40	0.69
56:1L:37:MIA:H112	56:1L:38:A:H1'	1.73	0.69
26:14:140:A:H8	26:14:1408:C:HO2'	1.41	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:14:330:A:H2	26:14:1210:A:HO2'	1.41	0.69
26:14:259:G:N2	26:14:621:A:H8	1.91	0.69
25:4K:13:A:O2'	25:4K:14:A:OP1	2.11	0.68
26:1H:635:C:O2'	26:1H:639:U:OP1	2.10	0.68
26:1H:770:G:OP2	61:1H:4379:HOH:O	2.11	0.68
31:41:65:GLY:HA2	51:M8:7:PRO:HG2	1.74	0.68
1:1G:975:A:H4'	1:1G:976:G:H5"	1.76	0.68
26:14:2153:G:N2	26:14:2154:G:O6	2.26	0.68
26:14:2693:A:H2'	26:14:2694:G:H8	1.57	0.68
42:95:48:GLY:HA3	42:95:51:VAL:C	2.18	0.68
42:95:62:LEU:HD23	42:95:93:GLU:HG2	1.75	0.68
26:1H:399:G:OP2	61:1H:4086:HOH:O	2.10	0.68
26:1H:1330:C:OP1	61:1H:3990:HOH:O	2.11	0.68
26:1H:1899:G:N2	26:1H:1902:C:H5	1.92	0.68
26:1H:2598:A:OP1	61:1H:3647:HOH:O	2.11	0.68
28:11:182:LEU:H	28:11:272:ALA:HB3	1.58	0.68
26:14:19:C:H2'	26:14:20:C:H6	1.57	0.68
26:14:2017:U:OP1	61:14:3673:HOH:O	2.12	0.68
32:59:159:GLU:O	32:59:163:TYR:OH	2.10	0.68
37:45:26:TYR:O	37:45:28:ALA:N	2.25	0.68
45:C5:29:GLU:OE1	45:C5:29:GLU:N	2.26	0.68
3:2E:77:ILE:HA	3:2E:84:ILE:HD12	1.75	0.68
26:14:1772:G:OP1	61:14:3567:HOH:O	2.09	0.68
26:14:2228:G:OP2	28:19:263:ARG:NH2	2.26	0.68
35:25:73:ASP:OD2	40:75:32:TYR:OH	2.09	0.68
1:13:588:G:OP2	61:13:1969:HOH:O	2.10	0.68
1:13:963:G:H21	10:1I:55:LYS:HZ1	1.42	0.68
1:13:1178:G:H5"	9:8E:93:ARG:NH2	2.09	0.68
26:1H:1221:C:H2'	26:1H:1222:C:H6	1.58	0.68
39:A8:89:ARG:HG2	39:A8:89:ARG:O	1.93	0.68
1:13:376:G:H5"	16:7I:5:ARG:HD2	1.75	0.68
26:1H:399:G:OP2	61:1H:4084:HOH:O	2.10	0.68
26:1H:547:A:H2'	26:1H:548:A:C8	2.29	0.68
1:1G:643:C:O2'	8:72:132:GLU:OE1	2.08	0.68
1:1G:1177:G:O2'	1:1G:1178:G:O4'	2.11	0.68
42:95:35:LEU:O	42:95:37:VAL:HG22	1.93	0.68
45:C5:62:GLU:CD	45:C5:63:LYS:H	2.01	0.68
1:13:1348:U:H3	1:13:1374:A:H2	1.42	0.68
26:1H:2032:G:H21	29:21:146:THR:CG2	2.05	0.68
32:51:153:LYS:HE2	32:51:153:LYS:H	1.59	0.68
40:B8:64:ARG:HB2	40:B8:73:GLU:HG2	1.76	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:C8:92:ARG:HA	41:C8:95:LEU:HB3	1.75	0.68
1:1G:560:U:O2'	1:1G:561:U:OP2	2.10	0.68
26:14:882:G:H22	26:14:894:C:H42	1.40	0.68
26:1H:1665:A:N6	61:1H:4131:HOH:O	2.25	0.68
2:12:178:ARG:NH1	2:12:196:LEU:O	2.27	0.68
56:1L:29:G:H4'	56:1L:29:G:OP1	1.92	0.68
26:14:1249:U:OP1	61:14:4028:HOH:O	2.11	0.68
10:1I:58:ASP:OD1	61:1I:201:HOH:O	2.12	0.68
11:2I:22:HIS:HB3	11:2I:29:ILE:HG23	1.75	0.68
13:4I:15:VAL:O	13:4I:19:LEU:HD22	1.94	0.68
29:21:152:LYS:HD3	34:58:77:GLY:HA3	1.76	0.68
40:75:24:PRO:HA	40:75:49:VAL:HG23	1.75	0.68
41:85:88:ILE:HG22	41:85:90:VAL:HG23	1.75	0.68
1:13:342:C:H2'	1:13:343:U:O4'	1.94	0.68
1:13:673:G:H2'	1:13:674:G:C8	2.27	0.68
14:5I:18:VAL:O	61:5I:201:HOH:O	2.11	0.68
26:1H:792:G:H5"	26:1H:793:A:H5'	1.75	0.68
26:1H:2127:G:H22	26:1H:2162:G:H1'	1.59	0.68
26:1H:2406:U:OP1	61:1H:3728:HOH:O	2.11	0.68
26:1H:2837:G:N7	61:1H:4290:HOH:O	2.26	0.68
29:21:64:LYS:O	29:21:70:ALA:HB2	1.94	0.68
35:68:47:ILE:HD13	35:68:48:PRO:HD2	1.74	0.68
55:Q8:34:TRP:CD1	55:Q8:36:LYS:H	2.12	0.68
1:13:376:G:O3'	16:7I:5:ARG:NH1	2.23	0.68
2:1E:165:VAL:HG23	2:1E:166:ASP:H	1.59	0.68
24:3K:7:A:N6	24:3K:49:C:N3	2.42	0.68
26:1H:270(L):U:O2	33:61:50:ARG:HG2	1.94	0.68
26:1H:1509:C:H3'	26:1H:1510:A:H5"	1.76	0.68
26:1H:1843:C:H5'	28:11:253:GLN:OE1	1.93	0.68
27:16:42:C:O3'	31:41:67:LYS:NZ	2.27	0.68
32:51:54:ARG:HD3	32:51:65:HIS:ND1	2.09	0.68
39:A8:26:LEU:HD12	39:A8:39:ILE:HD11	1.76	0.68
55:Q8:54:GLU:O	55:Q8:56:GLU:N	2.27	0.68
1:1G:1288:A:N3	1:1G:1352:C:O2'	2.26	0.68
7:62:72:ARG:HG2	7:62:142:GLU:OE2	1.93	0.68
26:14:607:U:OP1	30:39:102:PRO:HA	1.93	0.68
30:39:20:LEU:HG	30:39:199:TRP:HH2	1.59	0.68
1:13:1348:U:H2'	1:13:1349:A:H8	1.58	0.67
26:1H:330:A:O2'	26:1H:331:A:H8	1.76	0.67
26:1H:574:C:OP1	61:1H:3808:HOH:O	2.12	0.67
26:14:1664:A:OP2	61:14:3610:HOH:O	2.12	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:14:2415:G:H4'	36:35:67:MET:N	2.08	0.67
38:55:38:VAL:HG12	38:55:42:LYS:HD2	1.76	0.67
1:13:177:C:OP1	20:BI:65:LYS:NZ	2.22	0.67
26:1H:459:U:H5"	54:P8:40:TRP:CD2	2.29	0.67
26:1H:2864:G:OP1	40:B8:119:LYS:HD2	1.94	0.67
28:11:17:THR:HG22	28:11:204:ILE:HA	1.76	0.67
33:61:132:PRO:O	33:61:133:HIS:ND1	2.27	0.67
50:L8:26:LEU:HB2	50:L8:28:LEU:HD12	1.74	0.67
1:1G:371:G:H1	1:1G:390:C:H42	1.41	0.67
4:32:4:TYR:CE2	4:32:11:LEU:HD11	2.29	0.67
26:14:1864:U:OP1	26:14:2410:G:O2'	2.12	0.67
26:14:2801:A:H5"	26:14:2895:U:H4'	1.75	0.67
26:1H:1434:A:H61	26:1H:1558:A:N6	1.92	0.67
1:1G:1194:U:H2'	1:1G:1195:C:H6	1.59	0.67
1:1G:1326:C:OP1	21:1B:12:LYS:NZ	2.26	0.67
1:13:271:C:H2'	1:13:272:C:H6	1.60	0.67
26:1H:392:C:OP1	61:1H:3752:HOH:O	2.13	0.67
26:1H:1309:G:H4'	54:P8:7:PRO:HB2	1.76	0.67
26:1H:2150:U:H2'	26:1H:2151:G:C8	2.29	0.67
26:14:34:C:O2'	26:14:35:G:OP1	2.12	0.67
26:14:1141:U:H3'	34:15:63:THR:HG21	1.76	0.67
26:14:1716:U:H2'	26:14:1717:G:H8	1.59	0.67
30:39:157:VAL:HB	30:39:194:MET:HB3	1.76	0.67
31:49:76:SER:OG	31:49:84:LYS:N	2.27	0.67
33:69:65:ALA:O	33:69:69:LYS:N	2.27	0.67
43:A5:106:ILE:O	43:A5:106:ILE:HG13	1.93	0.67
1:13:265:G:N2	1:13:267:C:H5'	2.08	0.67
1:13:736:C:H2'	1:13:737:A:C8	2.29	0.67
12:3I:42:THR:HG22	12:3I:54:LYS:HD2	1.75	0.67
18:9I:53:ARG:HH21	18:9I:60:ALA:N	1.93	0.67
26:1H:583:G:OP2	41:C8:10:ARG:NH1	2.27	0.67
26:1H:900:A:H3'	26:1H:901:A:H8	1.58	0.67
26:1H:903:C:O2'	46:H8:169:GLU:OE1	2.13	0.67
42:D8:44:LYS:HZ3	42:D8:44:LYS:HA	1.60	0.67
1:1G:555:C:H2'	1:1G:556:C:C6	2.29	0.67
26:14:1593:G:H2'	26:14:1594:G:C8	2.29	0.67
32:59:152:ARG:HD2	32:59:153:LYS:HG3	1.76	0.67
37:45:35:VAL:HG12	37:45:36:ALA:H	1.60	0.67
55:M5:40:GLU:H	55:M5:43:GLN:HG3	1.58	0.67
1:13:601:C:H2'	1:13:602:A:C8	2.29	0.67
7:6E:16:LEU:HD13	9:8E:44:VAL:HG22	1.77	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1H:1520:U:H2'	26:1H:1521:G:O4'	1.94	0.67
26:1H:1534:G:H22	26:1H:1538:G:H22	1.42	0.67
37:88:86:GLY:HA3	37:88:87:LYS:HD3	1.77	0.67
2:12:5:ILE:HA	2:12:221:LEU:HD21	1.74	0.67
26:14:2414:G:N2	36:35:67:MET:HE1	2.08	0.67
28:19:148:GLU:HB2	28:19:151:LYS:HE3	1.76	0.67
45:C5:48:ALA:HB3	45:C5:59:GLY:C	2.20	0.67
1:13:838:G:H1	1:13:848:C:N4	1.93	0.67
1:13:1015:A:H2'	1:13:1016:A:C8	2.30	0.67
1:13:1318:A:H5"	19:AI:10:PHE:CD2	2.30	0.67
26:1H:138:G:N2	44:F8:44:GLU:OE2	2.18	0.67
38:98:20:LEU:HD21	38:98:40:LYS:HD3	1.77	0.67
57:3L:3:C:H2'	57:3L:4:C:O4'	1.95	0.67
26:14:196:A:O2'	26:14:805:G:O6	2.10	0.67
26:1H:2588:G:OP1	61:1H:3944:HOH:O	2.13	0.67
55:Q8:57:ARG:HD3	55:Q8:57:ARG:N	2.10	0.67
1:1G:179:A:H2'	1:1G:180:U:C6	2.29	0.67
1:1G:1154:G:H2'	1:1G:1155:G:C8	2.29	0.67
26:14:1828:G:OP2	61:14:3524:HOH:O	2.13	0.67
26:1H:252:G:OP2	36:78:50:ARG:NH1	2.27	0.67
26:1H:422:A:OP2	61:1H:4487:HOH:O	2.12	0.67
26:1H:860:U:H5	26:1H:917:A:H2	1.43	0.67
26:1H:2448:A:N1	61:1H:3878:HOH:O	2.28	0.67
29:21:105:THR:OG1	29:21:199:ARG:NH2	2.27	0.67
29:21:116:VAL:O	29:21:117:MET:HB3	1.94	0.67
1:1G:1213:A:N6	1:1G:1215:G:N3	2.43	0.67
1:1G:1343:G:H2'	1:1G:1344:C:C6	2.29	0.67
5:42:71:LEU:HD21	5:42:115:VAL:HG22	1.75	0.67
5:42:81:GLU:HB3	5:42:90:VAL:HG13	1.75	0.67
20:BA:87:LYS:O	20:BA:91:LEU:HG	1.95	0.67
26:14:2528:U:O3'	26:14:2529:G:N2	2.23	0.67
4:3E:83:SER:HA	4:3E:89:THR:HG23	1.75	0.67
19:AI:40:ILE:HD11	19:AI:62:ILE:HG23	1.77	0.67
19:AI:41:VAL:HB	19:AI:42:PRO:HA	1.76	0.67
26:1H:322:A:P	30:31:168:ARG:HH21	2.18	0.67
26:1H:2053:G:OP2	61:1H:3810:HOH:O	2.13	0.67
55:Q8:42:ARG:HG2	55:Q8:42:ARG:O	1.95	0.67
24:3K:35:A:H2'	24:3K:36:A:H8	1.59	0.66
26:1H:879:G:N1	26:1H:898:C:N3	2.43	0.66
26:1H:963:U:OP1	61:1H:3874:HOH:O	2.13	0.66
26:1H:1992:G:OP2	61:1H:4128:HOH:O	2.14	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1H:2788:C:O2'	26:1H:2809:A:N3	2.27	0.66
28:11:228:PRO:O	61:11:405:HOH:O	2.12	0.66
29:21:38:THR:HG23	29:21:41:LYS:H	1.60	0.66
34:58:96:GLU:C	34:58:98:VAL:H	2.02	0.66
1:1G:1218:C:OP2	14:5A:9:LYS:NZ	2.25	0.66
2:12:8:LYS:HE2	2:12:213:LEU:HD21	1.75	0.66
5:42:61:TYR:HA	5:42:64:ARG:HB2	1.77	0.66
57:3L:26:A:H61	57:3L:44:G:H1	1.43	0.66
26:14:323:G:HO2'	26:14:1205:U:H3	1.41	0.66
51:I5:22:ILE:HG12	51:I5:23:GLU:N	2.10	0.66
26:1H:1664:A:OP1	61:1H:4466:HOH:O	2.13	0.66
26:1H:1676:A:OP2	61:1H:3702:HOH:O	2.11	0.66
26:1H:2099:U:N3	26:1H:2190:G:O6	2.19	0.66
3:22:59:ARG:HG2	3:22:64:VAL:HG23	1.77	0.66
26:14:2033:A:H8	61:14:4058:HOH:O	1.78	0.66
2:1E:100:GLY:O	2:1E:104:ASN:N	2.26	0.66
3:2E:40:ARG:HH11	3:2E:40:ARG:HG3	1.60	0.66
26:1H:1102:C:H2'	26:1H:1103:A:C8	2.30	0.66
48:J8:91:LYS:O	48:J8:94:LEU:N	2.27	0.66
29:29:89:ASP:OD1	29:29:90:THR:N	2.28	0.66
1:1G:983:A:N1	1:1G:1222:G:N2	2.43	0.66
1:1G:1274:G:H2'	1:1G:1275:A:H8	1.60	0.66
26:14:1035:U:H2'	26:14:1036:G:C8	2.29	0.66
28:19:255:LYS:CE	28:19:255:LYS:H	2.08	0.66
26:1H:563:G:OP2	61:1H:3631:HOH:O	2.13	0.66
26:1H:2317:C:H2'	26:1H:2318:G:H5'	1.77	0.66
1:1G:261:U:OP2	20:BA:79:ARG:NH2	2.28	0.66
1:1G:1500:A:OP1	61:1G:1760:HOH:O	2.14	0.66
4:32:31:CYS:C	4:32:33:MET:N	2.54	0.66
8:72:114:THR:HG23	8:72:116:LYS:H	1.61	0.66
57:3L:76:A:H8	26:14:2394:C:H42	1.43	0.66
26:14:1061:U:H4'	26:14:1070:A:H1'	1.76	0.66
26:14:2016:U:O2	52:J5:7:PRO:HG2	1.96	0.66
26:1H:302:C:H2'	26:1H:303:U:C6	2.31	0.66
26:1H:1049:C:H2'	26:1H:1050:A:H5'	1.76	0.66
26:1H:2317:C:C2'	26:1H:2318:G:H5'	2.26	0.66
26:1H:2327:A:H2'	26:1H:2328:A:C8	2.31	0.66
30:31:167:ALA:HB1	30:31:173:VAL:HG11	1.77	0.66
1:1G:222:U:H2'	1:1G:223:U:C6	2.31	0.66
26:14:2115:G:O2'	26:14:2171:A:N6	2.28	0.66
27:16:87:G:N2	27:16:89(A):A:OP2	2.28	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:9A:36:ASN:O	18:9A:36:ASN:ND2	2.19	0.66
26:14:741:G:OP1	61:14:3555:HOH:O	2.13	0.66
26:14:1434:A:H61	26:14:1558:A:N6	1.93	0.66
46:D5:53:ILE:HG22	46:D5:71:VAL:HG13	1.75	0.66
26:1H:1670:C:OP1	61:1H:3662:HOH:O	2.13	0.66
26:1H:1900:A:H5'	26:1H:1900:A:C8	2.31	0.66
26:1H:2061:G:OP2	61:1H:3626:HOH:O	2.12	0.66
31:41:66:GLN:OE1	31:41:98:ARG:NH1	2.28	0.66
51:M8:52:THR:OG1	51:M8:53:GLU:N	2.28	0.66
1:1G:1131:G:H2'	1:1G:1132:C:H6	1.58	0.66
3:22:21:ARG:HB3	3:22:21:ARG:NH1	2.10	0.66
26:14:1024:G:H3'	26:14:1025:G:H5"	1.77	0.66
26:14:2062:A:OP2	61:14:3792:HOH:O	2.14	0.66
26:14:2818:G:OP2	38:55:42:LYS:NZ	2.28	0.66
37:45:22:LYS:N	37:45:23:GLY:HA3	2.09	0.66
39:65:50:SER:O	39:65:76:LYS:NZ	2.29	0.66
40:75:26:ASP:O	40:75:49:VAL:HG22	1.94	0.66
1:13:1297:C:OP1	13:4I:13:LYS:NZ	2.28	0.66
26:1H:563:G:OP2	61:1H:3632:HOH:O	2.14	0.66
26:1H:1210:A:H5'	26:1H:1210:A:H8	1.61	0.66
41:C8:69:CYS:SG	41:C8:79:PHE:HD2	2.18	0.66
45:G8:95:LYS:HB3	45:G8:97:ARG:HH12	1.61	0.66
1:1G:742:G:OP2	15:6A:35:ARG:NH2	2.27	0.66
1:1G:1235:U:O2'	1:1G:1305:G:O5'	2.13	0.66
1:1G:1478:C:H2'	1:1G:1479:C:H6	1.61	0.66
2:12:67:THR:HG21	2:12:155:LEU:HG	1.77	0.66
26:14:2074:U:OP1	61:14:3505:HOH:O	2.12	0.66
39:65:84:GLN:HA	39:65:110:LEU:HD12	1.77	0.66
1:13:674:G:H2'	1:13:675:A:H8	1.60	0.66
26:1H:646:A:H2'	26:1H:647:G:O4'	1.96	0.66
26:1H:1021:A:H8	26:1H:1022:G:H5"	1.59	0.66
26:1H:1899:G:H1	26:1H:1902:C:H41	1.44	0.66
28:11:96:HIS:CE1	28:11:102:LYS:HE2	2.30	0.66
3:22:3:ASN:HD22	3:22:3:ASN:H	1.44	0.66
9:82:24:GLY:HA2	9:82:59:PHE:O	1.96	0.66
20:BA:51:GLU:HA	20:BA:54:LYS:HB3	1.77	0.66
26:14:120:U:OP2	61:14:4042:HOH:O	2.13	0.66
26:14:1859:A:N6	26:14:1883:G:O2'	2.29	0.66
28:19:255:LYS:H	28:19:255:LYS:NZ	1.94	0.66
3:2E:32:LEU:HD13	3:2E:59:ARG:HD3	1.78	0.65
17:8I:68:ARG:H	17:8I:70:ARG:HH11	1.43	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1H:270(R):G:O6	61:1H:4355:HOH:O	2.11	0.65
26:1H:2292:C:OP1	39:A8:17:ARG:NH2	2.26	0.65
26:1H:2311:A:H1'	31:41:88:ILE:HD13	1.77	0.65
26:1H:2347:C:OP1	53:O8:39:TYR:OH	2.14	0.65
26:1H:2429:G:O6	36:78:61:ARG:NH1	2.28	0.65
32:51:107:VAL:HB	32:51:152:ARG:HG2	1.78	0.65
38:98:55:ALA:HA	38:98:80:PHE:HE1	1.60	0.65
1:1G:1255:G:OP1	10:1A:45:ARG:NH1	2.29	0.65
26:14:1022:G:H22	26:14:1142(A):A:H2	1.42	0.65
26:14:1112:G:H5'	32:59:3:ARG:HB3	1.78	0.65
26:14:1639:U:OP2	61:14:3519:HOH:O	2.13	0.65
39:65:34:HIS:CE1	39:65:54:LEU:HD13	2.30	0.65
12:3I:91:LYS:HG3	12:3I:91:LYS:O	1.96	0.65
20:BI:53:LEU:HA	20:BI:56:MET:HB3	1.78	0.65
26:1H:676:A:H8	26:1H:2069:G:H21	1.44	0.65
26:1H:1156:A:OP2	61:1H:3820:HOH:O	2.13	0.65
33:61:31:LEU:HD21	33:61:38:LEU:HG	1.76	0.65
41:C8:65:ILE:HD11	41:C8:95:LEU:HD22	1.78	0.65
1:1G:619:U:C6	4:32:135:LEU:HD21	2.31	0.65
1:1G:838:G:N2	1:1G:849:C:N3	2.44	0.65
1:1G:976:G:H5'	1:1G:1358:U:O2'	1.96	0.65
1:1G:1245:A:H61	1:1G:1292:U:H3	1.44	0.65
13:4A:13:LYS:HA	13:4A:44:ARG:NH1	2.09	0.65
23:2L:24:C:H2'	23:2L:25:U:C6	2.32	0.65
25:4L:12:A:H4'	25:4L:13:A:OP2	1.95	0.65
26:14:7:G:H2'	26:14:8:A:C8	2.31	0.65
26:14:1225:C:H4'	42:95:85:LYS:HB2	1.78	0.65
30:39:122:LYS:HB3	30:39:191:ARG:HB2	1.78	0.65
1:13:445:G:H1	1:13:489:C:H42	1.44	0.65
5:4E:144:THR:OG1	5:4E:147:ASP:OD1	2.13	0.65
6:5E:69:GLU:O	6:5E:72:VAL:HG12	1.96	0.65
9:8E:112:LYS:HA	9:8E:119:ALA:HB2	1.77	0.65
26:1H:878:A:N6	26:1H:899:A:O2'	2.28	0.65
26:14:2010:G:N7	61:14:3645:HOH:O	2.29	0.65
27:1J:70:C:H2'	27:1J:71:C:H6	1.61	0.65
1:13:1145:C:H4'	1:13:1146:A:H5'	1.77	0.65
24:3K:5:G:H1	24:3K:68:C:H42	1.44	0.65
26:1H:848:G:H2'	26:1H:849:A:C8	2.31	0.65
26:1H:1332:G:N2	26:1H:1610:A:C8	2.65	0.65
41:C8:94:ASN:O	41:C8:96:ALA:HB2	1.95	0.65
1:1G:962:C:H42	1:1G:973:G:H1	1.43	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:52:7:ASN:HD22	18:9A:76:LEU:HD11	1.61	0.65
10:1A:3:LYS:N	10:1A:74:ILE:O	2.28	0.65
13:4A:37:THR:HG21	13:4A:56:LEU:HD23	1.78	0.65
61:14:3840:HOH:O	30:39:55:GLY:HA2	1.97	0.65
32:59:144:VAL:O	32:59:148:ILE:HG12	1.97	0.65
3:2E:74:GLY:HA2	3:2E:77:ILE:HB	1.79	0.65
26:1H:443:A:H1'	26:1H:1201:C:O4'	1.96	0.65
26:1H:1332:G:OP1	61:1H:3971:HOH:O	2.14	0.65
26:1H:1533:C:H3'	26:1H:1534:G:H5"	1.76	0.65
28:11:237:GLU:OE1	61:11:409:HOH:O	2.14	0.65
1:1G:1054:C:O2'	1:1G:1055:A:O5'	2.15	0.65
26:14:2250:G:C6	37:45:82:ARG:HD2	2.32	0.65
26:14:2572:A:OP1	26:14:2574:G:O2'	2.15	0.65
29:29:11:MET:SD	29:29:24:THR:HG22	2.36	0.65
30:39:18:ARG:HG2	30:39:19:GLU:H	1.61	0.65
37:45:75:THR:HA	37:45:89:ASN:HA	1.77	0.65
1:13:559:A:OP1	5:4E:126:ARG:NH2	2.30	0.65
1:13:612:C:O2	1:13:629:G:N2	2.29	0.65
1:13:631:G:H2'	1:13:632:A:N3	2.10	0.65
2:1E:84:GLU:HB3	2:1E:219:VAL:HG21	1.79	0.65
4:3E:150:GLU:OE1	4:3E:150:GLU:N	2.29	0.65
26:1H:1557:C:OP2	26:1H:1558:A:O2'	2.08	0.65
1:1G:157:G:H1	1:1G:164:U:H3	1.42	0.65
26:14:1426:G:OP2	26:14:1427:A:O2'	2.15	0.65
26:14:1636:C:OP2	61:14:3629:HOH:O	2.15	0.65
26:14:2528:U:O2'	26:14:2530:A:OP1	2.10	0.65
34:15:34:LEU:HD21	34:15:120:LEU:HD13	1.79	0.65
43:A5:73:ALA:HB3	43:A5:106:ILE:HG12	1.79	0.65
1:13:1000:A:H2'	1:13:1001:G:C8	2.32	0.65
26:1H:193:U:OP1	61:1H:4178:HOH:O	2.13	0.65
41:C8:50:ARG:NH1	42:D8:72:VAL:HG12	2.12	0.65
43:E8:27:LYS:HB3	43:E8:31:GLU:HG3	1.77	0.65
4:32:60:GLU:OE2	4:32:199:ASN:N	2.29	0.65
7:62:79:ARG:HE	7:62:84:ASN:HB3	1.60	0.65
26:14:1154:G:OP1	41:85:58:ARG:HD3	1.97	0.65
26:1H:860:U:C5	26:1H:917:A:C2	2.85	0.65
26:1H:997:G:OP1	41:C8:92:ARG:HB2	1.97	0.65
26:1H:1406:U:H2'	26:1H:1407:C:C6	2.31	0.65
41:C8:92:ARG:C	41:C8:94:ASN:H	2.05	0.65
42:D8:65:GLY:HA3	42:D8:91:TYR:CE1	2.31	0.65
43:E8:95:ILE:O	43:E8:95:ILE:HG13	1.96	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:H8:163:LEU:HB3	46:H8:165:VAL:H	1.61	0.65
1:1G:114:U:H2'	1:1G:115:G:C8	2.31	0.65
1:1G:682:G:O6	61:1G:1773:HOH:O	2.13	0.65
1:1G:793:U:O2	1:1G:1516:G:H4'	1.97	0.65
55:M5:34:TRP:CG	55:M5:35:GLN:N	2.58	0.65
1:13:57:G:H2'	1:13:58:C:C6	2.31	0.65
26:1H:1515:C:H2'	26:1H:1516:U:H6	1.61	0.65
26:1H:2583:G:OP2	61:1H:3822:HOH:O	2.15	0.65
36:78:15:ARG:HB2	36:78:16:ARG:HB2	1.79	0.65
41:C8:49:HIS:HA	41:C8:52:ARG:HB3	1.79	0.65
57:3L:72:C:H3'	57:3L:73:A:H5"	1.78	0.65
26:14:848:G:H2'	26:14:849:A:C8	2.32	0.65
26:14:1485:G:H1	26:14:1504:C:H42	1.43	0.65
26:14:2292:C:OP1	39:65:17:ARG:NH2	2.30	0.65
26:14:2315:G:OP1	31:49:36:LYS:NZ	2.28	0.65
39:65:10:ARG:O	39:65:14:VAL:HG22	1.96	0.65
20:BI:73:HIS:HB3	20:BI:74:LYS:HG3	1.77	0.65
26:1H:607:U:N3	26:1H:621:A:H2	1.92	0.65
26:1H:2862:G:H2'	26:1H:2863:C:H6	1.61	0.65
26:1H:2865:U:O4	61:1H:4194:HOH:O	2.10	0.65
37:88:133:ARG:O	37:88:134:ARG:HB2	1.97	0.65
46:H8:120:ILE:HG13	46:H8:170:THR:HG22	1.78	0.65
1:1G:222:U:H2'	1:1G:223:U:H6	1.62	0.65
1:1G:1268:A:H2'	1:1G:1269:A:C8	2.32	0.65
2:12:19:HIS:HE1	2:12:206:ASP:HB2	1.62	0.65
4:3E:160:GLN:NE2	4:3E:160:GLN:O	2.30	0.64
5:4E:45:PHE:CE2	5:4E:47:LYS:HD2	2.32	0.64
10:1I:40:LEU:HB2	10:1I:69:ASN:HB2	1.79	0.64
26:1H:945:A:P	61:1H:4167:HOH:O	2.49	0.64
26:1H:1899:G:H22	26:1H:1902:C:H41	1.45	0.64
52:N8:40:LYS:HE2	52:N8:47:PRO:HD2	1.78	0.64
1:1G:1286:A:C8	1:1G:1287:A:H4'	2.32	0.64
4:32:71:SER:HB3	4:32:74:GLN:HG3	1.79	0.64
26:14:195:A:H61	26:14:198:C:H3'	1.60	0.64
26:14:1188:U:O2'	26:14:1189:A:H5'	1.97	0.64
26:14:1225:C:O2'	42:95:85:LYS:N	2.30	0.64
26:14:2056:G:OP2	61:14:4035:HOH:O	2.14	0.64
26:14:2871:C:N3	61:14:3622:HOH:O	2.30	0.64
1:13:154:C:N3	1:13:168:G:N2	2.44	0.64
2:1E:33:TYR:HB2	2:1E:43:ASP:HB2	1.77	0.64
26:1H:1417:C:P	61:1H:4059:HOH:O	2.54	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1H:1784:A:OP2	61:1H:4502:HOH:O	2.14	0.64
26:1H:2051:A:OP2	61:1H:4096:HOH:O	2.14	0.64
1:1G:179:A:H2'	1:1G:180:U:H6	1.61	0.64
1:1G:452:A:O2'	1:1G:453:A:O4'	2.12	0.64
1:1G:661:G:H1	1:1G:744:C:H42	1.45	0.64
26:14:741:G:P	61:14:3555:HOH:O	2.54	0.64
26:14:796:C:H2'	26:14:797:C:C6	2.33	0.64
35:25:67:LYS:HE3	35:25:68:GLU:OE1	1.98	0.64
2:1E:212:GLN:O	2:1E:216:SER:OG	2.13	0.64
13:4I:27:LYS:HD3	13:4I:31:LYS:HZ1	1.62	0.64
26:1H:2344:U:O2'	53:O8:37:ARG:HG2	1.96	0.64
34:58:1:MET:HE2	42:D8:12:TYR:HA	1.78	0.64
55:Q8:46:ARG:CZ	55:Q8:46:ARG:HB3	2.26	0.64
8:72:120:THR:HG23	8:72:123:GLU:H	1.63	0.64
26:14:945:A:OP1	61:14:3794:HOH:O	2.15	0.64
26:14:1030:G:OP2	37:45:128:LYS:NZ	2.29	0.64
26:14:2114:A:N6	26:14:2119:A:N7	2.45	0.64
26:14:2137:C:N4	26:14:2155:G:O6	2.19	0.64
26:14:2429:G:O6	36:35:61:ARG:NH2	2.30	0.64
9:8E:50:LEU:HD23	9:8E:85:LEU:HD11	1.78	0.64
20:BI:71:THR:HG22	20:BI:72:LEU:H	1.62	0.64
26:1H:2061:G:P	61:1H:3626:HOH:O	2.55	0.64
1:1G:1002:G:N2	1:1G:1038:C:N3	2.42	0.64
9:82:42:ARG:NH1	9:82:75:ASP:OD2	2.26	0.64
11:2A:100:ALA:O	11:2A:102:GLY:N	2.30	0.64
57:3L:52:G:H1	57:3L:62:C:H42	1.45	0.64
26:14:84:A:N6	26:14:102:G:O2'	2.23	0.64
26:14:93:C:H5'	26:14:94:G:OP2	1.97	0.64
26:14:2267:A:OP2	61:14:3912:HOH:O	2.14	0.64
26:14:2748:A:H2'	26:14:2749:A:C8	2.32	0.64
7:6E:111:ARG:NH1	7:6E:113:GLU:OE2	2.27	0.64
9:8E:24:GLY:HA2	9:8E:59:PHE:O	1.97	0.64
19:AI:5:LEU:HD13	19:AI:10:PHE:CD1	2.33	0.64
26:1H:1159:U:P	50:L8:30:ARG:HH12	2.20	0.64
26:1H:1430:C:H2'	26:1H:1431:U:C6	2.32	0.64
26:1H:1434:A:H61	26:1H:1558:A:H61	1.44	0.64
32:51:4:ILE:HG13	32:51:6:ARG:NE	2.13	0.64
55:Q8:5:LYS:O	55:Q8:6:THR:OG1	2.09	0.64
5:42:80:ILE:HG13	8:72:104:ARG:HH21	1.62	0.64
26:14:1225:C:O3'	42:95:85:LYS:HA	1.97	0.64
26:14:2128:C:H42	26:14:2160:G:H1	1.44	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:5E:39:LYS:HD3	6:5E:64:GLN:HG3	1.80	0.64
9:8E:3:GLN:OE1	9:8E:20:ARG:NH1	2.30	0.64
20:BI:89:ARG:NH2	20:BI:104:LEU:HD11	2.13	0.64
26:1H:2107:C:O2	26:1H:2182:G:N2	2.22	0.64
30:31:191:ARG:HB3	30:31:191:ARG:HH11	1.62	0.64
1:1G:407:G:OP1	4:32:115:ARG:NH2	2.30	0.64
5:42:70:PRO:HB3	5:42:144:THR:HG22	1.79	0.64
48:F5:82:LEU:HD23	48:F5:82:LEU:H	1.62	0.64
1:13:686:U:O4	1:13:703:G:H1'	1.97	0.64
1:13:1007:C:N4	1:13:1022:G:H1	1.95	0.64
2:1E:141:GLU:O	2:1E:145:LEU:HB2	1.97	0.64
26:1H:1697:G:OP2	26:1H:1698:A:O2'	2.12	0.64
46:H8:125:LEU:HG	46:H8:164:ALA:HB3	1.80	0.64
1:1G:987:G:N2	1:1G:1218:C:N3	2.44	0.64
1:1G:1308:U:OP2	13:4A:101:GLN:NE2	2.29	0.64
1:1G:1385:G:H2'	1:1G:1386:G:H8	1.63	0.64
3:22:6:HIS:HB3	14:5A:49:HIS:HD2	1.61	0.64
4:32:190:ASP:HB3	4:32:192:GLU:HG3	1.80	0.64
13:4A:84:ILE:HG12	19:AA:63:THR:HG21	1.79	0.64
26:14:1060:U:H4'	26:14:1061:U:H5"	1.80	0.64
26:14:2720:U:H3	26:14:2873:A:H2	1.45	0.64
37:45:51:ARG:HG2	37:45:51:ARG:HH11	1.60	0.64
45:C5:68:HIS:HB3	45:C5:71:LYS:HG3	1.78	0.64
1:13:1314:C:N4	19:AI:4:SER:O	2.25	0.64
26:1H:111:A:H4'	49:K8:69:ARG:NH2	2.13	0.64
26:1H:2135:A:N6	26:1H:2156:G:O2'	2.30	0.64
1:1G:41:G:H2'	1:1G:42:G:C8	2.33	0.64
1:1G:362:G:O2'	12:3A:33:ARG:NH2	2.30	0.64
8:72:99:GLU:CD	8:72:100:ILE:H	2.05	0.64
26:14:987:G:O2'	26:14:1000:A:N3	2.29	0.64
26:14:1278:A:OP1	38:55:36:THR:HG22	1.98	0.64
26:14:1977:A:OP2	61:14:4014:HOH:O	2.15	0.64
1:13:1286:A:H8	1:13:1287:A:H4'	1.63	0.64
15:6I:6:GLU:HA	15:6I:9:GLN:HB2	1.80	0.64
26:1H:259:G:N2	26:1H:621:A:H8	1.96	0.64
26:1H:796:C:H2'	26:1H:797:C:C6	2.32	0.64
26:1H:1061:U:H4'	26:1H:1070:A:H1'	1.79	0.64
26:1H:1678:G:H22	26:1H:1989:G:H22	1.46	0.64
26:1H:1858:G:H8	26:1H:1858:G:OP2	1.80	0.64
33:61:73:GLU:HG3	33:61:136:VAL:HG23	1.80	0.64
41:C8:88:ILE:O	41:C8:90:VAL:N	2.27	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:F8:12:VAL:HG13	44:F8:27:THR:O	1.98	0.64
1:1G:1292:U:H2'	1:1G:1293:G:C8	2.33	0.64
3:22:141:VAL:HA	3:22:144:SER:HB3	1.79	0.64
57:3L:48:C:C5	57:3L:59:U:H1'	2.32	0.64
46:D5:27:VAL:HG12	46:D5:87:ASP:HA	1.80	0.64
1:13:405:U:O4	4:3E:2:GLY:N	2.31	0.64
19:AI:41:VAL:HG11	19:AI:67:VAL:HA	1.79	0.64
26:1H:573:G:O2'	26:1H:574:C:H3'	1.97	0.64
26:1H:1359:A:C2	26:1H:1372:U:O4	2.50	0.64
26:1H:1495:A:OP2	61:1H:4397:HOH:O	2.15	0.64
32:51:4:ILE:HB	32:51:6:ARG:HG3	1.81	0.64
37:88:66:ILE:O	37:88:104:PHE:N	2.30	0.64
56:1L:38:A:H2'	56:1L:39:PSU:H6	1.63	0.64
26:14:38:A:H1'	30:39:48:THR:HB	1.80	0.64
26:14:1676:A:OP2	61:14:3536:HOH:O	2.14	0.64
1:13:1133:G:H2'	1:13:1134:G:C8	2.33	0.63
26:1H:1009:A:OP2	61:1H:4205:HOH:O	2.16	0.63
26:1H:2584:U:H2'	26:1H:2585:U:H2'	1.79	0.63
1:1G:1298:C:O2'	1:1G:1299:A:OP2	2.16	0.63
2:12:9:GLU:HB2	2:12:217:ARG:NH2	2.13	0.63
26:14:123:G:N2	26:14:128:C:O2	2.19	0.63
27:1J:9:G:P	39:65:25:ARG:HH22	2.21	0.63
28:19:32:SER:O	28:19:32:SER:OG	2.16	0.63
33:61:9:LEU:HD21	33:61:35:LEU:HD12	1.79	0.63
1:1G:1305:G:H22	1:1G:1331:G:C2'	2.11	0.63
33:69:38:LEU:HD12	33:69:38:LEU:H	1.63	0.63
1:13:233:C:H2'	1:13:234:C:H6	1.64	0.63
1:13:1372:U:H5"	9:8E:71:SER:HB2	1.81	0.63
10:1I:6:ILE:HG22	10:1I:98:ILE:HG13	1.79	0.63
13:4I:27:LYS:HA	13:4I:31:LYS:HZ3	1.62	0.63
19:AI:6:LYS:O	19:AI:7:LYS:HB3	1.98	0.63
24:3K:19:G:O2'	24:3K:57:G:N3	2.31	0.63
26:1H:550:G:O2'	26:1H:1220:A:N3	2.30	0.63
26:1H:1479:G:N7	26:1H:1510:A:N6	2.46	0.63
26:1H:2688:U:H5	26:1H:2720:U:OP2	1.81	0.63
28:11:72:LYS:NZ	28:11:99:ASP:OD2	2.26	0.63
26:14:2572:A:C8	29:29:144:ARG:HD2	2.33	0.63
49:G5:47:ASN:C	49:G5:49:LYS:H	2.06	0.63
1:13:412:A:H4'	1:13:413:G:O5'	1.98	0.63
17:8I:67:LYS:HA	17:8I:70:ARG:NH1	2.11	0.63
26:1H:422:A:P	61:1H:4487:HOH:O	2.55	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:78:19:VAL:HB	36:78:20:GLY:HA2	1.79	0.63
36:78:19:VAL:HG12	36:78:21:ARG:H	1.63	0.63
42:D8:21:ARG:HG2	42:D8:91:TYR:HE2	1.62	0.63
12:3A:36:VAL:O	12:3A:59:ARG:N	2.32	0.63
26:14:2318:G:H5'	26:14:2319:G:OP2	1.98	0.63
30:39:68:LYS:HB3	30:39:69:HIS:CD2	2.34	0.63
37:45:34:LEU:HB2	37:45:118:LEU:HD22	1.80	0.63
1:13:101:A:H2'	1:13:102:G:H8	1.62	0.63
1:13:209:U:H5'	1:13:210:U:OP2	1.99	0.63
1:13:1126:U:O4	1:13:1127:G:N1	2.32	0.63
26:1H:286:C:H2'	26:1H:287:C:H6	1.62	0.63
26:1H:557:U:H2'	26:1H:558:G:H8	1.61	0.63
26:1H:832:G:H5'	36:78:45:LEU:HD11	1.80	0.63
26:1H:1265:A:H8	26:1H:1265:A:OP1	1.80	0.63
29:21:101:ARG:CZ	29:21:171:GLU:HB2	2.29	0.63
37:88:104:PHE:HE2	37:88:125:LEU:HD11	1.63	0.63
41:C8:91:ASP:HB2	42:D8:11:GLN:OE1	1.98	0.63
26:14:892:G:N2	26:14:894:C:OP1	2.31	0.63
31:49:77:ILE:HG23	31:49:79:ASN:H	1.62	0.63
1:13:524:G:H2'	1:13:525:C:C6	2.32	0.63
1:13:854:G:N7	61:13:1887:HOH:O	2.31	0.63
40:B8:26:ASP:CB	40:B8:92:GLY:H	2.12	0.63
1:1G:625:G:H2'	1:1G:626:U:H6	1.63	0.63
1:1G:760:G:N2	17:8A:94:ASN:OD1	2.32	0.63
26:14:2119:A:N6	26:14:2170:A:N7	2.45	0.63
26:14:2611:U:O2'	52:J5:3:LYS:HG3	1.97	0.63
37:45:26:TYR:O	37:45:26:TYR:HD1	1.82	0.63
1:13:1133:G:H2'	1:13:1134:G:H8	1.63	0.63
1:13:1301:U:O2'	1:13:1302:U:H5'	1.99	0.63
1:13:1346:A:H5"	9:8E:120:ARG:NH1	2.13	0.63
6:5E:50:TYR:OH	18:9I:74:ARG:O	2.14	0.63
8:7E:64:LYS:HB3	8:7E:79:VAL:HG21	1.81	0.63
26:1H:761:A:OP1	61:1H:3683:HOH:O	2.16	0.63
26:1H:1156:A:C8	41:C8:51:LYS:HD3	2.33	0.63
26:1H:1602:U:O4	61:1H:4049:HOH:O	2.10	0.63
32:51:98:LEU:HD22	32:51:125:VAL:HG23	1.80	0.63
8:72:79:VAL:HG12	8:72:80:ILE:HG13	1.80	0.63
37:45:66:ILE:HG13	37:45:67:ARG:H	1.63	0.63
46:D5:163:LEU:HD23	46:D5:163:LEU:H	1.64	0.63
1:13:160:A:H1'	1:13:344:A:C8	2.34	0.63
26:1H:141:A:H8	26:1H:1595:G:H21	1.46	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:88:51:ARG:NH1	37:88:52:VAL:HG23	2.14	0.63
40:B8:54:ARG:HA	40:B8:59:THR:HB	1.80	0.63
46:H8:129:SER:H	46:H8:161:VAL:HG11	1.63	0.63
55:Q8:14:VAL:HG11	55:Q8:21:LYS:HZ1	1.64	0.63
4:32:176:LEU:HG	4:32:178:VAL:HG13	1.80	0.63
7:62:26:PHE:HD1	7:62:101:LEU:HD22	1.62	0.63
26:14:2120:G:H2'	26:14:2121:G:C8	2.33	0.63
26:14:2773:C:OP1	29:29:166:THR:OG1	2.15	0.63
29:29:23:VAL:HG11	29:29:183:LEU:HD23	1.79	0.63
30:39:192:LEU:HD23	30:39:193:VAL:H	1.63	0.63
42:95:71:LEU:N	42:95:86:GLY:HA2	2.14	0.63
1:13:542:G:O6	61:13:1928:HOH:O	2.12	0.63
1:13:963:G:N2	10:1I:55:LYS:HZ1	1.97	0.63
1:13:1117:G:H5"	9:8E:104:ARG:NH1	2.13	0.63
2:1E:162:ILE:O	2:1E:185:ILE:HG13	1.98	0.63
9:8E:26:VAL:HG13	9:8E:61:ALA:HB3	1.80	0.63
10:1I:84:GLN:HG3	10:1I:88:LEU:HD23	1.81	0.63
26:1H:49:A:N7	26:1H:120:U:C5	2.63	0.63
26:1H:1102:C:H2'	26:1H:1103:A:H8	1.63	0.63
26:1H:1425:G:O6	61:1H:4245:HOH:O	2.12	0.63
31:41:179:PRO:HG3	51:M8:38:LYS:HE3	1.81	0.63
33:61:131:LYS:HB3	33:61:132:PRO:HA	1.79	0.63
35:68:68:GLU:OE2	35:68:78:ARG:NH1	2.30	0.63
51:M8:6:HIS:HD1	51:M8:7:PRO:HD2	1.64	0.63
20:BA:49:ALA:HA	20:BA:52:ALA:HB3	1.81	0.63
26:14:123:G:N1	26:14:128:C:N3	2.39	0.63
26:14:994:C:OP1	41:85:53:ARG:NH2	2.31	0.63
36:35:47:ASP:HB3	36:35:49:ARG:N	2.14	0.63
36:35:64:LYS:CB	55:M5:30:ARG:HH22	2.12	0.63
39:65:11:LYS:HG3	39:65:91:PRO:HD3	1.80	0.63
46:D5:4:ARG:HA	46:D5:58:VAL:HB	1.81	0.63
48:F5:92:LYS:O	48:F5:94:LEU:N	2.31	0.63
53:K5:27:LYS:HZ3	53:K5:28:ARG:NH1	1.97	0.63
11:2I:21:ILE:HB	11:2I:84:VAL:HG12	1.81	0.62
22:1K:7:A:H61	22:1K:66:U:H3	1.45	0.62
22:1K:9:A:O2'	22:1K:10:G:OP1	2.15	0.62
26:1H:1794:U:H2'	26:1H:1795:C:C6	2.34	0.62
26:1H:2572:A:N7	29:21:144:ARG:HD2	2.13	0.62
26:1H:2646:C:OP2	26:1H:2732:G:O2'	2.14	0.62
37:88:81:VAL:O	37:88:82:ARG:HB2	1.98	0.62
40:B8:58:ASN:C	40:B8:58:ASN:HD22	2.07	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1G:766:A:OP2	61:1G:1770:HOH:O	2.16	0.62
5:42:61:TYR:O	5:42:65:ASN:N	2.25	0.62
26:14:654(B):C:H2'	26:14:654(C):G:C8	2.32	0.62
26:14:2037:G:H2'	26:14:2038:G:C8	2.33	0.62
31:49:120:LEU:HG	31:49:179:PRO:O	1.99	0.62
35:25:104:ARG:HH12	40:75:36:GLU:HB3	1.64	0.62
1:13:343:U:O2'	1:13:346:G:O6	2.17	0.62
1:13:631:G:C8	1:13:632:A:H2	2.18	0.62
26:1H:34:C:OP2	26:1H:34:C:H6	1.81	0.62
26:1H:1798:U:C5'	28:11:259:THR:HG22	2.30	0.62
30:31:9:ILE:HD11	30:31:125:LEU:H	1.63	0.62
36:78:114:ILE:HD11	36:78:130:PHE:CD2	2.34	0.62
40:B8:16:ARG:HE	40:B8:19:LEU:HD11	1.62	0.62
41:C8:68:ALA:O	41:C8:71:GLN:HB2	1.99	0.62
1:1G:564:C:O2'	8:72:91:ARG:NH2	2.32	0.62
4:32:98:GLU:OE2	4:32:103:ASN:ND2	2.31	0.62
26:14:751:A:P	61:14:3506:HOH:O	2.57	0.62
26:14:1342:A:H2	26:14:1602:U:N3	1.95	0.62
32:59:26:VAL:HG12	32:59:33:LEU:H	1.64	0.62
53:K5:9:LEU:N	53:K5:27:LYS:HG3	2.14	0.62
4:3E:81:GLU:OE1	4:3E:139:ARG:NH2	2.31	0.62
15:6I:6:GLU:CD	15:6I:6:GLU:H	2.06	0.62
26:1H:606:U:OP2	30:31:104:LYS:NZ	2.33	0.62
26:1H:805:G:OP2	36:78:41:ARG:HG2	1.98	0.62
39:A8:37:ALA:HB2	39:A8:101:LEU:HD21	1.82	0.62
1:1G:841:U:O2'	1:1G:842:C:H5"	1.99	0.62
1:1G:1057:G:H1	1:1G:1203:C:H42	1.47	0.62
3:22:155:GLY:HA3	3:22:196:LEU:HD13	1.81	0.62
29:29:25:VAL:HG12	29:29:26:ILE:H	1.63	0.62
42:95:80:GLN:HG3	42:95:81:TYR:H	1.64	0.62
52:J5:41:PRO:O	52:J5:44:THR:OG1	2.17	0.62
1:13:736:C:H2'	1:13:737:A:H8	1.62	0.62
12:3I:57:LYS:NZ	12:3I:67:THR:HG22	2.14	0.62
26:1H:994:C:OP1	41:C8:53:ARG:NH2	2.32	0.62
26:1H:2232:U:P	48:J8:40:ARG:HH12	2.22	0.62
26:1H:2315:G:OP1	31:41:36:LYS:NZ	2.32	0.62
37:88:5:ARG:HD3	37:88:5:ARG:N	2.13	0.62
1:1G:1294:G:H2'	1:1G:1295:G:H8	1.64	0.62
5:42:145:LYS:O	5:42:149:GLU:N	2.30	0.62
27:1J:4:C:H42	27:1J:116:G:H1	1.47	0.62
30:39:25:PRO:HB2	30:39:27:GLU:N	2.12	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:59:6:ARG:H	32:59:6:ARG:HD2	1.63	0.62
1:13:658:G:H2'	1:13:659:U:H6	1.64	0.62
1:13:1348:U:H4'	9:8E:120:ARG:HD2	1.80	0.62
6:5E:101:ALA:HB2	18:9I:28:GLU:HG2	1.82	0.62
26:1H:1113:U:H5'	32:51:2:SER:HB2	1.81	0.62
26:1H:1509:C:H2'	26:1H:1511:A:C8	2.35	0.62
26:1H:1575:C:H2'	26:1H:1576:U:C6	2.34	0.62
37:88:138:ASP:OD1	37:88:138:ASP:N	2.31	0.62
38:98:97:VAL:HG22	38:98:114:VAL:HG22	1.79	0.62
1:1G:485:G:O2'	1:1G:486:U:O5'	2.17	0.62
1:1G:501:C:H2'	1:1G:502:G:H8	1.64	0.62
1:1G:1118:C:H1'	1:1G:1179:A:C4	2.35	0.62
7:62:92:SER:HB2	7:62:95:ARG:H	1.64	0.62
26:14:491:G:H2'	26:14:492:A:C8	2.34	0.62
26:14:2250:G:C4	37:45:82:ARG:HG3	2.34	0.62
46:D5:139:VAL:HG13	46:D5:156:LYS:HE2	1.81	0.62
5:4E:110:LEU:HD13	5:4E:118:ILE:HD13	1.81	0.62
24:3K:76:A:H8	26:1H:2394:C:N4	1.95	0.62
26:1H:155:C:N4	26:1H:171:G:H1	1.93	0.62
26:1H:2383:G:O2'	26:1H:2384:G:H5'	1.99	0.62
35:68:4:PRO:O	35:68:5:GLN:HB2	1.98	0.62
39:A8:35:ILE:HD11	39:A8:101:LEU:HD23	1.82	0.62
44:F8:15:GLU:HG3	44:F8:16:LYS:N	2.14	0.62
26:14:19:C:H2'	26:14:20:C:C6	2.34	0.62
26:14:576:U:O4	61:14:3660:HOH:O	2.14	0.62
26:14:824:A:H1'	26:14:2358:G:N7	2.14	0.62
26:14:2331:G:O3'	47:E5:43:THR:HG22	2.00	0.62
35:25:8:LEU:HD13	35:25:82:ASN:HB3	1.82	0.62
37:45:25:ASP:HB3	37:45:102:VAL:HG23	1.81	0.62
1:13:737:A:H2'	1:13:738:C:C6	2.35	0.62
1:13:824:C:O2'	8:7E:1:MET:HB3	1.99	0.62
2:1E:126:GLU:HA	2:1E:129:GLU:HG2	1.81	0.62
13:4I:3:ARG:HE	13:4I:9:ILE:HD11	1.64	0.62
24:3K:19:G:C6	26:1H:2112:G:H1'	2.35	0.62
26:1H:612:G:N2	26:1H:616:A:O2'	2.33	0.62
37:88:12:GLN:HG2	37:88:73:PRO:HD2	1.81	0.62
1:1G:1258:G:H2'	1:1G:1259:C:H6	1.65	0.62
19:AA:41:VAL:HG12	19:AA:43:GLU:H	1.64	0.62
27:1J:6:C:H2'	27:1J:7:G:H5"	1.81	0.62
1:13:1530:G:H3'	1:13:1531:A:OP1	1.98	0.62
2:1E:53:ARG:NH2	2:1E:198:ASP:O	2.32	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1H:2233:U:H2'	26:1H:2234:G:C8	2.35	0.62
33:61:144:VAL:HG22	33:61:145:VAL:HG23	1.81	0.62
52:N8:33:CYS:HB2	52:N8:40:LYS:HD3	1.81	0.62
26:14:321:G:OP1	30:39:135:LYS:NZ	2.31	0.62
32:59:163:TYR:CE1	32:59:169:VAL:HG21	2.35	0.62
33:69:112:LYS:HA	33:69:114:LEU:H	1.65	0.62
40:75:23:ARG:HG3	40:75:120:ARG:NH1	2.15	0.62
41:85:100:VAL:O	41:85:101:ARG:HG2	1.99	0.62
55:M5:59:LYS:C	55:M5:60:LEU:HG	2.23	0.62
1:13:766:A:OP2	61:13:1804:HOH:O	2.16	0.62
1:13:793:U:H5'	1:13:794:A:H5"	1.82	0.62
1:13:1133:G:N2	1:13:1141:C:N3	2.47	0.62
1:13:1448:C:H42	1:13:1455:G:H1	1.46	0.62
10:1I:34:VAL:HG12	10:1I:74:ILE:HG23	1.80	0.62
26:1H:1332:G:H5'	26:1H:1332:G:H8	1.64	0.62
26:1H:1701:A:OP2	61:1H:4371:HOH:O	2.16	0.62
29:21:111:ARG:HD2	29:21:160:TYR:CE2	2.34	0.62
36:78:18:ARG:O	36:78:19:VAL:HG13	1.99	0.62
37:88:35:VAL:HG13	37:88:130:LYS:HB3	1.82	0.62
38:98:87:TYR:HE1	38:98:117:VAL:HG12	1.65	0.62
39:A8:59:LYS:HG2	39:A8:60:GLY:H	1.65	0.62
3:22:75:VAL:O	3:22:83:ARG:NH2	2.32	0.62
13:4A:17:VAL:HG13	13:4A:27:LYS:NZ	2.15	0.62
29:29:147:PRO:HB2	29:29:149:ARG:HG2	1.82	0.62
46:D5:7:ALA:HB3	46:D5:61:LEU:HA	1.81	0.62
46:D5:10:ARG:NE	46:D5:37:VAL:O	2.24	0.62
26:1H:1354:A:H4'	28:11:38:LYS:HE3	1.82	0.62
1:1G:1294:G:H2'	1:1G:1295:G:C8	2.35	0.62
27:1J:18:G:H2'	27:1J:19:G:C8	2.35	0.62
31:49:118:ARG:HB3	31:49:181:ARG:HG3	1.82	0.62
1:13:254:G:O3'	17:8I:69:LYS:NZ	2.29	0.61
1:13:1286:A:C8	1:13:1287:A:H4'	2.34	0.61
12:3I:11:VAL:HG13	17:8I:29:HIS:HD2	1.64	0.61
26:1H:1021:A:C8	26:1H:1021:A:H3'	2.35	0.61
26:1H:1221:C:H2'	26:1H:1222:C:C6	2.35	0.61
33:61:40:THR:O	33:61:44:LEU:HB2	2.00	0.61
42:D8:21:ARG:HG2	42:D8:91:TYR:CE2	2.35	0.61
53:O8:41:PRO:HB2	53:O8:43:CYS:HB2	1.82	0.61
1:1G:1108:G:H5'	3:22:176:HIS:CD2	2.34	0.61
1:1G:1268:A:H2'	1:1G:1269:A:H8	1.65	0.61
2:12:60:ASP:O	2:12:64:ARG:N	2.33	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:14:2542:A:H4'	26:14:2542:A:OP1	1.99	0.61
26:14:2588:G:P	61:14:3593:HOH:O	2.53	0.61
40:75:4:GLY:HA2	40:75:8:LYS:HB2	1.81	0.61
40:75:54:ARG:HA	40:75:59:THR:HB	1.82	0.61
5:4E:11:ILE:HG13	5:4E:31:LEU:HD13	1.81	0.61
13:4I:82:MET:HE3	13:4I:93:ARG:HG2	1.82	0.61
20:BI:26:ASN:HB2	20:BI:71:THR:HG23	1.80	0.61
20:BI:49:ALA:HB2	20:BI:99:LEU:HD23	1.82	0.61
26:1H:1021:A:H8	26:1H:1021:A:H3'	1.65	0.61
26:1H:1069:A:H4'	26:1H:1070:A:H5"	1.81	0.61
26:1H:1314:C:OP1	61:1H:3970:HOH:O	2.16	0.61
26:1H:1453:A:O2'	26:1H:1454:U:H2'	1.99	0.61
29:21:15:PHE:HA	29:21:19:ARG:O	1.99	0.61
7:62:149:ARG:HD3	11:2A:59:TYR:CE1	2.35	0.61
20:BA:45:GLN:HB2	20:BA:91:LEU:HD13	1.83	0.61
26:14:943:U:OP2	36:35:36:LYS:NZ	2.31	0.61
26:14:2137:C:O2	26:14:2155:G:N2	2.32	0.61
34:15:43:THR:N	34:15:48:MET:HE1	2.15	0.61
2:1E:226:ARG:HG3	2:1E:227:GLY:H	1.64	0.61
26:1H:639:U:O2'	26:1H:640:C:H5'	1.99	0.61
26:1H:1512:G:H2'	26:1H:1513:C:C6	2.34	0.61
48:J8:58:ILE:HG23	48:J8:87:PRO:HG3	1.83	0.61
4:32:24:GLU:N	4:32:24:GLU:OE2	2.32	0.61
26:14:878:A:H61	26:14:899:A:H1'	1.65	0.61
26:14:910:A:C5	37:45:13:GLN:HG3	2.34	0.61
26:14:2537:U:H2'	26:14:2538:C:C6	2.35	0.61
36:35:105:LEU:O	36:35:106:LEU:HB3	1.98	0.61
1:13:664:G:N2	1:13:741:G:H1	1.92	0.61
1:13:953:G:H2'	1:13:954:G:O4'	2.01	0.61
13:4I:27:LYS:HA	13:4I:31:LYS:NZ	2.15	0.61
26:1H:2334:G:H5'	39:A8:9:ARG:HG2	1.83	0.61
31:41:64:THR:HG22	31:41:66:GLN:N	2.16	0.61
43:E8:38:TYR:OH	52:N8:47:PRO:HG3	2.00	0.61
49:K8:22:GLU:OE2	49:K8:68:ARG:NH2	2.32	0.61
52:N8:41:PRO:HD2	52:N8:44:THR:HG21	1.83	0.61
53:O8:25:LYS:HB2	55:Q8:32:LEU:HD12	1.82	0.61
1:1G:376:G:H5"	16:7A:5:ARG:HD2	1.81	0.61
26:14:67:U:H3	26:14:74:A:H2	1.47	0.61
26:14:1434:A:H61	26:14:1558:A:H62	1.48	0.61
26:14:2190:G:H2'	26:14:2191:G:O4'	2.00	0.61
26:14:2261:C:H1'	26:14:2388:A:N3	2.15	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:75:56:GLY:O	40:75:59:THR:HG23	2.00	0.61
44:B5:32:PRO:HA	44:B5:77:LYS:HB2	1.81	0.61
1:13:201:C:N4	1:13:209:U:O2	2.33	0.61
1:13:963:G:H1	1:13:972:C:H42	1.47	0.61
1:13:1131:G:H2'	1:13:1132:C:C6	2.36	0.61
4:3E:22:LYS:HB2	4:3E:26:CYS:SG	2.40	0.61
18:9I:26:LEU:HD22	18:9I:42:ARG:HH22	1.66	0.61
43:E8:92:ARG:NH1	43:E8:94:ASP:OD1	2.30	0.61
4:32:76:ARG:HH21	4:32:80:GLU:HG2	1.65	0.61
20:BA:49:ALA:HB2	20:BA:92:LEU:HD22	1.81	0.61
26:14:631:A:OP2	55:M5:47:LYS:NZ	2.28	0.61
26:14:1154:G:OP2	41:85:58:ARG:NH1	2.34	0.61
30:39:7:TYR:CD1	30:39:18:ARG:HB2	2.35	0.61
1:13:1003:G:N2	1:13:1004:A:O2'	2.34	0.61
24:3K:35:A:H2'	24:3K:36:A:C8	2.36	0.61
31:41:129:GLY:O	31:41:161:THR:HG22	2.01	0.61
44:F8:1:MET:C	44:F8:3:THR:H	2.07	0.61
1:1G:1220:G:H5'	19:AA:35:SER:HA	1.82	0.61
26:14:1428:C:N4	26:14:1570:A:OP2	2.25	0.61
26:14:2557:G:H2'	26:14:2558:C:C6	2.36	0.61
29:29:151:TYR:HD2	29:29:154:LYS:HZ2	1.47	0.61
48:F5:86:SER:N	48:F5:87:PRO:HD2	2.15	0.61
1:13:156:G:H1'	1:13:166:G:N2	2.16	0.61
9:8E:49:PRO:HA	9:8E:52:ALA:HB3	1.82	0.61
24:3K:9:A:H62	24:3K:23:A:H62	1.49	0.61
32:51:150:ALA:O	32:51:153:LYS:NZ	2.33	0.61
41:C8:92:ARG:HA	41:C8:95:LEU:HD23	1.82	0.61
46:H8:73:GLN:HB2	46:H8:87:ASP:HB2	1.82	0.61
1:1G:1325:C:H5"	21:1B:17:THR:HG21	1.82	0.61
3:2E:58:GLU:HB2	3:2E:65:ALA:HB3	1.83	0.61
3:2E:175:LEU:HD23	3:2E:182:ILE:HD13	1.83	0.61
23:2K:21:U:O2	23:2K:21:U:H2'	2.00	0.61
26:1H:881:G:O6	26:1H:895:U:N3	2.29	0.61
26:1H:957:A:N1	26:1H:2458:G:H4'	2.16	0.61
26:1H:2830:G:H5"	26:1H:2830:G:H8	1.65	0.61
32:51:86:GLU:HG3	32:51:165:ALA:HB3	1.83	0.61
37:88:18:LYS:O	37:88:98:LYS:NZ	2.34	0.61
55:Q8:53:PRO:HB3	55:Q8:56:GLU:CG	2.31	0.61
1:1G:600:C:H2'	1:1G:601:C:C6	2.36	0.61
1:1G:933:G:O6	7:62:3:ARG:NH2	2.29	0.61
1:1G:1288:A:H4'	21:1B:13:ILE:HD13	1.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:2L:22:A:N6	23:2L:47:7MG:H2'	2.15	0.61
26:14:1006:C:H1'	34:15:106:MET:HE3	1.82	0.61
26:14:2567:G:H2'	26:14:2568:C:C6	2.35	0.61
51:I5:37:SER:C	51:I5:39:CYS:H	2.08	0.61
4:3E:15:GLU:OE1	4:3E:66:ARG:NH1	2.32	0.61
26:1H:265:A:C8	26:1H:266:G:H1'	2.36	0.61
26:1H:326:G:N7	61:1H:3850:HOH:O	2.31	0.61
26:1H:607:U:N3	26:1H:621:A:C2	2.68	0.61
26:1H:2032:G:H21	29:21:146:THR:HG23	1.66	0.61
26:1H:2287:A:N6	26:1H:2344:U:H3	1.98	0.61
29:21:24:THR:HG21	29:21:188:VAL:CG2	2.30	0.61
45:G8:40:GLU:HA	45:G8:42:VAL:H	1.65	0.61
55:Q8:14:VAL:HG21	55:Q8:21:LYS:HZ2	1.66	0.61
1:1G:1128:C:H4'	9:82:16:ARG:HH12	1.66	0.61
1:1G:1274:G:H2'	1:1G:1275:A:C8	2.35	0.61
23:2L:76:C:H2'	23:2L:77:A:C8	2.36	0.61
26:14:1677:A:H2'	26:14:1678:G:C8	2.36	0.61
26:14:2467:C:H4'	37:45:123:HIS:CE1	2.36	0.61
45:C5:99:CYS:SG	45:C5:100:ALA:N	2.73	0.61
46:D5:30:ASN:HA	46:D5:89:PHE:HE1	1.64	0.61
1:13:625:G:H4'	16:7I:16:HIS:ND1	2.16	0.61
1:13:1130:A:O2'	9:8E:3:GLN:NE2	2.28	0.61
6:5E:18:GLN:HA	6:5E:21:LEU:HD22	1.82	0.61
26:1H:1532:C:H2'	26:1H:1533:C:O4'	2.00	0.61
28:11:238:GLY:O	28:11:240:ALA:N	2.34	0.61
40:B8:3:ARG:HB2	40:B8:6:LEU:HB3	1.81	0.61
1:1G:1387:G:H2'	1:1G:1388:C:H6	1.64	0.61
26:14:2058:A:N6	61:14:4032:HOH:O	2.12	0.61
27:1J:9:G:OP1	39:65:25:ARG:NH2	2.33	0.61
29:29:103:ASP:OD2	29:29:199:ARG:NH2	2.34	0.61
36:35:65:ARG:HB2	36:35:65:ARG:NH1	2.10	0.61
36:35:71:VAL:HG13	36:35:72:PRO:HD3	1.83	0.61
41:85:52:ARG:HA	41:85:55:ARG:HD3	1.81	0.61
46:D5:157:LEU:HD12	46:D5:161:VAL:HG11	1.83	0.61
1:13:765:G:H5"	1:13:766:A:OP1	2.01	0.60
1:13:1423:G:P	35:68:49:ARG:HH22	2.24	0.60
4:3E:108:LEU:HD13	4:3E:174:LEU:HD13	1.83	0.60
26:1H:1055:G:H1'	26:1H:1085:A:C2	2.37	0.60
26:1H:1055:G:O2'	26:1H:1086:A:N6	2.33	0.60
33:61:80:PRO:HB2	33:61:146:ALA:HA	1.83	0.60
41:C8:96:ALA:H	41:C8:99:ALA:H	1.49	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1G:750:G:N3	15:6A:23:GLY:HA3	2.16	0.60
1:1G:1513:A:H2'	1:1G:1514:C:C6	2.37	0.60
19:AA:18:LYS:O	19:AA:22:LEU:HB2	2.01	0.60
26:14:800:A:H8	61:14:3727:HOH:O	1.82	0.60
26:14:1253:A:OP1	61:14:4007:HOH:O	2.16	0.60
26:14:2393:A:O3'	36:35:63:PRO:HD2	2.01	0.60
26:14:2420:C:N4	55:M5:31:HIS:HB3	2.15	0.60
9:8E:46:ALA:HB2	9:8E:74:ILE:HG23	1.83	0.60
19:AI:5:LEU:HB3	19:AI:10:PHE:HE1	1.66	0.60
26:1H:507:A:H5"	26:1H:508:G:H3'	1.82	0.60
26:1H:2199:A:H5'	26:1H:2199:A:C8	2.35	0.60
32:51:15:VAL:HG12	32:51:29:PRO:HD2	1.83	0.60
48:J8:90:ILE:HG22	48:J8:94:LEU:HD12	1.82	0.60
1:1G:438:G:H4'	4:32:123:HIS:CD2	2.35	0.60
1:1G:649:G:H2'	1:1G:650:G:H8	1.66	0.60
11:2A:85:ARG:HD3	11:2A:113:PRO:HD3	1.83	0.60
12:3A:111:LYS:H	12:3A:111:LYS:HD2	1.66	0.60
26:14:38:A:H2'	26:14:39:C:C6	2.36	0.60
27:1J:72:G:O2'	27:1J:104:A:N6	2.34	0.60
29:29:33:VAL:HG12	29:29:89:ASP:CB	2.30	0.60
33:69:102:SER:O	33:69:106:GLY:N	2.34	0.60
36:35:128:HIS:HA	36:35:147:LEU:HA	1.81	0.60
1:13:545:C:O2'	1:13:549:C:OP1	2.17	0.60
15:6I:7:GLU:OE1	15:6I:38:ARG:NH2	2.33	0.60
26:1H:805:G:P	61:1H:4480:HOH:O	2.55	0.60
26:1H:1110:G:O2'	26:1H:1111:A:O5'	2.18	0.60
26:1H:2080:G:H5"	26:1H:2080:G:H8	1.66	0.60
28:11:146:GLU:HB2	28:11:189:CYS:HB3	1.83	0.60
45:G8:40:GLU:HA	45:G8:42:VAL:N	2.16	0.60
1:1G:861:G:H2'	1:1G:862:C:H6	1.67	0.60
13:4A:3:ARG:HG2	13:4A:9:ILE:HG12	1.83	0.60
39:65:34:HIS:ND1	39:65:53:SER:OG	2.34	0.60
45:C5:76:CYS:HB2	45:C5:82:PRO:HG3	1.83	0.60
1:13:74:C:H42	1:13:96:G:H1	1.49	0.60
26:1H:692:C:O2'	28:11:38:LYS:HE2	2.00	0.60
31:41:173:LEU:HB3	31:41:178:PHE:CD2	2.36	0.60
46:H8:126:VAL:HA	46:H8:164:ALA:H	1.66	0.60
51:M8:48:ARG:HA	51:M8:48:ARG:HH11	1.65	0.60
1:1G:135:C:O2	16:7A:1:MET:HB3	2.00	0.60
1:1G:1251:A:H2'	1:1G:1252:A:C8	2.36	0.60
26:14:2393:A:H4'	36:35:62:LEU:H	1.67	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:65:67:ARG:NH1	39:65:67:ARG:HB2	2.16	0.60
1:13:392:G:H5'	16:7I:12:LYS:HD2	1.84	0.60
26:1H:730:C:H3'	61:1H:3684:HOH:O	2.01	0.60
26:1H:1575:C:H2'	26:1H:1576:U:H6	1.65	0.60
26:1H:1996:C:OP1	35:68:31:LYS:HE3	2.02	0.60
11:2A:21:ILE:HB	11:2A:84:VAL:HG12	1.83	0.60
26:14:152:G:H1	26:14:174:C:N4	1.99	0.60
26:14:1058:U:H2'	26:14:1059:G:C8	2.36	0.60
26:14:1386:C:H2'	26:14:1387:C:C6	2.36	0.60
26:14:2786:U:H4'	29:29:64:LYS:C	2.25	0.60
31:49:37:VAL:HG23	31:49:99:MET:HE3	1.82	0.60
55:M5:52:LYS:HE2	55:M5:52:LYS:O	2.02	0.60
16:7I:26:ARG:HE	16:7I:31:LYS:HB3	1.65	0.60
26:1H:1047:G:O2'	26:1H:1111:A:N6	2.34	0.60
26:1H:2572:A:C8	29:21:144:ARG:HD2	2.37	0.60
35:68:88:ASN:ND2	35:68:90:GLN:HB2	2.13	0.60
51:M8:36:CYS:SG	51:M8:39:CYS:HB3	2.41	0.60
1:1G:411:A:H62	1:1G:413:G:N2	2.00	0.60
1:1G:827:U:H3	1:1G:872:A:H62	1.48	0.60
13:4A:60:VAL:HG13	13:4A:64:TRP:HE1	1.66	0.60
23:2L:41:C:H2'	23:2L:42:C:C6	2.35	0.60
26:14:141:A:H8	26:14:1595:G:H21	1.49	0.60
27:1J:42:C:O2	31:49:93:THR:N	2.25	0.60
38:55:97:VAL:HG12	38:55:114:VAL:HG13	1.82	0.60
11:2I:54:ARG:NH1	24:3K:39:PSU:O2'	2.33	0.60
15:6I:6:GLU:OE1	15:6I:7:GLU:N	2.28	0.60
26:1H:323:G:C8	30:31:171:PRO:HG3	2.37	0.60
38:98:104:ARG:HH11	38:98:107:ASP:CG	2.09	0.60
1:1G:376:G:H1	1:1G:387:U:H3	1.50	0.60
9:82:13:ALA:HB2	9:82:68:GLY:HA3	1.84	0.60
13:4A:22:ILE:HB	13:4A:25:ILE:HG13	1.83	0.60
28:19:200:ASP:OD1	28:19:203:ASN:ND2	2.34	0.60
29:29:119:ARG:HG2	29:29:160:TYR:HB2	1.84	0.60
34:15:38:HIS:NE2	34:15:50:ASP:OD2	2.32	0.60
36:35:146:VAL:HG13	36:35:147:LEU:HD22	1.82	0.60
42:95:70:ILE:N	42:95:86:GLY:O	2.31	0.60
1:13:890:G:O2'	1:13:906:G:O6	2.14	0.60
26:1H:557:U:H2'	26:1H:558:G:C8	2.37	0.60
26:1H:744:G:OP1	61:1H:3699:HOH:O	2.17	0.60
26:1H:2262:U:OP1	26:1H:2387:U:O2'	2.20	0.60
37:88:21:THR:HA	37:88:98:LYS:HB2	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:F8:3:THR:OG1	44:F8:4:ALA:HA	2.02	0.60
44:F8:3:THR:HB	44:F8:6:ASP:HB2	1.83	0.60
44:F8:41:ASN:O	44:F8:45:THR:HG23	2.01	0.60
1:1G:458:C:H2'	1:1G:464:G:H8	1.66	0.60
1:1G:632:A:H1'	1:1G:633:G:OP2	2.01	0.60
1:1G:767:A:H3'	61:1G:1703:HOH:O	2.00	0.60
7:62:15:ASP:OD1	7:62:44:TYR:OH	2.20	0.60
41:85:49:HIS:HA	41:85:52:ARG:HB2	1.82	0.60
1:13:67:C:H2'	1:13:68:G:C8	2.36	0.60
26:1H:85:G:OP2	45:G8:9:LYS:HB2	2.00	0.60
29:21:23:VAL:HA	29:21:185:LYS:HA	1.82	0.60
1:1G:683:G:H2'	1:1G:684:A:C8	2.36	0.60
1:1G:1141:C:H2'	1:1G:1142:G:H8	1.67	0.60
2:12:179:LYS:HD3	2:12:180:LEU:HG	1.84	0.60
4:32:60:GLU:HG2	4:32:202:LEU:HB2	1.84	0.60
16:7A:53:VAL:HG13	16:7A:79:VAL:HG22	1.82	0.60
26:14:29:U:H2'	26:14:30:G:C8	2.37	0.60
26:14:918:A:O2'	27:1J:96:G:N2	2.34	0.60
26:14:2303:G:C2'	26:14:2304:G:H5'	2.32	0.60
33:69:63:ALA:HA	33:69:66:GLU:HG2	1.84	0.60
35:25:102:VAL:HB	35:25:106:LEU:HD12	1.84	0.60
1:13:1368:G:OP2	9:8E:112:LYS:HD2	2.02	0.60
26:1H:1204:A:H61	26:1H:1240:U:H2'	1.67	0.60
31:41:67:LYS:HE2	31:41:67:LYS:H	1.67	0.60
55:Q8:38:GLY:HA2	55:Q8:39:LYS:O	2.02	0.60
1:1G:409:G:H2'	1:1G:410:G:O4'	2.02	0.60
1:1G:1126:U:H4'	1:1G:1127:G:N7	2.16	0.60
26:14:1250:G:OP1	61:14:4029:HOH:O	2.17	0.60
26:14:1963:U:H5"	26:14:1963:U:O2	2.01	0.60
44:B5:67:GLY:C	44:B5:69:TYR:H	2.09	0.60
45:C5:30:VAL:HG12	45:C5:32:PRO:HD3	1.84	0.60
46:D5:110:GLY:HA2	46:D5:144:LEU:HD23	1.83	0.60
2:1E:5:ILE:HG13	2:1E:6:THR:HG22	1.84	0.59
17:8I:68:ARG:H	17:8I:70:ARG:NH1	1.99	0.59
26:1H:2795:G:H3'	26:1H:2797:U:H5"	1.84	0.59
30:31:101:LEU:HD22	30:31:102:PRO:HD2	1.84	0.59
53:O8:41:PRO:HB2	53:O8:43:CYS:H	1.67	0.59
55:Q8:38:GLY:HA2	55:Q8:39:LYS:C	2.26	0.59
1:1G:668:G:O4'	15:6A:49:ASP:HB2	2.02	0.59
19:AA:63:THR:OG1	19:AA:65:ASN:O	2.19	0.59
26:14:2331:G:H4'	47:E5:43:THR:H	1.67	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:14:2343:C:O2'	26:14:2373:G:O2'	2.10	0.59
27:1J:46:A:H2'	27:1J:47:C:C6	2.37	0.59
27:1J:46:A:H2'	27:1J:47:C:H6	1.67	0.59
27:1J:104:A:H2'	27:1J:105:G:O4'	2.02	0.59
1:13:674:G:H2'	1:13:675:A:C8	2.36	0.59
26:1H:309:G:H4'	45:G8:18:GLY:HA2	1.83	0.59
39:A8:24:LEU:HB2	39:A8:85:VAL:HG12	1.84	0.59
6:52:74:ASP:OD1	6:52:74:ASP:N	2.35	0.59
26:14:800:A:P	61:14:3727:HOH:O	2.59	0.59
26:14:882:G:H22	26:14:894:C:N4	1.99	0.59
26:14:2439:A:H5'	26:14:2439:A:C8	2.37	0.59
27:1J:40:U:H3	27:1J:43:C:H5"	1.67	0.59
33:69:78:THR:HG21	33:69:104:GLN:HG3	1.82	0.59
1:13:535:A:H5"	61:13:1846:HOH:O	2.02	0.59
1:13:1060:C:C5	3:2E:2:GLY:HA3	2.37	0.59
2:1E:88:ALA:HB2	2:1E:219:VAL:HG13	1.84	0.59
11:2I:21:ILE:HG12	11:2I:30:VAL:HG12	1.84	0.59
19:AI:50:ALA:HB1	19:AI:57:HIS:HB3	1.84	0.59
24:3K:71:G:O2'	26:1H:1851:U:O2'	2.20	0.59
26:1H:1103:A:H3'	26:1H:1104:C:H6	1.68	0.59
26:1H:1165:U:H2'	26:1H:1166:C:H6	1.66	0.59
26:1H:1168:G:C2	26:1H:1182:A:C2	2.91	0.59
30:31:129:PHE:HA	30:31:142:TRP:NE1	2.17	0.59
40:B8:24:PRO:HD3	40:B8:52:ILE:HD12	1.84	0.59
41:C8:92:ARG:CB	41:C8:95:LEU:HD23	2.32	0.59
44:F8:67:GLY:C	44:F8:69:TYR:H	2.09	0.59
13:4A:97:PRO:HB2	13:4A:101:GLN:HG3	1.83	0.59
16:7A:49:LEU:HD22	16:7A:73:LEU:HD13	1.85	0.59
56:1L:18:G:O2'	56:1L:19:G:OP1	2.19	0.59
26:14:1165:U:H2'	26:14:1166:C:C6	2.37	0.59
26:14:2130:U:H2'	26:14:2158:A:N1	2.18	0.59
28:19:65:ILE:HD11	28:19:67:PHE:CE1	2.37	0.59
31:49:33:ARG:CZ	31:49:162:THR:HG21	2.32	0.59
36:35:15:ARG:HB2	36:35:15:ARG:CZ	2.31	0.59
47:E5:51:VAL:N	47:E5:62:LEU:HD12	2.17	0.59
51:I5:22:ILE:HD13	51:I5:22:ILE:H	1.68	0.59
1:13:272:C:H2'	1:13:273:A:H8	1.66	0.59
13:4I:23:TYR:HD2	13:4I:67:GLU:HA	1.67	0.59
24:3K:8:U:H2'	24:3K:13:C:H41	1.67	0.59
26:1H:353:G:H2'	26:1H:354:G:H8	1.67	0.59
26:1H:524:U:H2'	26:1H:525:U:C6	2.36	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1H:637:A:H2'	36:78:117:GLU:OE1	2.01	0.59
26:1H:860:U:H1'	26:1H:2268:A:H5'	1.84	0.59
26:1H:1062:G:N2	26:1H:1076:C:N3	2.46	0.59
26:1H:1420:U:O2'	26:1H:1421:G:OP1	2.19	0.59
34:58:127:ASP:OD1	34:58:127:ASP:N	2.36	0.59
44:F8:24:GLY:O	44:F8:83:VAL:HG22	2.02	0.59
1:1G:1227:A:OP1	19:AA:80:TYR:OH	2.20	0.59
1:1G:1266:G:N2	1:1G:1270:C:N3	2.50	0.59
4:32:14:ARG:HG3	4:32:14:ARG:NH1	2.17	0.59
7:62:92:SER:HB3	7:62:94:ARG:HG2	1.84	0.59
57:3L:56:C:O2	26:14:2112:G:N2	2.35	0.59
26:14:218:A:C2	26:14:235:U:H4'	2.37	0.59
26:14:2656:U:H3	26:14:2665:A:H2	1.49	0.59
37:45:57:HIS:CD2	37:45:117:ALA:HB2	2.36	0.59
41:85:92:ARG:CZ	42:95:11:GLN:H	2.15	0.59
1:13:235:C:H5'	17:8I:70:ARG:HG2	1.84	0.59
1:13:598:U:H4'	8:7E:94:TYR:CD2	2.38	0.59
23:2K:62:C:H2'	23:2K:63:C:C6	2.33	0.59
26:1H:581:C:OP1	41:C8:33:ARG:HG3	2.01	0.59
26:1H:1997:G:P	61:1H:4031:HOH:O	2.50	0.59
26:1H:2791:C:N3	26:1H:2807:G:N2	2.48	0.59
35:68:71:ARG:HH21	35:68:77:ILE:HG21	1.66	0.59
41:C8:95:LEU:HD12	41:C8:96:ALA:CA	2.32	0.59
42:D8:3:ALA:HB1	42:D8:38:LEU:HD11	1.84	0.59
43:E8:18:ARG:HD3	43:E8:76:VAL:HG13	1.83	0.59
55:Q8:52:LYS:HA	55:Q8:54:GLU:HB2	1.85	0.59
1:1G:54:C:N4	1:1G:353:A:OP2	2.33	0.59
1:1G:146:G:H2'	1:1G:147:G:H8	1.67	0.59
4:32:8:VAL:HA	4:32:11:LEU:HD12	1.84	0.59
5:42:143:ARG:NH1	8:72:77:GLU:OE2	2.34	0.59
19:AA:23:ASN:HA	19:AA:27:GLU:CD	2.28	0.59
26:14:67:U:H2'	26:14:68:G:H8	1.68	0.59
26:14:279:C:H42	26:14:361:G:H1	1.50	0.59
26:14:654(E):C:H42	26:14:654(P):G:H22	1.50	0.59
32:59:42:ARG:NH1	32:59:53:GLU:O	2.36	0.59
36:35:62:LEU:HD12	55:M5:25:MET:CB	2.27	0.59
1:13:560:U:O2'	1:13:561:U:OP2	2.19	0.59
10:1I:5:ARG:HB2	10:1I:73:ASP:OD1	2.02	0.59
26:1H:2074:U:P	61:1H:3680:HOH:O	2.56	0.59
44:F8:80:ILE:HG13	44:F8:80:ILE:O	2.00	0.59
1:1G:438:G:C4'	4:32:123:HIS:HD2	2.16	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:AA:27:GLU:O	19:AA:47:HIS:NE2	2.29	0.59
26:14:2839:G:H5'	38:55:46:GLY:HA2	1.83	0.59
27:1J:5:C:H42	27:1J:115:G:H1	1.51	0.59
31:49:125:PHE:HB3	31:49:166:ASP:HB2	1.84	0.59
35:25:7:TYR:CE1	35:25:20:MET:HE3	2.34	0.59
42:95:85:LYS:CD	42:95:86:GLY:H	2.14	0.59
1:13:228:A:H2'	1:13:229:U:O4'	2.03	0.59
1:13:1279:A:O2'	1:13:1281:U:OP2	2.20	0.59
1:13:1312:G:O3'	19:AI:6:LYS:NZ	2.36	0.59
11:2I:107:SER:HA	18:9I:87:ARG:HD3	1.85	0.59
26:1H:2629:A:OP1	26:1H:2629:A:H4'	2.01	0.59
28:11:71:ASP:OD2	28:11:103:ARG:NH2	2.36	0.59
47:I8:63:VAL:HG23	47:I8:64:ASP:O	2.02	0.59
52:N8:46:CYS:HB2	52:N8:50:GLY:HA2	1.84	0.59
1:1G:362:G:H4'	12:3A:33:ARG:HH21	1.67	0.59
1:1G:1191:A:OP1	3:22:3:ASN:ND2	2.33	0.59
4:32:30:LYS:CB	4:32:35:ARG:HD2	2.32	0.59
26:14:873:G:N2	26:14:905:U:C2	2.71	0.59
32:59:23:ARG:HA	32:59:36:PRO:HA	1.84	0.59
36:35:47:ASP:HB3	36:35:49:ARG:H	1.67	0.59
46:D5:97:GLU:HB3	46:D5:125:LEU:HD21	1.83	0.59
1:13:1280:A:H3'	1:13:1281:U:H5'	1.85	0.59
8:7E:121:ASP:HB2	8:7E:125:ARG:NH2	2.17	0.59
29:21:50:GLY:HA2	29:21:77:ILE:HA	1.85	0.59
34:58:96:GLU:HG2	34:58:97:ARG:N	2.16	0.59
36:78:19:VAL:HG21	36:78:27:HIS:CG	2.38	0.59
46:H8:165:VAL:HB	46:H8:166:SER:HA	1.84	0.59
1:1G:1057:G:H1	1:1G:1203:C:N4	2.01	0.59
1:1G:1298:C:H4'	1:1G:1299:A:C8	2.37	0.59
2:12:163:PHE:CD2	2:12:185:ILE:HG13	2.33	0.59
17:8A:45:HIS:O	17:8A:73:VAL:HG12	2.02	0.59
19:AA:67:VAL:HG11	51:I5:56:VAL:HG23	1.84	0.59
26:14:1019:U:H3	26:14:1142(A):A:H62	1.51	0.59
34:15:96:GLU:H	34:15:96:GLU:CD	2.08	0.59
36:35:64:LYS:HB2	55:M5:30:ARG:HH22	1.67	0.59
39:65:34:HIS:HD1	39:65:53:SER:HG	1.47	0.59
46:D5:94:GLU:HB3	46:D5:96:VAL:HG23	1.85	0.59
3:2E:3:ASN:O	3:2E:4:LYS:HG2	2.03	0.59
17:8I:22:LEU:HD11	17:8I:39:SER:HB3	1.83	0.59
20:BI:97:ALA:O	20:BI:99:LEU:N	2.36	0.59
24:3K:56:C:N3	26:1H:2112:G:N2	2.51	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1H:639:U:H2'	26:1H:640:C:C6	2.38	0.59
26:1H:1705:G:C2'	26:1H:1706:U:H5'	2.33	0.59
26:1H:1970:A:P	61:1H:4003:HOH:O	2.60	0.59
37:88:72:LYS:HB3	37:88:94:VAL:HG23	1.85	0.59
57:3L:1:G:H1	57:3L:72:C:N4	1.88	0.59
26:14:491:G:H2'	26:14:492:A:H8	1.68	0.59
26:14:994:C:OP2	41:85:54:LYS:NZ	2.33	0.59
26:14:1843:C:H5'	28:19:253:GLN:OE1	2.01	0.59
38:55:54:LEU:HD23	38:55:66:VAL:HG23	1.84	0.59
1:13:973:G:H3'	1:13:974:A:H5"	1.85	0.59
26:1H:320:A:H2'	30:31:136:THR:HG21	1.84	0.59
26:1H:2402:C:H5	26:1H:2415:G:H22	1.50	0.59
26:1H:2704:C:H2'	26:1H:2705:A:C8	2.38	0.59
27:16:15:A:H1'	27:16:109:G:C8	2.38	0.59
29:21:33:VAL:O	29:21:69:LYS:HD2	2.03	0.59
42:D8:41:GLY:O	42:D8:45:THR:HA	2.02	0.59
45:G8:94:LYS:HA	45:G8:94:LYS:HZ3	1.67	0.59
26:14:1033:U:H3'	26:14:1033:U:H6	1.66	0.59
26:14:1055:G:O2'	26:14:1085:A:N1	2.33	0.59
26:14:1266:G:O5'	43:A5:15:ARG:NH2	2.35	0.59
1:13:244:U:H4'	1:13:245:C:O5'	2.02	0.58
26:1H:2314:C:H2'	26:1H:2315:G:H8	1.66	0.58
36:78:96:THR:C	36:78:98:GLU:H	2.11	0.58
41:C8:91:ASP:HB3	41:C8:94:ASN:HB2	1.86	0.58
1:1G:4:U:H3'	1:1G:5:U:H5'	1.85	0.58
4:32:18:LYS:HB3	4:32:33:MET:HG3	1.84	0.58
26:14:754:C:H2'	26:14:755:C:H6	1.67	0.58
46:D5:40:ASP:HB3	46:D5:43:GLU:HG3	1.85	0.58
4:3E:175:SER:HB3	4:3E:186:LEU:HD21	1.84	0.58
26:1H:671:C:OP1	36:78:42:SER:O	2.21	0.58
27:16:7:G:H4'	39:A8:29:PHE:CD2	2.38	0.58
35:68:93:PRO:HG3	35:68:114:ILE:HG12	1.85	0.58
40:B8:29:ARG:NH1	40:B8:46:GLU:OE2	2.36	0.58
2:12:68:ILE:HG12	2:12:161:ALA:HB3	1.85	0.58
57:3L:18:G:C2'	57:3L:57:G:H22	2.16	0.58
26:14:479:A:N3	26:14:481:G:H5"	2.17	0.58
26:14:2054:A:H5"	26:14:2055:C:O5'	2.03	0.58
26:14:2875:C:OP1	40:75:3:ARG:NH1	2.36	0.58
28:19:181:GLU:HA	28:19:272:ALA:HB1	1.85	0.58
36:35:55:ARG:HG2	36:35:56:SER:N	2.16	0.58
45:C5:87:LYS:CB	45:C5:94:LYS:HA	2.33	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:3K:8:U:H4'	24:3K:9:A:OP1	2.03	0.58
26:1H:995:C:O2	34:58:3:THR:OG1	2.21	0.58
26:1H:2058:A:OP1	61:1H:4269:HOH:O	2.17	0.58
26:1H:2683:C:OP1	40:B8:53:ARG:NH2	2.27	0.58
31:41:112:PRO:HG3	51:M8:38:LYS:HD2	1.85	0.58
45:G8:95:LYS:HE2	45:G8:97:ARG:HH22	1.68	0.58
1:1G:17:U:H2'	1:1G:18:C:C6	2.38	0.58
26:14:1754:C:OP1	40:75:96:ARG:NH1	2.35	0.58
26:14:2404:C:O3'	36:35:77:ARG:NH2	2.36	0.58
26:14:2776:A:OP1	26:14:2776:A:H3'	2.03	0.58
34:15:56:ASN:H	34:15:125:GLY:HA3	1.68	0.58
1:13:619:U:H3	4:3E:134:ASP:HB2	1.67	0.58
2:1E:21:ARG:HB2	2:1E:39:ILE:HA	1.86	0.58
5:4E:11:ILE:HD11	5:4E:31:LEU:HD22	1.84	0.58
13:4I:80:ARG:HH11	19:AI:65:ASN:HB2	1.69	0.58
26:1H:5:A:H2'	26:1H:6:A:C8	2.39	0.58
26:1H:286:C:H42	26:1H:355:G:H1	1.49	0.58
26:1H:899:A:HO2'	26:1H:900:A:H8	1.51	0.58
26:1H:1783:A:P	61:1H:4502:HOH:O	2.60	0.58
26:1H:2062:A:H2'	26:1H:2062:A:N3	2.18	0.58
26:1H:2431:U:OP2	61:1H:3933:HOH:O	2.17	0.58
26:1H:2591:C:OP1	28:11:239:ARG:HG3	2.03	0.58
46:H8:4:ARG:HB3	46:H8:58:VAL:HG23	1.84	0.58
49:K8:42:GLY:C	49:K8:44:LEU:H	2.09	0.58
1:1G:256:U:H2'	1:1G:257:G:C8	2.37	0.58
4:32:29:PRO:HD2	4:32:30:LYS:HE2	1.85	0.58
5:42:31:LEU:HD22	5:42:45:PHE:HB2	1.84	0.58
29:29:51:PHE:CE2	29:29:52:LEU:HG	2.39	0.58
5:4E:81:GLU:HG2	5:4E:90:VAL:HG23	1.85	0.58
17:8I:76:LEU:HD11	17:8I:79:SER:HB3	1.84	0.58
22:1K:26:A:H61	22:1K:44:G:N2	2.02	0.58
26:1H:1664:A:H5"	61:1H:4466:HOH:O	2.03	0.58
26:1H:2392:A:OP2	55:Q8:30:ARG:NH2	2.28	0.58
26:1H:2393:A:H2'	26:1H:2394:C:H6	1.68	0.58
26:1H:2492:U:H2'	26:1H:2493:U:C6	2.39	0.58
40:B8:2:ASN:O	40:B8:3:ARG:HG3	2.03	0.58
45:G8:49:VAL:HG21	45:G8:55:TYR:CE2	2.39	0.58
55:Q8:23:VAL:O	55:Q8:46:ARG:HB2	2.04	0.58
1:1G:192:U:H2'	1:1G:193:C:H6	1.68	0.58
1:1G:957:U:H1'	1:1G:960:U:H5	1.69	0.58
3:22:9:GLY:HA3	14:5A:49:HIS:HA	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:14:323:G:O2'	26:14:1205:U:N3	2.29	0.58
26:14:330:A:H2	26:14:1210:A:O2'	1.85	0.58
26:14:1079:C:H41	26:14:1088:A:H5"	1.68	0.58
28:19:12:SER:O	28:19:16:MET:HE3	2.03	0.58
43:A5:27:LYS:O	43:A5:71:VAL:HG23	2.04	0.58
1:13:804:U:H5"	1:13:805:C:OP2	2.04	0.58
1:13:1160:G:H1	1:13:1177:G:N2	2.02	0.58
3:2E:73:PRO:O	3:2E:76:VAL:HG13	2.02	0.58
10:1I:52:GLY:O	14:5I:41:ARG:NH2	2.37	0.58
1:1G:1372:U:H5"	9:82:71:SER:HB2	1.86	0.58
45:C5:52:SER:HA	45:C5:55:TYR:O	2.03	0.58
55:M5:34:TRP:CD1	55:M5:35:GLN:H	2.20	0.58
1:13:1346:A:OP1	9:8E:120:ARG:NH1	2.36	0.58
1:13:1435:G:H2'	1:13:1436:U:C6	2.39	0.58
8:7E:122:ARG:O	8:7E:126:LYS:HG3	2.04	0.58
18:9I:59:SER:HB3	18:9I:62:GLU:HG3	1.85	0.58
26:1H:585:G:P	61:1H:3853:HOH:O	2.59	0.58
26:1H:2210:G:H3'	26:1H:2211:G:C8	2.39	0.58
40:B8:60:THR:HG22	40:B8:77:PRO:HA	1.85	0.58
1:1G:690:G:H2'	1:1G:691:G:O4'	2.02	0.58
1:1G:1347:G:O2'	1:1G:1373:G:O6	2.20	0.58
10:1A:22:LYS:NZ	10:1A:88:LEU:O	2.36	0.58
26:14:218:A:H2	26:14:235:U:H4'	1.69	0.58
26:14:654(C):G:H2'	26:14:654(D):G:O4'	2.04	0.58
37:45:38:GLU:HB2	37:45:127:ILE:HG22	1.84	0.58
1:13:667:G:H4'	15:6I:51:HIS:CE1	2.38	0.58
1:13:1118:C:H1'	1:13:1179:A:C4	2.39	0.58
1:13:1226:C:O3'	13:4I:111:LYS:NZ	2.37	0.58
26:1H:11:G:H2'	26:1H:12:U:H5'	1.86	0.58
26:1H:1486:A:H2'	26:1H:1487:G:C8	2.39	0.58
28:11:242:ARG:O	61:11:401:HOH:O	2.17	0.58
32:51:30:LYS:HD2	32:51:81:GLU:H	1.67	0.58
41:C8:101:ARG:O	41:C8:103:PRO:HD3	2.04	0.58
1:1G:861:G:H2'	1:1G:862:C:C6	2.39	0.58
26:14:2468:G:H3'	26:14:2476:A:N1	2.19	0.58
34:15:19:GLU:HA	34:15:59:LYS:O	2.04	0.58
34:15:128:HIS:NE2	34:15:134:ARG:HD2	2.19	0.58
1:13:1322:C:O2'	1:13:1323:G:P	2.60	0.58
3:2E:7:PRO:O	3:2E:11:ARG:HG2	2.04	0.58
26:1H:1426:G:N1	61:1H:4248:HOH:O	2.32	0.58
26:1H:1607:C:H4'	26:1H:1608:A:O5'	2.04	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1H:1783:A:OP2	61:1H:4502:HOH:O	2.17	0.58
26:1H:2115:G:N2	26:1H:2172:U:O2	2.37	0.58
26:1H:2257:U:O2'	26:1H:2258:C:H5'	2.04	0.58
26:1H:2400:G:H2'	26:1H:2401:U:H6	1.68	0.58
27:16:101:A:H8	27:16:101:A:O5'	1.87	0.58
28:11:93:ALA:HB3	28:11:105:ILE:HG22	1.86	0.58
35:68:12:ASP:HB3	35:68:85:VAL:HG13	1.85	0.58
38:98:38:VAL:HB	38:98:39:PRO:HD3	1.86	0.58
38:98:72:ASP:O	38:98:76:VAL:HG23	2.04	0.58
40:B8:3:ARG:HD2	40:B8:6:LEU:HB3	1.86	0.58
42:D8:44:LYS:HA	42:D8:44:LYS:NZ	2.19	0.58
46:H8:63:ASP:HB2	46:H8:65:GLN:HG3	1.85	0.58
46:H8:105:VAL:HG22	46:H8:140:ASP:HB3	1.86	0.58
9:82:111:ARG:HD2	14:5A:61:TRP:C	2.29	0.58
26:14:1187:G:OP2	61:14:3681:HOH:O	2.17	0.58
26:14:2757:A:N1	32:59:67:LEU:HD22	2.18	0.58
48:F5:29:GLY:O	48:F5:30:VAL:HG22	2.04	0.58
48:F5:51:VAL:HG23	48:F5:58:ILE:HB	1.85	0.58
1:13:963:G:N2	10:1I:55:LYS:NZ	2.50	0.58
2:1E:185:ILE:CG2	2:1E:199:TYR:HB2	2.33	0.58
9:8E:112:LYS:HD3	9:8E:113:LYS:N	2.19	0.58
16:7I:5:ARG:HE	16:7I:22:THR:CG2	2.17	0.58
22:1K:27:G:N2	22:1K:43:C:O2	2.35	0.58
26:1H:277:C:H3'	26:1H:278:A:O4'	2.04	0.58
26:1H:818:G:H4'	26:1H:838:C:O3'	2.04	0.58
26:1H:1178:C:H4'	26:1H:1179:C:OP1	2.03	0.58
31:41:112:PRO:HD3	51:M8:38:LYS:HE2	1.85	0.58
55:Q8:47:LYS:HA	55:Q8:47:LYS:HZ2	1.66	0.58
1:1G:588:G:H1	1:1G:651:C:N4	1.94	0.58
10:1A:51:ARG:HB2	10:1A:60:ARG:HA	1.85	0.58
18:9A:22:VAL:HG12	18:9A:56:THR:HA	1.86	0.58
19:AA:33:THR:HG22	19:AA:49:ILE:HG22	1.85	0.58
33:69:14:ASP:O	33:69:17:GLN:HB2	2.04	0.58
42:95:35:LEU:HB2	42:95:37:VAL:HG13	1.85	0.58
1:13:323:U:H2'	1:13:324:G:O4'	2.03	0.57
1:13:1307:U:OP1	13:4I:101:GLN:NE2	2.37	0.57
12:3I:66:VAL:HG21	12:3I:98:TYR:HE2	1.69	0.57
20:BI:53:LEU:HD23	20:BI:100:ILE:HG22	1.85	0.57
22:1K:8:4SU:H6	22:1K:8:4SU:O5'	2.04	0.57
26:1H:1266:G:O4'	43:E8:15:ARG:NH2	2.37	0.57
26:1H:2176:A:H2'	26:1H:2177:C:H6	1.68	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1H:2887:U:H2'	26:1H:2888:C:C6	2.38	0.57
29:21:119:ARG:HD2	29:21:160:TYR:HB2	1.86	0.57
39:A8:14:VAL:O	39:A8:18:ILE:HD13	2.04	0.57
42:D8:34:GLU:HB2	42:D8:58:VAL:HG22	1.87	0.57
51:M8:34:GLU:HG2	51:M8:35:VAL:N	2.19	0.57
1:1G:1157:A:N6	1:1G:1178:G:H21	1.96	0.57
26:14:57:C:H2'	26:14:58:G:O4'	2.04	0.57
29:29:182:LEU:O	29:29:183:LEU:HD12	2.04	0.57
31:49:67:LYS:H	51:I5:6:HIS:CE1	2.22	0.57
38:55:104:ARG:HD2	38:55:109:ALA:HB3	1.86	0.57
42:95:80:GLN:C	42:95:81:TYR:HD1	2.12	0.57
46:D5:59:LEU:HD22	46:D5:61:LEU:HG	1.86	0.57
1:13:1446:A:OP1	1:13:1446:A:H4'	2.03	0.57
8:7E:10:LEU:HB3	8:7E:83:ILE:HD11	1.85	0.57
26:1H:2419:U:O4	55:Q8:29:LYS:NZ	2.25	0.57
30:31:107:LYS:HD2	30:31:206:ILE:HA	1.86	0.57
45:G8:39:VAL:O	45:G8:39:VAL:HG12	2.03	0.57
55:Q8:59:LYS:HB3	55:Q8:59:LYS:NZ	2.18	0.57
1:1G:45:U:H2'	1:1G:46:G:C8	2.39	0.57
1:1G:1127:G:N3	1:1G:1147:C:N4	2.51	0.57
1:1G:1129:C:C4	1:1G:1139:G:N1	2.73	0.57
2:12:21:ARG:HA	2:12:39:ILE:HA	1.85	0.57
4:32:13:ARG:C	4:32:15:GLU:H	2.12	0.57
20:BA:26:ASN:HB2	20:BA:71:THR:HG23	1.85	0.57
56:1L:19:G:N2	56:1L:56:C:N3	2.52	0.57
26:14:1057:A:H2'	26:14:1058:U:O4'	2.04	0.57
26:14:1176:G:H5'	26:14:1177:A:OP1	2.04	0.57
26:14:2557:G:H2'	26:14:2558:C:H6	1.68	0.57
29:29:37:ARG:NE	29:29:42:ASP:OD2	2.34	0.57
39:65:106:ARG:O	39:65:106:ARG:NH1	2.29	0.57
49:G5:43:GLN:OE1	49:G5:43:GLN:N	2.34	0.57
1:13:1106:G:H5"	3:2E:172:ARG:HG2	1.86	0.57
22:1K:47:U:H5'	22:1K:48:C:H5'	1.86	0.57
23:2K:20:G:C2	23:2K:58:A:N3	2.72	0.57
26:1H:1228:G:OP2	41:C8:16:LYS:NZ	2.34	0.57
26:1H:1405:U:H2'	26:1H:1406:U:C6	2.38	0.57
26:1H:1443:G:N2	26:1H:1549:C:O2	2.37	0.57
26:1H:2137:C:H42	26:1H:2154:G:N2	2.02	0.57
26:1H:2211:G:H4'	26:1H:2212:A:OP2	2.04	0.57
33:61:109:ILE:HB	33:61:130:TYR:CZ	2.39	0.57
36:78:114:ILE:HD12	36:78:134:ALA:HB1	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:E8:110:LYS:HG3	43:E8:111:HIS:H	1.69	0.57
1:1G:683:G:N2	1:1G:707:C:O2	2.30	0.57
1:1G:1326:C:OP1	21:1B:17:THR:OG1	2.16	0.57
17:8A:17:LYS:HD3	17:8A:47:PRO:HA	1.87	0.57
37:45:81:VAL:O	37:45:82:ARG:NH1	2.38	0.57
42:95:44:LYS:O	42:95:46:VAL:N	2.32	0.57
1:13:678:U:H2'	1:13:679:C:C6	2.39	0.57
1:13:1015:A:H2'	1:13:1016:A:H8	1.69	0.57
1:13:1302:U:OP2	13:4I:21:TYR:OH	2.14	0.57
26:1H:176:G:O2'	26:1H:177:G:H5'	2.03	0.57
26:1H:511:U:H5"	26:1H:512:G:OP2	2.04	0.57
26:1H:910:A:C4	37:88:13:GLN:NE2	2.72	0.57
26:1H:1287:A:C8	38:98:107:ASP:HB2	2.40	0.57
26:1H:2376:A:H2	39:A8:112:PHE:HB3	1.69	0.57
40:B8:108:ARG:HA	40:B8:111:ARG:HE	1.70	0.57
5:42:122:GLU:O	5:42:126:ARG:NH1	2.36	0.57
11:2A:98:LEU:O	11:2A:101:SER:OG	2.10	0.57
13:4A:5:ALA:HB3	13:4A:8:GLU:HB2	1.86	0.57
26:14:2387:U:OP1	47:E5:55:ARG:NH1	2.29	0.57
29:29:36:ARG:NH1	29:29:85:ASN:OD1	2.37	0.57
45:C5:19:LYS:HG3	45:C5:20:TYR:HD1	1.69	0.57
46:D5:157:LEU:HA	46:D5:161:VAL:HG11	1.85	0.57
10:1I:49:VAL:CG2	14:5I:41:ARG:HB2	2.33	0.57
26:1H:1257:C:OP1	30:31:75:HIS:HE1	1.87	0.57
32:51:101:ARG:HH22	32:51:122:THR:HA	1.68	0.57
43:E8:37:ARG:HD3	43:E8:38:TYR:CE1	2.39	0.57
48:J8:3:LYS:O	48:J8:12:PRO:HD3	2.05	0.57
52:N8:33:CYS:HB2	52:N8:40:LYS:CD	2.34	0.57
1:1G:536:C:H2'	1:1G:537:G:C8	2.40	0.57
1:1G:581:G:OP1	15:6A:61:GLY:HA3	2.05	0.57
1:1G:1317:C:O2	19:AA:37:ARG:NH2	2.38	0.57
3:22:40:ARG:HA	3:22:43:LEU:HB2	1.87	0.57
3:22:131:ARG:NH2	3:22:166:GLU:OE2	2.37	0.57
10:1A:40:LEU:HD13	10:1A:71:LEU:HD13	1.86	0.57
18:9A:22:VAL:HG22	18:9A:23:LYS:H	1.69	0.57
26:14:2441:C:OP2	26:14:2586:C:O2'	2.21	0.57
27:1J:90:C:P	37:45:16:ARG:HH21	2.27	0.57
30:39:125:LEU:HD12	30:39:196:LEU:HD21	1.85	0.57
32:59:6:ARG:H	32:59:6:ARG:HH11	1.53	0.57
32:59:97:ARG:NH2	32:59:98:LEU:O	2.37	0.57
37:45:110:THR:HG23	37:45:113:GLN:HE21	1.68	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:D5:155:LEU:HB2	46:D5:157:LEU:HD13	1.86	0.57
46:D5:158:PRO:HB2	46:D5:159:PRO:HD2	1.85	0.57
1:13:141:A:H2'	1:13:142:G:H8	1.69	0.57
1:13:1318:A:H1'	19:AI:37:ARG:HH21	1.69	0.57
3:2E:79:ARG:NH1	18:9A:87:ARG:HH12	2.02	0.57
26:1H:882:G:N2	26:1H:894:C:H42	2.02	0.57
26:1H:2559:C:O2'	26:1H:2560:C:H5'	2.04	0.57
32:51:4:ILE:HD13	32:51:4:ILE:H	1.70	0.57
34:58:15:LEU:HD12	34:58:136:GLU:HG2	1.86	0.57
45:G8:76:CYS:SG	45:G8:97:ARG:HG2	2.43	0.57
49:K8:58:ALA:O	49:K8:62:THR:HG22	2.04	0.57
1:1G:111:G:H8	1:1G:111:G:O5'	1.87	0.57
1:1G:1037:C:H2'	1:1G:1038:C:C6	2.39	0.57
26:14:67:U:H2'	26:14:68:G:C8	2.39	0.57
26:14:1324:G:N7	61:14:3652:HOH:O	2.33	0.57
27:1J:55:U:HO2'	31:49:29:TRP:CD1	2.22	0.57
31:49:56:ALA:HA	31:49:59:GLU:HB3	1.87	0.57
1:13:221:C:H2'	1:13:222:U:H6	1.69	0.57
1:13:555:C:OP2	12:3I:20:LYS:NZ	2.26	0.57
1:13:1187:G:O5'	9:8E:113:LYS:NZ	2.38	0.57
1:13:1190:G:OP1	3:2E:4:LYS:HA	2.04	0.57
1:13:1379:G:N7	7:6E:2:ALA:HB3	2.20	0.57
26:1H:1338:G:O2'	26:1H:1393:A:N1	2.37	0.57
26:1H:1364:G:N7	48:J8:2:SER:HB3	2.19	0.57
26:1H:1438:U:O2'	26:1H:1439:A:H5'	2.05	0.57
33:61:77:LEU:H	33:61:77:LEU:HD12	1.70	0.57
36:78:15:ARG:CB	36:78:16:ARG:HB2	2.35	0.57
36:78:60:MET:HA	55:Q8:13:ARG:NH1	2.19	0.57
37:88:21:THR:HG21	37:88:100:GLY:C	2.29	0.57
39:A8:56:LEU:C	39:A8:57:LYS:HG2	2.29	0.57
1:1G:604:G:H2'	1:1G:605:U:O4'	2.05	0.57
1:1G:1455:G:H5'	20:BA:32:ALA:HB2	1.86	0.57
2:12:84:GLU:HB3	2:12:219:VAL:HG11	1.87	0.57
10:1A:45:ARG:HB3	10:1A:65:LEU:HB3	1.86	0.57
26:14:1047:G:H2'	26:14:1110:G:H1	1.70	0.57
26:14:1141:U:OP1	34:15:25:ARG:NE	2.34	0.57
26:14:2062:A:O2'	26:14:2063:C:OP1	2.19	0.57
26:14:2064:C:H2'	26:14:2065:C:C6	2.40	0.57
27:1J:16:G:H2'	27:1J:17:C:C6	2.39	0.57
43:A5:13:SER:HB3	43:A5:16:LYS:HD2	1.86	0.57
1:13:1308:U:OP1	13:4I:98:VAL:HG23	2.05	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:13:1374:A:O2'	7:6E:28:ASN:HB3	2.04	0.57
4:3E:74:GLN:O	4:3E:78:LEU:HD13	2.05	0.57
26:1H:5:A:H2'	26:1H:6:A:H8	1.68	0.57
26:1H:1786:A:H2	26:1H:2606:C:H1'	1.69	0.57
26:1H:2001:A:H2'	26:1H:2002:G:C8	2.40	0.57
1:1G:142:G:H2'	1:1G:143:A:H8	1.70	0.57
7:62:26:PHE:O	7:62:30:ILE:HG13	2.05	0.57
26:14:71:A:H2	44:B5:31:HIS:NE2	2.00	0.57
26:14:2420:C:H41	55:M5:31:HIS:HB3	1.68	0.57
37:45:4:PRO:HG2	37:45:7:MET:HE3	1.87	0.57
1:13:659:U:H2'	1:13:660:G:H8	1.70	0.57
26:1H:1332:G:N2	26:1H:1610:A:H8	2.02	0.57
26:1H:1588:C:H2'	26:1H:1589:C:C6	2.37	0.57
26:1H:2275:C:H5'	26:1H:2275:C:H6	1.68	0.57
32:51:101:ARG:NH2	32:51:121:ILE:O	2.38	0.57
40:B8:26:ASP:HB3	40:B8:92:GLY:H	1.70	0.57
47:I8:23:VAL:HA	47:I8:38:VAL:HG22	1.86	0.57
1:1G:501:C:H2'	1:1G:502:G:C8	2.40	0.57
1:1G:652:U:H1'	1:1G:653:A:H2	1.69	0.57
1:1G:967:C:H3'	1:1G:968:A:H2'	1.87	0.57
2:12:221:LEU:HA	2:12:224:GLN:HB2	1.87	0.57
26:14:2850:A:C2	26:14:2851:A:C4	2.93	0.57
26:14:2865:U:C4	26:14:2866:U:C4	2.93	0.57
33:69:80:PRO:HA	33:69:143:SER:HA	1.87	0.57
34:15:28:THR:HG22	34:15:29:LYS:HZ3	1.70	0.57
39:65:106:ARG:NH1	39:65:107:GLU:OE1	2.37	0.57
1:13:963:G:N3	10:1I:55:LYS:NZ	2.52	0.57
1:13:983:A:OP1	14:5I:3:ARG:NH2	2.38	0.57
1:13:1060:C:HO2'	10:1I:56:HIS:HD1	1.52	0.57
14:5I:4:LYS:O	14:5I:7:ILE:HG13	2.05	0.57
26:1H:760:G:OP1	61:1H:3842:HOH:O	2.16	0.57
26:1H:2400:G:H2'	26:1H:2401:U:C6	2.39	0.57
31:41:104:GLU:CD	51:M8:23:GLU:HG3	2.30	0.57
1:1G:255:G:H2'	1:1G:256:U:C6	2.40	0.57
4:32:26:CYS:HA	4:32:31:CYS:CB	2.30	0.57
12:3A:49:ASN:ND2	12:3A:92:ASP:OD2	2.38	0.57
26:14:784:A:H5'	26:14:785:G:OP1	2.05	0.57
26:14:1000:A:C6	26:14:1001:A:N1	2.73	0.57
26:14:1292:U:H2'	26:14:1293:C:C6	2.38	0.57
27:1J:56:G:H4'	27:1J:57:A:C8	2.40	0.57
28:19:70:TRP:CD1	28:19:70:TRP:C	2.83	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:65:51:ALA:HB3	39:65:73:LEU:HG	1.87	0.57
41:85:19:LYS:O	41:85:22:LYS:HG3	2.05	0.57
1:13:401:C:OP2	4:3E:73:ARG:HD3	2.05	0.56
1:13:963:G:H21	10:1I:55:LYS:CE	2.18	0.56
1:13:991:U:HO2'	1:13:992:U:P	2.28	0.56
3:2E:14:ILE:HG13	3:2E:15:THR:N	2.20	0.56
4:3E:111:ALA:HB2	4:3E:120:LEU:HD12	1.87	0.56
26:1H:126:A:OP2	54:P8:19:ARG:HG3	2.04	0.56
26:1H:322:A:OP1	30:31:168:ARG:NH2	2.34	0.56
26:1H:569:U:C4	26:1H:570:G:C6	2.93	0.56
26:1H:1570:A:H2'	26:1H:1571:A:C8	2.39	0.56
26:1H:1794:U:H2'	26:1H:1795:C:H6	1.69	0.56
30:31:66:PRO:O	30:31:67:GLN:CB	2.52	0.56
31:41:16:ARG:O	31:41:20:ILE:HG13	2.05	0.56
41:C8:65:ILE:HD11	41:C8:95:LEU:HB2	1.86	0.56
41:C8:75:ASN:HB3	41:C8:77:SER:N	2.20	0.56
45:G8:87:LYS:HD3	45:G8:89:PHE:HD2	1.70	0.56
46:H8:9:TYR:HE1	46:H8:35:ARG:HD3	1.69	0.56
55:Q8:26:LYS:HB3	55:Q8:42:ARG:NH2	2.20	0.56
1:1G:20:U:H2'	1:1G:21:G:O4'	2.04	0.56
1:1G:736:C:H2'	1:1G:737:A:C8	2.39	0.56
1:1G:1129:C:N3	1:1G:1143:G:N2	2.52	0.56
2:12:97:TRP:CZ3	2:12:99:GLY:HA2	2.40	0.56
6:52:68:PRO:HG2	6:52:71:ARG:HG3	1.86	0.56
26:14:1639:U:P	61:14:3519:HOH:O	2.62	0.56
29:29:9:VAL:HG12	40:75:8:LYS:HZ1	1.70	0.56
30:39:49:ALA:O	30:39:92:PRO:HB2	2.03	0.56
33:69:130:TYR:HB3	33:69:136:VAL:HG13	1.87	0.56
36:35:97:PRO:HG3	36:35:112:LEU:HD12	1.86	0.56
37:45:29:PHE:HD2	37:45:65:PHE:CE2	2.22	0.56
1:13:1117:G:OP1	61:13:1923:HOH:O	2.18	0.56
5:4E:153:LYS:HD3	5:4E:154:GLY:N	2.19	0.56
26:1H:754:C:H2'	26:1H:755:C:H6	1.69	0.56
26:1H:1858:G:H2'	26:1H:1883:G:N2	2.20	0.56
26:1H:2074:U:H2'	26:1H:2075:U:C6	2.40	0.56
26:1H:2272:U:O4	61:1H:4281:HOH:O	2.17	0.56
26:1H:2313:C:H4'	31:41:91:ARG:HG3	1.86	0.56
34:58:38:HIS:O	41:C8:67:ALA:HB1	2.04	0.56
34:58:46:VAL:CG1	34:58:48:MET:HG3	2.35	0.56
50:L8:38:GLU:OE2	50:L8:38:GLU:N	2.27	0.56
53:O8:16:CYS:O	53:O8:17:LYS:HB2	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:3L:26:A:H3'	57:3L:27:G:H8	1.69	0.56
28:19:146:GLU:HB2	28:19:189:CYS:HB3	1.86	0.56
33:69:6:LEU:HD13	33:69:37:VAL:HG23	1.86	0.56
37:45:34:LEU:HD11	37:45:129:THR:HB	1.86	0.56
40:75:64:ARG:CB	40:75:73:GLU:HG2	2.35	0.56
48:F5:8:SER:HB3	48:F5:66:HIS:CD2	2.40	0.56
1:13:393:A:OP2	16:7I:12:LYS:NZ	2.19	0.56
1:13:468:A:H5"	16:7I:80:PHE:HB3	1.86	0.56
1:13:1497:G:C2'	1:13:1498:U:H5'	2.33	0.56
19:AI:5:LEU:HD13	19:AI:10:PHE:HD1	1.70	0.56
22:1K:9:A:H2	22:1K:11:C:H41	1.52	0.56
24:3K:9:A:H5"	24:3K:11:C:OP2	2.06	0.56
26:1H:125:G:C6	54:P8:10:ARG:HG3	2.40	0.56
26:1H:142:G:H1'	44:F8:37:THR:CG2	2.35	0.56
26:1H:336:C:OP1	45:G8:83:THR:HG23	2.05	0.56
26:1H:518:G:H2'	26:1H:519:U:C6	2.40	0.56
26:1H:2250:G:C4	37:88:82:ARG:HG2	2.40	0.56
28:11:10:THR:OG1	28:11:13:ARG:HB2	2.04	0.56
29:21:63:LEU:HD23	29:21:63:LEU:O	2.05	0.56
31:41:35:GLU:HG3	31:41:36:LYS:HB2	1.86	0.56
32:51:77:LYS:HE2	32:51:138:LYS:HD2	1.87	0.56
37:88:137:TYR:CE1	46:H8:83:PRO:HG3	2.40	0.56
48:J8:18:ILE:HG12	48:J8:37:ILE:HG12	1.86	0.56
51:M8:23:GLU:OE1	51:M8:24:THR:N	2.38	0.56
1:1G:36:C:OP1	12:3A:123:LYS:NZ	2.26	0.56
1:1G:130:A:C8	17:8A:63:ARG:HG3	2.40	0.56
1:1G:456:C:H2'	1:1G:457:C:H6	1.70	0.56
1:1G:1413:A:H2'	1:1G:1414:U:O4'	2.05	0.56
6:52:10:LEU:HD11	6:52:61:LEU:HD22	1.86	0.56
7:62:92:SER:O	7:62:96:GLN:HG3	2.05	0.56
13:4A:17:VAL:HG13	13:4A:27:LYS:HZ3	1.69	0.56
13:4A:33:ALA:O	13:4A:37:THR:OG1	2.13	0.56
26:14:547:A:N7	26:14:548:A:N6	2.53	0.56
26:14:1171:G:N2	26:14:1174:A:N1	2.53	0.56
26:14:1542:G:O6	26:14:1543:A:N6	2.37	0.56
26:14:1778:U:H2'	26:14:1784:A:N6	2.19	0.56
26:14:2239:G:P	61:14:3504:HOH:O	2.63	0.56
26:14:2257:U:O2'	26:14:2258:C:H5'	2.05	0.56
29:29:25:VAL:O	29:29:26:ILE:HG12	2.05	0.56
32:59:137:ASP:CB	32:59:140:LYS:HB2	2.34	0.56
33:69:52:ARG:HA	33:69:55:ALA:HB3	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:45:116:GLU:OE2	37:45:119:ARG:NE	2.38	0.56
39:65:42:ASP:O	39:65:43:GLU:HB2	2.05	0.56
45:C5:17:SER:OG	45:C5:18:GLY:O	2.23	0.56
55:M5:31:HIS:O	55:M5:32:LEU:HD12	2.05	0.56
1:13:658:G:H2'	1:13:659:U:C6	2.41	0.56
3:2E:128:PHE:HZ	3:2E:132:ARG:HD2	1.70	0.56
26:1H:563:G:P	61:1H:3632:HOH:O	2.64	0.56
26:1H:1216:G:OP2	41:C8:12:ARG:NH2	2.35	0.56
26:1H:1332:G:H21	26:1H:1610:A:H8	1.53	0.56
29:21:3:GLY:HA3	29:21:81:ILE:HG21	1.87	0.56
34:58:137:LYS:HE3	34:58:138:LEU:C	2.31	0.56
37:88:66:ILE:HG22	37:88:67:ARG:N	2.20	0.56
39:A8:5:THR:HG1	39:A8:8:GLU:HG3	1.69	0.56
42:D8:25:LEU:HD11	42:D8:94:LEU:HD11	1.87	0.56
52:N8:50:GLY:N	52:N8:56:LYS:HG3	2.17	0.56
1:1G:57:G:H2'	1:1G:58:C:C6	2.40	0.56
26:14:107:C:H2'	26:14:108:U:H6	1.70	0.56
26:14:273(C):C:H42	26:14:363(C):G:H1	1.53	0.56
26:14:667:U:O2	55:M5:2:PRO:HD2	2.05	0.56
26:14:754:C:H2'	26:14:755:C:C6	2.41	0.56
27:1J:44:G:H1'	27:1J:47:C:N4	2.20	0.56
35:25:3:GLN:HB2	35:25:4:PRO:HD2	1.87	0.56
37:45:89:ASN:C	37:45:89:ASN:HD22	2.13	0.56
46:D5:128:VAL:HG11	46:D5:133:ILE:HG23	1.88	0.56
50:H5:59:VAL:HG12	50:H5:60:GLU:H	1.68	0.56
55:M5:29:LYS:HB3	55:M5:44:LYS:HB3	1.88	0.56
1:13:1149:C:H2'	1:13:1150:U:C6	2.41	0.56
17:8I:100:LYS:HB3	17:8I:101:ARG:NH1	2.20	0.56
26:1H:1994:C:O2'	26:1H:1995:U:H5'	2.05	0.56
26:1H:2002:G:N7	61:1H:4267:HOH:O	2.31	0.56
26:1H:2285:C:OP2	53:O8:28:ARG:HG3	2.05	0.56
34:58:96:GLU:HB2	34:58:122:VAL:HG12	1.87	0.56
51:M8:40:HIS:CG	51:M8:45:GLY:HA3	2.41	0.56
55:Q8:34:TRP:CZ2	55:Q8:39:LYS:HB2	2.40	0.56
55:Q8:57:ARG:CB	55:Q8:59:LYS:HE2	2.32	0.56
1:1G:448:A:OP2	1:1G:485:G:N1	2.34	0.56
1:1G:512:U:H2'	1:1G:513:C:H6	1.70	0.56
1:1G:1291:G:H4'	9:82:39:GLY:HA3	1.88	0.56
16:7A:11:SER:H	16:7A:14:ASN:HB3	1.70	0.56
19:AA:66:MET:HE3	19:AA:66:MET:H	1.71	0.56
26:14:235:U:H2'	26:14:236:C:C6	2.41	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:14:446:G:OP2	61:14:3827:HOH:O	2.17	0.56
26:14:660:G:H21	36:35:12:ALA:HB2	1.70	0.56
26:14:1425:G:N2	26:14:1573:G:N7	2.54	0.56
26:14:2689:U:P	26:14:2719:G:H22	2.28	0.56
51:I5:23:GLU:HG3	51:I5:24:THR:H	1.71	0.56
51:I5:23:GLU:HG3	51:I5:24:THR:N	2.20	0.56
1:13:458:C:H2'	1:13:464:G:O4'	2.06	0.56
1:13:1300:G:N7	61:13:1951:HOH:O	2.33	0.56
2:1E:67:THR:HG21	2:1E:155:LEU:HG	1.87	0.56
2:1E:209:ARG:HG3	2:1E:240:GLN:HE22	1.71	0.56
26:1H:270(J):G:H2'	26:1H:270(K):C:O4'	2.06	0.56
26:1H:524:U:H2'	26:1H:525:U:H6	1.71	0.56
26:1H:654:A:H3'	26:1H:654:A:N3	2.20	0.56
26:1H:1187:G:O6	61:1H:4501:HOH:O	2.15	0.56
26:1H:1314:C:OP1	61:1H:3971:HOH:O	2.18	0.56
26:1H:1337:G:H2'	26:1H:1338:G:H8	1.70	0.56
26:1H:1534:G:N2	26:1H:1538:G:H22	2.03	0.56
26:1H:2128:C:H2'	26:1H:2129:C:C6	2.41	0.56
55:Q8:44:LYS:HG3	55:Q8:45:GLY:N	2.21	0.56
1:1G:512:U:H2'	1:1G:513:C:C6	2.40	0.56
1:1G:999:U:H2'	1:1G:1000:A:C8	2.40	0.56
1:1G:1203:C:H2'	1:1G:1204:A:O4'	2.06	0.56
15:6A:87:ILE:HG22	15:6A:88:ARG:N	2.18	0.56
20:BA:72:LEU:O	20:BA:73:HIS:HB2	2.06	0.56
26:14:71:A:H5'	26:14:71:A:C8	2.41	0.56
26:14:576:U:P	61:14:3663:HOH:O	2.63	0.56
26:14:673:C:H4'	30:39:82:ILE:HG12	1.88	0.56
26:14:2134:A:OP2	26:14:2157:G:N2	2.39	0.56
30:39:79:GLY:HA2	30:39:86:GLY:HA2	1.86	0.56
32:59:7:LEU:HD12	32:59:8:PRO:HD3	1.87	0.56
42:95:29:PRO:HA	42:95:61:VAL:HG11	1.87	0.56
1:13:1530:G:H3'	1:13:1531:A:P	2.46	0.56
19:AI:7:LYS:HB3	19:AI:7:LYS:NZ	2.21	0.56
24:3K:15:G:H22	24:3K:21:A:H8	1.53	0.56
26:1H:71:A:C2	44:F8:31:HIS:CE1	2.83	0.56
26:1H:82:G:O6	61:1H:4559:HOH:O	2.18	0.56
26:1H:389:G:H1	36:78:71:VAL:HG12	1.71	0.56
31:41:11:TYR:OH	31:41:16:ARG:NH1	2.39	0.56
41:C8:92:ARG:CA	41:C8:95:LEU:HD23	2.35	0.56
46:H8:126:VAL:HG12	46:H8:163:LEU:HA	1.87	0.56
1:1G:1055:A:N3	3:22:156:ARG:NH1	2.54	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:82:18:PHE:HD2	9:82:62:TYR:HD2	1.54	0.56
20:BA:25:ARG:HG3	20:BA:29:LYS:HE3	1.88	0.56
28:19:49:ILE:HD11	28:19:52:ARG:HA	1.87	0.56
1:13:872:A:C5	1:13:874:G:C8	2.93	0.56
1:13:1182:G:H4'	1:13:1183:A:H5"	1.87	0.56
1:13:1226:C:H4'	19:AI:80:TYR:OH	2.06	0.56
1:13:1510:U:H2'	1:13:1511:G:C8	2.41	0.56
8:7E:88:LYS:HB3	8:7E:89:PRO:HD2	1.87	0.56
19:AI:39:THR:HG22	19:AI:40:ILE:H	1.71	0.56
20:BI:35:THR:O	20:BI:38:LYS:HB2	2.06	0.56
26:1H:950:G:H2'	26:1H:951:C:C6	2.41	0.56
37:88:59:ARG:C	37:88:61:GLY:H	2.12	0.56
41:C8:34:LYS:HE2	41:C8:34:LYS:HA	1.87	0.56
45:G8:84:ARG:HD2	45:G8:84:ARG:C	2.29	0.56
45:G8:87:LYS:N	45:G8:94:LYS:HG2	2.19	0.56
46:H8:52:SER:O	46:H8:52:SER:OG	2.18	0.56
1:1G:355:C:O2'	1:1G:388:G:N3	2.39	0.56
1:1G:765:G:N2	1:1G:813:U:OP2	2.31	0.56
1:1G:983:A:H3'	1:1G:983:A:N3	2.21	0.56
1:1G:1095:U:P	1:1G:1108:G:H1	2.27	0.56
3:22:18:TRP:CD1	14:5A:54:PRO:HA	2.41	0.56
8:72:83:ILE:HG13	8:72:137:VAL:HG22	1.86	0.56
9:82:43:ALA:HA	9:82:74:ILE:HD13	1.88	0.56
12:3A:37:CYS:HA	12:3A:58:VAL:HA	1.86	0.56
12:3A:47:LYS:CG	12:3A:48:PRO:HD2	2.35	0.56
13:4A:3:ARG:HB2	51:I5:34:GLU:HG3	1.88	0.56
26:14:273(C):C:H5'	26:14:273(D):C:OP2	2.05	0.56
26:14:2378:A:O2'	39:65:21:THR:HG21	2.06	0.56
35:25:1:MET:HE2	35:25:32:TYR:CD1	2.41	0.56
36:35:95:VAL:HA	36:35:99:LEU:HD23	1.88	0.56
37:45:57:HIS:CG	37:45:117:ALA:HB2	2.40	0.56
46:D5:76:LEU:HA	46:D5:83:PRO:HA	1.88	0.56
1:13:200:G:H1	1:13:217:C:H42	1.53	0.56
1:13:757:U:H2'	1:13:758:G:O4'	2.04	0.56
1:13:1429:C:H2'	1:13:1430:C:C6	2.41	0.56
7:6E:122:HIS:HA	7:6E:125:MET:HE2	1.87	0.56
12:3I:57:LYS:HZ2	12:3I:67:THR:HG22	1.70	0.56
24:3K:13:C:H2'	24:3K:14:A:H8	1.71	0.56
24:3K:15:G:C6	24:3K:48:C:N4	2.74	0.56
26:1H:265:A:H1'	26:1H:266:G:O4'	2.05	0.56
26:1H:916:G:C2'	26:1H:917:A:H5"	2.36	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1H:1316:U:H2'	26:1H:1317:A:H8	1.69	0.56
26:1H:2298:A:H2'	26:1H:2299:G:O4'	2.06	0.56
26:1H:2577:A:P	61:1H:3811:HOH:O	2.64	0.56
29:21:78:LEU:HD23	29:21:78:LEU:O	2.05	0.56
35:68:98:VAL:HG13	35:68:117:LEU:HB3	1.87	0.56
37:88:135:ASP:HB3	37:88:137:TYR:H	1.70	0.56
44:F8:1:MET:HG2	44:F8:2:LYS:H	1.71	0.56
46:H8:141:VAL:HG21	46:H8:150:LEU:HD11	1.88	0.56
1:1G:985:C:N3	1:1G:1220:G:N2	2.52	0.56
1:1G:1028(A):C:O2	1:1G:1033:G:N2	2.39	0.56
1:1G:1114:C:H1'	14:5A:60:SER:HB2	1.88	0.56
5:42:151:LEU:HD13	8:72:77:GLU:HG2	1.88	0.56
20:BA:82:SER:OG	20:BA:86:ARG:NH2	2.39	0.56
21:1B:2:GLY:O	21:1B:4:GLY:N	2.39	0.56
26:14:1794:U:H2'	26:14:1795:C:C6	2.41	0.56
26:14:2074:U:P	61:14:3503:HOH:O	2.59	0.56
34:15:42:TRP:HA	34:15:48:MET:HE1	1.87	0.56
50:H5:7:LYS:HG3	50:H5:34:GLU:HG3	1.86	0.56
1:13:32:A:H2'	1:13:33:A:C8	2.41	0.56
1:13:1156:G:H2'	1:13:1157:A:H5"	1.88	0.56
2:1E:160:ASP:O	2:1E:183:PRO:HD2	2.06	0.56
20:BI:49:ALA:HB1	20:BI:99:LEU:HB2	1.87	0.56
26:1H:242:G:H5'	55:Q8:60:LEU:HD13	1.88	0.56
26:1H:1385:G:O6	26:1H:1403:C:N4	2.39	0.56
26:1H:1533:C:H2'	26:1H:1534:G:C2	2.41	0.56
34:58:34:LEU:HD21	34:58:120:LEU:HB2	1.88	0.56
36:78:39:LYS:HG3	36:78:45:LEU:HD22	1.86	0.56
38:98:27:SER:HB3	38:98:34:ILE:HD11	1.88	0.56
46:H8:40:ASP:HB3	46:H8:43:GLU:HB2	1.87	0.56
1:1G:191(F):U:H2'	1:1G:191:G:C8	2.41	0.56
1:1G:980:C:H3'	1:1G:981:U:C6	2.40	0.56
1:1G:991:U:O2	1:1G:993:G:H8	1.88	0.56
1:1G:1382:C:O2'	57:3L:34:G:N7	2.37	0.56
9:82:17:VAL:HA	9:82:63:ILE:HG12	1.88	0.56
13:4A:19:LEU:HB2	13:4A:25:ILE:HG21	1.88	0.56
13:4A:57:ARG:HH12	51:I5:17:GLY:HA3	1.70	0.56
19:AA:29:ARG:HH12	19:AA:47:HIS:HA	1.71	0.56
26:14:957:A:N6	26:14:2459:A:C8	2.73	0.56
26:14:996:A:N6	26:14:1160:G:C6	2.73	0.56
26:14:2507:C:H5"	26:14:2573:C:N4	2.21	0.56
27:1J:15:A:C5'	27:1J:16:G:H8	2.17	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:13:67:C:H2'	1:13:68:G:H8	1.71	0.55
1:13:247:G:OP2	17:8I:100:LYS:HB2	2.06	0.55
1:13:538:G:OP2	12:3I:115:LYS:HG3	2.06	0.55
12:3I:90:VAL:O	12:3I:91:LYS:HB3	2.06	0.55
14:5I:23:ARG:HD2	14:5I:28:GLY:O	2.06	0.55
26:1H:229:A:OP2	36:78:150:ALA:HB1	2.07	0.55
26:1H:363(A):A:H2'	26:1H:363(B):G:H8	1.71	0.55
26:1H:508:G:N3	26:1H:508:G:H5"	2.20	0.55
26:1H:986:C:H3'	61:1H:4017:HOH:O	2.06	0.55
26:1H:1257:C:H4'	30:31:83:PHE:CD1	2.42	0.55
26:1H:2308:G:N1	26:1H:2311:A:H2	2.01	0.55
28:11:164:GLN:NE2	28:11:166:GLN:OE1	2.36	0.55
41:C8:8:VAL:HG23	41:C8:11:ARG:NH2	2.20	0.55
46:H8:151:HIS:ND1	46:H8:168:GLU:HG3	2.21	0.55
50:L8:31:LEU:HB3	50:L8:32:GLN:OE1	2.07	0.55
5:42:141:GLN:HA	5:42:143:ARG:HH21	1.70	0.55
11:2A:12:ARG:NH2	11:2A:13:GLN:O	2.39	0.55
26:14:329:G:O6	45:C5:19:LYS:HG2	2.06	0.55
26:14:920:G:H2'	26:14:921:G:H8	1.70	0.55
26:14:1364:G:OP2	48:F5:2:SER:N	2.39	0.55
26:14:1636:C:P	61:14:3631:HOH:O	2.64	0.55
39:65:64:GLU:O	39:65:68:GLN:HG3	2.05	0.55
54:L5:24:THR:O	54:L5:28:ARG:HG3	2.06	0.55
1:13:1429:C:H2'	1:13:1430:C:H6	1.70	0.55
23:2K:48:U:O2'	23:2K:49:C:OP2	2.22	0.55
26:1H:309:G:N3	26:1H:329:G:O2'	2.38	0.55
26:1H:1509:C:N3	26:1H:1511:A:N6	2.54	0.55
26:1H:1693:U:H1'	28:11:14:ARG:NH2	2.21	0.55
26:1H:1899:G:H22	26:1H:1902:C:N4	2.04	0.55
26:1H:2062:A:P	61:1H:3859:HOH:O	2.63	0.55
28:11:70:TRP:CD1	28:11:70:TRP:C	2.84	0.55
28:11:102:LYS:C	28:11:103:ARG:HG2	2.31	0.55
32:51:149:ARG:NH1	32:51:167:GLU:OE2	2.37	0.55
39:A8:10:ARG:O	39:A8:14:VAL:HG13	2.05	0.55
39:A8:106:ARG:CZ	39:A8:107:GLU:HB2	2.36	0.55
46:H8:7:ALA:HB2	46:H8:59:LEU:HD22	1.88	0.55
55:Q8:8:LYS:H	55:Q8:8:LYS:HD2	1.70	0.55
3:22:39:ILE:O	3:22:43:LEU:HB2	2.06	0.55
7:62:94:ARG:O	7:62:97:GLN:HB3	2.06	0.55
12:3A:28:LYS:HE3	12:3A:33:ARG:HH12	1.70	0.55
28:19:166:GLN:HB3	28:19:174:ILE:HG22	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:69:2:LYS:HA	33:69:20:ASP:HA	1.88	0.55
36:35:85:LEU:HA	36:35:88:LEU:HB3	1.86	0.55
37:45:57:HIS:NE2	37:45:116:GLU:HB3	2.21	0.55
39:65:110:LEU:HB3	39:65:112:PHE:HE1	1.71	0.55
5:4E:147:ASP:HA	5:4E:150:ARG:NH1	2.21	0.55
19:AI:5:LEU:CB	19:AI:10:PHE:HE1	2.18	0.55
19:AI:41:VAL:O	51:M8:63:TYR:OH	2.24	0.55
26:1H:275:G:N7	26:1H:363:G:C4	2.74	0.55
26:1H:330:A:H2	26:1H:1210:A:O2'	1.88	0.55
26:1H:1038:C:H2'	26:1H:1039:G:O4'	2.07	0.55
26:1H:1061:U:N3	26:1H:1063:G:OP1	2.38	0.55
26:1H:1433:U:O2	26:1H:1561:G:C2	2.59	0.55
26:1H:1441:G:H2'	26:1H:1442:G:H8	1.71	0.55
26:1H:2419:U:C5'	53:O8:23:THR:HG21	2.31	0.55
26:1H:2469:A:H2	26:1H:2481:G:H21	1.51	0.55
29:21:111:ARG:HD2	29:21:160:TYR:CD2	2.41	0.55
30:31:12:LEU:O	30:31:127:GLU:N	2.39	0.55
30:31:39:TRP:O	30:31:43:LYS:HG2	2.06	0.55
42:D8:76:LYS:O	42:D8:79:VAL:HG12	2.06	0.55
47:I8:47:PRO:HG3	47:I8:53:MET:HB2	1.87	0.55
1:1G:766:A:OP2	61:1G:1765:HOH:O	2.18	0.55
1:1G:804:U:H5"	1:1G:805:C:OP2	2.07	0.55
26:14:30:G:H2'	26:14:31:C:C6	2.41	0.55
26:14:729:G:OP2	28:19:13:ARG:NH1	2.38	0.55
26:14:1266:G:O4'	43:A5:15:ARG:NH2	2.38	0.55
30:39:148:LEU:HD11	30:39:193:VAL:HG21	1.88	0.55
36:35:121:LYS:HG3	36:35:122:PRO:HD2	1.88	0.55
38:55:106:GLY:O	38:55:107:ASP:HB3	2.05	0.55
1:13:626:U:C2	1:13:627:G:C8	2.94	0.55
2:1E:163:PHE:CD1	2:1E:185:ILE:HB	2.42	0.55
13:4I:40:ASN:HB3	13:4I:43:THR:HG23	1.89	0.55
13:4I:108:ARG:HG3	13:4I:108:ARG:HH11	1.71	0.55
17:8I:45:HIS:HB2	17:8I:65:ILE:HD13	1.87	0.55
24:3K:33:U:C2	24:3K:35:A:H5'	2.42	0.55
26:1H:7:G:N2	26:1H:8:A:N3	2.54	0.55
26:1H:1329:U:H5"	26:1H:1330:C:H5	1.72	0.55
26:1H:1420:U:HO2'	26:1H:1421:G:P	2.29	0.55
26:1H:2019:A:N7	52:N8:9:LYS:HE3	2.21	0.55
26:1H:2820:A:OP1	38:98:2:ARG:NH2	2.38	0.55
26:1H:2852:G:H2'	26:1H:2853:C:O4'	2.06	0.55
31:41:107:LEU:HD21	31:41:178:PHE:CE1	2.41	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1G:250:A:H1'	1:1G:251:G:OP2	2.07	0.55
1:1G:1004:A:C6	1:1G:1025:U:H1'	2.41	0.55
1:1G:1157:A:H61	1:1G:1178:G:N2	1.94	0.55
1:1G:1328:C:O2'	13:4A:29:ARG:NE	2.35	0.55
1:1G:1508:G:H8	1:1G:1508:G:O5'	1.89	0.55
2:12:212:GLN:O	2:12:216:SER:N	2.26	0.55
4:32:173:TRP:CZ3	4:32:193:ASP:HB3	2.41	0.55
7:62:89:MET:HE3	7:62:155:ARG:HG3	1.89	0.55
56:1L:19:G:O2'	56:1L:57:G:N2	2.39	0.55
26:14:95:G:H4'	49:G5:46:GLN:HB2	1.87	0.55
26:14:138:G:N2	44:B5:44:GLU:OE2	2.29	0.55
26:14:2353:G:H4'	47:E5:33:ALA:HB3	1.87	0.55
27:1J:93:C:H2'	27:1J:94:C:H6	1.72	0.55
31:49:103:LEU:HD22	31:49:178:PHE:HZ	1.70	0.55
33:69:76:THR:HG23	33:69:77:LEU:H	1.72	0.55
1:13:345:C:O2'	1:13:346:G:N2	2.39	0.55
1:13:1157:A:N6	1:13:1178:G:H21	2.05	0.55
22:1K:76:A:H8	26:1H:2583:G:H21	1.47	0.55
26:1H:1378:A:O2'	26:1H:1379:A:H5"	2.06	0.55
26:1H:1534:G:H3'	26:1H:1534:G:N3	2.22	0.55
26:1H:1796:U:H2'	26:1H:1797:C:C6	2.41	0.55
26:1H:2373:G:H2'	26:1H:2374:C:C6	2.42	0.55
26:1H:2867:G:OP2	40:B8:119:LYS:NZ	2.26	0.55
35:68:7:TYR:HE1	35:68:20:MET:HE3	1.72	0.55
47:I8:36:ILE:O	47:I8:36:ILE:HD13	2.06	0.55
49:K8:47:ASN:O	49:K8:49:LYS:N	2.38	0.55
3:22:113:ALA:HA	3:22:202:ILE:HD11	1.89	0.55
26:14:614:U:H4'	26:14:615:G:OP1	2.05	0.55
27:1J:117:G:O5'	27:1J:117:G:H8	1.90	0.55
46:D5:144:LEU:HD23	46:D5:144:LEU:H	1.72	0.55
50:H5:44:ARG:O	50:H5:48:GLU:HG3	2.07	0.55
1:13:272:C:H2'	1:13:273:A:C8	2.42	0.55
1:13:1028:C:H42	1:13:1033:G:H1	1.54	0.55
8:7E:13:ILE:O	8:7E:17:THR:HG23	2.07	0.55
26:1H:34:C:OP2	26:1H:34:C:C6	2.60	0.55
26:1H:1021:A:C8	26:1H:1022:G:H5"	2.41	0.55
26:1H:1533:C:H3'	26:1H:1534:G:C5'	2.36	0.55
26:1H:2146:C:H4'	26:1H:2147:G:N7	2.21	0.55
26:1H:2147:G:H2'	26:1H:2148:G:H4'	1.88	0.55
27:16:7:G:O5'	39:A8:29:PHE:CE2	2.60	0.55
30:31:160:ASN:OD1	30:31:163:VAL:HG23	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:58:95:PRO:O	34:58:96:GLU:CD	2.50	0.55
37:88:21:THR:HG22	37:88:99:PRO:O	2.06	0.55
46:H8:124:ILE:HD12	46:H8:125:LEU:H	1.72	0.55
1:1G:1187:G:H5'	9:82:113:LYS:HZ3	1.71	0.55
1:1G:1387:G:H2'	1:1G:1388:C:C6	2.40	0.55
26:14:654(D):G:H22	26:14:654(Q):C:N4	2.05	0.55
26:14:2839:G:H21	38:55:92:GLY:HA2	1.71	0.55
42:95:37:VAL:HG21	42:95:57:VAL:H	1.72	0.55
1:13:377:G:H5'	16:7I:5:ARG:HH12	1.72	0.55
1:13:509:A:H5'	4:3E:54:TYR:HD2	1.72	0.55
1:13:805:C:O2'	1:13:806:C:H5'	2.07	0.55
4:3E:108:LEU:HD23	4:3E:110:PHE:HE1	1.71	0.55
19:AI:51:VAL:O	19:AI:57:HIS:HA	2.07	0.55
23:2K:24:C:H2'	23:2K:25:U:C6	2.42	0.55
26:1H:575:A:O3'	61:1H:4546:HOH:O	2.18	0.55
26:1H:600:G:N2	26:1H:605:C:O3'	2.39	0.55
26:1H:732:C:H3'	61:1H:4112:HOH:O	2.07	0.55
26:1H:1899:G:H1	26:1H:1902:C:N4	2.05	0.55
27:16:15:A:H3'	27:16:16:G:H5'	1.88	0.55
33:61:7:GLU:O	33:61:9:LEU:HD22	2.06	0.55
34:58:133:GLN:HG2	34:58:134:ARG:H	1.72	0.55
51:M8:4:GLY:C	51:M8:5:ILE:HG13	2.32	0.55
1:1G:406:G:H1	1:1G:436:C:H42	1.55	0.55
11:2A:32:ILE:HD11	11:2A:68:ALA:HB1	1.89	0.55
11:2A:32:ILE:HD13	11:2A:72:ALA:HB2	1.89	0.55
12:3A:27:LEU:HG	12:3A:33:ARG:HG2	1.88	0.55
26:14:433:C:C4	26:14:434:U:O4	2.60	0.55
26:14:519:U:H2'	26:14:520:G:H8	1.70	0.55
26:14:588:U:O4	26:14:670:A:H1'	2.07	0.55
26:14:2496:C:P	37:45:81:VAL:HG12	2.47	0.55
36:35:18:ARG:O	36:35:19:VAL:HG23	2.07	0.55
40:75:24:PRO:HD3	40:75:52:ILE:HD12	1.89	0.55
26:1H:66:C:H2'	26:1H:67:U:H6	1.72	0.55
26:1H:2393:A:H2'	26:1H:2394:C:C6	2.41	0.55
26:1H:2801:A:H5'	26:1H:2895:U:H1'	1.88	0.55
1:1G:1220:G:O3'	19:AA:36:ARG:HD3	2.06	0.55
9:82:102:LEU:O	9:82:103:THR:OG1	2.20	0.55
15:6A:79:ARG:HA	15:6A:82:ILE:HG22	1.87	0.55
16:7A:22:THR:HA	16:7A:33:ILE:HG13	1.88	0.55
26:14:979:G:H3'	26:14:980:A:C5'	2.36	0.55
26:14:1022:G:O2'	26:14:1023:U:OP2	2.24	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:14:2781:A:H5"	26:14:2782:G:H5'	1.89	0.55
27:1J:48:A:H4'	39:65:95:HIS:CD2	2.39	0.55
41:85:92:ARG:C	41:85:94:ASN:H	2.15	0.55
4:3E:98:GLU:O	4:3E:103:ASN:ND2	2.39	0.55
5:4E:91:LEU:HD12	5:4E:120:THR:HG22	1.89	0.55
26:1H:517:C:OP1	52:N8:16:ARG:NH2	2.32	0.55
26:1H:1152:C:H3'	61:1H:4023:HOH:O	2.07	0.55
26:1H:2346:A:O2'	53:O8:24:GLU:OE2	2.25	0.55
26:1H:2845:G:O2'	26:1H:2846:G:H5'	2.06	0.55
29:21:48:GLN:OE1	29:21:77:ILE:HG21	2.06	0.55
30:31:197:ASP:O	30:31:199:TRP:N	2.40	0.55
26:14:1970:A:P	61:14:3573:HOH:O	2.65	0.55
26:14:2280:G:O2'	26:14:2388:A:N1	2.37	0.55
26:14:2291:U:H2'	26:14:2292:C:C6	2.42	0.55
26:14:2448:A:N1	61:14:3799:HOH:O	2.33	0.55
1:13:165:C:H2'	1:13:166:G:H8	1.71	0.55
1:13:624:C:O3'	16:7I:10:GLY:HA2	2.06	0.55
1:13:1015:A:N3	1:13:1218:C:O2'	2.37	0.55
3:2E:128:PHE:CZ	3:2E:132:ARG:HD2	2.42	0.55
4:3E:129:ASN:ND2	4:3E:144:ASP:OD1	2.38	0.55
10:1I:26:ALA:HB1	10:1I:84:GLN:HG2	1.89	0.55
23:2K:17:C:H3'	23:2K:18:C:H2'	1.88	0.55
26:1H:731:C:P	61:1H:3685:HOH:O	2.63	0.55
26:1H:768:G:O2'	26:1H:1379:A:N6	2.40	0.55
34:58:129:PRO:O	34:58:134:ARG:NH1	2.40	0.55
47:I8:11:ARG:O	47:I8:14:ARG:NH2	2.40	0.55
1:1G:426:G:OP1	4:32:38:TYR:OH	2.21	0.55
21:1B:9:ARG:HE	21:1B:10:ARG:HG3	1.72	0.55
57:3L:71:G:O2'	26:14:1851:U:O2'	2.01	0.55
26:14:870:A:OP1	37:45:6:ARG:HD3	2.07	0.55
26:14:1204:A:C2	26:14:1241:A:N1	2.75	0.55
26:14:2839:G:H21	38:55:92:GLY:CA	2.20	0.55
29:29:68:ALA:C	29:29:70:ALA:H	2.15	0.55
31:49:97:ASP:HA	31:49:100:TRP:HD1	1.71	0.55
50:H5:46:ASN:O	50:H5:50:VAL:HG22	2.06	0.55
1:13:165:C:H2'	1:13:166:G:C8	2.42	0.54
1:13:555:C:H2'	1:13:556:C:C6	2.42	0.54
1:13:991:U:C4	1:13:1212:U:H1'	2.42	0.54
7:6E:89:MET:HE3	7:6E:155:ARG:HB2	1.89	0.54
9:8E:17:VAL:HG21	9:8E:80:GLY:HA3	1.89	0.54
10:1I:78:ASN:HB2	10:1I:81:THR:HG23	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:2I:78:GLN:O	11:2I:103:LEU:HA	2.08	0.54
22:1K:74:C:O2'	22:1K:75:C:O5'	2.23	0.54
23:2K:54:G:H2'	23:2K:55:5MU:C6	2.39	0.54
26:1H:2052:G:H4'	29:21:143:ASN:O	2.07	0.54
29:21:13:ARG:HH11	29:21:13:ARG:CG	2.19	0.54
34:58:26:LEU:O	34:58:30:ILE:HG13	2.06	0.54
37:88:11:LYS:HE2	37:88:86:GLY:HA2	1.89	0.54
49:K8:15:LYS:HA	49:K8:67:LYS:HZ1	1.71	0.54
49:K8:47:ASN:C	49:K8:49:LYS:H	2.15	0.54
51:M8:39:CYS:SG	51:M8:41:PRO:HD3	2.47	0.54
53:O8:9:LEU:N	53:O8:27:LYS:HA	2.23	0.54
53:O8:13:CYS:O	53:O8:21:TYR:HB3	2.07	0.54
55:Q8:46:ARG:HH11	55:Q8:46:ARG:CG	2.20	0.54
55:Q8:49:VAL:HG22	55:Q8:50:LEU:HA	1.87	0.54
1:1G:458:C:H2'	1:1G:464:G:C8	2.41	0.54
2:12:30:ARG:HH21	2:12:194:PRO:HB2	1.72	0.54
5:42:76:ILE:HG12	5:42:118:ILE:HG13	1.89	0.54
9:82:27:THR:HB	9:82:32:ASP:HA	1.87	0.54
11:2A:48:ILE:HD11	11:2A:64:ALA:HA	1.88	0.54
12:3A:46:LYS:HG2	12:3A:47:LYS:N	2.22	0.54
56:1L:18:G:O2'	56:1L:60:U:O4	2.24	0.54
26:14:574:C:OP2	61:14:3656:HOH:O	2.18	0.54
31:49:50:ALA:HB2	31:49:87:PRO:HG3	1.89	0.54
43:A5:18:ARG:HG3	43:A5:76:VAL:HG13	1.89	0.54
53:K5:51:GLU:HG2	53:K5:52:VAL:H	1.70	0.54
1:13:1291:G:OP1	7:6E:37:ASN:ND2	2.40	0.54
12:3I:87:GLY:HA2	12:3I:98:TYR:HA	1.88	0.54
17:8I:45:HIS:CE1	17:8I:47:PRO:HG3	2.41	0.54
19:AI:42:PRO:HD2	19:AI:43:GLU:OE1	2.07	0.54
26:1H:125:G:H5'	26:1H:125:G:H8	1.72	0.54
26:1H:620:G:H4'	26:1H:621:A:C5'	2.36	0.54
26:1H:888:C:H2'	26:1H:889:C:C2	2.42	0.54
26:1H:890:A:H3'	26:1H:892:G:H8	1.71	0.54
26:1H:960:A:H61	37:88:82:ARG:HH21	1.53	0.54
26:1H:1510:A:O2'	26:1H:1512:G:N7	2.37	0.54
26:1H:1639:U:H4'	26:1H:2699:C:H4'	1.90	0.54
26:1H:2127:G:N2	26:1H:2162:G:H1'	2.22	0.54
29:21:13:ARG:HG2	29:21:13:ARG:NH1	2.20	0.54
31:41:28:VAL:O	31:41:31:VAL:HG13	2.07	0.54
46:H8:103:ARG:HB2	46:H8:138:GLU:HA	1.90	0.54
1:1G:560:U:H4'	1:1G:561:U:O5'	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1G:980:C:H5'	1:1G:981:U:C5	2.42	0.54
10:1A:45:ARG:O	10:1A:65:LEU:N	2.34	0.54
19:AA:18:LYS:HG2	19:AA:31:ILE:HD13	1.88	0.54
26:14:596:G:H2'	26:14:597:U:O4'	2.07	0.54
26:14:997:G:OP1	41:85:93:LYS:HB2	2.07	0.54
26:14:2303:G:H2'	26:14:2304:G:H5'	1.89	0.54
27:1J:15:A:H5'	27:1J:16:G:C8	2.32	0.54
27:1J:44:G:H5"	27:1J:45:A:OP1	2.07	0.54
32:59:6:ARG:HH11	32:59:6:ARG:N	2.05	0.54
36:35:62:LEU:HD13	36:35:63:PRO:O	2.07	0.54
42:95:57:VAL:HG23	42:95:99:ILE:H	1.72	0.54
48:F5:15:ALA:O	48:F5:40:ARG:HG2	2.07	0.54
49:G5:13:ALA:HA	49:G5:16:LEU:HD23	1.89	0.54
1:13:411:A:C4	1:13:413:G:H1'	2.43	0.54
1:13:475:G:H2'	1:13:476:G:H8	1.73	0.54
1:13:606:G:N3	1:13:632:A:N6	2.55	0.54
1:13:920:U:H2'	1:13:921:U:C6	2.43	0.54
1:13:1060:C:OP1	14:5I:45:ARG:NH2	2.40	0.54
1:13:1368:G:H5"	9:8E:112:LYS:HB3	1.88	0.54
5:4E:147:ASP:OD1	5:4E:147:ASP:N	2.39	0.54
10:1I:54:PHE:CZ	10:1I:55:LYS:NZ	2.67	0.54
11:2I:87:THR:HG22	11:2I:88:GLY:H	1.72	0.54
22:1K:1:G:O6	22:1K:72:C:N4	2.41	0.54
28:11:145:VAL:HG12	28:11:146:GLU:O	2.07	0.54
42:D8:47:VAL:HG23	42:D8:48:GLY:N	2.22	0.54
53:O8:36:LEU:HB3	53:O8:50:ARG:HG2	1.90	0.54
1:1G:1246:C:O2	1:1G:1291:G:N2	2.29	0.54
1:1G:1315:U:H2'	1:1G:1316:G:O4'	2.07	0.54
1:1G:1367:C:H4'	10:1A:48:THR:HG21	1.87	0.54
4:32:112:VAL:HG12	4:32:116:GLN:OE1	2.06	0.54
4:32:150:GLU:C	4:32:152:SER:H	2.14	0.54
16:7A:70:ALA:O	16:7A:74:LEU:HD23	2.08	0.54
26:14:249:C:H4'	26:14:250:G:O5'	2.08	0.54
26:14:870:A:H5"	37:45:6:ARG:HB3	1.87	0.54
26:14:903:C:H2'	26:14:904:C:C6	2.42	0.54
26:14:972:G:OP2	26:14:973:A:O2'	2.23	0.54
26:14:1538:G:H2'	26:14:1539:G:H8	1.72	0.54
26:14:1783:A:H5'	26:14:2608:G:H4'	1.89	0.54
31:49:42:GLY:O	31:49:43:LEU:HD13	2.07	0.54
34:15:85:ILE:HD13	34:15:90:MET:HE3	1.90	0.54
35:25:71:ARG:NH2	35:25:122:LEU:O	2.39	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:55:24:GLN:OE1	38:55:36:THR:HG21	2.06	0.54
39:65:67:ARG:HB2	39:65:67:ARG:CZ	2.36	0.54
1:13:114:U:H2'	1:13:115:G:C8	2.42	0.54
1:13:712:A:O2'	1:13:713:G:H5'	2.07	0.54
1:13:737:A:H2'	1:13:738:C:H6	1.72	0.54
1:13:1194:U:H2'	1:13:1195:C:C6	2.43	0.54
3:2E:72:LYS:HB3	3:2E:75:VAL:HG23	1.90	0.54
4:3E:102:ASP:OD1	4:3E:103:ASN:N	2.41	0.54
13:4I:94:ARG:HH22	26:1H:887:A:H5'	1.71	0.54
26:1H:270(M):U:O2'	26:1H:270(N):G:O5'	2.22	0.54
26:1H:919:G:H4'	27:16:81:G:H4'	1.88	0.54
26:1H:1021:A:H3'	26:1H:1022:G:H5"	1.88	0.54
26:1H:2035:G:OP1	61:1H:3793:HOH:O	2.18	0.54
26:1H:2331:G:O3'	47:I8:43:THR:HG22	2.07	0.54
26:1H:2395:C:H5"	26:1H:2396:G:OP2	2.07	0.54
30:31:7:TYR:O	30:31:22:ALA:N	2.39	0.54
32:51:3:ARG:CZ	32:51:3:ARG:HA	2.37	0.54
39:A8:88:ASP:O	39:A8:90:GLY:N	2.40	0.54
53:O8:30:THR:HA	53:O8:31:PRO:C	2.32	0.54
1:1G:8:A:N7	4:32:209:ARG:HA	2.23	0.54
1:1G:1116:C:H42	1:1G:1184:G:H1	1.55	0.54
1:1G:1133:G:N2	1:1G:1141:C:O2	2.40	0.54
1:1G:1206:G:H4'	3:22:192:THR:O	2.07	0.54
1:1G:1372:U:H2'	1:1G:1373:G:O4'	2.06	0.54
2:12:145:LEU:O	2:12:149:LEU:HB2	2.07	0.54
3:22:18:TRP:H	3:22:18:TRP:HE3	1.55	0.54
4:32:30:LYS:HB2	4:32:35:ARG:HD2	1.89	0.54
6:52:70:ASP:OD1	6:52:70:ASP:N	2.39	0.54
7:62:84:ASN:OD1	7:62:84:ASN:N	2.38	0.54
11:2A:13:GLN:HA	11:2A:75:TYR:O	2.07	0.54
56:1L:35:A:H2'	56:1L:36:A:O4'	2.08	0.54
26:14:247:G:H4'	26:14:386:G:C5	2.43	0.54
26:14:311:A:C6	26:14:328:U:C4	2.96	0.54
26:14:890:A:H2'	26:14:892:G:H8	1.71	0.54
26:14:1317:A:H2'	26:14:1318:C:C6	2.43	0.54
26:14:1688:U:O2	26:14:1700:A:H5'	2.07	0.54
29:29:79:ARG:N	29:29:79:ARG:HD2	2.22	0.54
1:13:74:C:N4	1:13:96:G:H1	2.05	0.54
1:13:447:G:H8	1:13:447:G:O5'	1.91	0.54
1:13:523:A:H61	12:3I:92:ASP:HB2	1.72	0.54
1:13:1167:A:P	1:13:1167:A:H8	2.31	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1H:1218:C:H6	26:1H:1218:C:H5"	1.73	0.54
26:1H:1932:A:H2'	26:1H:1933:G:O4'	2.06	0.54
30:31:8:GLN:CD	30:31:8:GLN:N	2.66	0.54
38:98:78:LYS:O	38:98:83:ILE:HG13	2.07	0.54
41:C8:11:ARG:O	41:C8:15:LYS:HG3	2.07	0.54
43:E8:24:ILE:HD12	43:E8:24:ILE:O	2.08	0.54
45:G8:28:LYS:HB2	45:G8:40:GLU:OE1	2.08	0.54
47:I8:49:LYS:HB2	47:I8:80:HIS:HB3	1.89	0.54
1:1G:750:G:H1'	15:6A:22:THR:OG1	2.08	0.54
1:1G:957:U:H1'	1:1G:960:U:C5	2.42	0.54
1:1G:976:G:OP1	14:5A:31:ARG:HB3	2.08	0.54
1:1G:1086:U:H2'	1:1G:1087:G:H8	1.73	0.54
9:82:9:ARG:HG2	9:82:14:VAL:HG22	1.88	0.54
13:4A:78:ILE:HG23	13:4A:92:HIS:CE1	2.43	0.54
26:14:459:U:H5"	54:L5:40:TRP:CD2	2.42	0.54
26:14:1340:U:H4'	26:14:1394:U:O2'	2.07	0.54
26:14:1678:G:N2	26:14:1989:G:H22	2.04	0.54
26:14:2111:C:N4	26:14:2147:G:H21	2.06	0.54
44:B5:49:VAL:HB	44:B5:83:VAL:HG21	1.90	0.54
46:D5:7:ALA:O	46:D5:8:TYR:CG	2.60	0.54
1:13:57:G:H2'	1:13:58:C:H6	1.70	0.54
1:13:1014:A:C2	1:13:1219:U:H1'	2.42	0.54
1:13:1170:A:C8	1:13:1171:G:C8	2.96	0.54
2:1E:27:LYS:HD2	2:1E:193:ASP:HB2	1.89	0.54
7:6E:79:ARG:HG2	7:6E:84:ASN:OD1	2.08	0.54
15:6I:74:ASP:HB3	15:6I:77:ARG:HG2	1.88	0.54
16:7I:74:LEU:HA	16:7I:77:ALA:HB2	1.87	0.54
20:BI:57:ARG:NH1	20:BI:102:GLY:HA2	2.22	0.54
31:41:21:ARG:HG2	31:41:21:ARG:NH1	2.19	0.54
33:61:69:LYS:HG3	33:61:136:VAL:HB	1.89	0.54
37:88:81:VAL:C	37:88:82:ARG:HD2	2.33	0.54
1:1G:456:C:H42	1:1G:476:G:H1	1.53	0.54
1:1G:1193:G:O2'	5:42:25:ARG:NH2	2.40	0.54
5:42:9:LYS:HB2	5:42:112:LEU:HD11	1.89	0.54
8:72:109:ILE:HG22	8:72:137:VAL:HB	1.89	0.54
28:19:69:ARG:NH2	28:19:128:GLY:O	2.40	0.54
30:39:129:PHE:HA	30:39:142:TRP:NE1	2.22	0.54
30:39:172:TRP:CD1	30:39:172:TRP:H	2.26	0.54
35:25:111:PHE:HB3	35:25:114:ILE:HG13	1.90	0.54
36:35:50:ARG:HG2	36:35:50:ARG:HH11	1.73	0.54
1:13:128:G:H5'	17:8I:2:PRO:O	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1E:73:THR:O	2:1E:78:GLN:NE2	2.40	0.54
4:3E:148:VAL:HG21	4:3E:158:ILE:HG21	1.90	0.54
8:7E:9:MET:SD	8:7E:32:LYS:HG2	2.48	0.54
16:7I:21:VAL:O	16:7I:33:ILE:N	2.37	0.54
26:1H:270(I):G:H1	26:1H:270(Q):C:H42	1.53	0.54
26:1H:536:A:H2'	26:1H:537:C:C6	2.43	0.54
26:1H:779:U:O4	61:1H:4118:HOH:O	2.19	0.54
26:1H:1026:U:H1'	26:1H:1027:A:P	2.48	0.54
26:1H:1786:A:C2	26:1H:2606:C:H1'	2.43	0.54
27:16:15:A:H5'	27:16:16:G:C8	2.43	0.54
31:41:84:LYS:O	31:41:84:LYS:HG3	2.08	0.54
40:B8:24:PRO:HA	40:B8:49:VAL:HG22	1.89	0.54
2:12:73:THR:HB	2:12:96:ARG:H	1.73	0.54
26:14:276:A:N3	26:14:277:C:N4	2.55	0.54
26:14:889:C:H2'	26:14:890:A:H4'	1.90	0.54
29:29:11:MET:HA	29:29:24:THR:HA	1.90	0.54
30:39:7:TYR:HD1	30:39:18:ARG:H	1.56	0.54
30:39:53:THR:HG22	30:39:56:GLU:HG3	1.90	0.54
33:69:3:VAL:HG12	33:69:38:LEU:HA	1.89	0.54
33:69:130:TYR:C	33:69:131:LYS:HD2	2.32	0.54
39:65:3:ARG:HE	39:65:4:LEU:N	2.06	0.54
39:65:15:ARG:O	39:65:19:LYS:HD3	2.08	0.54
43:A5:96:ILE:HD11	43:A5:98:LYS:HD2	1.89	0.54
1:13:38:G:C2	1:13:397:A:C2	2.96	0.54
1:13:919:A:O2'	1:13:920:U:H5'	2.07	0.54
2:1E:18:GLY:N	2:1E:42:ILE:HG22	2.22	0.54
26:1H:1820:U:H4'	26:1H:1821:A:OP2	2.07	0.54
26:1H:2137:C:H42	26:1H:2154:G:H22	1.56	0.54
26:1H:2335:A:C8	26:1H:2337:G:C5	2.96	0.54
30:31:77:ASP:HB2	30:31:79:GLY:H	1.73	0.54
36:78:19:VAL:CG1	36:78:27:HIS:HB2	2.35	0.54
39:A8:42:ASP:O	39:A8:43:GLU:HB2	2.07	0.54
51:M8:24:THR:OG1	51:M8:25:TYR:N	2.41	0.54
52:N8:42:PRO:O	52:N8:44:THR:HB	2.08	0.54
55:Q8:32:LEU:HG	55:Q8:33:ASN:N	2.23	0.54
1:1G:562:C:H1'	12:3A:15:ARG:HD2	1.88	0.54
16:7A:21:VAL:HG22	16:7A:33:ILE:HB	1.89	0.54
26:14:821:A:O2'	26:14:946:G:OP2	2.24	0.54
26:14:993:G:N3	42:95:89:GLN:NE2	2.56	0.54
26:14:1819:A:H4'	26:14:1820:U:O5'	2.07	0.54
26:14:2693:A:H2'	26:14:2694:G:C8	2.41	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:49:124:SER:HB2	31:49:131:TYR:CE2	2.43	0.54
34:15:34:LEU:O	34:15:49:GLY:HA3	2.08	0.54
36:35:47:ASP:OD1	36:35:49:ARG:NE	2.27	0.54
41:85:92:ARG:NH1	42:95:11:GLN:H	2.06	0.54
51:I5:2:LYS:HB3	51:I5:6:HIS:HB2	1.90	0.54
1:13:945:G:C2	1:13:946:A:C8	2.96	0.54
1:13:1278:U:H5"	1:13:1279:A:O4'	2.07	0.54
3:2E:62:ASP:HB3	3:2E:97:LYS:HG2	1.90	0.54
4:3E:206:PHE:O	4:3E:209:ARG:HD2	2.08	0.54
8:7E:39:LEU:HB3	8:7E:45:ILE:HD11	1.89	0.54
8:7E:104:ARG:O	8:7E:107:LEU:HB2	2.08	0.54
11:2I:32:ILE:HD12	11:2I:72:ALA:HB2	1.88	0.54
26:1H:70:G:H21	26:1H:71:A:N6	2.05	0.54
26:1H:634:C:H2'	26:1H:635:C:C6	2.42	0.54
26:1H:1442:G:C2	26:1H:1550:C:O2	2.60	0.54
26:1H:2128:C:N4	26:1H:2160:G:H1	2.05	0.54
26:1H:2518:A:H5'	26:1H:2518:A:C8	2.42	0.54
26:1H:2700:C:C2'	26:1H:2701:C:H5'	2.37	0.54
37:88:34:LEU:HD11	37:88:129:THR:HB	1.90	0.54
37:88:135:ASP:HB2	37:88:138:ASP:OD1	2.08	0.54
45:G8:28:LYS:NZ	45:G8:64:GLU:OE2	2.40	0.54
46:H8:4:ARG:HB3	46:H8:58:VAL:CG2	2.38	0.54
47:I8:51:VAL:N	47:I8:62:LEU:HD12	2.23	0.54
1:1G:979:C:H3'	1:1G:980:C:C5'	2.38	0.54
1:1G:1401:G:OP1	25:4L:18:G:O2'	2.24	0.54
26:14:270(I):G:H2'	26:14:270(J):G:H8	1.71	0.54
26:14:528:A:C2	26:14:2042:A:H2'	2.43	0.54
26:14:579:G:H2'	26:14:580:C:C6	2.43	0.54
26:14:1646:C:O3'	61:14:3643:HOH:O	2.18	0.54
34:15:23:LEU:HD12	34:15:99:LEU:HD23	1.89	0.54
36:35:65:ARG:HH21	55:M5:15:LYS:HB3	1.73	0.54
37:45:36:ALA:HB2	37:45:103:MET:SD	2.47	0.54
1:13:1160:G:H1	1:13:1177:G:H22	1.54	0.54
2:1E:163:PHE:HD1	2:1E:185:ILE:HB	1.73	0.54
3:2E:40:ARG:HG3	3:2E:40:ARG:NH1	2.23	0.54
5:4E:126:ARG:HG3	5:4E:126:ARG:NH1	2.21	0.54
26:1H:956:G:OP1	37:88:85:LYS:HG3	2.08	0.54
26:1H:1579:A:H2'	26:1H:1580:A:O4'	2.08	0.54
26:1H:1678:G:C8	26:1H:1678:G:H5"	2.43	0.54
37:88:82:ARG:HD2	37:88:82:ARG:N	2.23	0.54
40:B8:5:ALA:HA	40:B8:8:LYS:HE2	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:H8:70:LEU:HD11	46:H8:98:MET:HE3	1.90	0.54
4:32:127:THR:HG21	4:32:149:ALA:HB2	1.89	0.54
15:6A:78:TYR:HD1	15:6A:79:ARG:HG3	1.72	0.54
26:14:1071:G:H1'	26:14:1089:G:H2'	1.90	0.54
26:14:2392:A:H2	26:14:2424:C:N4	2.00	0.54
26:14:2873:A:H8	38:55:6:SER:N	2.01	0.54
27:1J:66:A:N6	27:1J:107:U:H2'	2.23	0.54
28:19:43:ARG:HH11	28:19:43:ARG:CG	2.20	0.54
40:75:45:PHE:CE2	40:75:74:ARG:HB2	2.43	0.54
41:85:28:ARG:HH11	41:85:38:THR:HG1	1.52	0.54
51:I5:42:PHE:O	51:I5:43:TYR:HB3	2.08	0.54
8:7E:7:ALA:HB2	8:7E:85:ARG:HH11	1.72	0.53
26:1H:442:G:C4	26:1H:444:C:C5	2.96	0.53
26:1H:761:A:H5"	61:1H:3683:HOH:O	2.08	0.53
26:1H:1093:G:H1'	26:1H:1099:G:H1	1.72	0.53
26:1H:1339:G:N2	26:1H:1603:A:H1'	2.24	0.53
26:1H:1899:G:N2	26:1H:1902:C:H41	2.06	0.53
26:1H:2807:G:H3'	26:1H:2808:U:H5"	1.90	0.53
28:11:71:ASP:HB2	28:11:103:ARG:HH22	1.73	0.53
38:98:117:VAL:O	38:98:118:GLU:HB2	2.08	0.53
1:1G:998:G:H2'	1:1G:998(A):C:C6	2.43	0.53
1:1G:1237:C:O2'	1:1G:1300:G:N2	2.39	0.53
12:3A:37:CYS:SG	12:3A:81:SER:HB3	2.49	0.53
56:1L:76:A:H8	26:14:2583:G:H21	1.51	0.53
26:14:270(T):G:C6	26:14:270(U):C:C4	2.96	0.53
29:29:60:ASN:C	29:29:62:PRO:HD3	2.32	0.53
30:39:123:LEU:HB2	30:39:192:LEU:HB3	1.90	0.53
31:49:56:ALA:HB2	31:49:153:ARG:CZ	2.38	0.53
26:1H:528:A:C2	26:1H:2043:C:H4'	2.43	0.53
26:1H:762:U:H4'	26:1H:763:G:O5'	2.08	0.53
26:1H:1152:C:H4'	41:C8:77:SER:HA	1.90	0.53
26:1H:1312:U:H4'	26:1H:1313:U:O5'	2.08	0.53
26:1H:1512:G:H2'	26:1H:1513:C:H6	1.73	0.53
28:11:238:GLY:O	28:11:239:ARG:C	2.51	0.53
31:41:67:LYS:HE2	51:M8:6:HIS:HE1	1.73	0.53
33:61:124:GLY:H	33:61:142:VAL:HG23	1.73	0.53
39:A8:5:THR:OG1	39:A8:8:GLU:HG3	2.07	0.53
43:E8:71:VAL:HA	43:E8:107:LEU:HD12	1.89	0.53
55:Q8:30:ARG:HB2	55:Q8:30:ARG:CZ	2.37	0.53
1:1G:60:A:N6	1:1G:110:C:N3	2.55	0.53
1:1G:414:A:H2'	1:1G:415:A:O4'	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1G:529:G:O6	12:3A:49:ASN:HA	2.08	0.53
1:1G:1048:G:N2	1:1G:1209:C:N3	2.48	0.53
1:1G:1279:A:O2'	1:1G:1282:C:N4	2.41	0.53
1:1G:1478:C:H2'	1:1G:1479:C:C6	2.42	0.53
2:12:19:HIS:CE1	2:12:206:ASP:HB2	2.43	0.53
7:62:21:VAL:HG23	7:62:22:LEU:HD12	1.89	0.53
26:14:739:G:P	61:14:3751:HOH:O	2.65	0.53
26:14:1425:G:H2'	26:14:1426:G:C8	2.43	0.53
26:14:1485:G:H1	26:14:1504:C:N4	2.06	0.53
26:14:2447:G:OP2	61:14:3809:HOH:O	2.19	0.53
26:14:2619:C:OP1	29:29:152:LYS:HE2	2.07	0.53
43:A5:13:SER:O	43:A5:16:LYS:HB2	2.08	0.53
55:M5:14:VAL:HG13	55:M5:22:VAL:HG13	1.91	0.53
1:13:45:U:H2'	1:13:46:G:C8	2.44	0.53
1:13:112:G:OP1	16:7I:27:LYS:HD2	2.08	0.53
2:1E:17:PHE:HB3	2:1E:44:LEU:HD21	1.90	0.53
4:3E:18:LYS:HD3	4:3E:31:CYS:SG	2.49	0.53
4:3E:85:LYS:HG3	4:3E:86:LYS:N	2.22	0.53
6:5E:68:PRO:HG2	6:5E:71:ARG:HG3	1.90	0.53
13:4I:7:VAL:HB	31:41:115:ARG:CZ	2.38	0.53
23:2K:64:G:H2'	23:2K:65:G:H8	1.73	0.53
26:1H:217:G:P	61:1H:3763:HOH:O	2.63	0.53
26:1H:325:G:O2'	26:1H:326:G:H5'	2.09	0.53
26:1H:446:G:OP2	61:1H:3697:HOH:O	2.17	0.53
26:1H:484:C:H2'	26:1H:485:C:C6	2.43	0.53
26:1H:582:G:H2'	26:1H:583:G:C8	2.43	0.53
29:21:119:ARG:HG2	29:21:120:TRP:NE1	2.23	0.53
31:41:37:VAL:HG23	31:41:99:MET:HE3	1.90	0.53
39:A8:99:LYS:O	39:A8:103:GLU:HG2	2.07	0.53
46:H8:103:ARG:HG3	46:H8:136:PHE:CD2	2.44	0.53
1:1G:411:A:C5	1:1G:413:G:H1'	2.43	0.53
1:1G:986:A:H1'	19:AA:54:GLY:O	2.07	0.53
1:1G:1003:G:N2	1:1G:1037:C:O2	2.24	0.53
10:1A:24:VAL:HG13	10:1A:34:VAL:HG11	1.89	0.53
13:4A:81:LEU:HD13	13:4A:88:ARG:HD2	1.90	0.53
56:1L:37:MIA:H153	56:1L:37:MIA:HN6	1.73	0.53
23:2L:62:C:H2'	23:2L:63:C:H6	1.73	0.53
26:14:94:G:H21	49:G5:47:ASN:HD22	1.56	0.53
26:14:587:C:O2	36:35:33:ARG:NH1	2.41	0.53
26:14:1041:C:N4	26:14:1114:G:H22	2.03	0.53
26:14:2016:U:OP1	61:14:3885:HOH:O	2.19	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:1J:51:G:OP2	39:65:59:LYS:NZ	2.41	0.53
28:19:70:TRP:CH2	28:19:150:LYS:HA	2.44	0.53
30:39:178:PRO:HB3	30:39:198:ALA:HA	1.90	0.53
34:15:33:LEU:HD12	34:15:38:HIS:CD2	2.37	0.53
39:65:74:ALA:HB1	39:65:107:GLU:HB3	1.91	0.53
2:1E:166:ASP:C	2:1E:168:THR:H	2.16	0.53
4:3E:60:GLU:OE1	4:3E:63:LYS:NZ	2.23	0.53
26:1H:234:C:H2'	26:1H:235:U:C6	2.44	0.53
26:1H:847:U:C5	26:1H:933:A:N1	2.77	0.53
26:1H:969:U:OP1	50:L8:17:LYS:HG2	2.08	0.53
26:1H:1001:A:H2'	26:1H:1002:G:O4'	2.07	0.53
26:1H:2144:U:N3	26:1H:2146:C:O2	2.42	0.53
29:21:70:ALA:O	29:21:73:GLU:N	2.42	0.53
36:78:49:ARG:HE	55:Q8:57:ARG:HG2	1.73	0.53
44:F8:65:ARG:HG3	44:F8:67:GLY:H	1.73	0.53
1:1G:8:A:N6	4:32:209:ARG:HB2	2.23	0.53
1:1G:32:A:C2	1:1G:33:A:C4	2.96	0.53
1:1G:129(A):G:C6	1:1G:188:U:H4'	2.43	0.53
1:1G:130:A:O2'	1:1G:131:C:O5'	2.25	0.53
1:1G:694:A:O2'	57:3L:38:A:O2'	2.26	0.53
1:1G:977:A:HO2'	1:1G:981:U:H3	1.54	0.53
1:1G:1329:A:H2'	1:1G:1330:U:O4'	2.08	0.53
2:12:130:ARG:H	2:12:130:ARG:HE	1.54	0.53
56:1L:53:G:H1	56:1L:61:C:H42	1.55	0.53
26:14:96:G:H4'	49:G5:48:HIS:CE1	2.44	0.53
26:14:107:C:H2'	26:14:108:U:C6	2.43	0.53
26:14:305:U:H2'	26:14:306:U:C6	2.42	0.53
26:14:1204:A:H2	26:14:1241:A:N1	2.05	0.53
27:1J:94:C:H2'	27:1J:95:U:C6	2.44	0.53
35:25:4:PRO:O	35:25:5:GLN:HB2	2.07	0.53
42:95:71:LEU:O	42:95:72:VAL:HG12	2.08	0.53
1:13:1218:C:H2'	1:13:1219:U:C6	2.43	0.53
1:13:1238:A:N3	1:13:1241:G:O2'	2.41	0.53
1:13:1292:U:H2'	1:13:1293:G:C8	2.44	0.53
2:1E:60:ASP:HB3	2:1E:64:ARG:HH12	1.72	0.53
5:4E:148:VAL:HG21	8:7E:107:LEU:HD22	1.89	0.53
9:8E:112:LYS:HD3	9:8E:113:LYS:H	1.72	0.53
26:1H:270(Y):G:N1	61:1H:4468:HOH:O	2.27	0.53
26:1H:1316:U:H2'	26:1H:1317:A:C8	2.44	0.53
26:1H:1858:G:H2'	26:1H:1883:G:H22	1.73	0.53
27:16:54:G:O2'	27:16:55:U:H5'	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:31:96:ASP:OD1	30:31:98:SER:HB3	2.08	0.53
34:58:96:GLU:HB2	34:58:122:VAL:CG1	2.39	0.53
36:78:115:LEU:HA	36:78:134:ALA:HB2	1.90	0.53
46:H8:165:VAL:HB	46:H8:167:PRO:HD3	1.90	0.53
49:K8:14:ARG:HB3	49:K8:15:LYS:HE3	1.89	0.53
55:Q8:33:ASN:O	55:Q8:34:TRP:CG	2.62	0.53
4:32:158:ILE:HG22	4:32:162:LEU:HD12	1.91	0.53
26:14:666:G:H5"	36:35:47:ASP:O	2.09	0.53
26:14:1485:G:H2'	26:14:1486:A:H8	1.72	0.53
26:14:1788:C:C2	26:14:1789:A:C8	2.96	0.53
26:14:2777:G:OP2	26:14:2781:A:O2'	2.20	0.53
31:49:18:GLU:HG2	31:49:175:LEU:HD13	1.91	0.53
45:C5:18:GLY:O	45:C5:20:TYR:N	2.42	0.53
9:8E:21:PRO:HA	9:8E:59:PHE:HA	1.89	0.53
9:8E:47:LEU:H	9:8E:47:LEU:HD22	1.73	0.53
11:2I:69:ALA:HB1	11:2I:103:LEU:HD23	1.91	0.53
12:3I:66:VAL:HG21	12:3I:98:TYR:CE2	2.43	0.53
16:7I:20:VAL:HG21	16:7I:32:TYR:CD2	2.43	0.53
20:BI:30:LYS:NZ	20:BI:80:ARG:HH12	2.07	0.53
23:2K:8:4SU:O5'	23:2K:8:4SU:H6	2.08	0.53
26:1H:92:G:H2'	26:1H:93:C:H6	1.73	0.53
26:1H:608:A:H1'	26:1H:621:A:N6	2.23	0.53
26:1H:1022:G:N2	26:1H:1023:U:O4	2.41	0.53
26:1H:1799:G:H5'	26:1H:1819:A:H61	1.73	0.53
26:1H:2160:G:C2	26:1H:2161:C:H1'	2.44	0.53
26:1H:2251:G:OP1	61:1H:4387:HOH:O	2.19	0.53
26:1H:2784:C:O2'	29:21:37:ARG:NH1	2.41	0.53
35:68:1:MET:HE3	35:68:67:LYS:HE2	1.89	0.53
40:B8:51:ARG:HB2	40:B8:98:LYS:HD3	1.90	0.53
40:B8:112:ARG:HA	40:B8:115:ARG:CZ	2.38	0.53
43:E8:70:TYR:HD1	43:E8:70:TYR:H	1.55	0.53
44:F8:57:LEU:HG	44:F8:78:LYS:HG2	1.90	0.53
2:12:19:HIS:CG	2:12:20:GLU:H	2.27	0.53
3:22:61:ALA:C	3:22:63:ASN:H	2.16	0.53
11:2A:85:ARG:NE	11:2A:111:ASP:HB3	2.22	0.53
57:3L:52:G:H1	57:3L:62:C:N4	2.07	0.53
26:14:1485:G:H2'	26:14:1486:A:C8	2.44	0.53
26:14:2287:A:H61	26:14:2344:U:H3	1.55	0.53
33:69:110:ASP:H	33:69:130:TYR:HH	1.52	0.53
37:45:34:LEU:HD12	37:45:130:LYS:O	2.09	0.53
37:45:86:GLY:O	37:45:88:GLY:N	2.42	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:65:77:ALA:O	39:65:80:LEU:N	2.41	0.53
46:D5:108:PRO:HG3	46:D5:142:SER:HA	1.91	0.53
48:F5:83:GLU:OE1	48:F5:83:GLU:N	2.41	0.53
2:1E:112:VAL:O	2:1E:115:LEU:N	2.41	0.53
5:4E:76:ILE:HG13	5:4E:93:PRO:HB3	1.89	0.53
13:4I:13:LYS:O	13:4I:44:ARG:NE	2.42	0.53
14:5I:6:LEU:HB3	14:5I:23:ARG:NH2	2.24	0.53
26:1H:588:U:H2'	26:1H:589:C:C6	2.44	0.53
26:1H:2298:A:H62	26:1H:2318:G:H8	1.55	0.53
32:51:129:THR:O	32:51:129:THR:OG1	2.26	0.53
36:78:19:VAL:HG21	36:78:27:HIS:CB	2.39	0.53
40:B8:102:ILE:HA	40:B8:105:LEU:HD22	1.90	0.53
42:D8:43:GLU:HA	42:D8:44:LYS:HZ1	1.73	0.53
45:G8:40:GLU:HG2	45:G8:64:GLU:CD	2.33	0.53
53:O8:32:ASN:OD1	53:O8:32:ASN:N	2.42	0.53
1:1G:448:A:P	1:1G:485:G:H22	2.32	0.53
1:1G:742:G:P	15:6A:35:ARG:HH22	2.32	0.53
1:1G:974:A:P	14:5A:41:ARG:HH22	2.32	0.53
1:1G:991:U:O4	1:1G:1212:U:O2'	2.14	0.53
1:1G:1194:U:H2'	1:1G:1195:C:C6	2.42	0.53
1:1G:1449:C:H3'	1:1G:1450:U:H4'	1.90	0.53
2:12:69:LEU:HD23	2:12:70:PHE:H	1.74	0.53
26:14:108:U:H2'	26:14:109:G:C8	2.43	0.53
26:14:483:A:H5"	45:C5:49:VAL:HG22	1.91	0.53
26:14:495:G:H21	43:A5:61:ASN:HD21	1.55	0.53
26:14:646:A:H2'	26:14:647:G:O4'	2.08	0.53
26:14:747:U:C6	52:J5:2:ALA:HB3	2.44	0.53
26:14:2346:A:H5"	26:14:2383:G:O4'	2.09	0.53
27:1J:13:A:H5"	27:1J:15:A:C6	2.43	0.53
27:1J:39:A:N1	51:I5:1:MET:N	2.55	0.53
36:35:124:LYS:HE2	36:35:143:GLY:O	2.09	0.53
41:85:110:VAL:O	41:85:114:LYS:HG2	2.08	0.53
49:G5:24:LEU:HD13	49:G5:60:LEU:HD21	1.90	0.53
53:K5:29:ASN:ND2	53:K5:29:ASN:H	2.07	0.53
1:13:974:A:OP2	14:5I:41:ARG:NH1	2.42	0.53
1:13:1044:A:C5	1:13:1045:C:H1'	2.44	0.53
8:7E:85:ARG:HD3	8:7E:88:LYS:HG2	1.91	0.53
14:5I:29:ARG:HD3	14:5I:40:CYS:SG	2.49	0.53
22:1K:15:G:N2	22:1K:59:U:O2	2.42	0.53
26:1H:606:U:H4'	26:1H:658:C:H4'	1.89	0.53
26:1H:1107:G:H2'	26:1H:1108:U:C6	2.44	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1H:2341:G:H2'	26:1H:2342:C:C6	2.42	0.53
33:61:110:ASP:CB	33:61:112:LYS:H	2.22	0.53
41:C8:28:ARG:NH1	41:C8:38:THR:OG1	2.33	0.53
50:L8:37:LEU:HD12	50:L8:43:ILE:CG2	2.38	0.53
1:1G:535:A:H5"	61:1G:1733:HOH:O	2.08	0.53
1:1G:888:G:O2'	1:1G:1488:G:O2'	2.23	0.53
3:22:106:VAL:HB	3:22:109:PRO:HB3	1.91	0.53
5:42:126:ARG:HH11	5:42:126:ARG:HG3	1.74	0.53
9:82:82:ALA:HB1	9:82:96:LEU:HD21	1.91	0.53
26:14:1309:G:H4'	54:L5:7:PRO:HB2	1.89	0.53
26:14:1364:G:N7	48:F5:2:SER:HB2	2.24	0.53
26:14:1462:C:H4'	26:14:2703:C:H5'	1.91	0.53
26:14:2050:C:H1'	29:29:156:MET:HE2	1.89	0.53
45:C5:42:VAL:O	45:C5:65:ALA:N	2.35	0.53
54:L5:34:ARG:NH1	54:L5:41:ARG:O	2.41	0.53
1:13:352:C:P	61:13:1861:HOH:O	2.67	0.53
1:13:607:A:C2	16:7I:31:LYS:HG3	2.44	0.53
2:1E:6:THR:OG1	2:1E:7:VAL:N	2.42	0.53
4:3E:30:LYS:CB	4:3E:35:ARG:HE	2.21	0.53
12:3I:11:VAL:HG13	17:8I:29:HIS:CD2	2.43	0.53
26:1H:234:C:H2'	26:1H:235:U:H6	1.74	0.53
26:1H:389:G:N1	36:78:71:VAL:HG12	2.23	0.53
26:1H:576:U:O2'	26:1H:577:G:H5'	2.09	0.53
26:1H:1198:U:H2'	26:1H:1199:U:C6	2.44	0.53
26:1H:2153:G:O6	26:1H:2154:G:N2	2.42	0.53
35:68:112:MET:HA	35:68:115:VAL:HG22	1.91	0.53
39:A8:61:ASN:HB3	39:A8:64:GLU:HG3	1.90	0.53
40:B8:26:ASP:O	40:B8:49:VAL:HG13	2.08	0.53
41:C8:88:ILE:C	41:C8:90:VAL:H	2.17	0.53
1:1G:301:G:H8	1:1G:301:G:OP2	1.92	0.53
1:1G:1134:G:C2	1:1G:1135:U:H1'	2.43	0.53
1:1G:1360:A:H8	1:1G:1360:A:OP1	1.92	0.53
12:3A:49:ASN:N	12:3A:49:ASN:OD1	2.40	0.53
26:14:303:U:H2'	26:14:304:G:O4'	2.09	0.53
26:14:307:G:H21	26:14:330:A:N6	2.07	0.53
26:14:868:U:C2	26:14:869:G:C8	2.97	0.53
26:14:1317:A:H2'	26:14:1318:C:H6	1.73	0.53
26:14:2648:C:H2'	26:14:2649:U:C6	2.44	0.53
29:29:134:ILE:HD12	29:29:134:ILE:O	2.08	0.53
29:29:151:TYR:HD2	29:29:154:LYS:NZ	2.06	0.53
40:75:77:PRO:O	40:75:80:SER:HB2	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:D5:28:MET:O	46:D5:34:ASN:HA	2.09	0.53
2:1E:8:LYS:H	2:1E:8:LYS:HE2	1.74	0.53
4:3E:110:PHE:CE2	4:3E:148:VAL:HG23	2.44	0.53
6:5E:86:ARG:O	6:5E:87:ARG:HG2	2.09	0.53
8:7E:88:LYS:O	8:7E:92:ARG:HD3	2.08	0.53
9:8E:18:PHE:HD2	9:8E:62:TYR:HD2	1.57	0.53
26:1H:1159:U:OP1	50:L8:30:ARG:NH1	2.39	0.53
26:1H:2345:G:H4'	26:1H:2346:A:O5'	2.09	0.53
32:51:24:VAL:HG13	32:51:35:VAL:HB	1.91	0.53
32:51:154:PRO:HB3	32:51:163:TYR:CE2	2.44	0.53
41:C8:96:ALA:CB	41:C8:98:LEU:H	2.03	0.53
41:C8:110:VAL:O	41:C8:114:LYS:N	2.30	0.53
42:D8:16:PRO:HA	42:D8:96:ILE:HG22	1.91	0.53
46:H8:30:ASN:ND2	46:H8:90:VAL:HB	2.23	0.53
46:H8:130:PRO:O	46:H8:133:ILE:HG13	2.08	0.53
49:K8:30:ARG:HH11	49:K8:30:ARG:CG	2.22	0.53
54:P8:5:TRP:NE1	54:P8:7:PRO:HG3	2.24	0.53
55:Q8:9:GLY:O	55:Q8:13:ARG:HG2	2.08	0.53
26:14:2683:C:OP1	40:75:53:ARG:NH2	2.42	0.53
33:69:14:ASP:N	33:69:17:GLN:OE1	2.31	0.53
40:75:54:ARG:HG2	40:75:59:THR:HG21	1.89	0.53
42:95:71:LEU:H	42:95:86:GLY:HA2	1.73	0.53
42:95:85:LYS:HE3	42:95:88:ARG:H	1.73	0.53
48:F5:50:ARG:HD2	48:F5:57:GLU:OE1	2.08	0.53
1:13:222:U:H2'	1:13:223:U:C6	2.44	0.52
1:13:667:G:H4'	15:6I:51:HIS:ND1	2.25	0.52
1:13:1236:A:O2'	1:13:1304:G:H4'	2.09	0.52
1:13:1478:C:H2'	1:13:1479:C:C6	2.44	0.52
7:6E:45:ASP:O	7:6E:49:ILE:HG12	2.08	0.52
10:1I:32:ALA:HB3	10:1I:76:ASN:O	2.09	0.52
15:6I:82:ILE:HD13	15:6I:88:ARG:HB2	1.91	0.52
26:1H:286:C:H2'	26:1H:287:C:C6	2.42	0.52
26:1H:306:U:H2'	26:1H:307:G:O4'	2.08	0.52
26:1H:340:A:H2'	26:1H:341:G:O4'	2.09	0.52
26:1H:754:C:H2'	26:1H:755:C:C6	2.43	0.52
26:1H:1026:U:H1'	26:1H:1027:A:O5'	2.08	0.52
26:1H:1535:U:O2	26:1H:1535:U:H2'	2.09	0.52
26:1H:2058:A:H5"	26:1H:2059:A:OP2	2.09	0.52
26:1H:2572:A:N7	29:21:145:LYS:HB2	2.24	0.52
26:1H:2580:U:H4'	29:21:130:GLY:HA3	1.91	0.52
29:21:24:THR:N	29:21:184:VAL:O	2.41	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:21:103:ASP:OD1	29:21:201:THR:HG23	2.10	0.52
33:61:86:THR:HA	33:61:123:LEU:HD13	1.92	0.52
46:H8:92:SER:O	46:H8:130:PRO:HG2	2.09	0.52
1:1G:728:A:H2'	1:1G:729:A:C8	2.44	0.52
1:1G:1141:C:H2'	1:1G:1142:G:C8	2.44	0.52
1:1G:1170:A:H8	1:1G:1170:A:O5'	1.92	0.52
1:1G:1212:U:H4'	1:1G:1213:A:C8	2.44	0.52
1:1G:1321:C:H4'	13:4A:87:TYR:CZ	2.44	0.52
5:42:43:LEU:HD22	5:42:136:MET:HG3	1.92	0.52
8:72:73:ASP:HB2	8:72:75:ARG:NH2	2.24	0.52
13:4A:70:LEU:O	13:4A:74:VAL:HG23	2.09	0.52
14:5A:17:LYS:HD2	14:5A:18:VAL:N	2.24	0.52
14:5A:17:LYS:NZ	14:5A:18:VAL:HG13	2.24	0.52
26:14:142:G:H5"	26:14:1598:C:O2'	2.08	0.52
26:14:747:U:C5	52:J5:2:ALA:HB3	2.45	0.52
26:14:1298:C:OP2	61:14:3518:HOH:O	2.18	0.52
27:1J:15:A:H1'	27:1J:109:G:C5	2.44	0.52
28:19:71:ASP:CG	28:19:103:ARG:HH12	2.16	0.52
34:15:104:LYS:HA	34:15:107:LEU:HD12	1.91	0.52
46:D5:139:VAL:HG22	46:D5:156:LYS:HG2	1.91	0.52
51:I5:11:PRO:HA	51:I5:25:TYR:HA	1.91	0.52
1:13:271:C:H2'	1:13:272:C:C6	2.44	0.52
1:13:491:G:H2'	1:13:492:G:O4'	2.08	0.52
1:13:730:G:C5	1:13:731:G:H1'	2.44	0.52
1:13:872:A:C4	1:13:874:G:N7	2.77	0.52
26:1H:1111:A:N3	26:1H:1112:G:H1'	2.24	0.52
26:1H:2171:A:O2'	26:1H:2172:U:O5'	2.27	0.52
26:1H:2657:A:O3'	32:51:160:LYS:NZ	2.42	0.52
28:11:206:LEU:O	28:11:211:ARG:HD3	2.09	0.52
30:31:101:LEU:O	30:31:106:ARG:NH1	2.42	0.52
32:51:94:TYR:HA	32:51:106:THR:O	2.09	0.52
49:K8:59:ARG:O	49:K8:62:THR:HG23	2.09	0.52
55:Q8:46:ARG:NH2	55:Q8:48:PHE:HA	2.24	0.52
1:1G:192:U:H2'	1:1G:193:C:C6	2.43	0.52
1:1G:503:C:OP2	12:3A:116:SER:HB3	2.09	0.52
7:62:143:ARG:O	7:62:146:GLU:HB2	2.08	0.52
11:2A:59:TYR:CZ	11:2A:63:LEU:HD21	2.44	0.52
26:14:973:A:OP2	61:14:3697:HOH:O	2.19	0.52
26:14:1581:G:H2'	26:14:1582:C:O4'	2.09	0.52
26:14:1786:A:H2	26:14:2606:C:H1'	1.74	0.52
26:14:2068:U:H3	26:14:2430:A:H2	1.52	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:1J:89(A):A:C8	27:1J:90:C:H1'	2.44	0.52
28:19:11:PRO:C	28:19:13:ARG:H	2.16	0.52
28:19:11:PRO:O	28:19:13:ARG:N	2.42	0.52
30:39:123:LEU:O	30:39:193:VAL:HA	2.10	0.52
33:69:101:LEU:HD23	33:69:101:LEU:H	1.75	0.52
36:35:60:MET:C	36:35:61:ARG:HG2	2.34	0.52
40:75:21:GLU:O	40:75:91:ARG:NH2	2.42	0.52
42:95:85:LYS:CG	42:95:87:HIS:H	2.14	0.52
7:6E:5:ARG:NE	7:6E:7:ALA:HA	2.25	0.52
16:7I:3:LYS:HG3	16:7I:24:ALA:HB2	1.90	0.52
16:7I:13:HIS:C	16:7I:15:PRO:HD3	2.34	0.52
16:7I:71:ARG:O	16:7I:74:LEU:N	2.35	0.52
22:1K:44:G:H2'	22:1K:45:U:C6	2.44	0.52
26:1H:125:G:H5'	26:1H:125:G:C8	2.44	0.52
26:1H:218:A:H2	26:1H:235:U:H4'	1.74	0.52
26:1H:686:G:OP1	54:P8:11:LYS:NZ	2.41	0.52
26:1H:899:A:O2'	26:1H:900:A:O4'	2.25	0.52
26:1H:1430:C:H2'	26:1H:1431:U:H6	1.74	0.52
26:1H:2356:C:H2'	26:1H:2357:U:O4'	2.10	0.52
26:1H:2577:A:H1'	52:N8:3:LYS:HA	1.91	0.52
27:16:1:U:H2'	27:16:2:C:C6	2.44	0.52
27:16:99:A:H3'	61:16:317:HOH:O	2.09	0.52
31:41:11:TYR:HA	31:41:15:VAL:HB	1.91	0.52
31:41:16:ARG:N	31:41:17:PRO:HD2	2.24	0.52
34:58:128:HIS:HB2	34:58:129:PRO:HD2	1.92	0.52
35:68:10:VAL:HG11	35:68:16:ALA:HB3	1.91	0.52
49:K8:50:ILE:HD12	49:K8:50:ILE:N	2.24	0.52
52:N8:40:LYS:HG3	52:N8:47:PRO:HD2	1.91	0.52
53:O8:10:LEU:HD23	55:Q8:32:LEU:HD13	1.91	0.52
53:O8:51:GLU:HG2	53:O8:52:VAL:H	1.73	0.52
1:1G:677:U:H3	1:1G:713:G:H22	1.58	0.52
1:1G:934:C:O2'	1:1G:1344:C:OP2	2.26	0.52
1:1G:1412:C:H2'	1:1G:1413:A:C8	2.44	0.52
2:12:134:GLU:O	2:12:138:LEU:HG	2.09	0.52
12:3A:60:LEU:HD23	12:3A:64:TYR:HB3	1.89	0.52
19:AA:58:VAL:O	19:AA:60:VAL:HG12	2.09	0.52
57:3L:13:C:H2'	57:3L:14:A:H8	1.75	0.52
26:14:139:G:H1'	26:14:140:A:H2	1.74	0.52
26:14:250:G:OP1	36:35:60:MET:HE1	2.09	0.52
26:14:2191:G:O2'	26:14:2192:G:OP1	2.25	0.52
26:14:2637:U:H2'	26:14:2638:G:O4'	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:14:2802:G:H2'	26:14:2803:C:O4'	2.10	0.52
31:49:55:LYS:NZ	31:49:148:MET:HE3	2.25	0.52
34:15:30:ILE:O	34:15:34:LEU:HD22	2.09	0.52
39:65:89:ARG:O	39:65:92:TYR:N	2.42	0.52
39:65:102:ALA:HA	39:65:105:ALA:HB3	1.91	0.52
4:3E:67:ILE:HD13	4:3E:196:LEU:HD22	1.91	0.52
4:3E:192:GLU:H	4:3E:192:GLU:CD	2.14	0.52
6:5E:23:LYS:HB2	6:5E:23:LYS:NZ	2.25	0.52
26:1H:223:A:O4'	26:1H:422:A:H5'	2.10	0.52
26:1H:1444:G:C2	26:1H:1548:C:N3	2.78	0.52
45:G8:5:MET:HG3	45:G8:6:HIS:H	1.75	0.52
45:G8:20:TYR:CE1	45:G8:43:ASN:HA	2.45	0.52
1:1G:247:G:OP2	17:8A:100:LYS:HE2	2.08	0.52
2:12:98:LEU:O	2:12:101:MET:HG2	2.10	0.52
20:BA:60:GLU:OE1	20:BA:85:MET:HE1	2.09	0.52
26:14:1049:C:N4	26:14:2751:G:O6	2.40	0.52
26:14:1759:A:H4'	26:14:2715:C:O4'	2.09	0.52
26:14:2782:G:OP2	61:14:3881:HOH:O	2.19	0.52
27:1J:13:A:H5"	27:1J:15:A:N6	2.24	0.52
27:1J:116:G:C5'	39:65:55:ALA:HB2	2.39	0.52
36:35:13:ASN:C	36:35:15:ARG:H	2.16	0.52
1:13:323:U:H5'	20:BI:23:ARG:HB2	1.91	0.52
1:13:649:G:H2'	1:13:650:G:H8	1.74	0.52
1:13:1336:C:C6	1:13:1336:C:H5"	2.45	0.52
2:1E:100:GLY:N	2:1E:176:GLU:OE2	2.42	0.52
4:3E:106:TYR:HE1	4:3E:107:ARG:HH11	1.57	0.52
9:8E:43:ALA:HA	9:8E:74:ILE:HD13	1.91	0.52
12:3I:82:VAL:HG12	12:3I:106:ASP:OD2	2.09	0.52
12:3I:93:LEU:O	12:3I:96:VAL:HG13	2.09	0.52
22:1K:52:G:H5'	37:88:56:ARG:HH21	1.75	0.52
26:1H:7:G:H2'	26:1H:8:A:O4'	2.09	0.52
26:1H:250:G:H2'	26:1H:251:A:C8	2.45	0.52
26:1H:500:G:N1	26:1H:503:A:OP2	2.39	0.52
26:1H:1278:A:OP1	38:98:36:THR:HG22	2.09	0.52
26:1H:1412:A:H2'	26:1H:1413:G:C8	2.45	0.52
26:1H:1980:G:H4'	61:1H:3651:HOH:O	2.10	0.52
26:1H:2056:G:C2	26:1H:2057:A:C8	2.98	0.52
26:1H:2321:G:H5"	26:1H:2322:A:OP2	2.09	0.52
33:61:69:LYS:O	33:61:73:GLU:HB2	2.08	0.52
34:58:4:TYR:O	41:C8:64:ARG:NH1	2.37	0.52
52:N8:16:ARG:HG3	52:N8:17:ASP:N	2.25	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:P8:24:THR:HG23	54:P8:27:GLY:H	1.75	0.52
1:1G:292:G:OP2	1:1G:305:G:N2	2.30	0.52
1:1G:834:C:H2'	1:1G:835:U:H6	1.74	0.52
2:12:61:LEU:HD23	2:12:68:ILE:HD11	1.91	0.52
2:12:197:VAL:HG12	2:12:200:ILE:HG13	1.91	0.52
26:14:732:C:H3'	61:14:4081:HOH:O	2.09	0.52
36:35:121:LYS:HG2	36:35:123:LEU:HD21	1.92	0.52
37:45:26:TYR:O	37:45:26:TYR:CD1	2.62	0.52
51:I5:18:CYS:H	51:I5:19:GLY:HA2	1.75	0.52
26:1H:330:A:O2'	26:1H:331:A:C8	2.53	0.52
26:1H:1408:C:C2	26:1H:1595:G:N2	2.78	0.52
32:51:153:LYS:H	32:51:153:LYS:CE	2.22	0.52
36:78:13:ASN:ND2	36:78:13:ASN:O	2.40	0.52
43:E8:79:GLY:C	43:E8:100:THR:HG22	2.34	0.52
44:F8:31:HIS:CD2	44:F8:33:LYS:H	2.26	0.52
1:1G:1310:G:OP1	13:4A:77:ASN:ND2	2.36	0.52
1:1G:1312:G:H2'	1:1G:1313:U:O4'	2.10	0.52
2:12:190:THR:O	2:12:191:ASP:HB3	2.10	0.52
26:14:1430:C:H2'	26:14:1431:U:H6	1.75	0.52
26:14:1786:A:OP1	61:14:3563:HOH:O	2.18	0.52
26:14:2123:G:H1	26:14:2175:C:H42	1.57	0.52
27:1J:88:C:H3'	27:1J:89:G:C8	2.44	0.52
29:29:89:ASP:C	29:29:91:VAL:H	2.18	0.52
42:95:85:LYS:CG	42:95:86:GLY:H	2.23	0.52
1:13:381:C:H2'	1:13:382:A:O4'	2.08	0.52
1:13:1306:A:H61	1:13:1331:G:H1'	1.75	0.52
26:1H:821:A:H5"	26:1H:822:U:H6	1.74	0.52
26:1H:1103:A:H3'	26:1H:1104:C:C6	2.44	0.52
26:1H:1204:A:C2	26:1H:1241:A:N1	2.78	0.52
26:1H:1424:G:H2'	26:1H:1425:G:O4'	2.10	0.52
28:11:12:SER:O	28:11:16:MET:HB2	2.10	0.52
33:61:77:LEU:HD13	33:61:140:LEU:HB3	1.90	0.52
39:A8:88:ASP:C	39:A8:90:GLY:H	2.17	0.52
41:C8:92:ARG:HB3	41:C8:95:LEU:HD23	1.92	0.52
1:1G:34:C:H2'	1:1G:35:G:C8	2.45	0.52
1:1G:45:U:H2'	1:1G:46:G:H8	1.75	0.52
1:1G:625:G:H2'	1:1G:626:U:C6	2.43	0.52
4:32:13:ARG:O	4:32:15:GLU:N	2.42	0.52
26:14:747:U:OP1	52:J5:3:LYS:HD3	2.10	0.52
26:14:1430:C:H2'	26:14:1431:U:C6	2.44	0.52
26:14:2532:G:N2	26:14:2663:G:O2'	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:19:108:PRO:HG2	28:19:111:LEU:HG	1.92	0.52
32:59:20:ALA:O	32:59:22:GLY:N	2.41	0.52
36:35:89:ALA:HB1	36:35:121:LYS:HD2	1.92	0.52
38:55:20:LEU:HD21	38:55:40:LYS:HD3	1.92	0.52
42:95:29:PRO:HA	42:95:61:VAL:CG1	2.39	0.52
44:B5:5:TYR:CZ	49:G5:30:ARG:HG3	2.44	0.52
46:D5:19:ARG:NH1	46:D5:84:GLU:O	2.42	0.52
1:13:222:U:H2'	1:13:223:U:H6	1.74	0.52
1:13:1288:A:N1	1:13:1371:G:H1'	2.25	0.52
1:13:1346:A:N1	1:13:1374:A:H5"	2.25	0.52
2:1E:22:LYS:H	2:1E:40:HIS:CD2	2.28	0.52
2:1E:178:ARG:HB2	2:1E:178:ARG:HH11	1.74	0.52
26:1H:321:G:O3'	30:31:168:ARG:NH2	2.43	0.52
26:1H:638:G:C5	26:1H:651:G:C2	2.98	0.52
26:1H:863:A:H2'	26:1H:864:G:H8	1.74	0.52
26:1H:1828:G:P	61:1H:4514:HOH:O	2.64	0.52
26:1H:2250:G:C5	37:88:82:ARG:HG2	2.44	0.52
26:1H:2569:G:H8	26:1H:2569:G:H5"	1.75	0.52
27:16:42:C:H4'	31:41:67:LYS:HD2	1.91	0.52
32:51:6:ARG:HB3	32:51:65:HIS:CG	2.44	0.52
32:51:64:LEU:O	32:51:68:THR:OG1	2.28	0.52
37:88:39:PRO:HA	37:88:97:VAL:O	2.10	0.52
40:B8:87:ASP:OD1	40:B8:87:ASP:N	2.42	0.52
46:H8:126:VAL:HA	46:H8:164:ALA:N	2.25	0.52
47:I8:53:MET:HG3	47:I8:59:LEU:CD2	2.38	0.52
1:1G:973:G:OP1	10:1A:57:LYS:NZ	2.35	0.52
1:1G:1109:C:H2'	1:1G:1110:A:O4'	2.09	0.52
1:1G:1203:C:H2'	1:1G:1204:A:C8	2.44	0.52
1:1G:1320:C:H2'	1:1G:1321:C:C6	2.45	0.52
1:1G:1348:U:H4'	9:82:120:ARG:HD2	1.90	0.52
2:12:36:ARG:HB3	2:12:41:ILE:HD11	1.91	0.52
3:22:11:ARG:HB2	3:22:11:ARG:HH11	1.74	0.52
5:42:147:ASP:O	5:42:151:LEU:HG	2.10	0.52
6:52:7:ASN:N	6:52:7:ASN:OD1	2.42	0.52
8:72:121:ASP:OD1	8:72:122:ARG:N	2.43	0.52
9:82:117:HIS:O	9:82:118:LYS:HB2	2.08	0.52
10:1A:30:SER:OG	10:1A:81:THR:HG22	2.10	0.52
25:4L:14:A:H5'	25:4L:15:A:OP2	2.10	0.52
26:14:251:A:C5	26:14:252:G:H1'	2.44	0.52
26:14:661:C:H1'	36:35:12:ALA:HA	1.91	0.52
26:14:1382:G:N7	61:14:3818:HOH:O	2.34	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:14:1786:A:C2	26:14:2606:C:H1'	2.45	0.52
26:14:1800:C:OP2	28:19:183:ARG:NH2	2.42	0.52
26:14:2273:A:O2'	26:14:2274:A:H5'	2.09	0.52
26:14:2275:C:H6	26:14:2275:C:H5'	1.75	0.52
26:14:2287:A:C2	26:14:2289:G:C8	2.98	0.52
26:14:2319:G:H4'	26:14:2320:A:O4'	2.09	0.52
27:1J:38:C:N4	27:1J:44:G:H1	2.03	0.52
28:19:73:VAL:HG13	28:19:120:GLY:HA3	1.91	0.52
35:25:63:VAL:HB	35:25:102:VAL:HG12	1.91	0.52
36:35:85:LEU:HB2	36:35:88:LEU:HD23	1.92	0.52
44:B5:55:ASN:HB2	44:B5:80:ILE:HG13	1.91	0.52
1:13:626:U:N3	1:13:627:G:N7	2.58	0.52
1:13:648:A:N6	1:13:649:G:O6	2.43	0.52
4:3E:32:ALA:O	4:3E:35:ARG:N	2.43	0.52
24:3K:64:A:H2'	24:3K:65:G:H4'	1.90	0.52
26:1H:598:G:C5'	36:78:11:GLY:HA3	2.40	0.52
26:1H:1253:A:N6	61:1H:3711:HOH:O	2.15	0.52
26:1H:1401:G:H2'	26:1H:1402:C:C6	2.45	0.52
39:A8:38:GLN:HG3	39:A8:47:THR:HG21	1.91	0.52
1:1G:939:G:H1	1:1G:1344:C:H42	1.58	0.52
2:12:7:VAL:HG22	2:12:8:LYS:H	1.75	0.52
3:22:8:ILE:HG23	3:22:16:ARG:HG2	1.92	0.52
8:72:84:ARG:O	8:72:135:CYS:HB2	2.09	0.52
57:3L:18:G:H2'	57:3L:57:G:H22	1.75	0.52
57:3L:32:PSU:H5"	57:3L:33:U:OP2	2.10	0.52
57:3L:52:G:N2	57:3L:62:C:N3	2.55	0.52
26:14:276:A:H2'	26:14:277:C:C5	2.44	0.52
26:14:548:A:C6	26:14:549:G:H1'	2.45	0.52
36:35:101:VAL:HA	36:35:105:LEU:O	2.09	0.52
36:35:122:PRO:HB3	36:35:141:ALA:HB1	1.92	0.52
42:95:20:LEU:O	42:95:94:LEU:N	2.41	0.52
43:A5:62:HIS:HB2	43:A5:64:MET:HG3	1.91	0.52
45:C5:87:LYS:HB2	45:C5:94:LYS:HA	1.92	0.52
1:13:324:G:N2	1:13:326:G:H3'	2.25	0.52
1:13:349:A:O2'	1:13:350:G:H5'	2.10	0.52
13:4I:80:ARG:NH1	19:AI:65:ASN:O	2.43	0.52
25:4K:24:A:H2'	25:4K:25:A:C8	2.45	0.52
26:1H:155:C:H5'	26:1H:161:U:OP2	2.10	0.52
26:1H:910:A:H62	37:88:12:GLN:HA	1.74	0.52
26:1H:1113:U:OP1	32:51:2:SER:N	2.42	0.52
26:1H:1163:G:H2'	26:1H:1164:G:H8	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1H:1331:A:O2'	26:1H:1332:G:H8	1.92	0.52
26:1H:2287:A:N1	26:1H:2346:A:H2	2.08	0.52
26:1H:2793:G:H8	26:1H:2793:G:OP2	1.93	0.52
42:D8:59:ALA:HB2	42:D8:96:ILE:HD13	1.92	0.52
45:G8:82:PRO:HB3	45:G8:99:CYS:HB3	1.92	0.52
48:J8:83:GLU:CD	48:J8:85:LEU:HB2	2.34	0.52
1:1G:664:G:H22	1:1G:741:G:H1	1.58	0.52
1:1G:1120:G:H1	1:1G:1152:A:H61	1.57	0.52
1:1G:1126:U:N3	1:1G:1281:U:O4'	2.43	0.52
1:1G:1386:G:C2	1:1G:1387:G:C8	2.98	0.52
11:2A:82:VAL:HG13	11:2A:108:ILE:HG23	1.92	0.52
20:BA:26:ASN:HA	20:BA:29:LYS:HG3	1.92	0.52
26:14:2273:A:H2'	26:14:2274:A:H8	1.75	0.52
26:14:2541:A:H5"	26:14:2542:A:OP2	2.10	0.52
32:59:26:VAL:CG1	32:59:33:LEU:H	2.23	0.52
32:59:27:LYS:HA	32:59:32:GLU:HB3	1.91	0.52
35:25:47:ILE:HG13	35:25:48:PRO:HD2	1.92	0.52
45:C5:88:LYS:O	45:C5:89:PHE:HB3	2.09	0.52
1:13:926:G:H5'	1:13:927:G:O5'	2.09	0.51
10:1I:24:VAL:HG12	10:1I:25:GLU:HG3	1.90	0.51
19:AI:41:VAL:CG1	19:AI:67:VAL:HA	2.39	0.51
26:1H:11:G:C2'	26:1H:12:U:H5'	2.40	0.51
26:1H:942:G:OP2	36:78:39:LYS:HE2	2.10	0.51
26:1H:2418:A:OP1	55:Q8:39:LYS:HE2	2.10	0.51
27:16:54:G:H2'	27:16:55:U:H6	1.74	0.51
27:16:89:G:C6	27:16:89(A):A:C6	2.97	0.51
28:11:69:ARG:HH11	28:11:69:ARG:HG3	1.74	0.51
39:A8:103:GLU:O	39:A8:106:ARG:NE	2.43	0.51
43:E8:92:ARG:HB3	43:E8:92:ARG:HH11	1.74	0.51
1:1G:324:G:N7	61:1G:1752:HOH:O	2.34	0.51
1:1G:382:A:H2'	1:1G:383:A:C8	2.45	0.51
1:1G:407:G:P	4:32:115:ARG:HH21	2.32	0.51
1:1G:730:G:C5	1:1G:731:G:H1'	2.45	0.51
1:1G:1117:G:O3'	9:82:104:ARG:HD2	2.10	0.51
13:4A:89:GLY:HA2	13:4A:92:HIS:HB2	1.92	0.51
19:AA:51:VAL:HG23	19:AA:60:VAL:HG11	1.92	0.51
56:1L:2:C:N3	56:1L:72:C:N4	2.58	0.51
56:1L:10:G:H2'	56:1L:11:C:C6	2.44	0.51
26:14:2438:U:O3'	26:14:2439:A:H3'	2.10	0.51
26:14:2646:C:OP2	26:14:2732:G:O2'	2.23	0.51
27:1J:88:C:H3'	27:1J:89:G:N7	2.25	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:19:121:PRO:HA	28:19:131:LEU:HD23	1.91	0.51
36:35:59:LEU:O	36:35:59:LEU:HD22	2.10	0.51
42:95:35:LEU:C	42:95:37:VAL:HG13	2.34	0.51
1:13:1346:A:H5"	9:8E:120:ARG:HH12	1.75	0.51
2:1E:42:ILE:HD11	2:1E:202:PRO:HB2	1.91	0.51
5:4E:142:LEU:O	5:4E:143:ARG:NH1	2.44	0.51
15:6I:18:PHE:CZ	15:6I:21:ASP:HB2	2.45	0.51
22:1K:29:G:H1	22:1K:41:C:H42	1.57	0.51
26:1H:2308:G:H2'	26:1H:2308:G:N3	2.25	0.51
26:1H:2498:C:OP1	61:1H:3873:HOH:O	2.17	0.51
26:1H:2543:G:H2'	26:1H:2544:G:C8	2.44	0.51
28:11:147:LEU:HD22	28:11:155:LEU:HD11	1.92	0.51
32:51:23:ARG:HH12	32:51:25:LYS:HE3	1.75	0.51
34:58:35:ARG:O	34:58:42:TRP:HZ3	1.92	0.51
46:H8:98:MET:O	46:H8:125:LEU:HA	2.11	0.51
1:1G:984:C:H2'	1:1G:985:C:C6	2.45	0.51
2:12:162:ILE:O	2:12:185:ILE:HG12	2.10	0.51
2:12:236:TYR:HB2	2:12:239:VAL:HB	1.92	0.51
57:3L:8:4SU:H4'	57:3L:9:A:OP1	2.10	0.51
26:14:829:A:N7	26:14:2248:C:H5'	2.26	0.51
26:14:1894:C:O2'	26:14:1895:C:H5'	2.11	0.51
26:14:2212:A:H1'	26:14:2215:G:C5	2.45	0.51
26:14:2286:A:H8	26:14:2287:A:N6	2.08	0.51
26:14:2317:C:H2'	26:14:2318:G:O4'	2.11	0.51
26:14:2734:A:H2'	26:14:2735:G:O4'	2.10	0.51
38:55:107:ASP:C	38:55:107:ASP:OD1	2.53	0.51
55:M5:35:GLN:HG3	55:M5:35:GLN:O	2.11	0.51
1:13:377:G:H5'	16:7I:5:ARG:NH1	2.26	0.51
26:1H:1068:G:H1'	26:1H:1096:A:N3	2.25	0.51
31:41:5:VAL:H	51:M8:25:TYR:HE2	1.58	0.51
36:78:49:ARG:NE	55:Q8:57:ARG:HG2	2.25	0.51
36:78:62:LEU:O	55:Q8:13:ARG:HD3	2.10	0.51
1:1G:1321:C:N4	1:1G:1322:C:N4	2.58	0.51
2:12:22:LYS:HB3	2:12:40:HIS:CD2	2.45	0.51
2:12:27:LYS:HB2	2:12:194:PRO:HD2	1.92	0.51
3:22:47:LEU:HB3	3:22:52:LEU:HD13	1.92	0.51
12:3A:46:LYS:HG2	12:3A:47:LYS:HB2	1.92	0.51
56:1L:76:A:C8	26:14:2583:G:N2	2.78	0.51
26:14:235:U:H2'	26:14:236:C:H6	1.74	0.51
27:1J:40:U:C2'	27:1J:45:A:H61	2.24	0.51
34:15:72:TYR:HB2	34:15:85:ILE:HD12	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:K5:18:ARG:HH21	53:K5:44:ARG:HE	1.58	0.51
1:13:292:G:N7	1:13:293:G:H1'	2.26	0.51
1:13:1036:G:N7	1:13:1037:C:N4	2.58	0.51
1:13:1263:C:H2'	1:13:1264:C:C6	2.40	0.51
1:13:1367:C:H5'	10:1I:60:ARG:NH1	2.25	0.51
5:4E:41:VAL:HG22	5:4E:113:ALA:HB2	1.91	0.51
26:1H:729:G:C6	28:11:208:LYS:HB2	2.44	0.51
26:1H:1591:G:H2'	26:1H:1592:C:H6	1.75	0.51
26:1H:1692:U:O2'	26:1H:1693:U:H2'	2.10	0.51
26:1H:2111:C:H2'	26:1H:2118:U:H4'	1.91	0.51
26:1H:2635:C:H5"	29:21:78:LEU:HA	1.93	0.51
27:16:60:C:C2	27:16:61:G:C8	2.99	0.51
30:31:134:GLY:HA3	30:31:162:LEU:O	2.10	0.51
44:F8:3:THR:CB	44:F8:4:ALA:HA	2.40	0.51
55:Q8:34:TRP:C	55:Q8:34:TRP:HD1	2.15	0.51
1:1G:1286:A:C8	1:1G:1286:A:H3'	2.46	0.51
1:1G:1316:G:H4'	14:5A:18:VAL:HG11	1.93	0.51
1:1G:1505:G:H5'	61:1G:1759:HOH:O	2.09	0.51
26:14:2150:U:H2'	26:14:2151:G:H8	1.75	0.51
26:14:2320:A:H1'	26:14:2321:G:C6	2.45	0.51
26:14:2776:A:H4'	26:14:2777:G:O5'	2.11	0.51
30:39:89:VAL:HG12	30:39:90:PHE:H	1.75	0.51
1:13:789:U:H5	1:13:792:A:OP2	1.93	0.51
1:13:922:G:C6	1:13:923:A:C6	2.98	0.51
1:13:1078:U:O2'	5:4E:130:ASN:OD1	2.15	0.51
8:7E:54:ASP:HB2	8:7E:56:LYS:HE2	1.93	0.51
12:3I:8:ASN:O	12:3I:12:ARG:HG3	2.11	0.51
13:4I:7:VAL:HB	31:41:115:ARG:NH2	2.24	0.51
20:BI:67:ALA:HA	20:BI:72:LEU:O	2.11	0.51
20:BI:75:ASN:OD1	20:BI:75:ASN:N	2.36	0.51
22:1K:23:A:H2'	22:1K:24:G:O4'	2.11	0.51
26:1H:2336:A:H61	47:I8:43:THR:HB	1.74	0.51
28:11:112:GLN:NE2	28:11:115:GLN:OE1	2.44	0.51
31:41:10:LYS:HE2	31:41:175:LEU:O	2.11	0.51
37:88:130:LYS:NZ	46:H8:81:ARG:HG2	2.25	0.51
41:C8:32:PHE:HZ	41:C8:36:ARG:HH21	1.59	0.51
1:1G:987:G:H1	1:1G:1218:C:H42	1.57	0.51
1:1G:1111:A:H2'	1:1G:1112:C:C6	2.45	0.51
1:1G:1298:C:H41	7:62:114:ARG:HB3	1.75	0.51
1:1G:1386:G:C2	1:1G:1387:G:N7	2.78	0.51
5:42:34:VAL:O	5:42:41:VAL:HG12	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:82:26:VAL:HG22	9:82:61:ALA:N	2.26	0.51
13:4A:66:LEU:HA	13:4A:70:LEU:HB2	1.93	0.51
26:14:1298:C:P	61:14:3518:HOH:O	2.68	0.51
26:14:1473:G:C2	26:14:1474:C:C2	2.98	0.51
26:14:1678:G:H22	26:14:1989:G:N2	2.07	0.51
27:1J:13:A:N1	27:1J:69:G:O2'	2.31	0.51
30:39:187:VAL:HG12	36:35:3:LEU:HG	1.93	0.51
47:E5:53:MET:HG3	47:E5:59:LEU:HD21	1.93	0.51
8:7E:41:ARG:HH11	8:7E:41:ARG:HG3	1.75	0.51
20:BI:26:ASN:HB2	20:BI:71:THR:CG2	2.40	0.51
26:1H:280:C:N3	26:1H:361:G:C2	2.79	0.51
26:1H:883:G:H2'	26:1H:884:C:H4'	1.93	0.51
26:1H:1375:C:H2'	26:1H:1376:C:H6	1.74	0.51
31:41:9:ARG:HG2	31:41:13:GLU:CD	2.36	0.51
43:E8:86:LEU:HD12	43:E8:87:PRO:HD2	1.93	0.51
43:E8:97:LYS:HE2	43:E8:99:ARG:NH2	2.25	0.51
55:Q8:27:THR:O	55:Q8:29:LYS:HA	2.11	0.51
1:1G:429:U:H1'	1:1G:430:A:H5"	1.91	0.51
1:1G:485:G:HO2'	1:1G:486:U:P	2.34	0.51
1:1G:1053:G:O2'	1:1G:1054:C:OP2	2.28	0.51
8:72:86:ILE:HG12	8:72:135:CYS:HA	1.91	0.51
19:AA:7:LYS:HE3	19:AA:10:PHE:CE1	2.45	0.51
19:AA:66:MET:HA	19:AA:67:VAL:O	2.11	0.51
26:14:194:G:H2'	26:14:195:A:O4'	2.10	0.51
26:14:1053:C:H2'	26:14:1054:A:O4'	2.09	0.51
26:14:1111:A:H4'	32:59:3:ARG:HD3	1.92	0.51
26:14:1112:G:H2'	26:14:1113:U:C6	2.45	0.51
26:14:1582:C:O2'	26:14:1586:A:H8	1.92	0.51
26:14:1677:A:H2'	26:14:1678:G:H8	1.75	0.51
26:14:1716:U:H2'	26:14:1717:G:C8	2.42	0.51
26:14:1885:A:H5'	26:14:1886:C:OP2	2.11	0.51
26:14:2107:C:H42	26:14:2182:G:H1	1.58	0.51
26:14:2312:U:OP1	31:49:74:LYS:HD2	2.09	0.51
26:14:2785:C:O2'	29:29:64:LYS:NZ	2.44	0.51
45:C5:19:LYS:HZ2	45:C5:42:VAL:HG21	1.76	0.51
52:J5:4:HIS:O	52:J5:5:PRO:C	2.52	0.51
1:13:703:G:H4'	1:13:704:A:O5'	2.11	0.51
1:13:791:G:C6	1:13:792:A:C2	2.99	0.51
1:13:939:G:H2'	1:13:940:C:C6	2.45	0.51
1:13:1120:G:H2'	1:13:1121:U:H6	1.76	0.51
5:4E:6:PHE:CE1	5:4E:36:ASP:HB3	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:1I:6:ILE:HG12	10:1I:72:VAL:O	2.11	0.51
26:1H:50:U:H3'	26:1H:51:G:H5'	1.92	0.51
26:1H:2261:C:O2'	26:1H:2262:U:H5'	2.11	0.51
31:41:4:ASP:OD1	31:41:9:ARG:NH1	2.44	0.51
38:98:24:GLN:HE22	38:98:36:THR:HG21	1.74	0.51
44:F8:1:MET:C	44:F8:3:THR:N	2.69	0.51
46:H8:9:TYR:CE1	46:H8:35:ARG:HD3	2.45	0.51
55:Q8:39:LYS:O	55:Q8:40:GLU:CB	2.58	0.51
1:1G:164:U:H2'	1:1G:165:C:C6	2.45	0.51
1:1G:502:G:OP1	12:3A:118:SER:HB3	2.10	0.51
1:1G:583:A:H2'	1:1G:584:G:O4'	2.11	0.51
1:1G:978:A:O2'	1:1G:1322:C:N3	2.42	0.51
1:1G:1224:G:O2'	1:1G:1322:C:OP2	2.28	0.51
2:12:5:ILE:HG12	2:12:6:THR:HG22	1.92	0.51
6:52:81:ILE:HD11	28:19:125:ILE:HB	1.92	0.51
26:14:279:C:N4	26:14:361:G:H1	2.07	0.51
26:14:749:C:H5"	61:14:3784:HOH:O	2.10	0.51
26:14:1142:U:O2	26:14:1142:U:H2'	2.11	0.51
26:14:1291:C:H2'	26:14:1292:U:C6	2.46	0.51
26:14:1657:C:H2'	26:14:1658:C:C6	2.45	0.51
26:14:1849:G:H2'	26:14:1850:G:H8	1.75	0.51
26:14:2002:G:N7	61:14:3889:HOH:O	2.34	0.51
26:14:2275:C:H5'	26:14:2275:C:C6	2.45	0.51
28:19:267:SER:C	28:19:269:PHE:N	2.67	0.51
29:29:116:VAL:O	29:29:117:MET:HB3	2.11	0.51
35:25:49:ARG:HA	35:25:53:LYS:NZ	2.26	0.51
37:45:69:PHE:CD1	37:45:70:PRO:HD2	2.46	0.51
1:13:186(C):G:H2'	1:13:186(D):C:C6	2.45	0.51
1:13:448:A:OP2	1:13:485:G:N2	2.30	0.51
1:13:967:C:OP2	1:13:968:A:O2'	2.25	0.51
1:13:1120:G:H2'	1:13:1121:U:C6	2.46	0.51
9:8E:83:ARG:O	9:8E:86:VAL:HG12	2.11	0.51
26:1H:84:A:OP2	45:G8:8:LYS:NZ	2.39	0.51
26:1H:1088:A:H5'	26:1H:1089:G:H5'	1.91	0.51
26:1H:1803:A:H4'	28:11:259:THR:HG23	1.92	0.51
26:1H:1805:U:O2	28:11:50:THR:HB	2.10	0.51
26:1H:2364:C:H2'	26:1H:2365:G:O4'	2.11	0.51
26:1H:2760:C:O2'	26:1H:2761:G:H5'	2.11	0.51
26:1H:2875:C:H4'	40:B8:5:ALA:HB2	1.93	0.51
30:31:23:ASP:CG	30:31:24:LEU:H	2.18	0.51
32:51:6:ARG:HA	32:51:66:GLY:HA2	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:98:81:ASP:O	38:98:85:PRO:HG2	2.10	0.51
55:Q8:48:PHE:CZ	55:Q8:52:LYS:HG3	2.46	0.51
1:1G:757:U:H2'	1:1G:758:G:O4'	2.10	0.51
7:62:101:LEU:O	7:62:105:VAL:HG23	2.09	0.51
9:82:77:ILE:O	9:82:81:ILE:HG12	2.11	0.51
9:82:112:LYS:HE3	9:82:118:LYS:H	1.75	0.51
10:1A:4:ILE:HG12	10:1A:100:THR:HG22	1.92	0.51
11:2A:17:GLY:N	11:2A:79:SER:O	2.27	0.51
56:1L:68:C:H2'	56:1L:69:G:C8	2.46	0.51
25:4L:13:A:O2'	25:4L:14:A:OP1	2.27	0.51
26:14:1444(A):A:H2'	26:14:1444(A):A:N3	2.26	0.51
26:14:2015:A:H1'	52:J5:2:ALA:CB	2.40	0.51
26:14:2378:A:O5'	26:14:2378:A:H8	1.93	0.51
30:39:88:VAL:HG23	30:39:89:VAL:O	2.11	0.51
31:49:122:PRO:O	31:49:125:PHE:HD2	1.93	0.51
36:35:14:LYS:O	36:35:14:LYS:HD3	2.10	0.51
40:75:61:PHE:CE1	40:75:76:PHE:HB2	2.46	0.51
44:B5:8:ILE:O	49:G5:36:ARG:NH2	2.44	0.51
49:G5:21:LEU:O	49:G5:25:VAL:HG22	2.11	0.51
52:J5:16:ARG:HG3	52:J5:17:ASP:N	2.25	0.51
55:M5:52:LYS:NZ	55:M5:53:PRO:HA	2.25	0.51
1:13:659:U:H2'	1:13:660:G:C8	2.44	0.51
1:13:1148:U:H2'	1:13:1149:C:O4'	2.10	0.51
1:13:1161:C:H2'	1:13:1162:C:C6	2.45	0.51
1:13:1162:C:H2'	1:13:1163:C:C6	2.46	0.51
26:1H:213:A:H5"	26:1H:214:G:OP2	2.11	0.51
26:1H:916:G:H2'	26:1H:917:A:H5"	1.92	0.51
26:1H:1859:A:N6	26:1H:1883:G:O2'	2.44	0.51
26:1H:2757:A:N1	32:51:67:LEU:HD13	2.26	0.51
26:1H:2849:U:H4'	26:1H:2868:A:C2	2.46	0.51
27:16:39:A:H5"	27:16:39:A:H8	1.75	0.51
35:68:2:ILE:HD12	35:68:6:THR:HG21	1.92	0.51
38:98:33:ARG:NH1	38:98:113:LEU:HD21	2.25	0.51
46:H8:135:GLU:HG3	46:H8:136:PHE:HD1	1.76	0.51
2:12:47:THR:HG23	2:12:202:PRO:HG2	1.93	0.51
26:14:519:U:H2'	26:14:520:G:C8	2.46	0.51
26:14:521:G:H2'	26:14:522:G:H8	1.74	0.51
26:14:751:A:OP1	61:14:3506:HOH:O	2.19	0.51
26:14:1784:A:H4'	26:14:1785:A:O5'	2.11	0.51
26:14:2122:U:H2'	26:14:2123:G:O4'	2.10	0.51
26:14:2126:A:N1	26:14:2163:C:H1'	2.26	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:29:171:GLU:O	29:29:184:VAL:HA	2.11	0.51
30:39:107:LYS:HE2	30:39:205:ARG:HD2	1.92	0.51
32:59:81:GLU:HG2	32:59:83:TYR:H	1.76	0.51
34:15:97:ARG:HA	34:15:100:GLU:HB2	1.92	0.51
45:C5:83:THR:HG22	45:C5:84:ARG:H	1.75	0.51
48:F5:92:LYS:O	48:F5:93:GLU:C	2.53	0.51
4:3E:57:ARG:HB3	4:3E:206:PHE:HB2	1.92	0.51
8:7E:9:MET:HG3	8:7E:26:VAL:HG21	1.92	0.51
8:7E:127:LEU:HD23	8:7E:127:LEU:N	2.26	0.51
13:4I:22:ILE:HB	13:4I:25:ILE:HD12	1.93	0.51
15:6I:17:ARG:HG3	15:6I:17:ARG:NH1	2.25	0.51
19:AI:40:ILE:O	19:AI:41:VAL:HG22	2.11	0.51
20:BI:89:ARG:HG3	20:BI:104:LEU:HD21	1.92	0.51
26:1H:270(P):C:H2'	26:1H:270(Q):C:C6	2.45	0.51
26:1H:389:G:H22	36:78:72:PRO:HD3	1.75	0.51
26:1H:962:G:H2'	26:1H:963:U:C6	2.46	0.51
26:1H:1011:G:OP1	41:C8:77:SER:OG	2.20	0.51
26:1H:1432:C:H2'	26:1H:1433:U:O4'	2.11	0.51
26:1H:2315:G:H5"	26:1H:2316:C:OP2	2.11	0.51
42:D8:17:GLY:N	42:D8:96:ILE:O	2.22	0.51
43:E8:79:GLY:CA	43:E8:100:THR:HG22	2.41	0.51
46:H8:81:ARG:HG3	46:H8:81:ARG:O	2.10	0.51
54:P8:10:ARG:O	54:P8:14:LYS:HG3	2.10	0.51
1:1G:18:C:H6	1:1G:18:C:O5'	1.94	0.51
1:1G:176:C:H2'	1:1G:177:C:H6	1.76	0.51
1:1G:631:G:C3'	1:1G:632:A:H8	2.23	0.51
1:1G:1208:C:H2'	1:1G:1209:C:C6	2.46	0.51
1:1G:1298:C:H5"	7:62:114:ARG:HH22	1.77	0.51
3:22:7:PRO:O	3:22:11:ARG:NH1	2.44	0.51
3:22:152:ILE:HB	3:22:199:LYS:HB2	1.92	0.51
5:42:80:ILE:HG13	8:72:104:ARG:NH2	2.26	0.51
10:1A:61:GLU:HG3	14:5A:58:LYS:HE2	1.92	0.51
10:1A:78:ASN:OD1	10:1A:81:THR:HG23	2.11	0.51
57:3L:56:C:H2'	57:3L:57:G:H8	1.75	0.51
26:14:273(C):C:N4	26:14:363(C):G:H1	2.09	0.51
26:14:322:A:H3'	30:39:169:ASN:OD1	2.11	0.51
26:14:363(E):U:H5'	26:14:363(F):A:OP2	2.11	0.51
26:14:839:U:H2'	26:14:840:C:C6	2.46	0.51
26:14:1530:G:H2'	26:14:1531:C:O4'	2.11	0.51
26:14:2052:G:O4'	29:29:142:GLY:HA3	2.11	0.51
27:1J:38:C:N3	27:1J:44:G:N2	2.48	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:1J:63:G:H2'	27:1J:64:C:C6	2.46	0.51
27:1J:116:G:H5"	39:65:55:ALA:HB2	1.93	0.51
35:25:86:ILE:HG22	35:25:94:ARG:HG3	1.93	0.51
35:25:98:VAL:HG12	35:25:117:LEU:HB3	1.93	0.51
36:35:52:GLU:CD	36:35:57:THR:HA	2.37	0.51
37:45:78:PRO:HB2	37:45:79:LEU:HG	1.93	0.51
45:C5:17:SER:HG	45:C5:18:GLY:N	2.08	0.51
1:13:31:G:H3'	1:13:32:A:H5"	1.92	0.50
6:5E:67:MET:SD	6:5E:75:LEU:HD12	2.51	0.50
13:4I:16:ASP:HB3	13:4I:41:PRO:HB3	1.93	0.50
18:9I:38:GLU:HA	18:9I:41:LYS:NZ	2.24	0.50
26:1H:760:G:H5"	61:1H:3839:HOH:O	2.10	0.50
26:1H:1210:A:H5'	26:1H:1210:A:C8	2.44	0.50
26:1H:1530:G:O6	26:1H:1542:G:N2	2.44	0.50
26:1H:2209:C:O2	26:1H:2216:G:C2	2.63	0.50
29:21:78:LEU:O	29:21:79:ARG:HB2	2.11	0.50
31:41:98:ARG:HH21	51:M8:1:MET:HG3	1.76	0.50
1:1G:1051:C:H2'	1:1G:1052:U:C6	2.46	0.50
1:1G:1179:A:H2'	1:1G:1180:A:O4'	2.11	0.50
1:1G:1375:A:H4'	7:62:29:LYS:HE3	1.92	0.50
7:62:92:SER:CB	7:62:94:ARG:HG2	2.41	0.50
26:14:29:U:H2'	26:14:30:G:H8	1.76	0.50
26:14:823:G:H2'	26:14:824:A:C8	2.46	0.50
26:14:1250:G:OP2	36:35:21:ARG:NH1	2.44	0.50
26:14:1442:G:H2'	26:14:1443:G:C8	2.46	0.50
26:14:2032:G:H21	29:29:146:THR:HG23	1.75	0.50
26:14:2816:C:O3'	38:55:99:LYS:NZ	2.43	0.50
28:19:253:GLN:HG2	28:19:255:LYS:HZ3	1.76	0.50
30:39:192:LEU:HD22	30:39:194:MET:HG2	1.93	0.50
34:15:4:TYR:O	41:85:64:ARG:NH1	2.44	0.50
34:15:95:PRO:O	34:15:98:VAL:HG22	2.11	0.50
1:13:779:C:H2'	1:13:780:A:O4'	2.10	0.50
1:13:939:G:H5"	7:6E:102:ARG:NH2	2.26	0.50
1:13:1226:C:H2'	13:4I:103:THR:HB	1.93	0.50
5:4E:147:ASP:HA	5:4E:150:ARG:HH12	1.77	0.50
10:1I:45:ARG:HG2	10:1I:47:PHE:CZ	2.46	0.50
19:AI:36:ARG:NH1	19:AI:52:TYR:O	2.42	0.50
26:1H:311:A:C6	26:1H:328:U:C4	2.99	0.50
26:1H:459:U:H2'	26:1H:460:A:H8	1.76	0.50
26:1H:729:G:O5'	28:11:208:LYS:NZ	2.41	0.50
28:11:68:LYS:HB3	28:11:70:TRP:CZ3	2.47	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:31:196:LEU:C	30:31:197:ASP:O	2.53	0.50
31:41:112:PRO:HB3	51:M8:37:SER:N	2.25	0.50
45:G8:94:LYS:HG3	45:G8:95:LYS:H	1.77	0.50
1:1G:108:G:H5'	1:1G:109:A:H5"	1.91	0.50
1:1G:236:G:H2'	1:1G:237:C:O4'	2.11	0.50
1:1G:509:A:C8	1:1G:509:A:H3'	2.46	0.50
1:1G:1004:A:H8	1:1G:1036:G:H22	1.59	0.50
4:32:24:GLU:HG2	4:32:25:ARG:H	1.76	0.50
7:62:143:ARG:NH1	57:3L:41:C:O2'	2.45	0.50
10:1A:33:GLN:HB3	10:1A:75:ILE:HG12	1.93	0.50
23:2L:54:G:O2'	23:2L:55:5MU:H5"	2.12	0.50
26:14:780:G:H21	26:14:783:A:N6	2.07	0.50
26:14:1224:G:N2	26:14:1227:A:OP2	2.33	0.50
26:14:1450:C:H2'	26:14:1451:C:C6	2.46	0.50
26:14:2327:A:H2'	26:14:2328:A:H8	1.72	0.50
26:14:2335:A:C8	26:14:2337:G:C5	2.99	0.50
26:14:2720:U:N3	26:14:2873:A:H2	2.10	0.50
28:19:245:PRO:HG2	28:19:253:GLN:NE2	2.26	0.50
29:29:96:PHE:O	29:29:175:VAL:HG11	2.10	0.50
31:49:145:THR:C	31:49:147:ASP:H	2.18	0.50
37:45:25:ASP:OD1	37:45:25:ASP:N	2.44	0.50
37:45:97:VAL:HG21	37:45:103:MET:HE3	1.91	0.50
38:55:45:ARG:HA	38:55:95:THR:HG21	1.93	0.50
48:F5:91:LYS:HA	48:F5:91:LYS:NZ	2.24	0.50
51:I5:34:GLU:HG2	51:I5:35:VAL:H	1.76	0.50
1:13:375:U:O3'	16:7I:6:LEU:HB2	2.12	0.50
1:13:446:G:H1	1:13:488:C:N4	2.00	0.50
1:13:971:G:N2	1:13:1363:A:OP2	2.41	0.50
1:13:1432:G:OP1	40:B8:107:ASP:HB2	2.11	0.50
4:3E:173:TRP:CD1	4:3E:174:LEU:HG	2.47	0.50
22:1K:27:G:H2'	22:1K:28:G:H8	1.75	0.50
24:3K:9:A:N6	24:3K:23:A:H62	2.07	0.50
26:1H:801:G:OP2	61:1H:4223:HOH:O	2.18	0.50
26:1H:818:G:H5'	26:1H:839:U:OP1	2.10	0.50
26:1H:863:A:H2'	26:1H:864:G:C8	2.46	0.50
26:1H:2405:G:H5"	36:78:75:ILE:HD12	1.93	0.50
39:A8:27:SER:HA	39:A8:88:ASP:CB	2.39	0.50
41:C8:90:VAL:HG12	41:C8:91:ASP:N	2.26	0.50
1:1G:909:A:H2'	1:1G:910:C:O4'	2.10	0.50
1:1G:1187:G:H5'	9:82:113:LYS:NZ	2.26	0.50
2:12:131:PRO:HG2	2:12:134:GLU:HB2	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:62:69:VAL:HG12	7:62:103:TRP:HE3	1.76	0.50
13:4A:78:ILE:HG23	13:4A:92:HIS:ND1	2.26	0.50
26:14:1003:G:N2	26:14:1153:C:C2	2.78	0.50
26:14:1087:G:H2'	26:14:1089:G:H1'	1.91	0.50
26:14:1888:G:N3	26:14:1888:G:H5"	2.26	0.50
26:14:1979:C:H2'	26:14:1980:G:H5'	1.92	0.50
26:14:2306:C:H3'	26:14:2307:G:H5"	1.92	0.50
29:29:101:ARG:O	29:29:201:THR:OG1	2.30	0.50
41:85:66:ASN:HB2	41:85:76:TYR:HB2	1.92	0.50
51:I5:21:VAL:HG22	51:I5:22:ILE:H	1.75	0.50
1:13:429:U:H1'	1:13:430:A:H5"	1.93	0.50
1:13:982:U:H5"	14:5I:6:LEU:HD11	1.94	0.50
1:13:1164:G:C6	1:13:1165:C:C4	2.99	0.50
3:2E:52:LEU:HA	3:2E:70:VAL:HG12	1.93	0.50
8:7E:33:GLU:OE2	8:7E:50:ARG:NH1	2.44	0.50
8:7E:42:GLU:HG3	8:7E:109:ILE:HD12	1.93	0.50
16:7I:8:ARG:HB3	16:7I:28:ARG:NH1	2.26	0.50
26:1H:270(E):G:C6	26:1H:270(F):U:C4	2.99	0.50
26:1H:2513:G:N2	29:21:143:ASN:HD21	2.10	0.50
26:1H:2756:U:H4'	26:1H:2757:A:OP1	2.10	0.50
26:1H:2795:G:H3'	26:1H:2797:U:C5'	2.40	0.50
31:41:36:LYS:HG2	31:41:38:VAL:HG23	1.93	0.50
31:41:131:TYR:O	31:41:159:VAL:HG23	2.11	0.50
34:58:30:ILE:HG22	34:58:34:LEU:HD22	1.93	0.50
38:98:87:TYR:CE1	38:98:117:VAL:HG12	2.45	0.50
1:1G:539:A:H2'	1:1G:540:G:C8	2.46	0.50
1:1G:723:U:H4'	1:1G:724:G:OP2	2.11	0.50
1:1G:947:G:O3'	13:4A:109:THR:OG1	2.29	0.50
1:1G:977:A:O2'	1:1G:981:U:N3	2.43	0.50
1:1G:1131:G:C8	1:1G:1132:C:H5	2.27	0.50
3:22:34:LEU:HD13	14:5A:25:VAL:HG11	1.94	0.50
3:22:50:ALA:HB1	3:22:70:VAL:HG11	1.93	0.50
7:62:116:ALA:O	7:62:120:ILE:HG12	2.11	0.50
10:1A:40:LEU:HG	10:1A:41:PRO:HD2	1.92	0.50
57:3L:38:A:H5"	61:3L:203:HOH:O	2.12	0.50
26:14:2228:G:OP1	28:19:261:LYS:NZ	2.40	0.50
26:14:2685:G:OP2	40:75:51:ARG:NH1	2.43	0.50
28:19:136:ILE:HG22	28:19:140:THR:OG1	2.11	0.50
28:19:182:LEU:H	28:19:272:ALA:HB2	1.77	0.50
29:29:31:CYS:O	29:29:91:VAL:HG22	2.12	0.50
32:59:70:THR:O	32:59:74:ASN:ND2	2.36	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:25:49:ARG:HA	35:25:53:LYS:HZ3	1.76	0.50
36:35:98:GLU:HA	36:35:101:VAL:HG12	1.93	0.50
37:45:21:THR:HG22	37:45:23:GLY:HA3	1.93	0.50
46:D5:158:PRO:O	46:D5:161:VAL:HG22	2.10	0.50
48:F5:79:GLY:C	48:F5:80:LEU:HG	2.37	0.50
8:7E:38:ILE:HD11	8:7E:118:VAL:O	2.12	0.50
12:3I:66:VAL:HG22	12:3I:67:THR:H	1.76	0.50
26:1H:120:U:OP2	61:1H:4187:HOH:O	2.19	0.50
26:1H:444:C:H4'	30:31:49:ALA:HB2	1.93	0.50
26:1H:833:U:O2	36:78:55:ARG:NH2	2.43	0.50
26:1H:1069:A:N7	26:1H:1073:A:N6	2.59	0.50
26:1H:2125:G:N2	26:1H:2173:A:H62	2.09	0.50
26:1H:2308:G:N1	26:1H:2311:A:C2	2.68	0.50
27:16:66:A:H61	27:16:107:U:H2'	1.75	0.50
29:21:37:ARG:O	29:21:45:THR:HA	2.11	0.50
30:31:129:PHE:HA	30:31:142:TRP:CD1	2.45	0.50
36:78:106:LEU:O	36:78:107:LYS:C	2.55	0.50
44:F8:83:VAL:HG11	44:F8:89:ILE:HD12	1.93	0.50
1:1G:565:U:OP2	1:1G:566:G:O2'	2.22	0.50
1:1G:1108:G:H5'	3:22:176:HIS:HD2	1.76	0.50
1:1G:1385:G:H2'	1:1G:1386:G:C8	2.45	0.50
4:32:18:LYS:N	4:32:33:MET:HE2	2.26	0.50
26:14:639:U:H2'	26:14:640:C:C6	2.45	0.50
26:14:958:U:OP1	37:45:74:TYR:OH	2.25	0.50
26:14:1025:G:C4	26:14:1135:C:H1'	2.46	0.50
26:14:1033:U:H3'	26:14:1033:U:C6	2.46	0.50
26:14:1040:C:H2'	26:14:1041:C:C6	2.46	0.50
26:14:1171:G:O2'	26:14:1173:G:N3	2.44	0.50
26:14:1310:G:N7	61:14:3925:HOH:O	2.35	0.50
26:14:1412:A:H2'	26:14:1413:G:C8	2.46	0.50
26:14:2019:A:OP2	52:J5:9:LYS:NZ	2.44	0.50
26:14:2027:G:N7	61:14:4057:HOH:O	2.35	0.50
26:14:2272:U:H5"	26:14:2273:A:OP1	2.11	0.50
32:59:121:ILE:HA	32:59:134:SER:O	2.11	0.50
36:35:15:ARG:NH2	36:35:17:LYS:HE3	2.27	0.50
39:65:3:ARG:HE	39:65:4:LEU:H	1.59	0.50
40:75:4:GLY:N	40:75:7:ILE:HG22	2.27	0.50
1:13:141:A:H1'	1:13:182:U:O2	2.12	0.50
1:13:433:C:H2'	1:13:434:U:C6	2.47	0.50
1:13:690:G:H2'	1:13:691:G:O4'	2.12	0.50
1:13:1029:G:H1'	1:13:1032(A):G:N2	2.19	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:4E:35:GLY:HA3	5:4E:112:LEU:O	2.12	0.50
23:2K:9:G:N2	23:2K:47:7MG:OP2	2.45	0.50
26:1H:617:G:OP1	30:31:40:GLN:NE2	2.44	0.50
26:1H:773:U:C4'	28:11:47:GLY:HA3	2.41	0.50
26:1H:1109:C:O2'	26:1H:1110:G:O4'	2.30	0.50
26:1H:2116:G:N2	26:1H:2165:G:H22	2.10	0.50
26:1H:2292:C:H42	26:1H:2340:G:H1	1.60	0.50
27:16:29:A:H2'	27:16:30:C:O4'	2.11	0.50
32:51:154:PRO:HD3	32:51:162:ILE:O	2.11	0.50
43:E8:4:LYS:HE3	43:E8:6:ILE:HD11	1.93	0.50
45:G8:85:VAL:O	45:G8:86:ARG:HD3	2.11	0.50
55:Q8:6:THR:O	55:Q8:7:HIS:HB3	2.11	0.50
1:1G:561:U:HO2'	1:1G:562:C:P	2.35	0.50
1:1G:601:C:H2'	1:1G:602:A:C8	2.47	0.50
1:1G:1347:G:H22	1:1G:1373:G:H2'	1.77	0.50
3:22:150:LYS:HG3	3:22:169:ALA:HB2	1.93	0.50
7:62:79:ARG:HG2	7:62:84:ASN:HB3	1.93	0.50
17:8A:82:MET:O	17:8A:86:GLU:HG2	2.11	0.50
26:14:30:G:O6	61:14:3964:HOH:O	2.19	0.50
26:14:1057:A:H2	26:14:1082:U:H3	1.59	0.50
26:14:1210:A:H5'	26:14:1212:G:H5'	1.93	0.50
26:14:1423:G:OP1	26:14:1492:G:O2'	2.30	0.50
26:14:1751:C:O2'	26:14:1752:C:H5'	2.12	0.50
26:14:2015:A:H1'	52:J5:2:ALA:HB2	1.94	0.50
27:1J:40:U:N3	27:1J:43:C:H5"	2.27	0.50
33:69:6:LEU:HB2	33:69:36:ALA:HA	1.94	0.50
33:69:102:SER:OG	33:69:103:ARG:N	2.43	0.50
36:35:85:LEU:HA	36:35:88:LEU:HD23	1.93	0.50
40:75:11:GLU:OE1	40:75:11:GLU:N	2.45	0.50
1:13:1228:C:H2'	1:13:1229:A:H8	1.76	0.50
4:3E:98:GLU:HG2	4:3E:189:PRO:HG2	1.94	0.50
7:6E:63:LYS:NZ	7:6E:64:GLN:OE1	2.44	0.50
26:1H:654(H):G:H2'	26:1H:654(H):G:N3	2.27	0.50
26:1H:805:G:O2'	61:1H:4534:HOH:O	2.20	0.50
26:1H:1728:G:C6	26:1H:1730:U:OP2	2.64	0.50
26:1H:2611:U:H2'	52:N8:3:LYS:HG3	1.93	0.50
26:1H:2660:A:C2	26:1H:2661:G:H1'	2.47	0.50
26:1H:2700:C:O2'	26:1H:2701:C:H5'	2.12	0.50
32:51:10:PRO:HD3	32:51:69:ARG:HE	1.77	0.50
35:68:107:ARG:NH1	40:B8:36:GLU:HG2	2.27	0.50
35:68:107:ARG:HH12	40:B8:36:GLU:HG2	1.77	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:78:96:THR:C	36:78:98:GLU:N	2.69	0.50
52:N8:31:VAL:HB	52:N8:41:PRO:O	2.12	0.50
55:Q8:56:GLU:O	55:Q8:57:ARG:HG3	2.11	0.50
1:1G:656:C:O2'	15:6A:28:GLN:OE1	2.19	0.50
1:1G:1018:C:H2'	1:1G:1019:C:O4'	2.11	0.50
3:22:136:GLN:O	3:22:139:GLN:N	2.44	0.50
20:BA:33:ILE:O	20:BA:37:SER:OG	2.28	0.50
20:BA:73:HIS:HB3	20:BA:74:LYS:HG2	1.94	0.50
57:3L:58:A:H1'	57:3L:60:U:H5	1.77	0.50
26:14:1024:G:C3'	26:14:1025:G:H5"	2.40	0.50
26:14:2059:A:H5"	26:14:2060:A:OP2	2.11	0.50
27:1J:42:C:C4	31:49:91:ARG:NH2	2.80	0.50
30:39:158:THR:HB	30:39:195:ASP:HB2	1.93	0.50
37:45:97:VAL:HG11	37:45:103:MET:HE3	1.94	0.50
1:13:73:G:H2'	1:13:74:C:C6	2.46	0.50
1:13:685:G:O2'	1:13:686:U:H5'	2.11	0.50
1:13:825:G:H2'	1:13:826:C:H6	1.76	0.50
2:1E:118:LEU:HB3	2:1E:142:LEU:HD12	1.93	0.50
14:5I:27:CYS:HB2	14:5I:29:ARG:H	1.77	0.50
48:J8:91:LYS:O	48:J8:93:GLU:N	2.45	0.50
49:K8:21:LEU:HD13	49:K8:64:LEU:HA	1.94	0.50
55:Q8:35:GLN:C	55:Q8:37:SER:H	2.20	0.50
1:1G:79:G:H2'	1:1G:79:G:N3	2.27	0.50
1:1G:1069:C:O2'	1:1G:1192:C:O2	2.22	0.50
1:1G:1528:U:OP2	1:1G:1528:U:H6	1.95	0.50
2:12:9:GLU:HB2	2:12:217:ARG:HH22	1.76	0.50
3:22:186:PHE:HE2	3:22:188:LEU:HD22	1.76	0.50
26:14:138:G:H22	44:B5:44:GLU:CD	2.18	0.50
26:14:528:A:H8	26:14:528:A:H3'	1.76	0.50
26:14:1568:G:H5'	28:19:60:ARG:HA	1.94	0.50
26:14:2340:G:O2'	26:14:2341:G:H5'	2.12	0.50
26:14:2575:C:H2'	26:14:2578:G:O6	2.12	0.50
28:19:127:VAL:HA	28:19:193:VAL:HG22	1.93	0.50
28:19:267:SER:C	28:19:269:PHE:H	2.20	0.50
32:59:22:GLY:O	32:59:37:VAL:HG12	2.12	0.50
36:35:125:VAL:O	36:35:144:GLU:HB3	2.11	0.50
37:45:2:LEU:O	37:45:70:PRO:HG2	2.12	0.50
39:65:30:ARG:HG3	39:65:35:ILE:HD13	1.93	0.50
44:B5:26:TYR:O	44:B5:81:VAL:HG22	2.12	0.50
46:D5:152:ALA:HB2	46:D5:169:GLU:O	2.12	0.50
53:K5:21:TYR:HE2	53:K5:52:VAL:HG11	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:13:684:A:N6	1:13:685:G:C6	2.80	0.50
2:1E:71:VAL:HG23	2:1E:164:VAL:HA	1.93	0.50
7:6E:120:ILE:O	7:6E:124:LEU:HB2	2.12	0.50
26:1H:1268:A:OP1	61:1H:4448:HOH:O	2.19	0.50
26:1H:1339:G:H21	26:1H:1603:A:H1'	1.76	0.50
26:1H:1385:G:O2'	26:1H:1396:U:H6	1.95	0.50
26:1H:2392:A:H2	26:1H:2424:C:N4	2.06	0.50
26:1H:2518:A:H5'	26:1H:2518:A:H8	1.77	0.50
26:1H:2563:U:O2'	35:68:28:SER:HB2	2.12	0.50
31:41:47:LYS:HZ1	31:41:80:PHE:HD2	1.59	0.50
32:51:87:LEU:HB2	32:51:131:VAL:HG12	1.94	0.50
41:C8:61:TRP:CH2	41:C8:93:LYS:HB2	2.47	0.50
41:C8:79:PHE:CD1	41:C8:79:PHE:C	2.90	0.50
43:E8:73:ALA:HB3	43:E8:106:ILE:HB	1.93	0.50
48:J8:64:ALA:HA	48:J8:67:ILE:HG13	1.94	0.50
49:K8:35:LEU:CD1	49:K8:53:LEU:HD12	2.42	0.50
50:L8:35:ARG:HB3	50:L8:37:LEU:CD2	2.42	0.50
1:1G:375:U:OP1	16:7A:69:THR:OG1	2.19	0.50
1:1G:591:U:H2'	1:1G:592:G:C8	2.47	0.50
1:1G:1308:U:H5"	13:4A:98:VAL:HG22	1.93	0.50
1:1G:1344:C:HO2'	1:1G:1348:U:HO2'	1.59	0.50
26:14:290:G:H2'	26:14:291:C:O4'	2.12	0.50
26:14:350:U:H2'	26:14:351:G:O4'	2.11	0.50
26:14:2543:G:H2'	26:14:2544:G:C8	2.47	0.50
26:14:2712:U:H2'	26:14:2714:G:H5"	1.92	0.50
30:39:164:ARG:O	30:39:167:ALA:HB3	2.11	0.50
36:35:27:HIS:HB3	36:35:32:THR:HG23	1.94	0.50
37:45:51:ARG:HG2	37:45:51:ARG:NH1	2.26	0.50
51:I5:49:PHE:HD2	51:I5:50:VAL:HG22	1.77	0.50
1:13:917:G:H2'	1:13:918:A:C8	2.47	0.49
4:3E:110:PHE:HE2	4:3E:148:VAL:HG23	1.77	0.49
10:1I:5:ARG:NH1	10:1I:99:LYS:HD2	2.27	0.49
18:9I:26:LEU:HD13	18:9I:42:ARG:NH2	2.26	0.49
18:9I:31:LEU:H	18:9I:31:LEU:HD23	1.76	0.49
20:BI:10:LEU:HD11	20:BI:12:ALA:HB3	1.93	0.49
26:1H:618:G:H2'	26:1H:618(A):C:H6	1.76	0.49
26:1H:1429:G:O2'	26:1H:1430:C:H5'	2.11	0.49
27:16:44:G:C2	27:16:48:A:C2	3.00	0.49
32:51:42:ARG:HG2	32:51:44:VAL:HG23	1.94	0.49
34:58:96:GLU:C	34:58:98:VAL:N	2.69	0.49
36:78:121:LYS:O	36:78:123:LEU:N	2.41	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:98:63:ARG:HG3	38:98:80:PHE:HE2	1.77	0.49
41:C8:106:PHE:HA	41:C8:109:LEU:HD12	1.94	0.49
46:H8:100:VAL:HG11	46:H8:137:ILE:HG13	1.93	0.49
1:1G:142:G:H2'	1:1G:143:A:C8	2.47	0.49
1:1G:922:G:N3	1:1G:1398:A:H2	2.09	0.49
1:1G:1215:G:C5	1:1G:1216:G:C8	2.99	0.49
2:12:166:ASP:OD2	2:12:169:LYS:HB2	2.12	0.49
7:62:50:ILE:HB	7:62:58:PRO:HG3	1.94	0.49
9:82:89:ASN:O	9:82:92:TYR:HB2	2.12	0.49
26:14:26:G:C6	26:14:27:G:N1	2.79	0.49
26:14:1191:G:O2'	26:14:1192:G:H5'	2.12	0.49
29:29:89:ASP:O	29:29:91:VAL:N	2.39	0.49
30:39:32:LEU:O	30:39:36:VAL:HG23	2.12	0.49
32:59:30:LYS:HB3	32:59:79:VAL:O	2.10	0.49
37:45:63:LYS:HE2	37:45:65:PHE:CE2	2.46	0.49
46:D5:6:LYS:O	46:D5:62:PRO:HD3	2.12	0.49
46:D5:111:VAL:HG22	46:D5:112:ARG:HG2	1.94	0.49
1:13:295:C:H2'	1:13:296:U:O4'	2.12	0.49
1:13:827:U:C5	1:13:872:A:N1	2.74	0.49
8:7E:87:SER:HB2	8:7E:93:VAL:CB	2.39	0.49
12:3I:24:VAL:HB	12:3I:27:LEU:HD12	1.94	0.49
26:1H:458:G:O2'	26:1H:469:G:O6	2.21	0.49
26:1H:2123:G:H22	26:1H:2175:C:N4	2.10	0.49
26:1H:2157:G:O2'	26:1H:2158:A:O5'	2.29	0.49
26:1H:2235:G:H2'	26:1H:2236:C:C6	2.46	0.49
26:1H:2376:A:H2'	26:1H:2377:A:O4'	2.12	0.49
28:11:96:HIS:ND1	28:11:102:LYS:HE2	2.27	0.49
34:58:78:TYR:CD1	34:58:78:TYR:N	2.80	0.49
38:98:53:HIS:ND1	38:98:94:TYR:OH	2.41	0.49
39:A8:106:ARG:NH1	39:A8:107:GLU:HB2	2.27	0.49
40:B8:105:LEU:C	40:B8:107:ASP:H	2.20	0.49
41:C8:93:LYS:N	41:C8:95:LEU:HG	2.28	0.49
47:I8:60:PHE:CD1	47:I8:60:PHE:N	2.80	0.49
1:1G:456:C:H2'	1:1G:457:C:C6	2.47	0.49
1:1G:596:C:H2'	1:1G:597:G:H8	1.77	0.49
1:1G:748:C:H6	1:1G:748:C:O5'	1.95	0.49
2:12:213:LEU:HA	2:12:216:SER:HB3	1.93	0.49
26:14:234:C:H2'	26:14:235:U:C6	2.47	0.49
26:14:2657:A:O2'	32:59:160:LYS:HE3	2.11	0.49
33:69:76:THR:HG23	33:69:77:LEU:N	2.28	0.49
33:69:129:THR:HG22	33:69:137:PRO:HB3	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:B5:60:ARG:HH11	44:B5:60:ARG:HG2	1.77	0.49
1:13:4:U:O4	8:7E:105:ARG:HD2	2.12	0.49
2:1E:59:GLU:HB2	2:1E:221:LEU:HD11	1.94	0.49
4:3E:107:ARG:NH2	4:3E:194:LEU:HD13	2.28	0.49
5:4E:41:VAL:HG22	5:4E:113:ALA:CB	2.42	0.49
26:1H:481:G:H1'	26:1H:507:A:N1	2.27	0.49
26:1H:783:A:H8	26:1H:784:A:H4'	1.77	0.49
26:1H:890:A:H2'	26:1H:892:G:H5'	1.94	0.49
26:1H:2108:C:H2'	26:1H:2109:U:O4'	2.12	0.49
26:1H:2109:U:N3	26:1H:2110:G:O6	2.45	0.49
26:1H:2314:C:H2'	26:1H:2315:G:C8	2.47	0.49
32:51:125:VAL:HG12	32:51:127:GLU:O	2.12	0.49
37:88:85:LYS:HG2	37:88:86:GLY:N	2.27	0.49
44:F8:37:THR:O	44:F8:40:LYS:HB3	2.13	0.49
46:H8:63:ASP:OD2	46:H8:65:GLN:NE2	2.42	0.49
1:1G:79:G:H1	1:1G:90:C:N4	2.11	0.49
1:1G:300:A:H1'	1:1G:565:U:O2	2.12	0.49
1:1G:1130:A:N6	1:1G:1144:G:H21	2.10	0.49
3:22:175:LEU:H	3:22:175:LEU:HD12	1.77	0.49
10:1A:3:LYS:NZ	10:1A:75:ILE:O	2.45	0.49
10:1A:9:ARG:HH21	10:1A:95:GLU:HG2	1.77	0.49
57:3L:15:G:N1	57:3L:48:C:N4	2.60	0.49
26:14:1111:A:H4'	32:59:3:ARG:HH11	1.77	0.49
26:14:1790:C:H2'	26:14:1791:A:C5	2.47	0.49
26:14:2635:C:O2'	29:29:48:GLN:NE2	2.45	0.49
27:1J:23:G:C2	27:1J:24:G:O6	2.65	0.49
29:29:62:PRO:C	29:29:64:LYS:N	2.70	0.49
31:49:60:LEU:O	31:49:64:THR:HG22	2.12	0.49
35:25:63:VAL:HG12	35:25:106:LEU:HD11	1.93	0.49
42:95:71:LEU:CA	42:95:86:GLY:HA2	2.42	0.49
53:K5:21:TYR:CE2	53:K5:52:VAL:HG11	2.47	0.49
1:13:630:G:H2'	1:13:631:G:O4'	2.12	0.49
1:13:1004:A:C5'	1:13:1025:U:H3	2.20	0.49
1:13:1442:G:C6	1:13:1446:A:C6	3.01	0.49
2:1E:60:ASP:HB3	2:1E:64:ARG:NH1	2.27	0.49
2:1E:237:ALA:O	2:1E:239:VAL:N	2.45	0.49
7:6E:91:VAL:HG12	7:6E:95:ARG:HB3	1.94	0.49
9:8E:4:TYR:CE2	9:8E:88:TYR:HB2	2.47	0.49
9:8E:118:LYS:O	9:8E:119:ALA:HB3	2.12	0.49
10:1I:22:LYS:NZ	10:1I:88:LEU:O	2.45	0.49
26:1H:459:U:H5"	54:P8:40:TRP:CE2	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1H:498:G:O2'	26:1H:499:U:H5'	2.13	0.49
26:1H:1510:A:OP1	26:1H:1511:A:H5'	2.13	0.49
26:1H:1695:G:H2'	26:1H:1696:G:O4'	2.11	0.49
26:1H:2262:U:O2'	26:1H:2263:C:H5'	2.12	0.49
27:16:44:G:H1'	27:16:47:C:N4	2.28	0.49
29:21:36:ARG:HH22	29:21:88:GLY:H	1.60	0.49
44:F8:3:THR:CB	44:F8:6:ASP:HB2	2.42	0.49
1:1G:426:G:OP1	4:32:36:ARG:NH2	2.37	0.49
1:1G:626:U:C2	1:1G:627:G:C8	3.00	0.49
1:1G:981:U:O2'	14:5A:30:ALA:HB1	2.12	0.49
1:1G:1053:G:O2'	1:1G:1054:C:P	2.70	0.49
1:1G:1190:G:H5'	3:22:176:HIS:CE1	2.48	0.49
7:62:73:MET:HG3	7:62:89:MET:O	2.12	0.49
56:1L:36:A:H61	25:4L:19:U:H3	1.59	0.49
26:14:678:C:H2'	26:14:679:C:C6	2.46	0.49
26:14:921:G:C6	26:14:922:U:C4	3.01	0.49
26:14:1742:C:H5'	26:14:1743:G:OP2	2.12	0.49
26:14:1794:U:H2'	26:14:1795:C:H6	1.77	0.49
26:14:2127:G:O2'	26:14:2173:A:N1	2.42	0.49
32:59:9:ILE:HD12	32:59:49:VAL:HB	1.94	0.49
38:55:97:VAL:HA	38:55:113:LEU:O	2.12	0.49
44:B5:63:LYS:O	44:B5:63:LYS:HD2	2.11	0.49
48:F5:6:GLU:HG3	48:F5:61:ARG:O	2.13	0.49
1:13:1178:G:N2	1:13:1181:G:H8	2.11	0.49
2:1E:155:LEU:HD13	2:1E:157:ARG:O	2.11	0.49
3:2E:19:GLU:HA	3:2E:54:ARG:HH12	1.78	0.49
23:2K:13:C:H4'	26:1H:1924:C:H4'	1.94	0.49
26:1H:492:A:H2'	26:1H:493:G:O4'	2.13	0.49
26:1H:1971:A:H5'	26:1H:1972:A:H5"	1.94	0.49
26:1H:2377:A:H2'	26:1H:2378:A:C8	2.48	0.49
26:1H:2475:C:H4'	26:1H:2476:A:OP1	2.12	0.49
26:1H:2689:U:H5"	26:1H:2713:A:C2	2.47	0.49
33:61:57:ARG:O	33:61:61:ARG:HG2	2.12	0.49
46:H8:111:VAL:HG11	46:H8:146:ILE:HG12	1.94	0.49
55:Q8:57:ARG:HA	55:Q8:58:ILE:C	2.37	0.49
1:1G:446:G:H2'	1:1G:447:G:O4'	2.13	0.49
1:1G:1028(A):C:N4	1:1G:1028(B):C:H41	2.11	0.49
1:1G:1152:A:H2'	1:1G:1153:C:O4'	2.13	0.49
1:1G:1157:A:O2'	1:1G:1158:C:O5'	2.30	0.49
1:1G:1322:C:O2'	1:1G:1323:G:H5'	2.13	0.49
26:14:141:A:C8	26:14:1408:C:H1'	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:14:234:C:H2'	26:14:235:U:H6	1.77	0.49
26:14:975:G:H1'	26:14:990:A:C2	2.48	0.49
26:14:2567:G:H2'	26:14:2568:C:H6	1.77	0.49
27:1J:15:A:H1'	27:1J:109:G:C8	2.48	0.49
30:39:89:VAL:O	30:39:90:PHE:C	2.55	0.49
32:59:124:GLU:HG3	32:59:132:ARG:HD2	1.95	0.49
37:45:11:LYS:NZ	37:45:86:GLY:O	2.37	0.49
37:45:25:ASP:HB3	37:45:102:VAL:CG2	2.41	0.49
50:H5:3:ARG:HD2	50:H5:60:GLU:C	2.37	0.49
1:13:1305:G:O2'	1:13:1331:G:N2	2.46	0.49
2:1E:97:TRP:CZ3	2:1E:172:ILE:HB	2.47	0.49
2:1E:187:LEU:HA	2:1E:201:ILE:HB	1.94	0.49
3:2E:59:ARG:HA	3:2E:63:ASN:O	2.12	0.49
4:3E:172:PRO:HB2	4:3E:187:ARG:HH12	1.77	0.49
8:7E:82:HIS:HE1	8:7E:136:GLU:OE2	1.95	0.49
20:BI:26:ASN:O	20:BI:30:LYS:HB2	2.13	0.49
26:1H:1101:U:H2'	26:1H:1102:C:C6	2.48	0.49
26:1H:1252:G:H5"	61:1H:3758:HOH:O	2.12	0.49
36:78:98:GLU:O	36:78:101:VAL:HG22	2.13	0.49
36:78:113:LYS:HG2	36:78:115:LEU:HD23	1.95	0.49
37:88:22:LYS:HG3	37:88:22:LYS:O	2.13	0.49
40:B8:81:PRO:HG2	40:B8:82:LEU:HD12	1.93	0.49
1:1G:186(D):C:H2'	1:1G:186(E):C:C6	2.46	0.49
1:1G:735:C:H2'	1:1G:736:C:H6	1.78	0.49
1:1G:1127:G:N2	1:1G:1144:G:H22	2.10	0.49
2:12:128:GLU:O	2:12:130:ARG:HG2	2.13	0.49
4:32:148:VAL:HG12	4:32:152:SER:OG	2.12	0.49
5:42:24:ARG:HB2	5:42:26:PHE:CE1	2.47	0.49
57:3L:35:A:H2'	57:3L:36:A:H8	1.78	0.49
26:14:85:G:OP1	45:C5:30:VAL:HG21	2.12	0.49
26:14:362:U:H5'	26:14:363:G:OP2	2.13	0.49
26:14:452:G:N3	26:14:457:A:H2	2.10	0.49
26:14:1087:G:N3	26:14:1089:G:O2'	2.46	0.49
26:14:1111:A:O2'	32:59:2:SER:OG	2.27	0.49
26:14:1131:G:C2	26:14:1132:A:C4	3.01	0.49
26:14:1510:A:H2'	26:14:1511:A:O4'	2.12	0.49
26:14:1899:G:N2	26:14:1902:C:N4	2.46	0.49
26:14:2146:C:H4'	26:14:2147:G:C8	2.48	0.49
27:1J:70:C:H2'	27:1J:71:C:C6	2.47	0.49
28:19:273:ARG:O	28:19:273:ARG:HG2	2.13	0.49
1:13:108:G:C6	20:BI:15:ARG:HD2	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:13:110:C:O2'	16:7I:25:ARG:O	2.27	0.49
1:13:1131:G:H2'	1:13:1132:C:H6	1.76	0.49
1:13:1226:C:O2'	13:4I:111:LYS:NZ	2.45	0.49
1:13:1313:U:P	19:AI:6:LYS:HZ3	2.36	0.49
9:8E:17:VAL:HG11	9:8E:81:ILE:HD13	1.94	0.49
20:BI:29:LYS:O	20:BI:33:ILE:HG12	2.13	0.49
26:1H:459:U:H2'	26:1H:460:A:C8	2.46	0.49
26:1H:602:G:N2	26:1H:655:A:C8	2.65	0.49
26:1H:1173:G:C2	26:1H:1175:U:H5	2.30	0.49
26:1H:1359:A:H2'	26:1H:1360:A:H5'	1.94	0.49
26:1H:2017:U:O3'	52:N8:9:LYS:NZ	2.46	0.49
26:1H:2155:G:H2'	26:1H:2156:G:H5'	1.94	0.49
28:11:6:PHE:HE1	28:11:18:VAL:HG23	1.77	0.49
30:31:77:ASP:OD1	30:31:77:ASP:N	2.37	0.49
31:41:67:LYS:CE	51:M8:6:HIS:CE1	2.94	0.49
36:78:96:THR:O	36:78:98:GLU:N	2.42	0.49
40:B8:62:THR:HB	40:B8:75:ILE:HG12	1.94	0.49
48:J8:91:LYS:HA	48:J8:91:LYS:NZ	2.28	0.49
1:1G:200:G:H1	1:1G:217:C:H42	1.60	0.49
1:1G:280:C:H3'	1:1G:281:G:H5'	1.94	0.49
1:1G:1243:C:OP1	21:1B:8:THR:HG21	2.13	0.49
3:22:95:THR:HG21	3:22:97:LYS:HG2	1.94	0.49
4:32:79:PHE:HE1	4:32:204:ILE:HD13	1.77	0.49
7:62:113:GLU:O	7:62:119:ARG:HD3	2.12	0.49
13:4A:32:GLU:OE2	13:4A:33:ALA:N	2.45	0.49
56:1L:30:G:N2	56:1L:41:C:N3	2.61	0.49
23:2L:32:G:C5	23:2L:33:OMC:C5	3.01	0.49
26:14:634:C:H2'	26:14:635:C:C6	2.47	0.49
26:14:849:A:H2	50:H5:24:LYS:HB3	1.77	0.49
26:14:1693:U:O2'	28:19:14:ARG:NH2	2.46	0.49
26:14:2096:U:H3	26:14:2193:G:H1	1.59	0.49
26:14:2611:U:H6	26:14:2611:U:H5'	1.77	0.49
26:14:2753:A:H2'	26:14:2754:U:O4'	2.12	0.49
28:19:242:ARG:N	28:19:242:ARG:HD3	2.26	0.49
30:39:153:SER:OG	30:39:190:GLU:HB2	2.12	0.49
30:39:160:ASN:HB3	30:39:163:VAL:HB	1.93	0.49
34:15:65:LYS:NZ	34:15:65:LYS:HB3	2.28	0.49
39:65:7:TYR:CZ	39:65:91:PRO:HG3	2.47	0.49
46:D5:1:MET:N	46:D5:135:GLU:OE1	2.45	0.49
53:K5:52:VAL:HG22	53:K5:53:LYS:H	1.78	0.49
1:13:266:G:H5"	1:13:267:C:C5	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:13:453:A:H4'	16:7I:72:ARG:HB2	1.95	0.49
7:6E:115:ARG:O	7:6E:118:VAL:HG12	2.11	0.49
8:7E:23:SER:HA	8:7E:61:VAL:O	2.13	0.49
12:3I:90:VAL:HG11	12:3I:93:LEU:HG	1.95	0.49
12:3I:90:VAL:HB	12:3I:96:VAL:HG22	1.95	0.49
21:1F:5:ASP:O	21:1F:11:GLY:HA3	2.13	0.49
21:1F:9:ARG:O	21:1F:13:ILE:HG13	2.13	0.49
22:1K:52:G:H2'	22:1K:53:G:O4'	2.13	0.49
26:1H:141:A:C8	26:1H:1408:C:H1'	2.48	0.49
26:1H:764:A:N3	28:11:213:ARG:NH1	2.61	0.49
26:1H:817:C:H4'	26:1H:932:G:C5	2.47	0.49
26:1H:1170:G:N2	26:1H:1180:C:C2	2.80	0.49
26:1H:1754:C:H5	40:B8:96:ARG:NH2	2.10	0.49
26:1H:1914:C:H2'	26:1H:1915:U:O4'	2.12	0.49
26:1H:1986:A:OP1	61:1H:4238:HOH:O	2.20	0.49
26:1H:2503:A:P	61:1H:4545:HOH:O	2.68	0.49
26:1H:2784:C:H1'	29:21:37:ARG:HH12	1.76	0.49
30:31:178:PRO:HB3	30:31:198:ALA:HA	1.94	0.49
32:51:11:VAL:HB	32:51:12:PRO:HD2	1.94	0.49
45:G8:99:CYS:SG	45:G8:100:ALA:N	2.85	0.49
54:P8:8:ASN:OD1	54:P8:8:ASN:C	2.56	0.49
1:1G:539:A:OP2	12:3A:115:LYS:NZ	2.36	0.49
2:12:166:ASP:CG	2:12:169:LYS:HB2	2.38	0.49
4:32:61:LYS:HE2	4:32:206:PHE:CE2	2.47	0.49
17:8A:86:GLU:O	17:8A:90:ILE:HG12	2.13	0.49
20:BA:44:ALA:HB3	20:BA:91:LEU:HD12	1.95	0.49
26:14:450:G:N7	61:14:3736:HOH:O	2.34	0.49
26:14:469:G:O6	54:L5:39:ARG:NH1	2.46	0.49
26:14:1432:C:H2'	26:14:1433:U:O4'	2.12	0.49
26:14:2012:G:OP1	43:A5:11:ARG:NH2	2.46	0.49
26:14:2354:G:O2'	47:E5:36:ILE:HG23	2.12	0.49
26:14:2685:G:P	40:75:51:ARG:HH22	2.34	0.49
29:29:9:VAL:HG12	40:75:8:LYS:NZ	2.27	0.49
37:45:87:LYS:HB3	37:45:90:VAL:HG22	1.94	0.49
1:13:474:G:H2'	1:13:475:G:C8	2.47	0.49
4:3E:162:LEU:O	4:3E:165:MET:HB3	2.13	0.49
7:6E:28:ASN:HA	7:6E:31:MET:HE2	1.94	0.49
14:5I:21:TYR:OH	14:5I:23:ARG:NH2	2.45	0.49
22:1K:27:G:H2'	22:1K:28:G:C8	2.48	0.49
26:1H:150:C:O2'	26:1H:151:C:H5'	2.13	0.49
26:1H:287:C:H2'	26:1H:288:C:H6	1.78	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1H:1138:G:H2'	26:1H:1139:G:O4'	2.13	0.49
26:1H:1580:A:H8	26:1H:1580:A:OP2	1.96	0.49
26:1H:1582:C:O2'	26:1H:1586:A:C8	2.62	0.49
26:1H:2287:A:C2	26:1H:2346:A:H2	2.31	0.49
26:1H:2884:U:H2'	26:1H:2885:C:O4'	2.13	0.49
28:11:37:LEU:HD12	28:11:62:TYR:HB2	1.93	0.49
29:21:24:THR:HG21	29:21:188:VAL:HG21	1.95	0.49
29:21:77:ILE:C	29:21:79:ARG:H	2.20	0.49
37:88:51:ARG:HD2	37:88:66:ILE:HD11	1.95	0.49
49:K8:65:ASN:O	49:K8:69:ARG:HG3	2.12	0.49
1:1G:1299:A:C6	1:1G:1301:U:C2	3.01	0.49
2:12:19:HIS:CD2	2:12:20:GLU:HG2	2.48	0.49
3:22:44:GLU:HA	3:22:52:LEU:HD11	1.95	0.49
8:72:39:LEU:HB3	8:72:45:ILE:HG12	1.95	0.49
8:72:104:ARG:C	8:72:106:GLY:H	2.21	0.49
13:4A:37:THR:HG21	13:4A:56:LEU:HA	1.94	0.49
14:5A:17:LYS:HZ1	14:5A:18:VAL:HG13	1.76	0.49
19:AA:49:ILE:O	19:AA:60:VAL:HG13	2.13	0.49
19:AA:51:VAL:O	19:AA:57:HIS:HA	2.13	0.49
26:14:590:A:H2'	26:14:591:C:C6	2.48	0.49
26:14:920:G:H2'	26:14:921:G:C8	2.48	0.49
26:14:1754:C:H2'	26:14:1755:A:C8	2.48	0.49
26:14:2392:A:H8	36:35:61:ARG:HD2	1.77	0.49
27:1J:73:A:C4	27:1J:104:A:C2	3.01	0.49
30:39:40:GLN:NE2	30:39:182:ASN:HB2	2.21	0.49
36:35:63:PRO:HG3	55:M5:13:ARG:CZ	2.43	0.49
36:35:63:PRO:HD3	55:M5:13:ARG:NH1	2.28	0.49
44:B5:3:THR:O	44:B5:5:TYR:N	2.46	0.49
44:B5:84:ALA:O	44:B5:87:GLN:HG3	2.12	0.49
1:13:735:C:H2'	1:13:736:C:H6	1.78	0.49
1:13:1494:G:N7	59:13:1749:PAR:N32	2.60	0.49
17:8I:76:LEU:HD12	17:8I:77:VAL:H	1.78	0.49
19:AI:40:ILE:HD11	19:AI:62:ILE:HD13	1.95	0.49
20:BI:75:ASN:HA	20:BI:78:ALA:HB3	1.95	0.49
26:1H:6:A:H2'	26:1H:7:G:O4'	2.13	0.49
26:1H:1140:C:OP1	34:58:23:LEU:HB3	2.12	0.49
26:1H:1443:G:C2	26:1H:1549:C:O2	2.64	0.49
26:1H:1728:G:H3'	26:1H:1729:A:C5'	2.37	0.49
26:1H:1827:C:H5"	61:1H:4459:HOH:O	2.13	0.49
26:1H:1899:G:N2	26:1H:1902:C:C5	2.71	0.49
26:1H:2286:A:H2'	53:O8:31:PRO:HD3	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1H:2308:G:H22	26:1H:2311:A:H2	1.60	0.49
26:1H:2467:C:C2'	26:1H:2468:G:H5'	2.42	0.49
41:C8:97:ASP:O	41:C8:101:ARG:N	2.38	0.49
51:M8:38:LYS:O	51:M8:39:CYS:HB3	2.11	0.49
1:1G:652:U:O2'	1:1G:653:A:O5'	2.31	0.49
1:1G:720:C:O5'	1:1G:720:C:H6	1.96	0.49
1:1G:1095:U:H2'	1:1G:1096:C:O4'	2.13	0.49
1:1G:1260:C:H3'	1:1G:1260:C:H6	1.78	0.49
1:1G:1315:U:O2'	1:1G:1360:A:N3	2.43	0.49
4:32:9:CYS:SG	4:32:22:LYS:HD2	2.53	0.49
26:14:244:A:C2	26:14:255:A:C4	3.00	0.49
26:14:1385:G:O2'	26:14:1396:U:H6	1.95	0.49
26:14:2142:C:H2'	26:14:2143:C:C6	2.48	0.49
28:19:33:LEU:HD21	28:19:103:ARG:HA	1.95	0.49
36:35:75:ILE:HD13	36:35:75:ILE:H	1.78	0.49
37:45:37:LEU:HD11	37:45:130:LYS:HB2	1.94	0.49
44:B5:11:PRO:HG2	44:B5:13:LEU:HD21	1.94	0.49
1:13:170:U:H2'	1:13:171:A:H8	1.78	0.48
6:5E:41:GLU:CD	18:9I:35:ARG:HH22	2.21	0.48
12:3I:90:VAL:HG12	12:3I:92:ASP:H	1.78	0.48
13:4I:3:ARG:CZ	13:4I:7:VAL:HG13	2.43	0.48
15:6I:78:TYR:CZ	15:6I:82:ILE:HD11	2.47	0.48
17:8I:31:LEU:HD23	17:8I:32:TYR:CZ	2.48	0.48
26:1H:92:G:H2'	26:1H:93:C:C6	2.48	0.48
26:1H:468:G:N7	54:P8:39:ARG:NH2	2.60	0.48
26:1H:654(C):G:H2'	26:1H:654(D):G:O4'	2.13	0.48
26:1H:880:G:H1	26:1H:897:C:N4	2.06	0.48
26:1H:996:A:H5'	41:C8:93:LYS:HE2	1.95	0.48
26:1H:1138:G:N2	34:58:106:MET:HE3	2.11	0.48
26:1H:1405:U:H2'	26:1H:1406:U:H6	1.78	0.48
26:1H:1593:G:H2'	26:1H:1594:G:C8	2.48	0.48
30:31:63:LYS:NZ	30:31:75:HIS:O	2.46	0.48
34:58:25:ARG:HG2	34:58:25:ARG:HH11	1.76	0.48
34:58:57:ALA:C	34:58:59:LYS:H	2.19	0.48
42:D8:34:GLU:O	42:D8:36:PRO:HD3	2.12	0.48
42:D8:47:VAL:CG2	42:D8:48:GLY:N	2.76	0.48
46:H8:128:VAL:HG23	46:H8:161:VAL:HG21	1.95	0.48
48:J8:51:VAL:HG21	48:J8:74:VAL:HG21	1.95	0.48
1:1G:532:A:N6	1:1G:1206:G:O2'	2.46	0.48
1:1G:1028(A):C:H42	1:1G:1032(B):G:H22	1.59	0.48
1:1G:1392:G:H21	1:1G:1502:A:H8	1.61	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:22:73:PRO:HA	3:22:76:VAL:HG13	1.94	0.48
13:4A:84:ILE:C	13:4A:86:CYS:H	2.21	0.48
20:BA:86:ARG:CZ	20:BA:86:ARG:HB2	2.41	0.48
26:14:1019:U:H2'	26:14:1020:A:N7	2.27	0.48
26:14:1926:U:H2'	26:14:1928:A:OP2	2.13	0.48
26:14:2211:G:HO2'	26:14:2212:A:P	2.34	0.48
26:14:2320:A:N6	26:14:2333:A:H2'	2.28	0.48
26:14:2564:A:OP1	26:14:2648:C:H4'	2.12	0.48
26:14:2875:C:O2'	40:75:1:MET:HA	2.13	0.48
28:19:218:ARG:HB3	28:19:219:PRO:HD2	1.95	0.48
30:39:165:ARG:HG2	30:39:168:ARG:NH1	2.28	0.48
36:35:75:ILE:HG13	36:35:77:ARG:CZ	2.43	0.48
46:D5:70:LEU:O	46:D5:89:PHE:N	2.41	0.48
1:13:66:G:O4'	1:13:173:U:C4	2.65	0.48
1:13:501:C:H2'	1:13:502:G:H8	1.77	0.48
2:1E:226:ARG:HG3	2:1E:227:GLY:N	2.27	0.48
15:6I:47:LYS:HB3	15:6I:47:LYS:NZ	2.28	0.48
16:7I:19:ILE:HB	16:7I:36:ILE:O	2.13	0.48
24:3K:48:C:N4	24:3K:59:U:C2	2.81	0.48
26:1H:415:A:H2'	26:1H:416:C:O4'	2.13	0.48
26:1H:706:A:H5'	28:11:7:LYS:HD2	1.94	0.48
26:1H:751:A:H5'	43:E8:90:ARG:HA	1.95	0.48
26:1H:1429:G:H2'	26:1H:1430:C:C6	2.48	0.48
26:1H:1590:U:H2'	26:1H:1591:G:C8	2.48	0.48
27:16:32:C:C2	27:16:51:G:N2	2.81	0.48
30:31:63:LYS:HG2	30:31:65:TRP:O	2.13	0.48
36:78:88:LEU:HD12	36:78:95:VAL:HG11	1.95	0.48
40:B8:107:ASP:OD2	40:B8:109:GLU:HG3	2.12	0.48
41:C8:58:ARG:HA	41:C8:61:TRP:CE3	2.48	0.48
55:Q8:34:TRP:CD1	55:Q8:36:LYS:N	2.81	0.48
1:1G:176:C:O2'	1:1G:177:C:H5'	2.13	0.48
1:1G:363:A:OP1	12:3A:33:ARG:HG3	2.13	0.48
1:1G:377:G:OP1	16:7A:3:LYS:NZ	2.45	0.48
1:1G:1402:C:H2'	1:1G:1403:C:O4'	2.12	0.48
8:72:22:GLU:HG3	8:72:23:SER:HB3	1.95	0.48
26:14:2296:U:H4'	26:14:2297:C:OP1	2.11	0.48
28:19:32:SER:O	28:19:33:LEU:HB2	2.13	0.48
30:39:65:TRP:CZ3	30:39:72:ARG:HB3	2.48	0.48
34:15:35:ARG:HB2	34:15:42:TRP:HZ3	1.77	0.48
36:35:78:PRO:HA	36:35:110:TYR:CD2	2.48	0.48
39:65:101:LEU:HD12	39:65:105:ALA:HB2	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:C5:43:ASN:OD1	45:C5:43:ASN:N	2.45	0.48
46:D5:52:SER:O	46:D5:52:SER:OG	2.24	0.48
47:E5:48:GLY:HA3	47:E5:80:HIS:ND1	2.28	0.48
49:G5:47:ASN:N	49:G5:47:ASN:OD1	2.46	0.48
55:M5:34:TRP:CD1	55:M5:35:GLN:N	2.81	0.48
1:13:22:G:H2'	1:13:23:C:C6	2.48	0.48
8:7E:120:THR:OG1	8:7E:123:GLU:HG3	2.13	0.48
11:2I:87:THR:HA	11:2I:91:ARG:HH21	1.79	0.48
16:7I:17:TYR:HE2	16:7I:41:PRO:HG3	1.78	0.48
17:8I:28:PRO:HA	17:8I:35:VAL:HA	1.95	0.48
19:AI:14:HIS:CD2	19:AI:14:HIS:H	2.31	0.48
26:1H:433:C:H2'	26:1H:434:U:C6	2.48	0.48
26:1H:713:G:H2'	26:1H:714:U:C6	2.48	0.48
26:1H:960:A:H2'	26:1H:962:G:H5'	1.95	0.48
26:1H:1479:G:O2'	26:1H:1558:A:H5'	2.13	0.48
26:1H:1591:G:H2'	26:1H:1592:C:C6	2.49	0.48
26:1H:2766:G:H2'	26:1H:2766:G:N3	2.29	0.48
32:51:86:GLU:O	32:51:131:VAL:O	2.31	0.48
34:58:12:ARG:HB3	34:58:50:ASP:OD1	2.12	0.48
38:98:32:GLY:HA2	38:98:116:LEU:HD12	1.95	0.48
53:O8:17:LYS:O	53:O8:19:ARG:N	2.45	0.48
1:1G:397:A:H3'	1:1G:397:A:N3	2.28	0.48
1:1G:500:G:H2'	1:1G:501:C:C6	2.48	0.48
1:1G:1148:U:H2'	1:1G:1149:C:O4'	2.13	0.48
1:1G:1316:G:H5"	14:5A:17:LYS:NZ	2.27	0.48
2:12:7:VAL:O	2:12:217:ARG:NH2	2.43	0.48
2:12:8:LYS:CE	2:12:213:LEU:HD21	2.42	0.48
9:82:50:LEU:HB3	9:82:56:LEU:HA	1.95	0.48
26:14:1040:C:O2	26:14:1115:G:N2	2.34	0.48
26:14:1045:A:H1'	26:14:1047:G:N3	2.28	0.48
26:14:1666:G:OP1	35:25:66:LYS:HD3	2.12	0.48
26:14:1826:G:H4'	28:19:242:ARG:NH1	2.28	0.48
26:14:2250:G:C2	37:45:82:ARG:HB3	2.48	0.48
26:14:2400:G:H3'	26:14:2401:U:H6	1.78	0.48
26:14:2745:C:H4'	32:59:142:GLY:O	2.13	0.48
27:1J:103:U:HO2'	46:D5:29:TYR:HH	1.58	0.48
28:19:245:PRO:HG2	28:19:253:GLN:HE21	1.78	0.48
28:19:267:SER:O	28:19:268:ARG:HG2	2.13	0.48
29:29:12:THR:HG22	40:75:58:ASN:ND2	2.23	0.48
30:39:51:THR:HG23	30:39:92:PRO:HG2	1.95	0.48
31:49:14:GLU:O	31:49:17:PRO:HG2	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:25:68:GLU:CA	35:25:78:ARG:HB3	2.41	0.48
36:35:11:GLY:C	36:35:13:ASN:H	2.20	0.48
36:35:78:PRO:HA	36:35:110:TYR:HD2	1.78	0.48
40:75:88:ILE:HG21	40:75:91:ARG:CZ	2.42	0.48
46:D5:178:GLU:HG3	46:D5:179:ASP:H	1.78	0.48
53:K5:18:ARG:NH2	53:K5:43:CYS:O	2.43	0.48
1:13:10:A:OP2	5:4E:126:ARG:HD3	2.14	0.48
1:13:150:C:H2'	1:13:151:A:O4'	2.13	0.48
1:13:1052:U:O2'	1:13:1055:A:OP2	2.26	0.48
1:13:1057:G:H2'	1:13:1058:G:O4'	2.13	0.48
6:5E:16:GLN:HG2	6:5E:17:SER:N	2.28	0.48
11:2I:19:ALA:O	11:2I:82:VAL:HA	2.13	0.48
19:AI:5:LEU:HB3	19:AI:10:PHE:CE1	2.47	0.48
26:1H:194:G:H2'	26:1H:195:A:O4'	2.12	0.48
26:1H:882:G:H22	26:1H:894:C:H42	1.62	0.48
26:1H:1087:G:C5	26:1H:1089:G:H1'	2.48	0.48
26:1H:1478:G:O2'	26:1H:1558:A:H2	1.96	0.48
26:1H:1677:A:H2'	26:1H:1678:G:C8	2.48	0.48
26:1H:2887:U:H2'	26:1H:2888:C:H6	1.76	0.48
27:16:71:C:C2	27:16:72:G:C8	3.01	0.48
27:16:73:A:C4	27:16:104:A:C2	3.01	0.48
32:51:144:VAL:O	32:51:148:ILE:HG12	2.14	0.48
33:61:77:LEU:CD1	33:61:140:LEU:HB3	2.44	0.48
41:C8:14:HIS:O	41:C8:18:LEU:HD12	2.14	0.48
46:H8:13:GLU:HB3	46:H8:18:LEU:HD11	1.96	0.48
53:O8:44:ARG:O	53:O8:45:LYS:HG2	2.13	0.48
1:1G:428:G:C5	1:1G:430:A:C6	3.00	0.48
2:12:178:ARG:NH2	8:72:68:ARG:HH22	2.11	0.48
7:62:26:PHE:CE2	7:62:30:ILE:HD11	2.48	0.48
10:1A:22:LYS:HE2	10:1A:90:LEU:HD12	1.96	0.48
56:1L:76:A:H8	26:14:2583:G:N2	2.11	0.48
26:14:2208:U:H2'	26:14:2209:C:C6	2.48	0.48
26:14:2734:A:C8	26:14:2735:G:C8	3.01	0.48
26:14:2746:U:OP1	32:59:85:LYS:NZ	2.46	0.48
26:14:2823:A:OP1	29:29:159:HIS:NE2	2.38	0.48
29:29:26:ILE:HG22	29:29:27:LEU:C	2.38	0.48
32:59:99:VAL:HG13	32:59:100:GLY:H	1.77	0.48
33:69:138:ILE:HG12	33:69:139:GLN:O	2.13	0.48
39:65:86:ALA:O	39:65:87:PHE:HB2	2.13	0.48
42:95:18:LEU:O	42:95:96:ILE:HG12	2.14	0.48
49:G5:25:VAL:O	49:G5:29:LYS:HB2	2.12	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:J5:3:LYS:N	52:J5:3:LYS:HD2	2.24	0.48
52:J5:16:ARG:NH1	52:J5:17:ASP:OD1	2.46	0.48
1:13:353:A:H5'	1:13:353:A:C8	2.39	0.48
1:13:507:C:OP2	1:13:508:C:O2'	2.25	0.48
2:1E:239:VAL:O	2:1E:239:VAL:HG12	2.13	0.48
4:3E:61:LYS:HA	4:3E:203:VAL:HG22	1.94	0.48
19:AI:33:THR:HG23	19:AI:35:SER:H	1.78	0.48
26:1H:370:G:H4'	26:1H:371:A:OP2	2.13	0.48
26:1H:2111:C:O2'	26:1H:2119:A:OP1	2.31	0.48
31:41:121:ASN:HB2	31:41:181:ARG:HH22	1.78	0.48
33:61:41:GLU:O	33:61:45:LYS:HB2	2.13	0.48
36:78:126:VAL:HG13	36:78:145:PRO:HG2	1.94	0.48
40:B8:90:GLN:HG3	40:B8:91:ARG:N	2.28	0.48
44:F8:36:LYS:HG2	44:F8:54:VAL:HB	1.94	0.48
45:G8:84:ARG:HD2	45:G8:84:ARG:O	2.14	0.48
49:K8:48:HIS:N	49:K8:50:ILE:HD11	2.29	0.48
50:L8:43:ILE:O	50:L8:47:VAL:HG23	2.14	0.48
54:P8:22:MET:HE3	54:P8:22:MET:HB3	1.69	0.48
1:1G:1053:G:O6	1:1G:1199:U:H2'	2.12	0.48
1:1G:1172:C:H2'	1:1G:1173:G:H8	1.79	0.48
2:12:118:LEU:HB3	2:12:142:LEU:HD12	1.95	0.48
4:32:59:ARG:HA	4:32:62:GLN:HB2	1.95	0.48
4:32:111:ALA:HB2	4:32:120:LEU:HD12	1.96	0.48
7:62:46:ALA:O	7:62:50:ILE:HG12	2.14	0.48
8:72:99:GLU:OE2	8:72:100:ILE:N	2.44	0.48
10:1A:47:PHE:CZ	14:5A:37:PHE:HE2	2.32	0.48
14:5A:25:VAL:O	14:5A:26:ARG:HB3	2.13	0.48
16:7A:16:HIS:CD2	16:7A:16:HIS:N	2.82	0.48
57:3L:53:G:HO2'	57:3L:54:5MU:P	2.34	0.48
57:3L:76:A:H8	26:14:2394:C:N4	2.09	0.48
26:14:774:A:H2	26:14:787:U:HO2'	1.60	0.48
26:14:1011:G:O3'	41:85:75:ASN:ND2	2.46	0.48
26:14:1359:A:N7	26:14:1372:U:O4	2.45	0.48
26:14:2015:A:N3	52:J5:2:ALA:N	2.62	0.48
26:14:2689:U:H5"	26:14:2713:A:H2	1.78	0.48
41:85:88:ILE:HA	42:95:49:THR:O	2.13	0.48
49:G5:33:MET:O	49:G5:36:ARG:HB2	2.13	0.48
1:13:110:C:H2'	1:13:111:G:O4'	2.13	0.48
1:13:807:A:H2'	1:13:808:C:C6	2.47	0.48
1:13:1347:G:C8	9:8E:107:ARG:HB3	2.48	0.48
1:13:1347:G:OP2	9:8E:107:ARG:HG2	2.12	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:13:1405:G:O4'	1:13:1519:A:H4'	2.14	0.48
7:6E:31:MET:SD	7:6E:36:LYS:HG2	2.54	0.48
24:3K:10:G:H1	24:3K:25:C:H42	1.62	0.48
26:1H:405:U:O2	26:1H:405:U:H2'	2.13	0.48
26:1H:547:A:C6	26:1H:548:A:C6	3.02	0.48
26:1H:729:G:OP2	28:11:13:ARG:NH1	2.43	0.48
26:1H:1357:U:H2'	26:1H:1358:G:O4'	2.13	0.48
26:1H:1649:G:O2'	38:98:107:ASP:OD1	2.24	0.48
29:21:15:PHE:HB3	40:B8:81:PRO:HG3	1.95	0.48
30:31:66:PRO:HD2	30:31:70:THR:HG21	1.95	0.48
32:51:102:ALA:HB2	32:51:116:GLU:HG3	1.95	0.48
33:61:71:ILE:HG12	33:61:72:LEU:HD12	1.95	0.48
35:68:4:PRO:O	35:68:5:GLN:CB	2.62	0.48
36:78:85:LEU:HA	36:78:88:LEU:HD22	1.94	0.48
39:A8:28:VAL:HG11	39:A8:98:VAL:HG13	1.96	0.48
1:1G:66:G:C2	1:1G:67:C:C6	3.02	0.48
1:1G:517:G:N2	1:1G:530:G:OP1	2.36	0.48
1:1G:616:G:H2'	1:1G:617:G:H8	1.78	0.48
1:1G:957:U:H2'	1:1G:959:A:OP2	2.14	0.48
1:1G:972:C:O2'	10:1A:55:LYS:HB3	2.14	0.48
1:1G:1151:A:O2'	1:1G:1152:A:O5'	2.32	0.48
1:1G:1262:C:H2'	1:1G:1263:C:C6	2.49	0.48
9:82:70:LYS:O	9:82:74:ILE:HG13	2.14	0.48
18:9A:31:LEU:HD23	18:9A:31:LEU:H	1.78	0.48
57:3L:50:U:H2'	57:3L:51:U:H6	1.77	0.48
26:14:300:A:H2'	26:14:334:C:O2'	2.13	0.48
26:14:1036:G:OP1	32:59:59:ARG:N	2.39	0.48
26:14:1225:C:H4'	42:95:85:LYS:CB	2.43	0.48
26:14:1794:U:O2'	26:14:1795:C:H5'	2.14	0.48
30:39:25:PRO:HB2	30:39:27:GLU:C	2.38	0.48
31:49:130:ASN:HB3	31:49:160:VAL:HA	1.95	0.48
40:75:88:ILE:HG21	40:75:91:ARG:NH2	2.28	0.48
46:D5:111:VAL:HG23	46:D5:112:ARG:NH1	2.27	0.48
46:D5:174:VAL:HG13	46:D5:177:PRO:HG2	1.96	0.48
1:13:155:C:H2'	1:13:156:G:O4'	2.13	0.48
1:13:159:G:O2'	1:13:161:A:N7	2.36	0.48
1:13:1147:C:O2	9:8E:16:ARG:NH1	2.46	0.48
1:13:1378:C:O2	7:6E:76:ARG:NH1	2.47	0.48
4:3E:9:CYS:HB3	4:3E:32:ALA:HB2	1.96	0.48
4:3E:108:LEU:CD1	4:3E:174:LEU:HD13	2.44	0.48
6:5E:22:GLU:O	6:5E:26:ILE:HG13	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:2K:69:C:H2'	23:2K:70:C:C6	2.48	0.48
26:1H:90:U:H6	26:1H:90:U:OP1	1.97	0.48
26:1H:276:A:C5	26:1H:278:A:H2	2.30	0.48
26:1H:533:G:H5'	41:C8:24:TYR:CD1	2.49	0.48
26:1H:827:U:H5'	26:1H:828:U:O5'	2.13	0.48
26:1H:999:U:P	61:1H:4025:HOH:O	2.70	0.48
26:1H:1106:G:H2'	26:1H:1107:G:O4'	2.13	0.48
26:1H:1385:G:O2'	26:1H:1396:U:C6	2.63	0.48
26:1H:1813:G:H1'	28:11:50:THR:OG1	2.13	0.48
26:1H:1858:G:H1'	26:1H:1884:A:N6	2.28	0.48
26:1H:2262:U:H4'	26:1H:2328:A:C2	2.49	0.48
26:1H:2430:A:H8	26:1H:2431:U:C5	2.32	0.48
26:1H:2862:G:H2'	26:1H:2863:C:C6	2.46	0.48
29:21:51:PHE:O	29:21:74:PRO:HB2	2.13	0.48
32:51:8:PRO:HG2	32:51:69:ARG:NH2	2.28	0.48
41:C8:92:ARG:C	41:C8:94:ASN:N	2.71	0.48
42:D8:53:GLU:HG2	42:D8:54:GLY:N	2.29	0.48
1:1G:328:C:H4'	1:1G:329:A:H5"	1.95	0.48
1:1G:377:G:H1	1:1G:386:C:H42	1.61	0.48
1:1G:980:C:H3'	1:1G:981:U:H6	1.78	0.48
1:1G:1103:C:C2	1:1G:1104:G:C8	3.02	0.48
1:1G:1423:G:OP1	35:25:49:ARG:NH2	2.46	0.48
1:1G:1512:U:H2'	1:1G:1513:A:C8	2.49	0.48
5:42:141:GLN:HA	5:42:143:ARG:NH2	2.27	0.48
11:2A:18:ARG:HD2	11:2A:83:ILE:HD11	1.96	0.48
56:1L:30:G:H1	56:1L:40:C:H42	1.61	0.48
26:14:5:A:H2'	26:14:6:A:C8	2.49	0.48
26:14:1653:G:C6	38:55:9:LYS:HB2	2.48	0.48
26:14:2641:G:P	34:15:74:ARG:HH21	2.37	0.48
34:15:13:TRP:O	34:15:135:PRO:HD2	2.14	0.48
37:45:102:VAL:O	37:45:102:VAL:HG12	2.14	0.48
1:13:224:C:H2'	1:13:225:C:H6	1.79	0.48
1:13:536:C:H2'	1:13:537:G:C8	2.49	0.48
5:4E:33:VAL:CG1	5:4E:109:ILE:HG12	2.44	0.48
5:4E:68:GLU:O	5:4E:68:GLU:HG3	2.13	0.48
10:1I:27:ALA:HB1	10:1I:34:VAL:HG11	1.96	0.48
15:6I:36:ILE:HG23	15:6I:56:LEU:HD11	1.94	0.48
23:2K:24:C:H2'	23:2K:25:U:H6	1.79	0.48
26:1H:722:A:H2'	26:1H:723:G:C8	2.49	0.48
26:1H:748:G:C8	43:E8:89:ALA:HB1	2.49	0.48
26:1H:1385:G:HO2'	26:1H:1396:U:H6	1.55	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1H:1510:A:H2'	26:1H:1510:A:N3	2.27	0.48
30:31:37:VAL:HG21	36:78:6:LEU:HD21	1.96	0.48
34:58:104:LYS:HB2	34:58:117:PHE:CE1	2.49	0.48
36:78:43:GLY:N	61:78:305:HOH:O	2.33	0.48
36:78:90:ARG:HD3	36:78:91:PHE:HE1	1.79	0.48
38:98:10:LEU:O	38:98:11:ASN:C	2.56	0.48
41:C8:108:GLU:OE1	41:C8:112:ARG:NH1	2.46	0.48
46:H8:111:VAL:HG11	46:H8:146:ILE:CG1	2.44	0.48
49:K8:52:ASP:O	49:K8:56:GLN:HB2	2.14	0.48
51:M8:12:ALA:C	51:M8:24:THR:HG21	2.39	0.48
1:1G:191:G:H1'	20:BA:104:LEU:O	2.13	0.48
1:1G:520:A:N1	1:1G:536:C:H1'	2.29	0.48
1:1G:1120:G:H1	1:1G:1152:A:N6	2.11	0.48
1:1G:1148:U:OP1	9:82:7:THR:HG21	2.13	0.48
4:32:191:ARG:NH1	4:32:200:GLU:OE1	2.46	0.48
9:82:27:THR:OG1	9:82:31:GLN:O	2.20	0.48
20:BA:50:GLU:N	20:BA:100:ILE:HG12	2.29	0.48
23:2L:24:C:C2	23:2L:25:U:C5	3.02	0.48
57:3L:18:G:N2	57:3L:55:PSU:H1'	2.22	0.48
26:14:322:A:OP2	30:39:169:ASN:HB2	2.13	0.48
26:14:676:A:H8	26:14:2069:G:N2	2.01	0.48
26:14:2056:G:H1	52:J5:4:HIS:CB	2.25	0.48
26:14:2392:A:C8	36:35:61:ARG:HD2	2.49	0.48
26:14:2611:U:H3'	26:14:2611:U:OP2	2.14	0.48
26:14:2862:G:H2'	26:14:2863:C:H6	1.79	0.48
27:1J:65:C:H41	27:1J:108:C:C2'	2.26	0.48
30:39:182:ASN:O	30:39:186:ILE:HG12	2.13	0.48
32:59:54:ARG:HD2	32:59:56:SER:O	2.14	0.48
35:25:1:MET:HE2	35:25:32:TYR:CE1	2.49	0.48
35:25:19:ILE:HG22	35:25:43:VAL:HA	1.96	0.48
35:25:50:GLY:C	35:25:52:VAL:H	2.22	0.48
45:C5:47:LYS:HA	45:C5:60:PHE:HB3	1.96	0.48
49:G5:49:LYS:HB2	49:G5:49:LYS:HE3	1.68	0.48
1:13:1363:A:H1'	1:13:1365:G:N7	2.28	0.48
10:1I:80:LYS:O	10:1I:80:LYS:HD3	2.14	0.48
11:2I:99:GLN:HA	11:2I:105:VAL:CG1	2.42	0.48
12:3I:9:GLN:O	12:3I:13:LYS:HG2	2.14	0.48
24:3K:21:A:H2'	24:3K:22:G:O4'	2.13	0.48
26:1H:299:A:C2	26:1H:322:A:C4	3.01	0.48
26:1H:645:C:OP1	26:1H:645:C:H6	1.96	0.48
26:1H:844:C:H3'	26:1H:845:G:C8	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1H:1227:A:OP1	42:D8:84:LYS:HE3	2.14	0.48
26:1H:1533:C:C2	26:1H:1534:G:N2	2.81	0.48
26:1H:2001:A:OP1	38:98:9:LYS:NZ	2.47	0.48
26:1H:2125:G:H21	26:1H:2173:A:H62	1.61	0.48
26:1H:2492:U:H2'	26:1H:2493:U:H6	1.78	0.48
28:11:69:ARG:HD3	28:11:105:ILE:HD11	1.94	0.48
29:21:24:THR:HG21	29:21:188:VAL:HG22	1.94	0.48
31:41:35:GLU:C	31:41:99:MET:HE1	2.39	0.48
33:61:110:ASP:HB2	33:61:112:LYS:HG2	1.96	0.48
45:G8:11:ASP:O	45:G8:26:LYS:HG3	2.14	0.48
49:K8:55:ARG:O	49:K8:58:ALA:HB3	2.14	0.48
1:1G:979:C:OP1	1:1G:1223:C:N4	2.47	0.48
2:12:75:LYS:HD2	2:12:75:LYS:O	2.14	0.48
2:12:214:ILE:O	2:12:218:ALA:HB2	2.14	0.48
3:22:32:LEU:HD22	3:22:59:ARG:NH1	2.29	0.48
13:4A:94:ARG:NH2	19:AA:78:ARG:HH12	2.11	0.48
15:6A:70:LEU:HD23	15:6A:78:TYR:HA	1.96	0.48
57:3L:50:U:H2'	57:3L:51:U:C6	2.49	0.48
26:14:673:C:H5"	30:39:81:PRO:HD2	1.95	0.48
26:14:1149:G:H2'	26:14:1150:C:C6	2.49	0.48
26:14:1420:U:O2'	26:14:1421:G:OP1	2.29	0.48
26:14:1750:G:O2'	26:14:1751:C:H5'	2.13	0.48
26:14:2849:U:H1'	26:14:2866:U:O2	2.14	0.48
30:39:7:TYR:O	30:39:15:SER:HA	2.14	0.48
33:69:77:LEU:HD12	33:69:78:THR:H	1.78	0.48
55:M5:32:LEU:HB3	55:M5:33:ASN:OD1	2.13	0.48
1:13:101:A:H8	1:13:101:A:OP2	1.97	0.48
1:13:116:A:H61	1:13:313:A:H1'	1.77	0.48
1:13:600:C:O2	1:13:639:G:N2	2.47	0.48
1:13:881:G:OP2	12:3I:12:ARG:NH2	2.47	0.48
1:13:1018:C:H2'	1:13:1019:C:O4'	2.14	0.48
1:13:1145:C:H4'	1:13:1146:A:H8	1.79	0.48
1:13:1386:G:O2'	1:13:1387:G:H5'	2.13	0.48
12:3I:82:VAL:HG13	12:3I:105:TYR:HB3	1.95	0.48
13:4I:94:ARG:HD3	13:4I:94:ARG:HA	1.54	0.48
20:BI:61:SER:O	20:BI:65:LYS:HB2	2.13	0.48
26:1H:658:C:H2'	26:1H:659:C:C6	2.49	0.48
26:1H:804:A:P	61:1H:4481:HOH:O	2.70	0.48
26:1H:1266:G:O5'	43:E8:15:ARG:NH2	2.47	0.48
26:1H:1345:C:H2'	26:1H:1346:G:H8	1.77	0.48
26:1H:2553:G:H5"	26:1H:2554:U:OP2	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:51:101:ARG:NH2	32:51:122:THR:HA	2.29	0.48
36:78:82:GLY:HA2	36:78:113:LYS:O	2.13	0.48
39:A8:34:HIS:CB	39:A8:36:TYR:HE1	2.24	0.48
1:1G:407:G:C2	1:1G:436:C:C2	3.02	0.48
1:1G:570:G:H1'	1:1G:820:U:C4	2.49	0.48
1:1G:853:G:H2'	1:1G:854:G:H8	1.78	0.48
1:1G:872:A:O2'	1:1G:873:A:H5"	2.13	0.48
1:1G:1281:U:H3'	1:1G:1282:C:C5	2.49	0.48
3:22:11:ARG:NH2	3:22:182:ILE:HD11	2.28	0.48
3:22:140:ARG:NE	3:22:140:ARG:HA	2.29	0.48
10:1A:60:ARG:HE	10:1A:60:ARG:HB3	1.44	0.48
19:AA:66:MET:HA	19:AA:67:VAL:C	2.39	0.48
26:14:84:A:H2'	26:14:99:U:O4	2.14	0.48
26:14:399:G:OP2	61:14:3830:HOH:O	2.20	0.48
26:14:1021:A:H8	26:14:1021:A:H3'	1.79	0.48
29:29:51:PHE:O	29:29:52:LEU:HB2	2.14	0.48
40:75:8:LYS:HB2	40:75:8:LYS:NZ	2.29	0.48
42:95:12:TYR:CZ	42:95:22:VAL:HG23	2.49	0.48
42:95:35:LEU:HD12	42:95:37:VAL:HG11	1.95	0.48
1:13:964:A:N3	1:13:969:A:O2'	2.33	0.47
2:1E:25:ASN:ND2	2:1E:193:ASP:HB3	2.29	0.47
2:1E:189:ASP:HB3	2:1E:191:ASP:HB2	1.96	0.47
2:1E:223:ILE:HA	2:1E:226:ARG:HG2	1.96	0.47
3:2E:114:PRO:O	3:2E:118:GLN:HG3	2.14	0.47
7:6E:143:ARG:HG2	24:3K:41:C:H4'	1.94	0.47
10:1I:81:THR:O	10:1I:85:LEU:HG	2.14	0.47
26:1H:1042:G:H1	26:1H:1113:U:H3	1.62	0.47
26:1H:1174:A:C4	26:1H:1178:C:N4	2.82	0.47
26:1H:1448:G:N2	26:1H:1449:A:N6	2.62	0.47
27:16:116:G:H2'	27:16:117:G:O4'	2.14	0.47
31:41:42:GLY:O	31:41:43:LEU:HD13	2.14	0.47
42:D8:98:GLU:OE2	42:D8:100:ARG:HD3	2.13	0.47
46:H8:69:THR:HA	46:H8:89:PHE:O	2.13	0.47
47:I8:36:ILE:HD13	47:I8:36:ILE:C	2.39	0.47
1:1G:134:A:H61	16:7A:25:ARG:NH1	2.12	0.47
1:1G:198:G:H2'	1:1G:199:G:H8	1.79	0.47
1:1G:824:C:H2'	1:1G:825:G:C8	2.49	0.47
1:1G:994:A:N7	1:1G:1216:G:H4'	2.29	0.47
1:1G:994:A:C2	14:5A:5:ALA:HB2	2.49	0.47
1:1G:1263:C:N3	1:1G:1273:G:N2	2.62	0.47
6:52:96:PRO:HB3	18:9A:30:ASP:CG	2.39	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:14:250:G:P	36:35:60:MET:HE1	2.53	0.47
26:14:266:G:H2'	26:14:267:C:O5'	2.14	0.47
26:14:443:A:H1'	26:14:1201:C:O4'	2.13	0.47
26:14:480:A:H1'	45:C5:44:ILE:HG12	1.96	0.47
26:14:630:G:N2	26:14:633:A:OP2	2.40	0.47
26:14:839:U:H2'	26:14:840:C:H6	1.79	0.47
26:14:1020:A:N1	26:14:1141:U:O2'	2.41	0.47
26:14:1945:G:H2'	26:14:1946:U:C6	2.49	0.47
28:19:89:SER:HB2	28:19:159:ALA:HB2	1.95	0.47
30:39:25:PRO:C	30:39:27:GLU:N	2.72	0.47
35:25:119:PRO:HB2	40:75:68:TYR:CE2	2.49	0.47
41:85:108:GLU:HG2	41:85:112:ARG:HD2	1.95	0.47
1:13:359:U:OP1	33:69:87:LYS:HD2	2.15	0.47
1:13:748:C:H6	1:13:748:C:O5'	1.97	0.47
1:13:1331:G:OP2	13:4I:23:TYR:HD1	1.97	0.47
3:2E:94:LEU:HD12	3:2E:95:THR:HG23	1.96	0.47
4:3E:141:ARG:HB2	4:3E:141:ARG:CZ	2.43	0.47
9:8E:77:ILE:O	9:8E:81:ILE:HG12	2.13	0.47
10:1I:38:ILE:HG23	10:1I:71:LEU:HB3	1.96	0.47
15:6I:82:ILE:O	15:6I:86:GLY:N	2.47	0.47
20:BI:75:ASN:O	20:BI:79:ARG:HB2	2.14	0.47
21:1F:10:ARG:HA	21:1F:10:ARG:HE	1.78	0.47
26:1H:654(D):G:H22	26:1H:654(Q):C:N4	2.12	0.47
26:1H:1050:A:H2'	26:1H:1051:G:O4'	2.14	0.47
26:1H:1204:A:N6	26:1H:1240:U:H2'	2.29	0.47
26:1H:1494:A:C2'	26:1H:1495:A:H5'	2.44	0.47
26:1H:1754:C:OP1	40:B8:96:ARG:NH1	2.47	0.47
26:1H:2151:G:H2'	26:1H:2152:G:H8	1.79	0.47
26:1H:2309:A:C4	26:1H:2310:A:H8	2.32	0.47
27:16:119:A:H2'	27:16:119:A:N3	2.29	0.47
29:21:60:ASN:OD1	29:21:62:PRO:HD2	2.13	0.47
30:31:129:PHE:O	30:31:130:ALA:HB3	2.15	0.47
31:41:20:ILE:O	31:41:24:GLY:HA2	2.14	0.47
33:61:39:ALA:HB1	33:61:44:LEU:HD13	1.95	0.47
36:78:2:LYS:HD3	36:78:4:SER:HB2	1.96	0.47
36:78:59:LEU:O	55:Q8:13:ARG:HD2	2.14	0.47
39:A8:35:ILE:HG22	39:A8:97:ARG:HH21	1.79	0.47
1:1G:631:G:H3'	1:1G:632:A:C8	2.41	0.47
1:1G:745:C:H2'	1:1G:746:A:C8	2.49	0.47
1:1G:975:A:H4'	1:1G:976:G:C5'	2.42	0.47
1:1G:1028(A):C:N4	1:1G:1032(B):G:H22	2.12	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1G:1067:A:H4'	1:1G:1068:G:O5'	2.13	0.47
2:12:119:GLU:HA	2:12:122:PHE:HB3	1.95	0.47
15:6A:78:TYR:CZ	15:6A:82:ILE:HD12	2.49	0.47
26:14:239:U:H2'	26:14:240:G:O4'	2.13	0.47
26:14:483:A:H1'	45:C5:60:PHE:CE1	2.49	0.47
26:14:717:G:H2'	26:14:718:A:O4'	2.14	0.47
26:14:864:G:C6	26:14:865:C:N4	2.82	0.47
26:14:2685:G:N7	61:14:3614:HOH:O	2.35	0.47
28:19:201:HIS:O	28:19:204:ILE:HG23	2.14	0.47
29:29:9:VAL:HG23	29:29:26:ILE:O	2.14	0.47
29:29:81:ILE:HG22	29:29:82:ARG:N	2.26	0.47
8:7E:49:GLU:HG2	8:7E:62:TYR:HE2	1.79	0.47
9:8E:48:GLU:N	9:8E:49:PRO:HD2	2.28	0.47
26:1H:247:G:H4'	26:1H:386:G:C5	2.49	0.47
26:1H:978:G:C2	26:1H:986:C:C2	3.03	0.47
26:1H:1164:G:H2'	26:1H:1165:U:H6	1.75	0.47
26:1H:2275:C:H5'	26:1H:2275:C:C6	2.46	0.47
33:61:40:THR:HB	33:61:42:SER:H	1.80	0.47
46:H8:3:TYR:O	46:H8:58:VAL:HG22	2.14	0.47
1:1G:216:G:O2'	1:1G:217:C:O5'	2.31	0.47
1:1G:373:A:C2	1:1G:374:A:C8	3.02	0.47
1:1G:1171:G:H2'	1:1G:1172:C:C6	2.50	0.47
1:1G:1404:C:H2'	1:1G:1405:G:C8	2.49	0.47
2:12:32:ILE:HD12	2:12:41:ILE:O	2.14	0.47
12:3A:8:ASN:OD1	17:8A:34:LYS:HE2	2.13	0.47
12:3A:70:ILE:HD13	12:3A:77:LEU:HD12	1.96	0.47
21:1B:25:LYS:HA	21:1B:25:LYS:HD2	1.67	0.47
57:3L:36:A:N1	25:4L:14:A:H2	2.12	0.47
26:14:34:C:H2'	26:14:35:G:H5'	1.95	0.47
26:14:253:C:OP2	55:M5:5:LYS:NZ	2.28	0.47
26:14:491:G:O6	43:A5:49:LYS:HD3	2.15	0.47
26:14:1138:G:C4	26:14:1139:G:H1'	2.49	0.47
26:14:2129:C:H2'	26:14:2130:U:O4'	2.13	0.47
26:14:2535:G:H2'	26:14:2536:G:H8	1.79	0.47
30:39:128:ALA:O	30:39:129:PHE:C	2.56	0.47
38:55:87:TYR:HD1	38:55:90:ARG:HE	1.62	0.47
42:95:13:ARG:NH1	42:95:15:GLU:OE1	2.47	0.47
46:D5:127:LYS:O	46:D5:162:GLU:HB2	2.15	0.47
47:E5:23:VAL:HA	47:E5:38:VAL:HG22	1.96	0.47
1:13:401:C:O2'	1:13:621:A:N3	2.44	0.47
1:13:1464:G:H2'	1:13:1465:C:C6	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1H:66:C:H2'	26:1H:67:U:C6	2.50	0.47
26:1H:409:C:P	61:1H:3749:HOH:O	2.70	0.47
26:1H:1268:A:OP1	61:1H:4447:HOH:O	2.19	0.47
26:1H:1299:G:H3'	26:1H:1639:U:O4	2.14	0.47
26:1H:1317:A:H2'	26:1H:1318:C:H6	1.80	0.47
26:1H:1592:C:H2'	26:1H:1593:G:H8	1.80	0.47
36:78:147:LEU:O	36:78:148:LEU:HD23	2.15	0.47
49:K8:63:VAL:HA	49:K8:66:GLU:HG3	1.96	0.47
1:1G:11:G:N2	1:1G:525:C:O2'	2.38	0.47
1:1G:247:G:OP2	17:8A:100:LYS:HG2	2.14	0.47
1:1G:834:C:H2'	1:1G:835:U:C6	2.49	0.47
1:1G:983:A:H2	1:1G:984:C:C6	2.32	0.47
1:1G:1068:G:N7	1:1G:1094:G:C8	2.82	0.47
1:1G:1227:A:O2'	13:4A:115:LYS:HD2	2.14	0.47
1:1G:1295:G:O2'	13:4A:14:ARG:NH1	2.47	0.47
1:1G:1502:A:H4'	1:1G:1503:A:OP2	2.14	0.47
3:22:9:GLY:N	14:5A:49:HIS:O	2.47	0.47
12:3A:28:LYS:HE3	12:3A:33:ARG:NH1	2.29	0.47
56:1L:12:U:H3	56:1L:23:A:H61	1.61	0.47
56:1L:72:C:H2'	56:1L:73:A:H5"	1.96	0.47
26:14:108:U:H2'	26:14:109:G:H8	1.79	0.47
26:14:374:A:C2	26:14:401:A:C4	3.02	0.47
26:14:459:U:H2'	26:14:460:A:H8	1.79	0.47
26:14:902:C:H2'	26:14:903:C:C6	2.49	0.47
26:14:1275:A:N1	26:14:1295:C:O2'	2.44	0.47
26:14:1533:C:N3	26:14:1534:G:O2'	2.40	0.47
27:1J:21:G:H2'	27:1J:22:U:O4'	2.14	0.47
27:1J:88:C:P	27:1J:88:C:H6	2.38	0.47
30:39:20:LEU:HG	30:39:199:TRP:CH2	2.44	0.47
30:39:82:ILE:H	30:39:82:ILE:HG13	1.37	0.47
30:39:141:ALA:O	30:39:144:LYS:HB3	2.15	0.47
38:55:24:GLN:HB2	38:55:44:LEU:HD21	1.96	0.47
54:L5:5:TRP:NE1	54:L5:7:PRO:HG3	2.29	0.47
1:13:1356:G:O2'	1:13:1357:A:H5'	2.14	0.47
12:3I:85:ILE:HA	12:3I:85:ILE:HD13	1.44	0.47
16:7I:21:VAL:HG12	16:7I:33:ILE:HB	1.96	0.47
22:1K:76:A:H8	26:1H:2507:C:H1'	1.79	0.47
24:3K:14:A:C6	24:3K:22:G:C2	3.02	0.47
26:1H:475:U:C4	26:1H:481:G:O6	2.67	0.47
26:1H:493:G:H2'	26:1H:494:G:O4'	2.15	0.47
26:1H:880:G:H2'	26:1H:881:G:H8	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1H:2243:U:H2'	26:1H:2244:U:C6	2.49	0.47
26:1H:2475:C:H2'	26:1H:2477:C:OP2	2.13	0.47
27:16:100:G:OP1	61:16:315:HOH:O	2.20	0.47
30:31:125:LEU:HD21	30:31:199:TRP:CE3	2.50	0.47
31:41:47:LYS:NZ	31:41:81:LYS:HB2	2.30	0.47
40:B8:84:GLN:HE21	40:B8:85:LYS:HD2	1.78	0.47
44:F8:2:LYS:O	44:F8:3:THR:OG1	2.27	0.47
52:N8:30:LEU:HD23	52:N8:41:PRO:HA	1.95	0.47
1:1G:1040:U:H2'	1:1G:1041:A:C8	2.49	0.47
20:BA:67:ALA:HA	20:BA:73:HIS:HA	1.95	0.47
26:14:6:A:H2'	26:14:7:G:H5'	1.97	0.47
26:14:150:C:H2'	26:14:151:C:C6	2.50	0.47
26:14:1248:G:C8	41:85:3:ARG:HB2	2.49	0.47
26:14:1950:G:N1	26:14:1951:U:O4	2.47	0.47
26:14:2255:G:H21	47:E5:9:SER:HB2	1.79	0.47
26:14:2638:G:O2'	26:14:2639:A:H8	1.97	0.47
38:55:32:GLY:HA2	38:55:116:LEU:HD12	1.96	0.47
45:C5:39:VAL:HG23	45:C5:41:GLY:H	1.78	0.47
45:C5:52:SER:H	45:C5:57:GLN:N	2.12	0.47
45:C5:75:ILE:HG23	45:C5:76:CYS:N	2.29	0.47
1:13:486:U:H2'	1:13:487:A:H8	1.79	0.47
1:13:539:A:OP2	12:3I:115:LYS:HE2	2.14	0.47
1:13:1002:G:C4	1:13:1003:G:C8	3.02	0.47
3:2E:58:GLU:CB	3:2E:65:ALA:HB3	2.44	0.47
12:3I:110:VAL:CG2	12:3I:120:TYR:HB3	2.44	0.47
18:9I:59:SER:OG	18:9I:60:ALA:N	2.46	0.47
26:1H:483:A:O4'	45:G8:48:ALA:HB1	2.14	0.47
26:1H:720:C:H2'	26:1H:721:C:C6	2.49	0.47
26:1H:761:A:OP2	61:1H:4111:HOH:O	2.20	0.47
26:1H:1519:G:C2'	26:1H:1520:U:H5'	2.45	0.47
26:1H:2388:A:C2'	26:1H:2389:G:H5'	2.44	0.47
26:1H:2679:A:H4'	29:21:165:VAL:HG11	1.97	0.47
26:1H:2695:C:H2'	26:1H:2696:U:H6	1.79	0.47
40:B8:99:LEU:HB3	40:B8:101:PHE:HE1	1.78	0.47
44:F8:36:LYS:HE2	44:F8:54:VAL:O	2.14	0.47
47:I8:7:LEU:O	47:I8:11:ARG:HG2	2.14	0.47
1:1G:56:U:H2'	1:1G:57:G:C8	2.50	0.47
1:1G:468:A:C6	1:1G:474:G:H1'	2.50	0.47
4:32:126:ILE:HG22	4:32:127:THR:N	2.30	0.47
4:32:200:GLU:O	4:32:204:ILE:HG12	2.14	0.47
6:52:15:ASP:O	6:52:19:LEU:HB2	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:1B:2:GLY:O	21:1B:5:ASP:N	2.38	0.47
26:14:438:G:H2'	26:14:439:G:H8	1.80	0.47
26:14:1047:G:H21	26:14:1111:A:H62	1.63	0.47
26:14:1593:G:H2'	26:14:1594:G:H8	1.76	0.47
26:14:1939:U:OP1	26:14:2604:U:O2'	2.30	0.47
26:14:2111:C:N3	26:14:2118:U:O2'	2.46	0.47
26:14:2228:G:P	28:19:263:ARG:HH21	2.37	0.47
26:14:2458:G:O2'	26:14:2460:U:O4	2.20	0.47
30:39:129:PHE:HA	30:39:142:TRP:CD1	2.49	0.47
32:59:105:LEU:HG	32:59:113:VAL:HG13	1.95	0.47
42:95:76:LYS:HD2	42:95:80:GLN:O	2.13	0.47
46:D5:60:GLU:HA	46:D5:66:SER:HA	1.96	0.47
48:F5:49:VAL:HG21	48:F5:67:ILE:HD12	1.96	0.47
1:13:390:C:O3'	16:7I:28:ARG:NH2	2.48	0.47
1:13:593:G:H2'	1:13:594:G:H8	1.79	0.47
1:13:600:C:H2'	1:13:601:C:C6	2.49	0.47
1:13:1000:A:H2'	1:13:1001:G:H8	1.76	0.47
1:13:1020:U:H2'	1:13:1021:G:C8	2.50	0.47
1:13:1129:C:N4	1:13:1139:G:H1	2.13	0.47
1:13:1203:C:H2'	1:13:1204:A:O4'	2.15	0.47
1:13:1366:C:H2'	1:13:1367:C:C6	2.49	0.47
2:1E:11:LEU:HB3	2:1E:213:LEU:HD11	1.96	0.47
2:1E:76:GLN:O	2:1E:80:ILE:HD13	2.15	0.47
5:4E:72:GLN:O	5:4E:75:THR:HG22	2.14	0.47
6:5E:44:GLY:HA2	6:5E:59:TYR:CZ	2.50	0.47
9:8E:121:ARG:NH1	9:8E:122:ALA:O	2.44	0.47
10:1I:89:ASP:C	10:1I:91:PRO:HD3	2.40	0.47
20:BI:14:LYS:HG3	20:BI:17:ARG:HH21	1.79	0.47
24:3K:18:G:O2'	24:3K:19:G:OP1	2.29	0.47
24:3K:19:G:H4'	24:3K:57:G:H21	1.79	0.47
26:1H:270(G):C:H2'	26:1H:270(H):C:O4'	2.15	0.47
26:1H:392:C:P	61:1H:3752:HOH:O	2.72	0.47
26:1H:602:G:O2'	26:1H:604:G:O2'	2.28	0.47
26:1H:674:G:O2'	30:31:74:ARG:HD3	2.15	0.47
26:1H:945:A:OP2	26:1H:945:A:H4'	2.14	0.47
26:1H:1203:G:H3'	26:1H:1204:A:H5"	1.96	0.47
26:1H:1270:C:H5"	26:1H:1271:G:O5'	2.15	0.47
26:1H:2128:C:H2'	26:1H:2129:C:H6	1.80	0.47
26:1H:2176:A:H2'	26:1H:2177:C:C6	2.48	0.47
26:1H:2432:A:P	61:1H:3931:HOH:O	2.67	0.47
26:1H:2636:U:OP1	29:21:80:GLU:HG3	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1H:2734:A:H3'	26:1H:2735:G:H8	1.80	0.47
31:41:61:ALA:HA	31:41:66:GLN:O	2.14	0.47
31:41:94:LEU:N	31:41:94:LEU:HD23	2.30	0.47
32:51:10:PRO:HD2	32:51:50:VAL:O	2.14	0.47
34:58:23:LEU:HD12	34:58:23:LEU:HA	1.59	0.47
38:98:48:VAL:O	38:98:51:LEU:N	2.47	0.47
41:C8:65:ILE:CD1	41:C8:95:LEU:HD22	2.42	0.47
41:C8:79:PHE:C	41:C8:79:PHE:HD1	2.22	0.47
41:C8:88:ILE:HD11	41:C8:112:ARG:HB3	1.97	0.47
45:G8:34:LYS:O	45:G8:34:LYS:HG2	2.15	0.47
50:L8:38:GLU:H	50:L8:38:GLU:CD	2.13	0.47
54:P8:15:THR:HG22	54:P8:16:HIS:CE1	2.50	0.47
1:1G:90:C:H2'	1:1G:91:C:C6	2.50	0.47
1:1G:468:A:C5	1:1G:474:G:H1'	2.49	0.47
1:1G:619:U:N3	4:32:134:ASP:OD1	2.48	0.47
1:1G:633:G:H8	1:1G:633:G:O5'	1.96	0.47
1:1G:689:C:H3'	1:1G:690:G:H21	1.79	0.47
1:1G:727:G:N2	1:1G:730:G:OP2	2.41	0.47
1:1G:801:U:H2'	1:1G:802:A:H8	1.79	0.47
1:1G:1127:G:H1'	1:1G:1148:U:N3	2.29	0.47
1:1G:1349:A:P	9:82:118:LYS:HZ1	2.38	0.47
2:12:101:MET:O	2:12:105:PHE:HB2	2.15	0.47
3:22:21:ARG:O	3:22:58:GLU:HA	2.14	0.47
3:22:33:LEU:O	3:22:36:ASP:N	2.47	0.47
3:22:37:GLN:O	3:22:40:ARG:N	2.48	0.47
6:52:39:LYS:HE3	6:52:64:GLN:NE2	2.29	0.47
7:62:63:LYS:HG3	7:62:64:GLN:N	2.29	0.47
7:62:93:PRO:HG2	7:62:94:ARG:HD3	1.97	0.47
10:1A:24:VAL:HG21	10:1A:37:PRO:HG3	1.95	0.47
17:8A:59:ILE:HD13	17:8A:73:VAL:HA	1.97	0.47
19:AA:66:MET:N	19:AA:67:VAL:HB	2.29	0.47
57:3L:10:G:P	57:3L:46:7MG:H5'	2.55	0.47
26:14:92:G:H2'	26:14:93:C:C6	2.49	0.47
26:14:198:C:H5'	26:14:2244:U:OP1	2.15	0.47
26:14:528:A:H3'	26:14:528:A:C8	2.49	0.47
26:14:843:G:H1	26:14:935:C:H42	1.63	0.47
26:14:1839:G:H2'	26:14:1839:G:N3	2.28	0.47
26:14:1950:G:C2	26:14:1951:U:C5	3.02	0.47
26:14:2017:U:P	61:14:3670:HOH:O	2.72	0.47
26:14:2101:G:H2'	26:14:2102:U:O4'	2.14	0.47
26:14:2271:G:H5"	47:E5:20:ARG:NE	2.30	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:14:2400:G:H3'	26:14:2401:U:C6	2.50	0.47
26:14:2762:G:H5"	61:14:3913:HOH:O	2.14	0.47
26:14:2887:U:H2'	26:14:2888:C:C6	2.50	0.47
27:1J:64:C:H2'	27:1J:65:C:C6	2.50	0.47
27:1J:101:A:OP2	27:1J:101:A:H8	1.96	0.47
29:29:101:ARG:HG3	29:29:203:LYS:HD3	1.96	0.47
30:39:8:GLN:OE1	30:39:9:ILE:HB	2.15	0.47
30:39:46:ARG:HG2	30:39:46:ARG:NH1	2.27	0.47
34:15:61:ARG:HA	34:15:61:ARG:NE	2.29	0.47
34:15:134:ARG:O	34:15:134:ARG:HG2	2.14	0.47
35:25:98:VAL:CG1	35:25:117:LEU:HB3	2.45	0.47
37:45:35:VAL:HG12	37:45:36:ALA:N	2.29	0.47
39:65:89:ARG:O	39:65:90:GLY:C	2.57	0.47
41:85:88:ILE:HG22	41:85:90:VAL:CG2	2.45	0.47
42:95:19:LYS:H	42:95:19:LYS:HG3	1.47	0.47
42:95:71:LEU:H	42:95:86:GLY:CA	2.27	0.47
45:C5:67:LEU:HG	45:C5:71:LYS:HE3	1.97	0.47
48:F5:80:LEU:HD23	48:F5:82:LEU:HD21	1.96	0.47
1:13:1454:G:OP1	20:BI:39:LYS:NZ	2.37	0.47
2:1E:5:ILE:HG13	2:1E:6:THR:N	2.29	0.47
2:1E:82:ARG:HG3	2:1E:92:TYR:OH	2.15	0.47
2:1E:115:LEU:HD13	2:1E:145:LEU:HB3	1.96	0.47
5:4E:20:GLN:HG2	5:4E:21:ALA:H	1.79	0.47
15:6I:36:ILE:HG12	15:6I:59:MET:HE3	1.97	0.47
20:BI:10:LEU:HG	20:BI:12:ALA:H	1.80	0.47
23:2K:63:C:O2	23:2K:64:G:C8	2.67	0.47
26:1H:723:G:H2'	26:1H:724:U:O4'	2.14	0.47
26:1H:998:C:H3'	61:1H:4022:HOH:O	2.13	0.47
26:1H:1021:A:C8	26:1H:1021:A:C3'	2.98	0.47
26:1H:1668:A:OP1	35:68:5:GLN:HG3	2.15	0.47
26:1H:2154:G:O2'	26:1H:2155:G:H8	1.97	0.47
31:41:110:ALA:HA	31:41:140:ILE:O	2.14	0.47
37:88:14:ARG:HG2	37:88:41:TRP:HH2	1.79	0.47
45:G8:29:GLU:HB3	45:G8:38:ILE:CG2	2.44	0.47
48:J8:83:GLU:C	48:J8:85:LEU:H	2.23	0.47
1:1G:188:U:O2'	1:1G:189:U:H5'	2.15	0.47
1:1G:1080:A:H5'	5:42:14:ARG:HH22	1.80	0.47
1:1G:1499:A:H1'	1:1G:1520:G:H5'	1.97	0.47
3:22:77:ILE:HA	3:22:84:ILE:HB	1.97	0.47
4:32:9:CYS:O	4:32:12:CYS:HB2	2.15	0.47
4:32:138:TYR:CD1	4:32:138:TYR:C	2.93	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:42:14:ARG:O	5:42:16:THR:HG22	2.14	0.47
15:6A:55:GLY:O	15:6A:59:MET:HG3	2.15	0.47
20:BA:47:GLY:C	20:BA:49:ALA:H	2.23	0.47
26:14:125:G:H5"	54:L5:19:ARG:HD3	1.97	0.47
26:14:363:G:H2'	26:14:363(A):A:C8	2.40	0.47
26:14:469:G:C6	54:L5:39:ARG:NH1	2.83	0.47
26:14:654(J):A:H5'	26:14:654(K):C:OP2	2.14	0.47
26:14:996:A:H4'	41:85:92:ARG:CZ	2.45	0.47
26:14:1011:G:C2	26:14:1151:G:C2	3.03	0.47
26:14:1138:G:H21	34:15:106:MET:CE	2.28	0.47
26:14:1386:C:H2'	26:14:1387:C:H6	1.78	0.47
26:14:2469:A:H2	26:14:2481:G:H21	1.61	0.47
33:69:77:LEU:HA	33:69:141:LYS:HB2	1.97	0.47
35:25:88:ASN:HB3	35:25:94:ARG:HD3	1.96	0.47
40:75:77:PRO:HG2	40:75:80:SER:HB2	1.97	0.47
45:C5:100:ALA:O	45:C5:102:CYS:SG	2.73	0.47
46:D5:106:GLY:HA3	46:D5:140:ASP:OD1	2.15	0.47
1:13:838:G:H1	1:13:848:C:H42	1.62	0.47
1:13:1464:G:H2'	1:13:1465:C:H6	1.79	0.47
4:3E:92:VAL:O	4:3E:96:LEU:HD22	2.15	0.47
8:7E:36:LEU:HA	8:7E:39:LEU:HB2	1.97	0.47
9:8E:79:LEU:HD22	9:8E:83:ARG:HG3	1.97	0.47
11:2I:73:MET:HG3	11:2I:103:LEU:HD22	1.97	0.47
15:6I:39:LEU:HD13	15:6I:56:LEU:HB2	1.96	0.47
19:AI:65:ASN:OD1	19:AI:65:ASN:N	2.48	0.47
26:1H:466:A:H5"	26:1H:467:G:OP2	2.15	0.47
26:1H:960:A:C8	26:1H:962:G:C8	3.03	0.47
26:1H:2863:C:O2'	26:1H:2864:G:H5'	2.14	0.47
31:41:98:ARG:NH2	51:M8:1:MET:HG3	2.30	0.47
33:61:12:LEU:HG	33:61:19:VAL:HG21	1.97	0.47
41:C8:85:LYS:HA	41:C8:85:LYS:NZ	2.30	0.47
46:H8:117:LEU:HD22	46:H8:118:GLN:H	1.78	0.47
46:H8:128:VAL:CB	46:H8:161:VAL:HG21	2.45	0.47
52:N8:41:PRO:CD	52:N8:44:THR:HG21	2.44	0.47
1:1G:50:A:N1	1:1G:360:A:O2'	2.42	0.47
1:1G:516:U:O2'	1:1G:519:C:N3	2.46	0.47
1:1G:1157:A:H1'	1:1G:1181:G:H21	1.79	0.47
1:1G:1224:G:N1	1:1G:1322:C:H1'	2.29	0.47
1:1G:1298:C:H1'	1:1G:1299:A:C6	2.50	0.47
1:1G:1498:U:O2	1:1G:1499:A:N6	2.42	0.47
2:12:111:ARG:HA	2:12:111:ARG:HH11	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:52:2:ARG:HH21	6:52:69:GLU:HG3	1.80	0.47
23:2L:9:G:H21	23:2L:46:G:H3'	1.80	0.47
23:2L:38:A:H2'	23:2L:39:A:O4'	2.14	0.47
26:14:71:A:C2	44:B5:31:HIS:NE2	2.78	0.47
26:14:265:A:N6	26:14:427:U:O2'	2.45	0.47
26:14:333:G:H5"	26:14:334:C:OP2	2.15	0.47
26:14:442:G:C6	26:14:444:C:N4	2.83	0.47
26:14:1078:U:H1'	26:14:1088:A:C2	2.50	0.47
26:14:2527:C:N4	26:14:2528:U:C4	2.83	0.47
26:14:2655:G:N2	26:14:2665:A:OP2	2.38	0.47
28:19:141:VAL:HG23	28:19:162:SER:HB2	1.96	0.47
31:49:106:LEU:O	31:49:111:LEU:HG	2.14	0.47
31:49:135:LEU:HD23	31:49:140:ILE:HD11	1.97	0.47
36:35:64:LYS:HD2	55:M5:30:ARG:HH12	1.79	0.47
42:95:35:LEU:HB2	42:95:37:VAL:CG1	2.44	0.47
45:C5:40:GLU:N	45:C5:40:GLU:OE2	2.48	0.47
51:I5:53:GLU:OE2	51:I5:55:ARG:N	2.38	0.47
55:M5:29:LYS:HG2	55:M5:44:LYS:HB3	1.97	0.47
1:13:976:G:OP1	14:5I:32:SER:N	2.48	0.47
1:13:1286:A:N3	21:1F:18:TYR:OH	2.48	0.47
7:6E:92:SER:O	7:6E:96:GLN:HG3	2.15	0.47
7:6E:113:GLU:HG2	7:6E:119:ARG:HG2	1.96	0.47
11:2I:59:TYR:CZ	11:2I:63:LEU:HD11	2.49	0.47
12:3I:84:LEU:HB2	12:3I:105:TYR:CE2	2.50	0.47
26:1H:274:G:H8	26:1H:274:G:H3'	1.80	0.47
26:1H:618:G:H2'	26:1H:618(A):C:C6	2.50	0.47
26:1H:1058:U:H3	26:1H:1080:A:H61	1.63	0.47
26:1H:1671:U:OP2	61:1H:3662:HOH:O	2.19	0.47
26:1H:1830:C:C2'	26:1H:1831:G:H5'	2.45	0.47
27:16:43:C:P	31:41:67:LYS:HZ2	2.38	0.47
31:41:53:LEU:HD12	31:41:53:LEU:HA	1.69	0.47
32:51:166:GLY:O	32:51:167:GLU:HG2	2.15	0.47
41:C8:19:LYS:O	41:C8:22:LYS:HG3	2.15	0.47
45:G8:64:GLU:H	45:G8:64:GLU:HG2	1.40	0.47
55:Q8:33:ASN:O	55:Q8:34:TRP:CD1	2.68	0.47
55:Q8:47:LYS:NZ	55:Q8:47:LYS:CA	2.74	0.47
1:1G:1028:C:H2'	1:1G:1028(A):C:O4'	2.14	0.47
1:1G:1258:G:H2'	1:1G:1259:C:C6	2.47	0.47
1:1G:1286:A:H3'	1:1G:1286:A:H8	1.80	0.47
1:1G:1347:G:N2	1:1G:1373:G:H2'	2.30	0.47
2:12:92:TYR:CD1	2:12:151:GLY:HA3	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:52:33:TYR:OH	6:52:78:GLU:HG3	2.15	0.47
7:62:45:ASP:O	7:62:49:ILE:HG13	2.15	0.47
7:62:116:ALA:HA	7:62:119:ARG:NE	2.25	0.47
9:82:27:THR:HG1	9:82:28:VAL:H	1.63	0.47
13:4A:71:ARG:O	13:4A:75:ALA:N	2.48	0.47
18:9A:78:LEU:O	18:9A:79:LEU:HD23	2.15	0.47
26:14:35:G:H2'	26:14:36:G:O4'	2.15	0.47
26:14:71:A:OP2	26:14:71:A:H3'	2.14	0.47
26:14:515:A:N1	26:14:1260:G:O2'	2.44	0.47
26:14:1341:U:OP2	26:14:1394:U:O2'	2.27	0.47
26:14:2158:A:H1'	26:14:2159:G:C8	2.49	0.47
26:14:2294:C:OP2	39:65:89:ARG:NH2	2.48	0.47
26:14:2772:C:H2'	26:14:2773:C:C6	2.50	0.47
32:59:6:ARG:HD3	32:59:54:ARG:HH12	1.79	0.47
35:25:22:ILE:HA	35:25:22:ILE:HD13	1.46	0.47
45:C5:51:VAL:HA	45:C5:57:GLN:HA	1.96	0.47
46:D5:60:GLU:HB2	46:D5:66:SER:OG	2.15	0.47
46:D5:146:ILE:HG13	46:D5:147:GLY:H	1.79	0.47
1:13:438:G:H4'	4:3E:123:HIS:CD2	2.51	0.46
1:13:864:A:H5"	1:13:865:A:OP2	2.14	0.46
1:13:1032(A):G:H2'	1:13:1032(B):G:N7	2.30	0.46
1:13:1132:C:H2'	1:13:1133:G:C8	2.50	0.46
1:13:1236:A:HO2'	1:13:1304:G:H4'	1.80	0.46
7:6E:26:PHE:CE2	7:6E:30:ILE:HD11	2.49	0.46
16:7I:23:ASP:OD1	16:7I:25:ARG:HG3	2.15	0.46
26:1H:1019:U:O2'	26:1H:1021:A:C2	2.67	0.46
26:1H:1268:A:H2'	26:1H:1269:A:O4'	2.15	0.46
26:1H:1387:C:C2	26:1H:1388:G:C8	3.02	0.46
26:1H:1680:U:H2'	26:1H:1681:G:O4'	2.15	0.46
26:1H:2249:U:C5	61:1H:3722:HOH:O	2.67	0.46
29:21:131:ALA:HB1	29:21:135:HIS:HE1	1.80	0.46
34:58:40:PRO:CB	41:C8:68:ALA:HB2	2.44	0.46
37:88:35:VAL:HA	37:88:101:ARG:O	2.15	0.46
46:H8:128:VAL:HB	46:H8:161:VAL:HG21	1.97	0.46
55:Q8:7:HIS:HD1	55:Q8:10:ALA:H	1.62	0.46
55:Q8:8:LYS:HD2	55:Q8:8:LYS:N	2.30	0.46
1:1G:677:U:O2'	1:1G:678:U:H5'	2.15	0.46
1:1G:857:C:H2'	1:1G:858:G:O4'	2.15	0.46
1:1G:865:A:O5'	1:1G:865:A:H8	1.98	0.46
1:1G:1227:A:C8	1:1G:1227:A:H3'	2.49	0.46
1:1G:1265:G:H2'	1:1G:1266:G:O4'	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1G:1443:G:O2'	40:75:122:ASP:OD2	2.32	0.46
1:1G:1466:C:H2'	1:1G:1467:G:O4'	2.15	0.46
1:1G:1495:U:O4	59:1G:1697:PAR:N12	2.47	0.46
5:42:41:VAL:O	5:42:67:VAL:HG12	2.15	0.46
9:82:26:VAL:HG13	9:82:61:ALA:O	2.15	0.46
57:3L:8:4SU:H2'	57:3L:13:C:H41	1.80	0.46
57:3L:8:4SU:H2'	57:3L:13:C:N4	2.30	0.46
26:14:747:U:O2	26:14:2014:A:H1'	2.15	0.46
26:14:962:G:H2'	26:14:963:U:C6	2.50	0.46
26:14:1449(A):G:H2'	26:14:1450:C:C6	2.50	0.46
26:14:1511:A:H3'	26:14:1512:G:H8	1.80	0.46
26:14:1614:A:H2	61:14:3509:HOH:O	1.97	0.46
26:14:2104:G:H2'	26:14:2105:C:C6	2.50	0.46
26:14:2839:G:H5'	38:55:46:GLY:CA	2.44	0.46
29:29:57:LYS:HA	29:29:57:LYS:HD3	1.76	0.46
38:55:55:ALA:HB2	38:55:79:LEU:HD13	1.97	0.46
46:D5:130:PRO:HA	46:D5:133:ILE:HD11	1.97	0.46
46:D5:155:LEU:HD12	46:D5:163:LEU:HD13	1.96	0.46
1:13:156:G:H1	1:13:165:C:H42	1.63	0.46
1:13:1312:G:H5'	19:AI:6:LYS:NZ	2.30	0.46
2:1E:5:ILE:HG13	2:1E:6:THR:H	1.79	0.46
7:6E:16:LEU:HD21	9:8E:45:ALA:HB2	1.97	0.46
15:6I:6:GLU:CD	15:6I:6:GLU:N	2.69	0.46
15:6I:21:ASP:OD2	15:6I:24:SER:HB3	2.15	0.46
22:1K:54:5MU:H2'	22:1K:55:PSU:O4'	2.15	0.46
26:1H:356:G:H2'	26:1H:357:A:H8	1.79	0.46
26:1H:495:G:O2'	43:E8:62:HIS:HE1	1.98	0.46
26:1H:801:G:OP2	61:1H:4224:HOH:O	2.20	0.46
26:1H:1124:C:H2'	26:1H:1125:G:O4'	2.16	0.46
26:1H:1242:A:N1	36:78:4:SER:OG	2.40	0.46
26:1H:1494:A:O2'	26:1H:1495:A:H5'	2.16	0.46
26:1H:1728:G:H2'	26:1H:1731:G:O6	2.15	0.46
26:1H:2061:G:OP1	61:1H:3626:HOH:O	2.20	0.46
26:1H:2315:G:H2'	26:1H:2316:C:C6	2.50	0.46
26:1H:2378:A:H2'	39:A8:21:THR:HG21	1.97	0.46
26:1H:2698:U:H2'	26:1H:2699:C:C6	2.50	0.46
42:D8:79:VAL:HG13	42:D8:81:TYR:HB3	1.96	0.46
46:H8:7:ALA:HB3	46:H8:61:LEU:CB	2.45	0.46
50:L8:31:LEU:O	50:L8:32:GLN:HB2	2.14	0.46
55:Q8:14:VAL:O	55:Q8:15:LYS:HD3	2.15	0.46
1:1G:134:A:H61	16:7A:25:ARG:HH12	1.63	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1G:607:A:H2'	1:1G:608:A:O4'	2.15	0.46
1:1G:992:U:H3	1:1G:1044:A:H62	1.64	0.46
3:22:21:ARG:HB3	3:22:21:ARG:HH11	1.79	0.46
5:42:101:ILE:H	5:42:101:ILE:HD13	1.80	0.46
26:14:819:A:OP2	26:14:1187:G:N2	2.48	0.46
26:14:1257:C:H4'	30:39:83:PHE:CE1	2.49	0.46
26:14:2184:G:H2'	26:14:2185:C:C6	2.50	0.46
26:14:2209:C:H1'	26:14:2216:G:N2	2.29	0.46
26:14:2232:U:P	48:F5:40:ARG:HH12	2.39	0.46
26:14:2262:U:OP1	47:E5:19:LYS:HE2	2.14	0.46
26:14:2882:A:H5'	38:55:96:ARG:HG3	1.96	0.46
27:1J:9:G:H5'	39:65:25:ARG:HH12	1.80	0.46
32:59:6:ARG:HB2	32:59:66:GLY:HA2	1.98	0.46
37:45:74:TYR:O	37:45:89:ASN:HB2	2.15	0.46
46:D5:28:MET:HE2	46:D5:28:MET:HB3	1.59	0.46
1:13:167:G:H2'	1:13:168:G:C8	2.50	0.46
1:13:639:G:N2	1:13:640:A:C4	2.84	0.46
1:13:948:C:O2'	1:13:949:A:H5'	2.14	0.46
1:13:1124:G:H5'	10:1I:35:SER:HB2	1.97	0.46
1:13:1151:A:O2'	1:13:1152:A:H8	1.98	0.46
1:13:1160:G:H22	1:13:1177:G:N2	2.14	0.46
4:3E:126:ILE:HG22	4:3E:127:THR:N	2.31	0.46
4:3E:155:LEU:O	4:3E:158:ILE:N	2.49	0.46
8:7E:109:ILE:HD11	8:7E:120:THR:CG2	2.45	0.46
12:3I:28:LYS:HD3	12:3I:28:LYS:HA	1.58	0.46
18:9I:66:LEU:O	18:9I:70:ILE:HG13	2.15	0.46
19:AI:40:ILE:HD11	19:AI:62:ILE:CG2	2.44	0.46
22:1K:9:A:O2'	22:1K:10:G:H5'	2.15	0.46
26:1H:598:G:H2'	26:1H:599:G:O4'	2.15	0.46
26:1H:1443:G:N2	26:1H:1549:C:C2	2.84	0.46
26:1H:1678:G:N2	26:1H:1989:G:N2	2.56	0.46
26:1H:1771:C:H1'	26:1H:1786:A:C8	2.50	0.46
26:1H:1899:G:O2'	26:1H:1900:A:OP2	2.29	0.46
31:41:117:PHE:CZ	31:41:119:GLY:HA2	2.51	0.46
53:O8:9:LEU:HB3	53:O8:26:ASN:O	2.15	0.46
1:1G:235:C:H5'	17:8A:70:ARG:HG2	1.98	0.46
1:1G:1240:U:H1'	7:62:38:LEU:HD21	1.97	0.46
1:1G:1521:G:H2'	1:1G:1522:U:H6	1.80	0.46
9:82:23:ASN:HD22	9:82:23:ASN:H	1.63	0.46
13:4A:14:ARG:HD2	13:4A:42:ALA:HA	1.98	0.46
26:14:210:C:OP2	54:L5:29:LYS:NZ	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:14:1568:G:P	28:19:63:ARG:HH12	2.38	0.46
26:14:1750:G:H2'	26:14:1751:C:H6	1.80	0.46
26:14:2543:G:H1'	26:14:2766:G:H5'	1.96	0.46
26:14:2729:G:H2'	26:14:2730:C:H6	1.80	0.46
27:1J:41:U:O4	31:49:70:VAL:HG23	2.15	0.46
38:55:30:THR:HG22	38:55:31:HIS:CD2	2.50	0.46
49:G5:10:LEU:HD12	49:G5:10:LEU:HA	1.78	0.46
52:J5:18:ALA:O	52:J5:21:SER:HB3	2.15	0.46
2:1E:111:ARG:HG2	2:1E:111:ARG:NH1	2.11	0.46
4:3E:153:ARG:O	4:3E:181:MET:HE1	2.15	0.46
7:6E:12:LEU:HD21	7:6E:28:ASN:ND2	2.31	0.46
8:7E:54:ASP:O	8:7E:56:LYS:HG3	2.16	0.46
16:7I:38:TYR:CZ	16:7I:50:LYS:HB2	2.51	0.46
22:1K:74:C:O2'	22:1K:75:C:P	2.74	0.46
26:1H:192:C:O2'	26:1H:802:A:N3	2.45	0.46
26:1H:270(L):U:H3	33:61:50:ARG:NE	2.13	0.46
26:1H:1013:C:O2'	26:1H:1014:U:H5'	2.16	0.46
26:1H:1077:A:H3'	26:1H:1078:U:C5'	2.45	0.46
26:1H:1187:G:H5"	42:D8:81:TYR:CE2	2.49	0.46
26:1H:1630:G:H2'	26:1H:1630(A):C:C6	2.51	0.46
26:1H:2467:C:H4'	37:88:123:HIS:CD2	2.49	0.46
27:16:12:C:H2'	47:I8:73:GLY:HA3	1.96	0.46
29:21:13:ARG:O	29:21:14:ILE:HD13	2.15	0.46
31:41:7:LEU:HB2	31:41:104:GLU:CD	2.40	0.46
36:78:76:LYS:HD3	36:78:76:LYS:HA	1.68	0.46
38:98:81:ASP:OD1	38:98:81:ASP:N	2.48	0.46
42:D8:24:LYS:HA	42:D8:92:THR:HG23	1.96	0.46
46:H8:117:LEU:HD22	46:H8:118:GLN:N	2.31	0.46
55:Q8:57:ARG:CZ	55:Q8:57:ARG:O	2.63	0.46
1:1G:741:G:H2'	1:1G:742:G:O4'	2.15	0.46
1:1G:778:G:O2'	11:2A:119:CYS:HB3	2.15	0.46
1:1G:1036:G:H5'	1:1G:1037:C:OP2	2.14	0.46
1:1G:1227:A:H3'	1:1G:1227:A:H8	1.80	0.46
1:1G:1260:C:OP1	1:1G:1284:C:H4'	2.15	0.46
1:1G:1448:C:H2'	1:1G:1449:C:O4'	2.16	0.46
7:62:25:ALA:HA	7:62:28:ASN:ND2	2.30	0.46
10:1A:32:ALA:HA	10:1A:76:ASN:HB2	1.97	0.46
57:3L:36:A:C6	25:4L:14:A:H2	2.33	0.46
26:14:127:A:H5"	26:14:128:C:C6	2.51	0.46
26:14:1022:G:C6	26:14:1140:C:C4	3.04	0.46
26:14:1287:A:C5	26:14:1288:U:C4	3.03	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:14:1971:A:P	28:19:242:ARG:HH22	2.38	0.46
26:14:2074:U:H2'	26:14:2075:U:C6	2.50	0.46
26:14:2113:U:O4	26:14:2168:G:O2'	2.25	0.46
26:14:2427:C:H5"	26:14:2428:G:OP1	2.15	0.46
26:14:2872:G:C4	26:14:2873:A:C2	3.04	0.46
28:19:36:PRO:HA	28:19:61:LEU:HD12	1.97	0.46
29:29:35:GLN:O	29:29:48:GLN:HB2	2.15	0.46
31:49:104:GLU:HG2	51:I5:23:GLU:HG2	1.97	0.46
32:59:20:ALA:HB1	32:59:23:ARG:HG3	1.96	0.46
33:69:6:LEU:HD13	33:69:37:VAL:CG2	2.45	0.46
33:69:82:ARG:O	33:69:89:TYR:HD2	1.98	0.46
36:35:36:LYS:HB3	36:35:37:GLY:H	1.62	0.46
47:E5:26:TYR:O	47:E5:29:GLN:HB2	2.16	0.46
51:I5:16:CYS:HA	51:I5:33:VAL:HG13	1.98	0.46
52:J5:36:CYS:SG	52:J5:49:CYS:HB3	2.56	0.46
1:13:603:U:H2'	1:13:604:G:C8	2.50	0.46
1:13:659:U:C2	1:13:660:G:C8	3.02	0.46
1:13:963:G:H21	10:1I:55:LYS:HE2	1.79	0.46
1:13:973:G:H4'	10:1I:54:PHE:O	2.16	0.46
1:13:1226:C:H4'	19:AI:80:TYR:CZ	2.50	0.46
1:13:1351:U:H2'	1:13:1352:C:H6	1.81	0.46
3:2E:92:ALA:HA	3:2E:95:THR:OG1	2.15	0.46
4:3E:8:VAL:CG1	4:3E:21:LEU:HB2	2.46	0.46
5:4E:19:MET:HB3	5:4E:19:MET:HE3	1.60	0.46
5:4E:33:VAL:HG11	5:4E:109:ILE:HG12	1.98	0.46
18:9I:26:LEU:HB3	18:9I:42:ARG:HH22	1.79	0.46
19:AI:78:ARG:HD3	19:AI:78:ARG:C	2.41	0.46
26:1H:26:G:C6	26:1H:27:G:N1	2.83	0.46
26:1H:719:C:H2'	26:1H:720:C:H6	1.80	0.46
26:1H:1047:G:H2'	26:1H:1110:G:C2	2.50	0.46
26:1H:1301:A:H2	26:1H:1626:G:H21	1.61	0.46
26:1H:1337:G:C4	26:1H:1338:G:C8	3.04	0.46
26:1H:1364:G:OP2	48:J8:2:SER:OG	2.30	0.46
26:1H:1820:U:C2	28:11:202:LYS:HB3	2.51	0.46
26:1H:2291:U:H2'	26:1H:2292:C:C6	2.51	0.46
26:1H:2882:A:OP1	38:98:96:ARG:NH1	2.48	0.46
26:1H:2886:G:O2'	52:N8:31:VAL:HG22	2.16	0.46
28:11:108:PRO:HD2	28:11:111:LEU:HG	1.98	0.46
29:21:201:THR:HG22	29:21:203:LYS:H	1.80	0.46
31:41:107:LEU:HD21	31:41:178:PHE:CD1	2.51	0.46
32:51:4:ILE:HG21	32:51:6:ARG:HH11	1.75	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:68:104:ARG:NH1	40:B8:36:GLU:OE2	2.48	0.46
41:C8:66:ASN:HB2	41:C8:76:TYR:HB2	1.98	0.46
1:1G:406:G:C2	1:1G:407:G:C8	3.04	0.46
1:1G:742:G:H5"	15:6A:58:MET:HE1	1.97	0.46
1:1G:801:U:H2'	1:1G:802:A:C8	2.50	0.46
1:1G:1048:G:O4'	1:1G:1215:G:H4'	2.16	0.46
1:1G:1306:A:C6	1:1G:1307:U:C2	3.04	0.46
1:1G:1371:G:OP1	9:82:11:LYS:HB3	2.15	0.46
1:1G:1443:G:N2	40:75:119:LYS:HB2	2.31	0.46
4:32:105:VAL:HG13	4:32:110:PHE:HB2	1.98	0.46
4:32:156:GLU:H	4:32:156:GLU:HG3	1.54	0.46
7:62:50:ILE:HG21	7:62:58:PRO:HA	1.98	0.46
16:7A:49:LEU:HD11	16:7A:51:VAL:HG23	1.98	0.46
26:14:459:U:H2'	26:14:460:A:C8	2.50	0.46
26:14:1021:A:H3'	26:14:1021:A:C8	2.51	0.46
26:14:1427:A:H4'	26:14:1428:C:O4'	2.16	0.46
26:14:1753:G:N1	26:14:1756:G:C2	2.83	0.46
29:29:11:MET:HE3	29:29:186:GLY:HA2	1.97	0.46
29:29:120:TRP:CD2	29:29:155:LYS:HD3	2.50	0.46
30:39:85:GLY:C	61:39:302:HOH:O	2.58	0.46
37:45:110:THR:HG23	37:45:113:GLN:NE2	2.30	0.46
44:B5:36:LYS:HA	44:B5:39:ILE:HD12	1.97	0.46
1:13:501:C:H2'	1:13:502:G:C8	2.50	0.46
1:13:687:A:H2'	1:13:701:C:N4	2.30	0.46
12:3I:7:ILE:O	12:3I:11:VAL:HG23	2.14	0.46
26:1H:654(L):G:H3'	26:1H:654(M):C:H5"	1.98	0.46
26:1H:662:G:P	36:78:15:ARG:HE	2.39	0.46
26:1H:783:A:C8	26:1H:784:A:H4'	2.50	0.46
26:1H:852:G:H2'	26:1H:853:G:H8	1.80	0.46
26:1H:2591:C:P	28:11:239:ARG:HG3	2.56	0.46
26:1H:2646:C:H2'	26:1H:2647:U:O4'	2.16	0.46
28:11:239:ARG:HD3	28:11:239:ARG:HA	1.77	0.46
30:31:198:ALA:O	30:31:201:VAL:N	2.49	0.46
34:58:94:HIS:C	34:58:95:PRO:O	2.56	0.46
48:J8:21:ARG:HE	48:J8:21:ARG:HB3	1.43	0.46
1:1G:570:G:C2	1:1G:571:U:C4	3.04	0.46
1:1G:578:C:P	61:1G:1714:HOH:O	2.74	0.46
3:22:59:ARG:HH12	3:22:97:LYS:HZ2	1.63	0.46
10:1A:3:LYS:HD2	10:1A:77:PRO:HG3	1.98	0.46
13:4A:49:THR:HB	13:4A:52:GLU:H	1.79	0.46
15:6A:24:SER:O	15:6A:28:GLN:HG3	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:AA:41:VAL:H	19:AA:44:MET:HB2	1.81	0.46
19:AA:50:ALA:HB3	19:AA:57:HIS:HB3	1.98	0.46
26:14:236:C:H2'	26:14:237:C:C6	2.51	0.46
26:14:601:C:O2	26:14:605:C:H4'	2.15	0.46
26:14:656:G:H2'	26:14:657:U:O4'	2.16	0.46
26:14:1044:G:H4'	26:14:1048:A:H1'	1.97	0.46
26:14:1260:G:H2'	26:14:1261:C:C6	2.50	0.46
26:14:1288:U:C2	26:14:1327:C:O2	2.69	0.46
26:14:2321:G:N3	26:14:2321:G:H2'	2.30	0.46
26:14:2331:G:H5'	47:E5:44:ARG:HG3	1.97	0.46
26:14:2880:C:O2	38:55:93:GLY:N	2.25	0.46
28:19:65:ILE:HD11	28:19:67:PHE:CZ	2.50	0.46
34:15:28:THR:HA	34:15:106:MET:HE2	1.96	0.46
42:95:48:GLY:HA3	42:95:52:VAL:N	2.30	0.46
50:H5:9:VAL:HG22	50:H5:53:LEU:O	2.15	0.46
55:M5:23:VAL:HG23	55:M5:49:VAL:HG22	1.96	0.46
1:13:515:G:N2	1:13:537:G:C4	2.83	0.46
1:13:747:C:OP2	1:13:748:C:N4	2.47	0.46
1:13:972:C:OP1	61:13:1823:HOH:O	2.21	0.46
5:4E:71:LEU:HD22	5:4E:115:VAL:H	1.80	0.46
11:2I:98:LEU:O	11:2I:101:SER:OG	2.23	0.46
13:4I:67:GLU:CG	13:4I:71:ARG:HH21	2.29	0.46
19:AI:6:LYS:HE2	19:AI:6:LYS:HB3	1.40	0.46
20:BI:92:LEU:HD23	20:BI:92:LEU:HA	1.81	0.46
24:3K:38:A:C2'	24:3K:39:PSU:H5"	2.46	0.46
26:1H:298:G:H5"	26:1H:299:A:OP1	2.16	0.46
26:1H:389:G:O5'	26:1H:389:G:H8	1.99	0.46
26:1H:1588:C:O2'	26:1H:1589:C:H5'	2.16	0.46
26:1H:1787:A:O4'	26:1H:2589:A:H4'	2.16	0.46
26:1H:2688:U:C5	26:1H:2720:U:OP2	2.65	0.46
26:1H:2850:A:C2	26:1H:2851:A:C4	3.03	0.46
29:21:9:VAL:O	29:21:192:ASN:HB3	2.16	0.46
33:61:110:ASP:OD1	33:61:111:PRO:HA	2.15	0.46
36:78:138:LEU:HD12	36:78:144:GLU:CG	2.41	0.46
37:88:85:LYS:HG2	37:88:86:GLY:H	1.80	0.46
37:88:135:ASP:CB	37:88:137:TYR:H	2.28	0.46
38:98:9:LYS:HA	38:98:17:ARG:CD	2.45	0.46
45:G8:40:GLU:HB2	45:G8:41:GLY:HA2	1.98	0.46
46:H8:33:LEU:HD12	46:H8:33:LEU:HA	1.61	0.46
48:J8:73:LEU:HD13	48:J8:90:ILE:O	2.16	0.46
1:1G:35:G:C2	1:1G:550:G:N3	2.84	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1G:675:A:H2'	1:1G:676:A:O4'	2.16	0.46
1:1G:1130:A:H62	1:1G:1144:G:H21	1.62	0.46
1:1G:1238:A:N3	1:1G:1241:G:O2'	2.31	0.46
1:1G:1273:G:H3'	1:1G:1274:G:C8	2.51	0.46
1:1G:1396:A:H4'	1:1G:1397:C:OP2	2.15	0.46
3:22:42:LEU:O	3:22:46:GLU:HG3	2.15	0.46
6:52:11:ASN:HB3	6:52:14:LEU:CD1	2.45	0.46
11:2A:22:HIS:HB3	11:2A:29:ILE:HG12	1.98	0.46
17:8A:45:HIS:HA	17:8A:69:LYS:HZ1	1.81	0.46
18:9A:29:PHE:N	18:9A:29:PHE:HD1	2.14	0.46
26:14:861:A:C2	26:14:917:A:C4	3.04	0.46
26:14:1239:G:H2'	26:14:1240:U:O4'	2.15	0.46
26:14:1657:C:H2'	26:14:1658:C:H6	1.81	0.46
26:14:2687:U:C4	26:14:2688:U:C5	3.04	0.46
26:14:2697:G:H2'	26:14:2698:U:O4'	2.16	0.46
27:1J:52:A:N6	39:65:33:LYS:HG3	2.30	0.46
33:69:97:ILE:HD12	33:69:114:LEU:HD11	1.98	0.46
36:35:78:PRO:HB3	36:35:111:ARG:HH21	1.80	0.46
40:75:91:ARG:NH1	40:75:124:ASP:OD2	2.48	0.46
54:L5:12:ARG:NH2	54:L5:44:PRO:HB3	2.31	0.46
1:13:174:C:H5'	1:13:174:C:H6	1.81	0.46
1:13:451:A:N6	1:13:480:U:H2'	2.31	0.46
1:13:538:G:P	12:3I:115:LYS:HG3	2.55	0.46
1:13:620:C:H5"	61:13:1987:HOH:O	2.15	0.46
1:13:633:G:OP2	1:13:633:G:H8	1.97	0.46
1:13:1171:G:O2'	1:13:1172:C:H5'	2.16	0.46
1:13:1178:G:N2	1:13:1181:G:C8	2.84	0.46
1:13:1233:G:H2'	1:13:1234:C:C6	2.50	0.46
2:1E:162:ILE:HD11	2:1E:184:VAL:HG22	1.97	0.46
4:3E:79:PHE:O	4:3E:83:SER:HB2	2.16	0.46
6:5E:11:ASN:OD1	6:5E:12:PRO:HD2	2.15	0.46
7:6E:73:MET:HA	7:6E:90:GLU:HA	1.97	0.46
9:8E:95:LYS:HE2	9:8E:95:LYS:HB2	1.65	0.46
24:3K:75:C:O2'	24:3K:76:A:H2	1.99	0.46
26:1H:1138:G:H21	34:58:106:MET:CE	2.13	0.46
26:1H:1550:C:H2'	26:1H:1551:C:H6	1.81	0.46
26:1H:1858:G:H1'	26:1H:1884:A:H61	1.81	0.46
26:1H:2119:A:N6	26:1H:2170:A:C6	2.84	0.46
26:1H:2157:G:HO2'	26:1H:2158:A:P	2.39	0.46
30:31:33:LEU:HD12	30:31:33:LEU:HA	1.74	0.46
30:31:63:LYS:CE	30:31:67:GLN:HB2	2.45	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:41:101:ILE:HG13	51:M8:25:TYR:O	2.16	0.46
33:61:21:VAL:HG21	33:61:25:TYR:HD2	1.81	0.46
42:D8:43:GLU:OE2	42:D8:44:LYS:NZ	2.48	0.46
45:G8:55:TYR:N	45:G8:56:PRO:HD3	2.31	0.46
46:H8:76:LEU:HD13	46:H8:76:LEU:H	1.80	0.46
48:J8:8:SER:HB3	48:J8:66:HIS:CD2	2.51	0.46
52:N8:3:LYS:HB3	52:N8:3:LYS:HE3	1.63	0.46
53:O8:45:LYS:HD3	53:O8:45:LYS:HA	1.79	0.46
1:1G:1011:G:H2'	1:1G:1012:U:C6	2.51	0.46
3:22:73:PRO:O	3:22:76:VAL:HG22	2.16	0.46
5:42:40:ARG:HA	5:42:67:VAL:O	2.16	0.46
5:42:75:THR:OG1	5:42:117:ASP:O	2.26	0.46
11:2A:73:MET:HG2	11:2A:103:LEU:HD13	1.97	0.46
13:4A:94:ARG:HH22	19:AA:78:ARG:HH12	1.64	0.46
19:AA:14:HIS:ND1	19:AA:15:LEU:N	2.64	0.46
56:1L:9:A:H5'	56:1L:9:A:N3	2.31	0.46
26:14:270(Z):U:O3'	26:14:271(A):C:H6	1.98	0.46
26:14:302:C:H2'	26:14:303:U:C6	2.51	0.46
26:14:568:U:N3	61:14:3695:HOH:O	2.18	0.46
26:14:1857:G:O2'	26:14:1885:A:N6	2.48	0.46
26:14:2861:G:C2	26:14:2862:G:C4	3.03	0.46
29:29:170:LEU:HD13	29:29:170:LEU:HA	1.82	0.46
30:39:7:TYR:HD1	30:39:18:ARG:N	2.14	0.46
32:59:11:VAL:O	32:59:13:LYS:HG3	2.16	0.46
42:95:34:GLU:OE1	42:95:56:SER:HB2	2.16	0.46
44:B5:30:VAL:HG23	44:B5:77:LYS:HB3	1.97	0.46
46:D5:67:LEU:HA	46:D5:68:PRO:HD3	1.64	0.46
1:13:378:G:H2'	1:13:379:C:O4'	2.16	0.46
1:13:417:C:H2'	1:13:418:C:H6	1.81	0.46
9:8E:70:LYS:O	9:8E:74:ILE:HG13	2.16	0.46
16:7I:50:LYS:HD3	16:7I:51:VAL:H	1.80	0.46
22:1K:6:G:H1	22:1K:67:C:H42	1.64	0.46
24:3K:7:A:H5'	24:3K:8:U:OP2	2.16	0.46
24:3K:18:G:H1'	24:3K:58:A:C2	2.50	0.46
26:1H:208:C:H2'	26:1H:209:C:H6	1.81	0.46
26:1H:747:U:O2	26:1H:2014:A:H1'	2.16	0.46
26:1H:900:A:H3'	26:1H:901:A:C8	2.46	0.46
26:1H:960:A:H61	37:88:82:ARG:NH2	2.14	0.46
26:1H:1050:A:H1'	26:1H:2751:G:C8	2.51	0.46
26:1H:1435:G:H21	26:1H:1478:G:H5'	1.79	0.46
26:1H:1718:G:C2	26:1H:1725:G:C8	3.04	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1H:2068:U:N3	26:1H:2430:A:C2	2.84	0.46
26:1H:2137:C:N3	26:1H:2138:C:N4	2.64	0.46
26:1H:2516:G:O2'	26:1H:2517:C:H5'	2.15	0.46
26:1H:2801:A:H2'	26:1H:2802:G:H4'	1.98	0.46
27:16:29:A:H2'	27:16:30:C:C6	2.51	0.46
27:16:40:U:H1'	27:16:45:A:N6	2.31	0.46
32:51:15:VAL:CG1	32:51:29:PRO:HD2	2.44	0.46
33:61:95:LYS:HE2	33:61:95:LYS:HB3	1.81	0.46
40:B8:107:ASP:CG	40:B8:109:GLU:HG3	2.41	0.46
1:1G:618:C:H5'	1:1G:619:U:H5"	1.96	0.46
1:1G:999:U:O2	1:1G:1042:G:N2	2.49	0.46
1:1G:1084:G:H5'	1:1G:1102:A:OP2	2.15	0.46
1:1G:1157:A:H8	1:1G:1158:C:N4	2.14	0.46
1:1G:1503:A:C2	25:4L:13:A:N7	2.84	0.46
2:12:54:THR:HG23	2:12:199:TYR:HB3	1.98	0.46
57:3L:21:A:H61	57:3L:46:7MG:HN21	1.61	0.46
26:14:13:A:N1	26:14:525:U:H2'	2.30	0.46
26:14:557:U:O2'	34:15:45:ASN:O	2.33	0.46
26:14:933:A:C5	26:14:934:G:C8	3.04	0.46
26:14:1003:G:O2'	26:14:1010:A:N1	2.47	0.46
26:14:1210:A:H5'	26:14:1212:G:C5'	2.46	0.46
26:14:1614:A:N6	43:A5:88:ARG:H	2.14	0.46
28:19:270:ILE:O	28:19:271:ILE:HG23	2.15	0.46
29:29:111:ARG:HB2	29:29:160:TYR:O	2.16	0.46
32:59:20:ALA:CB	32:59:23:ARG:HG3	2.46	0.46
32:59:54:ARG:NH2	32:59:57:ASP:OD1	2.47	0.46
43:A5:59:VAL:HG21	43:A5:66:GLU:HB2	1.98	0.46
46:D5:104:PHE:O	46:D5:105:VAL:HB	2.15	0.46
51:I5:1:MET:HG2	51:I5:3:GLU:HG3	1.98	0.46
55:M5:14:VAL:CG1	55:M5:22:VAL:HG13	2.45	0.46
1:13:142:G:H2'	1:13:143:A:C8	2.51	0.46
1:13:329:A:C5	1:13:332:G:C6	3.04	0.46
1:13:553:A:H5"	12:3I:24:VAL:HG21	1.98	0.46
1:13:818:G:O2'	1:13:819:A:H5'	2.16	0.46
1:13:1075:C:O3'	2:1E:175:ARG:NH2	2.49	0.46
1:13:1523:G:OP1	11:2I:123:LYS:HE3	2.16	0.46
4:3E:143:GLY:N	4:3E:185:PHE:O	2.36	0.46
7:6E:73:MET:HG2	7:6E:90:GLU:HA	1.98	0.46
9:8E:34:ASN:O	9:8E:38:GLN:HB2	2.16	0.46
12:3I:53:ARG:HG3	12:3I:53:ARG:HH11	1.82	0.46
17:8I:66:SER:OG	17:8I:69:LYS:HB2	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1H:120:U:H3'	61:1H:4182:HOH:O	2.16	0.46
26:1H:587:C:N3	36:78:33:ARG:NH1	2.61	0.46
26:1H:890:A:H3'	26:1H:892:G:C8	2.51	0.46
26:1H:1033:U:H6	26:1H:1033:U:H5'	1.80	0.46
26:1H:1173:G:C2	26:1H:1175:U:C5	3.04	0.46
38:98:52:ILE:O	38:98:55:ALA:N	2.49	0.46
40:B8:62:THR:CG2	40:B8:75:ILE:HG12	2.46	0.46
46:H8:165:VAL:HB	46:H8:166:SER:CA	2.45	0.46
50:L8:54:VAL:O	50:L8:54:VAL:HG13	2.16	0.46
1:1G:15:G:H2'	1:1G:16:A:H8	1.81	0.46
1:1G:519:C:H2'	1:1G:520:A:O4'	2.16	0.46
1:1G:719:C:C5	1:1G:720:C:C4	3.04	0.46
1:1G:756:C:H2'	1:1G:757:U:O4'	2.15	0.46
1:1G:854:G:C2	1:1G:855:G:C8	3.04	0.46
1:1G:987:G:O5'	1:1G:987:G:H8	1.99	0.46
1:1G:1245:A:N6	1:1G:1292:U:H3	2.13	0.46
12:3A:58:VAL:O	12:3A:65:GLU:HA	2.15	0.46
17:8A:59:ILE:HG22	17:8A:71:PHE:CD2	2.51	0.46
26:14:993:G:OP1	41:85:50:ARG:NH2	2.49	0.46
26:14:1210:A:H5'	26:14:1212:G:O4'	2.16	0.46
26:14:1486:A:H2'	26:14:1487:G:C8	2.51	0.46
26:14:1647:G:H2'	61:14:3639:HOH:O	2.15	0.46
26:14:2031:A:C6	26:14:2498:C:H1'	2.51	0.46
26:14:2536:G:C6	26:14:2537:U:C4	3.04	0.46
29:29:81:ILE:HG21	29:29:84:PHE:HD2	1.80	0.46
31:49:61:ALA:HB2	31:49:68:PRO:HD3	1.98	0.46
34:15:91:LEU:O	34:15:95:PRO:HB3	2.15	0.46
37:45:66:ILE:HG13	37:45:67:ARG:N	2.30	0.46
42:95:97:LYS:HD2	42:95:97:LYS:HA	1.68	0.46
46:D5:152:ALA:HB3	46:D5:167:PRO:HA	1.96	0.46
1:13:224:C:H2'	1:13:225:C:C6	2.50	0.45
1:13:509:A:H3'	61:13:1946:HOH:O	2.16	0.45
1:13:739:C:C4	1:13:740:U:C5	3.04	0.45
1:13:859:A:H2'	1:13:860:A:H8	1.80	0.45
1:13:901:A:C5	1:13:902:G:H1'	2.52	0.45
1:13:1016:A:H2'	1:13:1017:G:O4'	2.16	0.45
1:13:1165:C:H2'	1:13:1166:G:O4'	2.16	0.45
1:13:1441:G:H21	1:13:1460:A:H62	1.65	0.45
2:1E:94:ASN:OD1	2:1E:95:GLN:N	2.44	0.45
3:2E:62:ASP:N	3:2E:62:ASP:OD1	2.49	0.45
12:3I:53:ARG:HG3	12:3I:93:LEU:HD21	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:8I:48:GLU:O	17:8I:50:LYS:HG2	2.16	0.45
26:1H:930:U:H4'	26:1H:931:G:O5'	2.16	0.45
26:1H:1203:G:OP2	26:1H:1204:A:H2'	2.15	0.45
26:1H:1925:C:C2'	26:1H:1926:U:H5'	2.45	0.45
26:1H:2562:U:H1'	35:68:23:ARG:NH1	2.30	0.45
26:1H:2636:U:P	29:21:79:ARG:HA	2.56	0.45
39:A8:29:PHE:CD1	39:A8:30:ARG:N	2.85	0.45
41:C8:39:LEU:HD23	41:C8:39:LEU:HA	1.62	0.45
1:1G:5:U:O2'	4:32:84:LYS:HG3	2.16	0.45
1:1G:382:A:H2'	1:1G:383:A:H8	1.80	0.45
1:1G:646:U:H2'	1:1G:647:C:C6	2.52	0.45
1:1G:942:G:C2	1:1G:1342:C:C2	3.04	0.45
1:1G:1149:C:H2'	1:1G:1150:U:O4'	2.15	0.45
3:22:70:VAL:HG21	3:22:76:VAL:HG11	1.98	0.45
3:22:73:PRO:O	3:22:77:ILE:HG13	2.16	0.45
4:32:121:VAL:O	4:32:134:ASP:HA	2.14	0.45
6:52:82:ARG:HE	6:52:82:ARG:HB3	1.69	0.45
12:3A:69:TYR:HB2	12:3A:96:VAL:HG11	1.98	0.45
26:14:271(A):C:O2'	26:14:271(B):G:H5'	2.16	0.45
26:14:706:A:H2'	26:14:707:G:O4'	2.16	0.45
26:14:720:C:H2'	26:14:721:C:H6	1.81	0.45
26:14:821:A:H62	26:14:972:G:H21	1.63	0.45
26:14:979:G:H3'	26:14:980:A:H5"	1.97	0.45
26:14:1011:G:C2	26:14:1013:C:C2	3.04	0.45
26:14:1116:C:H2'	26:14:1117:G:H8	1.80	0.45
26:14:1152:C:H4'	41:85:77:SER:HA	1.98	0.45
26:14:1871:A:H2'	26:14:1872:A:C8	2.51	0.45
26:14:1966:A:H4'	26:14:1967:C:OP1	2.16	0.45
26:14:2291:U:H5"	26:14:2380:C:O2'	2.17	0.45
26:14:2299:G:N1	26:14:2318:G:H8	2.15	0.45
26:14:2562:U:H4'	35:25:25:LEU:HD21	1.96	0.45
26:14:2689:U:H5"	26:14:2713:A:C2	2.51	0.45
37:45:117:ALA:HA	37:45:120:ILE:HB	1.98	0.45
40:75:29:ARG:HD3	40:75:44:ASP:OD2	2.15	0.45
41:85:108:GLU:OE1	41:85:112:ARG:NH1	2.49	0.45
45:C5:76:CYS:SG	45:C5:102:CYS:HB2	2.55	0.45
1:13:1075:C:OP1	2:1E:179:LYS:HE2	2.16	0.45
1:13:1443:G:O2'	40:B8:122:ASP:OD2	2.30	0.45
11:2I:43:SER:OG	11:2I:44:SER:N	2.49	0.45
12:3I:70:ILE:HD13	12:3I:77:LEU:HD12	1.97	0.45
24:3K:71:G:N2	26:1H:1852:C:OP1	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1H:59:U:O2'	26:1H:73:A:H2'	2.16	0.45
26:1H:1005:C:O2	26:1H:1005:C:H2'	2.17	0.45
26:1H:1110:G:HO2'	26:1H:1111:A:H8	1.60	0.45
26:1H:1142(A):A:C4	26:1H:1144:G:C8	3.03	0.45
26:1H:1204:A:H2	26:1H:1241:A:N1	2.14	0.45
26:1H:1265:A:O5'	61:1H:3615:HOH:O	2.21	0.45
26:1H:1292:U:H2'	26:1H:1293:C:C6	2.51	0.45
26:1H:1417:C:H42	26:1H:1581:G:H1	1.64	0.45
26:1H:1827:C:O2'	26:1H:1828:G:H5'	2.17	0.45
26:1H:2353:G:O6	26:1H:2365:G:C2	2.70	0.45
27:16:16:G:N2	27:16:69:G:H1'	2.31	0.45
28:11:232:PRO:HB3	28:11:244:ARG:CZ	2.46	0.45
33:61:1:MET:O	33:61:20:ASP:HA	2.16	0.45
38:98:91:GLN:NE2	38:98:91:GLN:H	2.13	0.45
46:H8:120:ILE:HG12	46:H8:172:ALA:HA	1.97	0.45
48:J8:87:PRO:O	48:J8:91:LYS:HB2	2.15	0.45
55:Q8:47:LYS:C	55:Q8:47:LYS:HD3	2.36	0.45
1:1G:273:A:H1'	17:8A:16:GLN:NE2	2.32	0.45
1:1G:1273:G:H3'	1:1G:1274:G:H8	1.81	0.45
1:1G:1306:A:N6	1:1G:1331:G:O2'	2.50	0.45
3:22:40:ARG:H	3:22:40:ARG:HG3	1.40	0.45
3:22:88:ARG:HB2	3:22:101:LEU:HD22	1.97	0.45
6:52:23:LYS:HB3	6:52:23:LYS:HE2	1.79	0.45
7:62:50:ILE:O	7:62:54:THR:HG23	2.16	0.45
8:72:97:VAL:HG22	8:72:129:VAL:C	2.41	0.45
11:2A:85:ARG:HA	11:2A:112:THR:OG1	2.15	0.45
16:7A:21:VAL:HG23	16:7A:33:ILE:HD12	1.98	0.45
17:8A:67:LYS:O	17:8A:68:ARG:HB3	2.16	0.45
26:14:329:G:OP2	45:C5:71:LYS:HD3	2.15	0.45
26:14:533:G:H2'	26:14:534:U:O4'	2.17	0.45
26:14:602:G:N2	26:14:655:A:C8	2.85	0.45
26:14:745:G:H2'	26:14:746:A:H5'	1.97	0.45
26:14:827:U:H2'	26:14:2430:A:H2	1.81	0.45
26:14:1385:G:C4	26:14:1386:C:C5	3.04	0.45
26:14:1676:A:OP2	61:14:3537:HOH:O	2.20	0.45
26:14:2414:G:H21	36:35:67:MET:CE	2.16	0.45
27:1J:2:C:H2'	27:1J:3:C:C6	2.51	0.45
31:49:68:PRO:HB2	31:49:90:LEU:HD12	1.97	0.45
34:15:47:ALA:O	34:15:119:ARG:NH2	2.49	0.45
46:D5:126:VAL:HA	46:D5:163:LEU:HA	1.98	0.45
55:M5:51:ALA:O	55:M5:52:LYS:HD3	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:13:22:G:H4'	1:13:885:G:C8	2.50	0.45
1:13:645:C:P	61:13:1972:HOH:O	2.73	0.45
1:13:741:G:H2'	1:13:742:G:O4'	2.15	0.45
1:13:933:G:OP2	7:6E:3:ARG:HB2	2.17	0.45
1:13:1139:G:H4'	1:13:1140:C:H5'	1.98	0.45
2:1E:4:GLU:OE2	2:1E:5:ILE:HG12	2.16	0.45
2:1E:21:ARG:C	2:1E:23:ARG:H	2.25	0.45
3:2E:142:MET:SD	3:2E:148:GLY:HA2	2.56	0.45
16:7I:5:ARG:HB3	16:7I:67:THR:OG1	2.16	0.45
24:3K:25:C:C4	24:3K:26:A:C8	3.05	0.45
26:1H:71:A:OP1	26:1H:72:U:H2'	2.16	0.45
26:1H:1528:A:N6	26:1H:1529:A:N1	2.64	0.45
26:1H:1889:A:N1	26:1H:2234:G:H1'	2.31	0.45
26:1H:2065:C:H2'	26:1H:2066:C:C6	2.51	0.45
26:1H:2341:G:H2'	26:1H:2342:C:H6	1.81	0.45
27:16:61:G:C6	27:16:62:C:C4	3.04	0.45
28:11:27:THR:HG23	28:11:28:GLU:HG2	1.98	0.45
28:11:70:TRP:CD1	28:11:70:TRP:O	2.69	0.45
45:G8:97:ARG:HD2	45:G8:97:ARG:N	2.30	0.45
46:H8:7:ALA:HB3	46:H8:61:LEU:HB3	1.97	0.45
46:H8:67:LEU:HD22	46:H8:90:VAL:HG11	1.98	0.45
1:1G:254:G:OP1	17:8A:67:LYS:O	2.34	0.45
1:1G:1068:G:N3	1:1G:1191:A:C2	2.85	0.45
3:22:84:ILE:HG12	3:22:88:ARG:NH2	2.31	0.45
3:22:121:ALA:HB2	3:22:198:VAL:HG21	1.99	0.45
5:42:10:MET:HE1	5:42:13:ILE:HD11	1.98	0.45
5:42:19:MET:HG3	5:42:20:GLN:N	2.30	0.45
7:62:131:LYS:NZ	7:62:131:LYS:HB3	2.30	0.45
11:2A:29:ILE:HG22	11:2A:44:SER:CB	2.34	0.45
11:2A:100:ALA:C	11:2A:102:GLY:H	2.24	0.45
13:4A:17:VAL:O	13:4A:20:THR:OG1	2.29	0.45
18:9A:29:PHE:N	18:9A:29:PHE:CD1	2.83	0.45
26:14:139:G:N2	26:14:141:A:N1	2.61	0.45
26:14:142:G:H2'	26:14:143:C:C6	2.51	0.45
26:14:2070:G:C2	26:14:2442:C:C2	3.04	0.45
26:14:2531:A:C2'	26:14:2532:G:H5'	2.46	0.45
26:14:2615:U:C2	52:J5:7:PRO:HA	2.52	0.45
26:14:2851:A:H2'	26:14:2852:G:O4'	2.16	0.45
29:29:8:LYS:HB3	29:29:192:ASN:HA	1.99	0.45
29:29:182:LEU:HD12	29:29:182:LEU:HA	1.69	0.45
32:59:82:GLY:HA3	32:59:135:GLY:O	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:69:129:THR:HA	33:69:137:PRO:HA	1.99	0.45
39:65:36:TYR:HA	39:65:52:SER:HB3	1.99	0.45
45:C5:86:ARG:NE	45:C5:87:LYS:O	2.47	0.45
48:F5:95:LEU:HD23	48:F5:95:LEU:HA	1.77	0.45
55:M5:29:LYS:HB3	55:M5:44:LYS:CB	2.46	0.45
1:13:448:A:P	1:13:485:G:H22	2.38	0.45
1:13:554:C:O2'	1:13:555:C:H5'	2.17	0.45
1:13:1319:A:OP2	19:AI:5:LEU:HD22	2.17	0.45
4:3E:107:ARG:NH1	4:3E:114:ARG:HH22	2.14	0.45
9:8E:112:LYS:HE3	9:8E:117:HIS:O	2.16	0.45
19:AI:37:ARG:H	19:AI:37:ARG:HG3	1.35	0.45
22:1K:60:U:H5'	22:1K:61:C:OP2	2.16	0.45
26:1H:184:C:H2'	26:1H:185:U:C6	2.51	0.45
26:1H:588:U:C2	30:31:90:PHE:CE1	3.04	0.45
26:1H:705:A:C8	26:1H:727:A:C2	3.05	0.45
26:1H:784:A:C5	28:11:229:VAL:HG21	2.51	0.45
26:1H:1071:G:H8	26:1H:1071:G:O5'	1.98	0.45
26:1H:1417:C:O5'	61:1H:4059:HOH:O	2.20	0.45
26:1H:2032:G:N2	29:21:146:THR:HG23	2.30	0.45
26:1H:2388:A:H2'	26:1H:2389:G:H5'	1.99	0.45
27:16:41:U:H5	31:41:70:VAL:O	1.99	0.45
28:11:68:LYS:HB3	28:11:70:TRP:CH2	2.52	0.45
33:61:10:GLU:HG3	33:61:10:GLU:O	2.16	0.45
33:61:139:GLN:C	33:61:140:LEU:HG	2.41	0.45
37:88:5:ARG:O	37:88:6:ARG:C	2.59	0.45
40:B8:20:PRO:HG2	40:B8:86:ILE:O	2.16	0.45
40:B8:29:ARG:HB2	40:B8:46:GLU:HG3	1.97	0.45
1:1G:186(A):C:H2'	1:1G:186(B):C:C6	2.51	0.45
1:1G:197:A:C6	1:1G:221:C:H4'	2.50	0.45
1:1G:728:A:C2	1:1G:729:A:C5	3.04	0.45
1:1G:1250:A:H4'	9:82:68:GLY:N	2.31	0.45
1:1G:1443:G:H22	40:75:119:LYS:HB2	1.80	0.45
6:52:8:ILE:N	6:52:8:ILE:HD12	2.31	0.45
21:1B:9:ARG:NE	21:1B:10:ARG:HG3	2.32	0.45
23:2L:14:A:C2	23:2L:23:G:C4	3.05	0.45
57:3L:15:G:H1	57:3L:48:C:H42	1.65	0.45
57:3L:15:G:H1	57:3L:48:C:N4	2.14	0.45
26:14:162:U:H4'	26:14:171:G:C4	2.51	0.45
26:14:336:C:OP1	45:C5:83:THR:HG23	2.15	0.45
26:14:528:A:H2	26:14:2043:C:H5'	1.81	0.45
26:14:952:G:C6	26:14:966:G:C6	3.05	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:14:1000:A:N6	26:14:1001:A:N1	2.65	0.45
26:14:1001:A:C8	26:14:1002:G:C8	3.04	0.45
26:14:1226:G:H5'	42:95:85:LYS:H	1.82	0.45
26:14:1359:A:H5'	26:14:1359:A:H8	1.81	0.45
26:14:2312:U:H3'	26:14:2312:U:H6	1.82	0.45
26:14:2394:C:P	36:35:63:PRO:HD2	2.56	0.45
34:15:34:LEU:HD21	34:15:120:LEU:CD1	2.46	0.45
36:35:59:LEU:HD21	55:M5:10:ALA:HA	1.98	0.45
42:95:12:TYR:OH	42:95:22:VAL:HG23	2.17	0.45
45:C5:86:ARG:HG3	45:C5:87:LYS:N	2.31	0.45
48:F5:76:ARG:HG3	48:F5:94:LEU:HD13	1.97	0.45
51:I5:18:CYS:SG	51:I5:19:GLY:HA2	2.57	0.45
51:I5:23:GLU:C	51:I5:24:THR:HG1	2.23	0.45
1:13:141:A:H2'	1:13:142:G:C8	2.49	0.45
1:13:148:G:H2'	1:13:149:A:H8	1.81	0.45
1:13:320:C:H42	1:13:333:G:H1	1.64	0.45
1:13:345:C:H5'	1:13:346:G:OP1	2.16	0.45
1:13:606:G:N2	1:13:632:A:N1	2.60	0.45
1:13:1151:A:O2'	1:13:1152:A:O5'	2.31	0.45
2:1E:11:LEU:O	2:1E:16:HIS:NE2	2.50	0.45
2:1E:91:PRO:HB3	2:1E:154:LEU:HB2	1.99	0.45
2:1E:178:ARG:HG3	8:7E:72:PRO:HA	1.98	0.45
2:1E:182:ILE:HA	2:1E:183:PRO:HD3	1.85	0.45
5:4E:6:PHE:HE1	5:4E:36:ASP:HB3	1.80	0.45
8:7E:87:SER:CB	8:7E:93:VAL:H	2.28	0.45
22:1K:62:C:H2'	22:1K:63:G:C8	2.51	0.45
26:1H:37:C:O2'	26:1H:38:A:H5'	2.17	0.45
26:1H:729:G:O4'	28:11:208:LYS:NZ	2.49	0.45
26:1H:880:G:O2'	26:1H:881:G:O5'	2.26	0.45
26:1H:1226:G:P	42:D8:69:LYS:HZ2	2.34	0.45
26:1H:2062:A:N6	26:1H:2503:A:H62	2.14	0.45
26:1H:2131:G:H5"	26:1H:2133:G:H4'	1.98	0.45
26:1H:2291:U:OP1	26:1H:2380:C:O2'	2.29	0.45
26:1H:2789:C:H1'	26:1H:2892:A:H2	1.80	0.45
29:21:32:PRO:HD2	29:21:50:GLY:O	2.16	0.45
36:78:38:GLN:O	36:78:44:GLY:HA2	2.17	0.45
36:78:71:VAL:CG1	36:78:72:PRO:HD3	2.46	0.45
37:88:85:LYS:CG	37:88:86:GLY:H	2.29	0.45
45:G8:83:THR:HG22	45:G8:84:ARG:HG3	1.98	0.45
46:H8:174:VAL:O	46:H8:175:VAL:HG23	2.17	0.45
1:1G:108:G:H5'	1:1G:109:A:C5'	2.45	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1G:890:G:O2'	1:1G:906:G:O6	2.28	0.45
3:22:11:ARG:HB2	3:22:11:ARG:NH1	2.31	0.45
6:52:69:GLU:O	6:52:72:VAL:HG12	2.16	0.45
7:62:95:ARG:HH21	7:62:99:LEU:HD11	1.80	0.45
12:3A:89:ARG:HG3	12:3A:97:ARG:HG2	1.99	0.45
13:4A:97:PRO:HA	13:4A:110:ARG:HD3	1.97	0.45
21:1B:6:ARG:HD3	21:1B:15:ARG:NH2	2.32	0.45
57:3L:72:C:C3'	57:3L:73:A:H5"	2.46	0.45
26:14:81:G:O6	61:14:3767:HOH:O	2.21	0.45
26:14:240:G:O2'	26:14:257:A:N6	2.44	0.45
26:14:651:G:H5'	55:M5:18:ALA:HB3	1.98	0.45
26:14:654:A:H8	26:14:654:A:OP1	1.99	0.45
26:14:829:A:N7	26:14:2247:A:O2'	2.46	0.45
26:14:1248:G:C5	41:85:3:ARG:HB2	2.52	0.45
26:14:2185:C:H2'	26:14:2186:G:C8	2.51	0.45
26:14:2616:C:C2'	26:14:2617:C:H5'	2.47	0.45
28:19:131:LEU:HB2	28:19:136:ILE:HD11	1.97	0.45
28:19:148:GLU:CB	28:19:151:LYS:HE3	2.44	0.45
45:C5:67:LEU:HD12	45:C5:67:LEU:HA	1.74	0.45
46:D5:94:GLU:O	46:D5:129:SER:HA	2.15	0.45
51:I5:9:LEU:HD22	51:I5:9:LEU:H	1.81	0.45
55:M5:60:LEU:HB2	55:M5:61:LEU:H	1.35	0.45
1:13:827:U:H5"	1:13:828:A:OP2	2.15	0.45
1:13:963:G:H5'	61:13:1902:HOH:O	2.15	0.45
1:13:1350:A:C5	1:13:1351:U:C4	3.05	0.45
3:2E:57:ILE:HG12	3:2E:66:VAL:HG22	1.97	0.45
10:1I:47:PHE:CZ	14:5I:37:PHE:HE2	2.35	0.45
13:4I:52:GLU:O	13:4I:56:LEU:HB2	2.16	0.45
13:4I:67:GLU:HG3	13:4I:71:ARG:HH21	1.82	0.45
16:7I:26:ARG:NE	16:7I:31:LYS:HB3	2.31	0.45
24:3K:19:G:N2	26:1H:2112:G:H21	2.14	0.45
24:3K:72:C:C3'	24:3K:73:A:H5"	2.40	0.45
26:1H:152:G:H2'	26:1H:153:C:C6	2.50	0.45
26:1H:739:G:P	61:1H:4509:HOH:O	2.74	0.45
26:1H:906:G:OP1	37:88:26:TYR:OH	2.31	0.45
26:1H:930:U:O2	26:1H:930:U:O4'	2.32	0.45
26:1H:1310:G:OP2	54:P8:9:ARG:HD2	2.15	0.45
26:1H:1778:U:P	61:1H:4513:HOH:O	2.75	0.45
26:1H:2396:G:H5"	48:J8:25:LYS:HE3	1.99	0.45
30:31:28:ILE:HG21	30:31:116:ASP:HB2	1.98	0.45
30:31:140:LEU:HD12	30:31:140:LEU:HA	1.77	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:78:39:LYS:CA	36:78:45:LEU:HD13	2.47	0.45
40:B8:118:ARG:HH21	40:B8:121:ILE:HG21	1.81	0.45
48:J8:23:LYS:HG2	48:J8:29:GLY:HA3	1.98	0.45
1:1G:41:G:H2'	1:1G:42:G:H8	1.80	0.45
1:1G:619:U:C5	4:32:135:LEU:HD21	2.51	0.45
1:1G:1509:C:H2'	1:1G:1510:U:O4'	2.17	0.45
4:32:150:GLU:HA	4:32:153:ARG:HG2	1.97	0.45
8:72:20:TYR:HA	8:72:65:TYR:CE2	2.52	0.45
57:3L:31:A:H5'	57:3L:32:PSU:OP2	2.17	0.45
26:14:128:C:H2'	26:14:129:C:H6	1.82	0.45
26:14:360:G:H2'	26:14:361:G:H8	1.81	0.45
26:14:607:U:N3	26:14:621:A:C2	2.78	0.45
26:14:819:A:C4	26:14:1189:A:C2	3.04	0.45
26:14:1796:U:H2'	26:14:1797:C:C6	2.52	0.45
26:14:2212:A:O2'	26:14:2213:U:O5'	2.32	0.45
26:14:2302:G:C4	26:14:2303:G:C8	3.05	0.45
27:1J:18:G:H1	27:1J:65:C:N4	2.07	0.45
38:55:38:VAL:HG22	38:55:112:ALA:HB2	1.99	0.45
40:75:53:ARG:HG3	40:75:53:ARG:O	2.17	0.45
44:B5:65:ARG:HG3	44:B5:67:GLY:N	2.26	0.45
45:C5:87:LYS:HB3	45:C5:94:LYS:HA	1.99	0.45
1:13:109:A:N7	1:13:326:G:H2'	2.32	0.45
1:13:115:G:C2	1:13:289:G:N7	2.85	0.45
1:13:153:C:H42	1:13:168:G:H22	1.65	0.45
1:13:721:G:C6	1:13:733:A:C2	3.05	0.45
1:13:1272:G:C6	1:13:1273:G:C5	3.05	0.45
1:13:1366:C:H2'	1:13:1367:C:H6	1.82	0.45
5:4E:142:LEU:C	5:4E:143:ARG:HG2	2.42	0.45
23:2K:16:C:O2'	23:2K:62:C:OP1	2.30	0.45
26:1H:3:U:H3	26:1H:2900:A:H61	1.65	0.45
26:1H:3:U:OP1	26:1H:2790:A:N6	2.50	0.45
26:1H:280:C:C2	26:1H:361:G:N2	2.85	0.45
26:1H:317:G:C2	26:1H:318:C:C2	3.05	0.45
26:1H:710:G:H2'	26:1H:711:G:C8	2.51	0.45
26:1H:821:A:H5"	26:1H:822:U:C6	2.52	0.45
26:1H:1940:U:C4	26:1H:1964:G:H4'	2.52	0.45
26:1H:1969:A:O2'	26:1H:1972:A:N3	2.48	0.45
26:1H:2002:G:C5	61:1H:4267:HOH:O	2.69	0.45
27:16:2:C:H2'	27:16:3:C:C6	2.52	0.45
40:B8:111:ARG:O	40:B8:112:ARG:HB3	2.16	0.45
45:G8:12:THR:OG1	45:G8:26:LYS:NZ	2.39	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:M8:2:LYS:HD3	51:M8:2:LYS:HA	1.89	0.45
53:O8:51:GLU:HG2	53:O8:52:VAL:N	2.32	0.45
1:1G:19:C:H5"	5:42:86:ALA:HB3	1.98	0.45
1:1G:421:U:O2'	1:1G:423:G:N7	2.48	0.45
1:1G:1028(A):C:H42	1:1G:1032(B):G:H1	1.65	0.45
1:1G:1497:G:O2'	1:1G:1498:U:H5'	2.17	0.45
3:22:40:ARG:O	3:22:44:GLU:N	2.49	0.45
3:22:113:ALA:HB3	3:22:114:PRO:HD3	1.97	0.45
4:32:18:LYS:H	4:32:33:MET:HE2	1.81	0.45
4:32:173:TRP:HZ3	4:32:193:ASP:HB3	1.82	0.45
8:72:86:ILE:HD11	8:72:136:GLU:HG2	1.99	0.45
9:82:3:GLN:C	9:82:4:TYR:HD1	2.25	0.45
12:3A:110:VAL:CG2	12:3A:120:TYR:HB3	2.47	0.45
13:4A:53:VAL:HG11	13:4A:57:ARG:HH21	1.81	0.45
15:6A:50:HIS:O	15:6A:53:HIS:HB3	2.16	0.45
20:BA:73:HIS:C	20:BA:74:LYS:HG2	2.42	0.45
26:14:483:A:C5'	45:C5:49:VAL:HG22	2.47	0.45
26:14:1028:A:N6	26:14:1125:G:H2'	2.32	0.45
26:14:1572:A:H2'	26:14:1573:G:O4'	2.16	0.45
26:14:2292:C:H4'	26:14:2375:G:H4'	1.99	0.45
29:29:33:VAL:HG11	29:29:36:ARG:NH2	2.32	0.45
30:39:146:ALA:HB1	30:39:148:LEU:HG	1.99	0.45
36:35:64:LYS:HB3	55:M5:30:ARG:HH22	1.81	0.45
41:85:28:ARG:HD3	41:85:38:THR:OG1	2.17	0.45
1:13:652:U:C4	1:13:752:G:N3	2.85	0.45
1:13:868:C:H2'	1:13:869:G:O4'	2.16	0.45
1:13:1316:G:N2	1:13:1318:A:H3'	2.32	0.45
2:1E:87:ARG:HH11	2:1E:233:SER:HB2	1.82	0.45
3:2E:151:VAL:HA	3:2E:199:LYS:O	2.16	0.45
7:6E:15:ASP:OD1	7:6E:16:LEU:N	2.50	0.45
7:6E:111:ARG:HD2	7:6E:123:GLU:HB2	1.99	0.45
12:3I:85:ILE:HG23	12:3I:85:ILE:HD12	1.69	0.45
26:1H:546:C:C4	26:1H:547:A:C6	3.04	0.45
26:1H:1219:G:OP2	41:C8:19:LYS:NZ	2.50	0.45
26:1H:1431:U:C2	26:1H:1563:G:N2	2.85	0.45
26:1H:1590:U:H2'	26:1H:1591:G:H8	1.80	0.45
30:31:112:MET:HE3	30:31:112:MET:HB3	1.42	0.45
32:51:15:VAL:HG12	32:51:28:GLY:HA3	1.98	0.45
34:58:41:ASP:C	41:C8:64:ARG:HD2	2.42	0.45
48:J8:85:LEU:HA	48:J8:87:PRO:HD2	1.98	0.45
50:L8:2:PRO:HB2	50:L8:3:ARG:H	1.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:M8:16:CYS:HG	51:M8:36:CYS:HG	1.64	0.45
1:1G:1004:A:H2	1:1G:1024:G:C8	2.34	0.45
1:1G:1028(A):C:H5	1:1G:1029:G:C5	2.34	0.45
1:1G:1040:U:H2'	1:1G:1041:A:H8	1.82	0.45
1:1G:1082:G:H8	1:1G:1082:G:OP2	2.00	0.45
1:1G:1210:C:H3'	1:1G:1211:U:H5"	1.98	0.45
2:12:77:ALA:O	2:12:81:VAL:HG23	2.15	0.45
6:52:15:ASP:OD1	6:52:18:GLN:N	2.42	0.45
7:62:16:LEU:HD11	9:82:42:ARG:HA	1.99	0.45
26:14:58:G:OP1	44:B5:75:ASP:HB2	2.15	0.45
26:14:274:G:C2'	26:14:275:G:H4'	2.42	0.45
26:14:375:C:H2'	26:14:376:C:C6	2.52	0.45
26:14:654(S):G:C2	26:14:654(T):A:C6	3.05	0.45
26:14:690:G:H2'	26:14:691:C:C6	2.51	0.45
26:14:729:G:C6	28:19:208:LYS:HB2	2.52	0.45
26:14:745:G:C2'	26:14:746:A:H5'	2.47	0.45
26:14:1184:G:C6	26:14:1185:C:C4	3.04	0.45
26:14:1336:A:H2'	26:14:1337:G:C8	2.51	0.45
26:14:1421:G:C2	26:14:1422:G:C8	3.04	0.45
26:14:1461:G:H2'	26:14:1462:C:C6	2.51	0.45
26:14:1628:G:H2'	26:14:1629:U:C6	2.51	0.45
26:14:1628:G:H2'	26:14:1629:U:H6	1.81	0.45
26:14:2078:C:C4	26:14:2079:U:C4	3.05	0.45
26:14:2520:C:H41	26:14:2542:A:N6	2.15	0.45
26:14:2562:U:H1'	35:25:23:ARG:NE	2.32	0.45
26:14:2849:U:H4'	26:14:2868:A:C2	2.52	0.45
28:19:16:MET:HG3	28:19:206:LEU:O	2.17	0.45
31:49:63:ILE:HD12	31:49:141:PHE:CD2	2.52	0.45
35:25:64:ARG:HH12	40:75:70:VAL:HG21	1.81	0.45
38:55:37:THR:OG1	38:55:40:LYS:HG3	2.17	0.45
38:55:70:LEU:HD23	38:55:70:LEU:HA	1.77	0.45
39:65:88:ASP:O	39:65:89:ARG:HB3	2.16	0.45
43:A5:17:VAL:O	43:A5:20:VAL:HG22	2.15	0.45
51:I5:12:ALA:HB1	51:I5:29:PRO:HA	1.99	0.45
54:L5:19:ARG:HG2	54:L5:19:ARG:HH11	1.81	0.45
1:13:346:G:H3'	1:13:346:G:N3	2.32	0.45
1:13:465:A:H2'	1:13:466:C:H5"	1.98	0.45
1:13:982:U:H4'	1:13:983:A:O5'	2.16	0.45
1:13:1014:A:H4'	19:AI:14:HIS:ND1	2.31	0.45
1:13:1022:G:H2'	1:13:1023:G:H8	1.82	0.45
1:13:1192:C:OP2	3:2E:4:LYS:NZ	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:4I:49:THR:C	13:4I:51:ALA:N	2.73	0.45
26:1H:102:G:OP1	49:K8:7:ARG:NH2	2.50	0.45
26:1H:274:G:H3'	26:1H:274:G:C8	2.52	0.45
26:1H:534:U:H5'	41:C8:42:ALA:HB1	1.99	0.45
26:1H:937:U:H2'	26:1H:938:G:O4'	2.17	0.45
26:1H:1337:G:H2'	26:1H:1338:G:C8	2.51	0.45
26:1H:1871:A:H2'	26:1H:1872:A:C8	2.52	0.45
26:1H:2663:G:C6	26:1H:2664:G:C4	3.04	0.45
30:31:89:VAL:HG12	30:31:90:PHE:CD2	2.51	0.45
30:31:130:ALA:H	30:31:132:VAL:HG13	1.81	0.45
31:41:107:LEU:O	51:M8:38:LYS:HD3	2.17	0.45
36:78:39:LYS:CG	36:78:45:LEU:HD22	2.47	0.45
44:F8:35:THR:N	44:F8:38:GLU:OE1	2.50	0.45
50:L8:46:ASN:O	50:L8:50:VAL:HG22	2.17	0.45
55:Q8:21:LYS:HD2	55:Q8:21:LYS:HA	1.59	0.45
55:Q8:34:TRP:CD1	55:Q8:35:GLN:N	2.85	0.45
1:1G:34:C:H2'	1:1G:35:G:H8	1.82	0.45
1:1G:596:C:H2'	1:1G:597:G:C8	2.51	0.45
1:1G:1171:G:H2'	1:1G:1172:C:H6	1.81	0.45
3:22:29:TYR:O	3:22:33:LEU:HB2	2.16	0.45
3:22:36:ASP:HA	3:22:39:ILE:HD12	1.99	0.45
9:82:112:LYS:HA	9:82:119:ALA:CB	2.39	0.45
23:2L:17:C:H3'	23:2L:18:C:H2'	1.99	0.45
23:2L:66:C:O2'	23:2L:67:C:H5'	2.17	0.45
26:14:675:A:N6	26:14:676:A:N6	2.65	0.45
26:14:818:G:H5'	26:14:839:U:OP1	2.17	0.45
26:14:1019:U:OP1	26:14:1035:U:O2'	2.25	0.45
26:14:1316:U:O2'	26:14:1317:A:H5'	2.17	0.45
26:14:1399:C:O2'	26:14:1400:G:H5'	2.17	0.45
26:14:1588:C:H5'	26:14:1589:C:OP2	2.17	0.45
26:14:1614:A:H61	43:A5:88:ARG:H	1.63	0.45
26:14:1652:A:OP1	38:55:8:ARG:NH1	2.50	0.45
26:14:1757:U:N3	26:14:1762:A:H2	2.03	0.45
26:14:1828:G:P	61:14:3570:HOH:O	2.70	0.45
26:14:2558:C:H2'	26:14:2559:C:O4'	2.17	0.45
26:14:2729:G:H2'	26:14:2730:C:C6	2.52	0.45
27:1J:40:U:O2'	27:1J:45:A:N6	2.34	0.45
29:29:81:ILE:HG21	29:29:84:PHE:CD2	2.52	0.45
30:39:116:ASP:O	30:39:120:GLU:HG2	2.17	0.45
30:39:168:ARG:HG3	30:39:175:THR:HG21	1.99	0.45
32:59:73:ALA:O	32:59:76:VAL:HB	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:69:109:ILE:HB	33:69:130:TYR:OH	2.17	0.45
35:25:63:VAL:O	35:25:64:ARG:HG3	2.17	0.45
43:A5:33:ARG:NE	43:A5:52:GLU:OE2	2.46	0.45
1:13:532:A:H2	1:13:1206:G:H21	1.64	0.45
1:13:963:G:C2	10:1I:55:LYS:NZ	2.83	0.45
1:13:1284:C:H2'	1:13:1285:A:N7	2.31	0.45
7:6E:79:ARG:NH1	7:6E:82:GLY:O	2.50	0.45
10:1I:16:LEU:HD12	10:1I:68:HIS:HB2	1.99	0.45
14:5I:3:ARG:O	14:5I:7:ILE:HG23	2.17	0.45
16:7I:72:ARG:O	16:7I:72:ARG:HG2	2.15	0.45
26:1H:443:A:N7	30:31:45:ARG:HG2	2.32	0.45
26:1H:1826:G:H4'	28:11:242:ARG:CZ	2.47	0.45
26:1H:1827:C:C2'	26:1H:1828:G:H5'	2.47	0.45
26:1H:1931:U:H5	26:1H:1969:A:N7	2.15	0.45
26:1H:2699:C:H2'	26:1H:2700:C:O4'	2.17	0.45
26:1H:2715:C:O2'	26:1H:2716:U:H5'	2.17	0.45
28:11:69:ARG:HG3	28:11:69:ARG:NH1	2.31	0.45
29:21:11:MET:HE2	29:21:11:MET:HB3	1.86	0.45
32:51:154:PRO:HB3	32:51:163:TYR:CZ	2.52	0.45
33:61:47:LEU:HA	33:61:50:ARG:HB2	1.98	0.45
37:88:43:THR:HG22	37:88:94:VAL:HG12	1.99	0.45
38:98:33:ARG:HD2	38:98:115:GLU:OE1	2.16	0.45
43:E8:33:ARG:NE	43:E8:52:GLU:OE1	2.30	0.45
47:I8:56:ASP:OD1	47:I8:58:THR:HB	2.17	0.45
49:K8:18:PRO:O	49:K8:22:GLU:HG3	2.17	0.45
1:1G:428:G:O4'	1:1G:430:A:C8	2.70	0.45
1:1G:600:C:H2'	1:1G:601:C:H6	1.79	0.45
1:1G:641:U:O3'	1:1G:642:A:H8	2.00	0.45
1:1G:1158:C:H2'	1:1G:1158:C:O2	2.16	0.45
1:1G:1428:A:H2'	1:1G:1429:C:C6	2.51	0.45
14:5A:26:ARG:O	14:5A:26:ARG:HG2	2.16	0.45
56:1L:11:C:H2'	56:1L:12:U:O4'	2.17	0.45
26:14:172:C:H2'	26:14:173:G:H8	1.82	0.45
26:14:288:C:H2'	26:14:289:A:C8	2.52	0.45
26:14:1268:A:H2'	26:14:1269:A:O4'	2.16	0.45
26:14:1607:C:H4'	26:14:1608:A:O5'	2.17	0.45
26:14:2019:A:N7	52:J5:9:LYS:HD2	2.32	0.45
26:14:2128:C:C4	26:14:2129:C:C4	3.05	0.45
26:14:2791:C:H42	26:14:2805:G:H1	1.65	0.45
26:14:2887:U:H2'	26:14:2888:C:H6	1.81	0.45
28:19:255:LYS:H	28:19:255:LYS:HZ1	1.65	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:29:203:LYS:C	29:29:205:ALA:H	2.25	0.45
32:59:18:GLU:HG3	32:59:25:LYS:HD2	1.99	0.45
33:69:70:GLU:O	33:69:74:ASN:ND2	2.50	0.45
36:35:144:GLU:CD	36:35:144:GLU:N	2.75	0.45
43:A5:50:VAL:HG22	43:A5:105:VAL:HG23	1.98	0.45
46:D5:24:LEU:HD12	46:D5:25:PRO:O	2.16	0.45
46:D5:40:ASP:OD2	46:D5:43:GLU:HG2	2.16	0.45
46:D5:59:LEU:HB3	46:D5:60:GLU:H	1.56	0.45
47:E5:27:GLU:HB2	47:E5:69:PHE:HD1	1.82	0.45
1:13:390:C:H2'	1:13:391:G:C8	2.52	0.44
1:13:588:G:H5"	8:7E:5:PRO:HG3	1.99	0.44
1:13:939:G:C6	1:13:940:C:N4	2.85	0.44
1:13:1176:A:N1	1:13:1177:G:C6	2.85	0.44
2:1E:174:VAL:HG13	2:1E:184:VAL:HG11	1.99	0.44
5:4E:80:ILE:HG12	5:4E:81:GLU:H	1.82	0.44
6:5E:23:LYS:HB2	6:5E:23:LYS:HZ3	1.80	0.44
22:1K:38:A:H5'	26:1H:1913:A:C6	2.52	0.44
26:1H:41:C:H42	26:1H:438:G:H1	1.65	0.44
26:1H:847:U:H5	26:1H:933:A:N1	2.16	0.44
26:1H:1022:G:O6	34:58:66:LYS:NZ	2.48	0.44
26:1H:1241:A:N3	26:1H:1241:A:O4'	2.49	0.44
26:1H:1878:G:H2'	26:1H:1879:C:C6	2.52	0.44
26:1H:2601:C:H3'	61:1H:4432:HOH:O	2.17	0.44
26:1H:2734:A:H8	26:1H:2734:A:H5"	1.83	0.44
26:1H:2749:A:H1'	32:51:63:SER:OG	2.17	0.44
27:16:112:G:H2'	27:16:113:C:C6	2.52	0.44
29:21:197:ILE:HD11	29:21:199:ARG:HE	1.83	0.44
31:41:173:LEU:HD22	31:41:178:PHE:CE2	2.52	0.44
35:68:64:ARG:HG2	35:68:79:PHE:CD2	2.51	0.44
37:88:3:MET:HG2	37:88:4:PRO:O	2.17	0.44
37:88:59:ARG:C	37:88:61:GLY:N	2.74	0.44
40:B8:6:LEU:HD13	40:B8:9:LEU:HB3	1.99	0.44
46:H8:77:ASP:N	46:H8:84:GLU:HG2	2.32	0.44
1:1G:15:G:C4	1:1G:16:A:C8	3.05	0.44
1:1G:434:U:H2'	1:1G:435:C:C6	2.52	0.44
1:1G:559:A:H4'	1:1G:560:U:H5"	1.99	0.44
1:1G:942:G:C2	1:1G:1342:C:O2	2.69	0.44
1:1G:1023:G:H3'	1:1G:1024:G:H5"	1.99	0.44
1:1G:1105:A:H2'	1:1G:1106:G:H8	1.81	0.44
5:42:79:GLU:OE1	8:72:104:ARG:HA	2.17	0.44
8:72:8:ASP:OD2	8:72:12:ARG:NH1	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:4A:29:ARG:HB3	13:4A:64:TRP:CZ2	2.52	0.44
16:7A:1:MET:HB2	16:7A:1:MET:HE3	1.32	0.44
18:9A:41:LYS:O	18:9A:41:LYS:HD3	2.17	0.44
57:3L:26:A:H3'	57:3L:27:G:C8	2.50	0.44
57:3L:36:A:C6	25:4L:14:A:C2	3.04	0.44
57:3L:67:C:H2'	57:3L:68:C:C6	2.52	0.44
26:14:110:G:C2	26:14:111:A:C8	3.05	0.44
26:14:248:G:H2'	61:14:3514:HOH:O	2.17	0.44
26:14:953:A:H2'	26:14:954:G:H8	1.82	0.44
26:14:996:A:C2	26:14:997:G:C8	3.04	0.44
26:14:1021:A:H62	26:14:1141:U:H3	1.64	0.44
26:14:1054:A:H2'	26:14:1055:G:H8	1.81	0.44
26:14:1204:A:O2'	26:14:1205:U:OP2	2.34	0.44
26:14:1328:G:H2'	26:14:1330:C:C4	2.52	0.44
26:14:1459:G:O2'	26:14:1460:A:H5'	2.17	0.44
26:14:1758:G:C2	26:14:2696:U:H5'	2.51	0.44
26:14:1949:G:O6	61:14:3903:HOH:O	2.20	0.44
26:14:1973:G:H2'	26:14:1974:C:C6	2.53	0.44
26:14:2123:G:H22	26:14:2175:C:H42	1.65	0.44
26:14:2238:G:H2'	26:14:2238:G:N3	2.32	0.44
28:19:176:ARG:HG2	28:19:176:ARG:HH11	1.82	0.44
29:29:62:PRO:C	29:29:64:LYS:H	2.24	0.44
29:29:89:ASP:CG	29:29:90:THR:H	2.16	0.44
30:39:9:ILE:HG23	30:39:11:VAL:O	2.16	0.44
30:39:205:ARG:HB2	30:39:205:ARG:NH1	2.32	0.44
38:55:29:LEU:HD23	38:55:70:LEU:HD11	1.98	0.44
38:55:79:LEU:HA	38:55:83:ILE:HB	1.98	0.44
39:65:67:ARG:O	39:65:71:ARG:N	2.40	0.44
40:75:4:GLY:O	40:75:5:ALA:C	2.60	0.44
42:95:71:LEU:HD13	42:95:71:LEU:HA	1.47	0.44
46:D5:30:ASN:HA	46:D5:89:PHE:CE1	2.48	0.44
46:D5:52:SER:C	46:D5:54:HIS:H	2.25	0.44
53:K5:47:THR:HG23	53:K5:48:VAL:N	2.32	0.44
55:M5:33:ASN:OD1	55:M5:33:ASN:N	2.50	0.44
1:13:820:U:H4'	1:13:821:G:OP2	2.17	0.44
1:13:1180:A:H5"	1:13:1181:G:OP1	2.18	0.44
1:13:1336:C:H5"	1:13:1336:C:H6	1.81	0.44
1:13:1358:U:OP1	14:5I:35:ARG:HG3	2.17	0.44
1:13:1390:U:H2'	1:13:1391:U:C6	2.52	0.44
1:13:1442:G:H2'	1:13:1443:G:H5'	2.00	0.44
4:3E:187:ARG:HH22	4:3E:193:ASP:CG	2.25	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:6E:62:PHE:HD1	7:6E:124:LEU:HD11	1.81	0.44
8:7E:45:ILE:HD12	8:7E:47:GLY:HA2	1.98	0.44
19:AI:10:PHE:CD1	19:AI:10:PHE:N	2.85	0.44
22:1K:76:A:C8	26:1H:2507:C:H1'	2.52	0.44
26:1H:197:A:N6	26:1H:2430:A:H2'	2.32	0.44
26:1H:818:G:OP2	61:1H:4498:HOH:O	2.21	0.44
26:1H:2352:A:C4	26:1H:2366:A:C2	3.05	0.44
26:1H:2619:C:H5'	29:21:150:VAL:O	2.17	0.44
30:31:9:ILE:HD12	30:31:10:PRO:HD2	1.99	0.44
33:61:5:LEU:HD23	33:61:5:LEU:HA	1.65	0.44
36:78:100:LEU:HD23	36:78:112:LEU:HD11	1.99	0.44
38:98:2:ARG:O	38:98:5:LYS:HG3	2.17	0.44
44:F8:89:ILE:HG21	44:F8:92:LEU:HD12	1.99	0.44
45:G8:93:GLY:O	45:G8:94:LYS:HB2	2.17	0.44
46:H8:104:PHE:CE2	46:H8:119:GLU:HB3	2.52	0.44
1:1G:109:A:H2'	1:1G:326:G:H21	1.81	0.44
1:1G:167:G:O2'	1:1G:168:G:H5'	2.17	0.44
1:1G:243:A:C2	1:1G:245:C:C2	3.05	0.44
1:1G:640:A:N3	8:72:115:SER:HB2	2.33	0.44
1:1G:942:G:N2	9:82:124:GLN:OE1	2.47	0.44
1:1G:1052:U:H5"	1:1G:1053:G:OP2	2.17	0.44
3:22:120:VAL:O	3:22:123:GLN:HB3	2.18	0.44
4:32:39:PRO:HA	4:32:40:PRO:HD3	1.81	0.44
5:42:133:TYR:O	5:42:137:GLU:HB2	2.17	0.44
10:1A:49:VAL:O	10:1A:60:ARG:HB2	2.17	0.44
56:1L:44:G:H2'	56:1L:45:U:C6	2.52	0.44
23:2L:8:4SU:O5'	23:2L:8:4SU:H6	2.17	0.44
23:2L:20:G:C2	23:2L:58:A:C2	3.05	0.44
26:14:1784:A:H4'	26:14:1785:A:C5'	2.47	0.44
26:14:2319:G:N1	26:14:2334:G:OP2	2.47	0.44
26:14:2651:C:H42	26:14:2669:G:H1	1.65	0.44
30:39:117:ARG:NH1	30:39:120:GLU:OE1	2.51	0.44
36:35:36:LYS:NZ	36:35:36:LYS:HB2	2.32	0.44
38:55:48:VAL:O	38:55:49:ASP:C	2.60	0.44
1:13:7:G:H5'	1:13:298:A:O4'	2.17	0.44
1:13:376:G:H5"	16:7I:5:ARG:HB2	1.99	0.44
1:13:464:G:O6	1:13:466:C:H4'	2.17	0.44
1:13:750:G:N3	15:6I:23:GLY:HA3	2.32	0.44
1:13:1013:G:N2	1:13:1016:A:OP2	2.50	0.44
1:13:1504:G:OP1	1:13:1507:A:H4'	2.17	0.44
2:1E:168:THR:OG1	2:1E:192:SER:HB2	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:8I:9:VAL:O	17:8I:21:VAL:HA	2.17	0.44
18:9I:67:ALA:O	18:9I:71:LYS:HG2	2.17	0.44
26:1H:315:G:C5	26:1H:316:C:C4	3.04	0.44
26:1H:356:G:H2'	26:1H:357:A:C8	2.52	0.44
26:1H:365:C:H2'	26:1H:366:C:O4'	2.18	0.44
26:1H:532:A:N7	26:1H:2021:C:O2'	2.48	0.44
26:1H:581:C:H2'	26:1H:582:G:H8	1.82	0.44
26:1H:783:A:C8	26:1H:783:A:H3'	2.52	0.44
26:1H:1528:A:C6	26:1H:1529:A:C6	3.05	0.44
26:1H:2667:C:H1'	32:51:109:PHE:CD1	2.51	0.44
26:1H:2818:G:OP2	38:98:42:LYS:NZ	2.51	0.44
29:21:38:THR:HG22	29:21:41:LYS:HB2	1.99	0.44
32:51:88:LEU:H	32:51:88:LEU:HG	1.60	0.44
35:68:87:ILE:HD12	35:68:91:LEU:HG	1.99	0.44
36:78:64:LYS:HE3	55:Q8:12:LYS:HD2	2.00	0.44
43:E8:74:ALA:HA	43:E8:104:THR:O	2.18	0.44
49:K8:48:HIS:CD2	49:K8:48:HIS:C	2.95	0.44
1:1G:73:G:H1	1:1G:97:U:H3	1.65	0.44
1:1G:109:A:H2'	1:1G:326:G:N2	2.33	0.44
1:1G:310:G:H5"	16:7A:31:LYS:HB2	1.98	0.44
1:1G:512:U:C2	1:1G:513:C:C5	3.06	0.44
1:1G:707:C:OP1	11:2A:85:ARG:NH1	2.50	0.44
1:1G:823:G:H21	8:72:1:MET:HE1	1.83	0.44
1:1G:994:A:C5	1:1G:1216:G:H4'	2.52	0.44
1:1G:1092:A:C2	1:1G:1183:A:H2	2.33	0.44
1:1G:1226:C:H4'	19:AA:80:TYR:OH	2.16	0.44
1:1G:1286:A:C8	1:1G:1286:A:C3'	3.01	0.44
1:1G:1327:C:H2'	1:1G:1328:C:C6	2.51	0.44
2:12:231:GLU:HA	2:12:232:PRO:HD3	1.80	0.44
3:22:14:ILE:HG12	3:22:15:THR:H	1.82	0.44
3:22:191:THR:HB	3:22:193:TYR:CE1	2.53	0.44
9:82:92:TYR:O	9:82:95:LYS:HD3	2.18	0.44
10:1A:32:ALA:HB2	10:1A:81:THR:HG21	1.98	0.44
10:1A:81:THR:OG1	10:1A:82:ILE:N	2.50	0.44
12:3A:92:ASP:O	12:3A:93:LEU:HD23	2.18	0.44
19:AA:40:ILE:HD13	19:AA:62:ILE:HG13	1.99	0.44
23:2L:44:A:H2'	23:2L:45:A:C8	2.52	0.44
26:14:76:C:O3'	49:G5:59:ARG:HG3	2.17	0.44
26:14:476:G:N1	26:14:479:A:OP2	2.50	0.44
26:14:706:A:OP1	28:19:7:LYS:HE3	2.17	0.44
26:14:1225:C:H4'	42:95:85:LYS:CG	2.47	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:14:1499:C:H2'	26:14:1500:G:H8	1.82	0.44
26:14:2415:G:O3'	36:35:66:GLY:HA3	2.18	0.44
26:14:2855:C:H2'	26:14:2856:C:H6	1.82	0.44
29:29:81:ILE:O	29:29:82:ARG:HB2	2.17	0.44
32:59:152:ARG:HG3	32:59:153:LYS:N	2.32	0.44
33:69:76:THR:HG21	33:69:139:GLN:O	2.17	0.44
34:15:1:MET:HB2	34:15:2:LYS:H	1.50	0.44
34:15:128:HIS:CE1	34:15:134:ARG:HD2	2.52	0.44
38:55:28:LEU:HD23	38:55:28:LEU:HA	1.81	0.44
42:95:5:VAL:HB	42:95:37:VAL:HG12	2.00	0.44
45:C5:33:LYS:NZ	45:C5:33:LYS:HB2	2.33	0.44
51:I5:14:ILE:HG22	51:I5:22:ILE:HA	1.99	0.44
55:M5:54:GLU:H	55:M5:54:GLU:HG3	1.52	0.44
1:13:407:G:H2'	1:13:408:A:C8	2.52	0.44
1:13:977:A:H1'	1:13:982:U:O4	2.17	0.44
1:13:1347:G:N2	1:13:1373:G:H2'	2.33	0.44
2:1E:68:ILE:O	2:1E:91:PRO:HD2	2.18	0.44
3:2E:88:ARG:H	3:2E:88:ARG:HG3	1.58	0.44
6:5E:25:ILE:HD13	6:5E:25:ILE:HA	1.77	0.44
7:6E:43:PHE:O	7:6E:46:ALA:HB3	2.18	0.44
7:6E:50:ILE:O	7:6E:54:THR:HG23	2.18	0.44
8:7E:95:VAL:HG12	8:7E:99:GLU:HB3	1.99	0.44
11:2I:34:ASP:HB2	11:2I:35:PRO:CD	2.48	0.44
18:9I:26:LEU:HD13	18:9I:42:ARG:HH21	1.83	0.44
23:2K:19:G:C2	23:2K:59:A:C5	3.06	0.44
26:1H:7:G:C2	26:1H:8:A:C4	3.06	0.44
26:1H:273(F):C:H3'	26:1H:274:G:H5"	2.00	0.44
26:1H:758:C:O2	26:1H:1981:A:H2	2.01	0.44
26:1H:803:U:C4	26:1H:804:A:N7	2.85	0.44
26:1H:1163:G:C2	26:1H:1164:G:C8	3.06	0.44
26:1H:1265:A:H3'	52:N8:19:ARG:NH1	2.32	0.44
26:1H:1903:G:OP1	28:11:241:PRO:HB2	2.16	0.44
26:1H:2469:A:O2'	37:88:56:ARG:HG3	2.17	0.44
26:1H:2716:U:O2'	26:1H:2717:G:H5'	2.17	0.44
29:21:3:GLY:HA3	29:21:81:ILE:CG2	2.47	0.44
29:21:166:THR:HG21	29:21:199:ARG:HH22	1.81	0.44
30:31:110:LEU:HD12	30:31:110:LEU:HA	1.79	0.44
32:51:20:ALA:HB1	32:51:21:PRO:HD2	1.97	0.44
35:68:98:VAL:HG11	35:68:114:ILE:HG23	1.98	0.44
39:A8:11:LYS:HD3	39:A8:91:PRO:HD3	1.99	0.44
44:F8:14:SER:O	44:F8:15:GLU:C	2.61	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:G8:84:ARG:NH2	61:G8:303:HOH:O	2.39	0.44
46:H8:117:LEU:H	46:H8:117:LEU:HD13	1.81	0.44
47:I8:64:ASP:HB2	47:I8:85:ALA:HB1	2.00	0.44
48:J8:91:LYS:HA	48:J8:91:LYS:HZ3	1.82	0.44
50:L8:7:LYS:HA	50:L8:33:GLN:O	2.17	0.44
50:L8:8:LEU:HD22	50:L8:31:LEU:CD2	2.48	0.44
51:M8:61:ARG:C	51:M8:63:TYR:H	2.25	0.44
1:1G:91:C:H2'	1:1G:92:G:C8	2.53	0.44
1:1G:526:C:C5	1:1G:527:G:H1'	2.52	0.44
1:1G:622:A:C8	1:1G:623:C:C6	3.06	0.44
1:1G:776:G:N2	1:1G:802:A:OP2	2.48	0.44
1:1G:1009:G:H8	1:1G:1009:G:OP2	2.01	0.44
2:12:42:ILE:HD13	2:12:43:ASP:N	2.33	0.44
4:32:59:ARG:O	4:32:63:LYS:N	2.41	0.44
4:32:100:ARG:HE	4:32:100:ARG:HB3	1.54	0.44
7:62:27:ILE:HA	7:62:30:ILE:HB	1.99	0.44
17:8A:75:ARG:HG3	17:8A:76:LEU:N	2.31	0.44
20:BA:59:ALA:O	20:BA:63:ILE:N	2.44	0.44
20:BA:59:ALA:HB3	20:BA:84:LEU:HD11	1.99	0.44
57:3L:51:U:H2'	57:3L:52:G:C8	2.52	0.44
26:14:1027:A:C2	26:14:2488:A:H5'	2.52	0.44
26:14:1858:G:O2'	26:14:1884:A:N6	2.50	0.44
26:14:1954:G:C2	26:14:2551:C:H5"	2.52	0.44
26:14:2068:U:N3	26:14:2430:A:H2	2.15	0.44
26:14:2459:A:C4	26:14:2460:U:C5	3.05	0.44
28:19:70:TRP:HZ3	28:19:146:GLU:CD	2.25	0.44
29:29:34:VAL:HG21	29:29:78:LEU:HD22	2.00	0.44
30:39:8:GLN:HA	30:39:15:SER:HA	2.00	0.44
30:39:81:PRO:HG3	30:39:89:VAL:HG22	1.99	0.44
31:49:16:ARG:NH2	31:49:28:VAL:O	2.49	0.44
34:15:28:THR:HG22	34:15:29:LYS:NZ	2.31	0.44
38:55:57:ARG:HH11	38:55:57:ARG:HG3	1.82	0.44
39:65:63:THR:O	39:65:66:ALA:HB3	2.17	0.44
41:85:95:LEU:HD11	42:95:11:GLN:O	2.17	0.44
45:C5:39:VAL:C	45:C5:40:GLU:OE2	2.60	0.44
48:F5:25:LYS:HE2	48:F5:25:LYS:HB3	1.67	0.44
51:I5:37:SER:HB3	51:I5:39:CYS:HB2	1.99	0.44
1:13:455:C:H42	1:13:477:G:H22	1.65	0.44
1:13:465:A:N7	1:13:467:G:C6	2.86	0.44
1:13:488:C:O2'	1:13:489:C:H5'	2.17	0.44
1:13:947:G:H2'	1:13:948:C:C6	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:13:1179:A:H4'	9:8E:103:THR:HA	2.00	0.44
1:13:1182:G:H4'	1:13:1183:A:C5'	2.48	0.44
1:13:1350:A:C6	1:13:1351:U:N3	2.86	0.44
8:7E:10:LEU:HD23	8:7E:10:LEU:N	2.32	0.44
8:7E:25:ASP:C	8:7E:26:VAL:HG12	2.42	0.44
16:7I:38:TYR:CE1	16:7I:50:LYS:HB2	2.52	0.44
26:1H:428:A:P	61:1H:3761:HOH:O	2.75	0.44
26:1H:511:U:C5	26:1H:512:G:C5	3.05	0.44
26:1H:1328:G:H2'	26:1H:1330:C:C5	2.52	0.44
26:1H:1388:G:H2'	26:1H:1389:G:C8	2.52	0.44
26:1H:1728:G:H8	26:1H:1732:A:N6	2.01	0.44
26:1H:2224:G:H4'	26:1H:2226:C:C2	2.53	0.44
26:1H:2376:A:C2	39:A8:112:PHE:HB3	2.51	0.44
26:1H:2496:C:OP1	37:88:82:ARG:HD3	2.17	0.44
26:1H:2749:A:H4'	32:51:62:LYS:HB3	1.99	0.44
26:1H:2830:G:H5"	26:1H:2830:G:C8	2.50	0.44
30:31:67:GLN:O	30:31:67:GLN:HG3	2.10	0.44
40:B8:42:ILE:HD12	40:B8:42:ILE:H	1.82	0.44
40:B8:50:ILE:O	40:B8:99:LEU:HD12	2.18	0.44
41:C8:95:LEU:HD12	41:C8:96:ALA:HA	1.99	0.44
49:K8:50:ILE:HD12	49:K8:50:ILE:H	1.81	0.44
55:Q8:50:LEU:O	55:Q8:51:ALA:HB3	2.18	0.44
55:Q8:57:ARG:HD3	55:Q8:57:ARG:H	1.82	0.44
1:1G:241:C:C2	1:1G:286:G:C2	3.05	0.44
1:1G:458:C:H42	1:1G:474:G:H1	1.66	0.44
3:22:21:ARG:HH12	10:1A:92:THR:HB	1.83	0.44
3:22:112:SER:HB3	3:22:115:LEU:HB2	1.99	0.44
5:42:7:GLU:HG2	5:42:8:GLU:N	2.33	0.44
9:82:99:LEU:HB3	9:82:101:PHE:CE1	2.53	0.44
20:BA:56:MET:HE2	20:BA:56:MET:HB3	1.82	0.44
56:1L:29:G:N2	56:1L:42:C:H1'	2.32	0.44
26:14:196:A:N3	26:14:196:A:H2'	2.33	0.44
26:14:513:A:C2	26:14:514:A:C4	3.05	0.44
26:14:784:A:H3'	61:14:4036:HOH:O	2.18	0.44
26:14:867:C:C5	26:14:868:U:H5	2.36	0.44
26:14:913:U:H4'	26:14:914:C:OP1	2.16	0.44
26:14:1027:A:H5'	27:1J:88:C:H41	1.83	0.44
26:14:1113:U:H5'	32:59:2:SER:HA	1.98	0.44
26:14:1416:G:O2'	26:14:1417:C:O4'	2.34	0.44
26:14:1491:G:O2'	28:19:101:GLU:HB2	2.17	0.44
26:14:1520:U:H2'	26:14:1521:G:O4'	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:14:2259:G:H1'	26:14:2427:C:H2'	1.98	0.44
27:1J:8:U:H6	27:1J:8:U:H5"	1.83	0.44
27:1J:42:C:N3	31:49:91:ARG:NH2	2.65	0.44
28:19:34:VAL:CG1	28:19:61:LEU:HG	2.48	0.44
28:19:49:ILE:CD1	28:19:52:ARG:HA	2.47	0.44
30:39:83:PHE:O	30:39:84:VAL:HB	2.17	0.44
34:15:137:LYS:HD3	34:15:137:LYS:HA	1.79	0.44
37:45:141:GLN:HG2	37:45:141:GLN:O	2.18	0.44
43:A5:78:GLU:OE2	43:A5:99:ARG:HD3	2.18	0.44
45:C5:30:VAL:O	45:C5:36:ALA:O	2.35	0.44
50:H5:52:HIS:CD2	50:H5:53:LEU:HG	2.53	0.44
1:13:130:A:O2'	1:13:131:C:O5'	2.31	0.44
1:13:607:A:H2	16:7I:31:LYS:HG3	1.83	0.44
1:13:942:G:C2	1:13:943:U:C6	3.06	0.44
1:13:1167:A:H8	1:13:1167:A:OP1	2.00	0.44
1:13:1170:A:H2'	1:13:1171:G:O4'	2.18	0.44
8:7E:87:SER:OG	8:7E:92:ARG:HA	2.17	0.44
12:3I:59:ARG:HA	12:3I:65:GLU:HA	1.99	0.44
14:5I:42:ILE:HG22	14:5I:46:GLU:OE1	2.18	0.44
22:1K:18:G:O2'	22:1K:19:G:OP1	2.29	0.44
26:1H:376:C:P	61:1H:3754:HOH:O	2.75	0.44
26:1H:427:U:H5"	26:1H:428:A:OP1	2.18	0.44
26:1H:582:G:H2'	26:1H:583:G:H8	1.82	0.44
26:1H:804:A:P	61:1H:4480:HOH:O	2.75	0.44
26:1H:1568:G:H5'	28:11:60:ARG:HA	2.00	0.44
26:1H:1945:G:H2'	26:1H:1946:U:C6	2.52	0.44
26:1H:2168:G:O2'	26:1H:2169:A:H5'	2.18	0.44
26:1H:2392:A:C8	36:78:61:ARG:HG2	2.44	0.44
27:16:60:C:N3	27:16:61:G:N7	2.66	0.44
42:D8:40:LEU:HD22	42:D8:47:VAL:HA	1.98	0.44
1:1G:841:U:H4'	1:1G:842:C:C6	2.52	0.44
1:1G:922:G:C6	1:1G:923:A:C6	3.06	0.44
1:1G:1029:G:O2'	1:1G:1031:G:OP2	2.35	0.44
1:1G:1280:A:H5'	1:1G:1281:U:OP2	2.18	0.44
8:72:68:ARG:HD3	8:72:69:ARG:O	2.17	0.44
16:7A:19:ILE:HB	16:7A:36:ILE:O	2.18	0.44
19:AA:7:LYS:HB2	19:AA:7:LYS:NZ	2.32	0.44
23:2L:22:A:H61	23:2L:47:7MG:H2'	1.82	0.44
26:14:242:G:O5'	55:M5:3:LYS:HE3	2.18	0.44
26:14:1071:G:N2	26:14:1087:G:H22	2.14	0.44
26:14:1678:G:N2	26:14:1989:G:N2	2.66	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:14:1970:A:OP1	26:14:1970:A:H4'	2.18	0.44
28:19:158:ALA:O	28:19:159:ALA:C	2.60	0.44
29:29:103:ASP:OD1	29:29:201:THR:HG23	2.17	0.44
30:39:130:ALA:H	30:39:142:TRP:CD1	2.36	0.44
30:39:155:LEU:HD23	30:39:186:ILE:HD13	1.99	0.44
31:49:32:PRO:HB2	31:49:172:LEU:HD22	2.00	0.44
31:49:145:THR:HG22	51:I5:31:ILE:HG21	2.00	0.44
33:69:41:GLU:H	33:69:41:GLU:HG3	1.48	0.44
34:15:125:GLY:HA3	34:15:126:PRO:HA	1.72	0.44
45:C5:18:GLY:O	45:C5:19:LYS:C	2.61	0.44
48:F5:52:ARG:HH11	48:F5:57:GLU:HG3	1.83	0.44
48:F5:73:LEU:HD23	48:F5:73:LEU:HA	1.80	0.44
54:L5:15:THR:HG22	54:L5:16:HIS:CE1	2.52	0.44
1:13:445:G:H1	1:13:489:C:N4	2.13	0.44
1:13:615:C:C2	1:13:616:G:C8	3.06	0.44
1:13:754:C:H6	15:6I:69:TYR:CE2	2.35	0.44
12:3I:117:ARG:O	12:3I:119:LYS:O	2.35	0.44
13:4I:15:VAL:HG23	13:4I:43:THR:O	2.17	0.44
14:5I:9:LYS:O	14:5I:12:ARG:HG3	2.18	0.44
26:1H:6:A:N3	34:58:131:GLN:HG3	2.33	0.44
26:1H:569:U:O4	26:1H:570:G:C6	2.71	0.44
26:1H:654(B):C:H2'	26:1H:654(C):G:C8	2.53	0.44
26:1H:878:A:N1	26:1H:899:A:H1'	2.33	0.44
26:1H:2031:A:C6	26:1H:2498:C:H1'	2.52	0.44
26:1H:2047:U:O2'	26:1H:2823:A:N1	2.45	0.44
26:1H:2327:A:H2'	26:1H:2328:A:H8	1.80	0.44
26:1H:2740:A:C6	26:1H:2764:A:C8	3.05	0.44
26:1H:2774:C:H2'	26:1H:2775:A:O4'	2.17	0.44
27:16:43:C:H5"	51:M8:1:MET:HG2	1.99	0.44
28:11:53:PHE:C	28:11:218:ARG:HG3	2.43	0.44
28:11:64:ILE:HD13	28:11:64:ILE:HG21	1.82	0.44
32:51:33:LEU:HD12	32:51:75:ALA:HA	1.99	0.44
38:98:109:ALA:HA	38:98:110:PRO:HD2	1.72	0.44
40:B8:3:ARG:O	40:B8:7:ILE:N	2.49	0.44
40:B8:5:ALA:O	40:B8:8:LYS:HG2	2.17	0.44
41:C8:101:ARG:C	41:C8:103:PRO:HD3	2.42	0.44
43:E8:88:ARG:HD2	43:E8:88:ARG:HA	1.68	0.44
50:L8:9:VAL:HG22	50:L8:54:VAL:HA	2.00	0.44
1:1G:352:C:P	61:1G:1723:HOH:O	2.75	0.44
1:1G:475:G:OP1	16:7A:81:ARG:NH1	2.50	0.44
1:1G:947:G:H2'	1:1G:948:C:O4'	2.16	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1G:1034:G:H8	1:1G:1034:G:O5'	2.01	0.44
1:1G:1063:C:H3'	1:1G:1064:G:H2'	1.99	0.44
1:1G:1149:C:OP2	9:82:9:ARG:NH1	2.50	0.44
1:1G:1246:C:H2'	1:1G:1247:U:H6	1.83	0.44
1:1G:1338:G:C6	1:1G:1339:A:C6	3.06	0.44
4:32:108:LEU:HD11	4:32:174:LEU:HB3	2.00	0.44
15:6A:10:LYS:HD2	15:6A:10:LYS:HA	1.56	0.44
15:6A:43:LEU:HA	15:6A:43:LEU:HD23	1.77	0.44
21:1B:8:THR:HG22	21:1B:11:GLY:N	2.23	0.44
56:1L:29:G:O6	56:1L:41:C:N4	2.51	0.44
26:14:1071:G:O2'	26:14:1089:G:H3'	2.18	0.44
26:14:1484:G:C6	26:14:1485:G:C5	3.05	0.44
26:14:1858:G:H2'	26:14:1883:G:N2	2.33	0.44
26:14:2105:C:H42	26:14:2184:G:H1	1.65	0.44
31:49:95:ARG:HG2	31:49:96:ARG:HG2	2.00	0.44
32:59:106:THR:HG22	32:59:112:PRO:HB3	1.99	0.44
37:45:27:VAL:HG12	46:D5:81:ARG:NH2	2.33	0.44
40:75:45:PHE:CD2	40:75:74:ARG:HD3	2.53	0.44
43:A5:12:ILE:HD13	43:A5:17:VAL:HB	1.99	0.44
43:A5:72:LYS:HB3	43:A5:106:ILE:HD11	1.99	0.44
45:C5:39:VAL:HG23	45:C5:41:GLY:N	2.32	0.44
1:13:31:G:O2'	1:13:48:C:N4	2.51	0.44
1:13:153:C:N4	1:13:168:G:H22	2.15	0.44
1:13:232:G:H2'	1:13:233:C:C6	2.52	0.44
1:13:413:G:N2	1:13:428:G:H1'	2.33	0.44
1:13:625:G:H2'	1:13:626:U:H6	1.82	0.44
1:13:1028(A):C:H42	1:13:1032(A):G:H1	1.65	0.44
1:13:1263:C:O2'	1:13:1264:C:H5'	2.18	0.44
1:13:1291:G:P	7:6E:37:ASN:HD22	2.40	0.44
2:1E:21:ARG:HD3	2:1E:38:GLY:C	2.42	0.44
8:7E:95:VAL:HG12	8:7E:99:GLU:CB	2.47	0.44
22:1K:56:C:O4'	26:1H:896:A:O2'	2.36	0.44
24:3K:18:G:HO2'	24:3K:19:G:P	2.41	0.44
26:1H:308:G:H2'	26:1H:309:G:C8	2.53	0.44
26:1H:700:G:H2'	26:1H:701:G:O4'	2.18	0.44
26:1H:1045:A:H4'	26:1H:1045:A:OP1	2.18	0.44
26:1H:2129:C:N3	26:1H:2160:G:N2	2.65	0.44
26:1H:2160:G:N1	26:1H:2161:C:H1'	2.33	0.44
26:1H:2310:A:N6	31:41:79:ASN:HB2	2.33	0.44
30:31:24:LEU:HA	30:31:25:PRO:HD2	1.70	0.44
34:58:133:GLN:H	34:58:133:GLN:CD	2.26	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:C8:79:PHE:HE2	41:C8:106:PHE:CZ	2.35	0.44
1:1G:195:A:C6	1:1G:196:A:N1	2.86	0.44
1:1G:284:G:H2'	1:1G:285:G:H8	1.82	0.44
1:1G:540:G:H2'	1:1G:541:G:O4'	2.17	0.44
1:1G:575:G:OP1	1:1G:575:G:H4'	2.18	0.44
1:1G:1176:A:C2'	1:1G:1177:G:H5'	2.47	0.44
1:1G:1281:U:H3'	1:1G:1282:C:H5	1.82	0.44
1:1G:1287:A:H2	1:1G:1353:G:N3	2.16	0.44
2:12:48:MET:HA	2:12:51:LEU:HB2	1.99	0.44
9:82:40:LEU:HB3	9:82:43:ALA:HB2	2.00	0.44
13:4A:94:ARG:NH2	19:AA:78:ARG:HH22	2.16	0.44
18:9A:22:VAL:C	18:9A:24:ALA:H	2.25	0.44
19:AA:66:MET:HE2	51:I5:59:PHE:HD2	1.82	0.44
23:2L:25:U:H2'	23:2L:26:C:O4'	2.18	0.44
57:3L:30:G:H2'	57:3L:31:A:C8	2.53	0.44
26:14:981:A:N1	26:14:2027:G:O2'	2.40	0.44
26:14:1538:G:H2'	26:14:1539:G:C8	2.52	0.44
26:14:2299:G:N1	26:14:2318:G:C8	2.86	0.44
26:14:2467:C:H4'	37:45:123:HIS:ND1	2.32	0.44
26:14:2495:G:O3'	37:45:81:VAL:HG12	2.18	0.44
26:14:2861:G:O2'	26:14:2862:G:H5'	2.18	0.44
28:19:145:VAL:HG13	28:19:191:ALA:HB2	1.99	0.44
29:29:29:GLY:H	29:29:51:PHE:HE1	1.65	0.44
30:39:182:ASN:ND2	30:39:185:ASP:OD2	2.43	0.44
31:49:29:TRP:C	31:49:31:VAL:N	2.75	0.44
33:69:76:THR:HG21	33:69:140:LEU:HA	2.00	0.44
33:69:110:ASP:OD1	33:69:111:PRO:HD2	2.18	0.44
34:15:120:LEU:O	34:15:121:LYS:HD2	2.17	0.44
35:25:35:VAL:HG11	35:25:103:ALA:HB3	1.99	0.44
39:65:74:ALA:HB1	39:65:107:GLU:CB	2.47	0.44
41:85:34:LYS:NZ	41:85:37:GLU:OE1	2.38	0.44
43:A5:15:ARG:O	43:A5:19:LEU:HD13	2.17	0.44
46:D5:158:PRO:HD2	46:D5:161:VAL:HG13	1.98	0.44
49:G5:64:LEU:HD21	49:G5:68:ARG:NH1	2.33	0.44
1:13:111:G:H8	1:13:111:G:O5'	2.01	0.44
1:13:341:C:O2'	1:13:342:C:H5'	2.17	0.44
1:13:428:G:C5	1:13:430:A:C6	3.06	0.44
1:13:650:G:N3	1:13:650:G:H2'	2.33	0.44
1:13:848:C:H6	1:13:848:C:O5'	2.00	0.44
1:13:1064:G:H4'	1:13:1065:U:OP1	2.17	0.44
1:13:1137:C:O2'	1:13:1138:G:N3	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:13:1285:A:H4'	1:13:1286:A:C5'	2.48	0.44
1:13:1455:G:H5"	20:BI:31:SER:HB2	1.99	0.44
2:1E:60:ASP:O	2:1E:64:ARG:HG2	2.17	0.44
2:1E:233:SER:OG	2:1E:234:PRO:HD2	2.18	0.44
13:4I:34:LEU:HD13	13:4I:39:ILE:HB	2.00	0.44
18:9I:58:LEU:HG	18:9I:62:GLU:OE1	2.18	0.44
24:3K:37:MIA:N1	24:3K:37:MIA:H152	2.33	0.44
26:1H:338:G:N2	26:1H:339:U:H1'	2.32	0.44
26:1H:528:A:N1	26:1H:2042:A:H2'	2.32	0.44
26:1H:556:G:H2'	26:1H:557:U:C6	2.53	0.44
26:1H:709:U:O2'	26:1H:710:G:H5'	2.18	0.44
26:1H:832:G:C5'	36:78:45:LEU:HD11	2.46	0.44
26:1H:1386:C:C2	26:1H:1387:C:C5	3.06	0.44
26:1H:2199:A:H5'	26:1H:2205:C:H5	1.83	0.44
26:1H:2488:A:H2'	26:1H:2489:G:O4'	2.18	0.44
36:78:60:MET:HE3	36:78:60:MET:HB3	1.73	0.44
36:78:107:LYS:HA	36:78:107:LYS:HD2	1.74	0.44
37:88:56:ARG:HA	37:88:56:ARG:HD2	1.64	0.44
41:C8:5:LYS:H	41:C8:5:LYS:HG3	1.69	0.44
41:C8:69:CYS:SG	41:C8:79:PHE:CD2	3.02	0.44
55:Q8:30:ARG:HB2	55:Q8:30:ARG:NH1	2.33	0.44
1:1G:21:G:H2'	1:1G:22:G:C8	2.53	0.44
1:1G:200:G:H1	1:1G:217:C:N4	2.16	0.44
1:1G:244:U:O4	1:1G:906:G:H1'	2.18	0.44
1:1G:362:G:H4'	12:3A:33:ARG:NH2	2.32	0.44
1:1G:885:G:O2'	1:1G:914:A:N1	2.35	0.44
1:1G:979:C:H5	1:1G:980:C:C6	2.36	0.44
1:1G:1275:A:H2'	1:1G:1276:G:H8	1.82	0.44
3:22:20:SER:HB2	3:22:40:ARG:HH12	1.81	0.44
4:32:31:CYS:O	4:32:33:MET:HG2	2.18	0.44
4:32:108:LEU:CD2	4:32:183:GLY:HA3	2.48	0.44
5:42:145:LYS:O	5:42:149:GLU:HG2	2.18	0.44
7:62:70:LYS:HG2	7:62:96:GLN:HB3	1.99	0.44
12:3A:60:LEU:HD13	12:3A:60:LEU:HA	1.79	0.44
15:6A:39:LEU:O	15:6A:39:LEU:HD22	2.18	0.44
19:AA:50:ALA:HB1	19:AA:58:VAL:N	2.32	0.44
23:2L:21:U:O2	23:2L:21:U:H2'	2.17	0.44
26:14:68:G:H2'	26:14:69:C:C6	2.52	0.44
26:14:301:G:C4	26:14:302:C:C5	3.06	0.44
26:14:332:A:O2'	26:14:334:C:OP2	2.32	0.44
26:14:848:G:H2'	26:14:849:A:H8	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:14:1047:G:N2	26:14:1111:A:H62	2.15	0.44
26:14:2448:A:P	61:14:3698:HOH:O	2.76	0.44
26:14:2639:A:C2	26:14:2778:A:C8	3.05	0.44
30:39:101:LEU:O	30:39:106:ARG:NH1	2.51	0.44
37:45:103:MET:O	37:45:104:PHE:HB2	2.18	0.44
40:75:118:ARG:NH1	40:75:121:ILE:HG21	2.33	0.44
43:A5:1:MET:HE3	43:A5:62:HIS:HB3	2.00	0.44
1:13:256:U:H2'	1:13:257:G:O4'	2.18	0.43
1:13:881:G:H2'	1:13:882:C:O4'	2.17	0.43
1:13:1077:G:N2	1:13:1080:A:OP2	2.44	0.43
1:13:1098:C:C2	1:13:1099:G:C8	3.07	0.43
1:13:1226:C:OP2	13:4I:103:THR:OG1	2.21	0.43
2:1E:44:LEU:HA	2:1E:47:THR:OG1	2.18	0.43
2:1E:87:ARG:NH1	2:1E:233:SER:HB2	2.32	0.43
2:1E:163:PHE:HA	2:1E:185:ILE:O	2.17	0.43
7:6E:125:MET:HE2	7:6E:125:MET:HB2	1.81	0.43
9:8E:89:ASN:C	9:8E:91:ASP:H	2.25	0.43
10:1I:90:LEU:N	10:1I:91:PRO:HD3	2.33	0.43
15:6I:18:PHE:CE1	15:6I:21:ASP:HB2	2.53	0.43
15:6I:63:ARG:HG2	15:6I:67:LEU:HD12	1.99	0.43
19:AI:18:LYS:HD2	19:AI:21:GLU:HG2	2.00	0.43
26:1H:139:G:N3	26:1H:141:A:N1	2.65	0.43
26:1H:662:G:H5'	36:78:15:ARG:HB3	1.99	0.43
26:1H:1471:A:C6	26:1H:1522:G:C2	3.06	0.43
26:1H:1472:A:H3'	26:1H:1473:G:H8	1.83	0.43
26:1H:2760:C:H2'	26:1H:2761:G:H8	1.82	0.43
29:21:21:VAL:HA	29:21:22:PRO:HD3	1.46	0.43
30:31:123:LEU:HD12	30:31:124:LEU:N	2.33	0.43
33:61:57:ARG:HA	33:61:60:GLU:HG2	1.99	0.43
39:A8:41:ASP:OD2	39:A8:44:LYS:HB2	2.18	0.43
1:1G:6:G:HO2'	1:1G:7:G:H5'	1.79	0.43
1:1G:678:U:H2'	1:1G:679:C:C6	2.53	0.43
1:1G:974:A:H5'	1:1G:975:A:OP1	2.17	0.43
1:1G:1157:A:O2'	1:1G:1158:C:P	2.76	0.43
4:32:106:TYR:HE2	4:32:112:VAL:O	2.01	0.43
4:32:153:ARG:HD3	4:32:153:ARG:HA	1.79	0.43
8:72:97:VAL:O	8:72:99:GLU:N	2.50	0.43
9:82:95:LYS:HE2	9:82:95:LYS:HB2	1.62	0.43
11:2A:106:LYS:H	11:2A:106:LYS:HG3	1.63	0.43
12:3A:21:LYS:HE3	12:3A:21:LYS:HB2	1.91	0.43
26:14:370:G:H4'	26:14:371:A:OP2	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:14:676:A:H1'	26:14:2443:C:H1'	1.99	0.43
26:14:1257:C:H4'	30:39:83:PHE:CD1	2.53	0.43
26:14:1826:G:H4'	28:19:242:ARG:CZ	2.48	0.43
26:14:2286:A:OP2	53:K5:28:ARG:HD2	2.17	0.43
26:14:2346:A:H8	53:K5:24:GLU:CD	2.26	0.43
26:14:2611:U:O2'	52:J5:3:LYS:CG	2.64	0.43
26:14:2747:G:C2	26:14:2754:U:C4	3.06	0.43
27:1J:3:C:H2'	27:1J:4:C:C6	2.53	0.43
27:1J:52:A:N6	39:65:33:LYS:HE2	2.33	0.43
39:65:27:SER:HA	39:65:88:ASP:CB	2.46	0.43
40:75:55:ASN:N	40:75:59:THR:HG22	2.32	0.43
46:D5:8:TYR:HA	46:D5:62:PRO:HG3	1.99	0.43
55:M5:7:HIS:CB	55:M5:58:ILE:HG22	2.48	0.43
1:13:13:U:O2	1:13:914:A:H3'	2.17	0.43
1:13:533:A:C2	1:13:536:C:C5	3.06	0.43
1:13:812:C:H4'	1:13:813:U:H5'	2.00	0.43
1:13:1334:G:H5"	1:13:1335:C:OP2	2.18	0.43
6:5E:41:GLU:O	6:5E:43:LEU:HD12	2.18	0.43
7:6E:79:ARG:NH1	7:6E:80:VAL:O	2.51	0.43
15:6I:82:ILE:HG22	15:6I:83:GLU:N	2.33	0.43
26:1H:66:C:O2'	26:1H:67:U:H5'	2.18	0.43
26:1H:449:A:C6	26:1H:450:G:C5	3.06	0.43
26:1H:1213:A:H1'	26:1H:1238:G:N3	2.33	0.43
26:1H:1317:A:H2'	26:1H:1318:C:C6	2.53	0.43
26:1H:1375:C:H2'	26:1H:1376:C:C6	2.53	0.43
26:1H:2334:G:H4'	26:1H:2335:A:OP2	2.17	0.43
26:1H:2508:G:H2'	26:1H:2509:G:H8	1.83	0.43
27:16:88:C:H2'	27:16:89:G:O4'	2.19	0.43
28:11:232:PRO:HB3	28:11:244:ARG:NH1	2.33	0.43
31:41:37:VAL:N	31:41:99:MET:HE3	2.33	0.43
31:41:96:ARG:O	31:41:97:ASP:HB2	2.18	0.43
32:51:10:PRO:HB2	32:51:50:VAL:HG13	2.00	0.43
32:51:43:VAL:HB	32:51:52:VAL:HG22	1.99	0.43
39:A8:34:HIS:HB2	39:A8:36:TYR:CE1	2.45	0.43
39:A8:48:LEU:CD2	39:A8:82:ILE:HD11	2.42	0.43
45:G8:35:TYR:CE2	45:G8:69:ALA:HB3	2.53	0.43
46:H8:48:PHE:HE1	46:H8:71:VAL:HG11	1.83	0.43
50:L8:5:LYS:HD2	50:L8:34:GLU:OE1	2.18	0.43
51:M8:39:CYS:C	51:M8:41:PRO:HD3	2.42	0.43
1:1G:29:G:H5'	1:1G:296:U:OP1	2.18	0.43
1:1G:38:G:H4'	1:1G:547:A:N6	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1G:411:A:N7	1:1G:413:G:N3	2.66	0.43
1:1G:1442:G:C6	1:1G:1446:A:N6	2.86	0.43
2:12:130:ARG:HE	2:12:130:ARG:N	2.16	0.43
7:62:60:LYS:HD2	7:62:60:LYS:HA	1.75	0.43
7:62:99:LEU:HD22	7:62:103:TRP:CZ2	2.53	0.43
19:AA:28:LYS:HG2	19:AA:29:ARG:H	1.83	0.43
26:14:585:G:H3'	61:14:4026:HOH:O	2.18	0.43
26:14:664:C:OP1	36:35:18:ARG:NH2	2.46	0.43
26:14:782:A:O2'	28:19:225:ALA:HB1	2.18	0.43
26:14:998:C:OP2	41:85:58:ARG:NH2	2.40	0.43
26:14:1358:G:N2	26:14:1372:U:C5	2.86	0.43
26:14:2292:C:H2'	26:14:2293:C:C6	2.53	0.43
27:1J:43:C:O4'	31:49:66:GLN:NE2	2.51	0.43
27:1J:89:G:H21	27:1J:89(A):A:H2	1.67	0.43
28:19:232:PRO:HA	61:19:301:HOH:O	2.18	0.43
29:29:116:VAL:O	29:29:117:MET:CB	2.66	0.43
30:39:178:PRO:HG2	30:39:179:GLU:OE2	2.18	0.43
31:49:20:ILE:HG23	31:49:25:TYR:HB2	2.00	0.43
31:49:172:LEU:O	31:49:176:LEU:HB2	2.18	0.43
33:69:75:LEU:HD22	33:69:76:THR:N	2.20	0.43
34:15:67:LEU:HG	34:15:88:GLU:HG2	1.99	0.43
36:35:19:VAL:HG13	36:35:21:ARG:N	2.22	0.43
38:55:81:ASP:O	38:55:82:GLU:HB3	2.17	0.43
39:65:6:ALA:HA	39:65:9:ARG:HB2	2.00	0.43
51:I5:8:LYS:HA	51:I5:8:LYS:HD3	1.48	0.43
53:K5:35:GLU:HG2	53:K5:51:GLU:HB2	1.99	0.43
54:L5:1:MET:HE2	54:L5:1:MET:HB3	1.79	0.43
1:13:74:C:H2'	1:13:75:C:O4'	2.18	0.43
1:13:1060:C:O2'	10:1I:56:HIS:ND1	2.42	0.43
1:13:1072:G:C5	1:13:1073:U:C4	3.06	0.43
1:13:1528:U:C2	1:13:1530:G:C8	3.06	0.43
2:1E:54:THR:HG21	2:1E:201:ILE:HD11	2.00	0.43
9:8E:112:LYS:CA	9:8E:119:ALA:HB2	2.47	0.43
13:4I:84:ILE:HD12	13:4I:84:ILE:HA	1.82	0.43
16:7I:77:ALA:HB3	16:7I:79:VAL:HG23	1.99	0.43
26:1H:243:U:O2'	26:1H:244:A:H5'	2.18	0.43
26:1H:617:G:OP2	30:31:43:LYS:HE2	2.17	0.43
26:1H:674:G:C1'	30:31:74:ARG:HD3	2.41	0.43
26:1H:907:U:O2'	37:88:101:ARG:NH2	2.45	0.43
26:1H:1171:G:N2	26:1H:1179:C:C2	2.86	0.43
26:1H:1388:G:H2'	26:1H:1389:G:H8	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1H:1441:G:H2'	26:1H:1442:G:C8	2.50	0.43
26:1H:1470:G:H5"	26:1H:1471:A:OP1	2.18	0.43
26:1H:1550:C:H2'	26:1H:1551:C:C6	2.53	0.43
26:1H:1677:A:H2'	26:1H:1678:G:H8	1.83	0.43
26:1H:2123:G:H2'	26:1H:2124:G:H8	1.83	0.43
26:1H:2598:A:P	61:1H:3647:HOH:O	2.60	0.43
26:1H:2705:A:O2'	26:1H:2852:G:OP1	2.26	0.43
26:1H:2734:A:H5"	26:1H:2734:A:C8	2.54	0.43
26:1H:2862:G:C4	26:1H:2863:C:C5	3.06	0.43
27:16:40:U:H1'	27:16:45:A:H61	1.83	0.43
29:21:50:GLY:HA2	29:21:76:ARG:O	2.18	0.43
37:88:32:TYR:OH	37:88:111:GLU:HB2	2.18	0.43
38:98:44:LEU:O	38:98:45:ARG:C	2.60	0.43
43:E8:19:LEU:HB3	52:N8:25:LEU:HD11	2.00	0.43
45:G8:15:VAL:HG21	45:G8:42:VAL:HG21	1.98	0.43
51:M8:9:LEU:HD12	51:M8:26:SER:C	2.42	0.43
1:1G:176:C:OP1	20:BA:29:LYS:NZ	2.51	0.43
1:1G:303:A:H2'	1:1G:304:U:O4'	2.19	0.43
1:1G:401:C:H2'	1:1G:402:G:C8	2.53	0.43
1:1G:537:G:H5"	12:3A:113:ARG:NH1	2.33	0.43
1:1G:616:G:C2	1:1G:617:G:N7	2.86	0.43
1:1G:1129:C:H4'	1:1G:1130:A:O5'	2.18	0.43
2:12:144:ARG:HG3	2:12:145:LEU:N	2.33	0.43
3:22:54:ARG:HE	3:22:54:ARG:HB2	1.70	0.43
4:32:33:MET:O	4:32:35:ARG:HG3	2.18	0.43
5:42:69:VAL:O	5:42:71:LEU:N	2.50	0.43
7:62:42:ILE:HG23	7:62:117:ALA:HB2	2.00	0.43
12:3A:26:ALA:O	12:3A:27:LEU:HD22	2.17	0.43
17:8A:10:VAL:HA	17:8A:20:THR:O	2.19	0.43
26:14:573:G:O2'	26:14:574:C:H3'	2.18	0.43
26:14:746:A:H2'	26:14:2612:C:H5"	1.99	0.43
26:14:1033:U:C6	26:14:1033:U:C3'	3.01	0.43
26:14:1519:G:C6	26:14:1520:U:N3	2.86	0.43
26:14:1818:U:H2'	28:19:157:ARG:HG3	2.00	0.43
26:14:2461:C:H2'	26:14:2462:U:C6	2.52	0.43
29:29:9:VAL:HA	40:75:3:ARG:CG	2.49	0.43
29:29:153:GLY:O	29:29:154:LYS:C	2.61	0.43
32:59:152:ARG:HG3	32:59:153:LYS:HB2	1.99	0.43
36:35:62:LEU:C	55:M5:13:ARG:HG2	2.43	0.43
47:E5:50:ASN:C	47:E5:62:LEU:HD12	2.42	0.43
47:E5:53:MET:HE2	47:E5:53:MET:HB3	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:13:974:A:OP2	14:5I:29:ARG:NH2	2.52	0.43
1:13:1372:U:OP1	9:8E:72:GLY:N	2.51	0.43
3:2E:43:LEU:O	3:2E:47:LEU:HB2	2.18	0.43
6:5E:62:TRP:CH2	6:5E:64:GLN:HG2	2.54	0.43
9:8E:89:ASN:HB2	9:8E:91:ASP:OD1	2.17	0.43
9:8E:126:SER:OG	9:8E:127:LYS:N	2.51	0.43
17:8I:52:LYS:HD2	17:8I:55:ASP:OD1	2.18	0.43
19:AI:43:GLU:H	19:AI:43:GLU:HG2	1.57	0.43
20:BI:74:LYS:HB3	20:BI:75:ASN:OD1	2.18	0.43
26:1H:130:C:O3'	26:1H:1349:A:H1'	2.19	0.43
26:1H:205:G:O2'	26:1H:206:U:P	2.76	0.43
26:1H:302:C:C2	26:1H:303:U:C5	3.06	0.43
26:1H:674:G:H1'	30:31:74:ARG:CD	2.41	0.43
26:1H:831:G:N2	36:78:53:GLY:O	2.51	0.43
26:1H:906:G:HO2'	37:88:67:ARG:HE	1.64	0.43
26:1H:1171:G:N1	26:1H:1178:C:N4	2.67	0.43
26:1H:1324:G:C4	26:1H:1328:G:O6	2.71	0.43
26:1H:1378:A:OP1	54:P8:10:ARG:NH2	2.51	0.43
26:1H:2109:U:H2'	26:1H:2110:G:C8	2.53	0.43
26:1H:2262:U:H4'	26:1H:2328:A:H2	1.83	0.43
26:1H:2368:C:H2'	26:1H:2369:A:H8	1.83	0.43
26:1H:2590:A:H2'	26:1H:2591:C:C6	2.53	0.43
26:1H:2619:C:O2'	26:1H:2620:C:H5'	2.18	0.43
27:16:15:A:H5'	27:16:16:G:H8	1.84	0.43
30:31:32:LEU:HD22	30:31:105:VAL:HG13	2.00	0.43
32:51:104:GLU:HB2	32:51:114:VAL:HG22	2.00	0.43
36:78:58:THR:HG21	55:Q8:52:LYS:HE3	1.99	0.43
39:A8:83:LYS:HE3	39:A8:110:LEU:HD23	2.00	0.43
45:G8:44:ILE:H	45:G8:44:ILE:HG13	1.49	0.43
46:H8:99:TYR:HD2	46:H8:123:ASP:HB3	1.84	0.43
48:J8:87:PRO:O	48:J8:88:LYS:C	2.60	0.43
49:K8:3:LEU:O	49:K8:6:VAL:HG13	2.19	0.43
1:1G:8:A:C5	4:32:209:ARG:HA	2.53	0.43
1:1G:340:U:H2'	1:1G:341:C:C6	2.53	0.43
1:1G:371:G:O2'	1:1G:373:A:N7	2.50	0.43
1:1G:487:A:H2'	1:1G:488:C:O4'	2.18	0.43
1:1G:867:G:O2'	1:1G:868:C:H5'	2.18	0.43
1:1G:1432:G:OP1	40:75:107:ASP:HB2	2.19	0.43
3:22:18:TRP:HE3	3:22:18:TRP:N	2.15	0.43
3:22:61:ALA:O	3:22:63:ASN:N	2.50	0.43
4:32:30:LYS:HB3	4:32:35:ARG:HD2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:52:30:LEU:HB3	6:52:35:ALA:HB3	2.00	0.43
6:52:100:ASN:ND2	18:9A:26:LEU:O	2.51	0.43
7:62:73:MET:HE3	7:62:73:MET:HB2	1.83	0.43
12:3A:117:ARG:HB3	12:3A:122:THR:HB	1.99	0.43
23:2L:55:5MU:C4	23:2L:56:PSU:C2	3.06	0.43
23:2L:65:G:C6	23:2L:66:C:C4	3.07	0.43
57:3L:15:G:O5'	57:3L:15:G:H8	2.01	0.43
26:14:84:A:O5'	45:C5:8:LYS:HD3	2.18	0.43
26:14:236:C:H2'	26:14:237:C:H6	1.84	0.43
26:14:376:C:H2'	26:14:377:C:C6	2.52	0.43
26:14:1054:A:H2'	26:14:1055:G:C8	2.52	0.43
26:14:1157:G:C2	26:14:1158:C:C2	3.06	0.43
26:14:1996:C:OP1	35:25:31:LYS:HE2	2.18	0.43
26:14:2298:A:H2'	26:14:2299:G:O4'	2.17	0.43
26:14:2371:G:H4'	53:K5:45:LYS:HG2	2.00	0.43
26:14:2392:A:N1	26:14:2424:C:N3	2.66	0.43
31:49:131:TYR:O	31:49:159:VAL:HG23	2.17	0.43
35:25:9:GLU:N	35:25:82:ASN:O	2.50	0.43
42:95:85:LYS:HD2	42:95:86:GLY:N	2.26	0.43
51:I5:43:TYR:O	51:I5:43:TYR:CG	2.71	0.43
1:13:190:G:HO2'	1:13:191(A):G:P	2.40	0.43
1:13:304:U:H2'	1:13:305:G:C8	2.54	0.43
1:13:973:G:OP1	10:1I:57:LYS:NZ	2.21	0.43
1:13:1064:G:OP1	1:13:1386:G:H4'	2.18	0.43
1:13:1091:U:O2	1:13:1093:A:C8	2.72	0.43
1:13:1118:C:H1'	1:13:1179:A:C5	2.53	0.43
1:13:1132:C:H2'	1:13:1133:G:O4'	2.18	0.43
1:13:1177:G:O2'	1:13:1178:G:O4'	2.26	0.43
2:1E:31:TYR:O	2:1E:42:ILE:HG13	2.18	0.43
4:3E:11:LEU:HD22	4:3E:66:ARG:HG2	2.01	0.43
7:6E:104:LEU:HD13	7:6E:104:LEU:HA	1.84	0.43
8:7E:86:ILE:HG22	8:7E:93:VAL:HG21	2.01	0.43
13:4I:23:TYR:HB3	13:4I:67:GLU:HB2	2.00	0.43
20:BI:45:GLN:HA	20:BI:91:LEU:HD22	1.99	0.43
20:BI:72:LEU:HD21	20:BI:77:ALA:HB2	2.00	0.43
26:1H:208:C:H2'	26:1H:209:C:C6	2.52	0.43
26:1H:286:C:N4	26:1H:355:G:H1	2.14	0.43
26:1H:1163:G:N3	26:1H:1164:G:C8	2.87	0.43
26:1H:1170:G:N2	26:1H:1180:C:O2	2.51	0.43
26:1H:1433:U:O2	26:1H:1561:G:N1	2.52	0.43
26:1H:1658:C:H5"	61:1H:3698:HOH:O	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1H:1727:U:H2'	26:1H:1728:G:O4'	2.18	0.43
26:1H:2502:G:N7	61:1H:3867:HOH:O	2.36	0.43
26:1H:2780:G:OP2	34:58:118:LYS:HD3	2.18	0.43
28:11:107:ALA:HA	28:11:108:PRO:HD3	1.82	0.43
29:21:29:GLY:N	29:21:51:PHE:HE1	2.04	0.43
30:31:114:VAL:HG21	30:31:202:PHE:CE1	2.53	0.43
30:31:124:LEU:HD12	30:31:125:LEU:O	2.18	0.43
30:31:136:THR:O	30:31:140:LEU:HB2	2.18	0.43
34:58:10:GLU:HA	34:58:11:PRO:HD3	1.74	0.43
34:58:65:LYS:HB2	34:58:65:LYS:HE3	1.38	0.43
35:68:86:ILE:HG22	35:68:94:ARG:HB2	2.00	0.43
38:98:4:LEU:HA	38:98:4:LEU:HD13	1.27	0.43
45:G8:94:LYS:HG3	45:G8:95:LYS:N	2.33	0.43
46:H8:55:HIS:ND1	46:H8:55:HIS:N	2.66	0.43
47:I8:26:TYR:O	47:I8:67:VAL:HG22	2.17	0.43
48:J8:15:ALA:O	48:J8:40:ARG:HG2	2.18	0.43
55:Q8:48:PHE:CG	55:Q8:49:VAL:N	2.79	0.43
55:Q8:54:GLU:C	55:Q8:56:GLU:N	2.76	0.43
1:1G:243:A:H4'	1:1G:244:U:O5'	2.18	0.43
1:1G:456:C:N4	1:1G:476:G:H1	2.15	0.43
1:1G:567:G:H2'	1:1G:568:G:O4'	2.19	0.43
1:1G:616:G:N3	1:1G:617:G:C8	2.87	0.43
1:1G:964:A:N3	1:1G:969:A:O2'	2.45	0.43
1:1G:972:C:O3'	10:1A:57:LYS:HG3	2.18	0.43
1:1G:1172:C:H2'	1:1G:1173:G:C8	2.54	0.43
1:1G:1275:A:H2'	1:1G:1276:G:C8	2.53	0.43
1:1G:1344:C:H5'	9:82:120:ARG:O	2.19	0.43
1:1G:1359:C:O2'	1:1G:1361:G:N7	2.51	0.43
1:1G:1517:G:C6	1:1G:1518:A:C5	3.07	0.43
2:12:193:ASP:OD2	2:12:196:LEU:HG	2.19	0.43
4:32:173:TRP:CD1	4:32:174:LEU:HG	2.53	0.43
5:42:37:ARG:HG2	5:42:112:LEU:HA	2.00	0.43
5:42:76:ILE:HG23	5:42:142:LEU:HD13	1.99	0.43
18:9A:18:ARG:HG3	18:9A:19:LYS:N	2.34	0.43
57:3L:9:A:C8	57:3L:11:C:N4	2.87	0.43
26:14:142:G:H2'	26:14:143:C:H6	1.84	0.43
26:14:882:G:H2'	26:14:883:G:H8	1.84	0.43
26:14:959:A:C6	26:14:960:A:N1	2.86	0.43
26:14:1204:A:N1	26:14:1241:A:C2	2.87	0.43
26:14:1329:U:H5"	26:14:1330:C:H5	1.83	0.43
26:14:1420:U:HO2'	26:14:1421:G:P	2.42	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:14:1946:U:H2'	26:14:1947:C:C6	2.53	0.43
26:14:2130:U:H2'	26:14:2158:A:C6	2.53	0.43
26:14:2402:C:H5	26:14:2415:G:H22	1.65	0.43
26:14:2859:G:C8	26:14:2859:G:H3'	2.54	0.43
46:D5:98:MET:HE3	46:D5:98:MET:HB2	1.68	0.43
51:I5:13:ARG:HA	51:I5:22:ILE:HB	1.99	0.43
1:13:114:U:O2'	1:13:115:G:H5'	2.18	0.43
1:13:645:C:OP2	61:13:1972:HOH:O	2.21	0.43
1:13:663:A:H2'	1:13:664:G:O4'	2.19	0.43
1:13:940:C:H2'	1:13:941:G:C8	2.53	0.43
1:13:1111:A:N1	3:2E:177:THR:HG23	2.33	0.43
1:13:1273:G:H5'	1:13:1274:G:OP2	2.18	0.43
1:13:1298:C:C5	7:6E:114:ARG:HD3	2.54	0.43
1:13:1315:U:H2'	1:13:1316:G:O4'	2.19	0.43
1:13:1374:A:C5	1:13:1375:A:C8	3.07	0.43
5:4E:110:LEU:CD1	5:4E:118:ILE:HD13	2.48	0.43
8:7E:121:ASP:OD1	8:7E:121:ASP:N	2.51	0.43
11:2I:79:SER:HB2	11:2I:106:LYS:HD2	2.00	0.43
16:7I:74:LEU:HB3	16:7I:79:VAL:HG21	2.00	0.43
20:BI:92:LEU:O	20:BI:96:GLY:HA3	2.19	0.43
22:1K:19:G:OP1	22:1K:60:U:N3	2.52	0.43
26:1H:10:G:N2	26:1H:2801:A:O2'	2.39	0.43
26:1H:382:G:H5"	26:1H:383:U:OP2	2.19	0.43
26:1H:581:C:H2'	26:1H:582:G:C8	2.54	0.43
26:1H:1243:G:O2'	36:78:7:ARG:NH2	2.52	0.43
26:1H:1790:C:H2'	26:1H:1791:A:C5	2.53	0.43
26:1H:1816:G:O6	28:11:35:LYS:NZ	2.31	0.43
26:1H:2056:G:N3	26:1H:2056:G:H2'	2.33	0.43
28:11:2:ALA:HA	28:11:20:ASP:CB	2.48	0.43
28:11:6:PHE:CE1	28:11:18:VAL:HG23	2.52	0.43
29:21:107:THR:O	29:21:190:GLY:HA3	2.19	0.43
31:41:21:ARG:HH11	31:41:21:ARG:CG	2.27	0.43
31:41:135:LEU:O	31:41:154:GLY:HA3	2.18	0.43
32:51:12:PRO:HG2	32:51:13:LYS:HG2	2.00	0.43
35:68:117:LEU:HA	35:68:117:LEU:HD23	1.83	0.43
36:78:97:PRO:HB3	36:78:112:LEU:HB2	1.99	0.43
39:A8:62:LYS:HB3	39:A8:97:ARG:HD2	2.01	0.43
44:F8:57:LEU:HD11	44:F8:78:LYS:HD2	2.00	0.43
44:F8:89:ILE:HG22	44:F8:92:LEU:HB2	2.01	0.43
46:H8:135:GLU:HG3	46:H8:136:PHE:CD1	2.54	0.43
55:Q8:32:LEU:HG	55:Q8:33:ASN:OD1	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:Q8:45:GLY:O	55:Q8:46:ARG:HB2	2.19	0.43
1:1G:617:G:C2	1:1G:618:C:C5	3.06	0.43
1:1G:828:A:H2'	1:1G:829:G:O4'	2.18	0.43
1:1G:830:G:H2'	1:1G:831:U:O4'	2.18	0.43
1:1G:892:A:C2	1:1G:907:A:C4	3.07	0.43
1:1G:1206:G:C6	1:1G:1207:G:C5	3.07	0.43
1:1G:1255:G:O3'	1:1G:1258:G:H1'	2.19	0.43
2:12:24:TRP:N	2:12:24:TRP:CD1	2.85	0.43
2:12:208:ILE:HA	2:12:211:ILE:HD12	2.00	0.43
3:22:91:LEU:HD11	3:22:101:LEU:CD1	2.49	0.43
4:32:31:CYS:O	4:32:31:CYS:SG	2.76	0.43
5:42:152:ARG:HD3	8:72:42:GLU:O	2.17	0.43
8:72:104:ARG:C	8:72:106:GLY:N	2.75	0.43
10:1A:6:ILE:HG22	10:1A:98:ILE:HG12	2.01	0.43
11:2A:19:ALA:O	11:2A:82:VAL:HA	2.19	0.43
21:1B:9:ARG:HG3	21:1B:10:ARG:H	1.83	0.43
21:1B:22:ARG:HA	21:1B:23:PRO:HD2	1.94	0.43
26:14:396:G:H8	26:14:396:G:O5'	2.01	0.43
26:14:818:G:H4'	26:14:838:C:O3'	2.19	0.43
26:14:968:G:H2'	26:14:969:U:O4'	2.18	0.43
26:14:1104:C:H2'	26:14:1105:U:C5	2.54	0.43
26:14:1338:G:N3	26:14:1393:A:H2	2.17	0.43
26:14:1636:C:OP1	61:14:3631:HOH:O	2.21	0.43
26:14:2426:A:H4'	26:14:2427:C:OP2	2.19	0.43
28:19:49:ILE:O	28:19:49:ILE:HG12	2.13	0.43
29:29:173:VAL:N	29:29:183:LEU:O	2.39	0.43
36:35:97:PRO:HD3	36:35:126:VAL:O	2.19	0.43
39:65:7:TYR:OH	39:65:91:PRO:HG3	2.19	0.43
42:95:28:GLU:O	42:95:61:VAL:HG11	2.19	0.43
44:B5:88:LYS:HE2	44:B5:90:GLU:OE2	2.19	0.43
1:13:431:A:H2'	1:13:432:A:O4'	2.19	0.43
1:13:474:G:C2	1:13:475:G:C4	3.07	0.43
1:13:475:G:H2'	1:13:476:G:C8	2.53	0.43
1:13:725:G:H2'	1:13:726:C:H6	1.83	0.43
1:13:1162:C:O5'	1:13:1162:C:H6	2.01	0.43
1:13:1343:G:O2'	9:8E:121:ARG:HD3	2.18	0.43
2:1E:17:PHE:HD1	2:1E:17:PHE:H	1.65	0.43
11:2I:34:ASP:HB3	11:2I:40:ILE:HD11	1.99	0.43
16:7I:52:ASP:CG	16:7I:55:ARG:HG3	2.43	0.43
19:AI:30:LEU:H	19:AI:30:LEU:HD13	1.84	0.43
24:3K:2:C:O3'	24:3K:3:C:O4'	2.37	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1H:37:C:H2'	26:1H:38:A:C8	2.54	0.43
26:1H:65:C:H2'	26:1H:66:C:H6	1.84	0.43
26:1H:270(N):G:H5'	33:61:53:ALA:HB1	1.99	0.43
26:1H:720:C:H2'	26:1H:721:C:H6	1.84	0.43
26:1H:1324:G:N2	26:1H:1331:A:C4	2.87	0.43
26:1H:2061:G:OP1	30:31:68:LYS:NZ	2.46	0.43
26:1H:2164:C:H5	26:1H:2165:G:C6	2.36	0.43
26:1H:2383:G:C2'	26:1H:2384:G:H5'	2.48	0.43
35:68:44:LYS:HD3	35:68:44:LYS:HA	1.87	0.43
55:Q8:60:LEU:N	55:Q8:61:LEU:HA	2.34	0.43
1:1G:554:C:H2'	1:1G:555:C:C6	2.54	0.43
1:1G:713:G:H2'	1:1G:714:G:C8	2.54	0.43
1:1G:834:C:H42	1:1G:852:G:H1	1.67	0.43
1:1G:1329:A:O2'	13:4A:24:GLY:HA2	2.17	0.43
1:1G:1330:U:H4'	13:4A:23:TYR:CE1	2.53	0.43
3:22:21:ARG:HB3	3:22:21:ARG:CZ	2.47	0.43
3:22:23:TYR:CD1	3:22:24:ALA:N	2.87	0.43
8:72:20:TYR:HA	8:72:65:TYR:CZ	2.54	0.43
9:82:112:LYS:HG2	9:82:119:ALA:HB2	2.01	0.43
12:3A:60:LEU:HB2	12:3A:64:TYR:CB	2.44	0.43
19:AA:50:ALA:CB	19:AA:57:HIS:HB3	2.48	0.43
20:BA:85:MET:HB2	20:BA:104:LEU:HD21	1.99	0.43
56:1L:22:G:OP2	56:1L:22:G:H8	2.01	0.43
56:1L:43:C:N3	56:1L:44:G:N2	2.67	0.43
56:1L:53:G:N2	56:1L:61:C:N3	2.50	0.43
57:3L:48:C:N4	57:3L:59:U:H1'	2.34	0.43
25:4L:19:U:O5'	25:4L:19:U:C6	2.72	0.43
26:14:77:C:OP1	49:G5:59:ARG:HD3	2.19	0.43
26:14:102:G:OP1	49:G5:7:ARG:NH2	2.51	0.43
26:14:252:G:P	36:35:50:ARG:NH2	2.92	0.43
26:14:270(F):U:H2'	26:14:270(G):C:C6	2.54	0.43
26:14:602:G:OP2	26:14:602:G:H8	2.01	0.43
26:14:637:A:H2'	36:35:117:GLU:OE2	2.18	0.43
26:14:702:G:C2	26:14:731:C:C2	3.07	0.43
26:14:757:U:H2'	26:14:758:C:O4'	2.18	0.43
26:14:817:C:H6	26:14:817:C:O5'	2.01	0.43
26:14:832:G:H5'	36:35:45:LEU:CD1	2.49	0.43
26:14:1006:C:C2	26:14:1138:G:N2	2.87	0.43
26:14:1142:U:H5"	26:14:1142(A):A:H5'	2.01	0.43
26:14:1147:C:H2'	26:14:1148:A:H8	1.83	0.43
26:14:1213:A:N3	26:14:1238:G:O2'	2.45	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:14:1533:C:C4	26:14:1534:G:H1'	2.54	0.43
26:14:1952:A:C6	35:25:22:ILE:HD12	2.54	0.43
26:14:2103:C:H2'	26:14:2104:G:C8	2.53	0.43
26:14:2211:G:H3'	26:14:2212:A:N3	2.33	0.43
26:14:2688:U:C5	26:14:2720:U:OP2	2.72	0.43
26:14:2836:U:H2'	26:14:2837:G:H8	1.70	0.43
30:39:28:ILE:O	30:39:29:ASN:C	2.62	0.43
34:15:21:LYS:O	34:15:60:ILE:HG13	2.18	0.43
36:35:90:ARG:HG3	36:35:91:PHE:H	1.84	0.43
39:65:41:ASP:OD1	39:65:44:LYS:HB2	2.18	0.43
41:85:91:ASP:C	41:85:93:LYS:H	2.26	0.43
47:E5:34:GLY:HA2	47:E5:61:ALA:O	2.18	0.43
48:F5:86:SER:N	48:F5:87:PRO:CD	2.82	0.43
52:J5:3:LYS:O	52:J5:4:HIS:C	2.60	0.43
1:13:21:G:OP1	61:13:1831:HOH:O	2.21	0.43
1:13:66:G:C2	1:13:67:C:C6	3.07	0.43
1:13:280:C:O2	17:8I:38:ARG:HG3	2.19	0.43
1:13:455:C:H42	1:13:477:G:H1	1.67	0.43
1:13:606:G:H22	1:13:631:G:H5"	1.84	0.43
1:13:704:A:H5"	1:13:705:U:OP2	2.19	0.43
1:13:828:A:H2'	1:13:829:G:O4'	2.18	0.43
4:3E:85:LYS:HE2	4:3E:85:LYS:HB2	1.65	0.43
5:4E:60:TYR:O	5:4E:64:ARG:HD3	2.19	0.43
9:8E:78:LYS:HE2	9:8E:101:PHE:CE1	2.54	0.43
16:7I:4:ILE:HA	16:7I:20:VAL:O	2.19	0.43
23:2K:52:C:H2'	23:2K:53:G:O4'	2.18	0.43
26:1H:163:U:O5'	26:1H:163:U:H6	2.00	0.43
26:1H:286:C:O2'	26:1H:287:C:H5'	2.18	0.43
26:1H:588:U:O4	26:1H:670:A:H1'	2.19	0.43
26:1H:644:A:C4	26:1H:646:A:C2	3.07	0.43
26:1H:734:A:O2'	26:1H:1635:G:H5'	2.18	0.43
26:1H:1300:U:H4'	26:1H:1301:A:H5'	2.01	0.43
26:1H:1478:G:H1'	26:1H:1557:C:O2'	2.18	0.43
26:1H:2418:A:P	55:Q8:39:LYS:HE2	2.59	0.43
26:1H:2729:G:H2'	26:1H:2730:C:C6	2.54	0.43
26:1H:2789:C:H3'	26:1H:2790:A:H5"	2.01	0.43
28:11:94:LEU:HD23	28:11:95:LEU:N	2.33	0.43
30:31:9:ILE:HD11	30:31:125:LEU:N	2.30	0.43
30:31:106:ARG:H	30:31:106:ARG:HG2	1.66	0.43
31:41:66:GLN:NE2	31:41:93:THR:O	2.51	0.43
31:41:67:LYS:HE2	31:41:67:LYS:N	2.32	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:41:179:PRO:HG3	51:M8:38:LYS:CE	2.46	0.43
33:61:127:VAL:HA	33:61:138:ILE:O	2.18	0.43
34:58:127:ASP:O	34:58:128:HIS:HB3	2.18	0.43
38:98:98:LEU:HD23	38:98:98:LEU:HA	1.86	0.43
39:A8:56:LEU:O	39:A8:58:LEU:HD23	2.19	0.43
40:B8:99:LEU:HD12	40:B8:99:LEU:H	1.84	0.43
45:G8:47:LYS:HG3	45:G8:48:ALA:O	2.19	0.43
47:I8:7:LEU:HA	47:I8:11:ARG:NH1	2.33	0.43
48:J8:75:GLU:O	48:J8:77:ALA:N	2.52	0.43
49:K8:15:LYS:H	49:K8:67:LYS:HE2	1.83	0.43
51:M8:60:GLN:HB2	51:M8:61:ARG:HD2	2.01	0.43
55:Q8:9:GLY:N	55:Q8:12:LYS:H	2.17	0.43
1:1G:1028(A):C:H42	1:1G:1032(B):G:N2	2.17	0.43
1:1G:1186:G:N2	1:1G:1187:G:H1'	2.34	0.43
1:1G:1256:A:N6	1:1G:1278:U:OP2	2.47	0.43
1:1G:1400:C:N4	23:2L:35:C:H1'	2.33	0.43
9:82:65:VAL:HG21	9:82:73:GLN:HB3	2.00	0.43
26:14:322:A:H5'	26:14:340:A:H1'	2.01	0.43
26:14:588:U:H2'	26:14:589:C:H6	1.76	0.43
26:14:820:A:O2'	26:14:821:A:H5'	2.19	0.43
26:14:1169:G:N3	26:14:1170:G:H1'	2.33	0.43
26:14:1366:A:H2'	26:14:1367:A:O4'	2.18	0.43
26:14:1387:C:C2	26:14:1388:G:C8	3.06	0.43
26:14:1643:G:N7	61:14:3984:HOH:O	2.37	0.43
26:14:1849:G:H2'	26:14:1850:G:C8	2.54	0.43
26:14:2016:U:H1'	52:J5:6:VAL:HG13	1.99	0.43
26:14:2033:A:P	61:14:4056:HOH:O	2.76	0.43
26:14:2638:G:OP2	29:29:82:ARG:NH2	2.52	0.43
27:1J:27:C:O3'	39:65:36:TYR:OH	2.36	0.43
29:29:29:GLY:HA2	29:29:180:ASN:HB3	2.00	0.43
31:49:117:PHE:HE1	31:49:120:LEU:HD23	1.83	0.43
32:59:120:GLY:O	32:59:135:GLY:HA2	2.19	0.43
41:85:88:ILE:C	41:85:90:VAL:H	2.27	0.43
42:95:80:GLN:HG3	42:95:81:TYR:N	2.31	0.43
44:B5:31:HIS:HA	44:B5:32:PRO:HD3	1.77	0.43
51:I5:37:SER:C	51:I5:39:CYS:N	2.75	0.43
1:13:179:A:H2'	1:13:180:U:C6	2.54	0.43
1:13:683:G:C6	1:13:684:A:C6	3.07	0.43
1:13:1455:G:OP1	20:BI:35:THR:OG1	2.34	0.43
3:2E:167:TRP:CD1	3:2E:167:TRP:C	2.95	0.43
5:4E:80:ILE:HG12	5:4E:81:GLU:N	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:5E:10:LEU:HD13	6:5E:61:LEU:HD13	1.99	0.43
8:7E:12:ARG:HD3	8:7E:26:VAL:HB	2.01	0.43
8:7E:85:ARG:NE	8:7E:87:SER:O	2.48	0.43
12:3I:89:ARG:HG3	12:3I:89:ARG:HH11	1.84	0.43
13:4I:69:GLU:HG3	31:41:118:ARG:NH2	2.33	0.43
19:AI:42:PRO:HD3	51:M8:63:TYR:HE2	1.84	0.43
26:1H:35:G:H2'	26:1H:36:G:O4'	2.19	0.43
26:1H:99:U:C6	26:1H:102:G:C2	3.07	0.43
26:1H:375:C:H42	26:1H:399:G:H1	1.66	0.43
26:1H:425:G:H2'	26:1H:426:C:H6	1.83	0.43
26:1H:710:G:H2'	26:1H:711:G:H8	1.84	0.43
26:1H:1178:C:H1'	26:1H:1179:C:C6	2.54	0.43
26:1H:1523:U:C2	26:1H:1524:G:C8	3.07	0.43
26:1H:2028:U:H2'	26:1H:2029:G:O4'	2.18	0.43
26:1H:2544:G:H8	26:1H:2544:G:O5'	2.02	0.43
36:78:62:LEU:HB3	55:Q8:23:VAL:HG21	1.99	0.43
37:88:106:VAL:HG21	37:88:114:ALA:HB1	2.00	0.43
40:B8:48:ILE:HD12	40:B8:110:ILE:HD11	1.99	0.43
41:C8:47:TYR:CD1	41:C8:47:TYR:C	2.97	0.43
41:C8:94:ASN:CA	41:C8:96:ALA:HB2	2.48	0.43
43:E8:58:ALA:HB1	43:E8:64:MET:HB2	2.01	0.43
55:Q8:7:HIS:CD2	55:Q8:57:ARG:HH22	2.36	0.43
1:1G:198:G:H2'	1:1G:199:G:C8	2.54	0.43
1:1G:457:C:H2'	1:1G:458:C:C6	2.54	0.43
1:1G:1119:C:OP2	9:82:9:ARG:NH2	2.52	0.43
1:1G:1331:G:OP1	1:1G:1331:G:H4'	2.19	0.43
4:32:126:ILE:HG22	4:32:127:THR:H	1.82	0.43
6:52:16:GLN:H	6:52:16:GLN:HG2	1.46	0.43
11:2A:34:ASP:HB2	11:2A:35:PRO:CD	2.49	0.43
15:6A:24:SER:OG	15:6A:27:VAL:HG23	2.18	0.43
26:14:146:G:H2'	26:14:147:U:O4'	2.19	0.43
26:14:857:C:H4'	47:E5:23:VAL:HG21	1.99	0.43
26:14:956:G:H5"	37:45:77:LYS:HD2	2.00	0.43
26:14:971:C:H2'	26:14:972:G:O4'	2.19	0.43
26:14:1171:G:N2	26:14:1178:C:H42	2.17	0.43
26:14:1203:G:H3'	26:14:1204:A:H5"	2.00	0.43
26:14:1453:A:O2'	26:14:1454:U:H2'	2.18	0.43
26:14:1784:A:H5"	61:14:3558:HOH:O	2.18	0.43
26:14:1856:G:N2	26:14:1886:C:O2	2.51	0.43
26:14:2211:G:H3'	26:14:2212:A:C2	2.54	0.43
26:14:2261:C:O2'	26:14:2262:U:H5'	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:14:2441:C:O2'	26:14:2442:C:H5'	2.19	0.43
26:14:2636:U:O2'	29:29:44:TYR:OH	2.26	0.43
26:14:2772:C:H2'	26:14:2773:C:H6	1.84	0.43
28:19:127:VAL:HG13	28:19:194:GLY:HA3	1.99	0.43
31:49:104:GLU:OE1	51:I5:23:GLU:HG2	2.18	0.43
33:69:77:LEU:HD22	33:69:141:LYS:HE3	2.00	0.43
35:25:47:ILE:HD12	35:25:47:ILE:HA	1.92	0.43
39:65:95:HIS:C	39:65:99:LYS:HB3	2.44	0.43
40:75:16:ARG:HG3	40:75:79:HIS:HA	2.01	0.43
44:B5:36:LYS:HG3	44:B5:56:THR:HG23	2.01	0.43
45:C5:40:GLU:HG3	45:C5:64:GLU:OE1	2.18	0.43
45:C5:75:ILE:O	45:C5:76:CYS:HB3	2.18	0.43
46:D5:102:LEU:HD22	46:D5:104:PHE:HE1	1.83	0.43
46:D5:138:GLU:O	46:D5:156:LYS:HG3	2.19	0.43
46:D5:148:ASP:CG	46:D5:175:VAL:HG11	2.44	0.43
1:13:60:A:N6	1:13:110:C:N3	2.67	0.43
1:13:142:G:C2	1:13:143:A:C5	3.07	0.43
1:13:157:G:H1	1:13:164:U:H3	1.65	0.43
1:13:237:C:C5'	17:8I:25:ARG:HH12	2.32	0.43
1:13:450:G:N7	1:13:481:G:C6	2.87	0.43
1:13:517:G:N1	1:13:533:A:OP2	2.45	0.43
1:13:1338:G:C6	1:13:1339:A:C6	3.06	0.43
2:1E:12:GLU:HA	2:1E:16:HIS:CD2	2.53	0.43
2:1E:27:LYS:HB2	2:1E:194:PRO:HD2	2.01	0.43
2:1E:165:VAL:HG23	2:1E:166:ASP:N	2.31	0.43
2:1E:189:ASP:HB2	2:1E:205:ASP:HB3	2.01	0.43
4:3E:135:LEU:HA	4:3E:136:PRO:HD2	1.83	0.43
8:7E:97:VAL:O	8:7E:100:ILE:HG13	2.19	0.43
10:1I:79:ARG:HA	10:1I:79:ARG:HD3	1.77	0.43
11:2I:105:VAL:O	11:2I:105:VAL:HG22	2.19	0.43
26:1H:140:A:C8	26:1H:1408:C:O2'	2.72	0.43
26:1H:639:U:C4	26:1H:640:C:N4	2.86	0.43
26:1H:729:G:C5	28:11:208:LYS:HB2	2.54	0.43
26:1H:780:G:N2	26:1H:783:A:N6	2.62	0.43
26:1H:1043:C:C4	26:1H:1044:G:N7	2.86	0.43
26:1H:1251:C:H5	61:1H:3852:HOH:O	2.02	0.43
26:1H:1386:C:OP2	26:1H:1396:U:H5	2.01	0.43
26:1H:2002:G:C6	61:1H:4267:HOH:O	2.70	0.43
26:1H:2067:G:H4'	61:1H:4534:HOH:O	2.18	0.43
26:1H:2287:A:C2	26:1H:2346:A:C2	3.07	0.43
26:1H:2592:G:C6	26:1H:2593:U:C4	3.07	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1H:2689:U:OP2	26:1H:2719:G:N2	2.39	0.43
26:1H:2784:C:H1'	29:21:37:ARG:NH1	2.34	0.43
31:41:124:SER:HB2	31:41:131:TYR:CE1	2.54	0.43
33:61:8:PRO:HA	33:61:14:ASP:HA	2.00	0.43
33:61:33:ARG:HB3	33:61:35:LEU:HD23	2.00	0.43
36:78:57:THR:HB	36:78:59:LEU:H	1.84	0.43
45:G8:76:CYS:CB	45:G8:97:ARG:HG2	2.49	0.43
46:H8:133:ILE:HA	46:H8:134:PRO:HD2	1.71	0.43
51:M8:43:TYR:CE2	51:M8:44:THR:HG23	2.54	0.43
55:Q8:5:LYS:O	55:Q8:6:THR:CB	2.67	0.43
1:1G:676:A:H1'	11:2A:115:PRO:HB3	2.01	0.43
1:1G:1246:C:H2'	1:1G:1247:U:C6	2.53	0.43
1:1G:1508:G:P	61:1G:1763:HOH:O	2.77	0.43
1:1G:1521:G:H2'	1:1G:1522:U:C6	2.54	0.43
4:32:188:LEU:HD23	4:32:188:LEU:HA	1.93	0.43
7:62:15:ASP:O	7:62:19:GLY:HA2	2.19	0.43
9:82:18:PHE:HD2	9:82:62:TYR:CD2	2.35	0.43
18:9A:36:ASN:HD22	18:9A:36:ASN:C	2.14	0.43
18:9A:45:SER:OG	18:9A:46:GLU:N	2.50	0.43
56:1L:14:A:C2	56:1L:22:G:H1'	2.54	0.43
26:14:71:A:H5'	26:14:71:A:H8	1.83	0.43
26:14:117:G:C6	26:14:119:A:C6	3.06	0.43
26:14:307:G:N2	26:14:309:G:H3'	2.34	0.43
26:14:529:A:H8	26:14:530:G:C6	2.36	0.43
26:14:1260:G:C6	26:14:1261:C:C4	3.06	0.43
26:14:2093:G:O5'	33:69:24:GLY:HA3	2.19	0.43
26:14:2314:C:H5'	31:49:38:VAL:HG11	2.01	0.43
26:14:2688:U:H5	26:14:2720:U:OP2	2.02	0.43
28:19:158:ALA:O	28:19:161:THR:HG23	2.18	0.43
33:69:40:THR:O	33:69:44:LEU:N	2.43	0.43
35:25:34:THR:OG1	35:25:35:VAL:N	2.52	0.43
35:25:122:LEU:HA	35:25:122:LEU:HD23	1.84	0.43
36:35:14:LYS:C	36:35:16:ARG:H	2.26	0.43
41:85:92:ARG:NH2	42:95:10:LYS:HA	2.30	0.43
42:95:23:GLU:OE1	42:95:91:TYR:HE1	2.02	0.43
42:95:94:LEU:HD23	42:95:94:LEU:HA	1.84	0.43
1:13:131:C:O2	1:13:131:C:H2'	2.19	0.42
1:13:153:C:H42	1:13:168:G:H1	1.67	0.42
1:13:626:U:N3	1:13:627:G:C8	2.87	0.42
1:13:1292:U:H5'	9:8E:38:GLN:OE1	2.19	0.42
3:2E:23:TYR:CD1	3:2E:23:TYR:C	2.98	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:2E:91:LEU:HB3	3:2E:99:VAL:HG11	2.01	0.42
5:4E:71:LEU:HA	5:4E:75:THR:O	2.19	0.42
8:7E:86:ILE:HG22	8:7E:87:SER:H	1.83	0.42
13:4I:23:TYR:CE2	13:4I:71:ARG:HG3	2.53	0.42
15:6I:39:LEU:O	15:6I:42:HIS:N	2.51	0.42
16:7I:83:GLU:HB3	16:7I:84:ALA:H	1.66	0.42
17:8I:18:THR:HG23	17:8I:69:LYS:HD2	2.01	0.42
19:AI:9:VAL:HG21	51:M8:63:TYR:O	2.19	0.42
22:1K:9:A:H2'	22:1K:9:A:N3	2.34	0.42
24:3K:18:G:H2'	24:3K:57:G:N2	2.34	0.42
26:1H:222:A:H8	26:1H:222:A:H2'	1.76	0.42
26:1H:709:U:H2'	26:1H:710:G:C8	2.54	0.42
26:1H:929:G:H8	26:1H:929:G:O5'	2.02	0.42
26:1H:1007:C:N4	61:1H:4589:HOH:O	2.51	0.42
26:1H:1026:U:C1'	26:1H:1027:A:P	3.07	0.42
26:1H:1396:U:O2	26:1H:1396:U:H2'	2.19	0.42
26:1H:1729:A:C6	26:1H:1731:G:C2	3.07	0.42
28:11:112:GLN:O	28:11:115:GLN:HG3	2.19	0.42
28:11:149:PRO:O	28:11:150:LYS:HB2	2.18	0.42
30:31:172:TRP:CD1	30:31:172:TRP:H	2.35	0.42
38:98:2:ARG:HB3	38:98:3:HIS:H	1.64	0.42
38:98:42:LYS:O	38:98:45:ARG:HD2	2.18	0.42
46:H8:70:LEU:HA	46:H8:70:LEU:HD23	1.68	0.42
46:H8:111:VAL:O	46:H8:114:GLY:HA2	2.18	0.42
55:Q8:48:PHE:CD1	55:Q8:49:VAL:N	2.87	0.42
1:1G:475:G:C6	1:1G:476:G:C5	3.06	0.42
1:1G:784:C:H2'	1:1G:785:G:O4'	2.18	0.42
1:1G:828:A:H61	1:1G:858:G:C2'	2.32	0.42
1:1G:848:C:H2'	1:1G:849:C:C6	2.53	0.42
1:1G:1033:G:H2'	1:1G:1034:G:O4'	2.19	0.42
1:1G:1190:G:H3'	3:22:3:ASN:OD1	2.19	0.42
1:1G:1490:C:H2'	1:1G:1491:G:O4'	2.18	0.42
2:12:146:GLN:O	2:12:149:LEU:N	2.52	0.42
3:22:87:LEU:HA	3:22:90:GLU:HG2	2.00	0.42
13:4A:28:ALA:C	13:4A:30:ALA:H	2.26	0.42
19:AA:25:LYS:HB3	19:AA:26:GLY:H	1.63	0.42
56:1L:36:A:C2	25:4L:20:C:C2	3.07	0.42
57:3L:14:A:N6	57:3L:22:G:C4	2.87	0.42
26:14:21:A:C2	26:14:520:G:C2	3.06	0.42
26:14:445:C:O2'	26:14:446:G:H5'	2.19	0.42
26:14:860:U:C2	26:14:2268:A:C8	3.07	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:14:1475:G:H5'	26:14:1476:C:OP2	2.19	0.42
26:14:1858:G:H8	26:14:1858:G:OP2	2.02	0.42
26:14:2128:C:H2'	26:14:2129:C:O4'	2.19	0.42
26:14:2271:G:H2'	26:14:2272:U:C6	2.54	0.42
26:14:2881:C:H2'	26:14:2882:A:O4'	2.18	0.42
29:29:112:GLY:O	29:29:159:HIS:HA	2.18	0.42
30:39:205:ARG:HB2	30:39:205:ARG:HH11	1.84	0.42
32:59:40:GLU:OE1	32:59:64:LEU:HD12	2.19	0.42
32:59:76:VAL:O	32:59:80:SER:N	2.52	0.42
39:65:62:LYS:O	39:65:65:VAL:HG12	2.19	0.42
49:G5:64:LEU:O	49:G5:64:LEU:HD23	2.19	0.42
51:I5:21:VAL:HG22	51:I5:22:ILE:HD13	2.01	0.42
1:13:37:U:O2'	1:13:500:G:H4'	2.19	0.42
1:13:127:G:O2'	17:8I:2:PRO:O	2.37	0.42
1:13:221:C:H2'	1:13:222:U:C6	2.52	0.42
1:13:567:G:H2'	1:13:568:G:O4'	2.19	0.42
1:13:859:A:H2'	1:13:860:A:C8	2.54	0.42
1:13:1273:G:H3'	1:13:1274:G:H8	1.84	0.42
1:13:1351:U:O4	9:8E:118:LYS:HE3	2.19	0.42
5:4E:145:LYS:HA	8:7E:107:LEU:HD21	2.01	0.42
9:8E:114:TYR:HE2	10:1I:59:SER:HA	1.85	0.42
26:1H:136:G:H2'	26:1H:137:C:C6	2.54	0.42
26:1H:1678:G:C8	26:1H:1678:G:C5'	3.02	0.42
26:1H:1820:U:O2	28:11:202:LYS:HB3	2.20	0.42
26:1H:2213:U:O4'	48:J8:52:ARG:NH2	2.52	0.42
26:1H:2309:A:C6	26:1H:2310:A:N7	2.87	0.42
26:1H:2593:U:H2'	26:1H:2594:C:C6	2.53	0.42
26:1H:2659:G:H4'	32:51:175:LYS:HD2	2.01	0.42
27:16:25:A:H2'	27:16:26:A:O4'	2.19	0.42
32:51:80:SER:C	32:51:81:GLU:HG3	2.43	0.42
32:51:124:GLU:HB3	32:51:132:ARG:HB3	2.02	0.42
34:58:133:GLN:O	34:58:134:ARG:HB2	2.19	0.42
35:68:108:GLU:H	35:68:108:GLU:HG3	1.67	0.42
1:1G:266:G:H2'	1:1G:266:G:N3	2.34	0.42
1:1G:568:G:N3	1:1G:574:A:H2	2.17	0.42
1:1G:1226:C:OP2	13:4A:91:ARG:NH1	2.51	0.42
1:1G:1256:A:N6	1:1G:1277:C:H3'	2.34	0.42
6:52:33:TYR:CE1	6:52:78:GLU:HG3	2.54	0.42
12:3A:67:THR:HG1	12:3A:96:VAL:H	1.64	0.42
13:4A:13:LYS:HG2	13:4A:14:ARG:N	2.33	0.42
13:4A:57:ARG:NH1	51:I5:34:GLU:O	2.51	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:4A:73:GLU:O	13:4A:77:ASN:HB2	2.19	0.42
20:BA:45:GLN:HA	20:BA:91:LEU:HB3	2.00	0.42
20:BA:61:SER:OG	20:BA:65:LYS:NZ	2.52	0.42
26:14:191:A:H2'	26:14:192:C:C6	2.54	0.42
26:14:275:G:H2'	26:14:276:A:C8	2.55	0.42
26:14:699:A:H2'	26:14:700:G:O4'	2.18	0.42
26:14:792:G:H5"	26:14:793:A:H5'	2.01	0.42
26:14:867:C:N4	26:14:868:U:O4	2.52	0.42
26:14:1152:C:H5"	41:85:80:ILE:HG22	2.00	0.42
26:14:1322:A:N1	26:14:1333:C:O2'	2.36	0.42
26:14:1641:A:H2'	26:14:1642:G:O4'	2.19	0.42
26:14:1903:G:OP1	28:19:241:PRO:HB2	2.18	0.42
26:14:2027:G:H2'	26:14:2028:U:O4'	2.18	0.42
26:14:2028:U:H2'	26:14:2029:G:O4'	2.19	0.42
26:14:2489:G:O2'	26:14:2490:G:H5'	2.19	0.42
26:14:2774:C:H2'	26:14:2775:A:O4'	2.20	0.42
26:14:2845:G:H2'	26:14:2846:G:C8	2.54	0.42
27:1J:66:A:C6	27:1J:107:U:H2'	2.53	0.42
27:1J:87:G:N2	27:1J:89:G:H3'	2.34	0.42
30:39:107:LYS:HA	30:39:107:LYS:HD3	1.54	0.42
33:69:75:LEU:HD21	33:69:141:LYS:CE	2.49	0.42
36:35:56:SER:O	36:35:57:THR:HB	2.19	0.42
1:13:113:G:H2'	1:13:114:U:C6	2.54	0.42
1:13:116:A:OP2	1:13:116:A:C8	2.72	0.42
1:13:530:G:O6	25:4K:21:C:H1'	2.19	0.42
1:13:593:G:H2'	1:13:594:G:C8	2.55	0.42
1:13:651:C:H2'	1:13:652:U:C6	2.55	0.42
1:13:938:A:N6	61:13:1962:HOH:O	2.46	0.42
1:13:1286:A:C2	21:1F:18:TYR:OH	2.71	0.42
1:13:1347:G:C4	1:13:1373:G:C6	3.07	0.42
2:1E:74:LYS:NZ	2:1E:205:ASP:O	2.52	0.42
2:1E:89:GLY:C	2:1E:90:MET:HE2	2.43	0.42
5:4E:68:GLU:O	5:4E:70:PRO:HD3	2.18	0.42
8:7E:100:ILE:HD13	8:7E:112:LEU:HD21	2.01	0.42
11:2I:30:VAL:HG21	11:2I:65:ALA:HA	2.01	0.42
13:4I:34:LEU:HA	13:4I:34:LEU:HD22	1.85	0.42
17:8I:45:HIS:NE2	17:8I:47:PRO:HG3	2.34	0.42
21:1F:6:ARG:H	21:1F:6:ARG:HG3	1.47	0.42
26:1H:18:C:O3'	41:C8:23:GLY:HA2	2.19	0.42
26:1H:250:G:C6	26:1H:251:A:C6	3.07	0.42
26:1H:1049:C:N3	26:1H:2751:G:O6	2.51	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1H:1058:U:H3	26:1H:1080:A:N6	2.17	0.42
26:1H:1125:G:OP2	26:1H:1126:A:O2'	2.35	0.42
26:1H:1188:U:C5'	42:D8:79:VAL:HG22	2.49	0.42
26:1H:1380:G:N2	26:1H:1570:A:C2	2.87	0.42
26:1H:2345:G:N3	26:1H:2381:C:H2'	2.34	0.42
26:1H:2590:A:OP2	28:11:238:GLY:HA2	2.20	0.42
26:1H:2791:C:H42	26:1H:2807:G:H1	1.67	0.42
28:11:44:ASN:O	28:11:46:GLN:O	2.37	0.42
36:78:101:VAL:HA	36:78:105:LEU:O	2.20	0.42
41:C8:75:ASN:HB3	41:C8:77:SER:H	1.83	0.42
45:G8:28:LYS:HD2	45:G8:40:GLU:CG	2.48	0.42
1:1G:90:C:H2'	1:1G:91:C:H6	1.83	0.42
1:1G:392:G:OP1	16:7A:8:ARG:NH2	2.50	0.42
1:1G:668:G:O2'	15:6A:46:HIS:HB3	2.19	0.42
1:1G:1261:A:C2	1:1G:1262:C:H1'	2.54	0.42
1:1G:1447:G:H2'	1:1G:1448:C:C6	2.54	0.42
3:22:113:ALA:HB2	3:22:202:ILE:HG13	2.01	0.42
6:52:91:VAL:HG12	6:52:92:LYS:O	2.18	0.42
7:62:49:ILE:HG22	7:62:53:LYS:HD2	2.00	0.42
7:62:69:VAL:HG13	7:62:134:ALA:O	2.19	0.42
13:4A:3:ARG:HB2	51:I5:34:GLU:CG	2.49	0.42
13:4A:40:ASN:OD1	13:4A:41:PRO:HD2	2.19	0.42
57:3L:23:A:H2'	57:3L:24:G:H8	1.85	0.42
57:3L:56:C:H2'	57:3L:57:G:C8	2.54	0.42
26:14:271(B):G:N7	26:14:421:U:H2'	2.34	0.42
26:14:881:G:N7	26:14:882:G:C2	2.87	0.42
26:14:1471:A:C2	26:14:1472:A:C4	3.08	0.42
26:14:1812:A:H2'	26:14:1813:G:C8	2.54	0.42
26:14:2208:U:H4'	28:19:151:LYS:HG2	2.01	0.42
26:14:2298:A:H1'	26:14:2321:G:N2	2.34	0.42
26:14:2388:A:C2'	26:14:2389:G:H5'	2.49	0.42
26:14:2650:U:H2'	26:14:2651:C:C6	2.54	0.42
28:19:13:ARG:HD2	28:19:13:ARG:HA	1.75	0.42
36:35:52:GLU:O	36:35:54:GLY:N	2.52	0.42
36:35:84:ASN:ND2	36:35:117:GLU:HB3	2.34	0.42
36:35:97:PRO:O	36:35:98:GLU:HB3	2.20	0.42
39:65:83:LYS:O	39:65:110:LEU:HD12	2.19	0.42
40:75:3:ARG:O	40:75:4:GLY:C	2.58	0.42
40:75:125:ARG:HA	40:75:125:ARG:HD3	1.74	0.42
42:95:48:GLY:N	42:95:52:VAL:HG22	2.34	0.42
46:D5:146:ILE:C	46:D5:148:ASP:H	2.27	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:I5:55:ARG:HB2	51:I5:56:VAL:H	1.66	0.42
1:13:687:A:N1	1:13:700:G:O2'	2.46	0.42
1:13:1417:G:N2	1:13:1482:G:H2'	2.34	0.42
3:2E:24:ALA:HB1	3:2E:28:GLN:HB2	2.01	0.42
3:2E:134:ILE:HD11	3:2E:153:VAL:HG21	2.01	0.42
4:3E:162:LEU:HD13	4:3E:181:MET:HG2	2.01	0.42
5:4E:36:ASP:OD2	5:4E:38:GLN:HB2	2.19	0.42
16:7I:74:LEU:O	16:7I:79:VAL:HB	2.18	0.42
17:8I:89:LEU:HA	17:8I:89:LEU:HD13	1.74	0.42
18:9I:53:ARG:HH21	18:9I:59:SER:C	2.27	0.42
24:3K:71:G:C2	24:3K:72:C:H1'	2.53	0.42
26:1H:686:G:H4'	26:1H:687:C:OP2	2.19	0.42
26:1H:910:A:N1	26:1H:2277:G:H1'	2.34	0.42
26:1H:1054:A:H2	26:1H:1105:U:H3	1.68	0.42
26:1H:1514:U:H2'	26:1H:1515:C:C6	2.55	0.42
26:1H:2401:U:H2'	26:1H:2402:C:H5"	2.02	0.42
27:16:70:C:N3	27:16:71:C:C5	2.87	0.42
28:11:53:PHE:O	28:11:218:ARG:N	2.48	0.42
31:41:79:ASN:OD1	31:41:79:ASN:N	2.50	0.42
34:58:30:ILE:O	34:58:34:LEU:HB2	2.19	0.42
34:58:39:ARG:NH1	34:58:41:ASP:OD2	2.51	0.42
35:68:63:VAL:HG12	35:68:106:LEU:HD11	2.00	0.42
38:98:51:LEU:HD23	38:98:51:LEU:HA	1.91	0.42
39:A8:36:TYR:N	39:A8:36:TYR:CD1	2.87	0.42
40:B8:16:ARG:HH21	40:B8:19:LEU:HD21	1.84	0.42
44:F8:1:MET:O	44:F8:3:THR:N	2.52	0.42
47:I8:47:PRO:CB	47:I8:51:VAL:HG12	2.50	0.42
50:L8:35:ARG:HB3	50:L8:37:LEU:HD21	2.02	0.42
1:1G:836:G:C6	1:1G:851:G:C6	3.07	0.42
1:1G:1011:G:N2	1:1G:1019:C:O2	2.51	0.42
1:1G:1099:G:H5'	1:1G:1100:C:OP2	2.19	0.42
1:1G:1376:U:H2'	1:1G:1377:A:C8	2.55	0.42
1:1G:1512:U:H2'	1:1G:1513:A:H8	1.84	0.42
2:12:215:LEU:HA	2:12:218:ALA:HB3	2.00	0.42
4:32:22:LYS:HD2	4:32:26:CYS:SG	2.58	0.42
9:82:119:ALA:O	9:82:120:ARG:HB2	2.18	0.42
13:4A:29:ARG:HD3	13:4A:64:TRP:CZ3	2.54	0.42
20:BA:55:ILE:HA	20:BA:55:ILE:HD13	1.71	0.42
56:1L:15:G:N2	56:1L:59:U:O2	2.53	0.42
23:2L:32:G:C4	23:2L:33:OMC:C5	3.08	0.42
26:14:515:A:H1'	26:14:581:C:H1'	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:14:605:C:O2	26:14:657:U:O2'	2.37	0.42
26:14:854:G:H2'	26:14:855:G:C8	2.54	0.42
26:14:999:U:O2'	26:14:1000:A:H5'	2.19	0.42
26:14:1025:G:C5	26:14:1135:C:H1'	2.55	0.42
26:14:1217:C:OP1	41:85:15:LYS:NZ	2.44	0.42
26:14:1470:G:N2	26:14:1522:G:OP2	2.53	0.42
26:14:1664:A:P	61:14:3613:HOH:O	2.68	0.42
26:14:1771:C:H1'	26:14:1786:A:C8	2.54	0.42
26:14:1824:G:N7	61:14:3851:HOH:O	2.37	0.42
26:14:2228:G:C5	26:14:2229:C:C4	3.07	0.42
26:14:2377:A:H2'	26:14:2378:A:C8	2.54	0.42
26:14:2489:G:C2'	26:14:2490:G:H5'	2.49	0.42
27:1J:56:G:H4'	27:1J:57:A:H8	1.81	0.42
29:29:73:GLU:HA	29:29:74:PRO:HD2	1.74	0.42
31:49:33:ARG:NH2	31:49:162:THR:HG21	2.34	0.42
34:15:15:LEU:HD23	34:15:134:ARG:HG3	2.00	0.42
37:45:59:ARG:H	37:45:59:ARG:HG3	1.42	0.42
39:65:87:PHE:CZ	39:65:102:ALA:HB2	2.54	0.42
41:85:92:ARG:O	41:85:94:ASN:N	2.53	0.42
46:D5:163:LEU:HD12	46:D5:165:VAL:HG23	2.01	0.42
1:13:1152:A:H4'	10:1I:13:HIS:CD2	2.54	0.42
3:2E:91:LEU:HB2	3:2E:99:VAL:HG21	2.00	0.42
4:3E:120:LEU:HD23	4:3E:120:LEU:HA	1.85	0.42
5:4E:24:ARG:HE	5:4E:24:ARG:HB3	1.72	0.42
7:6E:31:MET:HE1	7:6E:36:LYS:HZ2	1.84	0.42
20:BI:33:ILE:HG12	20:BI:33:ILE:H	1.55	0.42
26:1H:57:C:H2'	26:1H:58:G:O4'	2.19	0.42
26:1H:301:G:C2	26:1H:302:C:C2	3.08	0.42
26:1H:1207:C:H2'	26:1H:1208:C:H6	1.84	0.42
26:1H:1636:C:H2'	26:1H:1637:A:C8	2.54	0.42
26:1H:1799:G:H5'	26:1H:1819:A:N6	2.33	0.42
26:1H:2128:C:O2'	26:1H:2129:C:H5'	2.19	0.42
26:1H:2854:G:C2	26:1H:2855:C:C2	3.07	0.42
30:31:197:ASP:O	30:31:198:ALA:C	2.61	0.42
31:41:43:LEU:N	31:41:88:ILE:O	2.47	0.42
33:61:135:GLU:HB2	33:61:136:VAL:H	1.64	0.42
34:58:1:MET:C	34:58:2:LYS:HD3	2.44	0.42
35:68:80:ASP:OD2	40:B8:71:GLY:HA3	2.20	0.42
36:78:100:LEU:HA	36:78:100:LEU:HD12	1.60	0.42
41:C8:60:LEU:HD11	41:C8:64:ARG:CZ	2.49	0.42
44:F8:57:LEU:N	44:F8:57:LEU:HD23	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1G:407:G:H2'	1:1G:408:A:C8	2.53	0.42
1:1G:643:C:H2'	1:1G:644:G:H8	1.84	0.42
1:1G:1014:A:P	1:1G:1014:A:H8	2.43	0.42
1:1G:1086:U:O5'	1:1G:1086:U:H6	2.02	0.42
1:1G:1127:G:H22	1:1G:1144:G:N2	2.18	0.42
1:1G:1203:C:H2'	1:1G:1204:A:H8	1.84	0.42
2:12:71:VAL:HG23	2:12:164:VAL:HG13	2.01	0.42
3:22:134:ILE:HD13	3:22:134:ILE:HA	1.86	0.42
4:32:57:ARG:HH12	5:42:107:ARG:NH2	2.17	0.42
26:14:720:C:H2'	26:14:721:C:C6	2.55	0.42
26:14:2298:A:N6	26:14:2318:G:H2'	2.34	0.42
28:19:11:PRO:C	28:19:13:ARG:N	2.78	0.42
29:29:31:CYS:HB3	29:29:49:LEU:HB3	2.00	0.42
29:29:37:ARG:HE	29:29:42:ASP:CG	2.25	0.42
30:39:28:ILE:HA	30:39:112:MET:HG2	2.02	0.42
32:59:103:LEU:HD13	32:59:131:VAL:HG21	2.01	0.42
33:69:140:LEU:HA	33:69:140:LEU:HD12	1.68	0.42
36:35:13:ASN:C	36:35:15:ARG:N	2.78	0.42
36:35:15:ARG:O	36:35:15:ARG:NE	2.52	0.42
39:65:49:VAL:CG2	39:65:80:LEU:HD12	2.50	0.42
43:A5:95:ILE:HG12	43:A5:95:ILE:O	2.20	0.42
46:D5:29:TYR:HB3	46:D5:34:ASN:OD1	2.19	0.42
46:D5:94:GLU:HA	46:D5:95:PRO:HD3	1.92	0.42
1:13:723:U:H5'	1:13:724:G:OP2	2.19	0.42
1:13:814:A:N7	1:13:816:A:C4	2.87	0.42
1:13:1074:G:O2'	1:13:1101:A:N1	2.49	0.42
1:13:1103:C:H5"	2:1E:98:LEU:HD13	2.02	0.42
1:13:1513:A:H2'	1:13:1514:C:C6	2.54	0.42
2:1E:187:LEU:HD11	2:1E:204:ASN:O	2.20	0.42
2:1E:190:THR:C	2:1E:192:SER:N	2.77	0.42
3:2E:33:LEU:O	3:2E:36:ASP:HB2	2.19	0.42
4:3E:99:SER:O	4:3E:140:VAL:HG22	2.20	0.42
16:7I:58:TYR:CD1	16:7I:58:TYR:C	2.94	0.42
26:1H:794:G:H2'	26:1H:795:C:C6	2.54	0.42
26:1H:828:U:H4'	26:1H:831:G:N1	2.34	0.42
26:1H:1534:G:H22	26:1H:1538:G:N2	2.14	0.42
26:1H:2199:A:C8	26:1H:2199:A:C5'	3.01	0.42
26:1H:2469:A:H5'	26:1H:2469:A:N3	2.35	0.42
26:1H:2564:A:C2	26:1H:2647:U:H4'	2.54	0.42
27:16:79:C:O5'	27:16:79:C:H6	2.03	0.42
29:21:116:VAL:HG13	29:21:122:PHE:CD2	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:51:4:ILE:C	32:51:6:ARG:H	2.27	0.42
36:78:85:LEU:HA	36:78:88:LEU:CD2	2.50	0.42
36:78:121:LYS:HE3	36:78:121:LYS:HB3	1.37	0.42
36:78:135:LEU:HD23	36:78:135:LEU:HA	1.89	0.42
37:88:30:GLY:HA2	37:88:107:ALA:HB2	2.02	0.42
39:A8:108:GLY:O	39:A8:110:LEU:HD22	2.19	0.42
40:B8:45:PHE:CZ	40:B8:65:LYS:HG2	2.55	0.42
46:H8:28:MET:HB2	46:H8:37:VAL:HG11	2.02	0.42
55:Q8:46:ARG:CG	55:Q8:46:ARG:NH1	2.79	0.42
55:Q8:50:LEU:HG	55:Q8:51:ALA:H	1.85	0.42
1:1G:322:C:H5	1:1G:328:C:H5	1.66	0.42
1:1G:501:C:OP1	12:3A:117:ARG:NH2	2.29	0.42
1:1G:625:G:C4	1:1G:626:U:C5	3.08	0.42
1:1G:652:U:O2'	1:1G:653:A:N3	2.44	0.42
1:1G:1055:A:N6	1:1G:1206:G:C5	2.88	0.42
1:1G:1320:C:C4	1:1G:1321:C:N4	2.88	0.42
1:1G:1365:G:H2'	1:1G:1366:C:C6	2.55	0.42
2:12:136:VAL:O	2:12:139:LYS:HB3	2.19	0.42
5:42:20:GLN:CD	5:42:21:ALA:H	2.28	0.42
19:AA:32:LYS:HB3	19:AA:57:HIS:CD2	2.54	0.42
19:AA:71:LEU:HD23	19:AA:71:LEU:HA	1.84	0.42
20:BA:97:ALA:HA	20:BA:98:PRO:HD3	1.82	0.42
21:1B:9:ARG:HG3	21:1B:10:ARG:N	2.34	0.42
23:2L:17:C:OP2	23:2L:18:C:O2'	2.29	0.42
26:14:686:G:H2'	26:14:788:A:N1	2.35	0.42
26:14:686:G:N7	54:L5:5:TRP:CH2	2.87	0.42
26:14:832:G:N2	36:35:53:GLY:HA3	2.35	0.42
26:14:1060:U:H5'	26:14:1061:U:C6	2.54	0.42
26:14:1328:G:H2'	26:14:1330:C:C5	2.55	0.42
26:14:1683:C:H2'	26:14:1684:C:H6	1.84	0.42
26:14:1979:C:C2'	26:14:1980:G:H5'	2.49	0.42
26:14:2695:C:H2'	26:14:2696:U:H6	1.83	0.42
26:14:2747:G:C6	26:14:2754:U:C5	3.08	0.42
27:1J:2:C:H2'	27:1J:3:C:C5	2.55	0.42
34:15:35:ARG:CB	34:15:42:TRP:HZ3	2.33	0.42
37:45:19:GLY:O	37:45:99:PRO:HD2	2.18	0.42
40:75:45:PHE:CE2	40:75:74:ARG:HD3	2.54	0.42
42:95:17:GLY:H	42:95:96:ILE:HB	1.85	0.42
45:C5:17:SER:HB2	45:C5:71:LYS:HD2	2.02	0.42
47:E5:32:ARG:O	47:E5:34:GLY:N	2.46	0.42
1:13:22:G:C6	1:13:23:C:C4	3.07	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:13:444:C:H2'	1:13:445:G:C8	2.55	0.42
1:13:464:G:C6	1:13:466:C:H5'	2.55	0.42
1:13:724:G:C2	1:13:725:G:C8	3.07	0.42
1:13:917:G:H2'	1:13:918:A:H8	1.85	0.42
1:13:1117:G:H5"	9:8E:104:ARG:CZ	2.49	0.42
2:1E:22:LYS:C	2:1E:24:TRP:H	2.25	0.42
5:4E:20:GLN:OE1	5:4E:25:ARG:NH2	2.53	0.42
9:8E:92:TYR:HD1	9:8E:92:TYR:HA	1.69	0.42
11:2I:16:SER:O	11:2I:35:PRO:HG3	2.20	0.42
11:2I:20:TYR:HB2	11:2I:31:THR:HG23	2.02	0.42
13:4I:67:GLU:OE2	13:4I:68:GLY:N	2.52	0.42
16:7I:58:TYR:O	16:7I:61:SER:N	2.49	0.42
17:8I:70:ARG:C	17:8I:71:PHE:HD1	2.26	0.42
22:1K:76:A:O2'	26:1H:2506:U:H1'	2.19	0.42
24:3K:64:A:C2	24:3K:65:G:H1'	2.54	0.42
26:1H:86:C:H4'	26:1H:104:U:H1'	2.01	0.42
26:1H:322:A:OP2	30:31:169:ASN:HB2	2.20	0.42
26:1H:503:A:H4'	26:1H:504:U:H5"	2.02	0.42
26:1H:587:C:O2	36:78:33:ARG:NH1	2.53	0.42
26:1H:813:U:H2'	26:1H:814:C:C6	2.55	0.42
26:1H:1163:G:C2	26:1H:1164:G:N7	2.88	0.42
26:1H:1221:C:C2	26:1H:1222:C:C5	3.08	0.42
26:1H:1534:G:N2	26:1H:1538:G:N2	2.68	0.42
26:1H:1769:G:O2'	26:1H:1958:C:OP1	2.27	0.42
26:1H:2299:G:N2	26:1H:2318:G:H1'	2.34	0.42
26:1H:2432:A:C4	48:J8:33:LYS:HG2	2.55	0.42
26:1H:2692:C:OP1	26:1H:2871:C:H5'	2.20	0.42
26:1H:2713:A:H3'	26:1H:2714:G:H5"	2.00	0.42
26:1H:2815:C:H5'	52:N8:29:THR:HG21	2.02	0.42
31:41:37:VAL:HG21	31:41:103:LEU:HD21	2.02	0.42
37:88:85:LYS:CG	37:88:86:GLY:N	2.82	0.42
42:D8:9:GLY:O	42:D8:10:LYS:HG3	2.20	0.42
48:J8:78:LYS:O	48:J8:78:LYS:HG2	2.20	0.42
53:O8:34:LEU:H	53:O8:34:LEU:HD22	1.83	0.42
1:1G:15:G:H2'	1:1G:16:A:C8	2.55	0.42
1:1G:199:G:H2'	1:1G:200:G:H8	1.85	0.42
1:1G:362:G:C4'	12:3A:33:ARG:HH21	2.33	0.42
1:1G:374:A:C4	1:1G:375:U:C5	3.07	0.42
1:1G:642:A:N3	8:72:113:SER:OG	2.50	0.42
1:1G:868:C:H2'	1:1G:869:G:O4'	2.19	0.42
1:1G:991:U:OP2	1:1G:991:U:H6	2.03	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1G:1507:A:O3'	61:1G:1761:HOH:O	2.22	0.42
2:12:10:LEU:HD13	2:12:10:LEU:HA	1.82	0.42
3:22:129:ALA:HB3	3:22:132:ARG:HB3	2.01	0.42
4:32:150:GLU:C	4:32:152:SER:N	2.78	0.42
9:82:48:GLU:N	9:82:49:PRO:HD2	2.35	0.42
13:4A:86:CYS:SG	13:4A:88:ARG:HB3	2.60	0.42
26:14:513:A:C2	26:14:514:A:C5	3.08	0.42
26:14:635:C:H2'	26:14:636:G:O4'	2.20	0.42
26:14:649:G:C5	26:14:650:C:C4	3.07	0.42
26:14:1115:G:H2'	26:14:1116:C:C6	2.55	0.42
26:14:1187:G:P	61:14:3684:HOH:O	2.70	0.42
26:14:2168:G:N2	26:14:2170:A:C8	2.88	0.42
26:14:2294:C:P	39:65:89:ARG:NH2	2.93	0.42
29:29:151:TYR:CD2	29:29:154:LYS:NZ	2.79	0.42
41:85:91:ASP:O	41:85:93:LYS:N	2.53	0.42
43:A5:71:VAL:HA	43:A5:107:LEU:HD12	2.00	0.42
51:I5:22:ILE:O	51:I5:24:THR:HG23	2.19	0.42
52:J5:3:LYS:HD2	52:J5:3:LYS:HA	1.49	0.42
1:13:257:G:N1	1:13:258:G:C5	2.88	0.42
1:13:282:A:N3	1:13:282:A:H2'	2.34	0.42
1:13:329:A:C4	1:13:332:G:C5	3.07	0.42
1:13:595:G:H1'	1:13:596:C:H5	1.84	0.42
1:13:692:U:O2'	1:13:694:A:N7	2.36	0.42
1:13:739:C:O2	15:6I:42:HIS:HE1	2.02	0.42
2:1E:85:ALA:O	2:1E:90:MET:N	2.47	0.42
4:3E:50:ARG:H	4:3E:50:ARG:HG3	1.54	0.42
5:4E:133:TYR:HD1	5:4E:133:TYR:HA	1.58	0.42
8:7E:39:LEU:HD12	8:7E:39:LEU:HA	1.79	0.42
10:1I:6:ILE:HG22	10:1I:98:ILE:CG1	2.46	0.42
13:4I:11:ARG:HG2	13:4I:12:ASN:H	1.84	0.42
16:7I:21:VAL:HG12	16:7I:33:ILE:HD12	2.02	0.42
18:9I:37:VAL:HG12	18:9I:41:LYS:HE3	2.02	0.42
18:9I:52:PRO:O	18:9I:56:THR:HG23	2.19	0.42
26:1H:18:C:H4'	41:C8:23:GLY:O	2.20	0.42
26:1H:533:G:H5'	41:C8:24:TYR:CE1	2.53	0.42
26:1H:1253:A:C5	61:1H:3711:HOH:O	2.73	0.42
26:1H:1526:G:H2'	26:1H:1527:G:O4'	2.20	0.42
26:1H:1682:G:C2	26:1H:1683:C:C2	3.08	0.42
26:1H:1975:G:C2	26:1H:1976:U:C2	3.08	0.42
26:1H:2115:G:H1'	26:1H:2171:A:N1	2.34	0.42
26:1H:2443:C:OP1	30:31:68:LYS:HD3	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1H:2837:G:C6	26:1H:2838:G:N7	2.87	0.42
33:61:58:LEU:HD23	33:61:59:ALA:N	2.35	0.42
39:A8:59:LYS:HG2	39:A8:60:GLY:N	2.32	0.42
40:B8:105:LEU:O	40:B8:107:ASP:N	2.53	0.42
45:G8:29:GLU:HB3	45:G8:38:ILE:HG23	2.00	0.42
46:H8:80:ARG:H	46:H8:80:ARG:HG2	1.44	0.42
46:H8:141:VAL:HG21	46:H8:150:LEU:CD1	2.49	0.42
51:M8:12:ALA:O	51:M8:24:THR:HG21	2.20	0.42
1:1G:176:C:H2'	1:1G:177:C:C6	2.55	0.42
1:1G:283:C:C2	1:1G:284:G:C8	3.07	0.42
1:1G:373:A:N3	1:1G:374:A:C8	2.88	0.42
1:1G:519:C:OP2	12:3A:50:SER:OG	2.38	0.42
1:1G:750:G:H21	15:6A:23:GLY:HA3	1.84	0.42
1:1G:972:C:OP2	10:1A:57:LYS:HD2	2.20	0.42
1:1G:1043:C:H2'	1:1G:1044:A:H8	1.84	0.42
1:1G:1099:G:OP1	2:12:148:TYR:OH	2.37	0.42
1:1G:1287:A:H2'	1:1G:1288:A:C8	2.55	0.42
1:1G:1496:C:H2'	1:1G:1497:G:O4'	2.19	0.42
2:12:30:ARG:NH2	2:12:195:ASP:OD1	2.53	0.42
2:12:189:ASP:OD1	2:12:189:ASP:N	2.53	0.42
26:14:122:G:OP1	26:14:149:A:O2'	2.36	0.42
26:14:201:C:O2'	26:14:251:A:N1	2.49	0.42
26:14:664:C:P	36:35:18:ARG:HH21	2.42	0.42
26:14:768:G:H2'	26:14:769:G:H8	1.85	0.42
26:14:851:U:H5'	50:H5:49:LYS:HD2	2.02	0.42
26:14:1104:C:H2'	26:14:1105:U:C6	2.55	0.42
26:14:1327:C:O3'	38:55:105:ARG:NH2	2.53	0.42
26:14:1341:U:O4'	44:B5:57:LEU:HD22	2.20	0.42
26:14:1436:G:O2'	26:14:1477:A:H4'	2.20	0.42
26:14:2360:A:H2'	26:14:2361:A:O4'	2.20	0.42
26:14:2506:U:O5'	26:14:2506:U:H6	2.03	0.42
26:14:2766:G:H5"	26:14:2767:C:OP2	2.19	0.42
26:14:2767:C:H2'	26:14:2768:C:C6	2.54	0.42
26:14:2887:U:O2'	26:14:2888:C:H5'	2.20	0.42
27:1J:118:G:C6	27:1J:119:A:N7	2.88	0.42
29:29:199:ARG:HH12	29:29:202:LYS:NZ	2.17	0.42
31:49:37:VAL:HG22	31:49:159:VAL:HG12	2.02	0.42
31:49:108:ASN:O	51:I5:37:SER:HA	2.20	0.42
32:59:86:GLU:H	32:59:86:GLU:CD	2.28	0.42
32:59:138:LYS:HD2	32:59:138:LYS:HA	1.84	0.42
44:B5:66:LEU:HD23	44:B5:66:LEU:HA	1.86	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:C5:39:VAL:O	45:C5:40:GLU:HB2	2.20	0.42
1:13:173:U:C6	1:13:197:A:C2	3.07	0.42
1:13:376:G:OP1	16:7I:5:ARG:HB2	2.20	0.42
1:13:963:G:H1	1:13:972:C:N4	2.16	0.42
1:13:1348:U:N3	1:13:1374:A:C2	2.80	0.42
1:13:1438:G:H2'	1:13:1439:C:C6	2.54	0.42
2:1E:141:GLU:HG3	2:1E:145:LEU:HD23	2.00	0.42
2:1E:178:ARG:HD2	8:7E:71:GLY:O	2.20	0.42
2:1E:237:ALA:O	2:1E:239:VAL:HG23	2.20	0.42
8:7E:39:LEU:HB3	8:7E:45:ILE:CD1	2.49	0.42
12:3I:69:TYR:CD1	12:3I:90:VAL:HG21	2.55	0.42
13:4I:82:MET:O	13:4I:84:ILE:N	2.49	0.42
18:9I:76:LEU:HD13	18:9I:76:LEU:HA	1.85	0.42
26:1H:287:C:H2'	26:1H:288:C:C6	2.55	0.42
26:1H:333:G:H5"	26:1H:334:C:OP2	2.20	0.42
26:1H:631:A:H61	26:1H:2402:C:N4	2.18	0.42
26:1H:852:G:H2'	26:1H:853:G:C8	2.55	0.42
26:1H:996:A:C5	26:1H:1160:G:N2	2.88	0.42
26:1H:1165:U:C2	26:1H:1166:C:C5	3.08	0.42
26:1H:1414:G:C6	26:1H:1415:U:C4	3.08	0.42
26:1H:1621:U:H5"	26:1H:1622:G:OP1	2.19	0.42
26:1H:1652:A:OP1	38:98:8:ARG:NH1	2.53	0.42
26:1H:2127:G:H1	26:1H:2162:G:H1'	1.84	0.42
26:1H:2286:A:H4'	26:1H:2287:A:O4'	2.20	0.42
28:11:108:PRO:HG3	28:11:143:HIS:CE1	2.55	0.42
28:11:150:LYS:HA	28:11:150:LYS:HD3	1.94	0.42
29:21:37:ARG:HA	29:21:42:ASP:OD2	2.20	0.42
29:21:141:ILE:HD12	29:21:150:VAL:HG21	2.02	0.42
31:41:66:GLN:HA	51:M8:6:HIS:HE1	1.85	0.42
33:61:79:ILE:HD13	33:61:79:ILE:HA	1.70	0.42
33:61:79:ILE:HA	33:61:80:PRO:HD2	1.87	0.42
42:D8:15:GLU:HB3	42:D8:16:PRO:HD2	2.01	0.42
55:Q8:54:GLU:C	55:Q8:56:GLU:H	2.27	0.42
1:1G:659:U:H2'	1:1G:660:G:O4'	2.20	0.42
1:1G:674:G:N2	1:1G:717:C:O2	2.53	0.42
1:1G:1292:U:H2'	1:1G:1293:G:H8	1.84	0.42
1:1G:1308:U:H5"	13:4A:98:VAL:CG2	2.49	0.42
1:1G:1424:C:H2'	1:1G:1425:U:O4'	2.20	0.42
17:8A:10:VAL:HG23	17:8A:54:GLY:N	2.34	0.42
17:8A:63:ARG:HG2	17:8A:64:PRO:HD2	2.01	0.42
56:1L:21:A:N6	56:1L:46:G:N3	2.68	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:14:337:C:H2'	26:14:338:G:O4'	2.20	0.42
26:14:340:A:C8	26:14:341:G:C8	3.08	0.42
26:14:515:A:H2	26:14:1260:G:N3	2.18	0.42
26:14:576:U:H2'	26:14:577:G:C8	2.55	0.42
26:14:696:G:O2'	26:14:697:C:H5'	2.19	0.42
26:14:797:C:H2'	26:14:798:G:O4'	2.20	0.42
26:14:918:A:C2	27:1J:80:U:H4'	2.54	0.42
26:14:1358:G:O2'	26:14:1359:A:H5"	2.20	0.42
26:14:1543:A:H1'	26:14:1545:A:H1'	2.01	0.42
26:14:2562:U:H1'	35:25:23:ARG:HE	1.85	0.42
26:14:2577:A:H5"	26:14:2578:G:H5'	2.01	0.42
26:14:2724:C:N4	61:14:3617:HOH:O	2.06	0.42
27:1J:15:A:H1'	27:1J:109:G:C4	2.54	0.42
28:19:134:ARG:NH1	28:19:188:GLU:OE2	2.48	0.42
29:29:38:THR:HG23	29:29:40:GLU:HB2	2.02	0.42
30:39:31:HIS:CD2	30:39:31:HIS:C	2.97	0.42
30:39:69:HIS:CD2	30:39:69:HIS:N	2.88	0.42
30:39:123:LEU:C	30:39:125:LEU:H	2.18	0.42
37:45:33:GLY:O	37:45:132:VAL:HG12	2.20	0.42
42:95:15:GLU:HG2	42:95:16:PRO:HD2	2.00	0.42
42:95:80:GLN:C	42:95:81:TYR:CD1	2.96	0.42
43:A5:69:LEU:HA	43:A5:108:GLY:O	2.20	0.42
45:C5:104:GLY:HA2	45:C5:105:ALA:HA	1.69	0.42
54:L5:12:ARG:HH21	54:L5:44:PRO:HB3	1.84	0.42
1:13:122:G:H8	1:13:122:G:OP1	2.01	0.42
1:13:266:G:H8	1:13:266:G:H2'	1.77	0.42
1:13:600:C:C6	1:13:601:C:C5	3.08	0.42
1:13:883:C:C2'	1:13:884:U:H5'	2.50	0.42
1:13:963:G:N2	1:13:972:C:N3	2.46	0.42
1:13:992:U:H3	1:13:1044:A:H62	1.67	0.42
1:13:1326:C:H2'	1:13:1327:C:H6	1.85	0.42
2:1E:80:ILE:HD12	2:1E:80:ILE:H	1.84	0.42
3:2E:113:ALA:HA	3:2E:202:ILE:HD11	2.02	0.42
6:5E:44:GLY:HA2	6:5E:59:TYR:CE1	2.54	0.42
6:5E:79:LEU:HD23	6:5E:79:LEU:HA	1.78	0.42
8:7E:134:ILE:HG22	8:7E:135:CYS:SG	2.59	0.42
10:1I:3:LYS:N	10:1I:74:ILE:O	2.53	0.42
12:3I:12:ARG:HH11	12:3I:12:ARG:HD2	1.67	0.42
13:4I:65:LYS:NZ	51:M8:52:THR:HB	2.35	0.42
17:8I:68:ARG:N	17:8I:70:ARG:HH11	2.13	0.42
19:AI:25:LYS:HD3	19:AI:27:GLU:HB2	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1H:444:C:C4'	30:31:49:ALA:HB2	2.50	0.42
26:1H:527:C:H4'	26:1H:528:A:H5'	2.02	0.42
26:1H:789:A:OP1	26:1H:789:A:H3'	2.20	0.42
26:1H:1112:G:C6	26:1H:1113:U:C4	3.07	0.42
26:1H:1156:A:C8	41:C8:51:LYS:CD	3.03	0.42
26:1H:1296:G:O2'	26:1H:1297:C:H5'	2.20	0.42
26:1H:1314:C:P	61:1H:3971:HOH:O	2.78	0.42
26:1H:1485:G:C2	26:1H:1486:A:C4	3.08	0.42
26:1H:1525:G:C4	26:1H:1526:G:C8	3.08	0.42
26:1H:1658:C:H2'	26:1H:1659:U:C6	2.54	0.42
26:1H:1900:A:N1	26:1H:1970:A:C6	2.88	0.42
26:1H:2212:A:H1'	26:1H:2215:G:C6	2.54	0.42
28:11:92:ILE:HD12	28:11:104:TYR:CD1	2.55	0.42
28:11:121:PRO:HB3	28:11:135:PHE:CE2	2.54	0.42
28:11:236:GLY:O	28:11:237:GLU:HB2	2.20	0.42
28:11:261:LYS:HG3	28:11:262:ARG:N	2.35	0.42
30:31:177:ALA:HB1	30:31:178:PRO:HD2	2.02	0.42
30:31:206:ILE:HG21	30:31:206:ILE:HD13	1.78	0.42
34:58:23:LEU:HD13	34:58:60:ILE:HG13	2.02	0.42
38:98:117:VAL:HG22	38:98:118:GLU:H	1.85	0.42
48:J8:92:LYS:HG3	48:J8:95:LEU:HD12	2.01	0.42
51:M8:1:MET:HE3	51:M8:1:MET:HB3	1.73	0.42
52:N8:33:CYS:SG	52:N8:36:CYS:N	2.93	0.42
52:N8:41:PRO:HG2	52:N8:44:THR:HG21	2.01	0.42
1:1G:28:G:C6	1:1G:29:G:C5	3.08	0.42
1:1G:187:C:H2'	1:1G:188:U:O4'	2.20	0.42
1:1G:405:U:H5"	1:1G:406:G:O4'	2.20	0.42
1:1G:448:A:H2'	1:1G:449:C:O2	2.20	0.42
1:1G:750:G:C2	15:6A:23:GLY:HA3	2.54	0.42
1:1G:1030:C:O2	1:1G:1031:G:N1	2.52	0.42
1:1G:1072:G:C6	1:1G:1104:G:N1	2.88	0.42
1:1G:1236:A:H2'	1:1G:1237:C:C6	2.55	0.42
1:1G:1260:C:H3'	1:1G:1260:C:C6	2.55	0.42
1:1G:1326:C:H2'	1:1G:1327:C:C6	2.55	0.42
1:1G:1349:A:P	9:82:118:LYS:NZ	2.92	0.42
3:22:34:LEU:HD11	3:22:38:ARG:HH21	1.83	0.42
6:52:2:ARG:HE	6:52:69:GLU:CB	2.33	0.42
6:52:10:LEU:HD12	6:52:10:LEU:N	2.35	0.42
8:72:20:TYR:HD1	8:72:65:TYR:CD2	2.38	0.42
12:3A:32:PHE:HD1	12:3A:86:ARG:HA	1.84	0.42
13:4A:66:LEU:CA	13:4A:70:LEU:HB2	2.50	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:9A:66:LEU:O	18:9A:70:ILE:HG13	2.20	0.42
20:BA:54:LYS:HA	20:BA:57:ARG:NH1	2.35	0.42
26:14:221:A:C4	26:14:266:G:N7	2.88	0.42
26:14:273(C):C:H3'	26:14:273(D):C:H5"	2.02	0.42
26:14:582:G:H2'	26:14:583:G:C8	2.55	0.42
26:14:768:G:O2'	26:14:1379:A:N6	2.52	0.42
26:14:782:A:H5'	26:14:783:A:C2	2.55	0.42
26:14:1348:G:C6	26:14:1349:A:N1	2.88	0.42
26:14:1558:A:O2'	26:14:1559:G:OP2	2.28	0.42
26:14:2079:U:H2'	26:14:2080:G:O4'	2.20	0.42
26:14:2535:G:H2'	26:14:2536:G:C8	2.55	0.42
26:14:2578:G:O2'	26:14:2579:C:H5'	2.20	0.42
26:14:2747:G:O6	26:14:2755:C:H5"	2.20	0.42
27:1J:90:C:OP2	37:45:16:ARG:NH2	2.50	0.42
29:29:51:PHE:O	29:29:74:PRO:HB2	2.19	0.42
31:49:64:THR:OG1	31:49:94:LEU:HD21	2.19	0.42
32:59:88:LEU:HD13	32:59:164:TYR:O	2.20	0.42
34:15:56:ASN:OD1	34:15:56:ASN:N	2.52	0.42
36:35:78:PRO:HB3	36:35:111:ARG:NH2	2.35	0.42
38:55:48:VAL:HA	38:55:51:LEU:HB2	2.01	0.42
42:95:85:LYS:HG3	42:95:87:HIS:CA	2.50	0.42
46:D5:73:GLN:O	46:D5:86:VAL:HG22	2.19	0.42
48:F5:91:LYS:O	48:F5:92:LYS:C	2.63	0.42
53:K5:27:LYS:NZ	53:K5:27:LYS:HB3	2.35	0.42
1:13:724:G:O2'	1:13:725:G:H5'	2.19	0.41
1:13:1135:U:H2'	1:13:1137:C:C2	2.54	0.41
2:1E:219:VAL:HA	2:1E:222:ILE:HD12	2.01	0.41
3:2E:70:VAL:HG21	3:2E:76:VAL:HG11	2.01	0.41
3:2E:149:ALA:HA	3:2E:201:TYR:O	2.20	0.41
13:4I:13:LYS:NZ	13:4I:13:LYS:HA	2.35	0.41
20:BI:30:LYS:HA	20:BI:30:LYS:HD2	1.78	0.41
23:2K:76:C:H5"	23:2K:77:A:OP2	2.20	0.41
24:3K:60:U:H6	24:3K:60:U:O5'	2.01	0.41
26:1H:456:C:O2'	26:1H:457:A:OP2	2.32	0.41
26:1H:942:G:H4'	26:1H:1190:G:H5'	2.02	0.41
26:1H:1092:C:H2'	26:1H:1093:G:H5'	2.01	0.41
26:1H:1394:U:H4'	26:1H:1603:A:H4'	2.02	0.41
26:1H:1897:G:H2'	26:1H:1898:U:O4'	2.20	0.41
26:1H:2302:G:C6	26:1H:2315:G:C6	3.08	0.41
26:1H:2309:A:C5	26:1H:2310:A:C8	3.07	0.41
26:1H:2747:G:O2'	32:51:67:LEU:HD12	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:41:33:ARG:O	31:41:162:THR:HG23	2.20	0.41
32:51:30:LYS:HG3	32:51:80:SER:HA	2.02	0.41
32:51:88:LEU:HB3	32:51:130:ARG:HG3	2.02	0.41
41:C8:88:ILE:O	41:C8:88:ILE:HG22	2.20	0.41
46:H8:137:ILE:HG12	46:H8:158:PRO:HG2	2.01	0.41
49:K8:34:GLU:O	49:K8:38:GLN:HG3	2.20	0.41
55:Q8:58:ILE:HD13	55:Q8:58:ILE:HG21	1.64	0.41
1:1G:64:G:OP1	1:1G:64:G:H3'	2.20	0.41
1:1G:338:A:C5	1:1G:339:C:C5	3.08	0.41
1:1G:446:G:H1	1:1G:488:C:H42	1.67	0.41
1:1G:1151:A:OP1	10:1A:42:THR:N	2.48	0.41
1:1G:1269:A:H2	1:1G:1313:U:H1'	1.84	0.41
1:1G:1326:C:H2'	1:1G:1327:C:H6	1.84	0.41
1:1G:1355:G:H2'	1:1G:1356:G:C8	2.55	0.41
2:12:100:GLY:O	2:12:104:ASN:N	2.45	0.41
2:12:105:PHE:O	2:12:109:SER:N	2.36	0.41
3:22:65:ALA:HA	3:22:100:ALA:HB3	2.02	0.41
5:42:152:ARG:O	8:72:64:LYS:HD3	2.20	0.41
7:62:16:LEU:HD13	9:82:44:VAL:HG22	2.01	0.41
26:14:137(A):G:H2'	26:14:139:G:N7	2.35	0.41
26:14:566:U:H4'	26:14:809:G:OP2	2.20	0.41
26:14:1018:C:H2'	26:14:1019:U:C6	2.56	0.41
26:14:1140:C:H4'	26:14:1143:A:C6	2.55	0.41
26:14:1427:A:H4'	26:14:1428:C:O5'	2.19	0.41
26:14:2041:U:H2'	26:14:2042:A:O4'	2.20	0.41
26:14:2228:G:C6	26:14:2229:C:C4	3.08	0.41
26:14:2465:C:O2	26:14:2486:G:C2	2.73	0.41
26:14:2473:U:O2	26:14:2473:U:H2'	2.19	0.41
28:19:17:THR:O	28:19:211:ARG:NH2	2.50	0.41
30:39:198:ALA:O	30:39:201:VAL:HG12	2.19	0.41
34:15:133:GLN:O	34:15:134:ARG:HB3	2.20	0.41
35:25:10:VAL:CG1	35:25:19:ILE:HG12	2.45	0.41
36:35:93:GLY:O	36:35:123:LEU:HB2	2.20	0.41
37:45:25:ASP:HB3	37:45:102:VAL:CB	2.50	0.41
40:75:86:ILE:HD13	40:75:86:ILE:HG21	1.81	0.41
41:85:90:VAL:HA	42:95:39:LEU:HD22	2.02	0.41
41:85:92:ARG:C	41:85:94:ASN:N	2.78	0.41
46:D5:155:LEU:HB2	46:D5:157:LEU:CD1	2.49	0.41
1:13:51:A:OP2	1:13:52:G:H8	2.02	0.41
1:13:103:C:C2	1:13:104:G:C8	3.08	0.41
1:13:444:C:H2'	1:13:445:G:H8	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:13:1000:A:H4'	26:14:2137:C:OP1	2.19	0.41
1:13:1189:C:OP1	10:1I:51:ARG:NH2	2.36	0.41
1:13:1292:U:H2'	1:13:1293:G:H8	1.84	0.41
5:4E:11:ILE:HG12	5:4E:31:LEU:HB3	2.02	0.41
7:6E:138:LYS:HD3	7:6E:142:GLU:CD	2.45	0.41
8:7E:103:VAL:HG21	8:7E:110:ALA:HB2	2.02	0.41
12:3I:33:ARG:HD3	12:3I:62:SER:OG	2.20	0.41
13:4I:23:TYR:CD2	13:4I:67:GLU:HA	2.50	0.41
23:2K:56:PSU:O4	23:2K:58:A:C8	2.73	0.41
26:1H:265:A:C2	26:1H:428:A:C2	3.07	0.41
26:1H:627:A:H4'	26:1H:628:G:OP1	2.20	0.41
26:1H:644:A:H2'	26:1H:646:A:H2	1.84	0.41
26:1H:717:G:H2'	26:1H:718:A:O4'	2.19	0.41
26:1H:719:C:H2'	26:1H:720:C:C6	2.55	0.41
26:1H:1016:G:N7	61:1H:4320:HOH:O	2.36	0.41
26:1H:1136:G:N3	26:1H:1136:G:H2'	2.35	0.41
26:1H:1443:G:C2	26:1H:1549:C:C2	3.08	0.41
26:1H:1729:A:C4	26:1H:1731:G:C6	3.08	0.41
26:1H:2340:G:O2'	26:1H:2341:G:H5'	2.20	0.41
26:1H:2771:C:H2'	26:1H:2772:C:C6	2.55	0.41
29:21:49:LEU:HD12	29:21:49:LEU:HA	1.57	0.41
30:31:134:GLY:H	30:31:162:LEU:HB3	1.85	0.41
36:78:144:GLU:HA	36:78:145:PRO:HD3	1.79	0.41
37:88:72:LYS:HA	37:88:73:PRO:HD3	1.91	0.41
45:G8:89:PHE:HD1	45:G8:90:LEU:N	2.19	0.41
46:H8:103:ARG:HG3	46:H8:136:PHE:HD2	1.84	0.41
48:J8:85:LEU:HA	48:J8:85:LEU:HD13	1.52	0.41
1:1G:1502:A:H5"	1:1G:1504:G:N7	2.34	0.41
2:12:22:LYS:HB3	2:12:40:HIS:NE2	2.35	0.41
4:32:18:LYS:HD2	4:32:20:TYR:CZ	2.55	0.41
5:42:7:GLU:O	5:42:35:GLY:N	2.45	0.41
5:42:103:GLY:O	5:42:106:PRO:HD2	2.19	0.41
6:52:21:LEU:HD22	6:52:21:LEU:HA	1.68	0.41
16:7A:9:PHE:HB2	16:7A:16:HIS:O	2.19	0.41
16:7A:20:VAL:HG11	16:7A:32:TYR:CD2	2.54	0.41
26:14:51:G:O2'	26:14:119:A:N1	2.51	0.41
26:14:118:A:H1'	26:14:178:G:O4'	2.20	0.41
26:14:570:G:H5"	61:14:3692:HOH:O	2.21	0.41
26:14:654(J):A:N7	26:14:654(K):C:N4	2.67	0.41
26:14:810:U:O4	61:14:3675:HOH:O	2.21	0.41
26:14:868:U:N3	26:14:869:G:N7	2.69	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:14:918:A:C5	26:14:919:G:H1'	2.55	0.41
26:14:973:A:O4'	26:14:1188:U:C6	2.73	0.41
26:14:1026:U:H6	26:14:1026:U:H5"	1.84	0.41
26:14:1190:G:O2'	26:14:1191:G:H5'	2.20	0.41
26:14:2319:G:O6	39:65:4:LEU:HB3	2.20	0.41
26:14:2320:A:H61	26:14:2333:A:H2'	1.85	0.41
26:14:2758:A:C2	26:14:2759:G:H1'	2.54	0.41
27:1J:13:A:O2'	27:1J:15:A:O5'	2.38	0.41
30:39:123:LEU:HA	30:39:192:LEU:C	2.45	0.41
33:69:8:PRO:HD3	33:69:15:VAL:HG22	2.01	0.41
33:69:111:PRO:O	33:69:112:LYS:C	2.62	0.41
37:45:25:ASP:CB	37:45:102:VAL:H	2.34	0.41
37:45:134:ARG:N	37:45:135:ASP:OD1	2.52	0.41
40:75:91:ARG:O	40:75:116:ALA:HA	2.20	0.41
47:E5:36:ILE:HD11	47:E5:39:ARG:CG	2.48	0.41
48:F5:89:GLU:HA	48:F5:93:GLU:HG3	2.02	0.41
1:13:156:G:H1'	1:13:166:G:H22	1.84	0.41
1:13:355:C:H2'	1:13:356:A:O4'	2.21	0.41
1:13:714:G:H2'	1:13:715:A:C8	2.55	0.41
1:13:827:U:C4	1:13:870:U:C4	3.08	0.41
1:13:1157:A:C6	1:13:1180:A:C5	3.08	0.41
1:13:1372:U:H5"	9:8E:71:SER:CB	2.47	0.41
2:1E:76:GLN:NE2	2:1E:207:ALA:H	2.18	0.41
9:8E:18:PHE:HB2	9:8E:62:TYR:HB3	2.01	0.41
9:8E:102:LEU:HD23	9:8E:102:LEU:HA	1.90	0.41
12:3I:117:ARG:C	12:3I:119:LYS:O	2.63	0.41
13:4I:31:LYS:HD3	13:4I:31:LYS:N	2.36	0.41
17:8I:88:TYR:CD1	17:8I:88:TYR:C	2.96	0.41
26:1H:456:C:O5'	26:1H:456:C:H6	2.03	0.41
26:1H:515:A:C8	26:1H:516:C:C5	3.08	0.41
26:1H:649:G:C5	26:1H:650:C:C4	3.08	0.41
26:1H:969:U:O3'	50:L8:14:GLY:HA2	2.19	0.41
26:1H:1156:A:P	61:1H:3820:HOH:O	2.77	0.41
26:1H:1357:U:C4	26:1H:1358:G:C5	3.08	0.41
26:1H:1766:U:O2'	26:1H:1767:C:H5'	2.20	0.41
26:1H:1900:A:C8	26:1H:1900:A:C5'	3.01	0.41
26:1H:2210:G:H4'	26:1H:2211:G:OP2	2.20	0.41
26:1H:2436:G:C6	26:1H:2437:U:C4	3.08	0.41
29:21:46:ALA:HB2	29:21:82:ARG:HA	2.02	0.41
29:21:103:ASP:OD1	29:21:103:ASP:N	2.52	0.41
30:31:122:LYS:HD3	30:31:122:LYS:HA	1.74	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:B8:58:ASN:ND2	40:B8:58:ASN:O	2.53	0.41
41:C8:79:PHE:HD1	41:C8:79:PHE:O	2.02	0.41
45:G8:9:LYS:HA	45:G8:27:VAL:CG2	2.47	0.41
46:H8:30:ASN:OD1	46:H8:33:LEU:N	2.53	0.41
46:H8:125:LEU:HG	46:H8:164:ALA:CB	2.47	0.41
1:1G:453:A:C5	1:1G:454:C:C4	3.08	0.41
1:1G:1275:A:C4	1:1G:1276:G:C8	3.09	0.41
1:1G:1385:G:C4	1:1G:1386:G:C8	3.08	0.41
19:AA:29:ARG:NH1	19:AA:48:THR:H	2.18	0.41
56:1L:8:U:H2'	56:1L:9:A:H5"	2.01	0.41
26:14:21:A:C2'	26:14:22:C:H5'	2.50	0.41
26:14:185:U:H2'	26:14:186:G:O4'	2.19	0.41
26:14:537:C:H5'	26:14:539:G:OP2	2.20	0.41
26:14:817:C:H2'	26:14:818:G:O4'	2.20	0.41
26:14:990:A:H5'	26:14:990:A:C8	2.42	0.41
26:14:1035:U:H2'	26:14:1036:G:H8	1.83	0.41
26:14:1233:C:H2'	26:14:1234:U:H6	1.84	0.41
26:14:1324:G:C8	61:14:3652:HOH:O	2.71	0.41
26:14:1389:G:H2'	26:14:1390:U:O4'	2.20	0.41
26:14:1454:U:C5	26:14:2702:U:O4	2.74	0.41
26:14:1833:U:O2'	26:14:1969:A:N1	2.42	0.41
26:14:2271:G:H2'	26:14:2272:U:H6	1.85	0.41
26:14:2359:C:H2'	26:14:2360:A:C8	2.56	0.41
26:14:2506:U:H4'	26:14:2507:C:OP1	2.16	0.41
26:14:2552:U:C2	26:14:2554:U:H5'	2.55	0.41
27:1J:42:C:N4	31:49:91:ARG:HH22	2.18	0.41
30:39:5:ALA:N	30:39:18:ARG:O	2.46	0.41
30:39:63:LYS:NZ	30:39:67:GLN:HB2	2.35	0.41
30:39:89:VAL:HG12	30:39:90:PHE:N	2.34	0.41
31:49:29:TRP:HE3	31:49:33:ARG:NH1	2.18	0.41
32:59:111:HIS:HA	32:59:112:PRO:HD2	1.91	0.41
36:35:39:LYS:HB2	36:35:45:LEU:HD21	2.01	0.41
37:45:138:ASP:HB2	37:45:141:GLN:HG2	2.02	0.41
41:85:33:ARG:O	41:85:37:GLU:HG3	2.20	0.41
42:95:25:LEU:HD23	42:95:25:LEU:HA	1.81	0.41
42:95:37:VAL:CG2	42:95:57:VAL:H	2.33	0.41
44:B5:50:LYS:HA	44:B5:50:LYS:HD2	1.78	0.41
1:13:505:G:OP1	61:13:1853:HOH:O	2.22	0.41
1:13:589:C:H42	1:13:650:G:H1	1.69	0.41
1:13:738:C:OP1	6:5E:2:ARG:NH1	2.51	0.41
6:5E:17:SER:O	6:5E:21:LEU:HD13	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:5E:97:PHE:O	18:9I:31:LEU:HD23	2.19	0.41
7:6E:49:ILE:O	7:6E:53:LYS:HB2	2.20	0.41
10:1I:8:LEU:HD22	10:1I:96:ILE:HG22	2.03	0.41
12:3I:7:ILE:HD12	12:3I:7:ILE:HG23	1.74	0.41
13:4I:31:LYS:HD3	13:4I:31:LYS:H	1.85	0.41
13:4I:92:HIS:HA	13:4I:110:ARG:HH22	1.85	0.41
15:6I:17:ARG:HA	15:6I:17:ARG:HD2	1.72	0.41
16:7I:39:TYR:HB2	16:7I:49:LEU:HD13	2.02	0.41
18:9I:38:GLU:CD	18:9I:41:LYS:HZ1	2.19	0.41
19:AI:71:LEU:HD23	19:AI:71:LEU:HA	1.84	0.41
20:BI:29:LYS:HB2	20:BI:29:LYS:HE3	1.48	0.41
26:1H:172:C:H2'	26:1H:173:G:H8	1.85	0.41
26:1H:764:A:H5'	28:11:210:GLY:HA2	2.03	0.41
26:1H:860:U:H5	26:1H:917:A:N1	2.17	0.41
26:1H:887:A:H5'	26:1H:888:C:OP1	2.20	0.41
26:1H:945:A:P	61:1H:4160:HOH:O	2.77	0.41
26:1H:1534:G:C2'	26:1H:1535:U:H4'	2.45	0.41
26:1H:1786:A:H1'	26:1H:1938:A:N6	2.35	0.41
26:1H:2239:G:P	61:1H:3677:HOH:O	2.77	0.41
26:1H:2262:U:C2'	26:1H:2263:C:H5'	2.50	0.41
26:1H:2400:G:H5'	53:O8:19:ARG:HB2	2.02	0.41
26:1H:2779:U:O2	26:1H:2779:U:O4'	2.37	0.41
28:11:53:PHE:O	28:11:218:ARG:HG3	2.20	0.41
29:21:105:THR:HG21	29:21:164:ARG:NH1	2.35	0.41
29:21:170:LEU:HD21	29:21:187:ALA:HB3	2.01	0.41
32:51:152:ARG:HG3	32:51:161:GLY:HA2	2.03	0.41
40:B8:88:ILE:O	40:B8:88:ILE:HG13	2.20	0.41
41:C8:93:LYS:H	41:C8:95:LEU:CD2	2.34	0.41
55:Q8:38:GLY:N	55:Q8:41:ILE:HG13	2.34	0.41
1:1G:943:U:H1'	9:82:124:GLN:HE22	1.85	0.41
1:1G:995:C:H6	1:1G:995:C:O5'	2.03	0.41
1:1G:1242:C:O5'	1:1G:1242:C:H6	2.04	0.41
1:1G:1321:C:H4'	13:4A:87:TYR:CE1	2.55	0.41
2:12:9:GLU:HG2	2:12:48:MET:HG3	2.03	0.41
5:42:144:THR:HG23	5:42:147:ASP:OD2	2.20	0.41
9:82:113:LYS:HD2	9:82:113:LYS:N	2.34	0.41
10:1A:79:ARG:HH11	10:1A:79:ARG:H	1.67	0.41
15:6A:87:ILE:CG2	15:6A:88:ARG:H	2.24	0.41
16:7A:26:ARG:HE	16:7A:31:LYS:HB3	1.84	0.41
16:7A:40:ASP:HA	16:7A:41:PRO:HD2	1.73	0.41
17:8A:60:ILE:HG22	17:8A:62:SER:OG	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:3L:8:4SU:O5'	57:3L:8:4SU:H6	2.21	0.41
57:3L:64:A:C2	57:3L:65:G:H1'	2.54	0.41
26:14:819:A:H2'	26:14:820:A:H5'	2.01	0.41
26:14:1342:A:C2	26:14:1397:U:C2	3.08	0.41
26:14:1640:C:O2'	26:14:1641:A:H5'	2.21	0.41
26:14:2015:A:H1'	52:J5:2:ALA:HA	2.01	0.41
26:14:2056:G:O3'	52:J5:8:LYS:NZ	2.53	0.41
26:14:2320:A:C6	26:14:2333:A:C8	3.09	0.41
26:14:2432:A:H2'	26:14:2433:A:C8	2.56	0.41
27:1J:16:G:H2'	27:1J:17:C:H6	1.83	0.41
27:1J:87:G:H3'	27:1J:88:C:C5'	2.49	0.41
30:39:53:THR:HG22	30:39:56:GLU:CG	2.50	0.41
31:49:18:GLU:O	31:49:21:ARG:HB3	2.20	0.41
35:25:104:ARG:HB3	35:25:104:ARG:CZ	2.50	0.41
1:13:237:C:H5"	17:8I:25:ARG:NH1	2.35	0.41
1:13:380:G:C2	1:13:384:G:C6	3.08	0.41
1:13:413:G:H22	1:13:428:G:H1'	1.84	0.41
1:13:750:G:C2	1:13:751:U:C5	3.08	0.41
1:13:818:G:C2	1:13:820:U:O2'	2.73	0.41
1:13:838:G:OP2	1:13:842:C:N4	2.53	0.41
1:13:944:G:C2	1:13:1340:A:C6	3.09	0.41
1:13:983:A:H2	1:13:984:C:C6	2.39	0.41
1:13:1251:A:H2'	1:13:1252:A:C8	2.56	0.41
1:13:1326:C:H2'	1:13:1327:C:C6	2.56	0.41
7:6E:148:ASN:C	7:6E:150:ALA:N	2.77	0.41
19:AI:40:ILE:HG21	19:AI:40:ILE:HD13	1.85	0.41
20:BI:69:GLY:O	20:BI:73:HIS:CD2	2.72	0.41
20:BI:73:HIS:O	20:BI:76:ALA:HB3	2.20	0.41
22:1K:10:G:O2'	22:1K:11:C:OP1	2.34	0.41
24:3K:71:G:H1'	26:1H:1851:U:O2'	2.20	0.41
26:1H:32:C:C2'	26:1H:33:U:H5'	2.50	0.41
26:1H:304:G:H2'	26:1H:305:U:C6	2.56	0.41
26:1H:353:G:H2'	26:1H:354:G:C8	2.51	0.41
26:1H:821:A:H2'	26:1H:946:G:H5"	2.02	0.41
26:1H:1528:A:H2	26:1H:1542:G:C2	2.39	0.41
26:1H:1634:A:H5"	61:1H:4274:HOH:O	2.20	0.41
26:1H:1668:A:N6	26:1H:1676:A:H61	2.18	0.41
26:1H:2309:A:H8	26:1H:2309:A:O5'	2.03	0.41
26:1H:2808:U:H5'	26:1H:2891:G:O6	2.20	0.41
29:21:116:VAL:HG13	29:21:122:PHE:HB2	2.02	0.41
33:61:11:ASN:O	33:61:12:LEU:HB2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:78:86:LYS:HB3	36:78:118:GLY:CA	2.50	0.41
38:98:48:VAL:O	38:98:49:ASP:C	2.63	0.41
38:98:92:GLY:H	38:98:94:TYR:HE1	1.66	0.41
38:98:92:GLY:N	38:98:94:TYR:HE1	2.18	0.41
47:I8:34:GLY:O	47:I8:35:ASN:C	2.61	0.41
51:M8:18:CYS:HB3	51:M8:39:CYS:SG	2.61	0.41
53:O8:33:LYS:HB2	53:O8:33:LYS:NZ	2.34	0.41
54:P8:24:THR:HG23	54:P8:27:GLY:N	2.35	0.41
1:1G:186(C):G:C6	1:1G:186(D):C:C4	3.08	0.41
1:1G:743:U:H2'	1:1G:744:C:C6	2.55	0.41
1:1G:977:A:H1'	1:1G:982:U:O4	2.20	0.41
1:1G:1127:G:H22	1:1G:1144:G:H1	1.69	0.41
1:1G:1189:C:P	10:1A:51:ARG:HH22	2.43	0.41
1:1G:1299:A:N1	1:1G:1301:U:N3	2.69	0.41
1:1G:1316:G:N2	1:1G:1318:A:H3'	2.35	0.41
1:1G:1342:C:H4'	9:82:125:TYR:HB3	2.02	0.41
2:12:43:ASP:O	2:12:47:THR:OG1	2.38	0.41
2:12:91:PRO:HA	2:12:154:LEU:HD12	2.01	0.41
2:12:134:GLU:HA	2:12:137:ARG:HB2	2.03	0.41
4:32:168:ARG:HD3	4:32:168:ARG:HA	1.81	0.41
5:42:68:GLU:HG3	5:42:68:GLU:O	2.21	0.41
5:42:110:LEU:HD23	5:42:110:LEU:HA	1.79	0.41
6:52:33:TYR:CE2	6:52:74:ASP:HB2	2.56	0.41
8:72:12:ARG:NH1	8:72:27:PRO:HD2	2.36	0.41
10:1A:12:ASP:OD1	10:1A:13:HIS:N	2.54	0.41
11:2A:86:GLY:H	11:2A:112:THR:HG23	1.85	0.41
11:2A:120:ARG:HA	11:2A:121:PRO:HD3	1.78	0.41
57:3L:31:A:H3'	57:3L:32:PSU:O4'	2.21	0.41
57:3L:35:A:H2	25:4L:14:A:C6	2.38	0.41
26:14:39:C:O2	30:39:46:ARG:NH2	2.53	0.41
26:14:874:G:N2	26:14:904:C:C2	2.89	0.41
26:14:916:G:C2'	26:14:917:A:H5"	2.51	0.41
26:14:1542:G:O5'	26:14:1543:A:H5"	2.20	0.41
26:14:1839:G:H5"	26:14:1840:G:OP2	2.20	0.41
26:14:1839:G:C8	26:14:1927:A:H1'	2.55	0.41
26:14:2396:G:H4'	48:F5:30:VAL:H	1.86	0.41
26:14:2422:A:H8	26:14:2422:A:H2'	1.73	0.41
26:14:2590:A:OP2	28:19:237:GLU:HB3	2.19	0.41
26:14:2841:C:H2'	26:14:2842:G:C8	2.56	0.41
27:1J:7:G:H1	27:1J:113:C:H42	1.68	0.41
27:1J:109:G:C6	27:1J:110:G:C5	3.08	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:19:43:ARG:HA	28:19:49:ILE:HA	2.01	0.41
29:29:4:ILE:HD12	29:29:28:ALA:CB	2.51	0.41
33:69:38:LEU:HB2	33:69:40:THR:HG23	2.01	0.41
34:15:71:ILE:HD12	34:15:71:ILE:O	2.20	0.41
36:35:86:LYS:HG3	36:35:87:ASP:H	1.85	0.41
39:65:30:ARG:HE	39:65:30:ARG:HB3	1.62	0.41
41:85:47:TYR:HA	41:85:50:ARG:NH2	2.35	0.41
46:D5:170:THR:C	46:D5:172:ALA:H	2.28	0.41
47:E5:25:ARG:HD3	47:E5:25:ARG:HA	1.87	0.41
51:I5:16:CYS:HB2	51:I5:20:ASN:H	1.85	0.41
51:I5:56:VAL:HG22	51:I5:57:GLU:HG3	2.01	0.41
1:13:616:G:C2	1:13:617:G:C8	3.08	0.41
1:13:953:G:C2	1:13:954:G:H1'	2.56	0.41
1:13:1152:A:H2'	1:13:1153:C:H6	1.85	0.41
1:13:1392:G:N2	1:13:1502:A:H8	2.18	0.41
1:13:1406:U:H2'	1:13:1407:C:H5'	2.03	0.41
1:13:1448:C:N4	1:13:1455:G:H1	2.16	0.41
2:1E:69:LEU:HB3	2:1E:162:ILE:HG22	2.02	0.41
5:4E:10:MET:O	5:4E:10:MET:HG2	2.19	0.41
6:5E:3:ARG:HB3	6:5E:93:SER:HB2	2.02	0.41
13:4I:36:LYS:HB3	13:4I:36:LYS:HE3	1.88	0.41
13:4I:108:ARG:N	13:4I:108:ARG:HD2	2.36	0.41
16:7I:55:ARG:HE	16:7I:55:ARG:HB3	1.62	0.41
19:AI:44:MET:O	19:AI:47:HIS:HB2	2.20	0.41
26:1H:643:A:H2'	26:1H:644:A:C8	2.56	0.41
26:1H:1005:C:H5"	26:1H:1006:C:OP2	2.21	0.41
26:1H:1063:G:H22	26:1H:1076:C:H2'	1.86	0.41
26:1H:1268:A:C2	26:1H:2013:A:C4	3.08	0.41
26:1H:2062:A:N3	26:1H:2062:A:C2'	2.83	0.41
26:1H:2371:G:C4'	53:O8:45:LYS:HG3	2.51	0.41
29:21:134:ILE:C	29:21:134:ILE:HD12	2.45	0.41
31:41:39:ILE:HB	31:41:92:VAL:HG12	2.02	0.41
32:51:3:ARG:HA	32:51:3:ARG:NE	2.36	0.41
33:61:129:THR:HG22	33:61:137:PRO:HB3	2.03	0.41
33:61:131:LYS:HB3	33:61:132:PRO:CA	2.47	0.41
36:78:100:LEU:O	36:78:105:LEU:HD12	2.21	0.41
38:98:9:LYS:HA	38:98:17:ARG:NE	2.36	0.41
38:98:41:ALA:O	38:98:44:LEU:N	2.43	0.41
39:A8:67:ARG:CZ	39:A8:67:ARG:HB2	2.50	0.41
43:E8:79:GLY:HA3	43:E8:100:THR:HG22	2.02	0.41
44:F8:67:GLY:C	44:F8:69:TYR:N	2.76	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:J8:83:GLU:C	48:J8:85:LEU:N	2.75	0.41
49:K8:23:LYS:HZ2	49:K8:23:LYS:HG2	1.68	0.41
49:K8:31:GLU:HB3	49:K8:53:LEU:HD11	2.02	0.41
55:Q8:34:TRP:CG	55:Q8:35:GLN:N	2.85	0.41
1:1G:147:G:N2	1:1G:148:G:C4	2.88	0.41
1:1G:328:C:O2	1:1G:328:C:H2'	2.20	0.41
1:1G:1053:G:HO2'	1:1G:1054:C:P	2.44	0.41
1:1G:1073:U:H2'	1:1G:1074:G:C8	2.55	0.41
1:1G:1123:A:O3'	10:1A:36:GLY:HA3	2.20	0.41
1:1G:1216:G:H2'	1:1G:1217:C:C6	2.55	0.41
4:32:209:ARG:O	4:32:209:ARG:HG3	2.19	0.41
5:42:103:GLY:O	5:42:104:ALA:C	2.61	0.41
5:42:122:GLU:HG2	5:42:131:ILE:HD12	2.03	0.41
8:72:51:VAL:HG11	8:72:60:ARG:HE	1.84	0.41
13:4A:86:CYS:HA	19:AA:73:GLU:O	2.19	0.41
15:6A:32:LEU:O	15:6A:36:ILE:HG13	2.20	0.41
16:7A:52:ASP:OD2	16:7A:55:ARG:HG3	2.20	0.41
18:9A:19:LYS:HD2	18:9A:19:LYS:HA	1.78	0.41
26:14:24:G:H2'	26:14:25:U:O4'	2.20	0.41
26:14:270(E):G:C6	26:14:270(F):U:C4	3.08	0.41
26:14:571:A:H5'	26:14:2030:A:N7	2.36	0.41
26:14:774:A:H2	26:14:787:U:O2'	2.03	0.41
26:14:1449(A):G:O2'	26:14:1450:C:H5'	2.20	0.41
26:14:1499:C:H2'	26:14:1500:G:C8	2.56	0.41
26:14:2017:U:O2	52:J5:10:LYS:HB2	2.20	0.41
26:14:2388:A:H2'	26:14:2389:G:H5'	2.01	0.41
27:1J:0:A:H2'	27:1J:1:U:C6	2.55	0.41
27:1J:6:C:C2	27:1J:115:G:N2	2.89	0.41
27:1J:118:G:C5	27:1J:119:A:N7	2.89	0.41
29:29:9:VAL:HA	40:75:3:ARG:HG3	2.03	0.41
30:39:11:VAL:HG23	30:39:12:LEU:H	1.85	0.41
30:39:78:ILE:HA	30:39:83:PHE:CD2	2.56	0.41
31:49:43:LEU:HD12	31:49:45:GLU:OE1	2.19	0.41
31:49:105:LYS:NZ	51:I5:26:SER:HA	2.36	0.41
35:25:68:GLU:OE2	35:25:78:ARG:NH1	2.53	0.41
39:65:7:TYR:CE1	39:65:11:LYS:HD3	2.54	0.41
39:65:80:LEU:HD23	39:65:80:LEU:HA	1.78	0.41
42:95:57:VAL:HG23	42:95:99:ILE:N	2.35	0.41
45:C5:42:VAL:HG13	45:C5:65:ALA:HB3	2.02	0.41
50:H5:4:LEU:O	50:H5:36:VAL:HA	2.20	0.41
52:J5:46:CYS:SG	52:J5:48:GLU:HG2	2.61	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:13:337:C:H2'	1:13:338:A:C8	2.55	0.41
1:13:468:A:O2'	16:7I:82:GLN:HG2	2.21	0.41
1:13:604:G:H2'	1:13:605:U:O4'	2.20	0.41
1:13:828:A:N7	1:13:859:A:C8	2.89	0.41
3:2E:18:TRP:HB3	3:2E:20:SER:O	2.21	0.41
23:2K:64:G:N3	23:2K:65:G:C8	2.89	0.41
25:4K:24:A:H8	25:4K:24:A:O5'	2.04	0.41
26:1H:15:G:C2	26:1H:16:G:C8	3.08	0.41
26:1H:211:A:H2'	26:1H:212:G:O4'	2.21	0.41
26:1H:357:A:H2'	26:1H:358:U:H6	1.85	0.41
26:1H:1025:G:C4	26:1H:1135:C:H1'	2.55	0.41
26:1H:1257:C:H4'	30:31:83:PHE:CE1	2.55	0.41
26:1H:1550:C:O2'	26:1H:1551:C:H5'	2.20	0.41
26:1H:1675:C:H2'	26:1H:1676:A:O4'	2.20	0.41
26:1H:2557:G:H2'	26:1H:2558:C:C6	2.56	0.41
26:1H:2704:C:H2'	26:1H:2705:A:H8	1.83	0.41
26:1H:2820:A:P	38:98:2:ARG:NH2	2.94	0.41
26:1H:2830:G:N3	26:1H:2883:A:H2	2.18	0.41
26:1H:2851:A:H8	26:1H:2851:A:O5'	2.04	0.41
27:16:30:C:H2'	27:16:31:C:H5'	2.03	0.41
29:21:81:ILE:O	29:21:81:ILE:HG22	2.20	0.41
30:31:176:LEU:HD21	30:31:180:GLY:O	2.21	0.41
35:68:75:SER:CB	40:B8:74:ARG:HH12	2.34	0.41
36:78:38:GLN:O	36:78:41:ARG:HB2	2.21	0.41
36:78:96:THR:HG22	36:78:126:VAL:HG21	2.02	0.41
37:88:1:MET:O	37:88:2:LEU:HB2	2.21	0.41
37:88:2:LEU:HD12	37:88:2:LEU:HA	1.93	0.41
37:88:136:ALA:HB2	46:H8:52:SER:HB2	2.03	0.41
38:98:50:HIS:O	38:98:54:LEU:HD22	2.21	0.41
51:M8:59:PHE:HD1	51:M8:59:PHE:HA	1.73	0.41
53:O8:20:ASN:C	53:O8:21:TYR:CD1	2.99	0.41
55:Q8:40:GLU:HA	55:Q8:43:GLN:OE1	2.20	0.41
55:Q8:47:LYS:HA	55:Q8:47:LYS:CE	2.24	0.41
1:1G:328:C:H4'	1:1G:329:A:C5'	2.50	0.41
1:1G:332:G:C2	1:1G:333:G:C8	3.09	0.41
1:1G:565:U:H3'	1:1G:566:G:H2'	2.03	0.41
1:1G:689:C:C2'	1:1G:690:G:H5'	2.51	0.41
2:12:47:THR:HA	2:12:202:PRO:HG2	2.01	0.41
2:12:80:ILE:HG21	2:12:211:ILE:HG21	2.03	0.41
2:12:141:GLU:O	2:12:145:LEU:HB2	2.21	0.41
3:22:11:ARG:O	3:22:14:ILE:O	2.39	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:3A:18:VAL:O	12:3A:19:ARG:HB2	2.21	0.41
12:3A:41:ARG:HH11	12:3A:41:ARG:HB3	1.86	0.41
15:6A:26:GLU:H	15:6A:26:GLU:HG2	1.66	0.41
16:7A:37:GLY:HA2	16:7A:50:LYS:HD3	2.01	0.41
16:7A:58:TYR:O	16:7A:62:VAL:HG22	2.20	0.41
19:AA:42:PRO:HG3	51:I5:60:GLN:CD	2.45	0.41
26:14:396:G:O2'	48:F5:43:TYR:O	2.36	0.41
26:14:616:A:C4	30:39:180:GLY:HA2	2.55	0.41
26:14:868:U:C4	26:14:869:G:N7	2.88	0.41
26:14:1044:G:C2'	26:14:1045:A:H5"	2.51	0.41
26:14:1894:C:C2'	26:14:1895:C:H5'	2.51	0.41
26:14:2283:C:C2	26:14:2389:G:C2	3.08	0.41
26:14:2356:C:H4'	47:E5:20:ARG:HG3	2.03	0.41
26:14:2419:U:O4	55:M5:31:HIS:CG	2.73	0.41
26:14:2468:G:H3'	26:14:2476:A:C2	2.55	0.41
26:14:2543:G:C1'	26:14:2766:G:H5'	2.51	0.41
26:14:2771:C:H5"	29:29:202:LYS:HE2	2.02	0.41
27:1J:45:A:N3	27:1J:45:A:H2'	2.35	0.41
27:1J:51:G:C6	27:1J:52:A:C2	3.09	0.41
27:1J:57:A:C2'	27:1J:58:A:H5'	2.51	0.41
33:69:77:LEU:HD13	33:69:141:LYS:HD2	2.03	0.41
35:25:64:ARG:HH11	40:75:70:VAL:HG11	1.85	0.41
43:A5:96:ILE:HG12	43:A5:97:LYS:N	2.36	0.41
45:C5:59:GLY:O	45:C5:61:ILE:HG13	2.20	0.41
50:H5:50:VAL:HG12	50:H5:53:LEU:HD12	2.03	0.41
52:J5:2:ALA:C	52:J5:3:LYS:O	2.57	0.41
53:K5:33:LYS:HE2	53:K5:33:LYS:HB3	1.82	0.41
1:13:36:C:H1'	12:3I:118:SER:HB3	2.03	0.41
1:13:339:C:OP2	35:68:97:ARG:HD3	2.21	0.41
1:13:940:C:H2'	1:13:941:G:H8	1.86	0.41
1:13:1339:A:H2'	1:13:1340:A:O4'	2.20	0.41
1:13:1499:A:H1'	1:13:1520:G:O5'	2.21	0.41
2:1E:82:ARG:HB3	2:1E:83:MET:HE2	2.02	0.41
2:1E:97:TRP:CH2	2:1E:176:GLU:OE2	2.74	0.41
3:2E:84:ILE:HG23	3:2E:88:ARG:HE	1.85	0.41
4:3E:154:ASN:CG	4:3E:155:LEU:H	2.28	0.41
9:8E:89:ASN:O	9:8E:91:ASP:N	2.52	0.41
15:6I:56:LEU:HA	15:6I:59:MET:HE2	2.02	0.41
26:1H:451:C:H5'	61:1H:3916:HOH:O	2.20	0.41
26:1H:839:U:H2'	26:1H:840:C:C6	2.56	0.41
26:1H:1187:G:P	61:1H:3899:HOH:O	2.67	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1H:1309:G:P	54:P8:9:ARG:HD3	2.61	0.41
26:1H:1358:G:N2	26:1H:1372:U:C5	2.89	0.41
26:1H:1642:G:C2'	26:1H:1643:G:H5'	2.50	0.41
26:1H:1831:G:H2'	26:1H:1832:C:C6	2.55	0.41
26:1H:1919:A:H5"	26:1H:1920:C:OP2	2.21	0.41
26:1H:1931:U:O2	26:1H:1931:U:O4'	2.39	0.41
26:1H:2371:G:H4'	53:O8:45:LYS:HG3	2.03	0.41
26:1H:2436:G:C5	26:1H:2437:U:C5	3.09	0.41
28:11:105:ILE:HD12	28:11:105:ILE:HA	1.51	0.41
32:51:4:ILE:HD11	32:51:7:LEU:HD11	2.03	0.41
32:51:12:PRO:HD3	32:51:48:GLY:O	2.21	0.41
32:51:92:ILE:H	32:51:92:ILE:HG13	1.55	0.41
36:78:52:GLU:OE1	36:78:55:ARG:NE	2.49	0.41
38:98:29:LEU:O	38:98:78:LYS:HE3	2.21	0.41
39:A8:17:ARG:HH11	39:A8:17:ARG:HG3	1.86	0.41
44:F8:2:LYS:HG2	49:K8:26:ARG:HE	1.86	0.41
44:F8:61:GLY:N	44:F8:75:ASP:OD1	2.50	0.41
45:G8:40:GLU:HB3	45:G8:64:GLU:CB	2.51	0.41
46:H8:53:ILE:O	46:H8:53:ILE:HG13	2.19	0.41
48:J8:73:LEU:O	48:J8:76:ARG:HB2	2.19	0.41
1:1G:131:C:H2'	1:1G:132:C:C6	2.56	0.41
1:1G:191(F):U:H2'	1:1G:191:G:H8	1.85	0.41
1:1G:1050:G:C6	1:1G:1051:C:N4	2.89	0.41
1:1G:1265:G:C2	1:1G:1271:G:C2	3.09	0.41
1:1G:1290:G:C6	1:1G:1291:G:C5	3.09	0.41
1:1G:1324:A:C5	1:1G:1325:C:C5	3.09	0.41
2:12:239:VAL:HG12	2:12:240:GLN:HG3	2.02	0.41
3:22:81:GLY:HA2	3:22:85:ARG:HD3	2.02	0.41
3:22:188:LEU:HD13	3:22:188:LEU:HA	1.80	0.41
5:42:76:ILE:O	5:42:93:PRO:HB3	2.21	0.41
5:42:107:ARG:O	5:42:110:LEU:N	2.54	0.41
6:52:99:ALA:HB3	18:9A:29:PHE:CE1	2.56	0.41
8:72:100:ILE:HA	8:72:101:PRO:HD3	1.88	0.41
14:5A:4:LYS:C	14:5A:6:LEU:N	2.79	0.41
15:6A:5:LYS:O	15:6A:9:GLN:HG2	2.21	0.41
57:3L:8:4SU:O4'	57:3L:48:C:H2'	2.21	0.41
26:14:38:A:H2'	26:14:39:C:H6	1.83	0.41
26:14:414:C:H2'	26:14:415:A:C8	2.55	0.41
26:14:442:G:C4	26:14:444:C:C5	3.09	0.41
26:14:459:U:H4'	54:L5:40:TRP:CZ3	2.56	0.41
26:14:761:A:C5	61:14:4077:HOH:O	2.71	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:14:988:A:N6	50:H5:13:ILE:HG21	2.35	0.41
26:14:992:C:H2'	26:14:993:G:H8	1.85	0.41
26:14:1728:G:H2'	26:14:1731:G:H1	1.85	0.41
26:14:2211:G:H2'	26:14:2211:G:N3	2.34	0.41
26:14:2347:C:H4'	53:K5:39:TYR:HE2	1.86	0.41
26:14:2459:A:H2'	26:14:2459:A:N3	2.36	0.41
26:14:2622:C:H5'	29:29:159:HIS:ND1	2.35	0.41
26:14:2820:A:O5'	38:55:4:LEU:HD23	2.21	0.41
28:19:16:MET:HE3	28:19:16:MET:HB2	1.86	0.41
28:19:106:ILE:O	28:19:108:PRO:HD3	2.20	0.41
30:39:5:ALA:HB1	30:39:125:LEU:HD21	2.02	0.41
30:39:18:ARG:HG2	30:39:19:GLU:N	2.31	0.41
33:69:2:LYS:H	33:69:2:LYS:HG2	1.78	0.41
33:69:75:LEU:HD13	33:69:76:THR:C	2.45	0.41
39:65:26:LEU:HD22	39:65:87:PHE:CD1	2.55	0.41
39:65:62:LYS:HA	39:65:65:VAL:HG12	2.03	0.41
46:D5:67:LEU:HA	46:D5:67:LEU:HD23	1.91	0.41
46:D5:148:ASP:OD2	46:D5:175:VAL:HG11	2.20	0.41
50:H5:13:ILE:HD12	50:H5:13:ILE:H	1.85	0.41
1:13:16:A:C2	1:13:920:U:O2	2.74	0.41
1:13:131:C:H2'	1:13:132:C:C6	2.56	0.41
1:13:323:U:O3'	20:BI:22:ARG:HD3	2.21	0.41
1:13:375:U:OP1	16:7I:69:THR:HG21	2.20	0.41
1:13:456:C:H42	1:13:476:G:H1	1.68	0.41
1:13:575:G:H4'	1:13:576:G:C5'	2.51	0.41
1:13:825:G:O2'	1:13:826:C:H5'	2.21	0.41
1:13:1054:C:H5	1:13:1196:U:H2'	1.86	0.41
1:13:1129:C:O2	1:13:1130:A:N7	2.53	0.41
1:13:1348:U:H5	1:13:1373:G:N2	2.19	0.41
2:1E:26:PRO:C	2:1E:28:PHE:H	2.27	0.41
2:1E:28:PHE:O	2:1E:32:ILE:HG22	2.21	0.41
2:1E:178:ARG:HA	2:1E:178:ARG:HD3	1.94	0.41
2:1E:190:THR:C	2:1E:192:SER:H	2.28	0.41
3:2E:130:VAL:O	3:2E:134:ILE:HG12	2.20	0.41
3:2E:154:SER:OG	3:2E:165:THR:HB	2.21	0.41
4:3E:90:GLY:H	4:3E:204:ILE:HD11	1.86	0.41
7:6E:73:MET:HG2	7:6E:90:GLU:HB3	2.02	0.41
17:8I:45:HIS:O	17:8I:73:VAL:HG23	2.21	0.41
19:AI:40:ILE:HG22	19:AI:69:HIS:O	2.21	0.41
23:2K:64:G:C2	23:2K:65:G:C5	3.09	0.41
24:3K:9:A:H2'	24:3K:10:G:N7	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:3K:26:A:H2'	24:3K:27:G:H5'	2.03	0.41
24:3K:28:G:H1	24:3K:42:C:H42	1.67	0.41
26:1H:259:G:O2'	26:1H:621:A:O2'	2.17	0.41
26:1H:322:A:H5'	26:1H:340:A:H1'	2.03	0.41
26:1H:323:G:H5'	30:31:169:ASN:OD1	2.21	0.41
26:1H:363(B):G:H2'	26:1H:363(C):G:H8	1.86	0.41
26:1H:442:G:C6	26:1H:444:C:N4	2.89	0.41
26:1H:449:A:N6	26:1H:450:G:C6	2.89	0.41
26:1H:587:C:P	36:78:21:ARG:HH22	2.44	0.41
26:1H:784:A:O4'	28:11:227:ASN:ND2	2.54	0.41
26:1H:784:A:C8	26:1H:792:G:C5	3.09	0.41
26:1H:845:G:H8	26:1H:845:G:OP2	2.04	0.41
26:1H:1061:U:H3'	26:1H:1062:G:C5'	2.51	0.41
26:1H:1280:G:N2	26:1H:1291:C:C2	2.89	0.41
26:1H:1336:A:OP2	44:F8:64:LYS:NZ	2.53	0.41
26:1H:1448:G:H1'	26:1H:1528:A:H62	1.85	0.41
26:1H:1545(A):A:N7	26:1H:1546:C:C2	2.89	0.41
26:1H:1666:G:C2'	26:1H:1667:G:H5'	2.51	0.41
26:1H:1756:G:H4'	26:1H:1758:G:O4'	2.21	0.41
26:1H:2422:A:C5	26:1H:2424:C:C4	3.08	0.41
26:1H:2643:G:H2'	26:1H:2644:G:O4'	2.20	0.41
26:1H:2715:C:C2'	26:1H:2716:U:H5'	2.51	0.41
26:1H:2845:G:N2	26:1H:2871:C:O2	2.51	0.41
27:16:42:C:HO2'	31:41:67:LYS:HE3	1.84	0.41
27:16:99:A:C4	27:16:100:G:C8	3.09	0.41
29:21:1:MET:HG2	29:21:83:ASP:O	2.20	0.41
30:31:63:LYS:HE3	30:31:67:GLN:HB2	2.02	0.41
30:31:129:PHE:O	30:31:130:ALA:CB	2.69	0.41
31:41:47:LYS:NZ	31:41:80:PHE:HD2	2.17	0.41
34:58:35:ARG:HA	34:58:116:LEU:HD13	2.03	0.41
39:A8:32:LEU:HD23	39:A8:32:LEU:N	2.35	0.41
39:A8:63:THR:O	39:A8:66:ALA:HB3	2.21	0.41
39:A8:88:ASP:C	39:A8:90:GLY:N	2.78	0.41
43:E8:83:LYS:C	43:E8:84:ARG:HD2	2.46	0.41
43:E8:110:LYS:HG3	43:E8:111:HIS:N	2.34	0.41
45:G8:88:LYS:HD3	45:G8:88:LYS:HA	1.51	0.41
46:H8:28:MET:HE2	46:H8:28:MET:HB3	1.88	0.41
46:H8:102:LEU:HD23	46:H8:102:LEU:HA	1.83	0.41
46:H8:109:ALA:HB3	46:H8:144:LEU:HD13	2.03	0.41
47:I8:47:PRO:HB3	47:I8:51:VAL:HG12	2.02	0.41
48:J8:25:LYS:HE2	48:J8:25:LYS:HB3	1.48	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:J8:41:ARG:HG3	48:J8:43:TYR:CZ	2.55	0.41
48:J8:82:LEU:H	48:J8:82:LEU:HD22	1.85	0.41
48:J8:90:ILE:HG21	48:J8:90:ILE:HD13	1.71	0.41
49:K8:33:MET:O	49:K8:36:ARG:HB2	2.20	0.41
51:M8:60:GLN:C	51:M8:61:ARG:HD2	2.46	0.41
55:Q8:27:THR:CB	55:Q8:39:LYS:HZ2	2.33	0.41
1:1G:129(A):G:C2	1:1G:191(A):G:C8	3.08	0.41
1:1G:151:A:H2'	1:1G:152:A:O4'	2.19	0.41
1:1G:255:G:H2'	1:1G:256:U:H6	1.81	0.41
1:1G:359:U:H2'	1:1G:360:A:C8	2.56	0.41
1:1G:391:G:C6	1:1G:392:G:C5	3.08	0.41
1:1G:491:G:H2'	1:1G:492:G:O4'	2.20	0.41
1:1G:552:U:C2'	1:1G:553:A:H5'	2.51	0.41
1:1G:674:G:H2'	1:1G:675:A:C8	2.56	0.41
1:1G:745:C:OP1	1:1G:851:G:O2'	2.33	0.41
1:1G:750:G:N2	15:6A:23:GLY:HA3	2.36	0.41
1:1G:1072:G:H2'	1:1G:1073:U:O4'	2.21	0.41
1:1G:1125:U:C5	10:1A:5:ARG:NH1	2.89	0.41
1:1G:1181:G:H2'	1:1G:1182:G:O4'	2.21	0.41
1:1G:1241:G:H1	1:1G:1296:C:H42	1.68	0.41
1:1G:1329:A:H5"	13:4A:25:ILE:C	2.46	0.41
1:1G:1446:A:OP1	1:1G:1446:A:H4'	2.21	0.41
2:12:6:THR:OG1	2:12:217:ARG:HB3	2.20	0.41
2:12:219:VAL:HG23	2:12:222:ILE:HD12	2.02	0.41
4:32:18:LYS:HD2	4:32:20:TYR:CE1	2.55	0.41
4:32:61:LYS:HA	4:32:203:VAL:HG22	2.02	0.41
4:32:104:VAL:O	4:32:108:LEU:HB2	2.21	0.41
5:42:34:VAL:HB	5:42:62:ALA:HB1	2.03	0.41
6:52:44:GLY:HA2	6:52:59:TYR:CZ	2.56	0.41
7:62:78:ARG:O	7:62:84:ASN:HA	2.20	0.41
10:1A:8:LEU:HD22	10:1A:20:ALA:HB2	2.02	0.41
10:1A:50:ILE:HB	14:5A:41:ARG:HD2	2.03	0.41
13:4A:84:ILE:O	13:4A:86:CYS:N	2.54	0.41
14:5A:53:LEU:HD23	14:5A:53:LEU:HA	1.67	0.41
19:AA:12:ASP:HB3	19:AA:38:SER:CB	2.50	0.41
23:2L:48:U:O2'	23:2L:49:C:OP2	2.32	0.41
57:3L:11:C:H2'	57:3L:12:U:C6	2.56	0.41
26:14:30:G:C5	26:14:31:C:C4	3.08	0.41
26:14:286:C:H2'	26:14:287:C:C6	2.56	0.41
26:14:606:U:H4'	26:14:658:C:H4'	2.03	0.41
26:14:619:G:H5"	26:14:620:G:N2	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:14:867:C:C6	26:14:868:U:H5	2.39	0.41
26:14:1034:G:H2'	26:14:1035:U:O4'	2.20	0.41
26:14:1316:U:C2'	26:14:1317:A:H5'	2.51	0.41
26:14:1434:A:H2'	26:14:1435:G:C8	2.56	0.41
26:14:1945:G:H2'	26:14:1946:U:H6	1.85	0.41
26:14:2168:G:H2'	26:14:2168:G:N3	2.36	0.41
26:14:2244:U:O5'	26:14:2244:U:H6	2.04	0.41
26:14:2408:U:H2'	26:14:2409:G:H8	1.86	0.41
26:14:2415:G:C6	26:14:2416:C:C4	3.09	0.41
26:14:2563:U:O2	26:14:2565:A:C8	2.74	0.41
26:14:2607:G:H2'	26:14:2608:G:O4'	2.21	0.41
27:1J:66:A:C2	27:1J:108:C:C4	3.09	0.41
28:19:260:ARG:NH2	28:19:264:LYS:HD3	2.36	0.41
29:29:50:GLY:HA2	29:29:78:LEU:HD23	2.03	0.41
30:39:29:ASN:HA	30:39:30:PRO:HD3	1.63	0.41
30:39:31:HIS:CD2	30:39:31:HIS:O	2.74	0.41
31:49:127:GLY:HA2	31:49:166:ASP:CG	2.46	0.41
40:75:4:GLY:HA2	40:75:8:LYS:HZ3	1.85	0.41
40:75:62:THR:HG22	40:75:75:ILE:HG12	2.02	0.41
40:75:90:GLN:HG3	40:75:91:ARG:N	2.36	0.41
41:85:100:VAL:C	41:85:102:GLU:H	2.29	0.41
45:C5:87:LYS:HB2	45:C5:96:ILE:HD13	2.01	0.41
47:E5:72:ARG:HB3	47:E5:75:LEU:HB2	2.03	0.41
48:F5:18:ILE:HG12	48:F5:37:ILE:HD12	2.02	0.41
1:13:8:A:N7	4:3E:208:SER:HB3	2.37	0.41
1:13:243:A:H4'	1:13:244:U:H5"	2.03	0.41
1:13:255:G:C4	1:13:256:U:C5	3.09	0.41
1:13:310:G:OP2	16:7I:27:LYS:NZ	2.29	0.41
1:13:324:G:N1	1:13:327:A:OP2	2.51	0.41
1:13:375:U:C2	1:13:376:G:C8	3.09	0.41
1:13:560:U:H4'	1:13:561:U:H5"	2.03	0.41
1:13:1128:C:C6	1:13:1139:G:C6	3.09	0.41
1:13:1132:C:C2'	1:13:1133:G:H5'	2.51	0.41
1:13:1305:G:H8	1:13:1305:G:OP2	2.04	0.41
1:13:1352:C:OP1	21:1F:3:LYS:NZ	2.41	0.41
3:2E:7:PRO:O	3:2E:11:ARG:NH1	2.53	0.41
5:4E:35:GLY:H	5:4E:112:LEU:HD13	1.85	0.41
5:4E:69:VAL:O	5:4E:71:LEU:HG	2.20	0.41
8:7E:80:ILE:H	8:7E:80:ILE:HG12	1.73	0.41
9:8E:127:LYS:O	9:8E:127:LYS:HG2	2.20	0.41
16:7I:8:ARG:HD3	16:7I:17:TYR:CE1	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:9I:47:THR:HA	18:9I:83:GLU:HB2	2.02	0.41
26:1H:141:A:H8	26:1H:1408:C:H1'	1.86	0.41
26:1H:150:C:H2'	26:1H:151:C:C6	2.56	0.41
26:1H:234:C:C2	26:1H:235:U:C5	3.09	0.41
26:1H:1250:G:OP2	36:78:18:ARG:NH1	2.54	0.41
28:11:158:ALA:O	28:11:159:ALA:C	2.63	0.41
30:31:64:ILE:HA	30:31:64:ILE:HD13	1.50	0.41
30:31:149:ASP:OD1	30:31:149:ASP:N	2.49	0.41
34:58:3:THR:HG22	41:C8:64:ARG:NH1	2.35	0.41
39:A8:71:ARG:HE	39:A8:71:ARG:HB3	1.80	0.41
45:G8:54:LYS:O	45:G8:55:TYR:CG	2.74	0.41
51:M8:36:CYS:SG	51:M8:38:LYS:O	2.79	0.41
1:1G:162:A:H8	1:1G:162:A:O5'	2.04	0.41
1:1G:422:C:H6	1:1G:422:C:H2'	1.73	0.41
7:62:12:LEU:HA	7:62:12:LEU:HD12	1.68	0.41
15:6A:4:THR:C	15:6A:6:GLU:N	2.77	0.41
16:7A:74:LEU:HD12	16:7A:79:VAL:HG21	2.03	0.41
21:1B:6:ARG:HH11	21:1B:15:ARG:NH1	2.19	0.41
56:1L:29:G:H3'	56:1L:30:G:C8	2.56	0.41
56:1L:74:C:O2'	56:1L:75:C:OP2	2.38	0.41
23:2L:26:C:H2'	23:2L:27:G:O4'	2.21	0.41
26:14:49:A:H5"	26:14:51:G:O4'	2.20	0.41
26:14:363(A):A:H2'	26:14:363(A):A:N3	2.35	0.41
26:14:429:A:H2'	26:14:430:G:C8	2.56	0.41
26:14:947:G:H2'	26:14:948:G:C8	2.56	0.41
26:14:958:U:O2	27:1J:89(A):A:O2'	2.38	0.41
26:14:1174:A:H5'	26:14:1175:U:OP2	2.20	0.41
26:14:1488:G:C6	26:14:1489:U:N3	2.89	0.41
26:14:2357:U:P	47:E5:20:ARG:HH11	2.44	0.41
26:14:2414:G:OP1	48:F5:25:LYS:NZ	2.54	0.41
26:14:2885:C:N3	26:14:2886:G:H1'	2.36	0.41
27:1J:17:C:H2'	27:1J:18:G:O4'	2.21	0.41
27:1J:118:G:O6	27:1J:119:A:N6	2.54	0.41
29:29:44:TYR:HE2	29:29:80:GLU:OE1	2.03	0.41
32:59:9:ILE:HG22	32:59:51:ARG:HA	2.01	0.41
32:59:55:PRO:HG2	32:59:61:HIS:CG	2.56	0.41
32:59:154:PRO:HB3	32:59:162:ILE:O	2.21	0.41
33:69:58:LEU:O	33:69:62:LYS:N	2.53	0.41
33:69:130:TYR:O	33:69:131:LYS:HD2	2.21	0.41
34:15:35:ARG:HB2	34:15:42:TRP:CZ3	2.54	0.41
35:25:104:ARG:C	35:25:106:LEU:N	2.79	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:45:63:LYS:HE2	37:45:65:PHE:CZ	2.56	0.41
39:65:74:ALA:HB2	39:65:105:ALA:O	2.21	0.41
51:I5:2:LYS:HB3	51:I5:6:HIS:CD2	2.56	0.41
1:13:93:U:H2'	1:13:95:G:H5"	2.02	0.40
1:13:187:C:O2	1:13:191(A):G:C6	2.74	0.40
1:13:475:G:C4	1:13:476:G:C8	3.08	0.40
1:13:687:A:C2'	1:13:701:C:H41	2.34	0.40
1:13:1023:G:H3'	1:13:1024:G:C5'	2.47	0.40
1:13:1068:G:N7	1:13:1094:G:H2'	2.35	0.40
13:4I:50:GLU:O	13:4I:54:VAL:HG23	2.21	0.40
14:5I:13:THR:HG23	14:5I:20:ALA:HB2	2.04	0.40
17:8I:25:ARG:CZ	17:8I:27:PHE:HE2	2.34	0.40
20:BI:57:ARG:HH12	20:BI:102:GLY:HA2	1.85	0.40
26:1H:858:U:O2	26:1H:2268:A:H2'	2.21	0.40
26:1H:1045:A:H1'	26:1H:1047:G:C4	2.56	0.40
26:1H:1340:U:H4'	26:1H:1341:U:OP2	2.20	0.40
26:1H:1359:A:N1	26:1H:1372:U:C4	2.88	0.40
26:1H:1426:G:P	26:1H:1427:A:HO2'	2.36	0.40
26:1H:1524:G:C2	26:1H:1525:G:C4	3.08	0.40
26:1H:1641:A:N6	26:1H:1642:G:C2	2.90	0.40
26:1H:2028:U:C5	61:1H:4099:HOH:O	2.70	0.40
26:1H:2309:A:C6	26:1H:2310:A:C8	3.09	0.40
26:1H:2376:A:N1	39:A8:87:PHE:HD2	2.18	0.40
26:1H:2459:A:H2'	26:1H:2460:U:H5'	2.03	0.40
26:1H:2540:C:H2'	26:1H:2541:A:O4'	2.21	0.40
26:1H:2552:U:H2'	26:1H:2554:U:H5"	2.03	0.40
26:1H:2695:C:H2'	26:1H:2696:U:C6	2.56	0.40
29:21:105:THR:HG22	29:21:106:GLY:N	2.26	0.40
29:21:105:THR:O	29:21:196:VAL:HB	2.21	0.40
30:31:34:TRP:CZ2	36:78:8:PRO:HG3	2.56	0.40
33:61:131:LYS:N	33:61:131:LYS:HZ2	2.19	0.40
36:78:46:LYS:O	36:78:47:ASP:HB3	2.20	0.40
36:78:52:GLU:HG3	36:78:57:THR:HA	2.03	0.40
40:B8:129:ARG:HD3	40:B8:129:ARG:HA	1.86	0.40
43:E8:58:ALA:O	43:E8:64:MET:HB2	2.21	0.40
45:G8:100:ALA:HB1	45:G8:101:LYS:CB	2.45	0.40
46:H8:143:GLY:O	46:H8:145:GLU:HG2	2.21	0.40
48:J8:91:LYS:C	48:J8:93:GLU:N	2.78	0.40
50:L8:8:LEU:HD22	50:L8:31:LEU:HD22	2.02	0.40
54:P8:37:LYS:O	54:P8:37:LYS:HG3	2.21	0.40
55:Q8:48:PHE:O	55:Q8:49:VAL:HG12	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1G:589:C:N4	1:1G:650:G:H1	2.04	0.40
1:1G:779:C:H2'	1:1G:780:A:O4'	2.21	0.40
1:1G:960:U:O2	1:1G:1225:A:C8	2.74	0.40
1:1G:977:A:OP1	14:5A:31:ARG:HD3	2.20	0.40
1:1G:1062:U:H2'	1:1G:1063:C:C6	2.56	0.40
1:1G:1119:C:H2'	1:1G:1120:G:C8	2.56	0.40
1:1G:1165:C:H2'	1:1G:1166:G:O4'	2.19	0.40
1:1G:1187:G:H2'	1:1G:1188:A:C8	2.55	0.40
1:1G:1347:G:C8	9:82:107:ARG:HB3	2.56	0.40
2:12:97:TRP:HH2	2:12:176:GLU:OE2	2.05	0.40
3:22:51:GLY:O	3:22:70:VAL:HG13	2.21	0.40
5:42:9:LYS:HG2	5:42:108:ALA:HB1	2.03	0.40
7:62:69:VAL:HG21	7:62:104:LEU:HD13	2.02	0.40
8:72:104:ARG:HB3	8:72:107:LEU:HB2	2.03	0.40
9:82:26:VAL:HG22	9:82:61:ALA:H	1.85	0.40
13:4A:13:LYS:HG2	13:4A:14:ARG:H	1.85	0.40
23:2L:9:G:O4'	23:2L:47:7MG:H1'	2.21	0.40
57:3L:18:G:O2'	57:3L:57:G:N2	2.53	0.40
26:14:128:C:H2'	26:14:129:C:C6	2.56	0.40
26:14:528:A:C2	26:14:2043:C:H4'	2.57	0.40
26:14:719:C:O2'	26:14:720:C:H5'	2.20	0.40
26:14:868:U:N3	26:14:869:G:C5	2.89	0.40
26:14:883:G:H2'	26:14:884:C:C6	2.56	0.40
26:14:914:C:C4	26:14:915:C:C6	3.10	0.40
26:14:1268:A:C2	26:14:2013:A:C4	3.09	0.40
26:14:1780:A:P	61:14:4022:HOH:O	2.72	0.40
26:14:2187:G:C5	26:14:2188:C:C4	3.09	0.40
26:14:2420:C:OP1	55:M5:34:TRP:HB3	2.21	0.40
26:14:2854:G:C2	26:14:2864:G:C2	3.09	0.40
26:14:2873:A:C8	38:55:5:LYS:HA	2.56	0.40
27:1J:50:G:OP1	39:65:63:THR:HG23	2.21	0.40
27:1J:52:A:H62	39:65:33:LYS:HG3	1.86	0.40
28:19:70:TRP:O	28:19:73:VAL:HG23	2.21	0.40
30:39:154:VAL:HA	30:39:191:ARG:O	2.21	0.40
31:49:95:ARG:HG2	31:49:96:ARG:H	1.86	0.40
33:69:37:VAL:HG12	33:69:38:LEU:HD12	2.03	0.40
37:45:54:MET:HE3	37:45:121:ALA:HB2	2.02	0.40
39:65:29:PHE:O	39:65:35:ILE:HD12	2.22	0.40
39:65:77:ALA:HA	39:65:80:LEU:HB2	2.03	0.40
43:A5:4:LYS:HA	43:A5:105:VAL:O	2.21	0.40
54:L5:40:TRP:N	54:L5:40:TRP:CD1	2.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:M5:51:ALA:C	55:M5:52:LYS:HD3	2.46	0.40
1:13:129:U:N3	1:13:131:C:N4	2.69	0.40
1:13:403:C:O3'	4:3E:122:ARG:HD2	2.21	0.40
1:13:1080:A:H5"	5:4E:16:THR:HG21	2.03	0.40
1:13:1087:G:H2'	1:13:1088:G:C8	2.56	0.40
1:13:1365:G:H2'	1:13:1366:C:H6	1.87	0.40
1:13:1504:G:P	1:13:1504:G:H3'	2.62	0.40
20:BI:50:GLU:HG3	20:BI:100:ILE:HG12	2.02	0.40
22:1K:29:G:H1	22:1K:41:C:N4	2.19	0.40
23:2K:55:5MU:C4	23:2K:56:PSU:C2	3.09	0.40
24:3K:62:C:O5'	24:3K:62:C:H6	2.04	0.40
26:1H:259:G:N2	26:1H:621:A:C8	2.80	0.40
26:1H:270(I):G:H8	26:1H:270(I):G:O5'	2.03	0.40
26:1H:608:A:C4	26:1H:621:A:C6	3.09	0.40
26:1H:1013:C:H42	26:1H:1149:G:H1	1.69	0.40
26:1H:1239:G:H2'	26:1H:1240:U:O4'	2.21	0.40
26:1H:1588:C:C2	26:1H:1589:C:C5	3.10	0.40
26:1H:2126:A:H2'	26:1H:2126:A:N3	2.36	0.40
26:1H:2334:G:C2	39:A8:12:PHE:CD1	3.10	0.40
26:1H:2343:C:HO2'	26:1H:2373:G:HO2'	1.67	0.40
26:1H:2647:U:H2'	26:1H:2648:C:C6	2.56	0.40
26:1H:2693:A:H2'	26:1H:2694:G:H8	1.87	0.40
30:31:22:ALA:HB1	30:31:24:LEU:HD13	2.03	0.40
30:31:34:TRP:CH2	36:78:8:PRO:HB3	2.56	0.40
36:78:22:GLY:C	36:78:23:PRO:O	2.62	0.40
39:A8:110:LEU:O	39:A8:111:GLU:HB2	2.21	0.40
44:F8:5:TYR:CZ	49:K8:30:ARG:HB2	2.56	0.40
46:H8:28:MET:HB2	46:H8:37:VAL:CG1	2.51	0.40
52:N8:46:CYS:HA	52:N8:47:PRO:HD2	1.94	0.40
55:Q8:27:THR:HG23	55:Q8:31:HIS:NE2	2.36	0.40
1:1G:1028(A):C:N3	1:1G:1028(B):C:H5	2.19	0.40
1:1G:1239:A:H4'	1:1G:1240:U:C5'	2.51	0.40
1:1G:1401:G:C2	1:1G:1402:C:H1'	2.57	0.40
1:1G:1441:G:H5"	1:1G:1442:G:H5'	2.03	0.40
3:22:140:ARG:O	3:22:144:SER:HB2	2.21	0.40
6:52:7:ASN:HD21	18:9A:34:TYR:HE1	1.70	0.40
6:52:87:ARG:HH11	6:52:87:ARG:HG2	1.86	0.40
7:62:114:ARG:H	7:62:114:ARG:HG2	1.62	0.40
7:62:150:ALA:O	11:2A:57:THR:HG21	2.21	0.40
56:1L:16:U:H2'	56:1L:17:C:H5"	2.04	0.40
57:3L:76:A:O2'	26:14:2394:C:N3	2.45	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:4L:15:A:O5'	25:4L:15:A:H8	2.04	0.40
26:14:590:A:H2'	26:14:591:C:O4'	2.21	0.40
26:14:1018:C:H2'	26:14:1019:U:H6	1.86	0.40
26:14:1344:G:H4'	26:14:1384:A:C5	2.56	0.40
26:14:1379:A:H4'	26:14:1380:G:OP2	2.22	0.40
26:14:2094:G:OP1	33:69:22:LYS:HD2	2.21	0.40
26:14:2187:G:C6	26:14:2188:C:N3	2.90	0.40
26:14:2191:G:HO2'	26:14:2192:G:P	2.43	0.40
26:14:2889:C:H2'	26:14:2891:G:O4'	2.21	0.40
28:19:33:LEU:HA	28:19:33:LEU:HD12	1.71	0.40
29:29:170:LEU:HD11	29:29:185:LYS:O	2.21	0.40
37:45:135:ASP:O	37:45:137:TYR:HD1	2.04	0.40
40:75:105:LEU:O	40:75:110:ILE:HG13	2.21	0.40
40:75:123:GLN:O	40:75:127:ALA:N	2.48	0.40
1:13:50:A:H1'	1:13:52:G:C8	2.57	0.40
1:13:51:A:OP2	1:13:52:G:C8	2.75	0.40
1:13:222:U:C2	1:13:223:U:C5	3.09	0.40
1:13:539:A:H2'	1:13:540:G:C8	2.57	0.40
1:13:580:U:H2'	1:13:581:G:O4'	2.22	0.40
1:13:648:A:C6	1:13:649:G:C6	3.09	0.40
1:13:1527:C:H2'	1:13:1528:U:C6	2.56	0.40
2:1E:17:PHE:HD1	2:1E:17:PHE:N	2.19	0.40
3:2E:64:VAL:HG12	3:2E:66:VAL:HG23	2.03	0.40
5:4E:145:LYS:HE2	5:4E:145:LYS:HB3	1.89	0.40
6:5E:82:ARG:HB2	6:5E:85:VAL:HG23	2.03	0.40
11:2I:107:SER:HA	18:9I:87:ARG:CD	2.49	0.40
16:7I:80:PHE:N	16:7I:80:PHE:CD1	2.89	0.40
23:2K:44:A:C2	23:2K:45:A:C4	3.10	0.40
24:3K:22:G:C2	24:3K:23:A:C8	3.10	0.40
26:1H:142:G:O3'	44:F8:35:THR:HG21	2.22	0.40
26:1H:249:C:P	61:1H:3656:HOH:O	2.77	0.40
26:1H:265:A:H8	26:1H:266:G:H1'	1.85	0.40
26:1H:270(Y):G:C2	26:1H:270(Z):U:O4	2.74	0.40
26:1H:478:A:C6	26:1H:480:A:C6	3.09	0.40
26:1H:962:G:H2'	26:1H:963:U:H6	1.87	0.40
26:1H:1266:G:O2'	26:1H:2012:G:O6	2.34	0.40
26:1H:1808:U:H2'	26:1H:1809:A:O4'	2.21	0.40
26:1H:1861:G:C2	26:1H:1862:G:C8	3.09	0.40
26:1H:2308:G:N2	26:1H:2311:A:H2	2.20	0.40
26:1H:2392:A:N1	26:1H:2424:C:N3	2.69	0.40
26:1H:2615:U:OP1	61:1H:3614:HOH:O	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1H:2758:A:C2	26:1H:2759:G:H1'	2.57	0.40
27:16:0:A:N6	27:16:119:A:N1	2.61	0.40
29:21:101:ARG:HB3	29:21:201:THR:OG1	2.21	0.40
39:A8:34:HIS:CE1	39:A8:54:LEU:HD23	2.56	0.40
41:C8:57:PHE:O	41:C8:58:ARG:C	2.64	0.40
43:E8:42:ARG:HH11	43:E8:42:ARG:HD3	1.69	0.40
47:I8:51:VAL:HG23	47:I8:81:VAL:HG23	2.04	0.40
49:K8:21:LEU:HD23	49:K8:21:LEU:HA	1.73	0.40
52:N8:42:PRO:HB2	52:N8:43:HIS:ND1	2.36	0.40
55:Q8:39:LYS:HE3	55:Q8:43:GLN:NE2	2.36	0.40
1:1G:222:U:C2	1:1G:223:U:C5	3.09	0.40
1:1G:281:G:H8	1:1G:281:G:OP2	2.05	0.40
1:1G:324:G:C8	61:1G:1752:HOH:O	2.74	0.40
1:1G:833:U:O2'	1:1G:834:C:H5'	2.22	0.40
1:1G:921:U:O2	5:42:19:MET:HB3	2.20	0.40
1:1G:1132:C:C2	1:1G:1133:G:C8	3.09	0.40
1:1G:1205:U:O2'	3:22:195:VAL:HG13	2.22	0.40
2:12:32:ILE:HG13	2:12:33:TYR:N	2.36	0.40
2:12:189:ASP:HB3	2:12:203:GLY:O	2.21	0.40
4:32:33:MET:C	4:32:35:ARG:N	2.79	0.40
7:62:38:LEU:O	7:62:42:ILE:HG13	2.20	0.40
10:1A:51:ARG:HE	10:1A:61:GLU:HB2	1.86	0.40
12:3A:27:LEU:HD21	12:3A:60:LEU:HG	2.04	0.40
14:5A:12:ARG:H	14:5A:12:ARG:HG3	1.39	0.40
16:7A:74:LEU:CD1	16:7A:79:VAL:HG21	2.52	0.40
17:8A:23:VAL:O	17:8A:39:SER:HA	2.21	0.40
19:AA:31:ILE:HG23	19:AA:49:ILE:HG23	2.04	0.40
21:1B:12:LYS:HD2	21:1B:17:THR:O	2.21	0.40
23:2L:48:U:H4'	23:2L:49:C:H5'	2.02	0.40
26:14:307:G:H21	26:14:330:A:H62	1.68	0.40
26:14:443:A:N7	30:39:45:ARG:HD2	2.37	0.40
26:14:521:G:H2'	26:14:522:G:C8	2.55	0.40
26:14:528:A:H2	26:14:2043:C:C5'	2.34	0.40
26:14:613:U:O2	26:14:613:U:O4'	2.40	0.40
26:14:760:G:H2'	26:14:761:A:O4'	2.21	0.40
26:14:863:A:H2'	26:14:864:G:H8	1.86	0.40
26:14:1750:G:H2'	26:14:1751:C:C6	2.57	0.40
26:14:1848:A:C4	26:14:1849:G:C8	3.09	0.40
26:14:2057:A:P	61:14:4031:HOH:O	2.75	0.40
26:14:2111:C:C2	26:14:2118:U:H4'	2.56	0.40
27:1J:45:A:O4'	31:49:95:ARG:NH1	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:29:101:ARG:CZ	29:29:171:GLU:HB2	2.52	0.40
31:49:80:PHE:O	31:49:81:LYS:C	2.64	0.40
32:59:94:TYR:CD1	32:59:94:TYR:N	2.88	0.40
36:35:124:LYS:HA	36:35:143:GLY:O	2.21	0.40
45:C5:5:MET:HE3	45:C5:5:MET:HB3	1.99	0.40
55:M5:52:LYS:O	55:M5:52:LYS:CG	2.69	0.40
1:13:434:U:H2'	1:13:435:C:C6	2.57	0.40
1:13:632:A:H8	1:13:633:G:N9	2.20	0.40
1:13:858:G:O6	1:13:869:G:H3'	2.21	0.40
1:13:1159:U:O4'	1:13:1182:G:N2	2.55	0.40
1:13:1327:C:OP2	21:1F:12:LYS:NZ	2.52	0.40
1:13:1345:U:P	61:13:1941:HOH:O	2.76	0.40
1:13:1440:C:H2'	1:13:1441:G:O4'	2.22	0.40
1:13:1478:C:H2'	1:13:1479:C:H6	1.84	0.40
3:2E:79:ARG:HH21	11:2A:99:GLN:HG2	1.86	0.40
4:3E:18:LYS:HB2	4:3E:18:LYS:HE3	1.65	0.40
10:1I:32:ALA:HB1	10:1I:76:ASN:OD1	2.21	0.40
12:3I:76:ASN:ND2	12:3I:106:ASP:O	2.54	0.40
13:4I:89:GLY:O	13:4I:93:ARG:HG3	2.22	0.40
18:9I:32:ARG:HH11	18:9I:65:ILE:HD13	1.86	0.40
19:AI:58:VAL:HA	19:AI:59:PRO:HD3	1.90	0.40
20:BI:53:LEU:H	20:BI:53:LEU:HD22	1.86	0.40
20:BI:76:ALA:O	20:BI:80:ARG:HG2	2.21	0.40
22:1K:12:U:O2	22:1K:24:G:N2	2.55	0.40
24:3K:71:G:OP1	26:1H:1893:C:H4'	2.21	0.40
26:1H:172:C:H2'	26:1H:173:G:C8	2.57	0.40
26:1H:1486:A:O2'	26:1H:1487:G:H5'	2.21	0.40
26:1H:1655:A:H3'	26:1H:1656:C:H6	1.87	0.40
26:1H:1918:A:N3	26:1H:1919:A:N6	2.69	0.40
26:1H:2025:C:H2'	26:1H:2026:C:C6	2.56	0.40
26:1H:2608:G:H5"	26:1H:2609:U:OP1	2.21	0.40
26:1H:2846:G:N7	61:1H:4568:HOH:O	2.37	0.40
28:11:16:MET:HE3	28:11:211:ARG:HD2	2.03	0.40
30:31:23:ASP:CG	30:31:24:LEU:N	2.79	0.40
35:68:31:LYS:HB3	35:68:32:TYR:CE1	2.56	0.40
38:98:10:LEU:O	38:98:12:ARG:N	2.55	0.40
40:B8:16:ARG:NE	40:B8:19:LEU:HD11	2.32	0.40
40:B8:78:LEU:O	40:B8:78:LEU:HD22	2.21	0.40
43:E8:64:MET:HE2	43:E8:64:MET:HB3	1.91	0.40
43:E8:83:LYS:O	43:E8:84:ARG:HD2	2.22	0.40
45:G8:79:CYS:HB2	45:G8:80:GLY:H	1.68	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:H8:117:LEU:H	46:H8:117:LEU:CD1	2.34	0.40
47:I8:11:ARG:H	47:I8:11:ARG:HG3	1.37	0.40
1:1G:464:G:C6	1:1G:466:C:H5'	2.57	0.40
1:1G:465:A:N6	1:1G:467:G:C2	2.90	0.40
1:1G:624:C:O3'	16:7A:10:GLY:HA2	2.20	0.40
1:1G:957:U:H2'	1:1G:958:A:H3'	2.03	0.40
1:1G:999:U:H2'	1:1G:1000:A:H8	1.82	0.40
1:1G:1279:A:H5"	1:1G:1280:A:OP1	2.21	0.40
1:1G:1291:G:H2'	1:1G:1292:U:C6	2.57	0.40
1:1G:1320:C:H2'	1:1G:1321:C:H6	1.83	0.40
1:1G:1324:A:H2'	1:1G:1325:C:H6	1.86	0.40
2:12:187:LEU:HA	2:12:201:ILE:O	2.22	0.40
9:82:114:TYR:C	9:82:116:LYS:H	2.28	0.40
57:3L:52:G:O2'	57:3L:53:G:OP1	2.31	0.40
26:14:76:C:O2'	26:14:77:C:H5'	2.22	0.40
26:14:426:C:H2'	26:14:427:U:O4'	2.21	0.40
26:14:522:G:C2	26:14:523:C:C2	3.09	0.40
26:14:527:C:O2	26:14:527:C:O4'	2.39	0.40
26:14:528:A:O2'	26:14:529:A:H5'	2.22	0.40
26:14:550:G:O2'	26:14:1220:A:N3	2.41	0.40
26:14:612:G:H2'	26:14:613:U:O2	2.21	0.40
26:14:919:G:C6	26:14:920:G:C5	3.09	0.40
26:14:951:C:O2'	26:14:952:G:H5'	2.22	0.40
26:14:1655:A:H1'	29:29:113:PHE:CD1	2.56	0.40
26:14:1786:A:H1'	26:14:1938:A:N6	2.36	0.40
26:14:2128:C:H1'	26:14:2173:A:H2	1.86	0.40
26:14:2365:G:H4'	47:E5:60:PHE:CZ	2.56	0.40
26:14:2418:A:OP2	55:M5:29:LYS:NZ	2.47	0.40
26:14:2630:G:H21	26:14:2894:G:N2	2.20	0.40
26:14:2646:C:H2'	26:14:2647:U:O4'	2.22	0.40
26:14:2687:U:H2'	26:14:2688:U:O4'	2.21	0.40
29:29:7:VAL:HG12	29:29:193:GLY:HA2	2.04	0.40
30:39:117:ARG:HH12	36:35:1:MET:N	2.19	0.40
33:69:97:ILE:O	33:69:100:ALA:HB3	2.22	0.40
38:55:69:ASP:OD1	38:55:69:ASP:N	2.54	0.40
40:75:4:GLY:O	40:75:7:ILE:HG22	2.22	0.40
40:75:99:LEU:HA	40:75:99:LEU:HD23	1.83	0.40
41:85:91:ASP:C	41:85:93:LYS:N	2.79	0.40
42:95:71:LEU:HA	42:95:86:GLY:HA2	2.03	0.40
43:A5:89:ALA:O	43:A5:90:ARG:HB2	2.21	0.40
44:B5:18:TYR:C	44:B5:20:GLY:N	2.78	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:13:251:G:O6	1:13:271:C:N4	2.54	0.40
1:13:343:U:C2	1:13:347:G:N1	2.90	0.40
1:13:380:G:N2	1:13:384:G:C5	2.90	0.40
1:13:719:C:H1'	18:9I:49:LYS:HB3	2.03	0.40
1:13:1285:A:H4'	1:13:1286:A:O5'	2.22	0.40
2:1E:17:PHE:N	2:1E:17:PHE:CD1	2.88	0.40
13:4I:20:THR:HG23	13:4I:26:GLY:HA3	2.04	0.40
13:4I:66:LEU:O	13:4I:70:LEU:HB2	2.22	0.40
26:1H:6:A:O2'	34:58:129:PRO:HB3	2.21	0.40
26:1H:143:C:O2'	26:1H:144:C:H5'	2.22	0.40
26:1H:880:G:H22	26:1H:897:C:H42	1.68	0.40
26:1H:1026:U:HO2'	26:1H:1027:A:C5'	2.35	0.40
26:1H:1268:A:P	61:1H:4450:HOH:O	2.76	0.40
26:1H:1466:G:N2	26:1H:1547:C:N3	2.69	0.40
26:1H:2845:G:H2'	26:1H:2846:G:C8	2.57	0.40
27:16:11:C:OP2	27:16:12:C:H5	2.05	0.40
29:21:31:CYS:HA	29:21:32:PRO:HD3	1.72	0.40
29:21:120:TRP:CD1	29:21:155:LYS:HB3	2.57	0.40
30:31:53:THR:O	30:31:54:ARG:C	2.64	0.40
32:51:9:ILE:HG13	32:51:9:ILE:O	2.21	0.40
32:51:137:ASP:HB3	32:51:140:LYS:HB3	2.02	0.40
33:61:6:LEU:O	33:61:7:GLU:HB3	2.21	0.40
34:58:67:LEU:HA	34:58:87:LEU:HD12	2.04	0.40
36:78:91:PHE:N	36:78:91:PHE:CD1	2.90	0.40
45:G8:19:LYS:C	45:G8:21:LYS:H	2.30	0.40
46:H8:18:LEU:O	46:H8:21:ALA:HB3	2.22	0.40
49:K8:32:LEU:HA	49:K8:35:LEU:HD12	2.04	0.40
49:K8:42:GLY:C	49:K8:44:LEU:N	2.73	0.40
1:1G:4:U:C4	8:72:102:ARG:NE	2.90	0.40
1:1G:418:C:H2'	1:1G:419:C:O4'	2.21	0.40
1:1G:790:A:H2'	1:1G:791:G:C8	2.56	0.40
1:1G:1048:G:H1	1:1G:1209:C:N4	2.14	0.40
1:1G:1113:C:H2'	1:1G:1114:C:H6	1.86	0.40
1:1G:1301:U:O3'	13:4A:21:TYR:OH	2.34	0.40
1:1G:1329:A:H5"	13:4A:25:ILE:O	2.21	0.40
1:1G:1452:C:H4'	1:1G:1453:G:O5'	2.21	0.40
4:32:146:ILE:H	4:32:146:ILE:HD12	1.86	0.40
5:42:42:GLY:HA3	5:42:65:ASN:O	2.21	0.40
13:4A:3:ARG:HB2	51:I5:34:GLU:CD	2.46	0.40
23:2L:37:U:H2'	23:2L:38:A:O4'	2.22	0.40
23:2L:56:PSU:O4	23:2L:58:A:C8	2.74	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:14:302:C:H2'	26:14:303:U:H6	1.85	0.40
26:14:403:U:H4'	26:14:404:C:H5'	2.04	0.40
26:14:631:A:H2'	26:14:632:A:O4'	2.20	0.40
26:14:914:C:C5	26:14:915:C:C6	3.10	0.40
26:14:959:A:N6	26:14:960:A:N1	2.70	0.40
26:14:1337:G:H2'	26:14:1338:G:H8	1.87	0.40
26:14:1826:G:H2'	26:14:1827:C:O4'	2.21	0.40
26:14:2056:G:N3	26:14:2056:G:H2'	2.35	0.40
26:14:2611:U:O2	52:J5:3:LYS:HE3	2.20	0.40
26:14:2674:G:H2'	26:14:2675:A:C8	2.57	0.40
27:1J:24:G:H4'	27:1J:25:A:H5'	2.03	0.40
29:29:52:LEU:O	29:29:75:VAL:HG23	2.21	0.40
29:29:64:LYS:HB3	29:29:65:GLY:H	1.56	0.40
31:49:96:ARG:HG2	31:49:96:ARG:H	1.57	0.40
31:49:109:VAL:HG13	51:I5:33:VAL:HG23	2.03	0.40
37:45:43:THR:OG1	37:45:45:GLN:HG2	2.21	0.40
41:85:95:LEU:HD11	42:95:11:GLN:C	2.47	0.40
46:D5:109:ALA:O	46:D5:114:GLY:HA3	2.22	0.40
47:E5:36:ILE:HD12	47:E5:58:THR:HG23	2.03	0.40
53:K5:16:CYS:O	53:K5:17:LYS:HB2	2.22	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1H:277:C:O2'	49:G5:49:LYS:NZ[2_564]	2.14	0.06

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
2	12	235/256 (92%)	192 (82%)	37 (16%)	6 (3%)	4 12

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
2	1E	235/256 (92%)	197 (84%)	37 (16%)	1 (0%)	30 53
3	22	204/239 (85%)	180 (88%)	23 (11%)	1 (0%)	24 49
3	2E	203/239 (85%)	184 (91%)	19 (9%)	0	100 100
4	32	206/209 (99%)	179 (87%)	25 (12%)	2 (1%)	12 32
4	3E	206/209 (99%)	192 (93%)	12 (6%)	2 (1%)	12 32
5	42	149/162 (92%)	140 (94%)	9 (6%)	0	100 100
5	4E	149/162 (92%)	140 (94%)	8 (5%)	1 (1%)	18 40
6	52	99/101 (98%)	96 (97%)	3 (3%)	0	100 100
6	5E	99/101 (98%)	92 (93%)	7 (7%)	0	100 100
7	62	148/156 (95%)	137 (93%)	11 (7%)	0	100 100
7	6E	153/156 (98%)	144 (94%)	9 (6%)	0	100 100
8	72	136/138 (99%)	122 (90%)	12 (9%)	2 (2%)	8 23
8	7E	136/138 (99%)	125 (92%)	10 (7%)	1 (1%)	18 40
9	82	122/128 (95%)	113 (93%)	8 (7%)	1 (1%)	16 37
9	8E	125/128 (98%)	105 (84%)	19 (15%)	1 (1%)	16 37
10	1A	97/105 (92%)	88 (91%)	9 (9%)	0	100 100
10	1I	97/105 (92%)	89 (92%)	8 (8%)	0	100 100
11	2A	114/129 (88%)	102 (90%)	8 (7%)	4 (4%)	3 7
11	2I	114/129 (88%)	99 (87%)	14 (12%)	1 (1%)	14 34
12	3A	123/132 (93%)	101 (82%)	18 (15%)	4 (3%)	3 7
12	3I	123/132 (93%)	103 (84%)	20 (16%)	0	100 100
13	4A	115/126 (91%)	96 (84%)	18 (16%)	1 (1%)	14 34
13	4I	116/126 (92%)	96 (83%)	19 (16%)	1 (1%)	14 34
14	5A	56/61 (92%)	46 (82%)	9 (16%)	1 (2%)	6 19
14	5I	58/61 (95%)	47 (81%)	9 (16%)	2 (3%)	3 7
15	6A	86/89 (97%)	79 (92%)	7 (8%)	0	100 100
15	6I	86/89 (97%)	79 (92%)	7 (8%)	0	100 100
16	7A	82/88 (93%)	75 (92%)	7 (8%)	0	100 100
16	7I	82/88 (93%)	75 (92%)	7 (8%)	0	100 100
17	8A	98/105 (93%)	91 (93%)	7 (7%)	0	100 100
17	8I	98/105 (93%)	94 (96%)	4 (4%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
18	9A	70/88 (80%)	65 (93%)	5 (7%)	0	100 100
18	9I	70/88 (80%)	63 (90%)	6 (9%)	1 (1%)	9 24
19	AA	76/93 (82%)	59 (78%)	15 (20%)	2 (3%)	4 12
19	AI	79/93 (85%)	65 (82%)	11 (14%)	3 (4%)	2 6
20	BA	97/106 (92%)	84 (87%)	12 (12%)	1 (1%)	12 32
20	BI	97/106 (92%)	86 (89%)	10 (10%)	1 (1%)	12 32
21	1B	23/27 (85%)	21 (91%)	2 (9%)	0	100 100
21	1F	23/27 (85%)	22 (96%)	1 (4%)	0	100 100
28	11	270/276 (98%)	253 (94%)	12 (4%)	5 (2%)	6 17
28	19	271/276 (98%)	248 (92%)	16 (6%)	7 (3%)	4 12
29	21	203/206 (98%)	164 (81%)	30 (15%)	9 (4%)	2 4
29	29	203/206 (98%)	156 (77%)	35 (17%)	12 (6%)	1 2
30	31	200/210 (95%)	182 (91%)	15 (8%)	3 (2%)	8 23
30	39	206/210 (98%)	165 (80%)	34 (16%)	7 (3%)	3 7
31	41	179/182 (98%)	156 (87%)	21 (12%)	2 (1%)	11 29
31	49	179/182 (98%)	155 (87%)	22 (12%)	2 (1%)	11 29
32	51	172/180 (96%)	146 (85%)	18 (10%)	8 (5%)	2 4
32	59	168/180 (93%)	131 (78%)	30 (18%)	7 (4%)	2 5
33	61	144/148 (97%)	117 (81%)	23 (16%)	4 (3%)	4 11
33	69	144/148 (97%)	112 (78%)	29 (20%)	3 (2%)	5 16
34	15	136/140 (97%)	120 (88%)	15 (11%)	1 (1%)	18 40
34	58	136/140 (97%)	116 (85%)	16 (12%)	4 (3%)	3 10
35	25	120/122 (98%)	110 (92%)	8 (7%)	2 (2%)	7 20
35	68	120/122 (98%)	113 (94%)	7 (6%)	0	100 100
36	35	148/150 (99%)	117 (79%)	27 (18%)	4 (3%)	4 11
36	78	148/150 (99%)	113 (76%)	29 (20%)	6 (4%)	2 5
37	45	139/141 (99%)	111 (80%)	27 (19%)	1 (1%)	18 40
37	88	134/141 (95%)	112 (84%)	15 (11%)	7 (5%)	1 3
38	55	115/118 (98%)	108 (94%)	5 (4%)	2 (2%)	7 20
38	98	116/118 (98%)	104 (90%)	10 (9%)	2 (2%)	7 20
39	65	109/112 (97%)	88 (81%)	18 (16%)	3 (3%)	4 11

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
39	A8	109/112 (97%)	91 (84%)	16 (15%)	2 (2%)	6 19
40	75	135/146 (92%)	115 (85%)	17 (13%)	3 (2%)	5 15
40	B8	135/146 (92%)	119 (88%)	15 (11%)	1 (1%)	18 40
41	85	115/118 (98%)	102 (89%)	12 (10%)	1 (1%)	14 34
41	C8	115/118 (98%)	104 (90%)	9 (8%)	2 (2%)	7 20
42	95	99/101 (98%)	77 (78%)	17 (17%)	5 (5%)	1 3
42	D8	99/101 (98%)	94 (95%)	4 (4%)	1 (1%)	12 32
43	A5	111/113 (98%)	102 (92%)	7 (6%)	2 (2%)	6 19
43	E8	111/113 (98%)	100 (90%)	11 (10%)	0	100 100
44	B5	92/96 (96%)	83 (90%)	5 (5%)	4 (4%)	2 4
44	F8	92/96 (96%)	83 (90%)	7 (8%)	2 (2%)	5 15
45	C5	102/110 (93%)	75 (74%)	21 (21%)	6 (6%)	1 2
45	G8	102/110 (93%)	80 (78%)	15 (15%)	7 (7%)	1 1
46	D5	177/206 (86%)	134 (76%)	33 (19%)	10 (6%)	1 2
46	H8	173/206 (84%)	142 (82%)	25 (14%)	6 (4%)	3 7
47	E5	75/85 (88%)	67 (89%)	6 (8%)	2 (3%)	4 11
47	I8	78/85 (92%)	68 (87%)	9 (12%)	1 (1%)	9 26
48	F5	92/98 (94%)	87 (95%)	4 (4%)	1 (1%)	11 29
48	J8	95/98 (97%)	85 (90%)	8 (8%)	2 (2%)	5 16
49	G5	65/72 (90%)	61 (94%)	2 (3%)	2 (3%)	3 8
49	K8	65/72 (90%)	58 (89%)	4 (6%)	3 (5%)	2 4
50	H5	57/60 (95%)	53 (93%)	4 (7%)	0	100 100
50	L8	55/60 (92%)	51 (93%)	3 (6%)	1 (2%)	6 19
51	I5	58/71 (82%)	29 (50%)	25 (43%)	4 (7%)	1 1
51	M8	64/71 (90%)	43 (67%)	18 (28%)	3 (5%)	2 4
52	J5	57/60 (95%)	48 (84%)	8 (14%)	1 (2%)	6 19
52	N8	56/60 (93%)	48 (86%)	6 (11%)	2 (4%)	2 6
53	K5	43/54 (80%)	27 (63%)	14 (33%)	2 (5%)	2 4
53	O8	43/54 (80%)	28 (65%)	13 (30%)	2 (5%)	2 4
54	L5	44/49 (90%)	42 (96%)	2 (4%)	0	100 100
54	P8	43/49 (88%)	41 (95%)	2 (5%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
55	M5	58/65 (89%)	49 (84%)	6 (10%)	3 (5%)	1 3
55	Q8	58/65 (89%)	30 (52%)	21 (36%)	7 (12%)	0 0
All	All	11318/12054 (94%)	9776 (86%)	1313 (12%)	229 (2%)	6 16

All (229) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
29	21	83	ASP
36	78	57	THR
41	C8	89	GLU
41	C8	90	VAL
45	G8	54	LYS
49	K8	48	HIS
50	L8	54	VAL
52	N8	41	PRO
55	Q8	44	LYS
55	Q8	49	VAL
9	82	118	LYS
20	BA	73	HIS
28	19	237	GLU
29	29	25	VAL
30	39	28	ILE
30	39	84	VAL
37	45	27	VAL
38	55	107	ASP
46	D5	53	ILE
46	D5	165	VAL
46	D5	171	ILE
48	F5	30	VAL
51	I5	5	ILE
55	M5	35	GLN
4	3E	31	CYS
18	9I	22	VAL
29	21	60	ASN
29	21	78	LEU
32	51	168	PRO
32	51	169	VAL
37	88	6	ARG
37	88	66	ILE
37	88	79	LEU
44	F8	2	LYS

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Mol	Chain	Res	Type
46	H8	6	LYS
46	H8	60	GLU
46	H8	165	VAL
51	M8	50	VAL
52	N8	42	PRO
53	O8	17	LYS
55	Q8	55	ALA
2	12	7	VAL
11	2A	48	ILE
11	2A	100	ALA
11	2A	101	SER
12	3A	18	VAL
12	3A	26	ALA
19	AA	11	VAL
28	19	33	LEU
28	19	38	LYS
29	29	81	ILE
29	29	90	THR
36	35	15	ARG
39	65	87	PHE
39	65	89	ARG
42	95	45	THR
44	B5	4	ALA
45	C5	29	GLU
46	D5	105	VAL
49	G5	47	ASN
52	J5	57	VAL
55	M5	31	HIS
8	7E	86	ILE
14	5I	13	THR
28	11	239	ARG
29	21	118	LYS
30	31	67	GLN
34	58	97	ARG
34	58	128	HIS
37	88	2	LEU
45	G8	81	LYS
48	J8	75	GLU
48	J8	76	ARG
49	K8	43	GLN
55	Q8	8	LYS
4	32	32	ALA

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Mol	Chain	Res	Type
28	19	273	ARG
29	29	9	VAL
29	29	51	PHE
30	39	124	LEU
33	69	111	PRO
36	35	6	LEU
43	A5	44	ALA
44	B5	3	THR
45	C5	17	SER
46	D5	161	VAL
47	E5	33	ALA
49	G5	48	HIS
53	K5	17	LYS
13	4I	83	ASP
14	5I	14	PRO
19	AI	7	LYS
28	11	3	VAL
28	11	240	ALA
29	21	21	VAL
33	61	12	LEU
33	61	145	VAL
34	58	22	THR
36	78	42	SER
39	A8	4	LEU
39	A8	61	ASN
44	F8	68	ARG
45	G8	40	GLU
46	H8	59	LEU
47	I8	83	PRO
49	K8	47	ASN
2	12	73	THR
3	22	62	ASP
14	5A	29	ARG
28	19	239	ARG
29	29	26	ILE
30	39	167	ALA
32	59	92	ILE
33	69	145	VAL
36	35	110	TYR
39	65	111	GLU
40	75	2	ASN
40	75	94	ALA

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Mol	Chain	Res	Type
42	95	85	LYS
43	A5	93	ALA
44	B5	68	ARG
45	C5	19	LYS
46	D5	8	TYR
46	D5	116	VAL
51	I5	38	LYS
4	3E	155	LEU
11	2I	82	VAL
28	11	122	ASP
29	21	56	PRO
29	21	82	ARG
31	41	5	VAL
31	41	97	ASP
32	51	10	PRO
32	51	167	GLU
34	58	127	ASP
36	78	12	ALA
37	88	3	MET
37	88	60	ARG
38	98	2	ARG
40	B8	106	SER
45	G8	53	PRO
45	G8	84	ARG
46	H8	81	ARG
2	12	101	MET
8	72	22	GLU
8	72	73	ASP
11	2A	106	LYS
12	3A	47	LYS
29	29	187	ALA
30	39	25	PRO
38	55	3	HIS
40	75	126	ALA
41	85	93	LYS
47	E5	44	ARG
51	I5	26	SER
51	I5	33	VAL
5	4E	115	VAL
9	8E	112	LYS
28	11	123	ALA
29	21	22	PRO

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Mol	Chain	Res	Type
29	21	55	ASN
30	31	24	LEU
33	61	133	HIS
36	78	95	VAL
38	98	11	ASN
51	M8	43	TYR
53	O8	21	TYR
55	Q8	33	ASN
55	Q8	43	GLN
4	32	14	ARG
28	19	3	VAL
29	29	62	PRO
31	49	47	LYS
32	59	168	PRO
35	25	5	GLN
35	25	12	ASP
42	95	71	LEU
32	51	12	PRO
33	61	131	LYS
45	G8	76	CYS
29	29	91	VAL
30	39	89	VAL
30	39	132	VAL
34	15	128	HIS
44	B5	51	VAL
46	D5	141	VAL
2	1E	239	VAL
19	AI	9	VAL
19	AI	41	VAL
20	BI	63	ILE
30	31	132	VAL
36	78	19	VAL
42	D8	49	THR
2	12	39	ILE
2	12	71	VAL
12	3A	96	VAL
13	4A	84	ILE
29	29	59	VAL
29	29	77	ILE
32	59	167	GLU
42	95	72	VAL
46	D5	158	PRO

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Mol	Chain	Res	Type
55	M5	52	LYS
32	51	92	ILE
32	51	127	GLU
36	78	7	ARG
19	AA	67	VAL
31	49	5	VAL
32	59	4	ILE
32	59	8	PRO
32	59	131	VAL
45	C5	85	VAL
53	K5	52	VAL
45	G8	77	PRO
46	H8	53	ILE
55	Q8	58	ILE
28	19	240	ALA
29	29	52	LEU
32	59	169	VAL
42	95	99	ILE
45	C5	76	CYS
37	88	27	VAL
51	M8	5	ILE
2	12	32	ILE
33	69	144	VAL
36	35	63	PRO
45	C5	3	VAL
46	D5	176	PRO
32	51	173	PRO

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
2	12	205/220 (93%)	162 (79%)	43 (21%)	1 2
2	1E	205/220 (93%)	161 (78%)	44 (22%)	1 2
3	22	160/188 (85%)	125 (78%)	35 (22%)	1 2

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	2E	159/188 (85%)	124 (78%)	35 (22%)	1	2
4	32	180/181 (99%)	145 (81%)	35 (19%)	1	3
4	3E	180/181 (99%)	141 (78%)	39 (22%)	1	2
5	42	116/123 (94%)	89 (77%)	27 (23%)	1	2
5	4E	116/123 (94%)	90 (78%)	26 (22%)	1	2
6	52	90/90 (100%)	70 (78%)	20 (22%)	1	2
6	5E	90/90 (100%)	72 (80%)	18 (20%)	1	3
7	62	126/127 (99%)	100 (79%)	26 (21%)	1	3
7	6E	126/127 (99%)	98 (78%)	28 (22%)	1	2
8	72	119/119 (100%)	97 (82%)	22 (18%)	1	4
8	7E	119/119 (100%)	96 (81%)	23 (19%)	1	3
9	82	95/99 (96%)	79 (83%)	16 (17%)	2	6
9	8E	98/99 (99%)	70 (71%)	28 (29%)	0	0
10	1A	89/92 (97%)	67 (75%)	22 (25%)	1	1
10	1I	89/92 (97%)	73 (82%)	16 (18%)	2	4
11	2A	88/99 (89%)	69 (78%)	19 (22%)	1	2
11	2I	88/99 (89%)	75 (85%)	13 (15%)	3	9
12	3A	104/109 (95%)	79 (76%)	25 (24%)	1	1
12	3I	104/109 (95%)	87 (84%)	17 (16%)	2	7
13	4A	94/101 (93%)	72 (77%)	22 (23%)	1	2
13	4I	94/101 (93%)	71 (76%)	23 (24%)	1	1
14	5A	48/50 (96%)	40 (83%)	8 (17%)	2	6
14	5I	49/50 (98%)	37 (76%)	12 (24%)	1	1
15	6A	79/80 (99%)	65 (82%)	14 (18%)	2	4
15	6I	79/80 (99%)	60 (76%)	19 (24%)	1	1
16	7A	72/74 (97%)	59 (82%)	13 (18%)	2	4
16	7I	72/74 (97%)	57 (79%)	15 (21%)	1	3
17	8A	95/97 (98%)	81 (85%)	14 (15%)	3	9
17	8I	95/97 (98%)	76 (80%)	19 (20%)	1	3
18	9A	63/77 (82%)	53 (84%)	10 (16%)	2	8
18	9I	63/77 (82%)	55 (87%)	8 (13%)	4	13

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
19	AA	67/80 (84%)	49 (73%)	18 (27%)	0 0
19	AI	70/80 (88%)	50 (71%)	20 (29%)	0 0
20	BA	76/82 (93%)	64 (84%)	12 (16%)	2 8
20	BI	76/82 (93%)	52 (68%)	24 (32%)	0 0
21	1B	20/22 (91%)	19 (95%)	1 (5%)	22 47
21	1F	20/22 (91%)	18 (90%)	2 (10%)	7 20
28	11	214/218 (98%)	169 (79%)	45 (21%)	1 2
28	19	214/218 (98%)	163 (76%)	51 (24%)	1 1
29	21	165/166 (99%)	120 (73%)	45 (27%)	0 0
29	29	165/166 (99%)	118 (72%)	47 (28%)	0 0
30	31	161/166 (97%)	124 (77%)	37 (23%)	1 2
30	39	165/166 (99%)	119 (72%)	46 (28%)	0 0
31	41	155/156 (99%)	116 (75%)	39 (25%)	0 1
31	49	155/156 (99%)	126 (81%)	29 (19%)	1 4
32	51	145/148 (98%)	103 (71%)	42 (29%)	0 0
32	59	142/148 (96%)	106 (75%)	36 (25%)	0 1
33	61	122/124 (98%)	83 (68%)	39 (32%)	0 0
33	69	122/124 (98%)	84 (69%)	38 (31%)	0 0
34	15	117/119 (98%)	89 (76%)	28 (24%)	1 1
34	58	117/119 (98%)	92 (79%)	25 (21%)	1 2
35	25	100/100 (100%)	74 (74%)	26 (26%)	0 1
35	68	100/100 (100%)	82 (82%)	18 (18%)	2 4
36	35	116/116 (100%)	72 (62%)	44 (38%)	0 0
36	78	116/116 (100%)	74 (64%)	42 (36%)	0 0
37	45	111/111 (100%)	84 (76%)	27 (24%)	1 1
37	88	104/111 (94%)	78 (75%)	26 (25%)	0 1
38	55	100/101 (99%)	74 (74%)	26 (26%)	0 1
38	98	101/101 (100%)	70 (69%)	31 (31%)	0 0
39	65	87/88 (99%)	62 (71%)	25 (29%)	0 0
39	A8	87/88 (99%)	56 (64%)	31 (36%)	0 0
40	75	120/127 (94%)	80 (67%)	40 (33%)	0 0

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
40	B8	120/127 (94%)	77 (64%)	43 (36%)	0	0
41	85	93/94 (99%)	72 (77%)	21 (23%)	1	2
41	C8	93/94 (99%)	77 (83%)	16 (17%)	2	5
42	95	82/82 (100%)	54 (66%)	28 (34%)	0	0
42	D8	82/82 (100%)	62 (76%)	20 (24%)	1	1
43	A5	92/92 (100%)	66 (72%)	26 (28%)	0	0
43	E8	92/92 (100%)	66 (72%)	26 (28%)	0	0
44	B5	74/78 (95%)	56 (76%)	18 (24%)	1	1
44	F8	76/78 (97%)	57 (75%)	19 (25%)	0	1
45	C5	85/91 (93%)	62 (73%)	23 (27%)	0	0
45	G8	85/91 (93%)	56 (66%)	29 (34%)	0	0
46	D5	158/179 (88%)	121 (77%)	37 (23%)	1	2
46	H8	154/179 (86%)	117 (76%)	37 (24%)	1	1
47	E5	62/67 (92%)	52 (84%)	10 (16%)	2	7
47	I8	61/67 (91%)	45 (74%)	16 (26%)	0	1
48	F5	79/83 (95%)	57 (72%)	22 (28%)	0	0
48	J8	82/83 (99%)	60 (73%)	22 (27%)	0	0
49	G5	62/67 (92%)	41 (66%)	21 (34%)	0	0
49	K8	62/67 (92%)	33 (53%)	29 (47%)	0	0
50	H5	51/52 (98%)	36 (71%)	15 (29%)	0	0
50	L8	49/52 (94%)	35 (71%)	14 (29%)	0	0
51	I5	54/63 (86%)	44 (82%)	10 (18%)	1	4
51	M8	59/63 (94%)	42 (71%)	17 (29%)	0	0
52	J5	51/52 (98%)	37 (72%)	14 (28%)	0	0
52	N8	51/52 (98%)	38 (74%)	13 (26%)	0	1
53	K5	44/52 (85%)	34 (77%)	10 (23%)	1	2
53	O8	44/52 (85%)	30 (68%)	14 (32%)	0	0
54	L5	39/42 (93%)	32 (82%)	7 (18%)	2	4
54	P8	38/42 (90%)	31 (82%)	7 (18%)	1	4
55	M5	49/55 (89%)	34 (69%)	15 (31%)	0	0
55	Q8	50/55 (91%)	31 (62%)	19 (38%)	0	0

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	9552/9998 (96%)	7220 (76%)	2332 (24%)	1 1

All (2332) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	1E	6	THR
2	1E	8	LYS
2	1E	15	VAL
2	1E	17	PHE
2	1E	28	PHE
2	1E	41	ILE
2	1E	48	MET
2	1E	53	ARG
2	1E	67	THR
2	1E	71	VAL
2	1E	74	LYS
2	1E	83	MET
2	1E	93	VAL
2	1E	96	ARG
2	1E	107	THR
2	1E	108	ILE
2	1E	111	ARG
2	1E	113	HIS
2	1E	121	LEU
2	1E	127	ILE
2	1E	130	ARG
2	1E	136	VAL
2	1E	139	LYS
2	1E	144	ARG
2	1E	145	LEU
2	1E	150	SER
2	1E	153	ARG
2	1E	154	LEU
2	1E	155	LEU
2	1E	160	ASP
2	1E	162	ILE
2	1E	164	VAL
2	1E	172	ILE
2	1E	178	ARG
2	1E	185	ILE
2	1E	190	THR
2	1E	196	LEU

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Mol	Chain	Res	Type
2	1E	197	VAL
2	1E	200	ILE
2	1E	209	ARG
2	1E	213	LEU
2	1E	215	LEU
2	1E	217	ARG
2	1E	231	GLU
3	2E	3	ASN
3	2E	4	LYS
3	2E	5	ILE
3	2E	8	ILE
3	2E	14	ILE
3	2E	17	ASP
3	2E	21	ARG
3	2E	32	LEU
3	2E	36	ASP
3	2E	39	ILE
3	2E	49	SER
3	2E	52	LEU
3	2E	64	VAL
3	2E	68	VAL
3	2E	76	VAL
3	2E	77	ILE
3	2E	79	ARG
3	2E	84	ILE
3	2E	93	LYS
3	2E	95	THR
3	2E	98	ASN
3	2E	104	GLN
3	2E	116	VAL
3	2E	138	VAL
3	2E	144	SER
3	2E	151	VAL
3	2E	165	THR
3	2E	166	GLU
3	2E	167	TRP
3	2E	172	ARG
3	2E	179	ARG
3	2E	190	ARG
3	2E	192	THR
3	2E	196	LEU
3	2E	202	ILE

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Mol	Chain	Res	Type
4	3E	3	ARG
4	3E	5	ILE
4	3E	8	VAL
4	3E	15	GLU
4	3E	24	GLU
4	3E	28	SER
4	3E	31	CYS
4	3E	46	LYS
4	3E	49	ARG
4	3E	50	ARG
4	3E	58	LEU
4	3E	61	LYS
4	3E	70	ILE
4	3E	83	SER
4	3E	85	LYS
4	3E	86	LYS
4	3E	88	VAL
4	3E	91	SER
4	3E	96	LEU
4	3E	104	VAL
4	3E	108	LEU
4	3E	122	ARG
4	3E	127	THR
4	3E	132	ARG
4	3E	135	LEU
4	3E	141	ARG
4	3E	146	ILE
4	3E	155	LEU
4	3E	156	GLU
4	3E	163	GLU
4	3E	175	SER
4	3E	178	VAL
4	3E	179	GLU
4	3E	184	LYS
4	3E	188	LEU
4	3E	190	ASP
4	3E	192	GLU
4	3E	193	ASP
4	3E	194	LEU
5	4E	5	ASP
5	4E	6	PHE
5	4E	10	MET

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Mol	Chain	Res	Type
5	4E	11	ILE
5	4E	15	ARG
5	4E	16	THR
5	4E	31	LEU
5	4E	33	VAL
5	4E	41	VAL
5	4E	50	GLU
5	4E	53	LEU
5	4E	71	LEU
5	4E	72	GLN
5	4E	73	ASN
5	4E	76	ILE
5	4E	79	GLU
5	4E	80	ILE
5	4E	91	LEU
5	4E	92	LYS
5	4E	98	THR
5	4E	107	ARG
5	4E	112	LEU
5	4E	126	ARG
5	4E	147	ASP
5	4E	152	ARG
5	4E	153	LYS
6	5E	13	ASN
6	5E	19	LEU
6	5E	21	LEU
6	5E	23	LYS
6	5E	24	GLU
6	5E	25	ILE
6	5E	40	VAL
6	5E	45	LEU
6	5E	55	ASP
6	5E	64	GLN
6	5E	65	VAL
6	5E	74	ASP
6	5E	75	LEU
6	5E	78	GLU
6	5E	81	ILE
6	5E	89	MET
6	5E	91	VAL
6	5E	92	LYS
7	6E	6	ARG

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Mol	Chain	Res	Type
7	6E	13	GLN
7	6E	16	LEU
7	6E	23	VAL
7	6E	24	THR
7	6E	36	LYS
7	6E	38	LEU
7	6E	41	ARG
7	6E	47	CYS
7	6E	50	ILE
7	6E	53	LYS
7	6E	54	THR
7	6E	63	LYS
7	6E	79	ARG
7	6E	80	VAL
7	6E	89	MET
7	6E	90	GLU
7	6E	91	VAL
7	6E	94	ARG
7	6E	104	LEU
7	6E	111	ARG
7	6E	113	GLU
7	6E	115	ARG
7	6E	124	LEU
7	6E	135	VAL
7	6E	137	LYS
7	6E	138	LYS
7	6E	156	TRP
8	7E	1	MET
8	7E	10	LEU
8	7E	19	VAL
8	7E	25	ASP
8	7E	26	VAL
8	7E	35	ILE
8	7E	39	LEU
8	7E	41	ARG
8	7E	45	ILE
8	7E	53	VAL
8	7E	63	LEU
8	7E	68	ARG
8	7E	80	ILE
8	7E	83	ILE
8	7E	85	ARG

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Mol	Chain	Res	Type
8	7E	95	VAL
8	7E	111	ILE
8	7E	112	LEU
8	7E	122	ARG
8	7E	127	LEU
8	7E	129	VAL
8	7E	134	ILE
8	7E	137	VAL
9	8E	7	THR
9	8E	9	ARG
9	8E	10	ARG
9	8E	14	VAL
9	8E	16	ARG
9	8E	20	ARG
9	8E	31	GLN
9	8E	38	GLN
9	8E	42	ARG
9	8E	44	VAL
9	8E	47	LEU
9	8E	53	VAL
9	8E	63	ILE
9	8E	79	LEU
9	8E	86	VAL
9	8E	92	TYR
9	8E	95	LYS
9	8E	96	LEU
9	8E	105	ASP
9	8E	108	VAL
9	8E	109	VAL
9	8E	111	ARG
9	8E	112	LYS
9	8E	113	LYS
9	8E	117	HIS
9	8E	118	LYS
9	8E	124	GLN
9	8E	128	ARG
10	1I	4	ILE
10	1I	5	ARG
10	1I	6	ILE
10	1I	16	LEU
10	1I	24	VAL
10	1I	25	GLU

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Mol	Chain	Res	Type
10	1I	30	SER
10	1I	62	HIS
10	1I	67	THR
10	1I	70	ARG
10	1I	75	ILE
10	1I	76	ASN
10	1I	88	LEU
10	1I	92	THR
10	1I	96	ILE
10	1I	98	ILE
11	2I	28	THR
11	2I	29	ILE
11	2I	31	THR
11	2I	32	ILE
11	2I	36	ASP
11	2I	93	GLN
11	2I	96	ARG
11	2I	103	LEU
11	2I	105	VAL
11	2I	106	LYS
11	2I	109	VAL
11	2I	114	VAL
11	2I	120	ARG
12	3I	21	LYS
12	3I	33	ARG
12	3I	43	VAL
12	3I	46	LYS
12	3I	47	LYS
12	3I	50	SER
12	3I	60	LEU
12	3I	62	SER
12	3I	67	THR
12	3I	81	SER
12	3I	83	VAL
12	3I	85	ILE
12	3I	89	ARG
12	3I	90	VAL
12	3I	91	LYS
12	3I	96	VAL
12	3I	114	LYS
13	4I	4	ILE
13	4I	9	ILE

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Mol	Chain	Res	Type
13	4I	13	LYS
13	4I	19	LEU
13	4I	20	THR
13	4I	32	GLU
13	4I	34	LEU
13	4I	44	ARG
13	4I	45	VAL
13	4I	48	LEU
13	4I	49	THR
13	4I	56	LEU
13	4I	64	TRP
13	4I	67	GLU
13	4I	70	LEU
13	4I	86	CYS
13	4I	98	VAL
13	4I	101	GLN
13	4I	102	ARG
13	4I	106	ASN
13	4I	108	ARG
13	4I	110	ARG
13	4I	117	VAL
14	5I	4	LYS
14	5I	6	LEU
14	5I	12	ARG
14	5I	15	LYS
14	5I	18	VAL
14	5I	22	THR
14	5I	26	ARG
14	5I	33	VAL
14	5I	41	ARG
14	5I	44	LEU
14	5I	50	LYS
14	5I	58	LYS
15	6I	6	GLU
15	6I	10	LYS
15	6I	11	VAL
15	6I	17	ARG
15	6I	24	SER
15	6I	25	THR
15	6I	26	GLU
15	6I	35	ARG
15	6I	39	LEU

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Mol	Chain	Res	Type
15	6I	40	SER
15	6I	41	GLU
15	6I	47	LYS
15	6I	48	LYS
15	6I	59	MET
15	6I	66	LEU
15	6I	67	LEU
15	6I	68	ARG
15	6I	72	ARG
15	6I	87	ILE
16	7I	1	MET
16	7I	2	VAL
16	7I	11	SER
16	7I	20	VAL
16	7I	27	LYS
16	7I	35	LYS
16	7I	36	ILE
16	7I	45	THR
16	7I	50	LYS
16	7I	51	VAL
16	7I	54	GLU
16	7I	55	ARG
16	7I	67	THR
16	7I	69	THR
16	7I	72	ARG
17	8I	9	VAL
17	8I	10	VAL
17	8I	11	VAL
17	8I	19	VAL
17	8I	25	ARG
17	8I	35	VAL
17	8I	38	ARG
17	8I	48	GLU
17	8I	52	LYS
17	8I	53	LEU
17	8I	57	VAL
17	8I	60	ILE
17	8I	62	SER
17	8I	68	ARG
17	8I	74	LEU
17	8I	87	LYS
17	8I	89	LEU

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Mol	Chain	Res	Type
17	8I	92	ARG
17	8I	101	ARG
18	9I	18	ARG
18	9I	31	LEU
18	9I	32	ARG
18	9I	35	ARG
18	9I	53	ARG
18	9I	82	THR
18	9I	86	VAL
18	9I	88	LYS
19	AI	4	SER
19	AI	5	LEU
19	AI	7	LYS
19	AI	10	PHE
19	AI	14	HIS
19	AI	21	GLU
19	AI	22	LEU
19	AI	28	LYS
19	AI	29	ARG
19	AI	30	LEU
19	AI	31	ILE
19	AI	37	ARG
19	AI	43	GLU
19	AI	58	VAL
19	AI	60	VAL
19	AI	61	TYR
19	AI	65	ASN
19	AI	67	VAL
19	AI	77	THR
19	AI	78	ARG
20	BI	10	LEU
20	BI	13	LEU
20	BI	15	ARG
20	BI	18	GLN
20	BI	20	LEU
20	BI	29	LYS
20	BI	31	SER
20	BI	33	ILE
20	BI	37	SER
20	BI	41	ILE
20	BI	50	GLU
20	BI	51	GLU

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Mol	Chain	Res	Type
20	BI	53	LEU
20	BI	55	ILE
20	BI	60	GLU
20	BI	62	LEU
20	BI	68	LYS
20	BI	71	THR
20	BI	72	LEU
20	BI	75	ASN
20	BI	87	LYS
20	BI	99	LEU
20	BI	100	ILE
20	BI	105	SER
21	1F	6	ARG
21	1F	12	LYS
28	11	3	VAL
28	11	4	LYS
28	11	7	LYS
28	11	13	ARG
28	11	15	PHE
28	11	17	THR
28	11	27	THR
28	11	34	VAL
28	11	37	LEU
28	11	61	LEU
28	11	64	ILE
28	11	65	ILE
28	11	83	GLU
28	11	95	LEU
28	11	103	ARG
28	11	105	ILE
28	11	106	ILE
28	11	111	LEU
28	11	112	GLN
28	11	116	GLN
28	11	127	VAL
28	11	141	VAL
28	11	142	VAL
28	11	147	LEU
28	11	148	GLU
28	11	155	LEU
28	11	165	ILE
28	11	173	VAL

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Mol	Chain	Res	Type
28	11	192	THR
28	11	193	VAL
28	11	200	ASP
28	11	217	ARG
28	11	221	VAL
28	11	228	PRO
28	11	229	VAL
28	11	242	ARG
28	11	255	LYS
28	11	257	LEU
28	11	259	THR
28	11	261	LYS
28	11	265	PRO
28	11	266	SER
28	11	270	ILE
28	11	271	ILE
28	11	273	ARG
29	21	2	LYS
29	21	5	LEU
29	21	12	THR
29	21	13	ARG
29	21	14	ILE
29	21	16	ARG
29	21	25	VAL
29	21	26	ILE
29	21	33	VAL
29	21	34	VAL
29	21	40	GLU
29	21	41	LYS
29	21	42	ASP
29	21	45	THR
29	21	49	LEU
29	21	52	LEU
29	21	54	GLN
29	21	59	VAL
29	21	61	ARG
29	21	63	LEU
29	21	66	HIS
29	21	67	PHE
29	21	69	LYS
29	21	72	VAL
29	21	87	GLU

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Mol	Chain	Res	Type
29	21	89	ASP
29	21	92	THR
29	21	101	ARG
29	21	107	THR
29	21	116	VAL
29	21	128	SER
29	21	138	PRO
29	21	144	ARG
29	21	146	THR
29	21	166	THR
29	21	167	VAL
29	21	175	VAL
29	21	179	GLU
29	21	181	LEU
29	21	185	LYS
29	21	196	VAL
29	21	200	GLU
29	21	201	THR
29	21	202	LYS
29	21	203	LYS
30	31	7	TYR
30	31	8	GLN
30	31	9	ILE
30	31	12	LEU
30	31	13	SER
30	31	15	SER
30	31	24	LEU
30	31	28	ILE
30	31	32	LEU
30	31	33	LEU
30	31	38	ARG
30	31	57	VAL
30	31	64	ILE
30	31	77	ASP
30	31	78	ILE
30	31	88	VAL
30	31	98	SER
30	31	101	LEU
30	31	106	ARG
30	31	112	MET
30	31	117	ARG
30	31	127	GLU

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Mol	Chain	Res	Type
30	31	136	THR
30	31	158	THR
30	31	165	ARG
30	31	168	ARG
30	31	170	LEU
30	31	174	VAL
30	31	175	THR
30	31	176	LEU
30	31	181	LEU
30	31	183	VAL
30	31	191	ARG
30	31	192	LEU
30	31	200	GLU
30	31	201	VAL
30	31	204	ASN
31	41	14	GLU
31	41	20	ILE
31	41	21	ARG
31	41	26	GLN
31	41	28	VAL
31	41	31	VAL
31	41	34	LEU
31	41	43	LEU
31	41	45	GLU
31	41	52	ILE
31	41	58	GLN
31	41	62	LEU
31	41	63	ILE
31	41	64	THR
31	41	67	LYS
31	41	70	VAL
31	41	71	THR
31	41	76	SER
31	41	77	ILE
31	41	80	PHE
31	41	82	LEU
31	41	84	LYS
31	41	86	MET
31	41	88	ILE
31	41	90	LEU
31	41	94	LEU
31	41	99	MET

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Mol	Chain	Res	Type
31	41	101	ILE
31	41	104	GLU
31	41	116	ASP
31	41	128	ARG
31	41	133	LEU
31	41	135	LEU
31	41	159	VAL
31	41	161	THR
31	41	162	THR
31	41	165	THR
31	41	168	GLU
31	41	170	ARG
32	51	2	SER
32	51	3	ARG
32	51	4	ILE
32	51	6	ARG
32	51	7	LEU
32	51	10	PRO
32	51	24	VAL
32	51	26	VAL
32	51	37	VAL
32	51	40	GLU
32	51	41	MET
32	51	43	VAL
32	51	44	VAL
32	51	45	VAL
32	51	50	VAL
32	51	64	LEU
32	51	67	LEU
32	51	68	THR
32	51	71	LEU
32	51	72	ILE
32	51	77	LYS
32	51	80	SER
32	51	84	SER
32	51	88	LEU
32	51	92	ILE
32	51	97	ARG
32	51	103	LEU
32	51	116	GLU
32	51	122	THR
32	51	125	VAL

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Mol	Chain	Res	Type
32	51	129	THR
32	51	131	VAL
32	51	132	ARG
32	51	136	ILE
32	51	139	GLN
32	51	141	VAL
32	51	149	ARG
32	51	153	LYS
32	51	160	LYS
32	51	169	VAL
32	51	171	LEU
32	51	175	LYS
33	61	2	LYS
33	61	7	GLU
33	61	9	LEU
33	61	25	TYR
33	61	35	LEU
33	61	38	LEU
33	61	40	THR
33	61	44	LEU
33	61	45	LYS
33	61	48	GLU
33	61	56	LYS
33	61	60	GLU
33	61	64	GLU
33	61	71	ILE
33	61	73	GLU
33	61	74	ASN
33	61	77	LEU
33	61	78	THR
33	61	79	ILE
33	61	81	VAL
33	61	82	ARG
33	61	85	GLU
33	61	88	ILE
33	61	92	VAL
33	61	95	LYS
33	61	97	ILE
33	61	107	VAL
33	61	108	THR
33	61	110	ASP
33	61	120	ILE

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Mol	Chain	Res	Type
33	61	122	GLU
33	61	131	LYS
33	61	135	GLU
33	61	136	VAL
33	61	139	GLN
33	61	140	LEU
33	61	142	VAL
33	61	143	SER
33	61	145	VAL
34	58	1	MET
34	58	5	VAL
34	58	7	LYS
34	58	9	VAL
34	58	10	GLU
34	58	15	LEU
34	58	28	THR
34	58	29	LYS
34	58	34	LEU
34	58	58	ASP
34	58	60	ILE
34	58	61	ARG
34	58	65	LYS
34	58	67	LEU
34	58	70	LYS
34	58	87	LEU
34	58	90	MET
34	58	96	GLU
34	58	97	ARG
34	58	98	VAL
34	58	99	LEU
34	58	115	ARG
34	58	120	LEU
34	58	127	ASP
34	58	128	HIS
35	68	8	LEU
35	68	9	GLU
35	68	14	THR
35	68	20	MET
35	68	23	ARG
35	68	24	VAL
35	68	28	SER
35	68	31	LYS

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Mol	Chain	Res	Type
35	68	38	VAL
35	68	47	ILE
35	68	53	LYS
35	68	78	ARG
35	68	90	GLN
35	68	94	ARG
35	68	98	VAL
35	68	112	MET
35	68	113	LYS
35	68	120	GLU
36	78	1	MET
36	78	6	LEU
36	78	7	ARG
36	78	10	PRO
36	78	15	ARG
36	78	16	ARG
36	78	18	ARG
36	78	19	VAL
36	78	29	LYS
36	78	30	THR
36	78	32	THR
36	78	39	LYS
36	78	41	ARG
36	78	45	LEU
36	78	46	LYS
36	78	49	ARG
36	78	50	ARG
36	78	57	THR
36	78	61	ARG
36	78	75	ILE
36	78	76	LYS
36	78	77	ARG
36	78	83	VAL
36	78	88	LEU
36	78	99	LEU
36	78	100	LEU
36	78	105	LEU
36	78	106	LEU
36	78	111	ARG
36	78	112	LEU
36	78	114	ILE
36	78	115	LEU

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Mol	Chain	Res	Type
36	78	117	GLU
36	78	119	GLU
36	78	121	LYS
36	78	126	VAL
36	78	135	LEU
36	78	138	LEU
36	78	144	GLU
36	78	146	VAL
36	78	147	LEU
36	78	148	LEU
37	88	5	ARG
37	88	8	LYS
37	88	18	LYS
37	88	21	THR
37	88	22	LYS
37	88	25	ASP
37	88	35	VAL
37	88	45	GLN
37	88	51	ARG
37	88	52	VAL
37	88	55	VAL
37	88	56	ARG
37	88	59	ARG
37	88	60	ARG
37	88	82	ARG
37	88	87	LYS
37	88	98	LYS
37	88	102	VAL
37	88	103	MET
37	88	109	VAL
37	88	112	GLU
37	88	129	THR
37	88	134	ARG
37	88	138	ASP
37	88	139	GLU
37	88	141	GLN
38	98	2	ARG
38	98	4	LEU
38	98	9	LYS
38	98	10	LEU
38	98	17	ARG
38	98	18	LEU

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Mol	Chain	Res	Type
38	98	24	GLN
38	98	28	LEU
38	98	29	LEU
38	98	30	THR
38	98	33	ARG
38	98	34	ILE
38	98	36	THR
38	98	44	LEU
38	98	54	LEU
38	98	57	ARG
38	98	59	ASP
38	98	64	ARG
38	98	65	LEU
38	98	67	LEU
38	98	73	VAL
38	98	79	LEU
38	98	88	ARG
38	98	91	GLN
38	98	94	TYR
38	98	95	THR
38	98	100	LEU
38	98	105	ARG
38	98	111	LEU
38	98	117	VAL
38	98	118	GLU
39	A8	4	LEU
39	A8	8	GLU
39	A8	10	ARG
39	A8	14	VAL
39	A8	17	ARG
39	A8	19	LYS
39	A8	24	LEU
39	A8	32	LEU
39	A8	33	LYS
39	A8	35	ILE
39	A8	36	TYR
39	A8	46	VAL
39	A8	49	VAL
39	A8	50	SER
39	A8	52	SER
39	A8	54	LEU
39	A8	56	LEU

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Mol	Chain	Res	Type
39	A8	57	LYS
39	A8	58	LEU
39	A8	61	ASN
39	A8	69	VAL
39	A8	73	LEU
39	A8	80	LEU
39	A8	83	LYS
39	A8	89	ARG
39	A8	101	LEU
39	A8	103	GLU
39	A8	106	ARG
39	A8	107	GLU
39	A8	110	LEU
39	A8	112	PHE
40	B8	3	ARG
40	B8	6	LEU
40	B8	7	ILE
40	B8	10	VAL
40	B8	11	GLU
40	B8	12	SER
40	B8	13	ARG
40	B8	15	VAL
40	B8	19	LEU
40	B8	21	GLU
40	B8	23	ARG
40	B8	27	THR
40	B8	28	VAL
40	B8	30	VAL
40	B8	35	LYS
40	B8	40	THR
40	B8	42	ILE
40	B8	49	VAL
40	B8	50	ILE
40	B8	52	ILE
40	B8	55	ASN
40	B8	58	ASN
40	B8	59	THR
40	B8	62	THR
40	B8	64	ARG
40	B8	65	LYS
40	B8	74	ARG
40	B8	78	LEU

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Mol	Chain	Res	Type
40	B8	86	ILE
40	B8	87	ASP
40	B8	88	ILE
40	B8	89	VAL
40	B8	98	LYS
40	B8	99	LEU
40	B8	105	LEU
40	B8	106	SER
40	B8	108	ARG
40	B8	110	ILE
40	B8	111	ARG
40	B8	112	ARG
40	B8	115	ARG
40	B8	118	ARG
40	B8	136	GLN
41	C8	3	ARG
41	C8	5	LYS
41	C8	17	ILE
41	C8	27	LEU
41	C8	38	THR
41	C8	64	ARG
41	C8	74	LEU
41	C8	75	ASN
41	C8	79	PHE
41	C8	83	LEU
41	C8	85	LYS
41	C8	89	GLU
41	C8	104	GLN
41	C8	108	GLU
41	C8	111	GLU
41	C8	117	GLN
42	D8	1	MET
42	D8	5	VAL
42	D8	6	LYS
42	D8	7	THR
42	D8	12	TYR
42	D8	18	LEU
42	D8	20	LEU
42	D8	22	VAL
42	D8	34	GLU
42	D8	35	LEU
42	D8	39	LEU

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Mol	Chain	Res	Type
42	D8	40	LEU
42	D8	44	LYS
42	D8	47	VAL
42	D8	52	VAL
42	D8	70	ILE
42	D8	78	LYS
42	D8	85	LYS
42	D8	95	LEU
42	D8	100	ARG
43	E8	4	LYS
43	E8	11	ARG
43	E8	15	ARG
43	E8	16	LYS
43	E8	19	LEU
43	E8	20	VAL
43	E8	21	VAL
43	E8	24	ILE
43	E8	39	THR
43	E8	51	LEU
43	E8	52	GLU
43	E8	65	LEU
43	E8	66	GLU
43	E8	68	ARG
43	E8	69	LEU
43	E8	76	VAL
43	E8	78	GLU
43	E8	82	LEU
43	E8	92	ARG
43	E8	96	ILE
43	E8	97	LYS
43	E8	98	LYS
43	E8	99	ARG
43	E8	100	THR
43	E8	107	LEU
43	E8	111	HIS
44	F8	2	LYS
44	F8	12	VAL
44	F8	15	GLU
44	F8	23	GLU
44	F8	37	THR
44	F8	38	GLU
44	F8	45	THR

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Mol	Chain	Res	Type
44	F8	49	VAL
44	F8	54	VAL
44	F8	57	LEU
44	F8	60	ARG
44	F8	65	ARG
44	F8	72	LYS
44	F8	76	ARG
44	F8	80	ILE
44	F8	81	VAL
44	F8	87	GLN
44	F8	88	LYS
44	F8	89	ILE
45	G8	6	HIS
45	G8	7	VAL
45	G8	24	VAL
45	G8	27	VAL
45	G8	33	LYS
45	G8	38	ILE
45	G8	42	VAL
45	G8	44	ILE
45	G8	47	LYS
45	G8	50	ARG
45	G8	51	VAL
45	G8	52	SER
45	G8	54	LYS
45	G8	55	TYR
45	G8	57	GLN
45	G8	61	ILE
45	G8	63	LYS
45	G8	64	GLU
45	G8	67	LEU
45	G8	79	CYS
45	G8	82	PRO
45	G8	84	ARG
45	G8	85	VAL
45	G8	86	ARG
45	G8	88	LYS
45	G8	94	LYS
45	G8	98	VAL
45	G8	99	CYS
45	G8	106	LEU
46	H8	5	LEU

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Mol	Chain	Res	Type
46	H8	6	LYS
46	H8	11	GLU
46	H8	19	ARG
46	H8	23	LYS
46	H8	28	MET
46	H8	37	VAL
46	H8	42	VAL
46	H8	43	GLU
46	H8	53	ILE
46	H8	61	LEU
46	H8	71	VAL
46	H8	72	ARG
46	H8	76	LEU
46	H8	78	LYS
46	H8	80	ARG
46	H8	81	ARG
46	H8	86	VAL
46	H8	91	LEU
46	H8	93	ASP
46	H8	105	VAL
46	H8	116	VAL
46	H8	117	LEU
46	H8	118	GLN
46	H8	119	GLU
46	H8	121	HIS
46	H8	128	VAL
46	H8	135	GLU
46	H8	140	ASP
46	H8	144	LEU
46	H8	148	ASP
46	H8	154	ASP
46	H8	161	VAL
46	H8	166	SER
46	H8	168	GLU
46	H8	171	ILE
46	H8	175	VAL
47	I8	11	ARG
47	I8	19	LYS
47	I8	30	VAL
47	I8	36	ILE
47	I8	38	VAL
47	I8	41	ARG

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Mol	Chain	Res	Type
47	I8	44	ARG
47	I8	46	LYS
47	I8	51	VAL
47	I8	58	THR
47	I8	60	PHE
47	I8	66	VAL
47	I8	67	VAL
47	I8	70	GLN
47	I8	74	ARG
47	I8	82	ARG
48	J8	4	VAL
48	J8	19	GLN
48	J8	21	ARG
48	J8	25	LYS
48	J8	26	ARG
48	J8	30	VAL
48	J8	41	ARG
48	J8	46	LEU
48	J8	57	GLU
48	J8	62	VAL
48	J8	69	LYS
48	J8	74	VAL
48	J8	78	LYS
48	J8	80	LEU
48	J8	81	LYS
48	J8	82	LEU
48	J8	83	GLU
48	J8	90	ILE
48	J8	91	LYS
48	J8	92	LYS
48	J8	94	LEU
48	J8	97	LEU
49	K8	5	GLU
49	K8	6	VAL
49	K8	8	LYS
49	K8	12	GLU
49	K8	15	LYS
49	K8	16	LEU
49	K8	17	SER
49	K8	19	VAL
49	K8	20	GLU
49	K8	23	LYS

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Mol	Chain	Res	Type
49	K8	24	LEU
49	K8	30	ARG
49	K8	32	LEU
49	K8	41	ILE
49	K8	44	LEU
49	K8	45	SER
49	K8	46	GLN
49	K8	47	ASN
49	K8	48	HIS
49	K8	50	ILE
49	K8	53	LEU
49	K8	54	LYS
49	K8	55	ARG
49	K8	59	ARG
49	K8	62	THR
49	K8	64	LEU
49	K8	65	ASN
49	K8	66	GLU
49	K8	67	LYS
50	L8	3	ARG
50	L8	4	LEU
50	L8	6	VAL
50	L8	8	LEU
50	L8	28	LEU
50	L8	30	ARG
50	L8	31	LEU
50	L8	32	GLN
50	L8	36	VAL
50	L8	37	LEU
50	L8	38	GLU
50	L8	40	THR
50	L8	53	LEU
50	L8	58	VAL
51	M8	1	MET
51	M8	5	ILE
51	M8	15	ILE
51	M8	16	CYS
51	M8	34	GLU
51	M8	35	VAL
51	M8	37	SER
51	M8	39	CYS
51	M8	44	THR

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Mol	Chain	Res	Type
51	M8	48	ARG
51	M8	50	VAL
51	M8	52	THR
51	M8	55	ARG
51	M8	59	PHE
51	M8	61	ARG
51	M8	62	ARG
51	M8	65	ASP
52	N8	3	LYS
52	N8	6	VAL
52	N8	9	LYS
52	N8	16	ARG
52	N8	29	THR
52	N8	31	VAL
52	N8	35	GLU
52	N8	36	CYS
52	N8	40	LYS
52	N8	44	THR
52	N8	51	TYR
52	N8	55	ARG
52	N8	57	VAL
53	O8	10	LEU
53	O8	12	GLU
53	O8	21	TYR
53	O8	25	LYS
53	O8	26	ASN
53	O8	27	LYS
53	O8	30	THR
53	O8	32	ASN
53	O8	33	LYS
53	O8	36	LEU
53	O8	37	ARG
53	O8	39	TYR
53	O8	42	TRP
53	O8	47	THR
54	P8	4	THR
54	P8	8	ASN
54	P8	9	ARG
54	P8	19	ARG
54	P8	23	ARG
54	P8	29	LYS
54	P8	43	THR

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Mol	Chain	Res	Type
55	Q8	19	SER
55	Q8	21	LYS
55	Q8	22	VAL
55	Q8	23	VAL
55	Q8	30	ARG
55	Q8	31	HIS
55	Q8	34	TRP
55	Q8	35	GLN
55	Q8	41	ILE
55	Q8	42	ARG
55	Q8	43	GLN
55	Q8	46	ARG
55	Q8	47	LYS
55	Q8	49	VAL
55	Q8	52	LYS
55	Q8	57	ARG
55	Q8	59	LYS
55	Q8	60	LEU
55	Q8	61	LEU
2	12	5	ILE
2	12	10	LEU
2	12	17	PHE
2	12	22	LYS
2	12	23	ARG
2	12	42	ILE
2	12	44	LEU
2	12	47	THR
2	12	51	LEU
2	12	58	ILE
2	12	59	GLU
2	12	67	THR
2	12	69	LEU
2	12	71	VAL
2	12	75	LYS
2	12	78	GLN
2	12	83	MET
2	12	90	MET
2	12	103	THR
2	12	108	ILE
2	12	117	GLU
2	12	121	LEU
2	12	137	ARG

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Mol	Chain	Res	Type
2	12	138	LEU
2	12	139	LYS
2	12	145	LEU
2	12	155	LEU
2	12	164	VAL
2	12	165	VAL
2	12	170	GLU
2	12	172	ILE
2	12	178	ARG
2	12	179	LYS
2	12	185	ILE
2	12	187	LEU
2	12	196	LEU
2	12	200	ILE
2	12	204	ASN
2	12	205	ASP
2	12	209	ARG
2	12	213	LEU
2	12	219	VAL
2	12	223	ILE
3	22	3	ASN
3	22	5	ILE
3	22	11	ARG
3	22	16	ARG
3	22	18	TRP
3	22	22	TRP
3	22	28	GLN
3	22	40	ARG
3	22	43	LEU
3	22	47	LEU
3	22	52	LEU
3	22	54	ARG
3	22	67	THR
3	22	76	VAL
3	22	77	ILE
3	22	79	ARG
3	22	91	LEU
3	22	94	LEU
3	22	95	THR
3	22	97	LYS
3	22	98	ASN
3	22	103	VAL

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Mol	Chain	Res	Type
3	22	104	GLN
3	22	107	GLN
3	22	131	ARG
3	22	140	ARG
3	22	153	VAL
3	22	167	TRP
3	22	182	ILE
3	22	188	LEU
3	22	190	ARG
3	22	192	THR
3	22	198	VAL
3	22	202	ILE
3	22	207	VAL
4	32	5	ILE
4	32	8	VAL
4	32	13	ARG
4	32	14	ARG
4	32	24	GLU
4	32	28	SER
4	32	30	LYS
4	32	34	GLU
4	32	36	ARG
4	32	45	GLN
4	32	50	ARG
4	32	57	ARG
4	32	58	LEU
4	32	70	ILE
4	32	73	ARG
4	32	76	ARG
4	32	83	SER
4	32	96	LEU
4	32	108	LEU
4	32	115	ARG
4	32	119	GLN
4	32	122	ARG
4	32	126	ILE
4	32	127	THR
4	32	135	LEU
4	32	137	SER
4	32	140	VAL
4	32	145	GLU
4	32	168	ARG

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Mol	Chain	Res	Type
4	32	187	ARG
4	32	190	ASP
4	32	191	ARG
4	32	192	GLU
4	32	200	GLU
4	32	209	ARG
5	42	6	PHE
5	42	12	LEU
5	42	16	THR
5	42	19	MET
5	42	34	VAL
5	42	41	VAL
5	42	43	LEU
5	42	47	LYS
5	42	51	VAL
5	42	61	TYR
5	42	64	ARG
5	42	66	MET
5	42	68	GLU
5	42	72	GLN
5	42	75	THR
5	42	79	GLU
5	42	83	GLU
5	42	90	VAL
5	42	91	LEU
5	42	101	ILE
5	42	115	VAL
5	42	116	THR
5	42	118	ILE
5	42	120	THR
5	42	127	ASN
5	42	137	GLU
5	42	144	THR
6	52	2	ARG
6	52	3	ARG
6	52	7	ASN
6	52	14	LEU
6	52	16	GLN
6	52	21	LEU
6	52	25	ILE
6	52	27	GLN
6	52	28	ARG

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Mol	Chain	Res	Type
6	52	32	ASN
6	52	37	VAL
6	52	40	VAL
6	52	47	ARG
6	52	61	LEU
6	52	70	ASP
6	52	74	ASP
6	52	82	ARG
6	52	87	ARG
6	52	92	LYS
6	52	93	SER
7	62	4	ARG
7	62	8	GLU
7	62	9	VAL
7	62	23	VAL
7	62	27	ILE
7	62	29	LYS
7	62	30	ILE
7	62	32	ARG
7	62	35	LYS
7	62	52	GLU
7	62	54	THR
7	62	60	LYS
7	62	61	VAL
7	62	63	LYS
7	62	73	MET
7	62	78	ARG
7	62	84	ASN
7	62	87	VAL
7	62	91	VAL
7	62	94	ARG
7	62	104	LEU
7	62	114	ARG
7	62	118	VAL
7	62	131	LYS
7	62	137	LYS
7	62	140	ASP
8	72	19	VAL
8	72	22	GLU
8	72	23	SER
8	72	26	VAL
8	72	35	ILE

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Mol	Chain	Res	Type
8	72	39	LEU
8	72	51	VAL
8	72	73	ASP
8	72	77	GLU
8	72	79	VAL
8	72	84	ARG
8	72	85	ARG
8	72	86	ILE
8	72	91	ARG
8	72	92	ARG
8	72	97	VAL
8	72	99	GLU
8	72	100	ILE
8	72	107	LEU
8	72	109	ILE
8	72	112	LEU
8	72	116	LYS
9	82	7	THR
9	82	27	THR
9	82	31	GLN
9	82	38	GLN
9	82	42	ARG
9	82	47	LEU
9	82	81	ILE
9	82	85	LEU
9	82	93	ARG
9	82	95	LYS
9	82	99	LEU
9	82	104	ARG
9	82	109	VAL
9	82	113	LYS
9	82	117	HIS
9	82	118	LYS
10	1A	13	HIS
10	1A	17	ASP
10	1A	19	SER
10	1A	22	LYS
10	1A	35	SER
10	1A	40	LEU
10	1A	43	ARG
10	1A	44	VAL
10	1A	46	ARG

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Mol	Chain	Res	Type
10	1A	47	PHE
10	1A	48	THR
10	1A	55	LYS
10	1A	57	LYS
10	1A	59	SER
10	1A	62	HIS
10	1A	70	ARG
10	1A	72	VAL
10	1A	74	ILE
10	1A	79	ARG
10	1A	88	LEU
10	1A	96	ILE
10	1A	99	LYS
11	2A	12	ARG
11	2A	13	GLN
11	2A	14	VAL
11	2A	29	ILE
11	2A	30	VAL
11	2A	31	THR
11	2A	40	ILE
11	2A	63	LEU
11	2A	82	VAL
11	2A	83	ILE
11	2A	95	ILE
11	2A	98	LEU
11	2A	105	VAL
11	2A	106	LYS
11	2A	108	ILE
11	2A	109	VAL
11	2A	111	ASP
11	2A	114	VAL
11	2A	124	LYS
12	3A	6	THR
12	3A	13	LYS
12	3A	33	ARG
12	3A	37	CYS
12	3A	41	ARG
12	3A	42	THR
12	3A	43	VAL
12	3A	46	LYS
12	3A	47	LYS
12	3A	49	ASN

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Mol	Chain	Res	Type
12	3A	52	LEU
12	3A	54	LYS
12	3A	57	LYS
12	3A	60	LEU
12	3A	64	TYR
12	3A	66	VAL
12	3A	78	GLN
12	3A	83	VAL
12	3A	84	LEU
12	3A	85	ILE
12	3A	89	ARG
12	3A	96	VAL
12	3A	111	LYS
12	3A	118	SER
12	3A	122	THR
13	4A	4	ILE
13	4A	8	GLU
13	4A	9	ILE
13	4A	17	VAL
13	4A	19	LEU
13	4A	39	ILE
13	4A	47	ASP
13	4A	48	LEU
13	4A	49	THR
13	4A	55	ARG
13	4A	56	LEU
13	4A	64	TRP
13	4A	66	LEU
13	4A	77	ASN
13	4A	81	LEU
13	4A	82	MET
13	4A	88	ARG
13	4A	92	HIS
13	4A	101	GLN
13	4A	103	THR
13	4A	108	ARG
13	4A	117	VAL
14	5A	12	ARG
14	5A	18	VAL
14	5A	22	THR
14	5A	33	VAL
14	5A	35	ARG

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Mol	Chain	Res	Type
14	5A	44	LEU
14	5A	53	LEU
14	5A	58	LYS
15	6A	3	ILE
15	6A	10	LYS
15	6A	13	GLN
15	6A	26	GLU
15	6A	31	LEU
15	6A	32	LEU
15	6A	34	LEU
15	6A	38	ARG
15	6A	39	LEU
15	6A	45	VAL
15	6A	48	LYS
15	6A	66	LEU
15	6A	68	ARG
15	6A	88	ARG
16	7A	1	MET
16	7A	2	VAL
16	7A	4	ILE
16	7A	21	VAL
16	7A	29	ASP
16	7A	34	GLU
16	7A	45	THR
16	7A	62	VAL
16	7A	65	GLN
16	7A	67	THR
16	7A	69	THR
16	7A	73	LEU
16	7A	82	GLN
17	8A	7	THR
17	8A	10	VAL
17	8A	13	ASP
17	8A	25	ARG
17	8A	26	GLN
17	8A	38	ARG
17	8A	49	GLU
17	8A	53	LEU
17	8A	60	ILE
17	8A	68	ARG
17	8A	74	LEU
17	8A	79	SER

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Mol	Chain	Res	Type
17	8A	89	LEU
17	8A	100	LYS
18	9A	26	LEU
18	9A	29	PHE
18	9A	32	ARG
18	9A	36	ASN
18	9A	44	LEU
18	9A	47	THR
18	9A	53	ARG
18	9A	54	ARG
18	9A	58	LEU
18	9A	84	LYS
19	AA	7	LYS
19	AA	10	PHE
19	AA	11	VAL
19	AA	15	LEU
19	AA	20	LEU
19	AA	22	LEU
19	AA	23	ASN
19	AA	25	LYS
19	AA	33	THR
19	AA	49	ILE
19	AA	51	VAL
19	AA	53	ASN
19	AA	60	VAL
19	AA	66	MET
19	AA	71	LEU
19	AA	78	ARG
19	AA	81	ARG
19	AA	83	HIS
20	BA	8	ARG
20	BA	11	SER
20	BA	24	LEU
20	BA	29	LYS
20	BA	33	ILE
20	BA	37	SER
20	BA	55	ILE
20	BA	58	LYS
20	BA	68	LYS
20	BA	73	HIS
20	BA	75	ASN
20	BA	84	LEU

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Mol	Chain	Res	Type
21	1B	25	LYS
28	19	10	THR
28	19	18	VAL
28	19	24	ILE
28	19	28	GLU
28	19	32	SER
28	19	33	LEU
28	19	34	VAL
28	19	35	LYS
28	19	37	LEU
28	19	39	LYS
28	19	43	ARG
28	19	49	ILE
28	19	61	LEU
28	19	64	ILE
28	19	65	ILE
28	19	69	ARG
28	19	82	ILE
28	19	87	ASN
28	19	88	ARG
28	19	89	SER
28	19	94	LEU
28	19	105	ILE
28	19	106	ILE
28	19	111	LEU
28	19	112	GLN
28	19	136	ILE
28	19	138	VAL
28	19	141	VAL
28	19	147	LEU
28	19	155	LEU
28	19	173	VAL
28	19	174	ILE
28	19	192	THR
28	19	193	VAL
28	19	202	LYS
28	19	204	ILE
28	19	211	ARG
28	19	212	SER
28	19	217	ARG
28	19	239	ARG
28	19	242	ARG

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Mol	Chain	Res	Type
28	19	244	ARG
28	19	253	GLN
28	19	255	LYS
28	19	257	LEU
28	19	259	THR
28	19	260	ARG
28	19	262	ARG
28	19	266	SER
28	19	267	SER
28	19	271	ILE
29	29	4	ILE
29	29	5	LEU
29	29	7	VAL
29	29	9	VAL
29	29	19	ARG
29	29	23	VAL
29	29	25	VAL
29	29	37	ARG
29	29	40	GLU
29	29	44	TYR
29	29	45	THR
29	29	47	VAL
29	29	48	GLN
29	29	52	LEU
29	29	54	GLN
29	29	59	VAL
29	29	60	ASN
29	29	63	LEU
29	29	64	LYS
29	29	66	HIS
29	29	67	PHE
29	29	69	LYS
29	29	75	VAL
29	29	77	ILE
29	29	78	LEU
29	29	87	GLU
29	29	90	THR
29	29	93	VAL
29	29	107	THR
29	29	116	VAL
29	29	117	MET
29	29	119	ARG

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Mol	Chain	Res	Type
29	29	134	ILE
29	29	136	ARG
29	29	144	ARG
29	29	146	THR
29	29	154	LYS
29	29	170	LEU
29	29	174	ASP
29	29	175	VAL
29	29	178	GLU
29	29	181	LEU
29	29	185	LYS
29	29	188	VAL
29	29	197	ILE
29	29	200	GLU
29	29	201	THR
30	39	2	LYS
30	39	7	TYR
30	39	8	GLN
30	39	11	VAL
30	39	19	GLU
30	39	20	LEU
30	39	23	ASP
30	39	24	LEU
30	39	28	ILE
30	39	29	ASN
30	39	33	LEU
30	39	38	ARG
30	39	43	LYS
30	39	46	ARG
30	39	53	THR
30	39	57	VAL
30	39	62	ARG
30	39	67	GLN
30	39	68	LYS
30	39	69	HIS
30	39	70	THR
30	39	74	ARG
30	39	82	ILE
30	39	88	VAL
30	39	100	THR
30	39	105	VAL
30	39	106	ARG

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Mol	Chain	Res	Type
30	39	110	LEU
30	39	114	VAL
30	39	123	LEU
30	39	124	LEU
30	39	125	LEU
30	39	135	LYS
30	39	140	LEU
30	39	152	GLU
30	39	153	SER
30	39	158	THR
30	39	168	ARG
30	39	183	VAL
30	39	192	LEU
30	39	193	VAL
30	39	194	MET
30	39	196	LEU
30	39	201	VAL
30	39	203	GLN
30	39	205	ARG
31	49	3	LEU
31	49	7	LEU
31	49	19	LEU
31	49	20	ILE
31	49	26	GLN
31	49	28	VAL
31	49	35	GLU
31	49	39	ILE
31	49	40	ASN
31	49	48	GLU
31	49	53	LEU
31	49	64	THR
31	49	67	LYS
31	49	71	THR
31	49	74	LYS
31	49	77	ILE
31	49	81	LYS
31	49	82	LEU
31	49	90	LEU
31	49	101	ILE
31	49	109	VAL
31	49	120	LEU
31	49	130	ASN

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Mol	Chain	Res	Type
31	49	133	LEU
31	49	135	LEU
31	49	144	ILE
31	49	153	ARG
31	49	157	ILE
31	49	159	VAL
32	59	4	ILE
32	59	6	ARG
32	59	7	LEU
32	59	11	VAL
32	59	15	VAL
32	59	19	VAL
32	59	24	VAL
32	59	26	VAL
32	59	32	GLU
32	59	41	MET
32	59	44	VAL
32	59	45	VAL
32	59	50	VAL
32	59	70	THR
32	59	86	GLU
32	59	98	LEU
32	59	99	VAL
32	59	101	ARG
32	59	105	LEU
32	59	107	VAL
32	59	111	HIS
32	59	119	GLU
32	59	122	THR
32	59	123	PHE
32	59	124	GLU
32	59	127	GLU
32	59	129	THR
32	59	134	SER
32	59	136	ILE
32	59	139	GLN
32	59	144	VAL
32	59	152	ARG
32	59	155	SER
32	59	157	TYR
32	59	160	LYS
32	59	164	TYR

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Mol	Chain	Res	Type
33	69	2	LYS
33	69	7	GLU
33	69	9	LEU
33	69	15	VAL
33	69	23	PRO
33	69	37	VAL
33	69	41	GLU
33	69	44	LEU
33	69	51	ILE
33	69	54	GLN
33	69	56	LYS
33	69	58	LEU
33	69	61	ARG
33	69	68	LEU
33	69	75	LEU
33	69	76	THR
33	69	77	LEU
33	69	78	THR
33	69	79	ILE
33	69	81	VAL
33	69	82	ARG
33	69	86	THR
33	69	101	LEU
33	69	103	ARG
33	69	104	GLN
33	69	109	ILE
33	69	113	ARG
33	69	114	LEU
33	69	117	GLU
33	69	122	GLU
33	69	123	LEU
33	69	125	GLU
33	69	131	LYS
33	69	133	HIS
33	69	136	VAL
33	69	138	ILE
33	69	142	VAL
33	69	145	VAL
34	15	1	MET
34	15	5	VAL
34	15	9	VAL
34	15	10	GLU

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Mol	Chain	Res	Type
34	15	15	LEU
34	15	29	LYS
34	15	33	LEU
34	15	34	LEU
34	15	35	ARG
34	15	37	LYS
34	15	46	VAL
34	15	48	MET
34	15	56	ASN
34	15	60	ILE
34	15	63	THR
34	15	65	LYS
34	15	69	GLN
34	15	85	ILE
34	15	89	LYS
34	15	91	LEU
34	15	93	THR
34	15	94	HIS
34	15	99	LEU
34	15	104	LYS
34	15	106	MET
34	15	112	LEU
34	15	134	ARG
34	15	138	LEU
35	25	5	GLN
35	25	8	LEU
35	25	9	GLU
35	25	10	VAL
35	25	14	THR
35	25	19	ILE
35	25	22	ILE
35	25	24	VAL
35	25	28	SER
35	25	35	VAL
35	25	47	ILE
35	25	48	PRO
35	25	49	ARG
35	25	53	LYS
35	25	69	ILE
35	25	70	LYS
35	25	87	ILE
35	25	91	LEU

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Mol	Chain	Res	Type
35	25	94	ARG
35	25	97	ARG
35	25	104	ARG
35	25	105	GLU
35	25	113	LYS
35	25	114	ILE
35	25	116	SER
35	25	117	LEU
36	35	4	SER
36	35	6	LEU
36	35	10	PRO
36	35	14	LYS
36	35	15	ARG
36	35	18	ARG
36	35	19	VAL
36	35	21	ARG
36	35	27	HIS
36	35	30	THR
36	35	36	LYS
36	35	41	ARG
36	35	45	LEU
36	35	55	ARG
36	35	59	LEU
36	35	62	LEU
36	35	64	LYS
36	35	65	ARG
36	35	67	MET
36	35	71	VAL
36	35	74	GLU
36	35	75	ILE
36	35	81	GLN
36	35	85	LEU
36	35	88	LEU
36	35	90	ARG
36	35	98	GLU
36	35	102	ARG
36	35	105	LEU
36	35	106	LEU
36	35	110	TYR
36	35	112	LEU
36	35	114	ILE
36	35	121	LYS

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Mol	Chain	Res	Type
36	35	123	LEU
36	35	124	LYS
36	35	125	VAL
36	35	126	VAL
36	35	135	LEU
36	35	138	LEU
36	35	139	LYS
36	35	144	GLU
36	35	147	LEU
36	35	149	GLU
37	45	10	ARG
37	45	18	LYS
37	45	21	THR
37	45	22	LYS
37	45	27	VAL
37	45	45	GLN
37	45	56	ARG
37	45	59	ARG
37	45	64	ILE
37	45	75	THR
37	45	76	LYS
37	45	77	LYS
37	45	79	LEU
37	45	81	VAL
37	45	83	MET
37	45	85	LYS
37	45	89	ASN
37	45	90	VAL
37	45	91	GLU
37	45	103	MET
37	45	105	GLU
37	45	110	THR
37	45	112	GLU
37	45	113	GLN
37	45	127	ILE
37	45	134	ARG
37	45	139	GLU
38	55	9	LYS
38	55	15	SER
38	55	18	LEU
38	55	28	LEU
38	55	29	LEU

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Mol	Chain	Res	Type
38	55	34	ILE
38	55	35	THR
38	55	42	LYS
38	55	44	LEU
38	55	51	LEU
38	55	56	LYS
38	55	57	ARG
38	55	63	ARG
38	55	65	LEU
38	55	67	LEU
38	55	74	LYS
38	55	75	LEU
38	55	76	VAL
38	55	79	LEU
38	55	81	ASP
38	55	82	GLU
38	55	91	GLN
38	55	113	LEU
38	55	114	VAL
38	55	115	GLU
38	55	118	GLU
39	65	3	ARG
39	65	8	GLU
39	65	12	PHE
39	65	17	ARG
39	65	23	ARG
39	65	24	LEU
39	65	27	SER
39	65	31	SER
39	65	36	TYR
39	65	39	ILE
39	65	41	ASP
39	65	44	LYS
39	65	50	SER
39	65	58	LEU
39	65	69	VAL
39	65	73	LEU
39	65	78	LEU
39	65	82	ILE
39	65	83	LYS
39	65	88	ASP
39	65	93	LYS

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Mol	Chain	Res	Type
39	65	98	VAL
39	65	101	LEU
39	65	110	LEU
39	65	111	GLU
40	75	6	LEU
40	75	7	ILE
40	75	8	LYS
40	75	9	LEU
40	75	10	VAL
40	75	11	GLU
40	75	12	SER
40	75	13	ARG
40	75	19	LEU
40	75	21	GLU
40	75	23	ARG
40	75	27	THR
40	75	28	VAL
40	75	30	VAL
40	75	34	VAL
40	75	36	GLU
40	75	40	THR
40	75	42	ILE
40	75	50	ILE
40	75	59	THR
40	75	62	THR
40	75	63	VAL
40	75	64	ARG
40	75	66	VAL
40	75	67	SER
40	75	74	ARG
40	75	78	LEU
40	75	86	ILE
40	75	88	ILE
40	75	89	VAL
40	75	105	LEU
40	75	106	SER
40	75	108	ARG
40	75	112	ARG
40	75	113	LYS
40	75	120	ARG
40	75	124	ASP
40	75	132	LYS

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Mol	Chain	Res	Type
40	75	134	GLU
40	75	136	GLN
41	85	5	LYS
41	85	8	VAL
41	85	17	ILE
41	85	18	LEU
41	85	20	LEU
41	85	27	LEU
41	85	34	LYS
41	85	38	THR
41	85	55	ARG
41	85	64	ARG
41	85	74	LEU
41	85	75	ASN
41	85	78	THR
41	85	80	ILE
41	85	83	LEU
41	85	88	ILE
41	85	92	ARG
41	85	93	LYS
41	85	97	ASP
41	85	105	VAL
41	85	114	LYS
42	95	7	THR
42	95	10	LYS
42	95	14	VAL
42	95	15	GLU
42	95	19	LYS
42	95	28	GLU
42	95	32	THR
42	95	33	VAL
42	95	34	GLU
42	95	35	LEU
42	95	40	LEU
42	95	46	VAL
42	95	47	VAL
42	95	49	THR
42	95	61	VAL
42	95	62	LEU
42	95	66	ARG
42	95	71	LEU
42	95	74	LYS

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Mol	Chain	Res	Type
42	95	76	LYS
42	95	80	GLN
42	95	82	ARG
42	95	83	ARG
42	95	84	LYS
42	95	88	ARG
42	95	91	TYR
42	95	95	LEU
42	95	97	LYS
43	A5	11	ARG
43	A5	12	ILE
43	A5	14	PRO
43	A5	19	LEU
43	A5	23	LEU
43	A5	37	ARG
43	A5	39	THR
43	A5	41	LYS
43	A5	50	VAL
43	A5	51	LEU
43	A5	52	GLU
43	A5	59	VAL
43	A5	65	LEU
43	A5	67	ASP
43	A5	70	TYR
43	A5	71	VAL
43	A5	76	VAL
43	A5	92	ARG
43	A5	95	ILE
43	A5	96	ILE
43	A5	97	LYS
43	A5	98	LYS
43	A5	100	THR
43	A5	106	ILE
43	A5	107	LEU
43	A5	110	LYS
44	B5	3	THR
44	B5	12	VAL
44	B5	27	THR
44	B5	35	THR
44	B5	40	LYS
44	B5	43	VAL
44	B5	45	THR

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Mol	Chain	Res	Type
44	B5	48	LYS
44	B5	52	VAL
44	B5	54	VAL
44	B5	63	LYS
44	B5	66	LEU
44	B5	69	TYR
44	B5	70	LEU
44	B5	75	ASP
44	B5	76	ARG
44	B5	78	LYS
44	B5	93	GLU
45	C5	3	VAL
45	C5	24	VAL
45	C5	29	GLU
45	C5	33	LYS
45	C5	37	VAL
45	C5	43	ASN
45	C5	44	ILE
45	C5	47	LYS
45	C5	51	VAL
45	C5	55	TYR
45	C5	60	PHE
45	C5	62	GLU
45	C5	63	LYS
45	C5	67	LEU
45	C5	70	SER
45	C5	72	VAL
45	C5	84	ARG
45	C5	85	VAL
45	C5	88	LYS
45	C5	89	PHE
45	C5	97	ARG
45	C5	98	VAL
45	C5	99	CYS
46	D5	9	TYR
46	D5	11	GLU
46	D5	16	SER
46	D5	19	ARG
46	D5	24	LEU
46	D5	28	MET
46	D5	56	VAL
46	D5	57	ILE

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Mol	Chain	Res	Type
46	D5	59	LEU
46	D5	63	ASP
46	D5	70	LEU
46	D5	71	VAL
46	D5	72	ARG
46	D5	74	VAL
46	D5	76	LEU
46	D5	78	LYS
46	D5	82	ARG
46	D5	84	GLU
46	D5	86	VAL
46	D5	90	VAL
46	D5	92	SER
46	D5	98	MET
46	D5	100	VAL
46	D5	107	THR
46	D5	111	VAL
46	D5	116	VAL
46	D5	117	LEU
46	D5	119	GLU
46	D5	121	HIS
46	D5	123	ASP
46	D5	132	ASN
46	D5	133	ILE
46	D5	136	PHE
46	D5	161	VAL
46	D5	165	VAL
46	D5	168	GLU
46	D5	170	THR
47	E5	9	SER
47	E5	11	ARG
47	E5	12	ASN
47	E5	32	ARG
47	E5	36	ILE
47	E5	38	VAL
47	E5	43	THR
47	E5	49	LYS
47	E5	63	VAL
47	E5	84	LEU
48	F5	3	LYS
48	F5	4	VAL
48	F5	19	GLN

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Mol	Chain	Res	Type
48	F5	21	ARG
48	F5	27	GLU
48	F5	34	THR
48	F5	38	SER
48	F5	46	LEU
48	F5	56	GLN
48	F5	57	GLU
48	F5	62	VAL
48	F5	67	ILE
48	F5	72	GLU
48	F5	76	ARG
48	F5	78	LYS
48	F5	80	LEU
48	F5	82	LEU
48	F5	83	GLU
48	F5	85	LEU
48	F5	86	SER
48	F5	91	LYS
48	F5	92	LYS
49	G5	5	GLU
49	G5	6	VAL
49	G5	14	ARG
49	G5	15	LYS
49	G5	16	LEU
49	G5	17	SER
49	G5	19	VAL
49	G5	24	LEU
49	G5	26	ARG
49	G5	30	ARG
49	G5	40	SER
49	G5	44	LEU
49	G5	46	GLN
49	G5	47	ASN
49	G5	48	HIS
49	G5	53	LEU
49	G5	55	ARG
49	G5	59	ARG
49	G5	60	LEU
49	G5	65	ASN
49	G5	67	LYS
50	H5	5	LYS
50	H5	8	LEU

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Mol	Chain	Res	Type
50	H5	9	VAL
50	H5	10	LYS
50	H5	17	LYS
50	H5	24	LYS
50	H5	30	ARG
50	H5	32	GLN
50	H5	33	GLN
50	H5	35	ARG
50	H5	36	VAL
50	H5	38	GLU
50	H5	40	THR
50	H5	44	ARG
50	H5	54	VAL
51	I5	22	ILE
51	I5	27	THR
51	I5	32	TYR
51	I5	36	CYS
51	I5	38	LYS
51	I5	39	CYS
51	I5	44	THR
51	I5	53	GLU
51	I5	59	PHE
51	I5	60	GLN
52	J5	3	LYS
52	J5	4	HIS
52	J5	6	VAL
52	J5	11	THR
52	J5	16	ARG
52	J5	23	HIS
52	J5	25	LEU
52	J5	29	THR
52	J5	35	GLU
52	J5	44	THR
52	J5	45	VAL
52	J5	48	GLU
52	J5	55	ARG
52	J5	57	VAL
53	K5	10	LEU
53	K5	12	GLU
53	K5	18	ARG
53	K5	27	LYS
53	K5	28	ARG

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Mol	Chain	Res	Type
53	K5	29	ASN
53	K5	32	ASN
53	K5	34	LEU
53	K5	35	GLU
53	K5	47	THR
54	L5	1	MET
54	L5	2	LYS
54	L5	4	THR
54	L5	14	LYS
54	L5	32	LYS
54	L5	43	THR
54	L5	46	VAL
55	M5	6	THR
55	M5	11	LYS
55	M5	13	ARG
55	M5	15	LYS
55	M5	21	LYS
55	M5	23	VAL
55	M5	32	LEU
55	M5	33	ASN
55	M5	50	LEU
55	M5	52	LYS
55	M5	53	PRO
55	M5	57	ARG
55	M5	58	ILE
55	M5	59	LYS
55	M5	60	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (69) such sidechains are listed below:

Mol	Chain	Res	Type
4	3E	74	GLN
6	5E	13	ASN
7	6E	11	GLN
7	6E	106	GLN
7	6E	122	HIS
9	8E	89	ASN
11	2I	13	GLN
13	4I	92	HIS
13	4I	101	GLN
15	6I	50	HIS
19	AI	14	HIS

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Mol	Chain	Res	Type
20	BI	16	HIS
28	11	112	GLN
29	21	135	HIS
30	31	75	HIS
35	68	88	ASN
35	68	89	ASN
37	88	12	GLN
37	88	45	GLN
38	98	13	HIS
38	98	31	HIS
38	98	61	HIS
38	98	91	GLN
39	A8	84	GLN
40	B8	55	ASN
42	D8	80	GLN
44	F8	31	HIS
46	H8	34	ASN
46	H8	118	GLN
47	I8	29	GLN
2	12	19	HIS
2	12	37	ASN
3	22	176	HIS
5	42	73	ASN
6	52	64	GLN
7	62	84	ASN
7	62	96	GLN
9	82	29	ASN
10	1A	84	GLN
11	2A	38	ASN
11	2A	104	GLN
15	6A	46	HIS
15	6A	53	HIS
16	7A	13	HIS
28	19	116	GLN
29	29	121	ASN
30	39	40	GLN
30	39	160	ASN
31	49	123	ASN
33	69	54	GLN
33	69	104	GLN
34	15	128	HIS
34	15	131	GLN

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Mol	Chain	Res	Type
35	25	3	GLN
35	25	5	GLN
36	35	27	HIS
37	45	89	ASN
37	45	113	GLN
38	55	31	HIS
40	75	58	ASN
41	85	104	GLN
42	95	89	GLN
43	A5	61	ASN
44	B5	41	ASN
46	D5	151	HIS
47	E5	12	ASN
49	G5	46	GLN
49	G5	48	HIS
53	K5	29	ASN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	13	1495/1522 (98%)	329 (22%)	34 (2%)
1	1G	1496/1522 (98%)	354 (23%)	37 (2%)
22	1K	75/76 (98%)	33 (44%)	3 (4%)
23	2K	76/77 (98%)	21 (27%)	2 (2%)
23	2L	76/77 (98%)	16 (21%)	1 (1%)
24	3K	73/76 (96%)	41 (56%)	6 (8%)
25	4K	12/30 (40%)	4 (33%)	0
25	4L	11/30 (36%)	4 (36%)	1 (9%)
26	14	2908/2917 (99%)	726 (24%)	52 (1%)
26	1H	2911/2917 (99%)	704 (24%)	51 (1%)
27	16	121/122 (99%)	27 (22%)	1 (0%)
27	1J	121/122 (99%)	35 (28%)	2 (1%)
56	1L	75/76 (98%)	35 (46%)	3 (4%)
57	3L	75/76 (98%)	37 (49%)	4 (5%)
All	All	9525/9640 (98%)	2366 (24%)	197 (2%)

All (2366) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	13	5	U
1	13	6	G

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Mol	Chain	Res	Type
1	13	7	G
1	13	8	A
1	13	21	G
1	13	22	G
1	13	28	G
1	13	32	A
1	13	39	G
1	13	47	C
1	13	48	C
1	13	50	A
1	13	51	A
1	13	53	A
1	13	54	C
1	13	61	G
1	13	65	U
1	13	66	G
1	13	77	C
1	13	78	G
1	13	91	C
1	13	95	G
1	13	101	A
1	13	105	G
1	13	116	A
1	13	121	C
1	13	129(A)	G
1	13	131	C
1	13	142	G
1	13	144	G
1	13	147	G
1	13	150	C
1	13	151	A
1	13	157	G
1	13	159	G
1	13	163	C
1	13	168	G
1	13	172	A
1	13	173	U
1	13	174	C
1	13	188	U
1	13	189	U
1	13	190	G
1	13	191(A)	G

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Mol	Chain	Res	Type
1	13	195	A
1	13	197	A
1	13	199	G
1	13	201	C
1	13	208	U
1	13	210	U
1	13	216	G
1	13	217	C
1	13	222	U
1	13	227	G
1	13	231	G
1	13	244	U
1	13	245	C
1	13	247	G
1	13	251	G
1	13	262	A
1	13	266	G
1	13	267	C
1	13	281	G
1	13	288	A
1	13	289	G
1	13	316	G
1	13	317	G
1	13	318	G
1	13	321	A
1	13	324	G
1	13	328	C
1	13	329	A
1	13	330	C
1	13	332	G
1	13	342	C
1	13	345	C
1	13	346	G
1	13	347	G
1	13	352	C
1	13	353	A
1	13	354	G
1	13	367	U
1	13	372	C
1	13	373	A
1	13	383	A
1	13	384	G

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Mol	Chain	Res	Type
1	13	388	G
1	13	390	C
1	13	397	A
1	13	398	C
1	13	406	G
1	13	412	A
1	13	413	G
1	13	419	C
1	13	422	C
1	13	423	G
1	13	424	G
1	13	429	U
1	13	430	A
1	13	451	A
1	13	465	A
1	13	466	C
1	13	467	G
1	13	485	G
1	13	487	A
1	13	496	A
1	13	497	U
1	13	498	A
1	13	505	G
1	13	508	C
1	13	509	A
1	13	510	A
1	13	511	C
1	13	517	G
1	13	518	C
1	13	524	G
1	13	527	G
1	13	531	U
1	13	533	A
1	13	536	C
1	13	545	C
1	13	547	A
1	13	559	A
1	13	561	U
1	13	562	C
1	13	572	A
1	13	573	A
1	13	576	G

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Mol	Chain	Res	Type
1	13	577	G
1	13	596	C
1	13	607	A
1	13	630	G
1	13	631	G
1	13	632	A
1	13	639	G
1	13	650	G
1	13	653	A
1	13	655	A
1	13	660	G
1	13	662	G
1	13	665	A
1	13	666	G
1	13	687	A
1	13	688	G
1	13	693	G
1	13	704	A
1	13	723	U
1	13	724	G
1	13	728	A
1	13	748	C
1	13	749	C
1	13	755	G
1	13	759	A
1	13	766	A
1	13	767	A
1	13	777	A
1	13	792	A
1	13	793	U
1	13	794	A
1	13	805	C
1	13	813	U
1	13	817	C
1	13	821	G
1	13	827	U
1	13	828	A
1	13	841	U
1	13	842	C
1	13	843	U
1	13	848	C
1	13	859	A

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Mol	Chain	Res	Type
1	13	864	A
1	13	870	U
1	13	884	U
1	13	902	G
1	13	904	C
1	13	914	A
1	13	921	U
1	13	922	G
1	13	926	G
1	13	927	G
1	13	934	C
1	13	936	C
1	13	940	C
1	13	941	G
1	13	960	U
1	13	968	A
1	13	969	A
1	13	971	G
1	13	974	A
1	13	975	A
1	13	976	G
1	13	977	A
1	13	983	A
1	13	991	U
1	13	992	U
1	13	993	G
1	13	1004	A
1	13	1005	A
1	13	1006	C
1	13	1007	C
1	13	1008	C
1	13	1009	G
1	13	1012	U
1	13	1021	G
1	13	1024	G
1	13	1025	U
1	13	1028	C
1	13	1029	G
1	13	1032(A)	G
1	13	1033	G
1	13	1037	C
1	13	1040	U

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Mol	Chain	Res	Type
1	13	1042	G
1	13	1046	A
1	13	1049	U
1	13	1053	G
1	13	1054	C
1	13	1055	A
1	13	1064	G
1	13	1065	U
1	13	1066	C
1	13	1081	G
1	13	1094	G
1	13	1095	U
1	13	1101	A
1	13	1121	U
1	13	1122	U
1	13	1125	U
1	13	1126	U
1	13	1129	C
1	13	1130	A
1	13	1131	G
1	13	1132	C
1	13	1133	G
1	13	1136	U
1	13	1137	C
1	13	1138	G
1	13	1139	G
1	13	1144	G
1	13	1146	A
1	13	1149	C
1	13	1152	A
1	13	1154	G
1	13	1157	A
1	13	1158	C
1	13	1159	U
1	13	1171	G
1	13	1177	G
1	13	1178	G
1	13	1181	G
1	13	1191	A
1	13	1196	U
1	13	1197	G
1	13	1201	A

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Mol	Chain	Res	Type
1	13	1204	A
1	13	1212	U
1	13	1213	A
1	13	1214	C
1	13	1225	A
1	13	1226	C
1	13	1227	A
1	13	1236	A
1	13	1238	A
1	13	1240	U
1	13	1241	G
1	13	1253	G
1	13	1256	A
1	13	1257	U
1	13	1258	G
1	13	1270	C
1	13	1273	G
1	13	1278	U
1	13	1280	A
1	13	1281	U
1	13	1282	C
1	13	1285	A
1	13	1286	A
1	13	1287	A
1	13	1290	G
1	13	1299	A
1	13	1300	G
1	13	1302	U
1	13	1303	C
1	13	1317	C
1	13	1322	C
1	13	1323	G
1	13	1331	G
1	13	1335	C
1	13	1336	C
1	13	1337	G
1	13	1338	G
1	13	1340	A
1	13	1346	A
1	13	1347	G
1	13	1350	A
1	13	1353	G

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Mol	Chain	Res	Type
1	13	1358	U
1	13	1363	A
1	13	1364	U
1	13	1370	G
1	13	1377	A
1	13	1379	G
1	13	1381	U
1	13	1388	C
1	13	1398	A
1	13	1419	G
1	13	1422	G
1	13	1430	C
1	13	1442	G
1	13	1443	G
1	13	1446	A
1	13	1449	C
1	13	1451	A
1	13	1452	C
1	13	1453	G
1	13	1467	G
1	13	1469	G
1	13	1487	G
1	13	1492	A
1	13	1495	U
1	13	1497	G
1	13	1499	A
1	13	1503	A
1	13	1504	G
1	13	1505	G
1	13	1506	U
1	13	1517	G
1	13	1529	G
1	13	1530	G
22	1K	7	A
22	1K	9	A
22	1K	10	G
22	1K	11	C
22	1K	13	C
22	1K	14	A
22	1K	16	U
22	1K	17	C
22	1K	18	G

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Mol	Chain	Res	Type
22	1K	19	G
22	1K	21	A
22	1K	22	G
22	1K	24	G
22	1K	27	G
22	1K	29	G
22	1K	36	A
22	1K	44	G
22	1K	46	G
22	1K	47	U
22	1K	48	C
22	1K	49	C
22	1K	52	G
22	1K	53	G
22	1K	55	PSU
22	1K	59	U
22	1K	61	C
22	1K	64	A
22	1K	68	C
22	1K	70	G
22	1K	73	A
22	1K	74	C
22	1K	75	C
22	1K	76	A
23	2K	2	G
23	2K	6	G
23	2K	9	G
23	2K	13	C
23	2K	18	C
23	2K	20	G
23	2K	21	U
23	2K	22	A
23	2K	23	G
23	2K	27	G
23	2K	31	G
23	2K	35	C
23	2K	48	U
23	2K	49	C
23	2K	50	G
23	2K	53	G
23	2K	54	G
23	2K	59	A

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Mol	Chain	Res	Type
23	2K	62	C
23	2K	68	C
23	2K	77	A
24	3K	2	C
24	3K	3	C
24	3K	7	A
24	3K	8	U
24	3K	9	A
24	3K	10	G
24	3K	13	C
24	3K	14	A
24	3K	17	C
24	3K	19	G
24	3K	20	U
24	3K	21	A
24	3K	22	G
24	3K	24	G
24	3K	26	A
24	3K	33	U
24	3K	36	A
24	3K	37	MIA
24	3K	38	A
24	3K	39	PSU
24	3K	41	C
24	3K	42	C
24	3K	43	C
24	3K	45	U
24	3K	46	G
24	3K	47	U
24	3K	48	C
24	3K	49	C
24	3K	52	G
24	3K	55	U
24	3K	56	C
24	3K	58	A
24	3K	59	U
24	3K	60	U
24	3K	61	C
24	3K	65	G
24	3K	66	U
24	3K	69	G
24	3K	72	C

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Mol	Chain	Res	Type
24	3K	73	A
24	3K	76	A
25	4K	14	A
25	4K	15	A
25	4K	22	A
25	4K	25	A
26	1H	5	A
26	1H	9	U
26	1H	12	U
26	1H	27	G
26	1H	34	C
26	1H	39	C
26	1H	46	C
26	1H	51	G
26	1H	61	G
26	1H	63	U
26	1H	64	A
26	1H	71	A
26	1H	74	A
26	1H	75	G
26	1H	85	G
26	1H	93	C
26	1H	95	G
26	1H	118	A
26	1H	119	A
26	1H	120	U
26	1H	125	G
26	1H	126	A
26	1H	140	A
26	1H	151	C
26	1H	155	C
26	1H	163	U
26	1H	164	U
26	1H	171	G
26	1H	181	A
26	1H	188	G
26	1H	196	A
26	1H	197	A
26	1H	199	A
26	1H	200	U
26	1H	213	A
26	1H	214	G

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Mol	Chain	Res	Type
26	1H	215	G
26	1H	216	A
26	1H	222	A
26	1H	223	A
26	1H	224	G
26	1H	228	A
26	1H	229	A
26	1H	230	U
26	1H	233	A
26	1H	248	G
26	1H	249	C
26	1H	250	G
26	1H	252	G
26	1H	261	G
26	1H	266	G
26	1H	270(F)	U
26	1H	270(K)	C
26	1H	270(M)	U
26	1H	270(N)	G
26	1H	270(P)	C
26	1H	271(B)	G
26	1H	271(C)	U
26	1H	271	G
26	1H	274	G
26	1H	275	G
26	1H	278	A
26	1H	299	A
26	1H	304	G
26	1H	311	A
26	1H	323	G
26	1H	324	A
26	1H	329	G
26	1H	330	A
26	1H	340	A
26	1H	352	G
26	1H	354	G
26	1H	357	A
26	1H	363	G
26	1H	364	C
26	1H	370	G
26	1H	372	G
26	1H	375	C

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Mol	Chain	Res	Type
26	1H	380	U
26	1H	382	G
26	1H	386	G
26	1H	396	G
26	1H	399	G
26	1H	405	U
26	1H	407	G
26	1H	411	G
26	1H	427	U
26	1H	428	A
26	1H	431	U
26	1H	443	A
26	1H	444	C
26	1H	446	G
26	1H	448	U
26	1H	449	A
26	1H	451	C
26	1H	454	A
26	1H	455	C
26	1H	457	A
26	1H	459	U
26	1H	470	A
26	1H	471	A
26	1H	478	A
26	1H	481	G
26	1H	482	A
26	1H	494	G
26	1H	505	A
26	1H	508	G
26	1H	509	C
26	1H	513	A
26	1H	529	A
26	1H	530	G
26	1H	531	C
26	1H	532	A
26	1H	533	G
26	1H	545	G
26	1H	546	C
26	1H	547	A
26	1H	549	G
26	1H	556	G
26	1H	563	G

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Mol	Chain	Res	Type
26	1H	564	C
26	1H	567	A
26	1H	573	G
26	1H	575	A
26	1H	583	G
26	1H	587	C
26	1H	588	U
26	1H	603	A
26	1H	607	U
26	1H	609(A)	G
26	1H	613	U
26	1H	614	U
26	1H	615	G
26	1H	617	G
26	1H	618(A)	C
26	1H	621	A
26	1H	622	G
26	1H	626	U
26	1H	627	A
26	1H	637	A
26	1H	640	C
26	1H	644	A
26	1H	645	C
26	1H	646	A
26	1H	652	C
26	1H	654	A
26	1H	654(A)	A
26	1H	654(B)	C
26	1H	654(H)	G
26	1H	654(I)	C
26	1H	654(J)	A
26	1H	654(K)	C
26	1H	654(M)	C
26	1H	654(O)	G
26	1H	654(T)	A
26	1H	664	C
26	1H	669	G
26	1H	678	C
26	1H	686	G
26	1H	690	G
26	1H	717	G
26	1H	729	G

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Mol	Chain	Res	Type
26	1H	730	C
26	1H	731	C
26	1H	736	C
26	1H	752	A
26	1H	753	C
26	1H	764	A
26	1H	765	G
26	1H	770	G
26	1H	775	G
26	1H	776	G
26	1H	777	A
26	1H	779	U
26	1H	782	A
26	1H	784	A
26	1H	785	G
26	1H	789	A
26	1H	790	C
26	1H	791	C
26	1H	792	G
26	1H	805	G
26	1H	812	C
26	1H	824	A
26	1H	827	U
26	1H	828	U
26	1H	829	A
26	1H	831	G
26	1H	832	G
26	1H	845	G
26	1H	846	C
26	1H	847	U
26	1H	858	U
26	1H	859	G
26	1H	860	U
26	1H	866	A
26	1H	879	G
26	1H	880	G
26	1H	881	G
26	1H	882	G
26	1H	884	C
26	1H	885	C
26	1H	886	C
26	1H	887	A

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Mol	Chain	Res	Type
26	1H	888	C
26	1H	890	A
26	1H	892	G
26	1H	893	C
26	1H	894	C
26	1H	895	U
26	1H	896	A
26	1H	897	C
26	1H	898	C
26	1H	900	A
26	1H	901	A
26	1H	907	U
26	1H	910	A
26	1H	917	A
26	1H	918	A
26	1H	925	C
26	1H	932	G
26	1H	938	G
26	1H	940	G
26	1H	941	A
26	1H	946	G
26	1H	947	G
26	1H	952	G
26	1H	959	A
26	1H	961	C
26	1H	962	G
26	1H	968	G
26	1H	974	G
26	1H	974(A)	C
26	1H	975	G
26	1H	983	A
26	1H	990	A
26	1H	996	A
26	1H	1003	G
26	1H	1005	C
26	1H	1011	G
26	1H	1012	U
26	1H	1013	C
26	1H	1015	G
26	1H	1020	A
26	1H	1022	G
26	1H	1023	U

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Mol	Chain	Res	Type
26	1H	1025	G
26	1H	1026	U
26	1H	1027	A
26	1H	1028	A
26	1H	1031	G
26	1H	1033	U
26	1H	1037	G
26	1H	1046	A
26	1H	1047	G
26	1H	1054	A
26	1H	1057	A
26	1H	1061	U
26	1H	1062	G
26	1H	1064	C
26	1H	1067	A
26	1H	1068	G
26	1H	1070	A
26	1H	1071	G
26	1H	1072	C
26	1H	1073	A
26	1H	1075	C
26	1H	1076	C
26	1H	1077	A
26	1H	1078	U
26	1H	1079	C
26	1H	1080	A
26	1H	1081	U
26	1H	1082	U
26	1H	1084	A
26	1H	1085	A
26	1H	1086	A
26	1H	1087	G
26	1H	1088	A
26	1H	1090	U
26	1H	1095	A
26	1H	1096	A
26	1H	1097	U
26	1H	1104	C
26	1H	1106	G
26	1H	1107	G
26	1H	1111	A
26	1H	1112	G

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Mol	Chain	Res	Type
26	1H	1122	G
26	1H	1128	A
26	1H	1129	A
26	1H	1130	U
26	1H	1131	G
26	1H	1135	C
26	1H	1136	G
26	1H	1139	G
26	1H	1142	U
26	1H	1142(A)	A
26	1H	1144	G
26	1H	1151	G
26	1H	1156	A
26	1H	1171	G
26	1H	1176	G
26	1H	1178	C
26	1H	1179	C
26	1H	1180	C
26	1H	1194	A
26	1H	1195	G
26	1H	1204	A
26	1H	1205	U
26	1H	1210	A
26	1H	1218	C
26	1H	1220	A
26	1H	1225	C
26	1H	1228	G
26	1H	1237	A
26	1H	1244	G
26	1H	1250	G
26	1H	1253	A
26	1H	1256	G
26	1H	1265	A
26	1H	1267	U
26	1H	1268	A
26	1H	1269	A
26	1H	1271	G
26	1H	1272	A
26	1H	1274	A
26	1H	1300	U
26	1H	1301	A
26	1H	1313	U

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Mol	Chain	Res	Type
26	1H	1314	C
26	1H	1321	A
26	1H	1329	U
26	1H	1330	C
26	1H	1342	A
26	1H	1344	G
26	1H	1345	C
26	1H	1347	G
26	1H	1348	G
26	1H	1349	A
26	1H	1352	U
26	1H	1359	A
26	1H	1360	A
26	1H	1365	A
26	1H	1368	G
26	1H	1369	G
26	1H	1370	C
26	1H	1379	A
26	1H	1380	G
26	1H	1384	A
26	1H	1385	G
26	1H	1386	C
26	1H	1416	G
26	1H	1420	U
26	1H	1421	G
26	1H	1422	G
26	1H	1424	G
26	1H	1428	C
26	1H	1431	U
26	1H	1442	G
26	1H	1444(A)	A
26	1H	1449(A)	G
26	1H	1453	A
26	1H	1455	G
26	1H	1456	G
26	1H	1458	C
26	1H	1459	G
26	1H	1460	A
26	1H	1461	G
26	1H	1467	C
26	1H	1471	A
26	1H	1483	G

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Mol	Chain	Res	Type
26	1H	1490	A
26	1H	1493	C
26	1H	1495	A
26	1H	1497	U
26	1H	1507	A
26	1H	1508	A
26	1H	1509	C
26	1H	1510	A
26	1H	1511	A
26	1H	1522	G
26	1H	1526	G
26	1H	1534	G
26	1H	1535	U
26	1H	1536	A
26	1H	1537	C
26	1H	1538	G
26	1H	1540	G
26	1H	1543	A
26	1H	1544	C
26	1H	1545	A
26	1H	1547	C
26	1H	1548	C
26	1H	1554	A
26	1H	1555	G
26	1H	1558	A
26	1H	1559	G
26	1H	1560	G
26	1H	1566	A
26	1H	1569	A
26	1H	1577	C
26	1H	1578	U
26	1H	1580	A
26	1H	1586	A
26	1H	1594	G
26	1H	1608	A
26	1H	1609	A
26	1H	1610	A
26	1H	1611	C
26	1H	1612	C
26	1H	1616	A
26	1H	1617	C
26	1H	1622	G

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Mol	Chain	Res	Type
26	1H	1635	G
26	1H	1639	U
26	1H	1644	C
26	1H	1647	G
26	1H	1648	C
26	1H	1651	G
26	1H	1654	A
26	1H	1674	G
26	1H	1685	C
26	1H	1695	G
26	1H	1706	U
26	1H	1728	G
26	1H	1729	A
26	1H	1730	U
26	1H	1731	G
26	1H	1746	G
26	1H	1756	G
26	1H	1758	G
26	1H	1763	G
26	1H	1764	G
26	1H	1772	G
26	1H	1773	A
26	1H	1782	C
26	1H	1787	A
26	1H	1788	C
26	1H	1791	A
26	1H	1799	G
26	1H	1800	C
26	1H	1801	G
26	1H	1811	G
26	1H	1812	A
26	1H	1816	G
26	1H	1827	C
26	1H	1829	A
26	1H	1835	G
26	1H	1836	C
26	1H	1837	C
26	1H	1839	G
26	1H	1847	A
26	1H	1858	G
26	1H	1860	G
26	1H	1870	C

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Mol	Chain	Res	Type
26	1H	1878	G
26	1H	1889	A
26	1H	1897	G
26	1H	1900	A
26	1H	1901	A
26	1H	1905	C
26	1H	1906	G
26	1H	1913	A
26	1H	1914	C
26	1H	1916	A
26	1H	1919	A
26	1H	1926	U
26	1H	1929	G
26	1H	1930	G
26	1H	1931	U
26	1H	1936	A
26	1H	1937	A
26	1H	1938	A
26	1H	1951	U
26	1H	1952	A
26	1H	1955	U
26	1H	1959	G
26	1H	1961	C
26	1H	1963	U
26	1H	1965	C
26	1H	1967	C
26	1H	1969	A
26	1H	1970	A
26	1H	1971	A
26	1H	1972	A
26	1H	1993	U
26	1H	2020	A
26	1H	2021	C
26	1H	2023	G
26	1H	2030	A
26	1H	2031	A
26	1H	2033	A
26	1H	2043	C
26	1H	2051	A
26	1H	2055	C
26	1H	2056	G
26	1H	2058	A

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Mol	Chain	Res	Type
26	1H	2060	A
26	1H	2061	G
26	1H	2062	A
26	1H	2063	C
26	1H	2069	G
26	1H	2077	A
26	1H	2080	G
26	1H	2099	U
26	1H	2108	C
26	1H	2111	C
26	1H	2112	G
26	1H	2113	U
26	1H	2114	A
26	1H	2116	G
26	1H	2118	U
26	1H	2120	G
26	1H	2125	G
26	1H	2126	A
26	1H	2127	G
26	1H	2128	C
26	1H	2129	C
26	1H	2131	G
26	1H	2132	U
26	1H	2133	G
26	1H	2135	A
26	1H	2136	C
26	1H	2139	C
26	1H	2147	G
26	1H	2148	G
26	1H	2154	G
26	1H	2157	G
26	1H	2158	A
26	1H	2161	C
26	1H	2166	G
26	1H	2167	U
26	1H	2168	G
26	1H	2170	A
26	1H	2171	A
26	1H	2172	U
26	1H	2173	A
26	1H	2174	C
26	1H	2175	C

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Mol	Chain	Res	Type
26	1H	2176	A
26	1H	2181	G
26	1H	2185	C
26	1H	2190	G
26	1H	2198	A
26	1H	2199	A
26	1H	2205	C
26	1H	2210	G
26	1H	2212	A
26	1H	2213	U
26	1H	2215	G
26	1H	2224	G
26	1H	2225	A
26	1H	2226	C
26	1H	2237	G
26	1H	2238	G
26	1H	2239	G
26	1H	2240	C
26	1H	2250	G
26	1H	2254	C
26	1H	2263	C
26	1H	2267	A
26	1H	2273	A
26	1H	2275	C
26	1H	2280	G
26	1H	2283	C
26	1H	2286	A
26	1H	2287	A
26	1H	2298	A
26	1H	2305	A
26	1H	2307	G
26	1H	2308	G
26	1H	2310	A
26	1H	2312	U
26	1H	2314	C
26	1H	2315	G
26	1H	2318	G
26	1H	2319	G
26	1H	2320	A
26	1H	2321	G
26	1H	2325	G
26	1H	2326	C

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Mol	Chain	Res	Type
26	1H	2327	A
26	1H	2334	G
26	1H	2336	A
26	1H	2343	C
26	1H	2346	A
26	1H	2347	C
26	1H	2350	C
26	1H	2376	A
26	1H	2377	A
26	1H	2383	G
26	1H	2385	C
26	1H	2389	G
26	1H	2390	U
26	1H	2395	C
26	1H	2402	C
26	1H	2403	C
26	1H	2405	G
26	1H	2406	U
26	1H	2418	A
26	1H	2425	A
26	1H	2428	G
26	1H	2429	G
26	1H	2430	A
26	1H	2431	U
26	1H	2435	A
26	1H	2439	A
26	1H	2440	C
26	1H	2441	C
26	1H	2448	A
26	1H	2468	G
26	1H	2469	A
26	1H	2470	G
26	1H	2475	C
26	1H	2476	A
26	1H	2478	A
26	1H	2482	G
26	1H	2484	G
26	1H	2498	C
26	1H	2502	G
26	1H	2505	G
26	1H	2506	U
26	1H	2518	A

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Mol	Chain	Res	Type
26	1H	2529	G
26	1H	2553	G
26	1H	2554	U
26	1H	2556	C
26	1H	2566	A
26	1H	2567	G
26	1H	2573	C
26	1H	2582	G
26	1H	2590	A
26	1H	2594	C
26	1H	2601	C
26	1H	2602	A
26	1H	2608	G
26	1H	2609	U
26	1H	2611	U
26	1H	2612	C
26	1H	2615	U
26	1H	2629	A
26	1H	2630	G
26	1H	2634	G
26	1H	2636	U
26	1H	2654	A
26	1H	2660	A
26	1H	2665	A
26	1H	2666	C
26	1H	2667	C
26	1H	2673	G
26	1H	2682	U
26	1H	2689	U
26	1H	2701	C
26	1H	2702	U
26	1H	2703	C
26	1H	2704	C
26	1H	2705	A
26	1H	2707	G
26	1H	2712(A)	A
26	1H	2713	A
26	1H	2714	G
26	1H	2718	G
26	1H	2726	U
26	1H	2733	A
26	1H	2734	A

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Mol	Chain	Res	Type
26	1H	2744	G
26	1H	2756	U
26	1H	2757	A
26	1H	2758	A
26	1H	2764	A
26	1H	2765	A
26	1H	2766	G
26	1H	2778	A
26	1H	2779	U
26	1H	2781	A
26	1H	2787	C
26	1H	2789	C
26	1H	2790	A
26	1H	2791	C
26	1H	2793	G
26	1H	2794	C
26	1H	2795	G
26	1H	2797	U
26	1H	2799	A
26	1H	2801	A
26	1H	2802	G
26	1H	2807	G
26	1H	2808	U
26	1H	2820	A
26	1H	2821	A
26	1H	2830	G
26	1H	2833	G
26	1H	2834	G
26	1H	2835	A
26	1H	2847	U
26	1H	2872	G
26	1H	2891	G
26	1H	2892	A
26	1H	2893	G
26	1H	2894	G
26	1H	2895	U
26	1H	2899	G
26	1H	2902	C
27	16	0	A
27	16	1	U
27	16	3	C
27	16	5	C

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Mol	Chain	Res	Type
27	16	8	U
27	16	9	G
27	16	12	C
27	16	13	A
27	16	15	A
27	16	16	G
27	16	25	A
27	16	33	G
27	16	39	A
27	16	42	C
27	16	45	A
27	16	48	A
27	16	52	A
27	16	53	A
27	16	56	G
27	16	65	C
27	16	73	A
27	16	105	G
27	16	107	U
27	16	109	G
27	16	115	G
27	16	117	G
27	16	119	A
1	1G	5	U
1	1G	7	G
1	1G	9	G
1	1G	22	G
1	1G	31	G
1	1G	32	A
1	1G	39	G
1	1G	47	C
1	1G	48	C
1	1G	50	A
1	1G	51	A
1	1G	54	C
1	1G	65	U
1	1G	73	G
1	1G	76	G
1	1G	79	G
1	1G	80	G
1	1G	90	C
1	1G	91	C

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Mol	Chain	Res	Type
1	1G	101	A
1	1G	115	G
1	1G	116	A
1	1G	121	C
1	1G	131	C
1	1G	154	C
1	1G	163	C
1	1G	173	U
1	1G	174	C
1	1G	182	U
1	1G	186	C
1	1G	187	C
1	1G	188	U
1	1G	189	U
1	1G	190	G
1	1G	191(A)	G
1	1G	191(D)	U
1	1G	191(E)	G
1	1G	195	A
1	1G	196	A
1	1G	197	A
1	1G	198	G
1	1G	210	U
1	1G	216	G
1	1G	231	G
1	1G	244	U
1	1G	247	G
1	1G	250	A
1	1G	251	G
1	1G	266	G
1	1G	267	C
1	1G	274	A
1	1G	280	C
1	1G	281	G
1	1G	283	C
1	1G	289	G
1	1G	298	A
1	1G	308	C
1	1G	316	G
1	1G	318	G
1	1G	321	A
1	1G	328	C

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Mol	Chain	Res	Type
1	1G	329	A
1	1G	332	G
1	1G	345	C
1	1G	346	G
1	1G	347	G
1	1G	349	A
1	1G	350	G
1	1G	351	G
1	1G	352	C
1	1G	353	A
1	1G	354	G
1	1G	356	A
1	1G	363	A
1	1G	367	U
1	1G	369	C
1	1G	372	C
1	1G	384	G
1	1G	388	G
1	1G	397	A
1	1G	398	C
1	1G	406	G
1	1G	411	A
1	1G	412	A
1	1G	413	G
1	1G	414	A
1	1G	421	U
1	1G	422	C
1	1G	423	G
1	1G	424	G
1	1G	429	U
1	1G	430	A
1	1G	439	A
1	1G	442	C
1	1G	465	A
1	1G	466	C
1	1G	467	G
1	1G	475	G
1	1G	478	A
1	1G	484	G
1	1G	485	G
1	1G	486	U
1	1G	496	A

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Mol	Chain	Res	Type
1	1G	497	U
1	1G	502	G
1	1G	505	G
1	1G	509	A
1	1G	510	A
1	1G	511	C
1	1G	517	G
1	1G	518	C
1	1G	521	G
1	1G	527	G
1	1G	530	G
1	1G	531	U
1	1G	532	A
1	1G	533	A
1	1G	536	C
1	1G	547	A
1	1G	553	A
1	1G	559	A
1	1G	561	U
1	1G	562	C
1	1G	566	G
1	1G	567	G
1	1G	572	A
1	1G	573	A
1	1G	574	A
1	1G	576	G
1	1G	581	G
1	1G	596	C
1	1G	607	A
1	1G	608	A
1	1G	618	C
1	1G	630	G
1	1G	632	A
1	1G	633	G
1	1G	651	C
1	1G	653	A
1	1G	657	G
1	1G	665	A
1	1G	669	U
1	1G	670	G
1	1G	687	A
1	1G	688	G

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Mol	Chain	Res	Type
1	1G	723	U
1	1G	724	G
1	1G	731	G
1	1G	734	G
1	1G	749	C
1	1G	755	G
1	1G	760	G
1	1G	764	C
1	1G	777	A
1	1G	778	G
1	1G	792	A
1	1G	793	U
1	1G	794	A
1	1G	799	G
1	1G	809	G
1	1G	813	U
1	1G	816	A
1	1G	817	C
1	1G	821	G
1	1G	827	U
1	1G	828	A
1	1G	841	U
1	1G	842	C
1	1G	843	U
1	1G	848	C
1	1G	859	A
1	1G	873	A
1	1G	876	G
1	1G	885	G
1	1G	914	A
1	1G	916	G
1	1G	926	G
1	1G	927	G
1	1G	933	G
1	1G	934	C
1	1G	935	A
1	1G	936	C
1	1G	954	G
1	1G	958	A
1	1G	960	U
1	1G	961	U
1	1G	966	G

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Mol	Chain	Res	Type
1	1G	968	A
1	1G	969	A
1	1G	971	G
1	1G	972	C
1	1G	974	A
1	1G	975	A
1	1G	976	G
1	1G	977	A
1	1G	978	A
1	1G	980	C
1	1G	983	A
1	1G	984	C
1	1G	991	U
1	1G	992	U
1	1G	993	G
1	1G	995	C
1	1G	1004	A
1	1G	1006	C
1	1G	1009	G
1	1G	1013	G
1	1G	1023	G
1	1G	1024	G
1	1G	1025	U
1	1G	1028	C
1	1G	1028(B)	C
1	1G	1029	G
1	1G	1031	G
1	1G	1032(A)	G
1	1G	1033	G
1	1G	1035	A
1	1G	1036	G
1	1G	1038	C
1	1G	1040	U
1	1G	1046	A
1	1G	1047	G
1	1G	1050	G
1	1G	1051	C
1	1G	1053	G
1	1G	1054	C
1	1G	1055	A
1	1G	1056	U
1	1G	1064	G

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Mol	Chain	Res	Type
1	1G	1081	G
1	1G	1086	U
1	1G	1088	G
1	1G	1092	A
1	1G	1094	G
1	1G	1095	U
1	1G	1099	G
1	1G	1101	A
1	1G	1113	C
1	1G	1124	G
1	1G	1125	U
1	1G	1128	C
1	1G	1129	C
1	1G	1130	A
1	1G	1131	G
1	1G	1135	U
1	1G	1137	C
1	1G	1138	G
1	1G	1139	G
1	1G	1146	A
1	1G	1154	G
1	1G	1157	A
1	1G	1158	C
1	1G	1159	U
1	1G	1160	G
1	1G	1171	G
1	1G	1177	G
1	1G	1178	G
1	1G	1181	G
1	1G	1183	A
1	1G	1185	G
1	1G	1188	A
1	1G	1196	U
1	1G	1197	G
1	1G	1201	A
1	1G	1202	G
1	1G	1209	C
1	1G	1211	U
1	1G	1212	U
1	1G	1213	A
1	1G	1214	C
1	1G	1225	A

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Mol	Chain	Res	Type
1	1G	1227	A
1	1G	1232	U
1	1G	1238	A
1	1G	1240	U
1	1G	1241	G
1	1G	1256	A
1	1G	1257	U
1	1G	1258	G
1	1G	1260	C
1	1G	1263	C
1	1G	1267	C
1	1G	1269	A
1	1G	1274	G
1	1G	1275	A
1	1G	1278	U
1	1G	1279	A
1	1G	1280	A
1	1G	1281	U
1	1G	1286	A
1	1G	1287	A
1	1G	1288	A
1	1G	1293	G
1	1G	1297	C
1	1G	1298	C
1	1G	1299	A
1	1G	1300	G
1	1G	1301	U
1	1G	1303	C
1	1G	1305	G
1	1G	1312	G
1	1G	1317	C
1	1G	1319	A
1	1G	1320	C
1	1G	1322	C
1	1G	1323	G
1	1G	1331	G
1	1G	1335	C
1	1G	1336	C
1	1G	1337	G
1	1G	1338	G
1	1G	1346	A
1	1G	1347	G

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Mol	Chain	Res	Type
1	1G	1362(A)	C
1	1G	1363	A
1	1G	1364	U
1	1G	1370	G
1	1G	1379	G
1	1G	1382	C
1	1G	1386	G
1	1G	1396	A
1	1G	1397	C
1	1G	1398	A
1	1G	1399	C
1	1G	1400	C
1	1G	1401	G
1	1G	1406	U
1	1G	1419	G
1	1G	1442	G
1	1G	1443	G
1	1G	1446	A
1	1G	1447	G
1	1G	1450	U
1	1G	1451	A
1	1G	1452	C
1	1G	1453	G
1	1G	1454	G
1	1G	1469	G
1	1G	1492	A
1	1G	1498	U
1	1G	1499	A
1	1G	1502	A
1	1G	1503	A
1	1G	1504	G
1	1G	1506	U
1	1G	1507	A
1	1G	1517	G
1	1G	1519	A
1	1G	1520	G
1	1G	1525	G
1	1G	1528	U
1	1G	1529	G
1	1G	1530	G
1	1G	1531	A
56	1L	8	U

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Mol	Chain	Res	Type
56	1L	9	A
56	1L	11	C
56	1L	16	U
56	1L	17	C
56	1L	18	G
56	1L	19	G
56	1L	20	U
56	1L	21	A
56	1L	22	G
56	1L	25	C
56	1L	26	A
56	1L	27	G
56	1L	29	G
56	1L	31	A
56	1L	32	PSU
56	1L	34	G
56	1L	37	MIA
56	1L	38	A
56	1L	41	C
56	1L	46	G
56	1L	47	U
56	1L	48	C
56	1L	51	U
56	1L	57	G
56	1L	58	A
56	1L	60	U
56	1L	61	C
56	1L	68	C
56	1L	69	G
56	1L	70	G
56	1L	73	A
56	1L	74	C
56	1L	75	C
56	1L	76	A
23	2L	6	G
23	2L	15	G
23	2L	16	C
23	2L	17	C
23	2L	18	C
23	2L	19	G
23	2L	20	G
23	2L	21	U

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Mol	Chain	Res	Type
23	2L	23	G
23	2L	47	7MG
23	2L	48	U
23	2L	49	C
23	2L	50	G
23	2L	53	G
23	2L	55	5MU
23	2L	57	C
57	3L	2	C
57	3L	4	C
57	3L	9	A
57	3L	13	C
57	3L	16	U
57	3L	17	C
57	3L	18	G
57	3L	19	G
57	3L	20	U
57	3L	21	A
57	3L	22	G
57	3L	26	A
57	3L	31	A
57	3L	32	PSU
57	3L	33	U
57	3L	34	G
57	3L	37	A
57	3L	39	U
57	3L	40	C
57	3L	42	C
57	3L	44	G
57	3L	45	U
57	3L	46	7MG
57	3L	47	U
57	3L	48	C
57	3L	53	G
57	3L	54	5MU
57	3L	55	PSU
57	3L	58	A
57	3L	59	U
57	3L	60	U
57	3L	61	C
57	3L	62	C
57	3L	66	U

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Mol	Chain	Res	Type
57	3L	72	C
57	3L	73	A
57	3L	76	A
25	4L	13	A
25	4L	14	A
25	4L	20	C
25	4L	22	A
26	14	2	G
26	14	3	U
26	14	4	C
26	14	5	A
26	14	9	U
26	14	15	G
26	14	34	C
26	14	35	G
26	14	36	G
26	14	46	C
26	14	49	A
26	14	50	U
26	14	58	G
26	14	70	G
26	14	71	A
26	14	72	U
26	14	74	A
26	14	75	G
26	14	78	A
26	14	84	A
26	14	91	A
26	14	93	C
26	14	95	G
26	14	99	U
26	14	102	G
26	14	118	A
26	14	119	A
26	14	120	U
26	14	125	G
26	14	129	C
26	14	131	G
26	14	138	G
26	14	139	G
26	14	140	A
26	14	153	C

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Mol	Chain	Res	Type
26	14	154	G
26	14	155	C
26	14	161	U
26	14	162	U
26	14	173	G
26	14	174	C
26	14	181	A
26	14	182	A
26	14	196	A
26	14	199	A
26	14	201	C
26	14	205	G
26	14	215	G
26	14	216	A
26	14	221	A
26	14	222	A
26	14	225	A
26	14	229	A
26	14	233	A
26	14	248	G
26	14	249	C
26	14	250	G
26	14	252	G
26	14	265	A
26	14	267	C
26	14	270(K)	C
26	14	270(L)	U
26	14	270(M)	U
26	14	270(N)	G
26	14	270(O)	U
26	14	270(P)	C
26	14	271(B)	G
26	14	271	G
26	14	273(C)	C
26	14	273(D)	C
26	14	274	G
26	14	275	G
26	14	277	C
26	14	278	A
26	14	279	C
26	14	283	A
26	14	289	A

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Mol	Chain	Res	Type
26	14	290	G
26	14	298	G
26	14	299	A
26	14	310	A
26	14	311	A
26	14	324	A
26	14	327	G
26	14	329	G
26	14	330	A
26	14	352	G
26	14	362	U
26	14	363	G
26	14	363(A)	A
26	14	363(E)	U
26	14	363(F)	A
26	14	372	G
26	14	380	U
26	14	382	G
26	14	386	G
26	14	396	G
26	14	405	U
26	14	406	G
26	14	411	G
26	14	412	A
26	14	416	C
26	14	426	C
26	14	428	A
26	14	443	A
26	14	444	C
26	14	448	U
26	14	455	C
26	14	457	A
26	14	470	A
26	14	480	A
26	14	481	G
26	14	498	G
26	14	501	A
26	14	504	U
26	14	505	A
26	14	509	C
26	14	529	A
26	14	531	C

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Mol	Chain	Res	Type
26	14	532	A
26	14	533	G
26	14	537	C
26	14	546	C
26	14	549	G
26	14	556	G
26	14	563	G
26	14	564	C
26	14	573	G
26	14	575	A
26	14	584	C
26	14	586	A
26	14	587	C
26	14	603	A
26	14	606	U
26	14	607	U
26	14	609(A)	G
26	14	614	U
26	14	617	G
26	14	619	G
26	14	620	G
26	14	621	A
26	14	622	G
26	14	627	A
26	14	634	C
26	14	637	A
26	14	645	C
26	14	646	A
26	14	650	C
26	14	651	G
26	14	654	A
26	14	654(E)	C
26	14	654(G)	C
26	14	654(H)	G
26	14	654(I)	C
26	14	654(K)	C
26	14	654(L)	G
26	14	654(O)	G
26	14	654(T)	A
26	14	655	A
26	14	668	G
26	14	669	G

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Mol	Chain	Res	Type
26	14	686	G
26	14	701	G
26	14	708	C
26	14	717	G
26	14	722	A
26	14	730	C
26	14	731	C
26	14	732	C
26	14	738	G
26	14	740	U
26	14	750	A
26	14	752	A
26	14	753	C
26	14	764	A
26	14	765	G
26	14	770	G
26	14	775	G
26	14	776	G
26	14	779	U
26	14	782	A
26	14	784	A
26	14	785	G
26	14	789	A
26	14	792	G
26	14	800	A
26	14	805	G
26	14	812	C
26	14	814	C
26	14	816	C
26	14	819	A
26	14	820	A
26	14	827	U
26	14	828	U
26	14	830	G
26	14	831	G
26	14	832	G
26	14	840	C
26	14	846	C
26	14	848	G
26	14	859	G
26	14	860	U
26	14	863	A

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Mol	Chain	Res	Type
26	14	865	C
26	14	866	A
26	14	874	G
26	14	878	A
26	14	880	G
26	14	881	G
26	14	882	G
26	14	885	C
26	14	886	C
26	14	887	A
26	14	888	C
26	14	889	C
26	14	890	A
26	14	894	C
26	14	896	A
26	14	897	C
26	14	899	A
26	14	900	A
26	14	901	A
26	14	903	C
26	14	904	C
26	14	906	G
26	14	907	U
26	14	910	A
26	14	911	A
26	14	917	A
26	14	918	A
26	14	924	C
26	14	926	A
26	14	932	G
26	14	933	A
26	14	938	G
26	14	941	A
26	14	945	A
26	14	946	G
26	14	958	U
26	14	959	A
26	14	961	C
26	14	974	G
26	14	974(A)	C
26	14	977	G
26	14	980	A

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Mol	Chain	Res	Type
26	14	983	A
26	14	989	G
26	14	990	A
26	14	991	C
26	14	996	A
26	14	1002	G
26	14	1009	A
26	14	1011	G
26	14	1012	U
26	14	1013	C
26	14	1015	G
26	14	1017	G
26	14	1020	A
26	14	1022	G
26	14	1023	U
26	14	1025	G
26	14	1026	U
26	14	1037	G
26	14	1039	G
26	14	1043	C
26	14	1044	G
26	14	1045	A
26	14	1046	A
26	14	1047	G
26	14	1048	A
26	14	1051	G
26	14	1057	A
26	14	1060	U
26	14	1062	G
26	14	1064	C
26	14	1065	U
26	14	1067	A
26	14	1068	G
26	14	1070	A
26	14	1072	C
26	14	1073	A
26	14	1077	A
26	14	1079	C
26	14	1082	U
26	14	1083	U
26	14	1085	A
26	14	1086	A

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Mol	Chain	Res	Type
26	14	1087	G
26	14	1088	A
26	14	1090	U
26	14	1091	G
26	14	1093	G
26	14	1095	A
26	14	1096	A
26	14	1098	A
26	14	1105	U
26	14	1111	A
26	14	1112	G
26	14	1122	G
26	14	1128	A
26	14	1129	A
26	14	1130	U
26	14	1135	C
26	14	1136	G
26	14	1138	G
26	14	1139	G
26	14	1142	U
26	14	1142(A)	A
26	14	1143	A
26	14	1151	G
26	14	1155	A
26	14	1157	G
26	14	1160	G
26	14	1167	U
26	14	1170	G
26	14	1173	G
26	14	1174	A
26	14	1175	U
26	14	1177	A
26	14	1178	C
26	14	1187	G
26	14	1188	U
26	14	1204	A
26	14	1205	U
26	14	1212	G
26	14	1213	A
26	14	1220	A
26	14	1230	C
26	14	1244	G

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Mol	Chain	Res	Type
26	14	1253	A
26	14	1256	G
26	14	1268	A
26	14	1271	G
26	14	1272	A
26	14	1273	U
26	14	1293	C
26	14	1296	G
26	14	1298	C
26	14	1300	U
26	14	1301	A
26	14	1303	G
26	14	1314	C
26	14	1317	A
26	14	1318	C
26	14	1319	G
26	14	1321	A
26	14	1329	U
26	14	1332	G
26	14	1338	G
26	14	1345	C
26	14	1348	G
26	14	1349	A
26	14	1359	A
26	14	1360	A
26	14	1365	A
26	14	1368	G
26	14	1369	G
26	14	1370	C
26	14	1378	A
26	14	1379	A
26	14	1380	G
26	14	1384	A
26	14	1385	G
26	14	1386	C
26	14	1395	A
26	14	1400	G
26	14	1407	C
26	14	1416	G
26	14	1417	C
26	14	1419	A
26	14	1420	U

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Mol	Chain	Res	Type
26	14	1421	G
26	14	1422	G
26	14	1424	G
26	14	1427	A
26	14	1428	C
26	14	1437	C
26	14	1444(A)	A
26	14	1445	C
26	14	1449	A
26	14	1449(A)	G
26	14	1455	G
26	14	1458	C
26	14	1460	A
26	14	1461	G
26	14	1467	C
26	14	1471	A
26	14	1475	G
26	14	1478	G
26	14	1482	U
26	14	1483	G
26	14	1490	A
26	14	1492	G
26	14	1493	C
26	14	1494	A
26	14	1508	A
26	14	1509	C
26	14	1510	A
26	14	1515	C
26	14	1516	U
26	14	1520	U
26	14	1523	U
26	14	1533	C
26	14	1535	U
26	14	1537	C
26	14	1543	A
26	14	1547	C
26	14	1554	A
26	14	1558	A
26	14	1559	G
26	14	1560	G
26	14	1566	A
26	14	1569	A

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Mol	Chain	Res	Type
26	14	1578	U
26	14	1585	C
26	14	1586	A
26	14	1588	C
26	14	1594	G
26	14	1598	C
26	14	1608	A
26	14	1609	A
26	14	1616	A
26	14	1618	A
26	14	1620	G
26	14	1622	G
26	14	1647	G
26	14	1648	C
26	14	1654	A
26	14	1660	C
26	14	1671	U
26	14	1674	G
26	14	1682	G
26	14	1696	G
26	14	1700	A
26	14	1701	A
26	14	1703	G
26	14	1718	G
26	14	1725	G
26	14	1726	G
26	14	1728	G
26	14	1729	A
26	14	1730	U
26	14	1731	G
26	14	1743	G
26	14	1753	G
26	14	1754	C
26	14	1756	G
26	14	1762	A
26	14	1763	G
26	14	1764	G
26	14	1773	A
26	14	1780	A
26	14	1782	C
26	14	1791	A
26	14	1800	C

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Mol	Chain	Res	Type
26	14	1801	G
26	14	1811	G
26	14	1813	G
26	14	1816	G
26	14	1819	A
26	14	1820	U
26	14	1829	A
26	14	1839	G
26	14	1847	A
26	14	1848	A
26	14	1858	G
26	14	1878	G
26	14	1883	G
26	14	1899	G
26	14	1906	G
26	14	1913	A
26	14	1915	U
26	14	1917	U
26	14	1929	G
26	14	1930	G
26	14	1936	A
26	14	1937	A
26	14	1938	A
26	14	1952	A
26	14	1955	U
26	14	1960	A
26	14	1963	U
26	14	1964	G
26	14	1967	C
26	14	1970	A
26	14	1971	A
26	14	1972	A
26	14	1980	G
26	14	1985	G
26	14	1986	A
26	14	1993	U
26	14	2016	U
26	14	2020	A
26	14	2023	G
26	14	2031	A
26	14	2033	A
26	14	2043	C

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Mol	Chain	Res	Type
26	14	2048	G
26	14	2049	G
26	14	2055	C
26	14	2056	G
26	14	2059	A
26	14	2060	A
26	14	2061	G
26	14	2062	A
26	14	2063	C
26	14	2069	G
26	14	2071	A
26	14	2082	A
26	14	2093	G
26	14	2099	U
26	14	2100	G
26	14	2108	C
26	14	2111	C
26	14	2112	G
26	14	2113	U
26	14	2114	A
26	14	2117	A
26	14	2118	U
26	14	2126	A
26	14	2127	G
26	14	2128	C
26	14	2131	G
26	14	2132	U
26	14	2133	G
26	14	2136	C
26	14	2137	C
26	14	2140	C
26	14	2144	U
26	14	2145	C
26	14	2146	C
26	14	2147	G
26	14	2150	U
26	14	2157	G
26	14	2158	A
26	14	2165	G
26	14	2166	G
26	14	2167	U
26	14	2168	G

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Mol	Chain	Res	Type
26	14	2173	A
26	14	2174	C
26	14	2189	U
26	14	2191	G
26	14	2192	G
26	14	2198	A
26	14	2207	C
26	14	2210	G
26	14	2211	G
26	14	2212	A
26	14	2213	U
26	14	2215	G
26	14	2225	A
26	14	2226	C
26	14	2236	C
26	14	2238	G
26	14	2239	G
26	14	2245	U
26	14	2246	G
26	14	2249	U
26	14	2253	G
26	14	2267	A
26	14	2268	A
26	14	2269	A
26	14	2273	A
26	14	2275	C
26	14	2276	G
26	14	2278	A
26	14	2280	G
26	14	2281	C
26	14	2283	C
26	14	2286	A
26	14	2287	A
26	14	2294	C
26	14	2298	A
26	14	2307	G
26	14	2308	G
26	14	2310	A
26	14	2311	A
26	14	2318	G
26	14	2321	G
26	14	2325	G

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Mol	Chain	Res	Type
26	14	2327	A
26	14	2334	G
26	14	2335	A
26	14	2336	A
26	14	2342	C
26	14	2346	A
26	14	2347	C
26	14	2350	C
26	14	2353	G
26	14	2354	G
26	14	2355	C
26	14	2360	A
26	14	2372	G
26	14	2383	G
26	14	2385	C
26	14	2388	A
26	14	2389	G
26	14	2392	A
26	14	2395	C
26	14	2396	G
26	14	2401	U
26	14	2402	C
26	14	2403	C
26	14	2406	U
26	14	2407	G
26	14	2411	A
26	14	2413	G
26	14	2414	G
26	14	2418	A
26	14	2422	A
26	14	2424	C
26	14	2425	A
26	14	2428	G
26	14	2429	G
26	14	2430	A
26	14	2431	U
26	14	2435	A
26	14	2439	A
26	14	2440	C
26	14	2441	C
26	14	2447	G
26	14	2448	A

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Mol	Chain	Res	Type
26	14	2449	U
26	14	2469	A
26	14	2470	G
26	14	2472	G
26	14	2474	C
26	14	2475	C
26	14	2476	A
26	14	2477	C
26	14	2478	A
26	14	2482	G
26	14	2484	G
26	14	2486	G
26	14	2496	C
26	14	2497	A
26	14	2498	C
26	14	2502	G
26	14	2505	G
26	14	2506	U
26	14	2507	C
26	14	2518	A
26	14	2520	C
26	14	2528	U
26	14	2529	G
26	14	2532	G
26	14	2536	G
26	14	2542	A
26	14	2543	G
26	14	2554	U
26	14	2555	U
26	14	2566	A
26	14	2567	G
26	14	2569	G
26	14	2573	C
26	14	2579	C
26	14	2584	U
26	14	2585	U
26	14	2602	A
26	14	2603	G
26	14	2609	U
26	14	2611	U
26	14	2612	C
26	14	2613	U

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Mol	Chain	Res	Type
26	14	2615	U
26	14	2617	C
26	14	2630	G
26	14	2636	U
26	14	2641	G
26	14	2665	A
26	14	2667	C
26	14	2670	A
26	14	2673	G
26	14	2682	U
26	14	2689	U
26	14	2690	C
26	14	2700	C
26	14	2702	U
26	14	2703	C
26	14	2704	C
26	14	2707	G
26	14	2709	G
26	14	2712(A)	A
26	14	2713	A
26	14	2726	U
26	14	2733	A
26	14	2739	U
26	14	2744	G
26	14	2750	A
26	14	2751	G
26	14	2752	C
26	14	2754	U
26	14	2758	A
26	14	2761	G
26	14	2762	G
26	14	2764	A
26	14	2765	A
26	14	2766	G
26	14	2769	C
26	14	2777	G
26	14	2778	A
26	14	2779	U
26	14	2786	U
26	14	2787	C
26	14	2790	A
26	14	2791	C

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Mol	Chain	Res	Type
26	14	2794	C
26	14	2795	G
26	14	2797	U
26	14	2798	C
26	14	2818	G
26	14	2820	A
26	14	2821	A
26	14	2833	G
26	14	2834	G
26	14	2849	U
26	14	2860	A
26	14	2872	G
26	14	2873	A
26	14	2880	C
26	14	2885	C
26	14	2886	G
26	14	2894	G
26	14	2896	C
26	14	2898	U
27	1J	0	A
27	1J	7	G
27	1J	8	U
27	1J	13	A
27	1J	15	A
27	1J	16	G
27	1J	19	G
27	1J	22	U
27	1J	24	G
27	1J	29	A
27	1J	30	C
27	1J	40	U
27	1J	41	U
27	1J	42	C
27	1J	45	A
27	1J	47	C
27	1J	53	A
27	1J	58	A
27	1J	63	G
27	1J	64	C
27	1J	73	A
27	1J	75	G
27	1J	76	G

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Mol	Chain	Res	Type
27	1J	81	G
27	1J	88	C
27	1J	89	G
27	1J	89(A)	A
27	1J	90	C
27	1J	97	G
27	1J	99	A
27	1J	100	G
27	1J	101	A
27	1J	108	C
27	1J	109	G
27	1J	114	G

All (197) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	13	5	U
1	13	50	A
1	13	115	G
1	13	190	G
1	13	244	U
1	13	266	G
1	13	412	A
1	13	413	G
1	13	428	G
1	13	429	U
1	13	484	G
1	13	496	A
1	13	509	A
1	13	560	U
1	13	687	A
1	13	703	G
1	13	748	C
1	13	793	U
1	13	812	C
1	13	991	U
1	13	992	U
1	13	1027	C
1	13	1053	G
1	13	1054	C
1	13	1064	G
1	13	1065	U

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Mol	Chain	Res	Type
1	13	1285	A
1	13	1300	G
1	13	1302	U
1	13	1322	C
1	13	1336	C
1	13	1452	C
1	13	1498	U
1	13	1504	G
22	1K	9	A
22	1K	10	G
22	1K	18	G
23	2K	21	U
23	2K	48	U
24	3K	2	C
24	3K	8	U
24	3K	18	G
24	3K	46	G
24	3K	58	A
24	3K	60	U
26	1H	33	U
26	1H	125	G
26	1H	196	A
26	1H	199	A
26	1H	222	A
26	1H	229	A
26	1H	249	C
26	1H	271(B)	G
26	1H	404	C
26	1H	456	C
26	1H	481	G
26	1H	508	G
26	1H	587	C
26	1H	685	A
26	1H	752	A
26	1H	764	A
26	1H	776	G
26	1H	880	G
26	1H	974	G
26	1H	974(A)	C
26	1H	1022	G
26	1H	1026	U
26	1H	1060	U

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Mol	Chain	Res	Type
26	1H	1085	A
26	1H	1110	G
26	1H	1178	C
26	1H	1312	U
26	1H	1420	U
26	1H	1427	A
26	1H	1460	A
26	1H	1508	A
26	1H	1558	A
26	1H	1608	A
26	1H	1609	A
26	1H	1617	C
26	1H	1694	C
26	1H	1757	U
26	1H	1799	G
26	1H	1900	A
26	1H	2062	A
26	1H	2157	G
26	1H	2171	A
26	1H	2199	A
26	1H	2428	G
26	1H	2439	A
26	1H	2447	G
26	1H	2475	C
26	1H	2481	G
26	1H	2566	A
26	1H	2611	U
26	1H	2756	U
27	16	108	C
1	1G	64	G
1	1G	115	G
1	1G	197	A
1	1G	250	A
1	1G	266	G
1	1G	327	A
1	1G	328	C
1	1G	345	C
1	1G	412	A
1	1G	429	U
1	1G	485	G
1	1G	509	A
1	1G	560	U

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Mol	Chain	Res	Type
1	1G	561	U
1	1G	632	A
1	1G	687	A
1	1G	723	U
1	1G	748	C
1	1G	793	U
1	1G	812	C
1	1G	884	U
1	1G	913	A
1	1G	992	U
1	1G	1053	G
1	1G	1054	C
1	1G	1128	C
1	1G	1137	C
1	1G	1145	C
1	1G	1157	A
1	1G	1285	A
1	1G	1297	C
1	1G	1298	C
1	1G	1300	G
1	1G	1346	A
1	1G	1400	C
1	1G	1453	G
1	1G	1498	U
56	1L	10	G
56	1L	18	G
56	1L	19	G
23	2L	48	U
57	3L	8	4SU
57	3L	32	PSU
57	3L	52	G
57	3L	58	A
25	4L	12	A
26	14	34	C
26	14	49	A
26	14	101	G
26	14	128	C
26	14	199	A
26	14	278	A
26	14	310	A
26	14	503	A
26	14	575	A

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Mol	Chain	Res	Type
26	14	627	A
26	14	752	A
26	14	764	A
26	14	784	A
26	14	893	C
26	14	974	G
26	14	990	A
26	14	1022	G
26	14	1085	A
26	14	1141	U
26	14	1378	A
26	14	1396	U
26	14	1416	G
26	14	1420	U
26	14	1427	A
26	14	1460	A
26	14	1558	A
26	14	1608	A
26	14	1647	G
26	14	1819	A
26	14	1963	U
26	14	1984	G
26	14	2062	A
26	14	2157	G
26	14	2191	G
26	14	2211	G
26	14	2212	A
26	14	2225	A
26	14	2275	C
26	14	2335	A
26	14	2402	C
26	14	2406	U
26	14	2439	A
26	14	2447	G
26	14	2506	U
26	14	2602	A
26	14	2611	U
26	14	2629	A
26	14	2689	U
26	14	2776	A
26	14	2790	A
26	14	2859	G

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Mol	Chain	Res	Type
26	14	2893	G
27	1J	56	G
27	1J	88	C

5.4 Non-standard residues in protein, DNA, RNA chains (i)

28 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
57	4SU	3L	8	57	18,21,22	2.14	5 (27%)	25,30,33	2.03	5 (20%)
57	PSU	3L	32	57	18,21,22	1.33	2 (11%)	21,30,33	2.10	7 (33%)
22	4SU	1K	8	22	18,21,22	1.91	5 (27%)	25,30,33	2.23	5 (20%)
22	5MU	1K	54	22	19,22,23	4.00	5 (26%)	27,32,35	3.20	10 (37%)
23	7MG	2L	47	23	23,26,27	3.24	6 (26%)	27,39,42	2.79	11 (40%)
57	5MU	3L	54	57	19,22,23	4.03	5 (26%)	27,32,35	3.05	11 (40%)
56	PSU	1L	32	56	18,21,22	1.27	1 (5%)	21,30,33	1.87	5 (23%)
23	4SU	2K	8	23	18,21,22	1.81	3 (16%)	25,30,33	3.22	5 (20%)
56	MIA	1L	37	56	28,31,32	2.32	5 (17%)	38,44,47	3.18	12 (31%)
56	5MU	1L	54	56	19,22,23	4.10	5 (26%)	27,32,35	3.09	7 (25%)
23	7MG	2K	47	23	23,26,27	3.10	7 (30%)	27,39,42	2.65	9 (33%)
23	OMC	2L	33	23	19,22,23	1.80	3 (15%)	25,31,34	1.28	4 (16%)
57	7MG	3L	46	57	23,26,27	3.37	7 (30%)	27,39,42	2.78	11 (40%)
22	PSU	1K	39	22	18,21,22	1.21	2 (11%)	21,30,33	1.89	4 (19%)
57	PSU	3L	55	57	18,21,22	1.30	1 (5%)	21,30,33	1.56	4 (19%)
24	PSU	3K	39	24	18,21,22	1.29	1 (5%)	21,30,33	1.57	3 (14%)
24	PSU	3K	32	24	18,21,22	1.37	1 (5%)	21,30,33	1.86	4 (19%)
23	4SU	2L	8	23	18,21,22	2.06	5 (27%)	25,30,33	2.53	5 (20%)
23	5MU	2K	55	58,23	19,22,23	4.05	5 (26%)	27,32,35	3.41	8 (29%)
23	5MU	2L	55	23	19,22,23	4.13	5 (26%)	27,32,35	3.43	11 (40%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
23	PSU	2L	56	23	18,21,22	1.49	2 (11%)	21,30,33	1.88	2 (9%)
24	MIA	3K	37	58,24	28,31,32	2.51	6 (21%)	38,44,47	2.65	11 (28%)
23	PSU	2K	56	23	18,21,22	1.07	1 (5%)	21,30,33	2.18	4 (19%)
56	PSU	1L	39	56	18,21,22	1.14	1 (5%)	21,30,33	1.55	5 (23%)
22	PSU	1K	32	58,22	18,21,22	1.53	2 (11%)	21,30,33	1.86	4 (19%)
22	PSU	1K	55	22	18,21,22	1.45	2 (11%)	21,30,33	1.46	4 (19%)
23	OMC	2K	33	23	19,22,23	1.92	3 (15%)	25,31,34	1.15	2 (8%)
22	MIA	1K	37	22	28,31,32	2.38	4 (14%)	38,44,47	3.37	13 (34%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
57	4SU	3L	8	57	-	0/7/25/26	0/2/2/2
57	PSU	3L	32	57	-	1/7/25/26	0/2/2/2
22	4SU	1K	8	22	-	0/7/25/26	0/2/2/2
22	5MU	1K	54	22	-	0/7/25/26	0/2/2/2
23	7MG	2L	47	23	-	0/7/37/38	0/3/3/3
57	5MU	3L	54	57	-	2/7/25/26	0/2/2/2
56	PSU	1L	32	56	-	1/7/25/26	0/2/2/2
23	4SU	2K	8	23	-	0/7/25/26	0/2/2/2
56	MIA	1L	37	56	-	9/15/33/34	0/3/3/3
56	5MU	1L	54	56	-	0/7/25/26	0/2/2/2
23	7MG	2K	47	23	-	2/7/37/38	0/3/3/3
23	OMC	2L	33	23	-	0/9/27/28	0/2/2/2
57	7MG	3L	46	57	-	0/7/37/38	0/3/3/3
22	PSU	1K	39	22	-	0/7/25/26	0/2/2/2
57	PSU	3L	55	57	-	0/7/25/26	0/2/2/2
24	PSU	3K	39	24	-	4/7/25/26	0/2/2/2
24	PSU	3K	32	24	-	0/7/25/26	0/2/2/2
23	4SU	2L	8	23	-	2/7/25/26	0/2/2/2
23	5MU	2K	55	58,23	-	0/7/25/26	0/2/2/2
23	5MU	2L	55	23	-	3/7/25/26	0/2/2/2
23	PSU	2L	56	23	-	0/7/25/26	0/2/2/2
24	MIA	3K	37	58,24	-	7/15/33/34	0/3/3/3
23	PSU	2K	56	23	-	0/7/25/26	0/2/2/2
56	PSU	1L	39	56	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
22	PSU	1K	32	58,22	-	0/7/25/26	0/2/2/2
22	PSU	1K	55	22	-	3/7/25/26	0/2/2/2
23	OMC	2K	33	23	-	0/9/27/28	0/2/2/2
22	MIA	1K	37	22	-	2/15/33/34	0/3/3/3

All (100) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	2K	55	5MU	C2-N1	13.42	1.59	1.38
56	1L	54	5MU	C2-N1	13.39	1.59	1.38
23	2L	55	5MU	C2-N1	13.33	1.59	1.38
22	1K	54	5MU	C2-N1	12.46	1.58	1.38
57	3L	54	5MU	C2-N1	12.32	1.57	1.38
57	3L	46	7MG	C5-N7	8.99	1.47	1.35
22	1K	37	MIA	C13-C14	8.91	1.59	1.32
57	3L	46	7MG	C4-N9	-8.82	1.27	1.37
24	3K	37	MIA	C13-C14	8.69	1.58	1.32
23	2L	47	7MG	C4-N9	-8.47	1.27	1.37
56	1L	37	MIA	C13-C14	8.44	1.57	1.32
23	2K	47	7MG	C4-N9	-7.90	1.28	1.37
23	2L	47	7MG	C5-N7	7.86	1.45	1.35
24	3K	37	MIA	C6-N6	7.83	1.46	1.34
23	2K	47	7MG	C5-N7	7.52	1.45	1.35
22	1K	37	MIA	C6-N6	6.86	1.45	1.34
57	3L	8	4SU	C5-C4	6.63	1.50	1.42
57	3L	54	5MU	C6-N1	6.44	1.49	1.38
23	2K	55	5MU	C2-N3	6.42	1.49	1.38
56	1L	54	5MU	C2-N3	6.37	1.49	1.38
56	1L	54	5MU	C6-N1	6.35	1.48	1.38
57	3L	54	5MU	C2-N3	6.34	1.49	1.38
22	1K	54	5MU	C6-N1	6.31	1.48	1.38
23	2L	47	7MG	C4-N3	6.24	1.48	1.34
22	1K	54	5MU	C2-N3	6.23	1.48	1.38
23	2L	8	4SU	C5-C4	6.22	1.50	1.42
23	2L	55	5MU	C2-N3	6.20	1.48	1.38
23	2L	55	5MU	C4-C5	6.15	1.54	1.44
57	3L	54	5MU	C4-C5	6.04	1.54	1.44
56	1L	37	MIA	C6-N6	6.04	1.43	1.34
23	2L	55	5MU	C4-N3	-5.88	1.27	1.38
22	1K	8	4SU	C5-C4	5.82	1.49	1.42
23	2K	55	5MU	C6-N1	5.80	1.47	1.38
22	1K	54	5MU	C4-C5	5.70	1.54	1.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	2K	47	7MG	C4-N3	5.67	1.47	1.34
22	1K	54	5MU	C4-N3	-5.65	1.28	1.38
57	3L	46	7MG	C4-N3	5.63	1.47	1.34
57	3L	54	5MU	C4-N3	-5.57	1.28	1.38
56	1L	54	5MU	C4-N3	-5.56	1.28	1.38
23	2L	55	5MU	C6-N1	5.55	1.47	1.38
23	2K	8	4SU	C5-C4	5.48	1.49	1.42
23	2K	33	OMC	C2-N3	5.42	1.47	1.36
23	2K	55	5MU	C4-N3	-5.40	1.28	1.38
23	2L	33	OMC	C2-N3	5.01	1.46	1.36
22	1K	32	PSU	C6-C5	4.99	1.40	1.35
56	1L	54	5MU	C4-C5	4.98	1.52	1.44
23	2K	55	5MU	C4-C5	4.93	1.52	1.44
57	3L	46	7MG	C8-N7	4.93	1.66	1.42
22	1K	55	PSU	C6-C5	4.89	1.40	1.35
23	2L	47	7MG	C8-N7	4.88	1.65	1.42
24	3K	32	PSU	C6-C5	4.85	1.40	1.35
23	2K	47	7MG	C8-N7	4.84	1.65	1.42
23	2L	56	PSU	C6-C5	4.83	1.40	1.35
23	2L	47	7MG	C5-C4	-4.81	1.23	1.37
57	3L	46	7MG	C5-C4	-4.69	1.23	1.37
24	3K	39	PSU	C6-C5	4.52	1.40	1.35
56	1L	32	PSU	C6-C5	4.50	1.40	1.35
23	2K	47	7MG	C5-C4	-4.46	1.24	1.37
23	2K	33	OMC	C4-N4	4.36	1.44	1.33
57	3L	32	PSU	C6-C5	4.36	1.40	1.35
56	1L	37	MIA	C2-S10	4.34	1.79	1.75
57	3L	55	PSU	C6-C5	4.34	1.40	1.35
23	2L	33	OMC	C4-N4	4.26	1.44	1.33
57	3L	8	4SU	C2-N1	4.06	1.44	1.38
22	1K	39	PSU	C6-C5	4.00	1.39	1.35
22	1K	8	4SU	C2-N1	3.65	1.44	1.38
23	2K	33	OMC	C5-C4	3.64	1.51	1.42
23	2L	8	4SU	C2-N1	3.63	1.44	1.38
56	1L	39	PSU	C6-C5	3.62	1.39	1.35
24	3K	37	MIA	C2-S10	3.41	1.78	1.75
23	2L	47	7MG	C2-N2	3.37	1.42	1.34
23	2L	33	OMC	C5-C4	3.35	1.50	1.42
23	2K	56	PSU	C6-C5	3.28	1.38	1.35
23	2K	8	4SU	C2-N1	3.23	1.43	1.38
23	2L	8	4SU	C6-N1	3.22	1.45	1.38
57	3L	8	4SU	C6-N1	3.11	1.45	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
57	3L	46	7MG	C2-N2	3.05	1.41	1.34
23	2L	56	PSU	C2-N1	3.00	1.40	1.36
23	2K	47	7MG	C8-N9	2.89	1.47	1.45
22	1K	37	MIA	C15-C14	2.80	1.57	1.50
23	2K	47	7MG	C2-N2	2.80	1.40	1.34
23	2L	8	4SU	C4-N3	2.75	1.40	1.37
22	1K	32	PSU	C2-N1	2.73	1.40	1.36
22	1K	37	MIA	C5-N7	-2.63	1.34	1.39
22	1K	8	4SU	C6-N1	2.61	1.44	1.38
23	2K	8	4SU	C6-N1	2.59	1.44	1.38
57	3L	46	7MG	C5-C6	2.53	1.49	1.43
22	1K	55	PSU	C2-N1	2.34	1.39	1.36
24	3K	37	MIA	C5-C4	2.33	1.43	1.39
24	3K	37	MIA	C15-C14	2.29	1.56	1.50
24	3K	37	MIA	C5-N7	-2.29	1.34	1.39
57	3L	32	PSU	O4'-C1'	-2.28	1.40	1.43
57	3L	8	4SU	C4-N3	2.27	1.40	1.37
57	3L	8	4SU	C2-N3	2.25	1.41	1.38
22	1K	8	4SU	C2-N3	2.22	1.41	1.38
22	1K	8	4SU	C4-N3	2.21	1.39	1.37
56	1L	37	MIA	C5-N7	-2.13	1.35	1.39
22	1K	39	PSU	C4-C5	-2.09	1.38	1.44
23	2L	8	4SU	C2-N3	2.09	1.41	1.38
56	1L	37	MIA	C5-C4	2.05	1.42	1.39

All (186) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
22	1K	37	MIA	C11-S10-C2	11.78	111.09	102.25
22	1K	54	5MU	C5-C4-N3	11.12	124.99	115.32
23	2K	55	5MU	C5-C4-N3	11.01	124.89	115.32
56	1L	37	MIA	C11-S10-C2	10.99	110.49	102.25
23	2K	8	4SU	C4-N3-C2	-10.38	117.36	127.31
56	1L	54	5MU	C5-C4-N3	10.19	124.18	115.32
22	1K	37	MIA	C12-C13-C14	-9.80	109.42	127.01
57	3L	54	5MU	C5-C4-N3	9.25	123.36	115.32
24	3K	37	MIA	C12-C13-C14	-9.04	110.78	127.01
23	2K	8	4SU	C5-C4-N3	8.97	123.09	114.75
23	2L	55	5MU	C5-C4-N3	8.86	123.02	115.32
56	1L	37	MIA	C12-C13-C14	-8.41	111.91	127.01
23	2L	8	4SU	C4-N3-C2	-8.12	119.53	127.31
23	2L	47	7MG	C4-C5-N7	7.91	114.73	105.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
23	2K	47	7MG	C4-C5-N7	7.88	114.69	105.38
24	3K	37	MIA	C5-C4-N3	-7.70	119.06	127.18
56	1L	37	MIA	C5-C4-N3	-7.62	119.16	127.18
23	2L	55	5MU	C6-C5-C4	7.58	124.27	118.02
57	3L	46	7MG	C5-C4-N9	7.48	115.92	106.33
22	1K	37	MIA	C5-C4-N3	-7.26	119.53	127.18
22	1K	8	4SU	C4-N3-C2	-7.19	120.42	127.31
23	2K	55	5MU	O4-C4-C5	-7.08	116.82	124.92
23	2L	55	5MU	C4-N3-C2	-6.71	118.55	127.34
23	2K	55	5MU	C4-N3-C2	-6.60	118.69	127.34
57	3L	8	4SU	C4-N3-C2	-6.59	121.00	127.31
57	3L	46	7MG	C4-C5-N7	6.24	112.75	105.38
23	2L	55	5MU	C5-C6-N1	-6.22	116.55	123.31
23	2L	8	4SU	C5-C4-N3	6.01	120.34	114.75
23	2K	47	7MG	C5-C4-N9	5.98	114.00	106.33
22	1K	54	5MU	C4-N3-C2	-5.95	119.54	127.34
56	1L	54	5MU	O4-C4-C5	-5.76	118.33	124.92
23	2K	55	5MU	C6-C5-C4	5.72	122.74	118.02
23	2K	55	5MU	C5-C6-N1	-5.67	117.15	123.31
23	2L	47	7MG	C5-C4-N9	5.65	113.57	106.33
57	3L	54	5MU	C4-N3-C2	-5.52	120.10	127.34
23	2K	8	4SU	C5-C4-S4	-5.49	118.03	124.31
56	1L	54	5MU	C4-N3-C2	-5.44	120.20	127.34
23	2K	56	PSU	C4-N3-C2	-5.32	119.04	126.37
22	1K	37	MIA	N3-C4-N9	5.28	133.69	126.99
22	1K	54	5MU	C5-C6-N1	-5.24	117.63	123.31
23	2L	8	4SU	C5-C4-S4	-5.12	118.45	124.31
56	1L	37	MIA	N3-C4-N9	5.11	133.48	126.99
23	2L	55	5MU	C5M-C5-C6	-5.11	115.93	122.85
23	2L	56	PSU	C4-N3-C2	-5.05	119.42	126.37
57	3L	54	5MU	C5M-C5-C6	-5.02	116.06	122.85
23	2K	56	PSU	N1-C2-N3	4.97	120.42	115.17
22	1K	8	4SU	C5-C4-N3	4.92	119.33	114.75
56	1L	32	PSU	C4-N3-C2	-4.84	119.70	126.37
57	3L	46	7MG	C5-C6-N1	4.74	119.29	110.94
56	1L	54	5MU	C6-C5-C4	4.72	121.91	118.02
23	2L	47	7MG	C5-C6-N1	4.71	119.24	110.94
22	1K	54	5MU	O4-C4-C5	-4.71	119.53	124.92
24	3K	32	PSU	N1-C2-N3	4.68	120.10	115.17
56	1L	32	PSU	N1-C2-N3	4.67	120.09	115.17
22	1K	37	MIA	C5-N7-C8	4.67	110.78	103.45
24	3K	37	MIA	N3-C4-N9	4.63	132.87	126.99

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
57	3L	32	PSU	N1-C2-N3	4.63	120.05	115.17
23	2K	47	7MG	C6-C5-N7	-4.62	124.77	131.93
22	1K	39	PSU	C4-N3-C2	-4.62	120.01	126.37
22	1K	32	PSU	N1-C2-N3	4.60	120.02	115.17
57	3L	54	5MU	C6-C5-C4	4.58	121.79	118.02
57	3L	32	PSU	C4-N3-C2	-4.56	120.08	126.37
24	3K	32	PSU	C4-N3-C2	-4.56	120.09	126.37
23	2K	56	PSU	O2-C2-N1	-4.55	118.10	122.79
22	1K	39	PSU	N1-C2-N3	4.52	119.93	115.17
22	1K	32	PSU	C4-N3-C2	-4.47	120.21	126.37
22	1K	54	5MU	C5M-C5-C6	-4.45	116.83	122.85
56	1L	54	5MU	C5-C6-N1	-4.45	118.48	123.31
23	2K	8	4SU	N3-C2-N1	4.40	120.62	114.89
57	3L	8	4SU	C5-C4-N3	4.38	118.82	114.75
57	3L	54	5MU	C5-C6-N1	-4.33	118.61	123.31
56	1L	37	MIA	C15-C14-C13	-4.19	110.07	122.66
24	3K	37	MIA	C4-C5-N7	-4.18	105.80	110.58
22	1K	8	4SU	C5-C4-S4	-4.18	119.53	124.31
56	1L	39	PSU	C4-N3-C2	-4.16	120.65	126.37
57	3L	8	4SU	N3-C2-N1	4.13	120.27	114.89
23	2L	47	7MG	N9-C8-N7	-4.12	97.53	103.37
23	2L	56	PSU	N1-C2-N3	4.12	119.52	115.17
22	1K	37	MIA	C4-C5-N7	-4.11	105.89	110.58
57	3L	46	7MG	C2-N3-C4	4.10	119.36	112.30
56	1L	54	5MU	C5M-C5-C6	-4.06	117.36	122.85
23	2L	8	4SU	N3-C2-N1	4.05	120.17	114.89
23	2L	47	7MG	C6-C5-N7	-4.04	125.66	131.93
22	1K	37	MIA	N9-C8-N7	-4.04	108.21	113.94
57	3L	55	PSU	C4-N3-C2	-3.97	120.90	126.37
22	1K	54	5MU	C6-C5-C4	3.97	121.29	118.02
23	2L	55	5MU	N3-C2-N1	3.95	120.03	114.89
24	3K	39	PSU	N1-C2-N3	3.95	119.33	115.17
57	3L	54	5MU	C6-N1-C2	-3.92	117.40	121.30
23	2L	47	7MG	C2-N3-C4	3.89	119.00	112.30
24	3K	39	PSU	C4-N3-C2	-3.88	121.02	126.37
23	2K	47	7MG	C5-C6-N1	3.85	117.72	110.94
23	2K	55	5MU	C5M-C5-C6	-3.82	117.69	122.85
22	1K	8	4SU	N3-C2-N1	3.81	119.85	114.89
23	2L	55	5MU	C6-N1-C2	-3.78	117.54	121.30
24	3K	37	MIA	C5-N7-C8	3.76	109.36	103.45
56	1L	37	MIA	C6-C5-N7	3.76	136.53	132.43
57	3L	54	5MU	O4-C4-C5	-3.71	120.67	124.92

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
56	1L	37	MIA	C5-N7-C8	3.64	109.16	103.45
57	3L	46	7MG	N9-C8-N7	-3.64	98.22	103.37
23	2K	47	7MG	N9-C8-N7	-3.61	98.26	103.37
23	2L	55	5MU	O4-C4-C5	-3.57	120.83	124.92
56	1L	37	MIA	C4-C5-N7	-3.50	106.58	110.58
22	1K	32	PSU	C6-N1-C2	-3.48	119.46	122.69
56	1L	37	MIA	C2-N3-C4	3.47	121.38	112.29
57	3L	54	5MU	O2-C2-N1	-3.47	118.28	122.80
56	1L	54	5MU	C6-N1-C2	-3.47	117.85	121.30
23	2L	47	7MG	O6-C6-C5	-3.45	119.16	127.62
57	3L	46	7MG	N2-C2-N1	3.36	123.85	116.76
56	1L	37	MIA	C16-C14-C13	-3.36	112.58	122.66
23	2L	33	OMC	N4-C4-N3	3.31	123.84	117.91
22	1K	55	PSU	C4-N3-C2	-3.31	121.80	126.37
22	1K	37	MIA	C4-C5-C6	3.31	119.53	116.78
57	3L	55	PSU	N1-C2-N3	3.25	118.59	115.17
57	3L	32	PSU	O4'-C1'-C2'	3.24	109.64	105.15
24	3K	37	MIA	C16-C14-C13	-3.19	113.09	122.66
23	2L	47	7MG	C5-C4-N3	-3.18	122.17	128.13
57	3L	54	5MU	C5M-C5-C4	3.15	122.15	118.78
22	1K	37	MIA	C16-C14-C13	-3.07	113.43	122.66
22	1K	39	PSU	C6-N1-C2	-3.07	119.84	122.69
22	1K	55	PSU	N1-C2-N3	3.05	118.39	115.17
24	3K	32	PSU	C6-N1-C2	-3.04	119.87	122.69
23	2K	47	7MG	O6-C6-C5	-3.04	120.17	127.62
22	1K	37	MIA	C15-C14-C13	-3.03	113.57	122.66
23	2K	47	7MG	C5-C4-N3	-3.01	122.49	128.13
57	3L	46	7MG	N9-C4-N3	-2.99	121.08	125.46
23	2L	33	OMC	C5-C4-N4	-2.97	115.44	120.63
24	3K	37	MIA	C2-N3-C4	2.96	120.05	112.29
57	3L	54	5MU	N3-C2-N1	2.95	118.73	114.89
23	2K	33	OMC	N4-C4-N3	2.92	123.12	117.91
22	1K	54	5MU	C5M-C5-C4	2.90	121.88	118.78
56	1L	37	MIA	N3-C2-N1	-2.86	121.79	127.00
23	2L	8	4SU	O2-C2-N1	-2.84	119.10	122.80
23	2L	55	5MU	C1'-N1-C6	2.79	125.75	121.15
56	1L	39	PSU	N1-C2-N3	2.79	118.11	115.17
23	2K	47	7MG	C2-N1-C6	-2.78	120.06	125.11
24	3K	37	MIA	C15-C14-C13	-2.78	114.32	122.66
57	3L	46	7MG	C5-C4-N3	-2.73	123.01	128.13
23	2K	56	PSU	C6-N1-C2	-2.72	120.16	122.69
24	3K	37	MIA	C6-C5-N7	2.72	135.39	132.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
57	3L	46	7MG	C2-N1-C6	-2.71	120.20	125.11
23	2K	47	7MG	C2-N3-C4	2.67	116.91	112.30
22	1K	54	5MU	O2-C2-N1	-2.63	119.37	122.80
22	1K	55	PSU	C6-N1-C2	-2.63	120.25	122.69
57	3L	32	PSU	O2-C2-N1	-2.59	120.12	122.79
23	2L	47	7MG	C2-N1-C6	-2.59	120.42	125.11
57	3L	32	PSU	C6-N1-C2	-2.54	120.33	122.69
23	2L	55	5MU	O2-C2-N1	-2.53	119.51	122.80
57	3L	32	PSU	C3'-C2'-C1'	2.51	104.65	101.69
57	3L	46	7MG	O6-C6-C5	-2.51	121.47	127.62
23	2L	33	OMC	C1'-N1-C2	2.49	123.94	118.44
22	1K	54	5MU	O4-C4-N3	-2.46	115.48	120.11
57	3L	8	4SU	C5-C4-S4	-2.45	121.51	124.31
22	1K	37	MIA	C4-N9-C8	2.44	108.30	105.74
24	3K	37	MIA	C4-C5-C6	2.44	118.81	116.78
24	3K	32	PSU	O2-C2-N1	-2.44	120.28	122.79
57	3L	46	7MG	C6-C5-C4	-2.40	118.17	122.40
24	3K	39	PSU	C6-N1-C2	-2.40	120.46	122.69
23	2L	33	OMC	C1'-N1-C6	-2.38	115.69	120.78
22	1K	37	MIA	C2-N3-C4	2.36	118.46	112.29
23	2K	55	5MU	C6-N1-C2	-2.35	118.96	121.30
23	2K	33	OMC	C5-C4-N4	-2.31	116.59	120.63
57	3L	55	PSU	O4'-C1'-C2'	2.29	108.32	105.15
22	1K	55	PSU	O2-C2-N1	-2.27	120.44	122.79
57	3L	8	4SU	O2-C2-N1	-2.26	119.85	122.80
57	3L	55	PSU	O2-C2-N1	-2.26	120.46	122.79
22	1K	8	4SU	O2-C2-N1	-2.25	119.87	122.80
56	1L	32	PSU	C6-N1-C2	-2.25	120.60	122.69
56	1L	39	PSU	C6-C5-C4	-2.24	116.66	118.17
56	1L	32	PSU	O2-C2-N1	-2.21	120.51	122.79
57	3L	54	5MU	O4-C4-N3	-2.21	115.96	120.11
22	1K	32	PSU	O2-C2-N1	-2.14	120.58	122.79
56	1L	37	MIA	N9-C8-N7	-2.14	110.90	113.94
56	1L	32	PSU	O4'-C1'-C2'	2.14	108.11	105.15
57	3L	32	PSU	C6-C5-C4	2.12	119.61	118.17
23	2L	55	5MU	O4-C4-N3	-2.12	116.13	120.11
22	1K	39	PSU	O2-C2-N1	-2.07	120.66	122.79
24	3K	37	MIA	C5-C4-N9	2.06	108.06	105.81
56	1L	39	PSU	O2-C2-N1	-2.06	120.66	122.79
23	2L	47	7MG	N2-C2-N1	2.05	121.09	116.76
23	2L	47	7MG	N1-C2-N3	-2.05	119.57	123.32
23	2K	55	5MU	N3-C2-N1	2.04	117.55	114.89

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
22	1K	37	MIA	C1'-N9-C8	-2.04	122.57	127.09
56	1L	39	PSU	C5-C4-N3	2.04	121.03	116.55
23	2K	8	4SU	C1'-N1-C2	2.03	121.24	117.59
22	1K	54	5MU	C6-N1-C2	-2.03	119.28	121.30

There are no chirality outliers.

All (36) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
24	3K	37	MIA	C4'-C5'-O5'-P
24	3K	37	MIA	O4'-C4'-C5'-O5'
24	3K	37	MIA	C3'-C4'-C5'-O5'
24	3K	37	MIA	C5-C6-N6-C12
24	3K	37	MIA	C12-C13-C14-C15
56	1L	32	PSU	C2'-C1'-C5-C4
56	1L	37	MIA	O4'-C4'-C5'-O5'
56	1L	37	MIA	C5-C6-N6-C12
56	1L	37	MIA	N1-C2-S10-C11
56	1L	37	MIA	N3-C2-S10-C11
56	1L	37	MIA	N6-C12-C13-C14
56	1L	37	MIA	C12-C13-C14-C15
56	1L	37	MIA	C12-C13-C14-C16
22	1K	37	MIA	C12-C13-C14-C15
22	1K	37	MIA	C12-C13-C14-C16
57	3L	32	PSU	C4'-C5'-O5'-P
23	2K	47	7MG	O4'-C4'-C5'-O5'
24	3K	39	PSU	C3'-C4'-C5'-O5'
24	3K	39	PSU	O4'-C4'-C5'-O5'
23	2L	55	5MU	C3'-C4'-C5'-O5'
23	2L	55	5MU	O4'-C4'-C5'-O5'
24	3K	37	MIA	N1-C6-N6-C12
56	1L	37	MIA	C3'-C4'-C5'-O5'
22	1K	55	PSU	O4'-C4'-C5'-O5'
57	3L	54	5MU	O4'-C4'-C5'-O5'
56	1L	37	MIA	N1-C6-N6-C12
22	1K	55	PSU	C3'-C4'-C5'-O5'
57	3L	54	5MU	C3'-C4'-C5'-O5'
23	2K	47	7MG	C3'-C4'-C5'-O5'
23	2L	8	4SU	O4'-C4'-C5'-O5'
24	3K	39	PSU	O4'-C1'-C5-C4
22	1K	55	PSU	O4'-C1'-C5-C4
24	3K	37	MIA	C13-C12-N6-C6

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Mol	Chain	Res	Type	Atoms
23	2L	55	5MU	C4'-C5'-O5'-P
23	2L	8	4SU	C3'-C4'-C5'-O5'
24	3K	39	PSU	O4'-C1'-C5-C6

There are no ring outliers.

21 monomers are involved in 42 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
57	3L	8	4SU	5	0
57	3L	32	PSU	3	0
22	1K	8	4SU	1	0
22	1K	54	5MU	1	0
23	2L	47	7MG	3	0
57	3L	54	5MU	2	0
23	2K	8	4SU	1	0
56	1L	37	MIA	2	0
23	2K	47	7MG	3	0
23	2L	33	OMC	2	0
57	3L	46	7MG	3	0
57	3L	55	PSU	2	0
24	3K	39	PSU	2	0
23	2L	8	4SU	2	0
23	2K	55	5MU	3	0
23	2L	55	5MU	2	0
23	2L	56	PSU	2	0
24	3K	37	MIA	2	0
23	2K	56	PSU	2	0
56	1L	39	PSU	1	0
22	1K	55	PSU	1	0

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 1246 ligands modelled in this entry, 1244 are monoatomic - leaving 2 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The

Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
59	PAR	1G	1697	-	44,45,45	0.88	3 (6%)	63,67,67	1.66	14 (22%)
59	PAR	13	1749	-	44,45,45	0.71	1 (2%)	63,67,67	1.63	15 (23%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
59	PAR	1G	1697	-	-	6/18/94/94	0/4/4/4
59	PAR	13	1749	-	-	4/18/94/94	0/4/4/4

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
59	1G	1697	PAR	C24-N24	-2.80	1.43	1.47
59	1G	1697	PAR	C34-C24	-2.37	1.50	1.53
59	13	1749	PAR	C21-N21	-2.02	1.44	1.47
59	1G	1697	PAR	C31-C21	-2.02	1.51	1.53

All (29) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
59	1G	1697	PAR	C13-O52-C52	-4.74	106.75	117.98
59	1G	1697	PAR	C14-O33-C33	-4.26	107.88	117.98
59	13	1749	PAR	C14-O54-C54	3.94	121.42	113.72
59	1G	1697	PAR	O11-C11-C21	-3.40	102.51	108.08
59	1G	1697	PAR	C34-C24-N24	-3.36	104.17	111.05
59	13	1749	PAR	O61-C61-C51	-3.33	100.01	111.33
59	13	1749	PAR	C22-C12-C62	-3.28	105.17	110.08
59	1G	1697	PAR	O33-C14-C24	3.15	113.23	108.08
59	1G	1697	PAR	O52-C13-O43	-2.94	108.37	111.37
59	13	1749	PAR	C11-C21-C31	2.83	117.37	110.29
59	13	1749	PAR	O51-C51-C41	2.79	114.72	109.70
59	13	1749	PAR	C11-O51-C51	2.78	119.15	113.72
59	13	1749	PAR	O11-C42-C32	-2.74	102.64	109.18

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
59	13	1749	PAR	O54-C54-C44	2.69	114.54	109.70
59	13	1749	PAR	O52-C13-O43	-2.53	108.78	111.37
59	1G	1697	PAR	O62-C62-C52	2.50	116.35	109.94
59	13	1749	PAR	O34-C34-C44	-2.46	104.59	110.38
59	1G	1697	PAR	C14-O54-C54	2.37	118.34	113.72
59	13	1749	PAR	O43-C13-C23	-2.36	101.97	104.98
59	1G	1697	PAR	O51-C11-C21	2.32	115.21	110.08
59	1G	1697	PAR	C11-O51-C51	2.31	118.23	113.72
59	1G	1697	PAR	C41-C31-C21	-2.27	107.22	110.99
59	1G	1697	PAR	C62-C12-N12	-2.26	106.47	110.94
59	13	1749	PAR	C11-C21-N21	-2.21	106.23	110.20
59	1G	1697	PAR	O54-C54-C44	2.20	113.67	109.70
59	13	1749	PAR	C14-C24-C34	-2.17	104.87	110.29
59	13	1749	PAR	O11-C11-O51	-2.14	105.06	110.69
59	1G	1697	PAR	O11-C42-C32	-2.14	104.07	109.18
59	13	1749	PAR	C62-C52-C42	-2.07	107.07	111.72

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
59	13	1749	PAR	C33-C43-C53-O53
59	13	1749	PAR	O43-C43-C53-O53
59	1G	1697	PAR	C44-C54-C64-N64
59	13	1749	PAR	O43-C13-O52-C52
59	1G	1697	PAR	O43-C43-C53-O53
59	1G	1697	PAR	C42-C52-O52-C13
59	1G	1697	PAR	C62-C52-O52-C13
59	1G	1697	PAR	C52-C42-O11-C11
59	13	1749	PAR	C23-C33-O33-C14
59	1G	1697	PAR	C23-C33-O33-C14

There are no ring outliers.

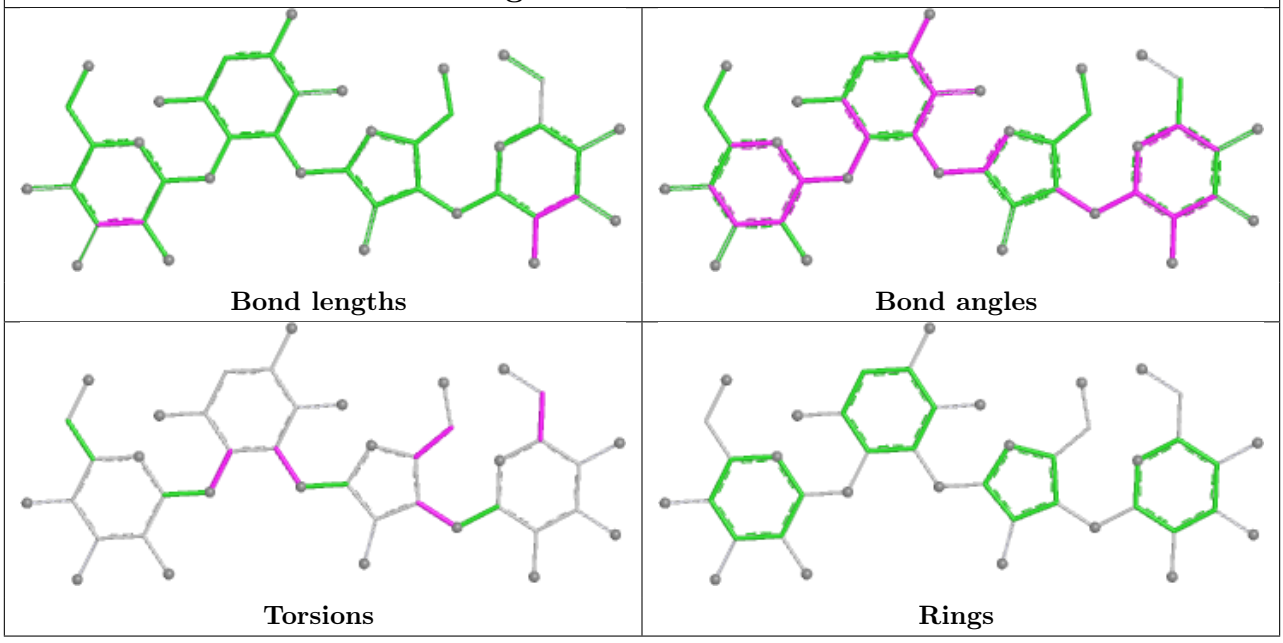
2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
59	1G	1697	PAR	2	0
59	13	1749	PAR	1	0

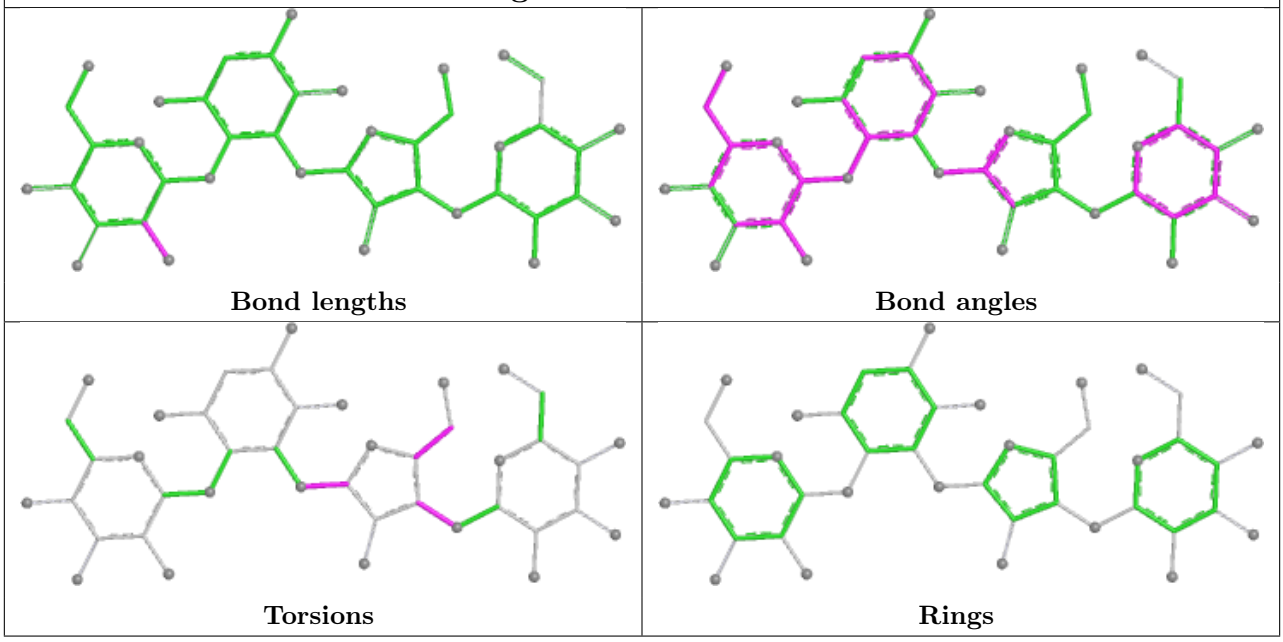
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In

addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

Ligand PAR 1G 1697



Ligand PAR 13 1749



5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	13	1
1	1G	1
25	4L	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	13	1530:G	O3'	1531:A	P	3.82
1	1G	1530:G	O3'	1531:A	P	3.28
1	4L	21:C	O3'	22:A	P	3.02

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95^{th} percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
1	13	1498/1522 (98%)	0.52	134 (8%) 15 14	53, 93, 174, 276	0
1	1G	1498/1522 (98%)	0.88	219 (14%) 6 5	69, 116, 188, 285	0
2	12	237/256 (92%)	1.88	88 (37%) 1 1	141, 173, 195, 205	0
2	1E	237/256 (92%)	1.28	58 (24%) 2 2	105, 141, 169, 176	0
3	22	206/239 (86%)	2.20	96 (46%) 0 0	136, 162, 182, 190	0
3	2E	205/239 (85%)	0.66	18 (8%) 15 14	82, 102, 138, 147	0
4	32	208/209 (99%)	1.26	50 (24%) 2 2	93, 114, 138, 145	0
4	3E	208/209 (99%)	1.03	23 (11%) 10 9	75, 100, 123, 134	0
5	42	151/162 (93%)	1.93	57 (37%) 1 0	111, 135, 154, 184	0
5	4E	151/162 (93%)	0.72	20 (13%) 7 7	72, 93, 117, 160	0
6	52	101/101 (100%)	0.65	8 (7%) 18 16	82, 100, 119, 142	0
6	5E	101/101 (100%)	0.83	9 (8%) 15 14	77, 96, 118, 141	0
7	62	152/156 (97%)	1.71	44 (28%) 1 1	112, 127, 147, 160	0
7	6E	155/156 (99%)	1.22	27 (17%) 4 3	92, 111, 146, 163	0
8	72	138/138 (100%)	1.37	32 (23%) 2 2	102, 132, 151, 155	0
8	7E	138/138 (100%)	0.84	21 (15%) 5 5	84, 101, 113, 121	0
9	82	124/128 (96%)	1.78	44 (35%) 1 1	115, 150, 165, 171	0
9	8E	127/128 (99%)	1.08	21 (16%) 4 4	80, 127, 148, 158	0
10	1A	99/105 (94%)	1.41	24 (24%) 2 2	131, 155, 176, 184	0
10	1I	99/105 (94%)	1.69	34 (34%) 1 1	73, 125, 159, 162	0
11	2A	116/129 (89%)	1.55	27 (23%) 2 2	85, 108, 130, 159	0
11	2I	116/129 (89%)	1.00	15 (12%) 7 7	69, 100, 127, 165	0
12	3A	125/132 (94%)	1.90	38 (30%) 1 1	83, 106, 134, 167	0
12	3I	125/132 (94%)	1.13	26 (20%) 2 2	60, 71, 107, 165	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
13	4A	117/126 (92%)	2.33	44 (37%) 1 0	118, 155, 179, 185	0
13	4I	118/126 (93%)	0.93	15 (12%) 8 7	74, 112, 132, 145	0
14	5A	58/61 (95%)	1.85	21 (36%) 1 1	134, 159, 174, 179	0
14	5I	60/61 (98%)	0.64	5 (8%) 17 15	80, 91, 106, 119	0
15	6A	88/89 (98%)	0.88	14 (15%) 5 4	87, 112, 127, 133	0
15	6I	88/89 (98%)	0.79	11 (12%) 8 7	69, 98, 116, 126	0
16	7A	84/88 (95%)	0.97	7 (8%) 17 15	87, 103, 126, 159	0
16	7I	84/88 (95%)	1.51	22 (26%) 1 1	93, 107, 141, 158	0
17	8A	100/105 (95%)	1.25	22 (22%) 2 2	93, 110, 128, 148	0
17	8I	100/105 (95%)	1.25	19 (19%) 3 3	83, 101, 113, 116	0
18	9A	72/88 (81%)	0.77	8 (11%) 10 9	92, 115, 144, 170	0
18	9I	72/88 (81%)	0.84	8 (11%) 10 9	83, 100, 136, 168	0
19	AA	78/93 (83%)	1.74	28 (35%) 1 1	150, 182, 192, 196	0
19	AI	81/93 (87%)	1.22	16 (19%) 3 3	88, 113, 138, 146	0
20	BA	99/106 (93%)	1.75	37 (37%) 1 1	85, 111, 137, 149	0
20	BI	99/106 (93%)	2.29	48 (48%) 0 0	102, 117, 153, 160	0
21	1B	25/27 (92%)	1.83	8 (32%) 1 1	119, 140, 152, 167	0
21	1F	25/27 (92%)	0.88	2 (8%) 18 16	88, 97, 113, 142	0
22	1K	70/76 (92%)	2.43	19 (27%) 1 1	76, 203, 246, 250	0
23	2K	72/77 (93%)	0.58	4 (5%) 30 25	68, 91, 119, 138	0
23	2L	72/77 (93%)	1.15	10 (13%) 6 6	80, 113, 149, 166	0
24	3K	72/76 (94%)	1.50	19 (26%) 1 1	71, 230, 258, 260	0
25	4K	13/30 (43%)	0.43	0 100 100	64, 80, 130, 131	0
25	4L	11/30 (36%)	1.01	1 (9%) 15 13	93, 124, 136, 143	0
26	14	2909/2917 (99%)	0.27	214 (7%) 20 18	50, 84, 241, 338	0
26	1H	2912/2917 (99%)	0.11	176 (6%) 27 23	37, 70, 222, 303	0
27	16	122/122 (100%)	0.13	3 (2%) 58 50	63, 87, 110, 193	0
27	1J	122/122 (100%)	1.13	20 (16%) 4 4	86, 120, 149, 192	0
28	11	272/276 (98%)	0.14	11 (4%) 42 35	38, 62, 78, 83	0
28	19	273/276 (98%)	0.61	30 (10%) 10 9	46, 71, 87, 97	0
29	21	205/206 (99%)	0.82	28 (13%) 6 6	50, 88, 129, 144	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
29	29	205/206 (99%)	1.26	46 (22%) 2 2	61, 93, 141, 174	0
30	31	202/210 (96%)	0.71	23 (11%) 10 9	43, 73, 113, 131	0
30	39	208/210 (99%)	1.08	33 (15%) 5 4	56, 103, 167, 189	0
31	41	181/182 (99%)	0.87	26 (14%) 6 5	78, 98, 131, 148	0
31	49	181/182 (99%)	1.29	40 (22%) 2 2	120, 142, 168, 178	0
32	51	174/180 (96%)	1.03	32 (18%) 3 3	77, 102, 120, 135	0
32	59	170/180 (94%)	2.14	71 (41%) 0 0	142, 193, 215, 227	0
33	61	146/148 (98%)	1.25	33 (22%) 2 2	71, 129, 146, 151	0
33	69	146/148 (98%)	2.41	67 (45%) 0 0	81, 122, 150, 157	0
34	15	138/140 (98%)	1.51	32 (23%) 2 2	77, 106, 136, 163	0
34	58	138/140 (98%)	1.16	20 (14%) 6 5	62, 89, 128, 145	0
35	25	122/122 (100%)	0.73	9 (7%) 20 18	66, 87, 103, 109	0
35	68	122/122 (100%)	0.51	12 (9%) 13 12	57, 72, 89, 100	0
36	35	150/150 (100%)	1.30	32 (21%) 2 2	58, 106, 138, 169	0
36	78	150/150 (100%)	0.62	11 (7%) 21 18	43, 77, 104, 157	0
37	45	141/141 (100%)	1.15	29 (20%) 2 2	75, 107, 136, 152	0
37	88	138/141 (97%)	0.48	8 (5%) 29 24	50, 76, 98, 128	0
38	55	117/118 (99%)	0.66	15 (12%) 7 7	59, 76, 91, 110	0
38	98	118/118 (100%)	0.91	18 (15%) 5 5	61, 81, 102, 110	0
39	65	111/112 (99%)	1.28	23 (20%) 2 2	91, 114, 131, 139	0
39	A8	111/112 (99%)	0.64	11 (9%) 13 11	73, 84, 108, 123	0
40	75	137/146 (93%)	0.99	18 (13%) 7 7	78, 95, 150, 184	0
40	B8	137/146 (93%)	1.29	29 (21%) 2 2	69, 89, 145, 175	0
41	85	117/118 (99%)	1.41	22 (18%) 3 3	66, 94, 138, 155	0
41	C8	117/118 (99%)	0.90	19 (16%) 4 4	52, 79, 111, 129	0
42	95	101/101 (100%)	1.96	33 (32%) 1 1	66, 124, 140, 157	0
42	D8	101/101 (100%)	1.66	26 (25%) 1 1	54, 103, 129, 140	0
43	A5	113/113 (100%)	0.59	5 (4%) 39 32	60, 72, 105, 150	0
43	E8	113/113 (100%)	0.69	13 (11%) 9 9	56, 72, 105, 146	0
44	B5	94/96 (97%)	0.57	7 (7%) 20 18	68, 83, 109, 120	0
44	F8	94/96 (97%)	0.28	6 (6%) 25 21	55, 69, 90, 108	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
45	C5	104/110 (94%)	1.76	42 (40%)	0	0	92, 115, 146, 153	0
45	G8	104/110 (94%)	1.10	19 (18%)	3	3	70, 90, 131, 142	0
46	D5	179/206 (86%)	1.50	49 (27%)	1	1	113, 151, 230, 237	0
46	H8	175/206 (84%)	1.17	31 (17%)	4	3	80, 119, 203, 216	0
47	E5	77/85 (90%)	1.10	11 (14%)	6	6	67, 88, 106, 145	0
47	I8	80/85 (94%)	0.67	12 (15%)	5	5	54, 67, 101, 108	0
48	F5	94/98 (95%)	1.37	27 (28%)	1	1	60, 79, 122, 132	0
48	J8	97/98 (98%)	0.55	14 (14%)	6	5	50, 69, 122, 149	0
49	G5	67/72 (93%)	1.00	11 (16%)	4	4	80, 100, 121, 144	0
49	K8	67/72 (93%)	0.85	12 (17%)	3	3	61, 77, 95, 125	0
50	H5	59/60 (98%)	1.31	13 (22%)	2	2	77, 100, 140, 153	0
50	L8	57/60 (95%)	0.95	7 (12%)	8	8	57, 78, 102, 109	0
51	I5	60/71 (84%)	1.47	17 (28%)	1	1	151, 187, 203, 206	0
51	M8	66/71 (92%)	1.65	19 (28%)	1	1	104, 144, 179, 189	0
52	J5	59/60 (98%)	1.23	14 (23%)	2	2	57, 81, 150, 183	0
52	N8	58/60 (96%)	1.19	13 (22%)	2	2	48, 97, 160, 163	0
53	K5	45/54 (83%)	2.71	28 (62%)	0	0	123, 152, 165, 172	0
53	O8	45/54 (83%)	1.59	13 (28%)	1	1	106, 137, 157, 161	0
54	L5	46/49 (93%)	-0.11	2 (4%)	40	32	45, 58, 72, 85	0
54	P8	45/49 (91%)	-0.14	2 (4%)	39	32	40, 48, 61, 75	0
55	M5	60/65 (92%)	0.87	12 (20%)	3	3	71, 79, 100, 124	0
55	Q8	60/65 (92%)	1.42	22 (36%)	1	1	56, 72, 98, 109	0
56	1L	72/76 (94%)	2.08	23 (31%)	1	1	122, 239, 257, 262	0
57	3L	71/76 (93%)	2.13	26 (36%)	1	1	82, 208, 243, 253	0
All	All	21028/21694 (96%)	0.83	3211 (15%)	5	5	37, 97, 186, 338	0

All (3211) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
22	1K	73	A	25.3
13	4A	6	GLY	20.3
27	1J	88	C	15.1
13	4A	7	VAL	14.7
11	2A	126	ARG	13.8

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Mol	Chain	Res	Type	RSRZ
57	3L	34	G	13.6
42	95	93	GLU	13.0
22	1K	76	A	13.0
11	2A	125	PHE	12.8
9	82	115	GLY	12.7
40	75	104	ASN	12.2
3	22	160	ALA	12.2
50	H5	17	LYS	11.1
29	29	76	ARG	11.1
1	1G	965	A	10.8
12	3A	13	LYS	10.7
33	69	35	LEU	10.6
3	22	158	GLY	10.6
40	B8	104	ASN	10.6
5	42	126	ARG	10.6
57	3L	17	C	10.4
26	14	1026	U	10.3
5	42	124	GLY	10.3
7	62	85	TYR	9.9
12	3A	16	GLU	9.9
2	12	163	PHE	9.9
31	41	26	GLN	9.8
33	69	34	GLY	9.7
34	15	84	LYS	9.6
38	98	69	ASP	9.5
1	13	311	C	9.5
41	85	20	LEU	9.2
33	69	6	LEU	9.2
51	I5	42	PHE	9.2
7	62	32	ARG	9.2
56	1L	31	A	9.1
34	58	72	TYR	9.1
28	19	5	LYS	9.0
34	15	74	ARG	9.0
56	1L	33	U	8.9
12	3A	14	GLY	8.8
13	4A	102	ARG	8.8
22	1K	72	C	8.8
1	1G	966	G	8.8
34	15	85	ILE	8.7
36	35	110	TYR	8.7
42	95	70	ILE	8.7

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Mol	Chain	Res	Type	RSRZ
42	D8	74	LYS	8.5
32	59	96	ALA	8.4
56	1L	76	A	8.4
7	62	86	GLN	8.4
11	2I	123	LYS	8.4
20	BI	18	GLN	8.3
11	2I	124	LYS	8.3
40	B8	1	MET	8.2
2	12	29	ALA	8.2
22	1K	75	C	8.2
23	2K	1	C	8.1
30	39	96	ASP	8.1
11	2A	124	LYS	8.0
1	1G	568	G	8.0
32	59	131	VAL	8.0
31	49	74	LYS	7.9
8	72	86	ILE	7.9
13	4A	4	ILE	7.9
13	4I	8	GLU	7.9
12	3I	17	LYS	7.8
12	3A	5	PRO	7.8
11	2A	120	ARG	7.8
48	F5	36	GLY	7.7
42	95	63	GLY	7.7
13	4A	8	GLU	7.6
50	H5	20	LYS	7.6
12	3A	15	ARG	7.6
53	K5	13	CYS	7.6
34	15	72	TYR	7.6
11	2A	123	LYS	7.5
22	1K	74	C	7.5
55	Q8	34	TRP	7.5
12	3A	28	LYS	7.5
13	4A	66	LEU	7.4
42	95	73	SER	7.4
32	59	100	GLY	7.3
7	62	33	ASP	7.3
23	2L	35	C	7.3
32	59	103	LEU	7.3
26	1H	2117	A	7.3
26	1H	2116	G	7.3
40	B8	106	SER	7.2

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Mol	Chain	Res	Type	RSRZ
48	F5	27	GLU	7.2
29	29	77	ILE	7.2
7	62	41	ARG	7.2
42	D8	73	SER	7.2
42	95	68	LYS	7.2
42	95	83	ARG	7.2
26	1H	1383	C	7.1
32	59	106	THR	7.1
4	3E	209	ARG	7.1
3	22	8	ILE	7.1
29	29	75	VAL	7.1
5	42	88	LYS	7.1
5	42	123	LEU	7.0
33	69	22	LYS	7.0
4	3E	31	CYS	7.0
40	75	6	LEU	7.0
15	6A	68	ARG	7.0
2	12	70	PHE	6.9
41	85	40	PHE	6.9
26	1H	2174	C	6.9
3	22	157	ILE	6.9
32	59	89	ILE	6.9
33	69	21	VAL	6.9
33	69	1	MET	6.8
26	1H	2189	U	6.8
3	22	155	GLY	6.8
34	58	71	ILE	6.8
41	85	17	ILE	6.8
22	1K	3	C	6.8
20	BI	72	LEU	6.8
42	95	74	LYS	6.8
2	12	165	VAL	6.7
57	3L	37	A	6.7
51	M8	58	ARG	6.7
32	59	93	GLY	6.7
8	7E	91	ARG	6.7
29	21	78	LEU	6.7
33	69	15	VAL	6.7
14	5A	6	LEU	6.7
22	1K	31	A	6.7
42	D8	75	PHE	6.6
13	4I	6	GLY	6.6

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Mol	Chain	Res	Type	RSRZ
1	1G	883	C	6.6
7	6E	32	ARG	6.6
29	29	52	LEU	6.6
33	69	36	ALA	6.6
39	65	55	ALA	6.6
51	M8	34	GLU	6.6
3	22	167	TRP	6.6
20	BI	14	LYS	6.6
10	1A	47	PHE	6.5
11	2A	122	LYS	6.5
11	2I	125	PHE	6.5
12	3I	16	GLU	6.5
24	3K	20	U	6.5
26	14	1537	C	6.5
32	51	171	LEU	6.5
56	1L	40	C	6.5
32	59	40	GLU	6.4
11	2A	121	PRO	6.4
2	12	71	VAL	6.4
9	82	75	ASP	6.4
26	1H	2170	A	6.4
34	15	83	LYS	6.4
8	72	93	VAL	6.3
26	1H	2476	A	6.3
43	E8	85	VAL	6.3
26	1H	2188	C	6.3
26	1H	2119	A	6.3
26	14	2790	A	6.3
20	BI	21	LYS	6.3
52	J5	26	THR	6.3
29	21	195	LEU	6.3
5	42	125	SER	6.3
26	1H	2190	G	6.3
42	D8	81	TYR	6.3
31	49	116	ASP	6.2
3	22	10	PHE	6.2
1	1G	377	G	6.2
56	1L	34	G	6.2
28	11	35	LYS	6.2
34	15	75	TYR	6.2
41	85	19	LYS	6.2
3	22	159	GLY	6.2

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Mol	Chain	Res	Type	RSRZ
1	1G	569	C	6.2
3	22	6	HIS	6.1
26	14	967	C	6.1
12	3I	7	ILE	6.1
20	BI	17	ARG	6.1
41	85	16	LYS	6.1
17	8I	36	ILE	6.1
32	59	104	GLU	6.1
26	1H	2477	C	6.1
49	K8	15	LYS	6.1
45	C5	29	GLU	6.0
7	62	77	SER	6.0
42	D8	78	LYS	6.0
26	1H	2113	U	6.0
4	3E	9	CYS	6.0
48	F5	28	GLY	6.0
19	AI	13	ASP	6.0
33	69	5	LEU	5.9
2	1E	228	GLY	5.9
4	32	23	GLY	5.9
33	69	9	LEU	5.9
1	1G	1251	A	5.9
17	8A	32	TYR	5.9
7	62	37	ASN	5.9
33	69	144	VAL	5.9
34	58	68	GLU	5.9
1	1G	1354	C	5.9
42	D8	79	VAL	5.9
12	3I	20	LYS	5.8
29	29	51	PHE	5.8
36	35	12	ALA	5.8
3	22	9	GLY	5.8
26	14	2173	A	5.8
8	72	84	ARG	5.8
41	C8	118	GLY	5.8
29	21	75	VAL	5.8
5	42	122	GLU	5.8
33	69	7	GLU	5.8
1	13	111	G	5.7
7	6E	83	ALA	5.7
5	42	12	LEU	5.7
2	12	26	PRO	5.7

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Mol	Chain	Res	Type	RSRZ
42	D8	84	LYS	5.7
1	1G	884	U	5.7
1	1G	824	C	5.7
7	62	13	GLN	5.7
20	BA	20	LEU	5.7
17	8A	7	THR	5.7
10	1I	5	ARG	5.7
31	41	35	GLU	5.7
41	85	44	ASN	5.7
8	72	4	ASP	5.7
2	12	164	VAL	5.7
1	1G	969	A	5.7
1	1G	562	C	5.7
1	1G	1367	C	5.7
10	1I	10	GLY	5.7
8	72	2	LEU	5.7
1	1G	876	G	5.6
11	2A	25	TYR	5.6
35	25	74	GLY	5.6
41	85	43	GLY	5.6
29	21	76	ARG	5.6
29	21	79	ARG	5.6
2	12	93	VAL	5.6
15	6I	62	GLN	5.6
22	1K	33	U	5.6
5	42	105	VAL	5.6
21	1F	16	GLY	5.6
1	1G	378	G	5.6
26	1H	2125	G	5.6
33	69	33	ARG	5.6
26	1H	2161	C	5.6
2	1E	31	TYR	5.6
7	62	78	ARG	5.6
34	58	88	GLU	5.6
45	C5	90	LEU	5.6
4	3E	22	LYS	5.6
26	1H	2709	G	5.6
3	22	30	ARG	5.5
46	D5	125	LEU	5.5
1	13	307	C	5.5
3	22	199	LYS	5.5
42	95	71	LEU	5.5

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Mol	Chain	Res	Type	RSRZ
1	1G	111	G	5.5
26	1H	1404	C	5.5
37	45	1	MET	5.5
50	L8	17	LYS	5.5
9	82	125	TYR	5.5
26	14	1538	G	5.5
8	72	92	ARG	5.5
30	31	131	GLY	5.4
42	95	75	PHE	5.4
13	4A	5	ALA	5.4
1	1G	962	C	5.4
2	1E	55	PHE	5.4
33	69	25	TYR	5.4
7	62	38	LEU	5.4
7	62	80	VAL	5.4
10	1A	59	SER	5.4
32	59	94	TYR	5.4
33	61	118	LYS	5.4
46	H8	66	SER	5.4
20	BI	80	ARG	5.4
1	1G	230	G	5.4
1	1G	825	G	5.4
8	72	133	LEU	5.4
32	51	114	VAL	5.3
45	C5	24	VAL	5.3
29	29	195	LEU	5.3
1	1G	110	C	5.3
28	19	38	LYS	5.3
13	4A	69	GLU	5.3
42	95	65	GLY	5.3
3	22	137	ALA	5.3
5	42	86	ALA	5.3
9	82	123	PRO	5.3
33	69	20	ASP	5.3
34	58	84	LYS	5.3
37	45	65	PHE	5.3
1	13	112	G	5.3
4	32	31	CYS	5.3
32	59	38	SER	5.3
13	4A	3	ARG	5.3
29	21	51	PHE	5.3
38	98	18	LEU	5.2

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Mol	Chain	Res	Type	RSRZ
44	B5	69	TYR	5.2
12	3I	19	ARG	5.2
12	3A	19	ARG	5.2
36	35	74	GLU	5.2
42	95	62	LEU	5.2
7	62	36	LYS	5.2
20	BI	79	ARG	5.2
56	1L	73	A	5.2
32	59	171	LEU	5.2
50	L8	20	LYS	5.2
12	3A	12	ARG	5.2
13	4I	100	GLY	5.2
32	59	99	VAL	5.2
3	22	17	ASP	5.2
32	51	172	LYS	5.2
26	1H	1032	A	5.1
29	21	55	ASN	5.1
43	A5	85	VAL	5.1
12	3A	10	LEU	5.1
12	3A	128	ALA	5.1
20	BA	9	ASN	5.1
13	4A	67	GLU	5.1
28	19	55	GLY	5.1
33	69	10	GLU	5.1
27	1J	116	G	5.1
53	K5	22	ALA	5.1
1	13	312	C	5.1
26	14	1306	C	5.1
34	15	73	THR	5.1
1	1G	1531	A	5.1
47	E5	21	LEU	5.1
4	32	5	ILE	5.1
52	N8	59	GLU	5.1
6	52	83	ASP	5.1
1	1G	953	G	5.1
1	1G	1117	G	5.1
3	22	178	LEU	5.1
48	F5	37	ILE	5.1
26	14	229	A	5.1
31	49	155	MET	5.1
20	BI	70	SER	5.1
12	3I	21	LYS	5.0

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Mol	Chain	Res	Type	RSRZ
1	1G	121	C	5.0
1	1G	1235	U	5.0
5	42	28	PHE	5.0
13	4A	9	ILE	5.0
40	75	101	PHE	5.0
1	1G	28	G	5.0
15	6I	65	ARG	5.0
42	D8	82	ARG	5.0
38	98	71	GLN	5.0
11	2A	117	ASN	5.0
11	2I	12	ARG	5.0
1	1G	1116	C	5.0
2	12	92	TYR	5.0
12	3A	11	VAL	5.0
51	M8	59	PHE	5.0
29	21	90	THR	5.0
8	72	1	MET	5.0
46	D5	68	PRO	5.0
51	I5	32	TYR	5.0
32	59	87	LEU	5.0
1	1G	882	C	4.9
1	1G	968	A	4.9
7	62	84	ASN	4.9
45	C5	77	PRO	4.9
53	K5	42	TRP	4.9
2	12	196	LEU	4.9
30	31	96	ASP	4.9
38	98	47	PHE	4.9
7	62	4	ARG	4.9
48	F5	84	GLY	4.9
56	1L	17	C	4.9
57	3L	33	U	4.9
34	58	129	PRO	4.9
3	22	141	VAL	4.9
47	E5	44	ARG	4.9
2	12	187	LEU	4.9
4	32	9	CYS	4.9
33	69	68	LEU	4.9
39	65	57	LYS	4.9
5	4E	128	PRO	4.8
2	1E	196	LEU	4.8
10	1A	65	LEU	4.8

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Mol	Chain	Res	Type	RSRZ
3	22	116	VAL	4.8
5	42	131	ILE	4.8
13	4A	65	LYS	4.8
31	49	75	LYS	4.8
12	3I	127	GLU	4.8
19	AA	68	GLY	4.8
20	BA	97	ALA	4.8
53	O8	22	ALA	4.8
55	M5	40	GLU	4.8
1	13	310	G	4.8
1	1G	963	G	4.8
4	3E	12	CYS	4.8
7	6E	5	ARG	4.8
10	1A	62	HIS	4.8
29	21	193	GLY	4.8
38	55	43	GLU	4.8
47	E5	22	GLY	4.8
33	61	20	ASP	4.8
11	2I	122	LYS	4.8
21	1B	2	GLY	4.8
45	C5	93	GLY	4.8
26	1H	1384	A	4.8
26	1H	2173	A	4.8
2	12	214	ILE	4.8
9	8E	126	SER	4.8
32	59	95	ARG	4.8
13	4A	101	GLN	4.8
26	1H	2708	G	4.8
42	D8	80	GLN	4.8
5	42	81	GLU	4.8
12	3A	27	LEU	4.7
39	65	56	LEU	4.7
52	N8	26	THR	4.7
1	13	308	C	4.7
9	82	71	SER	4.7
4	32	160	GLN	4.7
42	D8	77	ALA	4.7
7	62	151	TYR	4.7
8	7E	88	LYS	4.7
19	AI	78	ARG	4.7
32	59	133	VAL	4.7
38	55	8	ARG	4.7

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Mol	Chain	Res	Type	RSRZ
26	14	1046	A	4.7
46	H8	166	SER	4.7
57	3L	72	C	4.7
8	72	9	MET	4.7
34	15	86	PRO	4.7
42	95	91	TYR	4.7
4	32	112	VAL	4.7
39	65	5	THR	4.7
27	1J	117	G	4.7
26	14	2146	C	4.7
7	62	34	GLY	4.7
34	15	82	LEU	4.7
34	15	90	MET	4.7
33	69	137	PRO	4.7
4	3E	26	CYS	4.7
5	42	14	ARG	4.7
18	9I	32	ARG	4.7
33	69	12	LEU	4.7
41	85	42	ALA	4.7
27	1J	25	A	4.7
9	82	106	ALA	4.6
13	4A	72	ALA	4.6
20	BI	95	ALA	4.6
10	1A	49	VAL	4.6
12	3A	18	VAL	4.6
1	1G	506	G	4.6
56	1L	30	G	4.6
57	3L	35	A	4.6
56	1L	75	C	4.6
42	95	64	HIS	4.6
48	F5	85	LEU	4.6
16	7A	84	ALA	4.6
33	61	117	GLU	4.6
1	1G	90	C	4.6
32	59	64	LEU	4.6
5	42	128	PRO	4.6
29	29	7	VAL	4.6
42	D8	76	LYS	4.6
3	22	184	TYR	4.6
32	59	71	LEU	4.6
50	H5	18	ASP	4.6
1	1G	1202	G	4.6

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Mol	Chain	Res	Type	RSRZ
27	1J	89	G	4.6
51	I5	31	ILE	4.6
51	M8	56	VAL	4.6
18	9I	68	LYS	4.6
3	22	15	THR	4.5
31	41	25	TYR	4.5
4	3E	76	ARG	4.5
34	15	97	ARG	4.5
12	3A	26	ALA	4.5
9	82	65	VAL	4.5
33	69	136	VAL	4.5
26	14	561	G	4.5
36	35	35	HIS	4.5
53	O8	42	TRP	4.5
32	59	148	ILE	4.5
48	F5	15	ALA	4.5
29	29	150	VAL	4.5
35	68	31	LYS	4.5
1	13	1342	C	4.5
1	1G	312	C	4.5
26	14	2174	C	4.5
20	BA	13	LEU	4.5
21	1B	14	TRP	4.5
11	2A	87	THR	4.5
13	4A	100	GLY	4.5
17	8A	33	GLY	4.5
26	14	1885	A	4.5
20	BA	72	LEU	4.5
31	49	135	LEU	4.5
4	3E	139	ARG	4.5
1	1G	1115	C	4.5
56	1L	41	C	4.5
1	1G	1370	G	4.5
8	7E	93	VAL	4.5
33	69	14	ASP	4.5
23	2K	77	A	4.5
45	C5	92	ASN	4.5
3	22	152	ILE	4.4
36	35	46	LYS	4.4
1	1G	91	C	4.4
26	1H	961	C	4.4
26	1H	1463	C	4.4

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Mol	Chain	Res	Type	RSRZ
32	59	39	PRO	4.4
32	59	55	PRO	4.4
3	22	153	VAL	4.4
29	29	116	VAL	4.4
1	13	1385	G	4.4
34	15	76	SER	4.4
35	68	26	LYS	4.4
1	13	607	A	4.4
34	58	73	THR	4.4
20	BI	49	ALA	4.4
36	78	141	ALA	4.4
29	29	59	VAL	4.4
33	61	41	GLU	4.4
26	14	1886	C	4.4
7	62	79	ARG	4.4
40	75	112	ARG	4.4
17	8A	27	PHE	4.4
1	1G	561	U	4.4
26	14	1347	G	4.4
33	69	4	ILE	4.4
40	75	7	ILE	4.4
4	32	161	ASN	4.4
8	72	87	SER	4.4
20	BA	49	ALA	4.4
5	42	90	VAL	4.4
14	5A	55	GLY	4.4
26	14	1884	A	4.4
38	98	68	ARG	4.4
1	1G	1234	C	4.4
20	BI	76	ALA	4.4
5	4E	88	LYS	4.4
16	7I	31	LYS	4.4
32	59	4	ILE	4.4
1	13	1325	C	4.4
50	H5	2	PRO	4.4
35	68	1	MET	4.3
8	72	136	GLU	4.3
10	1A	61	GLU	4.3
40	75	11	GLU	4.3
4	3E	25	ARG	4.3
7	6E	4	ARG	4.3
1	1G	1250	A	4.3

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Mol	Chain	Res	Type	RSRZ
2	12	201	ILE	4.3
32	59	128	PRO	4.3
29	21	72	VAL	4.3
48	F5	86	SER	4.3
33	69	29	TYR	4.3
53	K5	39	TYR	4.3
2	12	127	ILE	4.3
1	13	965	A	4.3
1	1G	238	G	4.3
10	1A	58	ASP	4.3
37	45	103	MET	4.3
45	C5	98	VAL	4.3
3	22	164	ARG	4.3
7	6E	82	GLY	4.3
26	1H	1405	U	4.3
5	4E	123	LEU	4.3
14	5A	44	LEU	4.3
17	8I	37	LYS	4.3
42	95	81	TYR	4.3
30	31	66	PRO	4.3
26	1H	2171	A	4.3
33	69	37	VAL	4.3
15	6I	68	ARG	4.3
2	12	86	GLU	4.3
51	I5	47	GLN	4.3
26	14	1305	C	4.3
20	BA	80	ARG	4.3
30	39	93	LYS	4.3
32	51	115	VAL	4.3
5	4E	124	GLY	4.3
29	21	52	LEU	4.3
42	95	86	GLY	4.3
6	5E	95	GLU	4.3
1	1G	994	A	4.2
19	AI	56	GLN	4.2
1	1G	821	G	4.2
10	1I	4	ILE	4.2
26	14	2147	G	4.2
32	59	92	ILE	4.2
47	I8	9	SER	4.2
1	1G	311	C	4.2
9	82	10	ARG	4.2

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Mol	Chain	Res	Type	RSRZ
15	6A	65	ARG	4.2
45	G8	34	LYS	4.2
40	75	5	ALA	4.2
53	K5	52	VAL	4.2
34	15	80	GLY	4.2
53	K5	23	THR	4.2
8	72	88	LYS	4.2
28	19	35	LYS	4.2
26	1H	1382	G	4.2
3	22	120	VAL	4.2
17	8I	35	VAL	4.2
30	39	6	VAL	4.2
13	4I	5	ALA	4.2
33	61	34	GLY	4.2
6	5E	94	GLN	4.2
32	59	151	ILE	4.2
1	1G	262	A	4.2
1	1G	964	A	4.2
40	B8	51	ARG	4.2
33	69	18	VAL	4.2
46	D5	56	VAL	4.2
1	1G	454	C	4.2
26	1H	756	C	4.2
26	14	508	G	4.2
26	14	968	G	4.2
48	J8	92	LYS	4.2
3	22	16	ARG	4.2
13	4I	114	ARG	4.2
32	59	169	VAL	4.2
33	69	8	PRO	4.2
2	12	14	GLY	4.2
7	6E	81	GLY	4.2
52	J5	50	GLY	4.2
38	55	69	ASP	4.2
42	D8	70	ILE	4.2
49	G5	9	GLN	4.1
1	1G	73	G	4.1
33	69	11	ASN	4.1
20	BI	99	LEU	4.1
32	59	105	LEU	4.1
32	59	107	VAL	4.1
12	3I	81	SER	4.1

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Mol	Chain	Res	Type	RSRZ
1	1G	10	A	4.1
5	42	121	LYS	4.1
53	K5	9	LEU	4.1
13	4I	7	VAL	4.1
1	13	1386	G	4.1
1	1G	567	G	4.1
34	15	132	ALA	4.1
38	98	14	SER	4.1
14	5A	46	GLU	4.1
23	2L	36	A	4.1
26	1H	2062	A	4.1
36	35	39	LYS	4.1
2	12	193	ASP	4.1
19	AA	81	ARG	4.1
32	59	98	LEU	4.1
46	D5	155	LEU	4.1
9	82	109	VAL	4.1
20	BI	88	VAL	4.1
51	M8	32	TYR	4.1
18	9A	59	SER	4.1
2	1E	214	ILE	4.1
1	13	309	G	4.1
26	14	530	G	4.1
26	14	2659	G	4.1
53	K5	51	GLU	4.1
10	1I	73	ASP	4.1
19	AA	79	THR	4.1
20	BI	67	ALA	4.1
33	69	146	ALA	4.1
7	62	154	TYR	4.1
33	69	16	GLY	4.1
43	E8	96	ILE	4.1
38	98	17	ARG	4.1
8	7E	4	ASP	4.0
46	D5	33	LEU	4.0
19	AA	9	VAL	4.0
53	K5	41	PRO	4.0
40	B8	94	ALA	4.0
8	7E	90	GLY	4.0
53	K5	12	GLU	4.0
8	72	91	ARG	4.0
9	82	14	VAL	4.0

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Mol	Chain	Res	Type	RSRZ
11	2A	114	VAL	4.0
28	19	18	VAL	4.0
1	13	306	G	4.0
13	4A	2	ALA	4.0
16	7I	84	ALA	4.0
26	14	859	G	4.0
26	14	2664	G	4.0
3	2E	41	GLY	4.0
5	42	24	ARG	4.0
10	1I	95	GLU	4.0
40	B8	101	PHE	4.0
7	62	124	LEU	4.0
14	5A	39	LEU	4.0
1	13	1389	C	4.0
1	1G	1149	C	4.0
1	1G	1400	C	4.0
46	D5	58	VAL	4.0
3	22	7	PRO	4.0
17	8A	30	PRO	4.0
32	59	150	ALA	4.0
47	I8	6	ALA	4.0
5	42	13	ILE	4.0
3	22	18	TRP	4.0
33	61	7	GLU	4.0
29	29	181	LEU	4.0
31	49	139	LEU	4.0
33	61	6	LEU	4.0
33	69	69	LYS	4.0
36	35	76	LYS	4.0
39	65	33	LYS	4.0
20	BA	98	PRO	4.0
52	J5	28	PRO	4.0
3	22	168	ALA	4.0
50	L8	42	ALA	4.0
8	72	85	ARG	4.0
44	B5	68	ARG	4.0
11	2I	25	TYR	4.0
1	1G	1286	A	4.0
1	1G	576	G	4.0
39	65	52	SER	4.0
51	M8	66	SER	4.0
19	AA	11	VAL	4.0

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Mol	Chain	Res	Type	RSRZ
30	31	94	PRO	4.0
28	19	2	ALA	3.9
57	3L	16	U	3.9
36	35	47	ASP	3.9
5	42	15	ARG	3.9
8	7E	92	ARG	3.9
43	E8	84	ARG	3.9
48	F5	40	ARG	3.9
3	22	13	GLY	3.9
19	AA	82	GLY	3.9
2	12	215	LEU	3.9
53	K5	10	LEU	3.9
45	C5	34	LYS	3.9
3	22	198	VAL	3.9
27	1J	26	A	3.9
8	72	134	ILE	3.9
9	82	42	ARG	3.9
24	3K	19	G	3.9
26	14	1620	G	3.9
26	14	2792	G	3.9
31	49	118	ARG	3.9
2	1E	11	LEU	3.9
20	BA	24	LEU	3.9
41	C8	19	LYS	3.9
1	1G	1028(B)	C	3.9
2	12	33	TYR	3.9
12	3I	11	VAL	3.9
13	4A	10	PRO	3.9
34	15	71	ILE	3.9
13	4A	104	ARG	3.9
1	13	230	G	3.9
2	12	121	LEU	3.9
9	82	102	LEU	3.9
10	1I	65	LEU	3.9
12	3I	91	LYS	3.9
20	BI	20	LEU	3.9
26	1H	2115	G	3.9
10	1A	60	ARG	3.9
20	BI	22	ARG	3.9
48	F5	26	ARG	3.9
1	1G	26	A	3.9
17	8I	33	GLY	3.9

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Mol	Chain	Res	Type	RSRZ
4	32	80	GLU	3.9
40	75	109	GLU	3.9
45	C5	33	LYS	3.9
55	Q8	26	LYS	3.9
3	22	201	TYR	3.9
36	35	71	VAL	3.9
26	14	2271	G	3.9
38	98	21	TYR	3.9
39	65	20	ARG	3.9
20	BA	52	ALA	3.9
30	39	55	GLY	3.8
33	61	22	LYS	3.8
46	H8	67	LEU	3.8
31	49	137	GLU	3.8
7	6E	45	ASP	3.8
37	45	138	ASP	3.8
38	98	72	ASP	3.8
42	D8	37	VAL	3.8
33	61	39	ALA	3.8
1	13	124	G	3.8
22	1K	70	G	3.8
24	3K	6	G	3.8
53	K5	38	LYS	3.8
15	6A	20	GLY	3.8
10	1I	61	GLU	3.8
26	14	961	C	3.8
7	6E	33	ASP	3.8
1	1G	1236	A	3.8
26	1H	181	A	3.8
31	41	28	VAL	3.8
3	22	170	GLN	3.8
43	E8	92	ARG	3.8
2	1E	29	ALA	3.8
3	22	34	LEU	3.8
29	29	78	LEU	3.8
40	75	105	LEU	3.8
46	D5	91	LEU	3.8
48	J8	85	LEU	3.8
55	Q8	32	LEU	3.8
5	42	85	GLY	3.8
14	5A	38	GLY	3.8
3	22	186	PHE	3.8

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Mol	Chain	Res	Type	RSRZ
57	3L	5	G	3.8
7	6E	79	ARG	3.8
7	6E	156	TRP	3.8
26	1H	1084	A	3.8
31	41	2	PRO	3.8
19	AI	61	TYR	3.8
2	12	34	ALA	3.8
30	39	5	ALA	3.8
31	49	73	ALA	3.8
45	C5	105	ALA	3.8
9	82	69	GLY	3.8
28	19	6	PHE	3.8
2	1E	12	GLU	3.8
40	75	106	SER	3.8
46	H8	60	GLU	3.8
20	BA	25	ARG	3.8
46	H8	80	ARG	3.8
22	1K	34	G	3.8
56	1L	1	G	3.8
20	BI	68	LYS	3.8
26	1H	2712	U	3.8
26	14	387	U	3.8
46	D5	172	ALA	3.8
1	1G	574	A	3.8
2	12	102	LEU	3.8
40	B8	105	LEU	3.8
52	N8	25	LEU	3.8
20	BA	96	GLY	3.8
20	BA	71	THR	3.8
36	35	18	ARG	3.7
36	35	33	ARG	3.7
39	65	51	ALA	3.7
20	BA	75	ASN	3.7
26	14	614	U	3.7
26	1H	2112	G	3.7
26	1H	2162	G	3.7
26	14	1093	G	3.7
57	3L	6	G	3.7
4	3E	21	LEU	3.7
48	J8	98	LEU	3.7
3	2E	23	TYR	3.7
16	7I	39	TYR	3.7

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Mol	Chain	Res	Type	RSRZ
1	1G	89	U	3.7
26	14	958	U	3.7
2	1E	14	GLY	3.7
30	39	131	GLY	3.7
1	13	882	C	3.7
26	1H	2107	C	3.7
31	41	80	PHE	3.7
3	22	161	GLU	3.7
8	72	132	GLU	3.7
29	29	73	GLU	3.7
35	25	45	GLU	3.7
1	13	104	G	3.7
26	1H	2127	G	3.7
26	14	2663	G	3.7
16	7I	27	LYS	3.7
25	4L	22	A	3.7
5	4E	89	ILE	3.7
37	45	66	ILE	3.7
46	H8	58	VAL	3.7
2	12	98	LEU	3.7
42	D8	71	LEU	3.7
41	85	25	TRP	3.7
12	3A	8	ASN	3.7
12	3A	64	TYR	3.7
16	7I	32	TYR	3.7
31	49	85	GLY	3.7
1	1G	1196	U	3.7
53	K5	25	LYS	3.7
1	1G	877	C	3.7
57	3L	62	C	3.7
26	14	1519	G	3.7
2	12	44	LEU	3.7
10	1I	88	LEU	3.7
31	49	133	LEU	3.7
39	65	54	LEU	3.7
19	AA	13	ASP	3.7
33	69	27	ARG	3.7
28	11	30	GLU	3.7
34	58	100	GLU	3.7
40	B8	109	GLU	3.7
32	51	9	ILE	3.7
33	69	129	THR	3.7

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Mol	Chain	Res	Type	RSRZ
36	35	30	THR	3.7
46	D5	133	ILE	3.7
1	13	110	C	3.6
8	72	89	PRO	3.6
12	3I	5	PRO	3.6
20	BA	10	LEU	3.6
26	1H	949	C	3.6
26	1H	2114	A	3.6
27	1J	89(A)	A	3.6
26	14	550	G	3.6
4	32	76	ARG	3.6
20	BA	17	ARG	3.6
29	21	69	LYS	3.6
40	B8	25	GLY	3.6
2	1E	9	GLU	3.6
52	N8	51	TYR	3.6
30	39	4	VAL	3.6
31	49	39	ILE	3.6
13	4A	63	THR	3.6
53	O8	23	THR	3.6
20	BI	104	LEU	3.6
20	BA	92	LEU	3.6
46	H8	68	PRO	3.6
12	3I	128	ALA	3.6
1	13	123	C	3.6
1	1G	822	C	3.6
1	1G	967	C	3.6
1	1G	1172	C	3.6
57	3L	4	C	3.6
12	3A	20	LYS	3.6
20	BI	86	ARG	3.6
24	3K	36	A	3.6
53	O8	27	LYS	3.6
4	32	79	PHE	3.6
20	BI	69	GLY	3.6
39	65	36	TYR	3.6
40	B8	21	GLU	3.6
1	1G	823	G	3.6
1	1G	1171	G	3.6
1	1G	1392	G	3.6
14	5A	18	VAL	3.6
19	AA	67	VAL	3.6

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Mol	Chain	Res	Type	RSRZ
6	5E	89	MET	3.6
31	49	82	LEU	3.6
44	B5	85	PRO	3.6
34	58	92	ALA	3.6
3	22	131	ARG	3.6
4	32	208	SER	3.6
9	82	66	ARG	3.6
15	6I	89	GLY	3.6
26	1H	2527	C	3.6
1	1G	134	A	3.6
3	22	166	GLU	3.6
7	62	42	ILE	3.6
37	45	90	VAL	3.6
19	AA	53	ASN	3.6
3	22	12	LEU	3.6
32	59	21	PRO	3.6
51	I5	40	HIS	3.6
2	12	133	LYS	3.6
2	1E	220	ASP	3.6
4	3E	207	TYR	3.6
53	K5	21	TYR	3.6
1	1G	975	A	3.6
3	22	196	LEU	3.6
10	1A	48	THR	3.6
18	9I	31	LEU	3.6
33	69	38	LEU	3.6
43	E8	23	LEU	3.6
19	AI	76	PRO	3.6
4	32	22	LYS	3.5
4	32	49	ARG	3.5
7	62	2	ALA	3.5
42	95	80	GLN	3.5
26	1H	1033	U	3.5
1	1G	1353	G	3.5
2	12	81	VAL	3.5
34	58	67	LEU	3.5
9	82	114	TYR	3.5
45	G8	33	LYS	3.5
1	1G	135	C	3.5
1	1G	308	C	3.5
22	1K	2	C	3.5
26	14	2145	C	3.5

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Mol	Chain	Res	Type	RSRZ
26	14	2798	C	3.5
32	51	5	GLY	3.5
2	1E	229	VAL	3.5
31	41	137	GLU	3.5
34	15	98	VAL	3.5
40	75	10	VAL	3.5
22	1K	71	G	3.5
26	14	952	G	3.5
26	14	2101	G	3.5
35	68	80	ASP	3.5
49	G5	52	ASP	3.5
32	51	175	LYS	3.5
50	H5	21	ALA	3.5
1	13	1388	C	3.5
1	1G	655	A	3.5
1	1G	1397	C	3.5
7	62	50	ILE	3.5
55	Q8	48	PHE	3.5
14	5I	28	GLY	3.5
26	1H	2118	U	3.5
28	19	100	GLY	3.5
12	3I	18	VAL	3.5
33	69	145	VAL	3.5
12	3A	81	SER	3.5
14	5A	47	LEU	3.5
30	39	24	LEU	3.5
48	F5	17	SER	3.5
49	G5	61	LEU	3.5
52	N8	58	LEU	3.5
7	6E	60	LYS	3.5
52	J5	10	LYS	3.5
32	51	170	ARG	3.5
10	1I	81	THR	3.5
51	I5	43	TYR	3.5
4	32	164	ALA	3.5
13	4I	118	ALA	3.5
20	BI	106	ALA	3.5
20	BA	95	ALA	3.5
26	14	1475	G	3.5
33	69	65	ALA	3.5
12	3A	7	ILE	3.5
1	13	313	A	3.5

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Mol	Chain	Res	Type	RSRZ
1	13	395	C	3.5
1	13	883	C	3.5
1	1G	60	A	3.5
26	1H	1761	C	3.5
26	1H	2129	C	3.5
26	14	1472	A	3.5
26	14	2791	C	3.5
36	78	93	GLY	3.5
46	H8	90	VAL	3.5
1	13	884	U	3.5
13	4A	70	LEU	3.5
33	61	35	LEU	3.5
2	1E	171	ALA	3.5
9	82	117	HIS	3.5
19	AA	83	HIS	3.5
41	C8	86	ALA	3.5
1	13	606	G	3.4
1	1G	69	G	3.4
1	1G	1166	G	3.4
26	1H	232	G	3.4
2	1E	213	LEU	3.4
18	9A	88	LYS	3.4
20	BI	92	LEU	3.4
30	39	56	GLU	3.4
1	13	366	C	3.4
1	1G	526	C	3.4
26	1H	2172	U	3.4
27	1J	60	C	3.4
5	42	107	ARG	3.4
16	7I	26	ARG	3.4
20	BI	25	ARG	3.4
12	3A	48	PRO	3.4
29	29	151	TYR	3.4
2	12	25	ASN	3.4
40	B8	52	ILE	3.4
4	32	156	GLU	3.4
19	AA	78	ARG	3.4
26	1H	882	G	3.4
30	31	72	ARG	3.4
1	13	429	U	3.4
1	13	1286	A	3.4
26	1H	435	C	3.4

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Mol	Chain	Res	Type	RSRZ
26	1H	1403	C	3.4
13	4A	64	TRP	3.4
30	39	65	TRP	3.4
39	65	37	ALA	3.4
46	D5	121	HIS	3.4
48	F5	77	ALA	3.4
2	12	168	THR	3.4
41	85	45	TYR	3.4
2	12	41	ILE	3.4
54	L5	1	MET	3.4
28	11	34	VAL	3.4
31	41	139	LEU	3.4
32	51	113	VAL	3.4
45	G8	106	LEU	3.4
52	N8	60	VAL	3.4
4	3E	80	GLU	3.4
5	4E	122	GLU	3.4
5	4E	126	ARG	3.4
31	41	96	ARG	3.4
42	D8	36	PRO	3.4
26	14	2272	U	3.4
1	1G	112	G	3.4
26	1H	948	G	3.4
26	1H	2131	G	3.4
26	1H	2135	A	3.4
11	2I	81	ASP	3.4
36	78	57	THR	3.4
37	45	137	TYR	3.4
42	95	69	LYS	3.4
3	22	181	ASN	3.4
9	82	96	LEU	3.4
31	49	160	VAL	3.4
46	H8	70	LEU	3.4
48	J8	95	LEU	3.4
51	I5	45	GLY	3.4
2	1E	30	ARG	3.4
17	8I	86	GLU	3.4
45	C5	23	ARG	3.4
32	51	102	ALA	3.4
9	82	97	LYS	3.4
20	BI	11	SER	3.4
24	3K	33	U	3.4

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Mol	Chain	Res	Type	RSRZ
34	15	104	LYS	3.4
34	15	109	LYS	3.4
38	98	15	SER	3.4
48	F5	78	LYS	3.4
34	58	93	THR	3.4
36	78	68	GLN	3.4
1	1G	27	G	3.3
1	1G	68	G	3.3
1	1G	413	G	3.3
1	1G	328	C	3.3
20	BI	103	GLY	3.3
24	3K	17	C	3.3
26	1H	2175	C	3.3
26	14	1404	C	3.3
15	6A	54	ARG	3.3
36	35	16	ARG	3.3
46	H8	79	ARG	3.3
7	62	147	ALA	3.3
12	3A	47	LYS	3.3
29	29	152	LYS	3.3
32	59	72	ILE	3.3
1	13	1390	U	3.3
1	1G	239	U	3.3
2	12	24	TRP	3.3
47	E5	45	PHE	3.3
7	6E	38	LEU	3.3
29	29	5	LEU	3.3
55	M5	34	TRP	3.3
13	4A	74	VAL	3.3
4	32	171	GLY	3.3
12	3A	29	GLY	3.3
13	4A	99	ARG	3.3
20	BI	47	GLY	3.3
26	14	529	A	3.3
26	14	2758	A	3.3
3	2E	44	GLU	3.3
37	45	105	GLU	3.3
1	13	137	C	3.3
26	1H	591	C	3.3
1	13	1001	G	3.3
1	1G	108	G	3.3
24	3K	5	G	3.3

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Mol	Chain	Res	Type	RSRZ
32	51	117	PRO	3.3
33	61	134	PRO	3.3
40	B8	98	LYS	3.3
20	BA	106	ALA	3.3
10	1I	11	PHE	3.3
10	1I	47	PHE	3.3
32	51	123	PHE	3.3
28	19	40	THR	3.3
32	59	155	SER	3.3
36	35	32	THR	3.3
1	13	1425	U	3.3
1	1G	20	U	3.3
11	2A	75	TYR	3.3
20	BI	96	GLY	3.3
41	85	24	TYR	3.3
36	35	13	ASN	3.3
46	D5	34	ASN	3.3
13	4A	61	GLU	3.3
18	9A	62	GLU	3.3
1	1G	1201	A	3.3
20	BA	21	LYS	3.3
5	42	17	ALA	3.3
17	8A	36	ILE	3.3
26	1H	2700	C	3.3
29	21	187	ALA	3.3
26	14	1816	G	3.3
8	72	31	PHE	3.3
46	H8	150	LEU	3.3
12	3A	82	VAL	3.3
17	8A	68	ARG	3.3
32	59	129	THR	3.3
33	61	113	ARG	3.3
26	14	767	U	3.3
33	69	130	TYR	3.3
5	42	127	ASN	3.3
13	4A	62	ASN	3.3
10	1A	57	LYS	3.3
33	69	23	PRO	3.3
46	D5	171	ILE	3.3
57	3L	9	A	3.3
2	12	149	LEU	3.3
14	5A	53	LEU	3.3

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Mol	Chain	Res	Type	RSRZ
33	69	30	LEU	3.3
10	1A	63	PHE	3.3
9	82	9	ARG	3.3
19	AI	81	ARG	3.3
26	14	560	C	3.3
26	14	964	C	3.3
48	F5	20	ARG	3.3
56	1L	13	C	3.3
2	1E	224	GLN	3.3
12	3A	78	GLN	3.3
29	21	59	VAL	3.3
33	69	17	GLN	3.3
54	P8	36	GLN	3.3
1	1G	575	G	3.3
11	2A	86	GLY	3.3
26	1H	2123	G	3.3
26	1H	2334	G	3.3
26	14	1521	G	3.3
9	82	116	LYS	3.2
49	K8	12	GLU	3.2
5	4E	129	ILE	3.2
2	12	13	ALA	3.2
13	4A	75	ALA	3.2
20	BA	76	ALA	3.2
37	45	140	ALA	3.2
8	72	112	LEU	3.2
19	AA	71	LEU	3.2
31	41	34	LEU	3.2
20	BI	83	ARG	3.2
56	1L	38	A	3.2
3	22	130	VAL	3.2
9	82	108	VAL	3.2
1	1G	1352	C	3.2
3	22	165	THR	3.2
8	72	131	GLY	3.2
26	1H	2108	C	3.2
42	D8	49	THR	3.2
42	95	41	GLY	3.2
44	B5	86	GLY	3.2
53	K5	14	THR	3.2
17	8I	34	LYS	3.2
7	6E	44	TYR	3.2

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Mol	Chain	Res	Type	RSRZ
26	1H	2132	U	3.2
26	14	101	G	3.2
26	14	966	G	3.2
4	32	174	LEU	3.2
33	61	12	LEU	3.2
41	85	46	ALA	3.2
5	42	27	ARG	3.2
28	19	69	ARG	3.2
42	D8	83	ARG	3.2
14	5A	37	PHE	3.2
6	5E	92	LYS	3.2
10	1I	55	LYS	3.2
26	1H	2126	A	3.2
28	11	236	GLY	3.2
36	78	29	LYS	3.2
1	13	150	C	3.2
1	1G	237	C	3.2
13	4A	87	TYR	3.2
26	14	1735	C	3.2
17	8A	28	PRO	3.2
26	14	1621	U	3.2
14	5I	26	ARG	3.2
1	13	933	G	3.2
26	1H	1056	G	3.2
3	22	68	VAL	3.2
12	3A	9	GLN	3.2
45	C5	47	LYS	3.2
2	12	72	GLY	3.2
12	3I	29	GLY	3.2
29	21	50	GLY	3.2
26	14	1084	A	3.2
26	14	1103	A	3.2
26	14	2662	A	3.2
27	1J	59	A	3.2
32	59	86	GLU	3.2
57	3L	73	A	3.2
52	J5	46	CYS	3.2
4	32	83	SER	3.2
5	4E	125	SER	3.2
21	1B	13	ILE	3.2
40	B8	42	ILE	3.2
16	7I	29	ASP	3.2

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Mol	Chain	Res	Type	RSRZ
1	1G	154	C	3.2
3	2E	42	LEU	3.2
26	14	172	C	3.2
26	14	1049	C	3.2
46	D5	164	ALA	3.2
52	N8	24	ALA	3.2
53	K5	49	HIS	3.2
33	69	3	VAL	3.2
33	69	87	LYS	3.2
34	58	98	VAL	3.2
46	H8	175	VAL	3.2
46	D5	74	VAL	3.2
55	Q8	52	LYS	3.2
3	22	162	GLN	3.2
7	6E	106	GLN	3.2
1	13	953	G	3.2
1	1G	954	G	3.2
32	59	122	THR	3.2
2	1E	127	ILE	3.2
2	1E	201	ILE	3.2
13	4I	9	ILE	3.2
1	13	389	A	3.1
1	13	1531	A	3.1
7	62	59	LEU	3.1
30	31	99	TYR	3.1
30	31	13	SER	3.1
46	H8	153	SER	3.1
53	K5	11	LEU	3.1
4	3E	32	ALA	3.1
13	4A	118	ALA	3.1
29	29	114	ALA	3.1
45	G8	43	ASN	3.1
3	22	150	LYS	3.1
41	85	22	LYS	3.1
33	69	107	VAL	3.1
42	D8	46	VAL	3.1
48	F5	79	GLY	3.1
10	1A	42	THR	3.1
28	19	17	THR	3.1
55	Q8	27	THR	3.1
5	42	89	ILE	3.1
31	49	77	ILE	3.1

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Mol	Chain	Res	Type	RSRZ
34	58	85	ILE	3.1
1	13	122	G	3.1
1	13	799	G	3.1
8	7E	2	LEU	3.1
10	1A	66	ARG	3.1
13	4A	71	ARG	3.1
46	H8	82	ARG	3.1
47	I8	44	ARG	3.1
7	62	39	ALA	3.1
32	59	84	SER	3.1
48	J8	86	SER	3.1
2	12	55	PHE	3.1
37	45	104	PHE	3.1
34	58	69	GLN	3.1
4	3E	167	GLY	3.1
26	14	155	C	3.1
27	1J	6	C	3.1
45	G8	93	GLY	3.1
11	2A	48	ILE	3.1
34	15	100	GLU	3.1
46	D5	176	PRO	3.1
2	1E	217	ARG	3.1
2	12	142	LEU	3.1
3	22	115	LEU	3.1
8	72	10	LEU	3.1
37	45	79	LEU	3.1
41	C8	22	LYS	3.1
20	BI	97	ALA	3.1
30	31	42	ALA	3.1
30	39	49	ALA	3.1
30	39	97	TYR	3.1
41	85	21	ALA	3.1
17	8A	29	HIS	3.1
2	12	229	VAL	3.1
3	22	112	SER	3.1
4	32	26	CYS	3.1
11	2A	119	CYS	3.1
13	4A	117	VAL	3.1
16	7I	9	PHE	3.1
24	3K	22	G	3.1
26	1H	2124	G	3.1
26	1H	2191	G	3.1

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Mol	Chain	Res	Type	RSRZ
26	14	2125	G	3.1
26	14	2270	G	3.1
28	19	203	ASN	3.1
46	D5	165	VAL	3.1
1	13	1451	A	3.1
26	1H	405	U	3.1
26	1H	1516	U	3.1
47	I8	40	GLN	3.1
47	I8	42	GLY	3.1
23	2L	1	C	3.1
26	1H	886	C	3.1
4	3E	96	LEU	3.1
29	21	64	LYS	3.1
31	41	160	VAL	3.1
37	88	81	VAL	3.1
49	K8	52	ASP	3.1
4	32	2	GLY	3.1
29	29	106	GLY	3.1
32	59	5	GLY	3.1
1	13	105	G	3.1
1	1G	1029	G	3.1
1	1G	1061	G	3.1
26	14	2121	G	3.1
56	1L	14	A	3.1
3	22	5	ILE	3.1
3	2E	34	LEU	3.1
9	82	12	GLU	3.1
37	88	139	GLU	3.1
40	B8	114	LEU	3.1
5	4E	21	ALA	3.0
26	1H	1556	C	3.1
26	14	2161	C	3.1
11	2I	42	TRP	3.0
2	1E	15	VAL	3.0
9	8E	125	TYR	3.0
32	59	115	VAL	3.0
35	25	7	TYR	3.0
44	F8	52	VAL	3.0
16	7I	30	GLY	3.0
9	8E	81	ILE	3.0
42	95	21	ARG	3.0
2	1E	221	LEU	3.0

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Mol	Chain	Res	Type	RSRZ
3	22	91	LEU	3.0
3	22	111	LEU	3.0
32	51	116	GLU	3.0
33	61	9	LEU	3.0
36	35	45	LEU	3.0
1	1G	1150	U	3.0
23	2L	25	U	3.0
45	C5	83	THR	3.0
1	13	108	G	3.0
1	13	292	G	3.0
1	13	1343	G	3.0
1	13	1529	G	3.0
1	1G	11	G	3.0
1	1G	376	G	3.0
26	1H	1555	G	3.0
26	1H	2707	G	3.0
12	3I	129	ALA	3.0
2	12	152	PHE	3.0
5	42	45	PHE	3.0
17	8I	29	HIS	3.0
20	BI	16	HIS	3.0
37	88	104	PHE	3.0
1	13	1424	C	3.0
8	72	94	TYR	3.0
26	1H	2690	C	3.0
26	14	1304	C	3.0
31	49	146	TYR	3.0
56	1L	56	C	3.0
35	68	29	ASN	3.0
19	AA	49	ILE	3.0
29	29	50	GLY	3.0
34	15	81	GLY	3.0
38	55	103	ARG	3.0
42	95	9	GLY	3.0
7	6E	16	LEU	3.0
37	45	37	LEU	3.0
33	61	119	PRO	3.0
37	45	80	GLU	3.0
5	42	116	THR	3.0
20	BI	71	THR	3.0
26	1H	2122	U	3.0
23	2K	74	A	3.0

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Mol	Chain	Res	Type	RSRZ
27	16	1(M)	A	3.0
1	13	1033	G	3.0
1	1G	570	G	3.0
26	1H	1591	G	3.0
26	1H	2659	G	3.0
1	13	103	C	3.0
1	1G	74	C	3.0
2	12	80	ILE	3.0
20	BI	102	GLY	3.0
22	1K	13	C	3.0
26	14	1493	C	3.0
28	19	4	LYS	3.0
20	BA	70	SER	3.0
32	51	57	ASP	3.0
53	K5	36	LEU	3.0
45	G8	102	CYS	3.0
50	H5	12	PRO	3.0
1	13	1391	U	3.0
7	6E	2	ALA	3.0
26	1H	1406	U	3.0
26	14	1090	U	3.0
26	14	1520	U	3.0
14	5I	25	VAL	3.0
10	1I	60	ARG	3.0
19	AA	80	TYR	3.0
35	68	66	LYS	3.0
29	29	149	ARG	3.0
51	M8	62	ARG	3.0
52	J5	51	TYR	3.0
2	12	32	ILE	3.0
13	4A	78	ILE	3.0
2	12	51	LEU	3.0
34	15	69	GLN	3.0
39	A8	110	LEU	3.0
48	J8	84	GLY	3.0
55	M5	32	LEU	3.0
1	13	113	G	3.0
1	1G	1224	G	3.0
26	1H	2165	G	3.0
6	52	56	PRO	3.0
26	1H	2498	C	3.0
33	61	137	PRO	3.0

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Mol	Chain	Res	Type	RSRZ
56	1L	74	C	3.0
9	82	18	PHE	3.0
12	3A	80	HIS	3.0
29	29	159	HIS	3.0
30	39	83	PHE	3.0
39	65	19	LYS	2.9
4	32	141	ARG	2.9
13	4A	88	ARG	2.9
30	39	172	TRP	2.9
51	M8	55	ARG	2.9
40	B8	50	ILE	2.9
46	D5	53	ILE	2.9
46	D5	137	ILE	2.9
2	1E	51	LEU	2.9
3	22	52	LEU	2.9
33	69	75	LEU	2.9
34	58	138	LEU	2.9
34	15	78	TYR	2.9
41	85	39	LEU	2.9
34	15	131	GLN	2.9
45	C5	22	GLY	2.9
45	C5	103	GLY	2.9
55	Q8	43	GLN	2.9
3	22	109	PRO	2.9
10	1A	64	GLU	2.9
20	BI	98	PRO	2.9
15	6I	52	SER	2.9
1	1G	9	G	2.9
1	1G	231	G	2.9
26	1H	1816	G	2.9
26	14	2149	G	2.9
1	13	1230	C	2.9
2	1E	188	ALA	2.9
29	29	68	ALA	2.9
30	31	130	ALA	2.9
39	65	2	ALA	2.9
31	49	117	PHE	2.9
32	59	68	THR	2.9
1	1G	1159	U	2.9
3	22	38	ARG	2.9
4	32	122	ARG	2.9
12	3I	15	ARG	2.9

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Mol	Chain	Res	Type	RSRZ
16	7I	42	ARG	2.9
16	7I	75	ARG	2.9
46	D5	120	ILE	2.9
49	G5	57	ILE	2.9
5	42	35	GLY	2.9
31	41	146	TYR	2.9
53	O8	21	TYR	2.9
2	12	159	PRO	2.9
29	29	74	PRO	2.9
57	3L	38	A	2.9
38	98	43	GLU	2.9
8	72	135	CYS	2.9
12	3I	36	VAL	2.9
13	4I	2	ALA	2.9
46	H8	165	VAL	2.9
10	1A	67	THR	2.9
33	69	76	THR	2.9
51	M8	42	PHE	2.9
1	1G	875	C	2.9
1	1G	1249	C	2.9
3	22	156	ARG	2.9
1	1G	973	G	2.9
57	3L	19	G	2.9
51	I5	14	ILE	2.9
9	8E	47	LEU	2.9
9	8E	79	LEU	2.9
51	M8	63	TYR	2.9
33	61	111	PRO	2.9
17	8A	49	GLU	2.9
33	69	85	GLU	2.9
5	42	130	ASN	2.9
9	8E	75	ASP	2.9
2	12	225	ALA	2.9
7	62	35	LYS	2.9
28	11	32	SER	2.9
29	21	7	VAL	2.9
45	G8	98	VAL	2.9
48	F5	14	VAL	2.9
2	1E	163	PHE	2.9
13	4A	114	ARG	2.9
31	41	33	ARG	2.9
4	32	158	ILE	2.9

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Mol	Chain	Res	Type	RSRZ
28	11	64	ILE	2.9
4	32	11	LEU	2.9
32	59	88	LEU	2.9
37	88	37	LEU	2.9
1	13	562	C	2.9
26	14	1592	C	2.9
26	1H	1065	U	2.9
1	1G	21	G	2.9
24	3K	27	G	2.9
26	14	2148	G	2.9
33	69	54	GLN	2.9
3	22	23	TYR	2.9
30	31	97	TYR	2.9
39	A8	7	TYR	2.9
17	8I	49	GLU	2.9
35	68	108	GLU	2.9
55	Q8	56	GLU	2.9
2	12	22	LYS	2.9
4	3E	151	LYS	2.9
21	1B	3	LYS	2.9
41	C8	16	LYS	2.9
7	62	75	VAL	2.9
19	AA	58	VAL	2.9
32	59	50	VAL	2.9
46	H8	111	VAL	2.9
39	A8	12	PHE	2.9
26	1H	887	A	2.9
32	51	60	ARG	2.9
40	B8	111	ARG	2.9
12	3A	61	THR	2.9
12	3A	122	THR	2.9
8	72	6	ILE	2.9
17	8I	89	LEU	2.9
29	21	63	LEU	2.9
33	61	140	LEU	2.9
55	M5	16	ILE	2.9
29	21	194	GLY	2.8
2	12	97	TRP	2.8
7	6E	11	GLN	2.8
30	39	92	PRO	2.8
1	1G	1051	C	2.8
1	1G	1195	C	2.8

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Mol	Chain	Res	Type	RSRZ
26	14	1396	U	2.8
5	42	50	GLU	2.8
26	14	2136	C	2.8
9	8E	70	LYS	2.8
11	2A	11	LYS	2.8
29	29	145	LYS	2.8
49	K8	5	GLU	2.8
1	13	657	G	2.8
1	1G	1233	G	2.8
5	4E	132	ALA	2.8
10	1I	26	ALA	2.8
26	1H	2160	G	2.8
26	14	1473	G	2.8
32	59	113	VAL	2.8
29	29	79	ARG	2.8
33	61	115	ALA	2.8
40	B8	115	ARG	2.8
46	H8	113	ALA	2.8
47	E5	9	SER	2.8
2	1E	238	LEU	2.8
2	12	138	LEU	2.8
19	AA	40	ILE	2.8
51	M8	52	THR	2.8
26	1H	182	A	2.8
45	G8	99	CYS	2.8
4	32	109	GLY	2.8
10	1A	53	PRO	2.8
49	G5	56	GLN	2.8
9	8E	118	LYS	2.8
39	A8	11	LYS	2.8
49	K8	66	GLU	2.8
1	13	1132	C	2.8
1	13	1437	C	2.8
4	32	32	ALA	2.8
26	1H	2145	C	2.8
26	1H	2803	C	2.8
26	14	574	C	2.8
26	14	1386	C	2.8
26	14	2021	C	2.8
31	49	181	ARG	2.8
5	42	26	PHE	2.8
15	6A	15	PHE	2.8

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Mol	Chain	Res	Type	RSRZ
6	5E	83	ASP	2.8
16	7I	49	LEU	2.8
29	29	63	LEU	2.8
35	25	81	ASP	2.8
1	1G	29	G	2.8
1	1G	881	G	2.8
1	1G	1032(B)	G	2.8
1	1G	1373	G	2.8
26	1H	968	G	2.8
26	14	388	G	2.8
26	14	1051	G	2.8
26	14	2119	A	2.8
18	9A	61	LYS	2.8
34	58	70	LYS	2.8
43	E8	98	LYS	2.8
55	Q8	21	LYS	2.8
19	AA	76	PRO	2.8
32	59	126	PRO	2.8
34	58	40	PRO	2.8
4	32	207	TYR	2.8
13	4A	98	VAL	2.8
17	8I	32	TYR	2.8
17	8A	5	VAL	2.8
40	75	103	ARG	2.8
46	H8	72	ARG	2.8
46	D5	141	VAL	2.8
41	C8	116	ALA	2.8
2	12	155	LEU	2.8
9	8E	117	HIS	2.8
10	1I	90	LEU	2.8
32	51	103	LEU	2.8
33	69	31	LEU	2.8
35	25	13	ASN	2.8
1	13	314	C	2.8
1	1G	385	C	2.8
1	1G	826	C	2.8
1	1G	985	C	2.8
26	1H	2804	C	2.8
26	14	1407	C	2.8
2	12	124	SER	2.8
48	F5	38	SER	2.8
36	35	64	LYS	2.8

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Mol	Chain	Res	Type	RSRZ
43	E8	83	LYS	2.8
9	8E	68	GLY	2.8
44	F8	94	GLY	2.8
1	13	346	G	2.8
1	1G	1182	G	2.8
8	7E	89	PRO	2.8
24	3K	44	G	2.8
26	1H	2891	G	2.8
26	14	2532	G	2.8
52	J5	27	PRO	2.8
26	1H	529	A	2.8
26	1H	1046	A	2.8
26	14	1029	A	2.8
49	K8	11	GLU	2.8
13	4I	3	ARG	2.8
35	68	17	ARG	2.8
13	4A	54	VAL	2.8
19	AA	19	VAL	2.8
53	O8	48	VAL	2.8
3	22	50	ALA	2.8
4	32	4	TYR	2.8
5	42	84	PHE	2.8
45	C5	78	ALA	2.8
46	D5	99	TYR	2.8
26	14	1105	U	2.8
43	E8	86	LEU	2.8
49	K8	3	LEU	2.8
2	12	94	ASN	2.8
47	I8	43	THR	2.8
1	13	1076	C	2.8
1	1G	136	C	2.8
49	K8	4	SER	2.8
31	41	42	GLY	2.8
2	12	202	PRO	2.8
29	21	74	PRO	2.8
53	K5	31	PRO	2.8
5	4E	81	GLU	2.7
28	19	217	ARG	2.7
7	6E	75	VAL	2.7
11	2A	14	VAL	2.7
11	2A	105	VAL	2.7
53	K5	48	VAL	2.7

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Mol	Chain	Res	Type	RSRZ
4	32	173	TRP	2.7
1	13	631	G	2.7
2	12	17	PHE	2.7
26	14	849	A	2.7
26	14	1536	A	2.7
26	14	2751	G	2.7
27	1J	23	G	2.7
32	59	123	PHE	2.7
36	35	51	PHE	2.7
37	45	136	ALA	2.7
46	H8	104	PHE	2.7
9	82	74	ILE	2.7
10	1I	38	ILE	2.7
16	7A	32	TYR	2.7
1	13	1159	U	2.7
1	13	1196	U	2.7
1	13	1341	U	2.7
26	14	2118	U	2.7
15	6A	5	LYS	2.7
38	55	42	LYS	2.7
39	A8	41	ASP	2.7
47	E5	71	ASP	2.7
3	22	114	PRO	2.7
1	1G	995	C	2.7
24	3K	72	C	2.7
26	1H	4	C	2.7
26	1H	34	C	2.7
26	14	951	C	2.7
26	14	1476	C	2.7
31	49	138	GLN	2.7
37	88	38	GLU	2.7
57	3L	48	C	2.7
14	5A	56	VAL	2.7
5	4E	134	ALA	2.7
2	12	172	ILE	2.7
6	5E	97	PHE	2.7
37	45	2	LEU	2.7
39	65	58	LEU	2.7
41	85	41	ALA	2.7
41	85	96	ALA	2.7
55	M5	31	HIS	2.7
1	1G	228	A	2.7

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Mol	Chain	Res	Type	RSRZ
9	82	112	LYS	2.7
11	2I	11	LYS	2.7
13	4I	115	LYS	2.7
28	19	59	LYS	2.7
29	29	41	LYS	2.7
1	1G	1173	G	2.7
26	14	1517	G	2.7
6	52	84	ASN	2.7
51	I5	52	THR	2.7
21	1B	11	GLY	2.7
45	G8	41	GLY	2.7
20	BI	82	SER	2.7
38	98	22	ARG	2.7
15	6A	71	GLN	2.7
36	78	71	VAL	2.7
37	45	27	VAL	2.7
48	J8	70	VAL	2.7
1	1G	1113	C	2.7
7	62	127	ALA	2.7
13	4A	76	ALA	2.7
17	8I	27	PHE	2.7
22	1K	40	C	2.7
26	14	867	C	2.7
45	G8	89	PHE	2.7
46	H8	171	ILE	2.7
46	D5	5	LEU	2.7
48	F5	80	LEU	2.7
49	G5	60	LEU	2.7
57	3L	3	C	2.7
11	2A	51	LYS	2.7
33	69	2	LYS	2.7
34	15	70	LYS	2.7
41	C8	34	LYS	2.7
53	O8	13	CYS	2.7
55	M5	29	LYS	2.7
8	7E	1	MET	2.7
1	1G	313	A	2.7
1	1G	1225	A	2.7
56	1L	23	A	2.7
1	1G	560	U	2.7
1	1G	1391	U	2.7
4	3E	2	GLY	2.7

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Mol	Chain	Res	Type	RSRZ
20	BA	83	ARG	2.7
34	58	86	PRO	2.7
37	45	88	GLY	2.7
38	55	2	ARG	2.7
39	A8	109	GLY	2.7
50	H5	30	ARG	2.7
51	I5	41	PRO	2.7
1	13	181	G	2.7
1	13	238	G	2.7
1	13	293	G	2.7
1	13	630	G	2.7
1	1G	310	G	2.7
1	1G	505	G	2.7
2	12	126	GLU	2.7
10	1I	84	GLN	2.7
26	1H	2663	G	2.7
26	14	391	G	2.7
26	14	1623	G	2.7
27	1J	118	G	2.7
12	3A	40	VAL	2.7
33	69	41	GLU	2.7
33	69	92	VAL	2.7
46	D5	96	VAL	2.7
2	1E	44	LEU	2.7
17	8I	31	LEU	2.7
20	BA	66	ALA	2.7
43	E8	93	ALA	2.7
45	G8	48	ALA	2.7
45	C5	61	ILE	2.7
55	Q8	51	ALA	2.7
37	88	76	LYS	2.7
53	K5	17	LYS	2.7
35	25	1	MET	2.7
29	29	66	HIS	2.7
1	13	291	C	2.7
1	1G	1114	C	2.7
1	1G	1223	C	2.7
8	7E	94	TYR	2.7
26	1H	2699	C	2.7
26	14	1607	C	2.7
8	7E	85	ARG	2.7
20	BI	23	ARG	2.7

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Mol	Chain	Res	Type	RSRZ
50	H5	29	ARG	2.7
7	6E	84	ASN	2.7
29	21	71	GLY	2.7
36	35	34	GLY	2.7
47	I8	76	GLY	2.7
49	G5	18	PRO	2.7
52	J5	11	THR	2.7
26	1H	1762	A	2.7
2	12	112	VAL	2.7
28	19	3	VAL	2.7
51	I5	35	VAL	2.7
2	12	42	ILE	2.6
3	22	33	LEU	2.7
10	1I	23	ILE	2.6
16	7I	6	LEU	2.7
20	BI	43	LEU	2.7
3	22	26	LYS	2.6
12	3A	17	LYS	2.6
44	F8	53	LYS	2.6
48	F5	32	LYS	2.6
48	F5	39	LYS	2.6
50	L8	43	ILE	2.6
2	1E	13	ALA	2.6
29	29	204	ALA	2.6
1	13	1131	G	2.6
1	13	1224	G	2.6
1	1G	232	G	2.6
1	1G	1482	G	2.6
7	62	31	MET	2.6
26	1H	1062	G	2.6
26	14	669	G	2.6
26	14	1429	G	2.6
26	14	1591	G	2.6
7	6E	85	TYR	2.6
45	C5	102	CYS	2.6
30	39	205	ARG	2.6
49	K8	14	ARG	2.6
49	K8	69	ARG	2.6
1	13	1228	C	2.6
26	14	1599	C	2.6
26	14	1625	C	2.6
9	82	67	GLY	2.6

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Mol	Chain	Res	Type	RSRZ
52	N8	32	PRO	2.6
1	1G	961	U	2.6
28	19	99	ASP	2.6
34	15	87	LEU	2.6
37	45	102	VAL	2.6
41	C8	83	LEU	2.6
46	H8	5	LEU	2.6
47	I8	46	LYS	2.6
50	H5	58	VAL	2.6
53	K5	15	GLU	2.6
3	22	14	ILE	2.6
26	14	1471	A	2.6
32	51	4	ILE	2.6
39	65	35	ILE	2.6
2	1E	48	MET	2.6
3	22	169	ALA	2.6
28	19	77	ALA	2.6
34	15	117	PHE	2.6
52	N8	53	ALA	2.6
19	AI	14	HIS	2.6
1	13	231	G	2.6
6	52	47	ARG	2.6
26	1H	593	G	2.6
26	1H	928	G	2.6
26	1H	2805	G	2.6
26	14	154	G	2.6
26	14	352	G	2.6
26	14	1539	G	2.6
26	14	1555	G	2.6
45	G8	35	TYR	2.6
56	1L	28	G	2.6
11	2A	115	PRO	2.6
12	3I	14	GLY	2.6
16	7I	66	PRO	2.6
18	9A	57	GLY	2.6
29	21	32	PRO	2.6
30	39	66	PRO	2.6
36	35	8	PRO	2.6
45	C5	25	GLY	2.6
48	F5	22	GLY	2.6
1	13	63	C	2.6
2	1E	187	LEU	2.6

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Mol	Chain	Res	Type	RSRZ
2	12	9	GLU	2.6
3	22	207	VAL	2.6
15	6A	31	LEU	2.6
26	1H	277	C	2.6
26	1H	1574	C	2.6
26	1H	2701	C	2.6
26	14	2568	C	2.6
27	16	12	C	2.6
32	59	67	LEU	2.6
34	15	138	LEU	2.6
41	C8	20	LEU	2.6
42	95	52	VAL	2.6
42	95	94	LEU	2.6
44	B5	52	VAL	2.6
48	J8	97	LEU	2.6
52	N8	57	VAL	2.6
3	22	202	ILE	2.6
10	1I	74	ILE	2.6
16	7I	19	ILE	2.6
1	1G	229	U	2.6
1	1G	1450	U	2.6
9	82	105	ASP	2.6
51	M8	65	ASP	2.6
2	1E	122	PHE	2.6
7	62	40	ALA	2.6
9	82	101	PHE	2.6
39	65	112	PHE	2.6
40	75	94	ALA	2.6
1	13	1227	A	2.6
1	1G	325	A	2.6
1	1G	1287	A	2.6
12	3I	22	SER	2.6
26	1H	2662	A	2.6
7	62	153	HIS	2.6
28	19	250	TRP	2.6
9	8E	114	TYR	2.6
36	35	78	PRO	2.6
37	45	33	GLY	2.6
52	N8	34	PRO	2.6
38	55	9	LYS	2.6
1	13	1002	G	2.6
2	1E	154	LEU	2.6

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Mol	Chain	Res	Type	RSRZ
3	22	101	LEU	2.6
4	32	19	LEU	2.6
2	12	39	ILE	2.6
3	22	106	VAL	2.6
26	1H	2121	G	2.6
26	14	2550	G	2.6
26	14	2655	G	2.6
36	78	30	THR	2.6
42	D8	38	LEU	2.6
42	95	72	VAL	2.6
51	M8	21	VAL	2.6
51	M8	35	VAL	2.6
51	I5	9	LEU	2.6
57	3L	27	G	2.6
12	3A	127	GLU	2.6
39	A8	43	GLU	2.6
53	K5	26	ASN	2.6
1	1G	643	C	2.6
1	1G	989	C	2.6
2	12	79	ASP	2.6
19	AI	75	ALA	2.6
20	BA	94	ALA	2.6
26	14	393	C	2.6
26	14	1104	C	2.6
26	14	1221	C	2.6
1	13	170	U	2.6
26	1H	1590	U	2.6
9	8E	121	ARG	2.6
47	I8	41	ARG	2.6
24	3K	14	A	2.6
26	14	821	A	2.6
26	14	2170	A	2.6
26	14	2542	A	2.6
4	3E	138	TYR	2.6
16	7I	41	PRO	2.6
18	9A	84	LYS	2.6
28	19	39	LYS	2.6
29	21	62	PRO	2.6
10	1I	85	LEU	2.6
12	3A	52	LEU	2.6
30	31	12	LEU	2.6
30	39	20	LEU	2.6

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Mol	Chain	Res	Type	RSRZ
31	49	19	LEU	2.6
40	75	99	LEU	2.6
3	2E	39	ILE	2.6
3	22	99	VAL	2.6
32	59	19	VAL	2.6
33	61	4	ILE	2.6
46	D5	126	VAL	2.6
46	D5	139	VAL	2.6
53	O8	40	CYS	2.6
3	2E	37	GLN	2.6
38	55	71	GLN	2.6
45	G8	105	ALA	2.6
45	C5	100	ALA	2.6
26	14	654(D)	G	2.5
26	14	1091	G	2.5
2	1E	40	HIS	2.5
3	22	31	HIS	2.5
26	14	2122	U	2.5
26	14	2506	U	2.5
1	13	328	C	2.5
23	2L	72	C	2.5
26	14	4	C	2.5
9	82	11	LYS	2.5
45	G8	94	LYS	2.5
1	1G	873	A	2.5
8	72	5	PRO	2.5
26	1H	984	A	2.5
9	82	8	GLY	2.5
10	1A	37	PRO	2.5
26	1H	2712(A)	A	2.5
31	49	87	PRO	2.5
38	55	92	GLY	2.5
41	C8	43	GLY	2.5
42	95	36	PRO	2.5
52	J5	32	PRO	2.5
56	1L	9	A	2.5
14	5A	28	GLY	2.5
19	AI	22	LEU	2.5
33	69	72	LEU	2.5
45	C5	59	GLY	2.5
40	B8	100	TYR	2.5
45	C5	55	TYR	2.5

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Mol	Chain	Res	Type	RSRZ
48	J8	94	LEU	2.5
55	Q8	60	LEU	2.5
3	22	124	ILE	2.5
7	62	125	MET	2.5
18	9I	75	ILE	2.5
29	29	25	VAL	2.5
30	31	132	VAL	2.5
30	39	36	VAL	2.5
31	49	114	ILE	2.5
32	59	41	MET	2.5
5	42	54	ALA	2.5
31	49	50	ALA	2.5
41	C8	96	ALA	2.5
55	Q8	55	ALA	2.5
12	3I	89	ARG	2.5
16	7I	28	ARG	2.5
35	25	12	ASP	2.5
36	35	111	ARG	2.5
12	3I	28	LYS	2.5
43	A5	83	LYS	2.5
45	C5	54	LYS	2.5
48	J8	91	LYS	2.5
1	13	579	G	2.5
1	1G	326	G	2.5
26	1H	654(P)	G	2.5
26	1H	696	G	2.5
26	14	1348	G	2.5
26	14	2661	G	2.5
1	1G	1369	C	2.5
26	1H	982	C	2.5
31	41	94	LEU	2.5
33	69	134	PRO	2.5
34	15	129	PRO	2.5
2	12	208	ILE	2.5
7	6E	42	ILE	2.5
13	4I	4	ILE	2.5
46	H8	174	VAL	2.5
1	1G	563	A	2.5
1	1G	983	A	2.5
1	1G	1169	A	2.5
26	1H	5	A	2.5
26	14	1177	A	2.5

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Mol	Chain	Res	Type	RSRZ
2	12	59	GLU	2.5
17	8A	58	GLU	2.5
29	29	40	GLU	2.5
39	65	43	GLU	2.5
46	D5	2	GLU	2.5
52	J5	59	GLU	2.5
29	29	67	PHE	2.5
39	65	29	PHE	2.5
29	29	70	ALA	2.5
2	12	30	ARG	2.5
4	3E	118	ARG	2.5
17	8I	25	ARG	2.5
36	35	77	ARG	2.5
41	C8	36	ARG	2.5
52	N8	23	HIS	2.5
2	12	205	ASP	2.5
4	32	30	LYS	2.5
7	6E	29	LYS	2.5
20	BA	74	LYS	2.5
1	13	294	U	2.5
1	13	1125	U	2.5
1	1G	1364	U	2.5
23	2L	37	U	2.5
26	14	1405	U	2.5
8	7E	133	LEU	2.5
33	61	116	LEU	2.5
39	A8	48	LEU	2.5
45	C5	56	PRO	2.5
10	1I	50	ILE	2.5
31	49	157	ILE	2.5
37	45	30	GLY	2.5
38	98	106	GLY	2.5
47	E5	36	ILE	2.5
46	D5	71	VAL	2.5
1	13	569	C	2.5
16	7A	39	TYR	2.5
22	1K	17	C	2.5
26	1H	2164	C	2.5
26	14	279	C	2.5
1	13	1133	G	2.5
1	1G	1220	G	2.5
26	14	880	G	2.5

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Mol	Chain	Res	Type	RSRZ
26	14	2112	G	2.5
32	59	157	TYR	2.5
56	1L	29	G	2.5
2	12	28	PHE	2.5
7	6E	56	GLN	2.5
9	8E	61	ALA	2.5
13	4A	49	THR	2.5
20	BI	89	ARG	2.5
26	1H	2031	A	2.5
26	14	394	A	2.5
26	14	819	A	2.5
26	14	1384	A	2.5
36	35	79	ARG	2.5
47	E5	77	ARG	2.5
10	1I	80	LYS	2.5
14	5A	58	LYS	2.5
46	D5	87	ASP	2.5
2	12	101	MET	2.5
20	BI	13	LEU	2.5
39	65	110	LEU	2.5
40	B8	99	LEU	2.5
2	12	232	PRO	2.5
38	55	110	PRO	2.5
1	1G	1257	U	2.5
2	1E	18	GLY	2.5
2	12	222	ILE	2.5
5	42	11	ILE	2.5
28	11	100	GLY	2.5
5	4E	90	VAL	2.5
32	59	17	VAL	2.5
3	22	193	TYR	2.5
30	31	83	PHE	2.5
38	55	21	TYR	2.5
46	D5	29	TYR	2.5
9	82	76	ALA	2.5
15	6I	63	ARG	2.5
16	7A	26	ARG	2.5
30	31	95	ARG	2.5
43	E8	11	ARG	2.5
49	G5	7	ARG	2.5
1	13	754	C	2.5
37	45	21	THR	2.5

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Mol	Chain	Res	Type	RSRZ
13	4A	46	LYS	2.5
19	AI	6	LYS	2.5
45	C5	63	LYS	2.5
55	M5	59	LYS	2.5
1	13	227	G	2.5
1	1G	331	G	2.5
24	3K	15	G	2.5
26	1H	563	G	2.5
26	1H	975	G	2.5
26	1H	1063	G	2.5
26	1H	1074	G	2.5
26	14	171	G	2.5
57	3L	63	G	2.5
20	BI	9	ASN	2.5
53	K5	40	CYS	2.5
2	1E	142	LEU	2.4
11	2A	103	LEU	2.4
18	9A	58	LEU	2.4
20	BA	53	LEU	2.4
28	11	37	LEU	2.4
33	69	101	LEU	2.4
5	42	49	PRO	2.4
34	15	79	PRO	2.4
3	22	145	GLY	2.4
2	12	150	SER	2.4
32	59	37	VAL	2.4
33	69	19	VAL	2.4
40	B8	89	VAL	2.4
46	D5	86	VAL	2.4
51	M8	37	SER	2.4
26	1H	767	U	2.4
26	14	1406	U	2.4
4	32	209	ARG	2.4
9	8E	59	PHE	2.4
13	4I	102	ARG	2.4
16	7A	25	ARG	2.4
17	8A	75	ARG	2.4
30	31	65	TRP	2.4
37	45	139	GLU	2.4
41	C8	40	PHE	2.4
45	C5	60	PHE	2.4
3	22	163	ALA	2.4

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Mol	Chain	Res	Type	RSRZ
5	4E	133	TYR	2.4
14	5A	4	LYS	2.4
15	6I	71	GLN	2.4
36	78	140	ALA	2.4
45	C5	65	ALA	2.4
48	J8	78	LYS	2.4
5	4E	135	THR	2.4
46	D5	69	THR	2.4
1	1G	153	C	2.4
1	1G	1325	C	2.4
26	1H	1295	C	2.4
26	1H	1537	C	2.4
26	14	129	C	2.4
26	14	737	C	2.4
27	1J	108	C	2.4
17	8I	76	LEU	2.4
17	8A	98	LEU	2.4
31	41	135	LEU	2.4
36	35	3	LEU	2.4
46	D5	117	LEU	2.4
1	1G	1229	A	2.4
26	1H	2030	A	2.4
1	1G	22	G	2.4
1	1G	644	G	2.4
1	1G	987	G	2.4
15	6A	2	PRO	2.4
26	1H	929	G	2.4
26	1H	1091	G	2.4
26	14	2210	G	2.4
32	51	10	PRO	2.4
32	59	112	PRO	2.4
35	68	86	ILE	2.4
44	F8	85	PRO	2.4
9	8E	8	GLY	2.4
10	1I	101	VAL	2.4
28	19	98	VAL	2.4
42	95	8	GLY	2.4
3	2E	179	ARG	2.4
4	3E	115	ARG	2.4
38	55	27	SER	2.4
40	B8	80	SER	2.4
49	G5	4	SER	2.4

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Mol	Chain	Res	Type	RSRZ
50	L8	29	ARG	2.4
2	1E	4	GLU	2.4
2	1E	27	LYS	2.4
2	12	27	LYS	2.4
3	22	206	GLU	2.4
26	14	380	U	2.4
26	14	2041	U	2.4
30	31	56	GLU	2.4
34	15	37	LYS	2.4
37	45	91	GLU	2.4
5	42	48	ALA	2.4
32	59	102	ALA	2.4
32	59	156	ALA	2.4
33	69	83	ALA	2.4
7	62	44	TYR	2.4
5	42	98	THR	2.4
19	AA	77	THR	2.4
42	95	92	THR	2.4
2	12	69	LEU	2.4
3	22	87	LEU	2.4
4	32	21	LEU	2.4
32	59	33	LEU	2.4
41	C8	95	LEU	2.4
46	H8	28	MET	2.4
2	1E	185	ILE	2.4
1	13	390	C	2.4
1	13	822	C	2.4
1	1G	25	C	2.4
1	1G	1362(A)	C	2.4
2	12	194	PRO	2.4
5	42	80	ILE	2.4
31	49	144	ILE	2.4
26	14	837	C	2.4
26	14	1504	C	2.4
26	14	2039	C	2.4
29	29	62	PRO	2.4
33	69	132	PRO	2.4
48	F5	18	ILE	2.4
26	1H	1544	C	2.4
55	M5	53	PRO	2.4
2	12	151	GLY	2.4
2	12	191	ASP	2.4

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Mol	Chain	Res	Type	RSRZ
3	22	2	GLY	2.4
3	22	70	VAL	2.4
4	32	56	VAL	2.4
4	32	69	GLY	2.4
5	42	34	VAL	2.4
5	42	51	VAL	2.4
8	7E	95	VAL	2.4
11	2A	118	GLY	2.4
29	29	196	VAL	2.4
32	59	45	VAL	2.4
46	D5	27	VAL	2.4
26	1H	1472	A	2.4
26	14	2273	A	2.4
3	22	21	ARG	2.4
18	9A	21	LYS	2.4
20	BA	79	ARG	2.4
21	1B	22	ARG	2.4
30	39	62	ARG	2.4
34	58	74	ARG	2.4
1	1G	80	G	2.4
1	1G	1181	G	2.4
1	1G	1197	G	2.4
17	8I	24	GLU	2.4
19	AI	38	SER	2.4
24	3K	63	G	2.4
26	14	1131	G	2.4
26	14	2100	G	2.4
57	3L	1	G	2.4
14	5I	5	ALA	2.4
18	9I	20	ALA	2.4
39	A8	2	ALA	2.4
48	F5	42	GLN	2.4
1	13	560	U	2.4
26	14	562	U	2.4
7	6E	154	TYR	2.4
13	4A	103	THR	2.4
33	69	77	LEU	2.4
49	G5	44	LEU	2.4
20	BA	100	ILE	2.4
33	61	97	ILE	2.4
33	69	79	ILE	2.4
29	29	55	ASN	2.4

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Mol	Chain	Res	Type	RSRZ
3	22	80	GLY	2.4
3	22	103	VAL	2.4
5	42	41	VAL	2.4
13	4I	111	LYS	2.4
13	4A	85	GLY	2.4
42	D8	58	VAL	2.4
14	5A	50	LYS	2.4
31	49	115	ARG	2.4
40	B8	33	LYS	2.4
41	C8	93	LYS	2.4
43	A5	92	ARG	2.4
46	D5	179	ASP	2.4
1	1G	1230	C	2.4
26	1H	654(G)	C	2.4
26	1H	737	C	2.4
26	14	915	C	2.4
1	13	196	A	2.4
1	1G	109	A	2.4
1	1G	958	A	2.4
16	7A	83	GLU	2.4
24	3K	26	A	2.4
26	1H	21	A	2.4
26	1H	655	A	2.4
26	14	532	A	2.4
45	C5	91	GLU	2.4
45	G8	65	ALA	2.4
46	H8	172	ALA	2.4
19	AA	35	SER	2.4
33	69	91	SER	2.4
47	E5	16	SER	2.4
1	13	561	U	2.4
1	13	1171	G	2.4
1	1G	952	U	2.4
1	1G	1187	G	2.4
1	1G	1232	U	2.4
4	32	106	TYR	2.4
10	1I	48	THR	2.4
14	5A	21	TYR	2.4
26	1H	180	G	2.4
26	1H	2661	G	2.4
26	14	1622	G	2.4
26	14	2486	G	2.4

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Mol	Chain	Res	Type	RSRZ
28	19	192	THR	2.4
53	O8	47	THR	2.4
5	42	53	LEU	2.4
30	31	101	LEU	2.4
36	35	148	LEU	2.4
45	C5	75	ILE	2.4
46	D5	57	ILE	2.4
8	72	74	PRO	2.4
4	32	77	ASN	2.3
5	42	82	VAL	2.3
7	62	61	VAL	2.3
9	82	118	LYS	2.3
12	3I	23	LYS	2.3
19	AI	25	LYS	2.3
53	O8	26	ASN	2.3
53	K5	50	ARG	2.3
55	Q8	49	VAL	2.3
3	22	171	GLY	2.3
55	M5	57	ARG	2.3
14	5I	27	CYS	2.3
5	42	83	GLU	2.3
8	7E	124	ALA	2.3
9	8E	119	ALA	2.3
11	2A	89	ALA	2.3
15	6A	16	ALA	2.3
32	59	127	GLU	2.3
33	61	98	ALA	2.3
52	J5	14	ALA	2.3
1	13	1362(A)	C	2.3
2	12	146	GLN	2.3
9	82	73	GLN	2.3
17	8I	16	GLN	2.3
17	8I	26	GLN	2.3
26	1H	645	C	2.3
26	1H	2710	C	2.3
26	14	1383	C	2.3
26	14	1474	C	2.3
35	68	5	GLN	2.3
55	M5	35	GLN	2.3
1	13	262	A	2.3
1	13	1229	A	2.3
17	8A	15	MET	2.3

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Mol	Chain	Res	Type	RSRZ
26	1H	571	A	2.3
26	1H	2602	A	2.3
10	1A	71	LEU	2.3
32	51	98	LEU	2.3
33	61	114	LEU	2.3
53	K5	47	THR	2.3
1	1G	1052	U	2.3
26	14	858	U	2.3
26	14	2172	U	2.3
14	5A	7	ILE	2.3
28	19	204	ILE	2.3
51	M8	14	ILE	2.3
2	12	74	LYS	2.3
30	39	52	LYS	2.3
48	F5	23	LYS	2.3
53	O8	38	LYS	2.3
1	13	438	G	2.3
1	13	1026	G	2.3
3	2E	38	ARG	2.3
4	32	170	VAL	2.3
9	82	104	ARG	2.3
26	1H	1678	G	2.3
31	49	28	VAL	2.3
32	51	97	ARG	2.3
51	M8	33	VAL	2.3
56	1L	24	G	2.3
57	3L	44	G	2.3
9	8E	115	GLY	2.3
45	C5	104	GLY	2.3
5	42	6	PHE	2.3
31	49	23	PHE	2.3
10	1I	58	ASP	2.3
13	4A	73	GLU	2.3
19	AI	12	ASP	2.3
2	12	186	ALA	2.3
48	J8	77	ALA	2.3
50	L8	21	ALA	2.3
17	8A	16	GLN	2.3
33	61	17	GLN	2.3
46	H8	76	LEU	2.3
49	K8	16	LEU	2.3
1	13	1362	C	2.3

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Mol	Chain	Res	Type	RSRZ
10	1A	50	ILE	2.3
13	4A	43	THR	2.3
17	8I	51	TYR	2.3
26	1H	884	C	2.3
26	14	1387	C	2.3
27	1J	4	C	2.3
31	49	145	THR	2.3
37	45	64	ILE	2.3
47	I8	10	THR	2.3
1	1G	389	A	2.3
26	1H	2169	A	2.3
26	14	2269	A	2.3
55	Q8	41	ILE	2.3
37	45	130	LYS	2.3
42	D8	19	LYS	2.3
42	D8	69	LYS	2.3
44	B5	33	LYS	2.3
26	14	395	U	2.3
28	19	249	PRO	2.3
33	61	27	ARG	2.3
50	L8	2	PRO	2.3
12	3A	66	VAL	2.3
32	51	11	VAL	2.3
29	21	88	GLY	2.3
32	59	48	GLY	2.3
3	22	3	ASN	2.3
2	1E	17	PHE	2.3
1	13	1392	G	2.3
1	1G	92	G	2.3
1	1G	1368	G	2.3
4	3E	81	GLU	2.3
20	BI	94	ALA	2.3
26	1H	391	G	2.3
26	1H	592	G	2.3
35	68	45	GLU	2.3
2	12	158	LEU	2.3
4	32	157	LEU	2.3
9	82	85	LEU	2.3
36	78	148	LEU	2.3
39	A8	24	LEU	2.3
43	E8	82	LEU	2.3
38	98	61	HIS	2.3

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Mol	Chain	Res	Type	RSRZ
2	12	216	SER	2.3
4	3E	137	SER	2.3
45	C5	94	LYS	2.3
3	2E	184	TYR	2.3
21	1F	15	ARG	2.3
43	A5	84	ARG	2.3
1	13	134	A	2.3
1	1G	132	C	2.3
2	1E	239	VAL	2.3
1	13	1040	U	2.3
1	1G	263	A	2.3
1	1G	559	A	2.3
8	72	95	VAL	2.3
22	1K	49	C	2.3
23	2K	72	C	2.3
26	1H	390	A	2.3
26	1H	1070	A	2.3
26	1H	1379	A	2.3
26	1H	1498	C	2.3
26	1H	2176	A	2.3
26	14	32	C	2.3
26	14	2138	C	2.3
27	1J	27	C	2.3
41	C8	90	VAL	2.3
50	H5	59	VAL	2.3
1	1G	955	U	2.3
3	22	51	GLY	2.3
9	8E	6	GLY	2.3
20	BA	69	GLY	2.3
40	B8	47	GLY	2.3
10	1I	63	PHE	2.3
19	AI	10	PHE	2.3
31	49	178	PHE	2.3
45	C5	43	ASN	2.3
51	I5	49	PHE	2.3
10	1I	27	ALA	2.3
20	BI	52	ALA	2.3
30	39	141	ALA	2.3
32	59	165	ALA	2.3
55	Q8	25	MET	2.3
33	61	110	ASP	2.3
36	35	38	GLN	2.3

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Mol	Chain	Res	Type	RSRZ
36	35	59	LEU	2.3
43	A5	82	LEU	2.3
46	D5	70	LEU	2.3
46	D5	154	ASP	2.3
12	3A	21	LYS	2.3
45	C5	87	LYS	2.3
49	K8	8	LYS	2.3
1	1G	1032(A)	G	2.3
26	1H	2187	G	2.3
26	14	298	G	2.3
9	8E	16	ARG	2.3
11	2I	87	THR	2.3
21	1B	15	ARG	2.3
36	78	65	ARG	2.3
45	C5	97	ARG	2.3
2	1E	202	PRO	2.3
4	32	178	VAL	2.3
36	35	63	PRO	2.3
46	D5	39	VAL	2.3
8	72	90	GLY	2.3
11	2A	49	GLY	2.3
31	41	44	GLY	2.3
33	61	124	GLY	2.3
27	1J	41	U	2.3
1	13	195	A	2.2
1	1G	137	C	2.2
1	1G	224	C	2.2
1	1G	578	C	2.2
1	1G	1045	C	2.2
26	14	1556	C	2.2
26	14	1847	A	2.2
47	I8	57	PHE	2.2
5	42	104	ALA	2.2
9	8E	110	GLU	2.2
33	61	36	ALA	2.2
33	69	63	ALA	2.2
2	1E	10	LEU	2.2
19	AA	22	LEU	2.2
28	19	37	LEU	2.2
42	95	20	LEU	2.2
46	D5	18	LEU	2.2
47	I8	7	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
48	F5	82	LEU	2.2
3	22	28	GLN	2.2
3	22	118	GLN	2.2
9	82	124	GLN	2.2
12	3I	13	LYS	2.2
31	49	26	GLN	2.2
54	L5	2	LYS	2.2
8	72	13	ILE	2.2
20	BI	41	ILE	2.2
4	32	73	ARG	2.2
7	6E	76	ARG	2.2
15	6A	72	ARG	2.2
30	31	106	ARG	2.2
40	B8	112	ARG	2.2
4	32	12	CYS	2.2
2	1E	190	THR	2.2
2	1E	164	VAL	2.2
2	12	91	PRO	2.2
3	2E	109	PRO	2.2
4	3E	152	SER	2.2
12	3A	39	VAL	2.2
15	6I	60	VAL	2.2
17	8A	35	VAL	2.2
31	41	37	VAL	2.2
32	59	114	VAL	2.2
42	D8	50	PRO	2.2
6	5E	50	TYR	2.2
30	39	7	TYR	2.2
50	H5	15	TYR	2.2
1	13	890	G	2.2
1	13	1142	G	2.2
1	13	1182	G	2.2
26	1H	2151	G	2.2
26	14	954	G	2.2
26	14	1883	G	2.2
15	6I	20	GLY	2.2
32	51	14	GLY	2.2
46	H8	136	PHE	2.2
1	1G	1056	U	2.2
26	14	271(C)	U	2.2
2	12	61	LEU	2.2
3	22	47	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
5	42	91	LEU	2.2
7	62	146	GLU	2.2
28	19	90	ALA	2.2
30	31	35	GLU	2.2
30	39	128	ALA	2.2
31	49	46	ALA	2.2
31	41	152	LEU	2.2
31	49	3	LEU	2.2
32	51	104	GLU	2.2
32	51	119	GLU	2.2
33	69	48	GLU	2.2
33	69	66	GLU	2.2
47	E5	33	ALA	2.2
1	13	121	C	2.2
1	1G	307	C	2.2
1	1G	383	A	2.2
8	7E	46	LYS	2.2
16	7A	49	LEU	2.2
1	1G	656	C	2.2
19	AA	70	LYS	2.2
33	69	123	LEU	2.2
26	1H	2363	C	2.2
26	14	1349	A	2.2
26	14	2111	C	2.2
26	14	2799	A	2.2
26	14	2828	C	2.2
33	69	131	LYS	2.2
38	98	70	LEU	2.2
41	85	84	LYS	2.2
42	D8	40	LEU	2.2
46	D5	163	LEU	2.2
22	1K	48	C	2.2
2	1E	96	ARG	2.2
4	32	25	ARG	2.2
4	32	144	ASP	2.2
9	82	121	ARG	2.2
11	2A	54	ARG	2.2
53	O8	46	HIS	2.2
4	32	29	PRO	2.2
9	82	44	VAL	2.2
31	49	159	VAL	2.2
36	78	97	PRO	2.2

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Mol	Chain	Res	Type	RSRZ
36	35	58	THR	2.2
44	F8	3	THR	2.2
46	H8	69	THR	2.2
50	H5	16	PRO	2.2
17	8A	42	TYR	2.2
19	AA	52	TYR	2.2
19	AA	84	GLY	2.2
46	D5	136	PHE	2.2
5	42	47	LYS	2.2
1	13	760	G	2.2
1	13	823	G	2.2
1	1G	1164	G	2.2
3	2E	161	GLU	2.2
3	22	180	ALA	2.2
16	7I	77	ALA	2.2
20	BI	48	LYS	2.2
26	14	382	G	2.2
26	14	1343	G	2.2
26	14	1401	G	2.2
26	14	2455	G	2.2
28	19	215	LEU	2.2
31	41	43	LEU	2.2
31	49	53	LEU	2.2
32	51	58	GLU	2.2
32	51	87	LEU	2.2
40	75	135	ALA	2.2
48	F5	24	ALA	2.2
55	Q8	29	LYS	2.2
23	2L	19	G	2.2
26	1H	2506	U	2.2
2	12	211	ILE	2.2
32	59	130	ARG	2.2
37	45	141	GLN	2.2
40	B8	103	ARG	2.2
55	Q8	35	GLN	2.2
26	1H	1177	A	2.2
26	1H	1554	A	2.2
26	14	1045	A	2.2
26	14	2114	A	2.2
1	13	1189	C	2.2
1	1G	234	C	2.2
1	1G	984	C	2.2

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Mol	Chain	Res	Type	RSRZ
26	1H	2163	C	2.2
26	14	1092	C	2.2
2	1E	193	ASP	2.2
30	39	23	ASP	2.2
3	2E	141	VAL	2.2
4	32	172	PRO	2.2
5	4E	82	VAL	2.2
5	42	33	VAL	2.2
6	5E	88	VAL	2.2
7	62	71	PRO	2.2
13	4A	45	VAL	2.2
32	51	173	PRO	2.2
32	59	26	VAL	2.2
38	55	39	PRO	2.2
51	I5	50	VAL	2.2
52	N8	41	PRO	2.2
5	42	23	GLY	2.2
16	7I	17	TYR	2.2
18	9I	48	GLY	2.2
37	45	26	TYR	2.2
37	45	83	MET	2.2
20	BA	105	SER	2.2
40	B8	12	SER	2.2
29	29	64	LYS	2.2
30	31	93	LYS	2.2
33	61	95	LYS	2.2
46	D5	36	LYS	2.2
8	7E	10	LEU	2.2
17	8A	31	LEU	2.2
28	11	111	LEU	2.2
34	58	87	LEU	2.2
34	15	116	LEU	2.2
38	98	20	LEU	2.2
40	B8	6	LEU	2.2
2	12	141	GLU	2.2
8	7E	22	GLU	2.2
8	7E	132	GLU	2.2
28	19	130	ALA	2.2
2	1E	80	ILE	2.2
2	12	58	ILE	2.2
9	82	16	ARG	2.2
9	82	77	ILE	2.2

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Mol	Chain	Res	Type	RSRZ
20	BA	89	ARG	2.2
24	3K	45	U	2.2
26	14	969	U	2.2
45	G8	97	ARG	2.2
31	41	27	ASN	2.2
32	59	74	ASN	2.2
1	13	159	G	2.2
1	13	493	G	2.2
1	13	1050	G	2.2
1	13	1143	G	2.2
1	1G	587	G	2.2
1	1G	725	G	2.2
1	1G	755	G	2.2
1	1G	1058	G	2.2
1	1G	1127	G	2.2
1	1G	1272	G	2.2
22	1K	27	G	2.2
24	3K	28	G	2.2
26	1H	2168	G	2.2
26	14	1171	G	2.2
26	14	2802	G	2.2
27	1J	61	G	2.2
33	69	133	HIS	2.2
1	1G	1280	A	2.2
2	12	125	PRO	2.2
4	32	37	PRO	2.2
6	52	51	PRO	2.2
6	52	55	ASP	2.2
11	2I	121	PRO	2.2
24	3K	64	A	2.2
26	1H	872	A	2.2
26	1H	2320	A	2.2
31	41	31	VAL	2.2
32	51	15	VAL	2.2
53	O8	52	VAL	2.2
1	1G	1063	C	2.2
1	1G	1218	C	2.2
26	1H	654(B)	C	2.2
26	1H	1064	C	2.2
26	1H	1407	C	2.2
26	14	955	C	2.2
26	14	1145	C	2.2

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Mol	Chain	Res	Type	RSRZ
26	14	1518	C	2.2
57	3L	2	C	2.2
57	3L	61	C	2.2
10	1I	100	THR	2.2
3	22	205	GLY	2.2
8	7E	66	GLY	2.2
11	2I	52	GLY	2.2
13	4A	68	GLY	2.2
37	88	41	TRP	2.2
42	D8	44	LYS	2.2
45	G8	104	GLY	2.2
53	K5	27	LYS	2.2
3	2E	112	SER	2.2
30	39	50	SER	2.2
39	A8	112	PHE	2.2
9	8E	13	ALA	2.2
11	2A	15	ALA	2.2
38	55	102	GLU	2.2
42	D8	59	ALA	2.2
51	I5	34	GLU	2.2
10	1I	82	ILE	2.1
14	5A	29	ARG	2.1
16	7I	72	ARG	2.1
30	39	95	ARG	2.1
31	41	20	ILE	2.1
7	6E	13	GLN	2.1
41	C8	117	GLN	2.1
1	13	239	U	2.1
1	1G	950	U	2.1
7	62	148	ASN	2.1
26	14	2144	U	2.1
41	85	49	HIS	2.1
43	E8	111	HIS	2.1
5	42	55	VAL	2.1
8	7E	67	PRO	2.1
8	72	51	VAL	2.1
19	AI	9	VAL	2.1
29	29	86	PRO	2.1
46	H8	108	PRO	2.1
7	62	144	MET	2.1
19	AA	12	ASP	2.1
1	13	347	G	2.1

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Mol	Chain	Res	Type	RSRZ
1	13	1000	A	2.1
1	13	1124	G	2.1
1	13	1187	G	2.1
1	13	1324	A	2.1
1	1G	1371	G	2.1
2	1E	168	THR	2.1
2	12	99	GLY	2.1
2	12	190	THR	2.1
3	2E	15	THR	2.1
20	BI	65	LYS	2.1
26	1H	654(D)	G	2.1
26	14	173	G	2.1
26	14	866	A	2.1
26	14	944	G	2.1
26	14	1624	G	2.1
26	14	2126	A	2.1
27	16	25	A	2.1
29	29	115	GLY	2.1
31	49	65	GLY	2.1
35	25	96	THR	2.1
37	88	77	LYS	2.1
38	98	26	LYS	2.1
56	1L	35	A	2.1
3	2E	167	TRP	2.1
1	13	656	C	2.1
1	13	877	C	2.1
3	2E	91	LEU	2.1
5	4E	112	LEU	2.1
9	82	79	LEU	2.1
10	1A	54	PHE	2.1
20	BA	99	LEU	2.1
3	22	29	TYR	2.1
23	2L	24	C	2.1
26	14	654(E)	C	2.1
26	14	1109	C	2.1
26	14	1403	C	2.1
31	49	111	LEU	2.1
41	C8	18	LEU	2.1
41	85	18	LEU	2.1
45	C5	14	LEU	2.1
3	22	53	ALA	2.1
3	22	71	ALA	2.1

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Mol	Chain	Res	Type	RSRZ
10	1I	32	ALA	2.1
46	D5	109	ALA	2.1
2	12	134	GLU	2.1
11	2I	120	ARG	2.1
15	6I	87	ILE	2.1
40	75	110	ILE	2.1
19	AA	57	HIS	2.1
5	42	73	ASN	2.1
1	13	1240	U	2.1
1	1G	429	U	2.1
1	1G	960	U	2.1
2	1E	165	VAL	2.1
10	1I	24	VAL	2.1
12	3I	82	VAL	2.1
19	AI	41	VAL	2.1
26	14	822	U	2.1
26	14	1415	U	2.1
26	14	1535	U	2.1
32	51	112	PRO	2.1
52	J5	60	VAL	2.1
55	M5	22	VAL	2.1
46	D5	98	MET	2.1
10	1I	22	LYS	2.1
2	1E	195	ASP	2.1
2	1E	227	GLY	2.1
5	42	42	GLY	2.1
20	BA	102	GLY	2.1
21	1B	16	GLY	2.1
29	29	92	THR	2.1
30	31	100	THR	2.1
3	22	43	LEU	2.1
3	22	188	LEU	2.1
6	52	97	PHE	2.1
15	6A	39	LEU	2.1
40	B8	22	PHE	2.1
48	J8	80	LEU	2.1
2	1E	237	ALA	2.1
11	2I	75	TYR	2.1
14	5A	30	ALA	2.1
18	9I	72	ARG	2.1
19	AA	24	ALA	2.1
26	14	196	A	2.1

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Mol	Chain	Res	Type	RSRZ
26	14	1220	A	2.1
27	1J	1(M)	A	2.1
30	39	72	ARG	2.1
32	51	101	ARG	2.1
32	59	6	ARG	2.1
36	35	89	ALA	2.1
39	65	17	ARG	2.1
42	95	66	ARG	2.1
1	13	755	G	2.1
1	1G	309	G	2.1
2	1E	42	ILE	2.1
2	12	108	ILE	2.1
11	2I	83	ILE	2.1
23	2L	46	G	2.1
26	1H	880	G	2.1
26	1H	2793	G	2.1
27	1J	85	G	2.1
29	29	176	ILE	2.1
31	49	35	GLU	2.1
40	B8	48	ILE	2.1
57	3L	15	G	2.1
1	13	106	C	2.1
1	1G	186(D)	C	2.1
26	1H	1218	C	2.1
26	1H	1592	C	2.1
26	1H	2128	C	2.1
26	14	280	C	2.1
26	14	965	C	2.1
26	14	2658	C	2.1
57	3L	56	C	2.1
10	1I	62	HIS	2.1
15	6A	51	HIS	2.1
2	12	197	VAL	2.1
3	22	142	MET	2.1
8	72	101	PRO	2.1
9	82	95	LYS	2.1
36	35	121	LYS	2.1
40	75	1	MET	2.1
48	F5	16	ASN	2.1
51	I5	21	VAL	2.1
53	K5	20	ASN	2.1
1	13	820	U	2.1

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Mol	Chain	Res	Type	RSRZ
1	13	999	U	2.1
6	5E	55	ASP	2.1
10	1A	88	LEU	2.1
12	3I	35	GLY	2.1
30	39	207	GLY	2.1
42	95	48	GLY	2.1
44	B5	94	GLY	2.1
45	G8	90	LEU	2.1
51	M8	17	GLY	2.1
55	Q8	38	GLY	2.1
7	62	5	ARG	2.1
20	BA	23	ARG	2.1
31	41	115	ARG	2.1
35	68	97	ARG	2.1
46	D5	35	ARG	2.1
55	Q8	42	ARG	2.1
20	BA	12	ALA	2.1
9	82	62	TYR	2.1
10	1I	97	GLU	2.1
17	8I	95	TYR	2.1
28	19	97	TYR	2.1
32	59	136	ILE	2.1
33	69	135	GLU	2.1
46	H8	137	ILE	2.1
1	1G	974	A	2.1
1	1G	986	A	2.1
26	1H	1069	A	2.1
3	22	37	GLN	2.1
1	13	410	G	2.1
1	1G	879	C	2.1
1	1G	1017	G	2.1
1	1G	1124	G	2.1
1	1G	1362	C	2.1
10	1A	34	VAL	2.1
19	AA	7	LYS	2.1
22	1K	4	C	2.1
26	1H	654(E)	C	2.1
26	1H	1428	C	2.1
26	1H	2526	G	2.1
26	1H	2532	G	2.1
26	1H	2706	G	2.1
26	14	34	C	2.1

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Mol	Chain	Res	Type	RSRZ
28	11	38	LYS	2.1
29	29	69	LYS	2.1
37	45	35	VAL	2.1
41	85	15	LYS	2.1
45	C5	19	LYS	2.1
45	C5	95	LYS	2.1
55	Q8	39	LYS	2.1
55	M5	52	LYS	2.1
57	3L	25	C	2.1
7	6E	80	VAL	2.1
2	1E	167	PRO	2.1
45	C5	82	PRO	2.1
30	39	133	ASN	2.1
4	32	194	LEU	2.1
15	6A	57	LEU	2.1
17	8A	6	LEU	2.1
33	61	38	LEU	2.1
1	13	261	U	2.1
10	1A	11	PHE	2.1
14	5A	36	PHE	2.1
26	14	1094	U	2.1
29	21	186	GLY	2.1
46	H8	64	GLY	2.1
56	1L	20	U	2.1
5	42	25	ARG	2.1
30	31	62	ARG	2.1
31	49	21	ARG	2.1
32	59	3	ARG	2.1
32	59	97	ARG	2.1
39	65	3	ARG	2.1
7	62	145	ALA	2.1
8	72	83	ILE	2.1
14	5A	5	ALA	2.1
20	BI	100	ILE	2.1
28	19	247	ALA	2.1
29	21	4	ILE	2.1
29	29	81	ILE	2.1
30	39	78	ILE	2.1
31	41	77	ILE	2.1
33	61	94	ALA	2.1
45	C5	64	GLU	2.1
5	42	61	TYR	2.1

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Mol	Chain	Res	Type	RSRZ
2	1E	192	SER	2.0
3	22	154	SER	2.0
4	32	33	MET	2.0
12	3A	46	LYS	2.0
17	8A	99	SER	2.0
20	BI	61	SER	2.0
29	29	54	GLN	2.0
31	41	74	LYS	2.0
46	D5	16	SER	2.0
46	D5	66	SER	2.0
45	G8	68	HIS	2.0
1	1G	535	A	2.0
6	52	88	VAL	2.0
7	62	69	VAL	2.0
18	9I	22	VAL	2.0
27	1J	119	A	2.0
30	39	11	VAL	2.0
32	59	52	VAL	2.0
32	59	144	VAL	2.0
33	61	142	VAL	2.0
42	95	51	VAL	2.0
42	95	79	VAL	2.0
52	J5	34	PRO	2.0
1	13	1129	C	2.0
1	1G	390	C	2.0
1	1G	1214	C	2.0
2	1E	25	ASN	2.0
2	12	213	LEU	2.0
24	3K	4	C	2.0
26	1H	654(F)	C	2.0
26	1H	914	C	2.0
26	14	392	C	2.0
26	14	2456	C	2.0
31	49	34	LEU	2.0
32	51	7	LEU	2.0
39	65	32	LEU	2.0
43	E8	57	ASN	2.0
46	D5	67	LEU	2.0
1	13	102	G	2.0
1	13	391	G	2.0
1	13	1139	G	2.0
4	32	168	ARG	2.0

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Mol	Chain	Res	Type	RSRZ
17	8A	38	ARG	2.0
26	1H	654(C)	G	2.0
26	1H	1002	G	2.0
26	1H	1559	G	2.0
26	14	654(P)	G	2.0
3	22	39	ILE	2.0
3	22	77	ILE	2.0
23	2L	48	U	2.0
26	1H	271(C)	U	2.0
26	14	1590	U	2.0
26	14	2357	U	2.0
2	1E	218	ALA	2.0
7	62	121	ALA	2.0
20	BI	66	ALA	2.0
35	25	80	ASP	2.0
5	4E	83	GLU	2.0
16	7I	48	TRP	2.0
3	2E	193	TYR	2.0
32	59	85	LYS	2.0
33	69	45	LYS	2.0
41	85	13	LYS	2.0
45	C5	46	LYS	2.0
8	7E	129	VAL	2.0
29	21	198	VAL	2.0
32	59	24	VAL	2.0
34	15	101	HIS	2.0
38	55	6	SER	2.0
39	65	53	SER	2.0
45	C5	39	VAL	2.0
55	Q8	37	SER	2.0
12	3A	37	CYS	2.0
15	6I	19	PRO	2.0
42	95	29	PRO	2.0
1	1G	1349	A	2.0
2	1E	121	LEU	2.0
5	42	112	LEU	2.0
7	62	22	LEU	2.0
26	14	390	A	2.0
30	39	124	LEU	2.0
32	51	105	LEU	2.0
50	H5	26	LEU	2.0
52	J5	58	LEU	2.0

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Mol	Chain	Res	Type	RSRZ
2	1E	137	ARG	2.0
5	4E	27	ARG	2.0
11	2A	91	ARG	2.0
12	3I	33	ARG	2.0
13	4I	108	ARG	2.0
20	BA	22	ARG	2.0
30	31	133	ASN	2.0
40	75	54	ARG	2.0
41	C8	94	ASN	2.0
44	F8	68	ARG	2.0
47	E5	35	ASN	2.0
54	P8	23	ARG	2.0
28	11	238	GLY	2.0
1	1G	295	C	2.0
1	1G	386	C	2.0
10	1A	4	ILE	2.0
26	1H	2658	C	2.0
26	1H	2791	C	2.0
26	14	1146	C	2.0
26	14	1147	C	2.0
26	14	2752	C	2.0
3	22	189	ALA	2.0
5	42	30	ALA	2.0
12	3A	56	ALA	2.0
16	7I	69	THR	2.0
29	29	24	THR	2.0
29	29	157	ALA	2.0
38	98	19	ALA	2.0
42	95	77	ALA	2.0
51	I5	24	THR	2.0
55	Q8	6	THR	2.0
1	13	1393	U	2.0
1	1G	486	U	2.0
26	14	383	U	2.0
26	14	1033	U	2.0
26	14	1516	U	2.0
26	14	2797	U	2.0
1	13	46	G	2.0
1	1G	260	G	2.0
1	1G	654	G	2.0
1	1G	1002	G	2.0
1	1G	1231	G	2.0

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Mol	Chain	Res	Type	RSRZ
20	BI	34	LYS	2.0
26	1H	1059	G	2.0
26	1H	2550	G	2.0
26	14	711	G	2.0
26	14	2899	G	2.0
29	21	73	GLU	2.0
45	C5	101	LYS	2.0
7	62	66	VAL	2.0
9	82	41	VAL	2.0
46	H8	56	VAL	2.0
46	D5	90	VAL	2.0
48	J8	49	VAL	2.0
49	G5	25	VAL	2.0
51	M8	50	VAL	2.0

6.2 Non-standard residues in protein, DNA, RNA chains (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	7MG	3L	46	24/25	0.44	0.17	147,158,169,181	0
57	PSU	3L	55	20/21	0.55	0.22	121,143,168,174	0
22	PSU	1K	55	20/21	0.57	0.18	112,129,148,149	0
56	PSU	1L	32	20/21	0.62	0.47	124,129,142,152	0
57	PSU	3L	32	20/21	0.67	0.19	119,134,142,142	0
57	4SU	3L	8	20/21	0.70	0.13	153,160,176,185	0
57	5MU	3L	54	21/22	0.71	0.20	115,149,174,177	0
56	5MU	1L	54	21/22	0.74	0.17	134,151,174,175	0
23	5MU	2L	55	21/22	0.78	0.12	101,107,114,117	0
22	4SU	1K	8	20/21	0.79	0.11	129,144,162,164	0
56	PSU	1L	39	20/21	0.80	0.25	110,121,135,138	0
23	7MG	2L	47	24/25	0.80	0.15	107,115,120,123	0
24	MIA	3K	37	29/30	0.83	0.27	103,119,131,151	0
22	5MU	1K	54	21/22	0.84	0.12	106,112,129,132	0
23	PSU	2L	56	20/21	0.85	0.10	96,107,114,116	0
22	PSU	1K	32	20/21	0.86	0.40	89,96,103,114	0
23	5MU	2K	55	21/22	0.86	0.12	81,93,97,102	0
24	PSU	3K	39	20/21	0.86	0.12	113,120,126,127	0
23	PSU	2K	56	20/21	0.86	0.13	84,91,100,103	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
23	4SU	2L	8	20/21	0.88	0.12	94,105,113,115	0
23	7MG	2K	47	24/25	0.89	0.12	82,93,103,108	0
24	PSU	3K	32	20/21	0.89	0.11	108,124,131,143	0
56	MIA	1L	37	29/30	0.91	0.20	102,116,122,128	0
22	PSU	1K	39	20/21	0.92	0.17	72,86,90,90	0
23	4SU	2K	8	20/21	0.92	0.13	75,84,93,98	0
23	OMC	2L	33	21/22	0.94	0.10	87,93,96,103	0
22	MIA	1K	37	29/30	0.94	0.17	70,75,87,93	0
23	OMC	2K	33	21/22	0.96	0.13	65,68,74,78	0

6.3 Carbohydrates (i)

There are no oligosaccharides in this entry.

6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	13	1710	1/1	-0.03	0.44	148,148,148,148	0
58	MG	14	3253	1/1	0.31	0.26	151,151,151,151	0
58	MG	14	3051	1/1	0.35	0.45	102,102,102,102	0
58	MG	14	3287	1/1	0.44	0.46	96,96,96,96	0
58	MG	1G	1665	1/1	0.45	0.44	127,127,127,127	0
58	MG	14	3178	1/1	0.48	0.48	88,88,88,88	0
58	MG	14	3160	1/1	0.49	0.41	82,82,82,82	0
58	MG	14	3028	1/1	0.53	0.40	99,99,99,99	0
58	MG	1G	1607	1/1	0.56	0.18	85,85,85,85	0
58	MG	13	1704	1/1	0.56	0.42	102,102,102,102	0
58	MG	1H	3020	1/1	0.59	0.41	90,90,90,90	0
58	MG	14	3239	1/1	0.59	0.45	98,98,98,98	0
58	MG	1J	202	1/1	0.59	0.49	88,88,88,88	0
58	MG	1H	3299	1/1	0.60	0.37	98,98,98,98	0
58	MG	1G	1679	1/1	0.60	0.39	120,120,120,120	0
58	MG	1H	3343	1/1	0.61	0.40	99,99,99,99	0
58	MG	1H	3334	1/1	0.62	0.38	95,95,95,95	0
58	MG	1G	1660	1/1	0.62	0.36	98,98,98,98	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	1H	3247	1/1	0.62	0.37	92,92,92,92	0
58	MG	14	3293	1/1	0.63	0.31	94,94,94,94	0
58	MG	14	3165	1/1	0.63	0.35	83,83,83,83	0
58	MG	13	1670	1/1	0.64	0.28	91,91,91,91	0
58	MG	1H	3162	1/1	0.64	0.46	89,89,89,89	0
58	MG	14	3167	1/1	0.65	0.37	86,86,86,86	0
58	MG	3E	302	1/1	0.66	0.39	108,108,108,108	0
58	MG	14	3050	1/1	0.66	0.44	94,94,94,94	0
58	MG	49	201	1/1	0.66	0.26	128,128,128,128	0
58	MG	1H	3025	1/1	0.67	0.26	90,90,90,90	0
58	MG	14	3199	1/1	0.68	0.39	96,96,96,96	0
58	MG	1H	3224	1/1	0.68	0.38	92,92,92,92	0
58	MG	13	1627	1/1	0.68	0.42	90,90,90,90	0
58	MG	14	3016	1/1	0.68	0.24	91,91,91,91	0
58	MG	13	1701	1/1	0.68	0.43	99,99,99,99	0
58	MG	14	3294	1/1	0.68	0.27	94,94,94,94	0
58	MG	1H	3325	1/1	0.68	0.43	92,92,92,92	0
58	MG	14	3198	1/1	0.68	0.33	94,94,94,94	0
58	MG	13	1622	1/1	0.69	0.31	66,66,66,66	0
58	MG	14	3246	1/1	0.69	0.28	85,85,85,85	0
58	MG	1G	1649	1/1	0.69	0.35	101,101,101,101	0
58	MG	1H	3345	1/1	0.69	0.33	81,81,81,81	0
58	MG	14	3019	1/1	0.70	0.43	84,84,84,84	0
58	MG	1G	1624	1/1	0.70	0.20	85,85,85,85	0
58	MG	1J	204	1/1	0.70	0.56	94,94,94,94	0
58	MG	1H	3051	1/1	0.70	0.40	97,97,97,97	0
58	MG	1G	1676	1/1	0.71	0.33	95,95,95,95	0
58	MG	1H	3342	1/1	0.71	0.38	89,89,89,89	0
58	MG	14	3073	1/1	0.71	0.37	91,91,91,91	0
58	MG	1H	3074	1/1	0.71	0.34	88,88,88,88	0
58	MG	13	1626	1/1	0.71	0.38	90,90,90,90	0
58	MG	1H	3262	1/1	0.71	0.39	96,96,96,96	0
58	MG	1H	3337	1/1	0.72	0.24	86,86,86,86	0
58	MG	13	1671	1/1	0.72	0.24	95,95,95,95	0
58	MG	13	1662	1/1	0.72	0.60	115,115,115,115	0
58	MG	1G	1626	1/1	0.72	0.37	99,99,99,99	0
58	MG	14	3259	1/1	0.72	0.21	102,102,102,102	0
58	MG	14	3285	1/1	0.72	0.29	104,104,104,104	0
58	MG	25	201	1/1	0.72	0.42	102,102,102,102	0
58	MG	C5	201	1/1	0.72	0.30	105,105,105,105	0
58	MG	1G	1678	1/1	0.73	0.28	108,108,108,108	0
58	MG	16	205	1/1	0.73	0.31	81,81,81,81	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	1H	3054	1/1	0.73	0.54	92,92,92,92	0
58	MG	14	3140	1/1	0.73	0.43	69,69,69,69	0
58	MG	1H	3169	1/1	0.73	0.38	85,85,85,85	0
58	MG	14	3023	1/1	0.73	0.47	90,90,90,90	0
58	MG	2K	103	1/1	0.73	0.36	88,88,88,88	0
58	MG	14	3168	1/1	0.73	0.36	92,92,92,92	0
58	MG	1G	1627	1/1	0.74	0.22	88,88,88,88	0
58	MG	2A	202	1/1	0.74	0.18	98,98,98,98	0
58	MG	13	1713	1/1	0.74	0.40	88,88,88,88	0
58	MG	88	201	1/1	0.74	0.31	84,84,84,84	0
58	MG	13	1693	1/1	0.74	0.40	94,94,94,94	0
58	MG	1H	3098	1/1	0.74	0.40	71,71,71,71	0
58	MG	16	201	1/1	0.74	0.27	79,79,79,79	0
58	MG	14	3170	1/1	0.74	0.24	84,84,84,84	0
58	MG	13	1648	1/1	0.75	0.35	78,78,78,78	0
58	MG	14	3122	1/1	0.75	0.36	79,79,79,79	0
58	MG	1H	3290	1/1	0.75	0.35	84,84,84,84	0
58	MG	13	1712	1/1	0.75	0.29	80,80,80,80	0
58	MG	1H	3310	1/1	0.75	0.24	105,105,105,105	0
58	MG	13	1661	1/1	0.75	0.39	97,97,97,97	0
58	MG	14	3299	1/1	0.76	0.35	76,76,76,76	0
58	MG	1H	3021	1/1	0.76	0.29	68,68,68,68	0
58	MG	1H	3177	1/1	0.76	0.35	86,86,86,86	0
58	MG	1H	3322	1/1	0.76	0.19	88,88,88,88	0
58	MG	1G	1663	1/1	0.76	0.20	112,112,112,112	0
58	MG	14	3193	1/1	0.76	0.40	89,89,89,89	0
58	MG	1G	1601	1/1	0.77	0.45	90,90,90,90	0
58	MG	14	3169	1/1	0.77	0.37	92,92,92,92	0
58	MG	1H	3185	1/1	0.77	0.19	72,72,72,72	0
58	MG	3L	101	1/1	0.77	0.18	99,99,99,99	0
58	MG	14	3011	1/1	0.77	0.31	70,70,70,70	0
58	MG	1H	3196	1/1	0.77	0.38	102,102,102,102	0
58	MG	14	3158	1/1	0.77	0.37	95,95,95,95	0
58	MG	14	3227	1/1	0.77	0.29	84,84,84,84	0
58	MG	1H	3266	1/1	0.77	0.32	91,91,91,91	0
58	MG	1H	3166	1/1	0.77	0.29	64,64,64,64	0
58	MG	1G	1629	1/1	0.77	0.30	96,96,96,96	0
60	ZN	G8	202	1/1	0.77	0.19	164,164,164,164	0
58	MG	14	3148	1/1	0.78	0.39	65,65,65,65	0
58	MG	1H	3230	1/1	0.78	0.38	91,91,91,91	0
58	MG	1H	3161	1/1	0.78	0.30	89,89,89,89	0
58	MG	1H	3055	1/1	0.78	0.31	85,85,85,85	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	1G	1674	1/1	0.78	0.33	98,98,98,98	0
58	MG	13	1690	1/1	0.78	0.28	90,90,90,90	0
58	MG	14	3042	1/1	0.78	0.18	87,87,87,87	0
58	MG	13	1678	1/1	0.78	0.29	89,89,89,89	0
58	MG	16	206	1/1	0.78	0.20	74,74,74,74	0
58	MG	1G	1636	1/1	0.78	0.38	106,106,106,106	0
58	MG	14	3118	1/1	0.78	0.26	72,72,72,72	0
58	MG	2L	103	1/1	0.78	0.29	93,93,93,93	0
58	MG	14	3130	1/1	0.78	0.42	85,85,85,85	0
58	MG	1H	3294	1/1	0.78	0.16	61,61,61,61	0
58	MG	14	3272	1/1	0.79	0.35	85,85,85,85	0
58	MG	1G	1677	1/1	0.79	0.45	97,97,97,97	0
58	MG	1G	1638	1/1	0.79	0.32	84,84,84,84	0
58	MG	1G	1619	1/1	0.79	0.48	92,92,92,92	0
58	MG	14	3034	1/1	0.79	0.36	82,82,82,82	0
58	MG	13	1675	1/1	0.79	0.21	78,78,78,78	0
58	MG	14	3301	1/1	0.79	0.28	87,87,87,87	0
58	MG	1H	3033	1/1	0.79	0.40	78,78,78,78	0
58	MG	13	1688	1/1	0.79	0.30	97,97,97,97	0
58	MG	2K	102	1/1	0.79	0.22	80,80,80,80	0
58	MG	14	3089	1/1	0.79	0.42	81,81,81,81	0
58	MG	14	3255	1/1	0.79	0.34	92,92,92,92	0
58	MG	1G	1616	1/1	0.79	0.40	86,86,86,86	0
58	MG	14	3047	1/1	0.80	0.23	92,92,92,92	0
58	MG	1G	1645	1/1	0.80	0.32	142,142,142,142	0
58	MG	1H	3035	1/1	0.80	0.33	89,89,89,89	0
58	MG	1H	3046	1/1	0.80	0.15	84,84,84,84	0
58	MG	14	3077	1/1	0.80	0.27	77,77,77,77	0
58	MG	13	1708	1/1	0.80	0.41	90,90,90,90	0
58	MG	14	3115	1/1	0.80	0.30	66,66,66,66	0
58	MG	1H	3313	1/1	0.80	0.27	78,78,78,78	0
58	MG	1H	3016	1/1	0.80	0.43	97,97,97,97	0
58	MG	1J	203	1/1	0.80	0.22	100,100,100,100	0
58	MG	1H	3268	1/1	0.80	0.32	71,71,71,71	0
58	MG	1J	205	1/1	0.80	0.23	78,78,78,78	0
58	MG	1H	3282	1/1	0.80	0.31	98,98,98,98	0
58	MG	13	1687	1/1	0.80	0.22	98,98,98,98	0
58	MG	14	3039	1/1	0.80	0.26	74,74,74,74	0
58	MG	1G	1606	1/1	0.80	0.34	83,83,83,83	0
58	MG	1G	1659	1/1	0.81	0.54	95,95,95,95	0
58	MG	13	1695	1/1	0.81	0.21	83,83,83,83	0
58	MG	14	3026	1/1	0.81	0.29	71,71,71,71	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	14	3260	1/1	0.81	0.29	100,100,100,100	0
58	MG	13	1664	1/1	0.81	0.36	74,74,74,74	0
58	MG	14	3282	1/1	0.81	0.41	88,88,88,88	0
58	MG	14	3284	1/1	0.81	0.34	94,94,94,94	0
58	MG	13	1665	1/1	0.81	0.38	88,88,88,88	0
58	MG	1G	1623	1/1	0.81	0.25	91,91,91,91	0
58	MG	1H	3302	1/1	0.81	0.23	77,77,77,77	0
58	MG	1H	3309	1/1	0.81	0.21	70,70,70,70	0
58	MG	13	1705	1/1	0.81	0.25	91,91,91,91	0
58	MG	13	1657	1/1	0.81	0.38	89,89,89,89	0
58	MG	13	1682	1/1	0.81	0.34	73,73,73,73	0
58	MG	14	3184	1/1	0.81	0.24	91,91,91,91	0
58	MG	1H	3280	1/1	0.81	0.33	82,82,82,82	0
58	MG	1G	1642	1/1	0.81	0.22	92,92,92,92	0
58	MG	14	3095	1/1	0.81	0.39	83,83,83,83	0
58	MG	14	3003	1/1	0.81	0.38	77,77,77,77	0
58	MG	1G	1602	1/1	0.81	0.22	93,93,93,93	0
58	MG	1H	3211	1/1	0.81	0.34	78,78,78,78	0
58	MG	14	3137	1/1	0.82	0.16	78,78,78,78	0
58	MG	1H	3024	1/1	0.82	0.40	77,77,77,77	0
58	MG	13	1608	1/1	0.82	0.33	85,85,85,85	0
58	MG	1H	3031	1/1	0.82	0.33	90,90,90,90	0
58	MG	14	3271	1/1	0.82	0.31	86,86,86,86	0
58	MG	14	3064	1/1	0.82	0.33	86,86,86,86	0
58	MG	14	3070	1/1	0.82	0.27	79,79,79,79	0
58	MG	14	3072	1/1	0.82	0.44	74,74,74,74	0
58	MG	3E	301	1/1	0.82	0.22	109,109,109,109	0
58	MG	13	1651	1/1	0.82	0.39	79,79,79,79	0
58	MG	14	3083	1/1	0.82	0.16	88,88,88,88	0
58	MG	1H	3132	1/1	0.82	0.26	62,62,62,62	0
58	MG	14	3094	1/1	0.82	0.38	76,76,76,76	0
58	MG	1H	3134	1/1	0.82	0.31	50,50,50,50	0
58	MG	1H	3041	1/1	0.82	0.21	88,88,88,88	0
58	MG	1H	3236	1/1	0.82	0.22	79,79,79,79	0
58	MG	14	3222	1/1	0.82	0.33	75,75,75,75	0
58	MG	2L	102	1/1	0.82	0.38	85,85,85,85	0
58	MG	14	3235	1/1	0.82	0.40	80,80,80,80	0
58	MG	13	1653	1/1	0.82	0.26	87,87,87,87	0
58	MG	14	3131	1/1	0.82	0.37	87,87,87,87	0
58	MG	14	3252	1/1	0.82	0.13	91,91,91,91	0
58	MG	1H	3319	1/1	0.83	0.38	83,83,83,83	0
58	MG	14	3229	1/1	0.83	0.31	91,91,91,91	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	1H	3099	1/1	0.83	0.29	63,63,63,63	0
58	MG	1H	3271	1/1	0.83	0.41	80,80,80,80	0
58	MG	14	3102	1/1	0.83	0.16	73,73,73,73	0
58	MG	1H	3326	1/1	0.83	0.20	90,90,90,90	0
58	MG	1H	3330	1/1	0.83	0.30	75,75,75,75	0
58	MG	1H	3331	1/1	0.83	0.20	67,67,67,67	0
58	MG	1H	3273	1/1	0.83	0.27	84,84,84,84	0
58	MG	1H	3275	1/1	0.83	0.39	82,82,82,82	0
58	MG	14	3262	1/1	0.83	0.18	78,78,78,78	0
58	MG	14	3268	1/1	0.83	0.36	87,87,87,87	0
58	MG	1H	3004	1/1	0.83	0.30	68,68,68,68	0
58	MG	1H	3006	1/1	0.83	0.29	57,57,57,57	0
58	MG	1G	1644	1/1	0.83	0.26	110,110,110,110	0
58	MG	14	3033	1/1	0.83	0.50	76,76,76,76	0
58	MG	1H	3285	1/1	0.83	0.20	80,80,80,80	0
58	MG	1H	3492	1/1	0.83	0.26	82,82,82,82	0
58	MG	1H	3156	1/1	0.83	0.36	78,78,78,78	0
58	MG	13	1673	1/1	0.83	0.28	73,73,73,73	0
58	MG	1G	1661	1/1	0.83	0.20	99,99,99,99	0
58	MG	1H	3045	1/1	0.83	0.29	72,72,72,72	0
58	MG	41	202	1/1	0.83	0.27	81,81,81,81	0
58	MG	1H	3077	1/1	0.83	0.21	54,54,54,54	0
58	MG	13	1703	1/1	0.83	0.30	89,89,89,89	0
58	MG	1H	3172	1/1	0.83	0.30	79,79,79,79	0
58	MG	1H	3174	1/1	0.83	0.29	70,70,70,70	0
58	MG	14	3203	1/1	0.83	0.36	83,83,83,83	0
58	MG	14	3217	1/1	0.83	0.27	101,101,101,101	0
58	MG	1H	3314	1/1	0.83	0.22	84,84,84,84	0
58	MG	1H	3029	1/1	0.84	0.39	72,72,72,72	0
58	MG	1G	1633	1/1	0.84	0.46	82,82,82,82	0
58	MG	1G	1634	1/1	0.84	0.18	84,84,84,84	0
58	MG	1H	3195	1/1	0.84	0.31	81,81,81,81	0
58	MG	1H	3023	1/1	0.84	0.40	88,88,88,88	0
58	MG	14	3258	1/1	0.84	0.18	82,82,82,82	0
58	MG	1H	3118	1/1	0.84	0.16	53,53,53,53	0
58	MG	14	3166	1/1	0.84	0.38	81,81,81,81	0
58	MG	1H	3122	1/1	0.84	0.18	68,68,68,68	0
58	MG	1G	1608	1/1	0.84	0.26	72,72,72,72	0
58	MG	14	3001	1/1	0.84	0.39	89,89,89,89	0
58	MG	1G	1647	1/1	0.84	0.17	94,94,94,94	0
58	MG	13	1645	1/1	0.84	0.27	69,69,69,69	0
58	MG	1H	3234	1/1	0.84	0.26	67,67,67,67	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	1G	1622	1/1	0.84	0.40	81,81,81,81	0
58	MG	13	1667	1/1	0.84	0.28	82,82,82,82	0
58	MG	1H	3287	1/1	0.84	0.37	77,77,77,77	0
58	MG	14	3200	1/1	0.84	0.28	94,94,94,94	0
58	MG	14	3027	1/1	0.84	0.34	81,81,81,81	0
58	MG	1H	3097	1/1	0.84	0.22	69,69,69,69	0
58	MG	14	3406	1/1	0.84	0.17	112,112,112,112	0
58	MG	14	3220	1/1	0.84	0.17	66,66,66,66	0
58	MG	14	3121	1/1	0.84	0.34	75,75,75,75	0
58	MG	1G	1672	1/1	0.84	0.36	88,88,88,88	0
58	MG	1H	3178	1/1	0.84	0.16	63,63,63,63	0
58	MG	14	3233	1/1	0.84	0.14	63,63,63,63	0
58	MG	14	3234	1/1	0.84	0.29	80,80,80,80	0
58	MG	14	3035	1/1	0.84	0.34	72,72,72,72	0
58	MG	14	3238	1/1	0.84	0.19	86,86,86,86	0
58	MG	1H	3321	1/1	0.85	0.19	72,72,72,72	0
58	MG	14	3123	1/1	0.85	0.32	78,78,78,78	0
58	MG	13	1656	1/1	0.85	0.30	79,79,79,79	0
58	MG	14	3029	1/1	0.85	0.39	87,87,87,87	0
58	MG	1H	3274	1/1	0.85	0.26	83,83,83,83	0
58	MG	1H	3188	1/1	0.85	0.34	73,73,73,73	0
58	MG	14	3142	1/1	0.85	0.33	88,88,88,88	0
58	MG	14	3143	1/1	0.85	0.34	85,85,85,85	0
58	MG	13	1638	1/1	0.85	0.28	62,62,62,62	0
58	MG	1G	1671	1/1	0.85	0.17	82,82,82,82	0
58	MG	1H	3146	1/1	0.85	0.26	67,67,67,67	0
58	MG	1H	3151	1/1	0.85	0.28	73,73,73,73	0
58	MG	14	3048	1/1	0.85	0.28	76,76,76,76	0
58	MG	13	1658	1/1	0.85	0.22	92,92,92,92	0
58	MG	1H	3289	1/1	0.85	0.29	89,89,89,89	0
58	MG	14	3063	1/1	0.85	0.27	70,70,70,70	0
58	MG	14	3277	1/1	0.85	0.15	104,104,104,104	0
58	MG	4K	101	1/1	0.85	0.26	73,73,73,73	0
58	MG	14	3283	1/1	0.85	0.44	82,82,82,82	0
58	MG	14	3172	1/1	0.85	0.21	72,72,72,72	0
58	MG	14	3174	1/1	0.85	0.24	84,84,84,84	0
58	MG	13	1660	1/1	0.85	0.21	86,86,86,86	0
58	MG	14	3179	1/1	0.85	0.30	72,72,72,72	0
58	MG	1G	1631	1/1	0.85	0.23	82,82,82,82	0
58	MG	1H	3084	1/1	0.85	0.25	69,69,69,69	0
58	MG	14	3197	1/1	0.85	0.31	73,73,73,73	0
58	MG	13	1637	1/1	0.85	0.24	66,66,66,66	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	1H	3308	1/1	0.85	0.23	75,75,75,75	0
58	MG	1H	3012	1/1	0.85	0.26	78,78,78,78	0
58	MG	13	1646	1/1	0.85	0.24	61,61,61,61	0
58	MG	1H	3267	1/1	0.85	0.25	71,71,71,71	0
58	MG	29	304	1/1	0.85	0.32	95,95,95,95	0
58	MG	13	1654	1/1	0.85	0.29	76,76,76,76	0
58	MG	13	1702	1/1	0.85	0.12	81,81,81,81	0
58	MG	1G	1604	1/1	0.85	0.23	98,98,98,98	0
58	MG	1G	1657	1/1	0.85	0.15	107,107,107,107	0
58	MG	1G	1675	1/1	0.86	0.29	90,90,90,90	0
58	MG	13	1636	1/1	0.86	0.35	77,77,77,77	0
58	MG	1H	3159	1/1	0.86	0.26	73,73,73,73	0
58	MG	14	3159	1/1	0.86	0.19	73,73,73,73	0
58	MG	14	3049	1/1	0.86	0.41	86,86,86,86	0
58	MG	1H	3116	1/1	0.86	0.32	51,51,51,51	0
58	MG	16	202	1/1	0.86	0.28	81,81,81,81	0
58	MG	14	3057	1/1	0.86	0.29	62,62,62,62	0
58	MG	1G	1682	1/1	0.86	0.29	103,103,103,103	0
58	MG	1H	3202	1/1	0.86	0.32	58,58,58,58	0
58	MG	7A	101	1/1	0.86	0.20	90,90,90,90	0
58	MG	1H	3022	1/1	0.86	0.26	88,88,88,88	0
58	MG	11	304	1/1	0.86	0.26	73,73,73,73	0
58	MG	14	3074	1/1	0.86	0.30	73,73,73,73	0
58	MG	1H	3216	1/1	0.86	0.19	71,71,71,71	0
58	MG	1H	3318	1/1	0.86	0.33	85,85,85,85	0
58	MG	1H	3010	1/1	0.86	0.47	87,87,87,87	0
58	MG	14	3196	1/1	0.86	0.37	65,65,65,65	0
58	MG	14	3292	1/1	0.86	0.19	84,84,84,84	0
58	MG	2I	201	1/1	0.86	0.28	77,77,77,77	0
58	MG	1H	3283	1/1	0.86	0.14	73,73,73,73	0
58	MG	1H	3323	1/1	0.86	0.32	78,78,78,78	0
58	MG	14	3103	1/1	0.86	0.27	78,78,78,78	0
58	MG	14	3020	1/1	0.86	0.21	75,75,75,75	0
58	MG	5I	101	1/1	0.86	0.14	81,81,81,81	0
58	MG	1H	3286	1/1	0.86	0.17	71,71,71,71	0
58	MG	1H	3027	1/1	0.86	0.27	76,76,76,76	0
58	MG	1H	3246	1/1	0.86	0.32	75,75,75,75	0
58	MG	2K	101	1/1	0.86	0.21	66,66,66,66	0
58	MG	1H	3154	1/1	0.86	0.25	59,59,59,59	0
58	MG	1H	3155	1/1	0.86	0.21	58,58,58,58	0
58	MG	1G	1673	1/1	0.86	0.41	92,92,92,92	0
58	MG	1H	3301	1/1	0.86	0.13	59,59,59,59	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	1H	3102	1/1	0.87	0.27	60,60,60,60	0
58	MG	14	3037	1/1	0.87	0.37	82,82,82,82	0
58	MG	14	3181	1/1	0.87	0.32	79,79,79,79	0
58	MG	14	3182	1/1	0.87	0.59	86,86,86,86	0
58	MG	1H	3332	1/1	0.87	0.13	74,74,74,74	0
58	MG	1H	3110	1/1	0.87	0.14	45,45,45,45	0
58	MG	13	1681	1/1	0.87	0.27	66,66,66,66	0
58	MG	1H	3340	1/1	0.87	0.37	82,82,82,82	0
58	MG	1H	3341	1/1	0.87	0.31	96,96,96,96	0
58	MG	1H	3279	1/1	0.87	0.21	67,67,67,67	0
58	MG	13	1672	1/1	0.87	0.21	72,72,72,72	0
58	MG	1H	3186	1/1	0.87	0.41	74,74,74,74	0
58	MG	14	3208	1/1	0.87	0.18	83,83,83,83	0
58	MG	14	3215	1/1	0.87	0.25	73,73,73,73	0
58	MG	14	3059	1/1	0.87	0.19	55,55,55,55	0
58	MG	14	3062	1/1	0.87	0.26	75,75,75,75	0
58	MG	1H	3019	1/1	0.87	0.28	85,85,85,85	0
58	MG	14	3223	1/1	0.87	0.26	80,80,80,80	0
58	MG	1H	3520	1/1	0.87	0.26	97,97,97,97	0
58	MG	1G	1662	1/1	0.87	0.37	83,83,83,83	0
58	MG	1H	3191	1/1	0.87	0.33	70,70,70,70	0
58	MG	1H	3130	1/1	0.87	0.16	59,59,59,59	0
58	MG	16	204	1/1	0.87	0.19	67,67,67,67	0
58	MG	14	3236	1/1	0.87	0.20	86,86,86,86	0
58	MG	14	3075	1/1	0.87	0.20	89,89,89,89	0
58	MG	13	1612	1/1	0.87	0.35	89,89,89,89	0
58	MG	14	3240	1/1	0.87	0.29	83,83,83,83	0
58	MG	14	3245	1/1	0.87	0.35	77,77,77,77	0
58	MG	14	3080	1/1	0.87	0.32	62,62,62,62	0
58	MG	13	1674	1/1	0.87	0.09	77,77,77,77	0
58	MG	11	301	1/1	0.87	0.14	50,50,50,50	0
58	MG	1H	3138	1/1	0.87	0.26	65,65,65,65	0
58	MG	1H	3292	1/1	0.87	0.34	84,84,84,84	0
58	MG	14	3096	1/1	0.87	0.24	73,73,73,73	0
58	MG	13	1652	1/1	0.87	0.17	85,85,85,85	0
58	MG	98	202	1/1	0.87	0.44	95,95,95,95	0
58	MG	14	3267	1/1	0.87	0.11	79,79,79,79	0
58	MG	1H	3298	1/1	0.87	0.37	68,68,68,68	0
58	MG	1H	3218	1/1	0.87	0.14	55,55,55,55	0
58	MG	2A	201	1/1	0.87	0.25	91,91,91,91	0
58	MG	14	3273	1/1	0.87	0.15	62,62,62,62	0
58	MG	13	1677	1/1	0.87	0.31	74,74,74,74	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	1H	3227	1/1	0.87	0.35	87,87,87,87	0
58	MG	2K	104	1/1	0.87	0.37	80,80,80,80	0
58	MG	13	1694	1/1	0.87	0.16	78,78,78,78	0
58	MG	1G	1609	1/1	0.87	0.23	81,81,81,81	0
58	MG	14	3286	1/1	0.87	0.43	71,71,71,71	0
58	MG	1G	1612	1/1	0.87	0.30	83,83,83,83	0
58	MG	1G	1614	1/1	0.87	0.29	91,91,91,91	0
58	MG	13	1624	1/1	0.87	0.24	68,68,68,68	0
58	MG	14	3145	1/1	0.87	0.34	87,87,87,87	0
58	MG	14	3013	1/1	0.87	0.37	56,56,56,56	0
58	MG	1H	3244	1/1	0.87	0.13	98,98,98,98	0
58	MG	14	3302	1/1	0.87	0.25	83,83,83,83	0
58	MG	1H	3078	1/1	0.87	0.26	67,67,67,67	0
58	MG	13	1698	1/1	0.87	0.14	80,80,80,80	0
58	MG	1H	3252	1/1	0.87	0.23	60,60,60,60	0
58	MG	14	3025	1/1	0.87	0.31	81,81,81,81	0
58	MG	1H	3091	1/1	0.87	0.25	77,77,77,77	0
58	MG	29	301	1/1	0.87	0.37	64,64,64,64	0
58	MG	1H	3030	1/1	0.87	0.20	67,67,67,67	0
58	MG	1H	3167	1/1	0.87	0.19	56,56,56,56	0
58	MG	13	1699	1/1	0.87	0.16	61,61,61,61	0
58	MG	1H	3269	1/1	0.87	0.18	72,72,72,72	0
58	MG	1H	3032	1/1	0.87	0.34	82,82,82,82	0
58	MG	1H	3203	1/1	0.88	0.39	79,79,79,79	0
58	MG	1G	1646	1/1	0.88	0.57	95,95,95,95	0
58	MG	1H	3316	1/1	0.88	0.18	81,81,81,81	0
58	MG	1H	3206	1/1	0.88	0.27	54,54,54,54	0
58	MG	1H	3208	1/1	0.88	0.30	70,70,70,70	0
58	MG	1H	3015	1/1	0.88	0.17	73,73,73,73	0
58	MG	1H	3164	1/1	0.88	0.28	58,58,58,58	0
58	MG	14	3124	1/1	0.88	0.32	76,76,76,76	0
58	MG	14	3126	1/1	0.88	0.44	79,79,79,79	0
58	MG	14	3031	1/1	0.88	0.32	78,78,78,78	0
58	MG	1H	3034	1/1	0.88	0.29	73,73,73,73	0
58	MG	1H	3221	1/1	0.88	0.28	63,63,63,63	0
58	MG	14	3242	1/1	0.88	0.34	78,78,78,78	0
58	MG	14	3244	1/1	0.88	0.19	68,68,68,68	0
58	MG	14	3139	1/1	0.88	0.27	63,63,63,63	0
58	MG	1H	3281	1/1	0.88	0.30	98,98,98,98	0
58	MG	14	3250	1/1	0.88	0.23	72,72,72,72	0
58	MG	13	1635	1/1	0.88	0.19	48,48,48,48	0
58	MG	1H	3040	1/1	0.88	0.40	76,76,76,76	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	14	3254	1/1	0.88	0.27	92,92,92,92	0
58	MG	1H	3089	1/1	0.88	0.24	72,72,72,72	0
58	MG	14	3043	1/1	0.88	0.27	76,76,76,76	0
58	MG	14	3151	1/1	0.88	0.49	91,91,91,91	0
58	MG	14	3154	1/1	0.88	0.18	68,68,68,68	0
58	MG	14	3044	1/1	0.88	0.19	57,57,57,57	0
58	MG	14	3265	1/1	0.88	0.43	90,90,90,90	0
58	MG	1H	3135	1/1	0.88	0.37	61,61,61,61	0
58	MG	1H	3026	1/1	0.88	0.30	80,80,80,80	0
58	MG	14	3161	1/1	0.88	0.31	74,74,74,74	0
58	MG	1H	3338	1/1	0.88	0.22	80,80,80,80	0
58	MG	1G	1620	1/1	0.88	0.23	77,77,77,77	0
58	MG	14	3276	1/1	0.88	0.28	80,80,80,80	0
58	MG	1H	3140	1/1	0.88	0.15	69,69,69,69	0
58	MG	13	1609	1/1	0.88	0.38	81,81,81,81	0
58	MG	1H	3291	1/1	0.88	0.26	86,86,86,86	0
58	MG	1G	1681	1/1	0.88	0.18	75,75,75,75	0
58	MG	1G	1625	1/1	0.88	0.14	129,129,129,129	0
58	MG	13	1644	1/1	0.88	0.31	78,78,78,78	0
58	MG	1H	3248	1/1	0.88	0.30	75,75,75,75	0
58	MG	14	3289	1/1	0.88	0.20	78,78,78,78	0
58	MG	14	3290	1/1	0.88	0.48	79,79,79,79	0
58	MG	1G	1628	1/1	0.88	0.30	88,88,88,88	0
58	MG	13	1659	1/1	0.88	0.38	68,68,68,68	0
58	MG	1H	3255	1/1	0.88	0.33	83,83,83,83	0
58	MG	1H	3259	1/1	0.88	0.53	82,82,82,82	0
58	MG	14	3185	1/1	0.88	0.18	81,81,81,81	0
58	MG	14	3191	1/1	0.88	0.23	70,70,70,70	0
58	MG	14	3076	1/1	0.88	0.23	73,73,73,73	0
58	MG	13	1649	1/1	0.88	0.32	79,79,79,79	0
58	MG	14	3078	1/1	0.88	0.19	63,63,63,63	0
58	MG	1G	1635	1/1	0.88	0.38	92,92,92,92	0
58	MG	14	3082	1/1	0.88	0.27	63,63,63,63	0
58	MG	1H	3264	1/1	0.88	0.27	67,67,67,67	0
58	MG	1H	3109	1/1	0.88	0.14	46,46,46,46	0
58	MG	14	3015	1/1	0.88	0.35	80,80,80,80	0
58	MG	14	3212	1/1	0.88	0.22	75,75,75,75	0
58	MG	13	1683	1/1	0.88	0.18	76,76,76,76	0
58	MG	1H	3059	1/1	0.88	0.24	56,56,56,56	0
60	ZN	C5	202	1/1	0.88	0.14	181,181,181,181	0
58	MG	14	3106	1/1	0.89	0.22	62,62,62,62	0
58	MG	14	3226	1/1	0.89	0.17	67,67,67,67	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	14	3111	1/1	0.89	0.23	92,92,92,92	0
58	MG	1G	1637	1/1	0.89	0.43	79,79,79,79	0
58	MG	14	3230	1/1	0.89	0.44	82,82,82,82	0
58	MG	1H	3257	1/1	0.89	0.11	69,69,69,69	0
58	MG	13	1650	1/1	0.89	0.22	72,72,72,72	0
58	MG	1H	3042	1/1	0.89	0.23	64,64,64,64	0
58	MG	16	207	1/1	0.89	0.11	88,88,88,88	0
58	MG	16	209	1/1	0.89	0.28	65,65,65,65	0
58	MG	1H	3119	1/1	0.89	0.23	91,91,91,91	0
58	MG	14	3127	1/1	0.89	0.28	54,54,54,54	0
58	MG	1H	3083	1/1	0.89	0.34	68,68,68,68	0
58	MG	1G	1651	1/1	0.89	0.37	77,77,77,77	0
58	MG	1G	1653	1/1	0.89	0.15	78,78,78,78	0
58	MG	1H	3165	1/1	0.89	0.22	60,60,60,60	0
58	MG	1H	3212	1/1	0.89	0.19	70,70,70,70	0
58	MG	1H	3123	1/1	0.89	0.26	49,49,49,49	0
58	MG	1H	3217	1/1	0.89	0.20	54,54,54,54	0
58	MG	13	1709	1/1	0.89	0.41	84,84,84,84	0
58	MG	1H	3085	1/1	0.89	0.10	69,69,69,69	0
58	MG	14	3045	1/1	0.89	0.36	70,70,70,70	0
58	MG	14	3046	1/1	0.89	0.26	68,68,68,68	0
58	MG	1G	1605	1/1	0.89	0.36	83,83,83,83	0
58	MG	14	3261	1/1	0.89	0.28	84,84,84,84	0
58	MG	1G	1667	1/1	0.89	0.21	92,92,92,92	0
58	MG	14	3263	1/1	0.89	0.14	76,76,76,76	0
58	MG	14	3264	1/1	0.89	0.22	77,77,77,77	0
58	MG	13	1616	1/1	0.89	0.20	65,65,65,65	0
58	MG	1H	3324	1/1	0.89	0.36	76,76,76,76	0
58	MG	14	3162	1/1	0.89	0.22	81,81,81,81	0
58	MG	14	3270	1/1	0.89	0.61	95,95,95,95	0
58	MG	14	3163	1/1	0.89	0.43	71,71,71,71	0
58	MG	1H	3226	1/1	0.89	0.21	89,89,89,89	0
58	MG	13	1711	1/1	0.89	0.37	76,76,76,76	0
58	MG	1H	3327	1/1	0.89	0.28	77,77,77,77	0
58	MG	14	3060	1/1	0.89	0.22	58,58,58,58	0
58	MG	1G	1613	1/1	0.89	0.18	87,87,87,87	0
58	MG	1H	3229	1/1	0.89	0.19	50,50,50,50	0
58	MG	1H	3052	1/1	0.89	0.33	83,83,83,83	0
58	MG	14	3066	1/1	0.89	0.33	59,59,59,59	0
58	MG	1H	3232	1/1	0.89	0.15	72,72,72,72	0
58	MG	13	1620	1/1	0.89	0.24	72,72,72,72	0
58	MG	1H	3235	1/1	0.89	0.38	83,83,83,83	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	1H	3183	1/1	0.89	0.22	60,60,60,60	0
58	MG	13	1680	1/1	0.89	0.21	97,97,97,97	0
58	MG	13	1605	1/1	0.89	0.40	76,76,76,76	0
58	MG	14	3189	1/1	0.89	0.18	46,46,46,46	0
58	MG	1H	3106	1/1	0.89	0.23	49,49,49,49	0
58	MG	1H	3073	1/1	0.89	0.38	73,73,73,73	0
58	MG	1H	3250	1/1	0.89	0.37	86,86,86,86	0
58	MG	14	3385	1/1	0.89	0.09	91,91,91,91	0
58	MG	14	3081	1/1	0.89	0.31	80,80,80,80	0
58	MG	1H	3491	1/1	0.89	0.09	105,105,105,105	0
58	MG	1H	3295	1/1	0.89	0.33	87,87,87,87	0
58	MG	14	3085	1/1	0.89	0.23	52,52,52,52	0
58	MG	14	3008	1/1	0.89	0.17	65,65,65,65	0
58	MG	14	3090	1/1	0.89	0.24	68,68,68,68	0
58	MG	1G	1632	1/1	0.89	0.53	83,83,83,83	0
58	MG	14	3214	1/1	0.89	0.09	75,75,75,75	0
58	MG	1H	3251	1/1	0.89	0.24	79,79,79,79	0
58	MG	3K	101	1/1	0.89	0.10	80,80,80,80	0
58	MG	1H	3157	1/1	0.89	0.28	84,84,84,84	0
58	MG	16	203	1/1	0.89	0.28	81,81,81,81	0
58	MG	1H	3075	1/1	0.90	0.14	76,76,76,76	0
58	MG	13	1633	1/1	0.90	0.20	49,49,49,49	0
58	MG	14	3237	1/1	0.90	0.28	79,79,79,79	0
58	MG	13	1618	1/1	0.90	0.19	63,63,63,63	0
58	MG	1H	3120	1/1	0.90	0.34	70,70,70,70	0
58	MG	13	1614	1/1	0.90	0.21	86,86,86,86	0
58	MG	1H	3228	1/1	0.90	0.25	83,83,83,83	0
58	MG	1H	3047	1/1	0.90	0.39	76,76,76,76	0
58	MG	1G	1610	1/1	0.90	0.16	88,88,88,88	0
58	MG	1H	3050	1/1	0.90	0.29	63,63,63,63	0
58	MG	14	3157	1/1	0.90	0.29	71,71,71,71	0
58	MG	13	1631	1/1	0.90	0.19	82,82,82,82	0
58	MG	1H	3133	1/1	0.90	0.18	53,53,53,53	0
58	MG	13	1689	1/1	0.90	0.26	118,118,118,118	0
58	MG	1H	3092	1/1	0.90	0.23	57,57,57,57	0
58	MG	1H	3136	1/1	0.90	0.20	73,73,73,73	0
58	MG	1G	1680	1/1	0.90	0.42	101,101,101,101	0
58	MG	1H	3094	1/1	0.90	0.15	54,54,54,54	0
58	MG	14	3065	1/1	0.90	0.31	62,62,62,62	0
58	MG	1H	3187	1/1	0.90	0.33	78,78,78,78	0
58	MG	1H	3139	1/1	0.90	0.28	52,52,52,52	0
58	MG	1H	3293	1/1	0.90	0.09	67,67,67,67	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	1H	3346	1/1	0.90	0.28	80,80,80,80	0
58	MG	14	3266	1/1	0.90	0.32	84,84,84,84	0
58	MG	1H	3400	1/1	0.90	0.17	54,54,54,54	0
58	MG	1H	3403	1/1	0.90	0.17	72,72,72,72	0
58	MG	14	3269	1/1	0.90	0.18	77,77,77,77	0
58	MG	14	3175	1/1	0.90	0.21	87,87,87,87	0
58	MG	1H	3428	1/1	0.90	0.14	74,74,74,74	0
58	MG	1G	1630	1/1	0.90	0.11	78,78,78,78	0
58	MG	14	3002	1/1	0.90	0.35	64,64,64,64	0
58	MG	13	1663	1/1	0.90	0.29	62,62,62,62	0
58	MG	13	1691	1/1	0.90	0.14	75,75,75,75	0
58	MG	14	3281	1/1	0.90	0.14	84,84,84,84	0
58	MG	14	3009	1/1	0.90	0.21	66,66,66,66	0
58	MG	1H	3499	1/1	0.90	0.08	105,105,105,105	0
58	MG	1H	3513	1/1	0.90	0.12	82,82,82,82	0
58	MG	1H	3297	1/1	0.90	0.25	78,78,78,78	0
58	MG	1H	3148	1/1	0.90	0.32	78,78,78,78	0
58	MG	14	3017	1/1	0.90	0.36	63,63,63,63	0
58	MG	1H	3254	1/1	0.90	0.32	78,78,78,78	0
58	MG	1H	3056	1/1	0.90	0.58	97,97,97,97	0
58	MG	14	3022	1/1	0.90	0.41	78,78,78,78	0
58	MG	1G	1639	1/1	0.90	0.23	80,80,80,80	0
58	MG	14	3204	1/1	0.90	0.18	63,63,63,63	0
58	MG	14	3297	1/1	0.90	0.18	75,75,75,75	0
58	MG	14	3206	1/1	0.90	0.12	50,50,50,50	0
58	MG	14	3104	1/1	0.90	0.16	74,74,74,74	0
58	MG	14	3209	1/1	0.90	0.47	81,81,81,81	0
58	MG	14	3370	1/1	0.90	0.09	106,106,106,106	0
58	MG	1H	3256	1/1	0.90	0.19	58,58,58,58	0
58	MG	1H	3307	1/1	0.90	0.20	60,60,60,60	0
58	MG	1H	3152	1/1	0.90	0.29	71,71,71,71	0
58	MG	1H	3100	1/1	0.90	0.32	64,64,64,64	0
58	MG	1H	3037	1/1	0.90	0.34	62,62,62,62	0
58	MG	1H	3104	1/1	0.90	0.19	68,68,68,68	0
58	MG	1H	3265	1/1	0.90	0.31	79,79,79,79	0
58	MG	1H	3063	1/1	0.90	0.17	64,64,64,64	0
58	MG	1H	3214	1/1	0.90	0.18	67,67,67,67	0
58	MG	13	1647	1/1	0.90	0.16	87,87,87,87	0
58	MG	55	201	1/1	0.90	0.19	58,58,58,58	0
58	MG	14	3129	1/1	0.90	0.30	69,69,69,69	0
58	MG	14	3038	1/1	0.90	0.39	86,86,86,86	0
58	MG	1H	3028	1/1	0.90	0.40	64,64,64,64	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	14	3177	1/1	0.91	0.20	84,84,84,84	0
58	MG	1H	3137	1/1	0.91	0.24	71,71,71,71	0
58	MG	1H	3192	1/1	0.91	0.24	71,71,71,71	0
58	MG	1H	3076	1/1	0.91	0.23	51,51,51,51	0
58	MG	14	3117	1/1	0.91	0.28	57,57,57,57	0
58	MG	16	208	1/1	0.91	0.24	77,77,77,77	0
58	MG	1H	3163	1/1	0.91	0.26	65,65,65,65	0
58	MG	14	3186	1/1	0.91	0.39	85,85,85,85	0
58	MG	1G	1664	1/1	0.91	0.13	92,92,92,92	0
58	MG	14	3190	1/1	0.91	0.13	53,53,53,53	0
58	MG	1H	3233	1/1	0.91	0.26	70,70,70,70	0
58	MG	1G	1666	1/1	0.91	0.13	84,84,84,84	0
58	MG	14	3125	1/1	0.91	0.21	70,70,70,70	0
58	MG	1H	3198	1/1	0.91	0.21	70,70,70,70	0
58	MG	21	301	1/1	0.91	0.29	54,54,54,54	0
58	MG	13	1606	1/1	0.91	0.22	88,88,88,88	0
58	MG	14	3024	1/1	0.91	0.27	82,82,82,82	0
58	MG	13	1629	1/1	0.91	0.19	69,69,69,69	0
58	MG	14	3133	1/1	0.91	0.17	77,77,77,77	0
58	MG	1H	3080	1/1	0.91	0.16	56,56,56,56	0
58	MG	14	3280	1/1	0.91	0.49	87,87,87,87	0
58	MG	14	3138	1/1	0.91	0.09	94,94,94,94	0
58	MG	P8	101	1/1	0.91	0.21	73,73,73,73	0
58	MG	1H	3147	1/1	0.91	0.27	63,63,63,63	0
58	MG	1H	3209	1/1	0.91	0.19	57,57,57,57	0
58	MG	1H	3347	1/1	0.91	0.33	78,78,78,78	0
58	MG	14	3144	1/1	0.91	0.40	81,81,81,81	0
58	MG	14	3032	1/1	0.91	0.29	82,82,82,82	0
58	MG	14	3079	1/1	0.91	0.29	73,73,73,73	0
58	MG	1H	3048	1/1	0.91	0.52	81,81,81,81	0
58	MG	14	3152	1/1	0.91	0.31	75,75,75,75	0
58	MG	1H	3150	1/1	0.91	0.27	69,69,69,69	0
58	MG	14	3155	1/1	0.91	0.26	65,65,65,65	0
58	MG	1H	3101	1/1	0.91	0.31	72,72,72,72	0
58	MG	14	3298	1/1	0.91	0.12	93,93,93,93	0
58	MG	14	3232	1/1	0.91	0.11	52,52,52,52	0
58	MG	13	1700	1/1	0.91	0.28	92,92,92,92	0
58	MG	14	3084	1/1	0.91	0.17	81,81,81,81	0
58	MG	1H	3066	1/1	0.91	0.23	48,48,48,48	0
58	MG	14	3087	1/1	0.91	0.20	48,48,48,48	0
58	MG	14	3387	1/1	0.91	0.08	93,93,93,93	0
58	MG	1H	3011	1/1	0.91	0.27	72,72,72,72	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	1H	3044	1/1	0.91	0.30	61,61,61,61	0
58	MG	14	3093	1/1	0.91	0.24	63,63,63,63	0
58	MG	1H	3036	1/1	0.91	0.33	65,65,65,65	0
58	MG	1H	3258	1/1	0.91	0.17	64,64,64,64	0
58	MG	1H	3225	1/1	0.91	0.18	79,79,79,79	0
58	MG	14	3097	1/1	0.91	0.31	77,77,77,77	0
58	MG	14	3099	1/1	0.91	0.16	55,55,55,55	0
58	MG	14	3247	1/1	0.91	0.12	85,85,85,85	0
58	MG	14	3248	1/1	0.91	0.30	79,79,79,79	0
58	MG	1H	3112	1/1	0.91	0.28	71,71,71,71	0
58	MG	1H	3160	1/1	0.91	0.31	79,79,79,79	0
58	MG	1G	1658	1/1	0.91	0.11	92,92,92,92	0
58	MG	14	3116	1/1	0.92	0.32	80,80,80,80	0
58	MG	14	3055	1/1	0.92	0.18	54,54,54,54	0
58	MG	14	3007	1/1	0.92	0.32	68,68,68,68	0
58	MG	14	3256	1/1	0.92	0.13	57,57,57,57	0
58	MG	14	3257	1/1	0.92	0.20	58,58,58,58	0
58	MG	14	3120	1/1	0.92	0.31	54,54,54,54	0
58	MG	1H	3197	1/1	0.92	0.18	63,63,63,63	0
58	MG	13	1643	1/1	0.92	0.35	78,78,78,78	0
58	MG	1G	1618	1/1	0.92	0.15	78,78,78,78	0
58	MG	1H	3061	1/1	0.92	0.28	56,56,56,56	0
58	MG	14	3014	1/1	0.92	0.33	77,77,77,77	0
58	MG	13	1601	1/1	0.92	0.23	52,52,52,52	0
58	MG	1H	3175	1/1	0.92	0.15	65,65,65,65	0
58	MG	14	3067	1/1	0.92	0.14	81,81,81,81	0
58	MG	13	1692	1/1	0.92	0.22	79,79,79,79	0
58	MG	13	1611	1/1	0.92	0.32	71,71,71,71	0
58	MG	1H	3179	1/1	0.92	0.22	67,67,67,67	0
58	MG	14	3021	1/1	0.92	0.23	73,73,73,73	0
58	MG	1H	3270	1/1	0.92	0.37	77,77,77,77	0
58	MG	1H	3181	1/1	0.92	0.06	63,63,63,63	0
58	MG	14	3205	1/1	0.92	0.15	58,58,58,58	0
58	MG	1G	1669	1/1	0.92	0.23	80,80,80,80	0
58	MG	13	1742	1/1	0.92	0.12	95,95,95,95	0
58	MG	14	3279	1/1	0.92	0.26	74,74,74,74	0
58	MG	13	1630	1/1	0.92	0.09	67,67,67,67	0
58	MG	14	3211	1/1	0.92	0.16	81,81,81,81	0
58	MG	1H	3249	1/1	0.92	0.50	76,76,76,76	0
58	MG	14	3213	1/1	0.92	0.29	75,75,75,75	0
58	MG	1H	3277	1/1	0.92	0.21	70,70,70,70	0
58	MG	14	3147	1/1	0.92	0.24	81,81,81,81	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	14	3216	1/1	0.92	0.08	63,63,63,63	0
58	MG	1H	3344	1/1	0.92	0.13	70,70,70,70	0
58	MG	13	1666	1/1	0.92	0.23	82,82,82,82	0
58	MG	L8	101	1/1	0.92	0.22	79,79,79,79	0
58	MG	13	1706	1/1	0.92	0.57	81,81,81,81	0
58	MG	14	3224	1/1	0.92	0.29	77,77,77,77	0
58	MG	13	1707	1/1	0.92	0.39	80,80,80,80	0
58	MG	1H	3253	1/1	0.92	0.13	76,76,76,76	0
58	MG	1G	1603	1/1	0.92	0.12	87,87,87,87	0
58	MG	1H	3317	1/1	0.92	0.24	84,84,84,84	0
58	MG	1H	3422	1/1	0.92	0.09	66,66,66,66	0
58	MG	1H	3190	1/1	0.92	0.32	69,69,69,69	0
58	MG	1H	3460	1/1	0.92	0.09	81,81,81,81	0
58	MG	2L	101	1/1	0.92	0.25	88,88,88,88	0
58	MG	13	1641	1/1	0.92	0.17	69,69,69,69	0
58	MG	1H	3128	1/1	0.92	0.25	66,66,66,66	0
58	MG	1J	201	1/1	0.92	0.44	76,76,76,76	0
58	MG	1G	1648	1/1	0.92	0.32	79,79,79,79	0
58	MG	1H	3129	1/1	0.92	0.21	63,63,63,63	0
58	MG	1H	3509	1/1	0.92	0.09	68,68,68,68	0
58	MG	14	3107	1/1	0.92	0.21	58,58,58,58	0
58	MG	14	3171	1/1	0.92	0.40	80,80,80,80	0
58	MG	13	1642	1/1	0.92	0.24	64,64,64,64	0
58	MG	14	3173	1/1	0.92	0.25	79,79,79,79	0
58	MG	14	3112	1/1	0.92	0.22	65,65,65,65	0
58	MG	14	3114	1/1	0.92	0.28	79,79,79,79	0
58	MG	14	3176	1/1	0.92	0.08	58,58,58,58	0
58	MG	14	3251	1/1	0.92	0.47	84,84,84,84	0
58	MG	14	3005	1/1	0.92	0.39	60,60,60,60	0
58	MG	1G	1670	1/1	0.93	0.16	88,88,88,88	0
58	MG	1H	3053	1/1	0.93	0.24	66,66,66,66	0
58	MG	14	3030	1/1	0.93	0.13	70,70,70,70	0
58	MG	1H	3210	1/1	0.93	0.25	67,67,67,67	0
58	MG	1H	3127	1/1	0.93	0.16	50,50,50,50	0
58	MG	1H	3043	1/1	0.93	0.19	77,77,77,77	0
58	MG	1K	101	1/1	0.93	0.08	85,85,85,85	0
58	MG	14	3100	1/1	0.93	0.21	66,66,66,66	0
58	MG	1H	3288	1/1	0.93	0.09	58,58,58,58	0
58	MG	13	1669	1/1	0.93	0.13	68,68,68,68	0
58	MG	1H	3329	1/1	0.93	0.41	85,85,85,85	0
58	MG	1H	3184	1/1	0.93	0.28	78,78,78,78	0
58	MG	14	3040	1/1	0.93	0.36	82,82,82,82	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	14	3180	1/1	0.93	0.28	74,74,74,74	0
58	MG	1H	3131	1/1	0.93	0.19	57,57,57,57	0
58	MG	1H	3220	1/1	0.93	0.16	74,74,74,74	0
58	MG	14	3183	1/1	0.93	0.20	66,66,66,66	0
58	MG	13	1679	1/1	0.93	0.14	75,75,75,75	0
58	MG	1H	3081	1/1	0.93	0.27	90,90,90,90	0
58	MG	1H	3060	1/1	0.93	0.18	52,52,52,52	0
58	MG	88	202	1/1	0.93	0.08	64,64,64,64	0
58	MG	98	201	1/1	0.93	0.22	56,56,56,56	0
58	MG	1H	3296	1/1	0.93	0.12	72,72,72,72	0
58	MG	1H	3107	1/1	0.93	0.13	52,52,52,52	0
58	MG	14	3195	1/1	0.93	0.40	70,70,70,70	0
58	MG	1H	3038	1/1	0.93	0.42	73,73,73,73	0
58	MG	1H	3039	1/1	0.93	0.28	75,75,75,75	0
58	MG	14	3056	1/1	0.93	0.30	58,58,58,58	0
58	MG	1H	3193	1/1	0.93	0.14	60,60,60,60	0
58	MG	14	3278	1/1	0.93	0.12	89,89,89,89	0
58	MG	14	3058	1/1	0.93	0.20	58,58,58,58	0
58	MG	13	1676	1/1	0.93	0.06	88,88,88,88	0
58	MG	14	3128	1/1	0.93	0.12	58,58,58,58	0
58	MG	14	3004	1/1	0.93	0.53	78,78,78,78	0
58	MG	14	3061	1/1	0.93	0.18	58,58,58,58	0
58	MG	1H	3303	1/1	0.93	0.13	76,76,76,76	0
58	MG	14	3132	1/1	0.93	0.07	44,44,44,44	0
58	MG	14	3006	1/1	0.93	0.22	62,62,62,62	0
58	MG	14	3134	1/1	0.93	0.20	62,62,62,62	0
58	MG	1H	3306	1/1	0.93	0.36	78,78,78,78	0
58	MG	1H	3113	1/1	0.93	0.28	68,68,68,68	0
58	MG	1H	3070	1/1	0.93	0.25	68,68,68,68	0
58	MG	14	3010	1/1	0.93	0.35	78,78,78,78	0
58	MG	14	3069	1/1	0.93	0.17	60,60,60,60	0
58	MG	14	3296	1/1	0.93	0.22	74,74,74,74	0
58	MG	14	3218	1/1	0.93	0.21	71,71,71,71	0
58	MG	1G	1654	1/1	0.93	0.22	85,85,85,85	0
58	MG	14	3012	1/1	0.93	0.27	69,69,69,69	0
58	MG	1G	1656	1/1	0.93	0.13	140,140,140,140	0
58	MG	1H	3072	1/1	0.93	0.24	61,61,61,61	0
58	MG	14	3319	1/1	0.93	0.09	65,65,65,65	0
58	MG	14	3326	1/1	0.93	0.11	61,61,61,61	0
58	MG	1H	3200	1/1	0.93	0.15	35,35,35,35	0
58	MG	14	3372	1/1	0.93	0.07	76,76,76,76	0
58	MG	1H	3443	1/1	0.93	0.07	66,66,66,66	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	14	3228	1/1	0.93	0.19	85,85,85,85	0
58	MG	13	1625	1/1	0.93	0.25	82,82,82,82	0
58	MG	14	3407	1/1	0.93	0.09	117,117,117,117	0
58	MG	14	3153	1/1	0.93	0.28	60,60,60,60	0
58	MG	14	3018	1/1	0.93	0.26	50,50,50,50	0
58	MG	1H	3469	1/1	0.93	0.09	99,99,99,99	0
58	MG	14	3156	1/1	0.93	0.33	63,63,63,63	0
58	MG	1H	3243	1/1	0.93	0.24	81,81,81,81	0
58	MG	1G	1615	1/1	0.93	0.10	85,85,85,85	0
58	MG	29	303	1/1	0.93	0.22	73,73,73,73	0
58	MG	1H	3315	1/1	0.93	0.20	80,80,80,80	0
58	MG	1H	3096	1/1	0.93	0.08	50,50,50,50	0
58	MG	1H	3205	1/1	0.93	0.26	68,68,68,68	0
58	MG	5I	102	1/1	0.93	0.31	90,90,90,90	0
58	MG	1G	1668	1/1	0.93	0.10	84,84,84,84	0
58	MG	14	3088	1/1	0.93	0.24	45,45,45,45	0
58	MG	1H	3176	1/1	0.93	0.19	82,82,82,82	0
58	MG	1H	3194	1/1	0.94	0.28	40,40,40,40	0
58	MG	1H	3068	1/1	0.94	0.12	50,50,50,50	0
58	MG	1H	3369	1/1	0.94	0.15	55,55,55,55	0
58	MG	14	3275	1/1	0.94	0.20	86,86,86,86	0
58	MG	14	3068	1/1	0.94	0.30	60,60,60,60	0
58	MG	1H	3392	1/1	0.94	0.06	94,94,94,94	0
58	MG	1H	3103	1/1	0.94	0.33	58,58,58,58	0
58	MG	13	1632	1/1	0.94	0.22	71,71,71,71	0
58	MG	1H	3153	1/1	0.94	0.26	72,72,72,72	0
58	MG	1H	3071	1/1	0.94	0.17	39,39,39,39	0
58	MG	1G	1643	1/1	0.94	0.21	74,74,74,74	0
58	MG	13	1696	1/1	0.94	0.11	70,70,70,70	0
58	MG	1H	3459	1/1	0.94	0.09	73,73,73,73	0
58	MG	13	1619	1/1	0.94	0.14	75,75,75,75	0
58	MG	13	1728	1/1	0.94	0.12	95,95,95,95	0
58	MG	13	1634	1/1	0.94	0.16	47,47,47,47	0
58	MG	1H	3095	1/1	0.94	0.17	49,49,49,49	0
58	MG	1G	1650	1/1	0.94	0.38	81,81,81,81	0
58	MG	3L	102	1/1	0.94	0.09	151,151,151,151	0
58	MG	14	3241	1/1	0.94	0.19	80,80,80,80	0
58	MG	1H	3114	1/1	0.94	0.14	66,66,66,66	0
58	MG	14	3295	1/1	0.94	0.22	79,79,79,79	0
58	MG	14	3243	1/1	0.94	0.18	70,70,70,70	0
58	MG	14	3187	1/1	0.94	0.25	47,47,47,47	0
58	MG	1G	1611	1/1	0.94	0.13	91,91,91,91	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	1H	3500	1/1	0.94	0.09	54,54,54,54	0
58	MG	1H	3003	1/1	0.94	0.19	49,49,49,49	0
58	MG	1H	3117	1/1	0.94	0.33	43,43,43,43	0
58	MG	14	3249	1/1	0.94	0.25	65,65,65,65	0
58	MG	1H	3519	1/1	0.94	0.11	101,101,101,101	0
58	MG	14	3337	1/1	0.94	0.09	73,73,73,73	0
58	MG	14	3091	1/1	0.94	0.27	57,57,57,57	0
58	MG	1H	3239	1/1	0.94	0.10	67,67,67,67	0
58	MG	1H	3240	1/1	0.94	0.28	77,77,77,77	0
58	MG	14	3386	1/1	0.94	0.06	94,94,94,94	0
58	MG	1H	3017	1/1	0.94	0.35	66,66,66,66	0
58	MG	14	3395	1/1	0.94	0.10	75,75,75,75	0
58	MG	14	3397	1/1	0.94	0.08	52,52,52,52	0
58	MG	14	3404	1/1	0.94	0.09	66,66,66,66	0
58	MG	1H	3213	1/1	0.94	0.09	43,43,43,43	0
58	MG	1H	3300	1/1	0.94	0.47	72,72,72,72	0
58	MG	14	3052	1/1	0.94	0.16	59,59,59,59	0
58	MG	14	3054	1/1	0.94	0.19	51,51,51,51	0
58	MG	1H	3272	1/1	0.94	0.13	68,68,68,68	0
58	MG	14	3207	1/1	0.94	0.06	68,68,68,68	0
58	MG	1H	3336	1/1	0.94	0.08	62,62,62,62	0
58	MG	1H	3245	1/1	0.94	0.28	81,81,81,81	0
58	MG	29	302	1/1	0.94	0.23	57,57,57,57	0
58	MG	1H	3018	1/1	0.94	0.31	73,73,73,73	0
58	MG	1H	3304	1/1	0.94	0.07	71,71,71,71	0
58	MG	14	3108	1/1	0.94	0.17	50,50,50,50	0
58	MG	1H	3305	1/1	0.94	0.24	75,75,75,75	0
58	MG	1H	3079	1/1	0.94	0.16	53,53,53,53	0
58	MG	13	1621	1/1	0.94	0.17	74,74,74,74	0
58	MG	1H	3005	1/1	0.94	0.09	53,53,53,53	0
58	MG	1H	3219	1/1	0.94	0.25	70,70,70,70	0
58	MG	1H	3171	1/1	0.95	0.12	58,58,58,58	0
58	MG	13	1736	1/1	0.95	0.07	116,116,116,116	0
58	MG	14	3110	1/1	0.95	0.16	55,55,55,55	0
58	MG	14	3041	1/1	0.95	0.25	66,66,66,66	0
58	MG	1H	3173	1/1	0.95	0.33	65,65,65,65	0
58	MG	14	3113	1/1	0.95	0.53	62,62,62,62	0
58	MG	13	1655	1/1	0.95	0.08	77,77,77,77	0
58	MG	1H	3082	1/1	0.95	0.11	61,61,61,61	0
58	MG	1H	3111	1/1	0.95	0.16	44,44,44,44	0
58	MG	1H	3348	1/1	0.95	0.27	73,73,73,73	0
58	MG	1H	3142	1/1	0.95	0.21	39,39,39,39	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	1H	3215	1/1	0.95	0.19	60,60,60,60	0
58	MG	14	3194	1/1	0.95	0.17	61,61,61,61	0
58	MG	1H	3145	1/1	0.95	0.32	76,76,76,76	0
58	MG	13	1602	1/1	0.95	0.22	49,49,49,49	0
58	MG	1H	3406	1/1	0.95	0.08	49,49,49,49	0
58	MG	14	3274	1/1	0.95	0.39	88,88,88,88	0
58	MG	13	1628	1/1	0.95	0.08	58,58,58,58	0
58	MG	14	3053	1/1	0.95	0.12	45,45,45,45	0
58	MG	1H	3260	1/1	0.95	0.14	35,35,35,35	0
58	MG	1H	3440	1/1	0.95	0.07	52,52,52,52	0
58	MG	1H	3261	1/1	0.95	0.21	64,64,64,64	0
58	MG	1H	3447	1/1	0.95	0.10	55,55,55,55	0
58	MG	1H	3453	1/1	0.95	0.06	105,105,105,105	0
58	MG	5E	201	1/1	0.95	0.12	67,67,67,67	0
58	MG	1H	3149	1/1	0.95	0.10	61,61,61,61	0
58	MG	1H	3462	1/1	0.95	0.06	79,79,79,79	0
58	MG	1H	3088	1/1	0.95	0.14	77,77,77,77	0
58	MG	14	3135	1/1	0.95	0.15	54,54,54,54	0
58	MG	14	3136	1/1	0.95	0.18	49,49,49,49	0
58	MG	1H	3474	1/1	0.95	0.07	100,100,100,100	0
58	MG	1H	3223	1/1	0.95	0.19	60,60,60,60	0
58	MG	14	3291	1/1	0.95	0.09	70,70,70,70	0
58	MG	1H	3065	1/1	0.95	0.19	43,43,43,43	0
58	MG	1H	3493	1/1	0.95	0.16	79,79,79,79	0
58	MG	1H	3311	1/1	0.95	0.20	81,81,81,81	0
58	MG	1H	3312	1/1	0.95	0.25	73,73,73,73	0
58	MG	1H	3503	1/1	0.95	0.19	73,73,73,73	0
58	MG	1H	3007	1/1	0.95	0.32	64,64,64,64	0
58	MG	14	3146	1/1	0.95	0.13	64,64,64,64	0
58	MG	1H	3067	1/1	0.95	0.20	46,46,46,46	0
58	MG	1H	3189	1/1	0.95	0.14	61,61,61,61	0
58	MG	1H	3009	1/1	0.95	0.35	73,73,73,73	0
58	MG	1G	1641	1/1	0.95	0.10	98,98,98,98	0
58	MG	1H	3069	1/1	0.95	0.17	52,52,52,52	0
58	MG	14	3332	1/1	0.95	0.07	64,64,64,64	0
58	MG	13	1686	1/1	0.95	0.34	80,80,80,80	0
58	MG	14	3338	1/1	0.95	0.07	74,74,74,74	0
58	MG	14	3366	1/1	0.95	0.09	94,94,94,94	0
58	MG	14	3367	1/1	0.95	0.07	103,103,103,103	0
58	MG	1H	3126	1/1	0.95	0.17	60,60,60,60	0
58	MG	13	1697	1/1	0.95	0.06	73,73,73,73	0
58	MG	14	3379	1/1	0.95	0.11	106,106,106,106	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	1H	3276	1/1	0.95	0.11	55,55,55,55	0
58	MG	13	1610	1/1	0.95	0.32	66,66,66,66	0
58	MG	1H	3014	1/1	0.95	0.13	58,58,58,58	0
58	MG	14	3389	1/1	0.95	0.07	75,75,75,75	0
58	MG	14	3392	1/1	0.95	0.10	77,77,77,77	0
58	MG	14	3394	1/1	0.95	0.07	53,53,53,53	0
58	MG	13	1603	1/1	0.95	0.27	50,50,50,50	0
58	MG	1H	3238	1/1	0.95	0.09	52,52,52,52	0
58	MG	13	1668	1/1	0.95	0.18	66,66,66,66	0
58	MG	1G	1652	1/1	0.95	0.39	81,81,81,81	0
58	MG	14	3164	1/1	0.95	0.31	78,78,78,78	0
58	MG	1H	3328	1/1	0.95	0.20	56,56,56,56	0
58	MG	13	1604	1/1	0.95	0.36	81,81,81,81	0
58	MG	1G	1655	1/1	0.95	0.07	86,86,86,86	0
58	MG	41	201	1/1	0.95	0.13	67,67,67,67	0
58	MG	1H	3284	1/1	0.95	0.27	74,74,74,74	0
58	MG	1H	3241	1/1	0.95	0.24	71,71,71,71	0
58	MG	1H	3242	1/1	0.95	0.33	77,77,77,77	0
58	MG	1H	3333	1/1	0.95	0.09	71,71,71,71	0
58	MG	1H	3201	1/1	0.95	0.17	41,41,41,41	0
58	MG	13	1613	1/1	0.95	0.24	83,83,83,83	0
58	MG	13	1723	1/1	0.95	0.08	70,70,70,70	0
58	MG	1H	3105	1/1	0.95	0.24	71,71,71,71	0
58	MG	1H	3339	1/1	0.95	0.13	75,75,75,75	0
59	PAR	13	1749	42/42	0.95	0.08	52,62,69,75	0
59	PAR	1G	1697	42/42	0.95	0.09	75,80,88,91	0
58	MG	13	1639	1/1	0.95	0.18	55,55,55,55	0
58	MG	1H	3207	1/1	0.95	0.23	56,56,56,56	0
58	MG	1H	3386	1/1	0.96	0.06	50,50,50,50	0
58	MG	13	1607	1/1	0.96	0.47	71,71,71,71	0
58	MG	13	1617	1/1	0.96	0.16	60,60,60,60	0
58	MG	14	3101	1/1	0.96	0.08	65,65,65,65	0
58	MG	1H	3168	1/1	0.96	0.20	64,64,64,64	0
58	MG	13	1684	1/1	0.96	0.40	94,94,94,94	0
58	MG	14	3149	1/1	0.96	0.14	62,62,62,62	0
58	MG	14	3150	1/1	0.96	0.21	50,50,50,50	0
58	MG	1H	3415	1/1	0.96	0.07	63,63,63,63	0
58	MG	14	3300	1/1	0.96	0.17	63,63,63,63	0
58	MG	14	3105	1/1	0.96	0.17	45,45,45,45	0
58	MG	1H	3121	1/1	0.96	0.19	35,35,35,35	0
58	MG	14	3201	1/1	0.96	0.11	69,69,69,69	0
58	MG	14	3202	1/1	0.96	0.07	64,64,64,64	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	1G	1685	1/1	0.96	0.09	88,88,88,88	0
58	MG	14	3333	1/1	0.96	0.06	67,67,67,67	0
58	MG	1G	1689	1/1	0.96	0.06	84,84,84,84	0
58	MG	14	3109	1/1	0.96	0.09	62,62,62,62	0
58	MG	14	3361	1/1	0.96	0.07	76,76,76,76	0
58	MG	14	3365	1/1	0.96	0.10	83,83,83,83	0
58	MG	13	1733	1/1	0.96	0.06	104,104,104,104	0
58	MG	1H	3335	1/1	0.96	0.06	59,59,59,59	0
58	MG	1H	3231	1/1	0.96	0.29	74,74,74,74	0
58	MG	1G	1617	1/1	0.96	0.12	74,74,74,74	0
58	MG	14	3375	1/1	0.96	0.08	89,89,89,89	0
58	MG	1H	3057	1/1	0.96	0.12	44,44,44,44	0
58	MG	14	3071	1/1	0.96	0.19	42,42,42,42	0
58	MG	1H	3125	1/1	0.96	0.17	47,47,47,47	0
58	MG	13	1735	1/1	0.96	0.07	84,84,84,84	0
58	MG	14	3036	1/1	0.96	0.33	67,67,67,67	0
58	MG	14	3390	1/1	0.96	0.12	109,109,109,109	0
58	MG	1H	3158	1/1	0.96	0.08	44,44,44,44	0
58	MG	1H	3049	1/1	0.96	0.28	69,69,69,69	0
58	MG	1H	3465	1/1	0.96	0.06	76,76,76,76	0
58	MG	21	302	1/1	0.96	0.07	68,68,68,68	0
58	MG	14	3400	1/1	0.96	0.12	65,65,65,65	0
58	MG	1H	3466	1/1	0.96	0.06	67,67,67,67	0
58	MG	1H	3143	1/1	0.96	0.14	50,50,50,50	0
58	MG	78	201	1/1	0.96	0.14	80,80,80,80	0
58	MG	1H	3008	1/1	0.96	0.27	68,68,68,68	0
58	MG	1H	3475	1/1	0.96	0.11	109,109,109,109	0
58	MG	1H	3484	1/1	0.96	0.12	73,73,73,73	0
58	MG	1H	3485	1/1	0.96	0.05	87,87,87,87	0
58	MG	14	3086	1/1	0.96	0.36	67,67,67,67	0
58	MG	14	3231	1/1	0.96	0.06	70,70,70,70	0
58	MG	1H	3488	1/1	0.96	0.13	69,69,69,69	0
58	MG	1H	3180	1/1	0.96	0.18	77,77,77,77	0
58	MG	1H	3062	1/1	0.96	0.11	44,44,44,44	0
58	MG	1H	3087	1/1	0.96	0.14	75,75,75,75	0
58	MG	1H	3222	1/1	0.96	0.09	58,58,58,58	0
58	MG	14	3092	1/1	0.96	0.24	48,48,48,48	0
58	MG	1H	3001	1/1	0.96	0.29	53,53,53,53	0
58	MG	1H	3002	1/1	0.96	0.14	60,60,60,60	0
58	MG	14	3288	1/1	0.96	0.17	78,78,78,78	0
60	ZN	3E	303	1/1	0.96	0.33	97,97,97,97	0
58	MG	1G	1640	1/1	0.96	0.09	83,83,83,83	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	1H	3504	1/1	0.96	0.08	66,66,66,66	0
58	MG	1H	3349	1/1	0.97	0.08	40,40,40,40	0
58	MG	1H	3352	1/1	0.97	0.07	45,45,45,45	0
58	MG	1G	1621	1/1	0.97	0.07	90,90,90,90	0
58	MG	1G	1687	1/1	0.97	0.07	104,104,104,104	0
58	MG	1G	1688	1/1	0.97	0.12	102,102,102,102	0
58	MG	1H	3354	1/1	0.97	0.06	49,49,49,49	0
58	MG	1G	1690	1/1	0.97	0.04	104,104,104,104	0
58	MG	1G	1691	1/1	0.97	0.12	89,89,89,89	0
58	MG	1G	1692	1/1	0.97	0.06	83,83,83,83	0
58	MG	1G	1695	1/1	0.97	0.11	96,96,96,96	0
58	MG	1G	1696	1/1	0.97	0.04	109,109,109,109	0
58	MG	1H	3494	1/1	0.97	0.09	82,82,82,82	0
58	MG	1H	3496	1/1	0.97	0.05	59,59,59,59	0
58	MG	1H	3359	1/1	0.97	0.05	60,60,60,60	0
58	MG	1H	3361	1/1	0.97	0.10	64,64,64,64	0
58	MG	14	3210	1/1	0.97	0.21	51,51,51,51	0
58	MG	1H	3364	1/1	0.97	0.05	47,47,47,47	0
58	MG	1H	3115	1/1	0.97	0.17	37,37,37,37	0
58	MG	1H	3506	1/1	0.97	0.09	44,44,44,44	0
58	MG	1H	3508	1/1	0.97	0.06	55,55,55,55	0
58	MG	14	3141	1/1	0.97	0.20	46,46,46,46	0
58	MG	1H	3374	1/1	0.97	0.08	90,90,90,90	0
58	MG	1H	3510	1/1	0.97	0.17	51,51,51,51	0
58	MG	1H	3511	1/1	0.97	0.06	82,82,82,82	0
58	MG	1H	3378	1/1	0.97	0.06	79,79,79,79	0
58	MG	14	3221	1/1	0.97	0.12	72,72,72,72	0
58	MG	1H	3514	1/1	0.97	0.04	77,77,77,77	0
58	MG	1H	3518	1/1	0.97	0.07	94,94,94,94	0
58	MG	1H	3383	1/1	0.97	0.06	61,61,61,61	0
58	MG	14	3225	1/1	0.97	0.31	57,57,57,57	0
58	MG	1H	3170	1/1	0.97	0.35	77,77,77,77	0
58	MG	14	3307	1/1	0.97	0.07	49,49,49,49	0
58	MG	14	3315	1/1	0.97	0.06	57,57,57,57	0
58	MG	1H	3013	1/1	0.97	0.23	52,52,52,52	0
58	MG	14	3321	1/1	0.97	0.06	55,55,55,55	0
58	MG	1H	3394	1/1	0.97	0.15	70,70,70,70	0
58	MG	1H	3058	1/1	0.97	0.12	36,36,36,36	0
58	MG	13	1745	1/1	0.97	0.11	107,107,107,107	0
58	MG	14	3334	1/1	0.97	0.06	49,49,49,49	0
58	MG	1H	3237	1/1	0.97	0.35	72,72,72,72	0
58	MG	1H	3408	1/1	0.97	0.05	49,49,49,49	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	14	3346	1/1	0.97	0.05	74,74,74,74	0
58	MG	14	3352	1/1	0.97	0.14	99,99,99,99	0
58	MG	14	3353	1/1	0.97	0.06	82,82,82,82	0
58	MG	14	3354	1/1	0.97	0.05	56,56,56,56	0
58	MG	1H	3414	1/1	0.97	0.15	64,64,64,64	0
58	MG	1H	3086	1/1	0.97	0.13	54,54,54,54	0
58	MG	1H	3420	1/1	0.97	0.07	50,50,50,50	0
58	MG	1K	102	1/1	0.97	0.20	72,72,72,72	0
58	MG	14	3369	1/1	0.97	0.05	102,102,102,102	0
58	MG	11	303	1/1	0.97	0.05	41,41,41,41	0
58	MG	1H	3426	1/1	0.97	0.06	88,88,88,88	0
58	MG	13	1747	1/1	0.97	0.05	96,96,96,96	0
58	MG	14	3377	1/1	0.97	0.04	107,107,107,107	0
58	MG	1H	3430	1/1	0.97	0.04	73,73,73,73	0
58	MG	14	3380	1/1	0.97	0.05	76,76,76,76	0
58	MG	1H	3431	1/1	0.97	0.08	94,94,94,94	0
58	MG	1H	3437	1/1	0.97	0.06	54,54,54,54	0
58	MG	1H	3439	1/1	0.97	0.07	51,51,51,51	0
58	MG	1H	3263	1/1	0.97	0.08	56,56,56,56	0
58	MG	13	1748	1/1	0.97	0.07	82,82,82,82	0
58	MG	13	1615	1/1	0.97	0.38	84,84,84,84	0
58	MG	14	3393	1/1	0.97	0.14	76,76,76,76	0
58	MG	1H	3199	1/1	0.97	0.09	44,44,44,44	0
58	MG	I8	101	1/1	0.97	0.07	56,56,56,56	0
58	MG	1H	3454	1/1	0.97	0.10	67,67,67,67	0
58	MG	14	3398	1/1	0.97	0.08	70,70,70,70	0
58	MG	1H	3456	1/1	0.97	0.06	80,80,80,80	0
58	MG	14	3402	1/1	0.97	0.08	76,76,76,76	0
58	MG	14	3403	1/1	0.97	0.08	66,66,66,66	0
58	MG	1H	3458	1/1	0.97	0.06	45,45,45,45	0
58	MG	14	3405	1/1	0.97	0.08	75,75,75,75	0
58	MG	1H	3124	1/1	0.97	0.15	39,39,39,39	0
58	MG	1H	3064	1/1	0.97	0.10	43,43,43,43	0
58	MG	1H	3144	1/1	0.97	0.22	49,49,49,49	0
58	MG	1H	3464	1/1	0.97	0.05	84,84,84,84	0
58	MG	1H	3182	1/1	0.97	0.31	61,61,61,61	0
58	MG	1H	3093	1/1	0.97	0.07	53,53,53,53	0
58	MG	13	1716	1/1	0.97	0.06	73,73,73,73	0
58	MG	1H	3320	1/1	0.97	0.23	71,71,71,71	0
58	MG	13	1640	1/1	0.97	0.14	64,64,64,64	0
58	MG	1H	3477	1/1	0.97	0.17	62,62,62,62	0
58	MG	1H	3478	1/1	0.97	0.05	91,91,91,91	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	1H	3479	1/1	0.97	0.05	79,79,79,79	0
58	MG	1H	3480	1/1	0.97	0.05	88,88,88,88	0
58	MG	14	3188	1/1	0.97	0.15	53,53,53,53	0
58	MG	1H	3481	1/1	0.97	0.12	132,132,132,132	0
58	MG	J5	101	1/1	0.97	0.10	52,52,52,52	0
58	MG	13	1740	1/1	0.97	0.05	70,70,70,70	0
58	MG	14	3119	1/1	0.97	0.14	49,49,49,49	0
58	MG	14	3192	1/1	0.97	0.12	59,59,59,59	0
58	MG	13	1741	1/1	0.97	0.05	82,82,82,82	0
60	ZN	32	301	1/1	0.97	0.26	112,112,112,112	0
60	ZN	5A	101	1/1	0.97	0.06	143,143,143,143	0
58	MG	13	1685	1/1	0.97	0.08	74,74,74,74	0
58	MG	1H	3470	1/1	0.98	0.09	73,73,73,73	0
58	MG	1H	3471	1/1	0.98	0.05	63,63,63,63	0
58	MG	14	3335	1/1	0.98	0.05	80,80,80,80	0
58	MG	1H	3472	1/1	0.98	0.10	72,72,72,72	0
58	MG	14	3098	1/1	0.98	0.35	71,71,71,71	0
58	MG	14	3344	1/1	0.98	0.06	64,64,64,64	0
58	MG	13	1743	1/1	0.98	0.04	60,60,60,60	0
58	MG	14	3350	1/1	0.98	0.05	92,92,92,92	0
58	MG	13	1744	1/1	0.98	0.04	89,89,89,89	0
58	MG	1H	3417	1/1	0.98	0.04	66,66,66,66	0
58	MG	1H	3418	1/1	0.98	0.05	70,70,70,70	0
58	MG	14	3355	1/1	0.98	0.07	64,64,64,64	0
58	MG	14	3358	1/1	0.98	0.08	82,82,82,82	0
58	MG	1H	3204	1/1	0.98	0.06	41,41,41,41	0
58	MG	14	3363	1/1	0.98	0.04	54,54,54,54	0
58	MG	1H	3421	1/1	0.98	0.06	46,46,46,46	0
58	MG	1H	3367	1/1	0.98	0.06	54,54,54,54	0
58	MG	1H	3483	1/1	0.98	0.04	90,90,90,90	0
58	MG	1H	3423	1/1	0.98	0.04	59,59,59,59	0
58	MG	1H	3424	1/1	0.98	0.05	73,73,73,73	0
58	MG	1H	3425	1/1	0.98	0.05	49,49,49,49	0
58	MG	14	3374	1/1	0.98	0.11	86,86,86,86	0
58	MG	1H	3489	1/1	0.98	0.06	53,53,53,53	0
58	MG	13	1623	1/1	0.98	0.17	62,62,62,62	0
58	MG	1H	3371	1/1	0.98	0.04	45,45,45,45	0
58	MG	14	3219	1/1	0.98	0.05	51,51,51,51	0
58	MG	14	3382	1/1	0.98	0.05	81,81,81,81	0
58	MG	14	3383	1/1	0.98	0.08	66,66,66,66	0
58	MG	1H	3373	1/1	0.98	0.09	75,75,75,75	0
58	MG	13	1746	1/1	0.98	0.06	84,84,84,84	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	1H	3434	1/1	0.98	0.05	63,63,63,63	0
58	MG	1H	3497	1/1	0.98	0.06	42,42,42,42	0
58	MG	1H	3498	1/1	0.98	0.06	47,47,47,47	0
58	MG	14	3391	1/1	0.98	0.06	97,97,97,97	0
58	MG	1H	3435	1/1	0.98	0.04	82,82,82,82	0
58	MG	1H	3436	1/1	0.98	0.04	67,67,67,67	0
58	MG	1H	3501	1/1	0.98	0.09	42,42,42,42	0
58	MG	1H	3375	1/1	0.98	0.08	81,81,81,81	0
58	MG	14	3396	1/1	0.98	0.04	53,53,53,53	0
58	MG	1H	3376	1/1	0.98	0.05	67,67,67,67	0
58	MG	1H	3505	1/1	0.98	0.05	41,41,41,41	0
58	MG	13	1738	1/1	0.98	0.06	84,84,84,84	0
58	MG	1H	3507	1/1	0.98	0.05	43,43,43,43	0
58	MG	13	1739	1/1	0.98	0.05	85,85,85,85	0
58	MG	1H	3384	1/1	0.98	0.04	34,34,34,34	0
58	MG	1H	3448	1/1	0.98	0.07	51,51,51,51	0
58	MG	1H	3449	1/1	0.98	0.04	74,74,74,74	0
58	MG	1H	3450	1/1	0.98	0.05	62,62,62,62	0
58	MG	1H	3451	1/1	0.98	0.06	55,55,55,55	0
58	MG	1H	3452	1/1	0.98	0.06	74,74,74,74	0
58	MG	13	1724	1/1	0.98	0.15	96,96,96,96	0
58	MG	1H	3389	1/1	0.98	0.07	74,74,74,74	0
58	MG	1H	3390	1/1	0.98	0.18	56,56,56,56	0
58	MG	13	1734	1/1	0.98	0.05	100,100,100,100	0
58	MG	1H	3393	1/1	0.98	0.10	58,58,58,58	0
58	MG	13	1725	1/1	0.98	0.04	77,77,77,77	0
58	MG	1H	3398	1/1	0.98	0.04	57,57,57,57	0
58	MG	1H	3351	1/1	0.98	0.05	53,53,53,53	0
58	MG	1G	1686	1/1	0.98	0.05	84,84,84,84	0
58	MG	1H	3278	1/1	0.98	0.10	106,106,106,106	0
58	MG	14	3310	1/1	0.98	0.04	56,56,56,56	0
58	MG	14	3314	1/1	0.98	0.05	58,58,58,58	0
58	MG	1H	3353	1/1	0.98	0.08	40,40,40,40	0
58	MG	14	3316	1/1	0.98	0.04	62,62,62,62	0
58	MG	14	3317	1/1	0.98	0.05	48,48,48,48	0
58	MG	1H	3467	1/1	0.98	0.06	69,69,69,69	0
58	MG	16	210	1/1	0.98	0.05	73,73,73,73	0
58	MG	1H	3468	1/1	0.98	0.04	63,63,63,63	0
58	MG	2K	105	1/1	0.98	0.04	81,81,81,81	0
58	MG	13	1726	1/1	0.99	0.03	93,93,93,93	0
58	MG	14	3309	1/1	0.99	0.04	59,59,59,59	0
58	MG	1H	3380	1/1	0.99	0.03	77,77,77,77	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	14	3311	1/1	0.99	0.04	65,65,65,65	0
58	MG	14	3312	1/1	0.99	0.05	88,88,88,88	0
58	MG	14	3313	1/1	0.99	0.03	48,48,48,48	0
58	MG	1H	3432	1/1	0.99	0.05	70,70,70,70	0
58	MG	1H	3433	1/1	0.99	0.07	73,73,73,73	0
58	MG	1H	3381	1/1	0.99	0.10	62,62,62,62	0
58	MG	1H	3502	1/1	0.99	0.05	66,66,66,66	0
58	MG	14	3318	1/1	0.99	0.05	47,47,47,47	0
58	MG	1H	3382	1/1	0.99	0.04	71,71,71,71	0
58	MG	14	3320	1/1	0.99	0.04	42,42,42,42	0
58	MG	1H	3141	1/1	0.99	0.06	40,40,40,40	0
58	MG	14	3322	1/1	0.99	0.03	72,72,72,72	0
58	MG	14	3323	1/1	0.99	0.07	65,65,65,65	0
58	MG	14	3324	1/1	0.99	0.08	62,62,62,62	0
58	MG	14	3325	1/1	0.99	0.06	76,76,76,76	0
58	MG	1H	3350	1/1	0.99	0.03	51,51,51,51	0
58	MG	14	3327	1/1	0.99	0.09	58,58,58,58	0
58	MG	14	3328	1/1	0.99	0.04	49,49,49,49	0
58	MG	14	3329	1/1	0.99	0.04	54,54,54,54	0
58	MG	14	3330	1/1	0.99	0.04	53,53,53,53	0
58	MG	14	3331	1/1	0.99	0.03	56,56,56,56	0
58	MG	1H	3438	1/1	0.99	0.05	55,55,55,55	0
58	MG	1H	3385	1/1	0.99	0.05	45,45,45,45	0
58	MG	13	1727	1/1	0.99	0.04	55,55,55,55	0
58	MG	1H	3442	1/1	0.99	0.05	54,54,54,54	0
58	MG	14	3336	1/1	0.99	0.05	60,60,60,60	0
58	MG	1H	3387	1/1	0.99	0.05	65,65,65,65	0
58	MG	1H	3444	1/1	0.99	0.06	82,82,82,82	0
58	MG	14	3339	1/1	0.99	0.10	62,62,62,62	0
58	MG	14	3340	1/1	0.99	0.10	67,67,67,67	0
58	MG	14	3342	1/1	0.99	0.06	49,49,49,49	0
58	MG	1H	3512	1/1	0.99	0.04	44,44,44,44	0
58	MG	14	3345	1/1	0.99	0.08	51,51,51,51	0
58	MG	1H	3446	1/1	0.99	0.04	59,59,59,59	0
58	MG	14	3347	1/1	0.99	0.04	48,48,48,48	0
58	MG	14	3348	1/1	0.99	0.04	76,76,76,76	0
58	MG	14	3349	1/1	0.99	0.11	62,62,62,62	0
58	MG	1H	3388	1/1	0.99	0.08	59,59,59,59	0
58	MG	14	3351	1/1	0.99	0.13	87,87,87,87	0
58	MG	1H	3515	1/1	0.99	0.07	83,83,83,83	0
58	MG	1H	3516	1/1	0.99	0.03	86,86,86,86	0
58	MG	1H	3517	1/1	0.99	0.11	57,57,57,57	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	13	1718	1/1	0.99	0.05	69,69,69,69	0
58	MG	14	3356	1/1	0.99	0.03	65,65,65,65	0
58	MG	14	3357	1/1	0.99	0.03	69,69,69,69	0
58	MG	13	1729	1/1	0.99	0.09	86,86,86,86	0
58	MG	14	3359	1/1	0.99	0.04	73,73,73,73	0
58	MG	14	3360	1/1	0.99	0.04	69,69,69,69	0
58	MG	1H	3391	1/1	0.99	0.08	60,60,60,60	0
58	MG	14	3362	1/1	0.99	0.04	56,56,56,56	0
58	MG	13	1730	1/1	0.99	0.03	67,67,67,67	0
58	MG	14	3364	1/1	0.99	0.07	75,75,75,75	0
58	MG	1H	3355	1/1	0.99	0.04	57,57,57,57	0
58	MG	1H	3356	1/1	0.99	0.02	52,52,52,52	0
58	MG	1H	3395	1/1	0.99	0.04	36,36,36,36	0
58	MG	14	3368	1/1	0.99	0.04	89,89,89,89	0
58	MG	1H	3455	1/1	0.99	0.06	66,66,66,66	0
58	MG	1H	3396	1/1	0.99	0.04	69,69,69,69	0
58	MG	14	3371	1/1	0.99	0.04	79,79,79,79	0
58	MG	1H	3457	1/1	0.99	0.10	82,82,82,82	0
58	MG	14	3373	1/1	0.99	0.09	64,64,64,64	0
58	MG	1H	3397	1/1	0.99	0.08	49,49,49,49	0
58	MG	1H	3357	1/1	0.99	0.04	35,35,35,35	0
58	MG	14	3376	1/1	0.99	0.07	119,119,119,119	0
58	MG	1H	3399	1/1	0.99	0.09	52,52,52,52	0
58	MG	14	3378	1/1	0.99	0.07	71,71,71,71	0
58	MG	16	212	1/1	0.99	0.12	81,81,81,81	0
58	MG	1H	3461	1/1	0.99	0.05	51,51,51,51	0
58	MG	14	3381	1/1	0.99	0.04	91,91,91,91	0
58	MG	11	302	1/1	0.99	0.04	35,35,35,35	0
58	MG	13	1732	1/1	0.99	0.03	78,78,78,78	0
58	MG	14	3384	1/1	0.99	0.03	68,68,68,68	0
58	MG	1H	3463	1/1	0.99	0.09	66,66,66,66	0
58	MG	1H	3401	1/1	0.99	0.07	47,47,47,47	0
58	MG	1H	3402	1/1	0.99	0.03	53,53,53,53	0
58	MG	14	3388	1/1	0.99	0.08	79,79,79,79	0
58	MG	1H	3360	1/1	0.99	0.03	46,46,46,46	0
58	MG	1H	3404	1/1	0.99	0.05	48,48,48,48	0
58	MG	13	1719	1/1	0.99	0.03	67,67,67,67	0
58	MG	1H	3407	1/1	0.99	0.03	43,43,43,43	0
58	MG	1H	3362	1/1	0.99	0.08	41,41,41,41	0
58	MG	1H	3410	1/1	0.99	0.04	33,33,33,33	0
58	MG	1H	3411	1/1	0.99	0.03	46,46,46,46	0
58	MG	G8	201	1/1	0.99	0.13	73,73,73,73	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	1H	3473	1/1	0.99	0.05	85,85,85,85	0
58	MG	1H	3412	1/1	0.99	0.05	50,50,50,50	0
58	MG	14	3399	1/1	0.99	0.07	77,77,77,77	0
58	MG	1H	3413	1/1	0.99	0.03	50,50,50,50	0
58	MG	1H	3476	1/1	0.99	0.04	70,70,70,70	0
58	MG	13	1721	1/1	0.99	0.05	83,83,83,83	0
58	MG	1H	3366	1/1	0.99	0.04	56,56,56,56	0
58	MG	1H	3416	1/1	0.99	0.08	67,67,67,67	0
58	MG	13	1722	1/1	0.99	0.08	76,76,76,76	0
58	MG	1H	3368	1/1	0.99	0.04	56,56,56,56	0
58	MG	1H	3482	1/1	0.99	0.03	54,54,54,54	0
58	MG	1H	3419	1/1	0.99	0.07	47,47,47,47	0
58	MG	1H	3090	1/1	0.99	0.07	37,37,37,37	0
58	MG	1G	1683	1/1	0.99	0.06	61,61,61,61	0
58	MG	1G	1684	1/1	0.99	0.06	70,70,70,70	0
58	MG	1H	3370	1/1	0.99	0.05	55,55,55,55	0
58	MG	1H	3486	1/1	0.99	0.20	50,50,50,50	0
58	MG	1H	3487	1/1	0.99	0.09	100,100,100,100	0
58	MG	13	1715	1/1	0.99	0.07	89,89,89,89	0
58	MG	13	1737	1/1	0.99	0.03	93,93,93,93	0
58	MG	1H	3490	1/1	0.99	0.04	64,64,64,64	0
58	MG	13	1714	1/1	0.99	0.03	45,45,45,45	0
58	MG	1H	3108	1/1	0.99	0.07	50,50,50,50	0
58	MG	1G	1693	1/1	0.99	0.07	82,82,82,82	0
58	MG	1G	1694	1/1	0.99	0.04	67,67,67,67	0
58	MG	13	1717	1/1	0.99	0.04	76,76,76,76	0
58	MG	1H	3427	1/1	0.99	0.03	41,41,41,41	0
60	ZN	5I	103	1/1	0.99	0.03	91,91,91,91	0
58	MG	1H	3495	1/1	0.99	0.04	47,47,47,47	0
58	MG	1H	3377	1/1	0.99	0.05	61,61,61,61	0
58	MG	14	3303	1/1	0.99	0.07	53,53,53,53	0
58	MG	14	3305	1/1	0.99	0.04	69,69,69,69	0
58	MG	16	213	1/1	1.00	0.03	66,66,66,66	0
58	MG	1H	3379	1/1	1.00	0.06	72,72,72,72	0
58	MG	1H	3409	1/1	1.00	0.08	41,41,41,41	0
58	MG	13	1731	1/1	1.00	0.03	68,68,68,68	0
58	MG	1H	3429	1/1	1.00	0.07	72,72,72,72	0
58	MG	14	3304	1/1	1.00	0.05	50,50,50,50	0
58	MG	1H	3363	1/1	1.00	0.06	40,40,40,40	0
58	MG	14	3306	1/1	1.00	0.01	52,52,52,52	0
58	MG	14	3341	1/1	1.00	0.11	41,41,41,41	0
58	MG	1H	3441	1/1	1.00	0.02	51,51,51,51	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	14	3343	1/1	1.00	0.01	47,47,47,47	0
58	MG	14	3401	1/1	1.00	0.02	45,45,45,45	0
58	MG	14	3308	1/1	1.00	0.02	46,46,46,46	0
58	MG	13	1720	1/1	1.00	0.03	82,82,82,82	0
58	MG	1H	3365	1/1	1.00	0.04	44,44,44,44	0
58	MG	1H	3405	1/1	1.00	0.02	43,43,43,43	0
58	MG	1H	3445	1/1	1.00	0.03	44,44,44,44	0
58	MG	1H	3358	1/1	1.00	0.02	43,43,43,43	0
58	MG	16	211	1/1	1.00	0.02	70,70,70,70	0
58	MG	1H	3372	1/1	1.00	0.05	64,64,64,64	0

6.5 Other polymers (i)

There are no such residues in this entry.