Full wwPDB X-ray Structure Validation Report ⓘ

Mar 24, 2026 – 12:38 PM UTC

PDB ID	:	6GSJ / pdb_00006gsj
Title	:	Structure of T. thermophilus 70S ribosome complex with mRNA, tRNAfMet and cognate tRNAThr in the A-site
Authors	:	Rozov, A.; Yusupov, M.; Yusupova, G.
Deposited on	:	2018-06-14
Resolution	:	2.96 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:

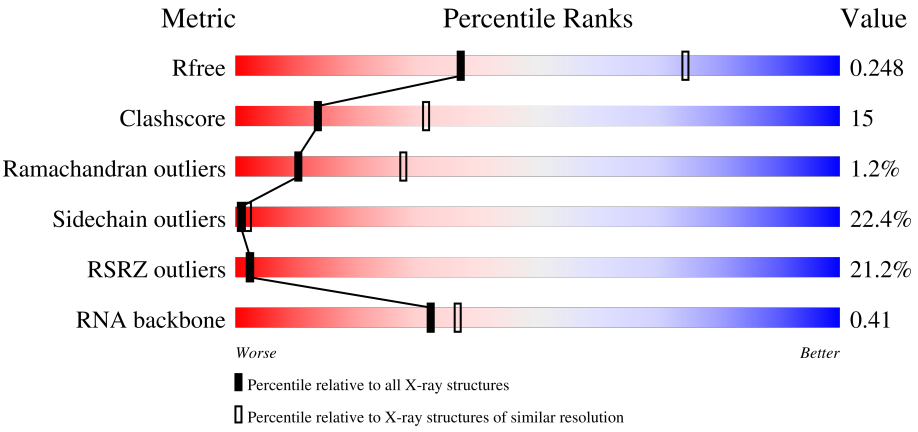
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (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 2.96 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	20% 45% 40% 13% •
1	1G	1522	17% 48% 38% 12% •
2	12	256	34% 30% 38% 11% • 19%
2	1E	256	20% 38% 38% 13% • 10%

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Mol	Chain	Length	Quality of chain
3	22	239	33% 37% 36% 10% 18%
3	2E	239	24% 54% 28% 5% 14%
4	32	209	22% 54% 35% 9%
4	3E	209	16% 52% 39% 8%
5	42	162	28% 42% 38% 13% 7%
5	4E	162	18% 56% 28% 8% 8%
6	52	101	24% 65% 26% 9%
6	5E	101	20% 66% 28% 5%
7	62	156	29% 45% 38% 6% 12%
7	6E	156	15% 57% 33% 8%
8	72	138	27% 54% 34% 11%
8	7E	138	9% 55% 30% 14%
9	82	128	25% 43% 41% 9% 5%
9	8E	128	24% 43% 45% 11%
10	1A	105	42% 35% 47% 12% 6%
10	1I	105	32% 51% 28% 10% 10%
11	2A	129	12% 51% 29% 7% 12%
11	2I	129	12% 47% 30% 8% 14%
12	3A	132	26% 51% 32% 10% 8%
12	3I	132	21% 47% 38% 8% 8%
13	4A	126	26% 35% 37% 13% 13%
13	4I	126	17% 40% 40% 13% 6%
14	5A	61	36% 39% 41% 16%
14	5I	61	11% 46% 39% 13%
15	6A	89	9% 75% 22%

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Mol	Chain	Length	Quality of chain
15	6I	89	20% 54% 35% 9%
16	7A	88	5% 63% 30% 5%
16	7I	88	16% 50% 39% 6% 6%
17	8A	105	13% 61% 28% 6% 6%
17	8I	105	20% 55% 30% 9% 5%
18	9A	88	3% 48% 22% 9% 22%
18	9I	88	14% 39% 33% 6% 23%
19	AA	93	29% 22% 31% 14% 30%
19	AI	93	11% 43% 33% 11% 11%
20	BA	106	21% 62% 28% 7%
20	BI	106	26% 38% 46% 8% 8%
21	1B	27	4% 37% 41% 19%
21	1F	27	7% 44% 37% 15%
22	1K	76	34% 20% 46% 30%
22	1L	76	34% 22% 37% 38%
23	2K	77	23% 56% 34% 9%
23	2L	77	16% 42% 42% 13%
24	3K	76	34% 24% 42% 29% 5%
25	4K	27	11% 26% 11% 30% 33%
25	4L	27	19% 7% 22% 48%
26	14	2917	17% 48% 38% 10%
26	1H	2917	15% 51% 37% 10%
27	16	122	6% 50% 42% 7%
27	1J	122	7% 39% 43% 18%
28	11	276	9% 63% 27% 7%

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Mol	Chain	Length	Quality of chain
28	19	276	11% 60% 30% 9%
29	21	206	27% 50% 34% 14%
29	29	206	38% 49% 35% 14%
30	31	210	16% 55% 35% 6%
30	39	210	35% 40% 40% 15%
31	41	182	25% 46% 42% 11%
31	49	182	20% 47% 41% 10%
32	51	180	23% 54% 29% 11%
32	59	180	63% 35% 44% 14% 6%
33	61	148	21% 46% 36% 13%
33	69	148	36% 49% 39% 10%
34	15	140	27% 52% 32% 14%
34	58	140	19% 48% 36% 11%
35	25	122	11% 60% 33% 7%
35	68	122	6% 66% 28% 6%
36	35	150	41% 44% 34% 20%
36	78	150	33% 42% 45% 9%
37	45	141	36% 48% 35% 14%
37	88	141	32% 52% 37% 11%
38	55	118	19% 49% 36% 14%
38	98	118	33% 44% 47% 9%
39	65	112	16% 32% 52% 14%
39	A8	112	11% 40% 45% 14%
40	75	146	21% 45% 40% 10%
40	B8	146	34% 41% 38% 13% 7%

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Mol	Chain	Length	Quality of chain
41	85	118	39% 47% 42% 8%
41	C8	118	16% 53% 36% 8%
42	95	101	32% 54% 34% 10%
42	D8	101	34% 51% 39% 9%
43	A5	113	19% 59% 34% 5%
43	E8	113	19% 64% 26% 8%
44	B5	96	5% 58% 30% 9%
44	F8	96	15% 65% 28% 6%
45	C5	110	20% 29% 14% 5% 53%
45	G8	110	23% 43% 35% 9% 12%
46	D5	206	28% 35% 39% 11% 14%
46	H8	206	17% 34% 35% 11% 17%
47	E5	85	29% 54% 26% 9% 11%
47	I8	85	7% 49% 35% 6% 9%
48	F5	98	33% 48% 34% 13%
48	J8	98	32% 48% 37% 11%
49	G5	72	11% 36% 42% 14%
49	K8	72	19% 40% 38% 11% 6% 6%
50	H5	60	33% 55% 38%
50	L8	60	15% 63% 27% 5%
51	M8	71	15% 31% 38% 11% 15%
52	J5	60	32% 53% 33% 7% 7%
52	N8	60	12% 40% 30% 10% 20%
53	L5	49	8% 63% 35%
53	P8	49	2% 53% 39%

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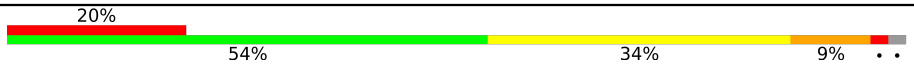
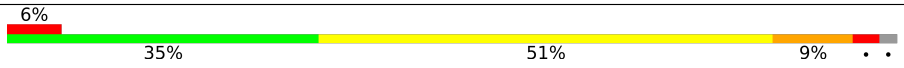
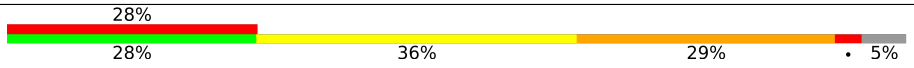
Mol	Chain	Length	Quality of chain
54	M5	65	
54	Q8	65	
55	3L	76	

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	MG	13	1632	-	-	-	X
56	MG	13	1665	-	-	-	X
56	MG	13	1666	-	-	-	X
56	MG	13	1668	-	-	-	X
56	MG	13	1684	-	-	-	X
56	MG	13	1686	-	-	-	X
56	MG	13	1741	-	-	-	X
56	MG	14	3029	-	-	-	X
56	MG	14	3041	-	-	-	X
56	MG	14	3042	-	-	-	X
56	MG	14	3077	-	-	-	X
56	MG	14	3096	-	-	-	X
56	MG	14	3210	-	-	-	X
56	MG	14	3245	-	-	-	X
56	MG	14	3248	-	-	-	X
56	MG	14	3268	-	-	-	X
56	MG	14	3272	-	-	-	X
56	MG	14	3280	-	-	-	X
56	MG	14	3285	-	-	-	X
56	MG	14	3298	-	-	-	X
56	MG	16	206	-	-	-	X
56	MG	16	209	-	-	-	X
56	MG	16	210	-	-	-	X
56	MG	1G	1626	-	-	-	X
56	MG	1G	1646	-	-	-	X
56	MG	1G	1690	-	-	-	X
56	MG	1G	1701	-	-	-	X
56	MG	1H	3026	-	-	-	X
56	MG	1H	3041	-	-	-	X
56	MG	1H	3054	-	-	-	X
56	MG	1H	3101	-	-	-	X
56	MG	1H	3129	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
56	MG	1H	3153	-	-	-	X
56	MG	1H	3165	-	-	-	X
56	MG	1H	3198	-	-	-	X
56	MG	1H	3205	-	-	-	X
56	MG	1H	3227	-	-	-	X
56	MG	1H	3238	-	-	-	X
56	MG	1H	3269	-	-	-	X
56	MG	1H	3276	-	-	-	X
56	MG	1H	3303	-	-	-	X
56	MG	1H	3328	-	-	-	X
56	MG	1H	3334	-	-	-	X
56	MG	1H	3356	-	-	-	X
56	MG	1H	3386	-	-	-	X
56	MG	1H	3401	-	-	-	X
56	MG	1H	3405	-	-	-	X
56	MG	1H	3421	-	-	-	X
56	MG	1J	201	-	-	-	X
56	MG	35	203	-	-	-	X
56	MG	88	201	-	-	-	X

2 Entry composition (i)

There are 59 unique types of molecules in this entry. The entry contains 294252 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	1500	Total	C	N	O	P	0	0	0
			32246	14352	5978	10416	1500			
1	1G	1490	Total	C	N	O	P	0	0	0
			32028	14255	5932	10351	1490			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	1E	231	Total	C	N	O	S	0	0	0
			1874	1199	334	336	5			
2	12	207	Total	C	N	O	S	0	0	0
			1696	1083	306	303	4			

- 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	197	Total	C	N	O	S	0	0	0
			1546	978	299	268	1			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	3E	207	Total	C	N	O	S	0	0	0
			1698	1064	338	289	7			
4	32	207	Total	C	N	O	S	0	0	0
			1698	1064	338	289	7			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	4E	149	Total	C	N	O	S	0	0	0
			1142	722	216	200	4			
5	42	150	Total	C	N	O	S	0	0	0
			1141	719	217	201	4			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	5E	100	Total	C	N	O	S	0	0	0
			837	528	154	152	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	154	Total	C	N	O	S	0	0	0
			1242	770	250	216	6			
7	62	138	Total	C	N	O	S	0	0	0
			1110	689	221	194	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	137	Total	C	N	O	S	0	0	0
			1107	700	214	191	2			

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
9	8E	126	Total	C	N	O	0	0	0
			1000	634	196	170			
9	82	121	Total	C	N	O	0	0	0
			953	605	186	162			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	1I	94	Total	C	N	O	S	0	0	0
			749	468	147	133	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	111	Total	C	N	O	S	0	0	0
			823	512	154	154	3			
11	2A	113	Total	C	N	O	S	0	0	0
			835	520	156	156	3			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	3I	122	Total	C	N	O	S	0	0	0
			956	603	193	159	1			
12	3A	122	Total	C	N	O	S	0	0	0
			956	603	193	159	1			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	4I	119	Total	C	N	O	S	0	0	0
			942	582	194	164	2			
13	4A	109	Total	C	N	O	S	0	0	0
			879	544	181	152	2			

- 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	59	Total	C	N	O	S	0	0	0
			486	309	103	70	4			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
15	6I	87	Total	C	N	O	S	0	0	0
			729	457	146	124	2			
15	6A	87	Total	C	N	O	S	0	0	0
			729	457	146	124	2			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
16	7I	83	Total	C	N	O	S	0	0	0
			700	443	139	117	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	99	Total	C	N	O	S	0	0	0
			823	528	151	142	2			

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
18	9I	68	Total	C	N	O	0	0	0
			549	352	105	92			
18	9A	69	Total	C	N	O	0	0	0
			554	355	106	93			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	AI	83	Total	C	N	O	S	0	0	0
			665	424	124	115	2			
19	AA	65	Total	C	N	O	S	0	0	0
			510	324	92	92	2			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	BI	97	Total	C	N	O	S	0	0	0
			746	461	157	126	2			
20	BA	103	Total	C	N	O	S	0	0	0
			778	481	163	132	2			

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
21	1F	23	Total	C	N	O	0	0	0
			199	122	48	29			
21	1B	22	Total	C	N	O	0	0	0
			188	116	44	28			

- Molecule 22 is a RNA chain called tRNAThr.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	1K	74	Total	C	N	O	P	0	0	0
			1593	712	285	522	74			
22	1L	74	Total	C	N	O	P	0	0	0
			1593	712	285	522	74			

- Molecule 23 is a RNA chain called tRNAfMet.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
23	2K	77	Total	C	N	O	P	S	0	0	0
			1646	735	297	536	77	1			
23	2L	77	Total	C	N	O	P	S	0	0	0
			1646	735	297	536	77	1			

- Molecule 24 is a RNA chain called tRNAThr.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
24	3K	72	Total	C	N	O	P	0	0	0
			1537	686	276	503	72			

- Molecule 25 is a RNA chain called RNA (27-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
25	4K	18	Total	C	N	O	P	0	0	0
			391	176	80	117	18			
25	4L	14	Total	C	N	O	P	0	0	0
			303	137	63	89	14			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	1H	2850	Total	C	N	O	P	0	0	0
			61381	27319	11475	19737	2850			
26	14	2811	Total	C	N	O	P	0	0	0
			60561	26951	11337	19462	2811			

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1H	161	U	UNK	conflict	GB 55771382
1H	654A	A	G	conflict	GB 55771382
1H	654E	C	G	conflict	GB 55771382
1H	654P	G	C	conflict	GB 55771382
1H	654T	A	C	conflict	GB 55771382
1H	1058	U	G	conflict	GB 55771382
1H	1080	A	C	conflict	GB 55771382
14	158	U	UNK	conflict	GB 55771382
14	654A	A	G	conflict	GB 55771382
14	654E	C	G	conflict	GB 55771382
14	654P	G	C	conflict	GB 55771382
14	654T	A	C	conflict	GB 55771382
14	1058	U	G	conflict	GB 55771382
14	1080	A	C	conflict	GB 55771382

- 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	273	Total	C	N	O	S	0	0	0
			2120	1338	421	358	3			
28	19	274	Total	C	N	O	S	0	0	0
			2125	1341	422	359	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
			1556	984	297	269	6			
29	29	204	Total	C	N	O	S	0	0	0
			1563	988	299	270	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	204	Total	C	N	O	S	0	0	0
			1602	1022	299	279	2			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
31	41	179	Total	C	N	O	S	0	0	0
			1457	931	265	257	4			
31	49	180	Total	C	N	O	S	0	0	0
			1459	931	266	258	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
			1328	842	249	236	1			
32	59	169	Total	C	N	O	S	0	0	0
			1295	823	241	230	1			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
33	61	145	Total	C	N	O	S	0	0	0
			1131	723	200	207	1			
33	69	145	Total	C	N	O	S	0	0	0
			1131	723	200	207	1			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
34	58	125	Total	C	N	O	S	0	0	0
			995	645	183	163	4			
34	15	137	Total	C	N	O	S	0	0	0
			1096	707	205	181	3			

- 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			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
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	148	Total	C	N	O	S	0	0	0
			1127	701	230	193	3			
36	35	147	Total	C	N	O	S	0	0	0
			1122	698	229	192	3			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
37	88	141	Total	C	N	O	S	0	0	0
			1117	712	211	187	7			
37	45	138	Total	C	N	O	S	0	0	0
			1099	702	208	183	6			

- 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	118	Total	C	N	O	S	0	0	0
			967	604	203	159	1			

- 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	110	Total	C	N	O	0	0	0
			876	553	175	148			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
40	B8	136	Total	C	N	O	S	0	0	0
			1128	702	231	194	1			
40	75	140	Total	C	N	O	S	0	0	0
			1164	723	238	202	1			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
41	C8	115	Total	C	N	O	S	0	0	0
			950	603	199	147	1			
41	85	116	Total	C	N	O	S	0	0	0
			959	608	201	149	1			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
42	D8	100	Total	C	N	O	S	0	0	0
			774	499	141	133	1			
42	95	100	Total	C	N	O	S	0	0	0
			770	496	140	133	1			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
43	E8	110	Total	C	N	O	S	0	0	0
			876	552	171	151	2			
43	A5	111	Total	C	N	O	S	0	0	0
			886	558	174	152	2			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
44	F8	95	Total	C	N	O	S	0	0	0
			750	488	135	126	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	97	Total	C	N	O	S	0	0	0
			734	472	140	117	5			
45	C5	52	Total	C	N	O	S	0	0	0
			396	258	72	65	1			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
46	H8	170	Total	C	N	O	S	0	0	0
			1365	870	246	246	3			
46	D5	177	Total	C	N	O	S	0	0	0
			1411	901	253	255	2			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
47	I8	77	Total	C	N	O	S	0	0	0
			611	378	129	103	1			
47	E5	76	Total	C	N	O	S	0	0	0
			603	372	128	102	1			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
48	J8	96	Total	C	N	O	S	0	0	0
			747	469	148	129	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	68	Total	C	N	O	S	0	0	0
			575	358	116	100	1			
49	G5	69	Total	C	N	O	S	0	0	0
			576	358	116	101	1			

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
50	L8	58	Total	C	N	O	0	0	0
			459	293	89	77			
50	H5	58	Total	C	N	O	0	0	0
			459	293	89	77			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
51	M8	60	Total	C	N	O	S	0	0	0
			475	300	84	86	5			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
52	N8	48	Total	C	N	O	S	0	0	0
			369	229	75	60	5			
52	J5	56	Total	C	N	O	S	0	0	0
			434	272	87	70	5			

- Molecule 53 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
53	P8	47	Total	C	N	O	S	0	0	0
			401	246	99	54	2			
53	L5	48	Total	C	N	O	S	0	0	0
			406	249	100	55	2			

- Molecule 54 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
54	Q8	64	Total	C	N	O	S	0	0	0
			516	331	102	81	2			
54	M5	64	Total	C	N	O	S	0	0	0
			516	331	102	81	2			

- Molecule 55 is a RNA chain called tRNAThr.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
55	3L	72	Total	C	N	O	P	0	0	0
			1538	687	276	503	72			

- Molecule 56 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	13	205	Total	Mg	0	0
			205	205		
56	3E	1	Total	Mg	0	0
			1	1		
56	5E	1	Total	Mg	0	0
			1	1		
56	2I	1	Total	Mg	0	0
			1	1		
56	5I	2	Total	Mg	0	0
			2	2		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
56	8I	1	Total Mg 1 1	0	0
56	BI	2	Total Mg 2 2	0	0
56	1K	1	Total Mg 1 1	0	0
56	2K	2	Total Mg 2 2	0	0
56	1H	622	Total Mg 622 622	0	0
56	16	15	Total Mg 15 15	0	0
56	11	1	Total Mg 1 1	0	0
56	21	4	Total Mg 4 4	0	0
56	31	2	Total Mg 2 2	0	0
56	41	1	Total Mg 1 1	0	0
56	68	2	Total Mg 2 2	0	0
56	78	2	Total Mg 2 2	0	0
56	88	3	Total Mg 3 3	0	0
56	98	1	Total Mg 1 1	0	0
56	D8	1	Total Mg 1 1	0	0
56	I8	2	Total Mg 2 2	0	0
56	P8	1	Total Mg 1 1	0	0
56	Q8	1	Total Mg 1 1	0	0
56	1G	155	Total Mg 155 155	0	0
56	42	1	Total Mg 1 1	0	0
56	2A	1	Total Mg 1 1	0	0

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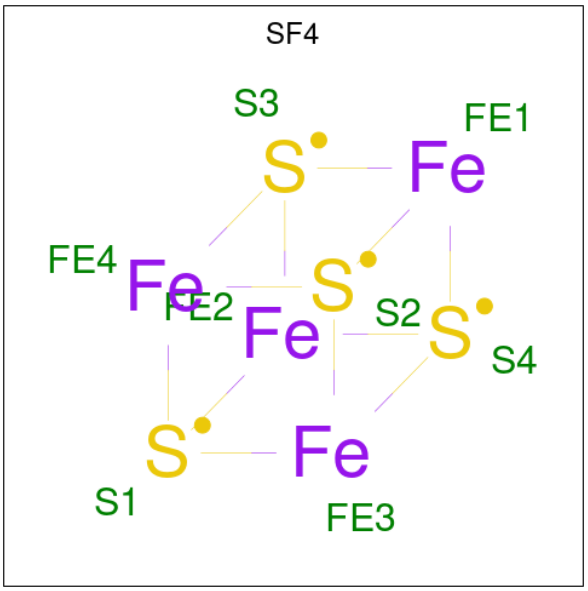
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
56	4A	1	Total Mg 1 1	0	0
56	9A	1	Total Mg 1 1	0	0
56	BA	2	Total Mg 2 2	0	0
56	1B	1	Total Mg 1 1	0	0
56	2L	2	Total Mg 2 2	0	0
56	4L	1	Total Mg 1 1	0	0
56	14	435	Total Mg 435 435	0	0
56	1J	6	Total Mg 6 6	0	0
56	19	1	Total Mg 1 1	0	0
56	29	3	Total Mg 3 3	0	0
56	39	1	Total Mg 1 1	0	0
56	25	1	Total Mg 1 1	0	0
56	35	3	Total Mg 3 3	0	0
56	45	2	Total Mg 2 2	0	0
56	55	1	Total Mg 1 1	0	0
56	85	1	Total Mg 1 1	0	0
56	E5	1	Total Mg 1 1	0	0

- Molecule 57 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe_4S_4).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
57	3E	1	Total Fe S 8 4 4	0	0
57	32	1	Total Fe S 8 4 4	0	0

- Molecule 58 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
58	5I	1	Total Zn 1 1	0	0
58	5A	1	Total Zn 1 1	0	0

- Molecule 59 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
59	13	339	Total O 339 339	0	0
59	1E	1	Total O 1 1	0	0
59	3E	2	Total O 2 2	0	0
59	4E	2	Total O 2 2	0	0
59	6E	1	Total O 1 1	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
59	8E	2	Total O 2 2	0	0
59	1I	3	Total O 3 3	0	0
59	3I	1	Total O 1 1	0	0
59	4I	2	Total O 2 2	0	0
59	5I	1	Total O 1 1	0	0
59	6I	1	Total O 1 1	0	0
59	7I	3	Total O 3 3	0	0
59	1F	2	Total O 2 2	0	0
59	1K	1	Total O 1 1	0	0
59	4K	2	Total O 2 2	0	0
59	1H	1047	Total O 1047 1047	0	0
59	16	19	Total O 19 19	0	0
59	11	11	Total O 11 11	0	0
59	21	8	Total O 8 8	0	0
59	31	7	Total O 7 7	0	0
59	58	3	Total O 3 3	0	0
59	78	6	Total O 6 6	0	0
59	D8	1	Total O 1 1	0	0
59	E8	1	Total O 1 1	0	0
59	G8	1	Total O 1 1	0	0
59	I8	2	Total O 2 2	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
59	J8	1	Total O 1 1	0	0
59	L8	4	Total O 4 4	0	0
59	P8	1	Total O 1 1	0	0
59	Q8	2	Total O 2 2	0	0
59	1G	289	Total O 289 289	0	0
59	32	2	Total O 2 2	0	0
59	42	1	Total O 1 1	0	0
59	52	4	Total O 4 4	0	0
59	1A	1	Total O 1 1	0	0
59	7A	4	Total O 4 4	0	0
59	9A	2	Total O 2 2	0	0
59	BA	2	Total O 2 2	0	0
59	2L	6	Total O 6 6	0	0
59	4L	3	Total O 3 3	0	0
59	14	730	Total O 730 730	0	0
59	19	10	Total O 10 10	0	0
59	29	2	Total O 2 2	0	0
59	39	5	Total O 5 5	0	0
59	15	1	Total O 1 1	0	0
59	25	6	Total O 6 6	0	0
59	35	6	Total O 6 6	0	0

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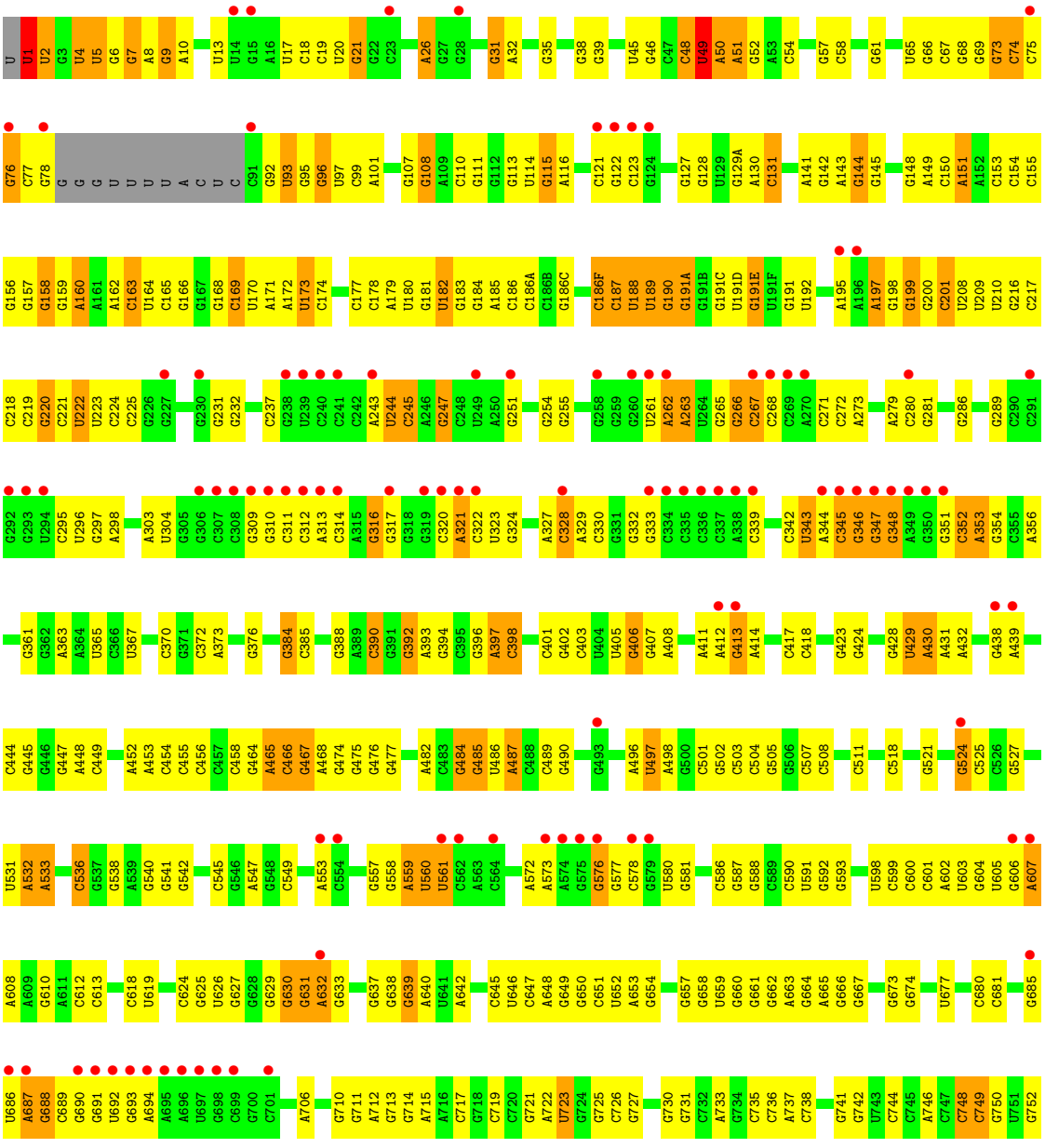
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
59	45	4	Total O 4 4	0	0
59	75	1	Total O 1 1	0	0
59	95	1	Total O 1 1	0	0
59	B5	3	Total O 3 3	0	0
59	H5	3	Total O 3 3	0	0
59	M5	2	Total O 2 2	0	0

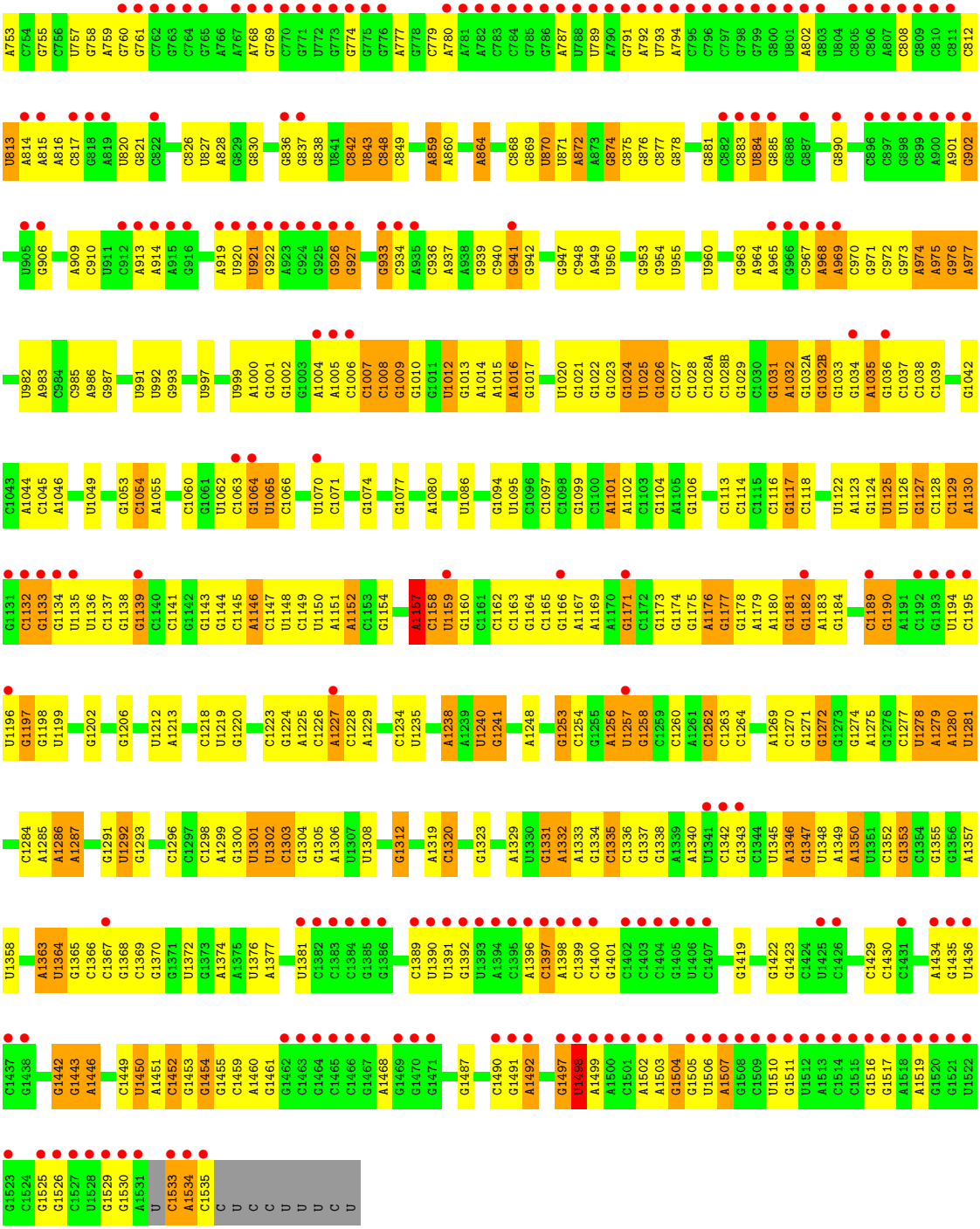
3 Residue-property plots (i)

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

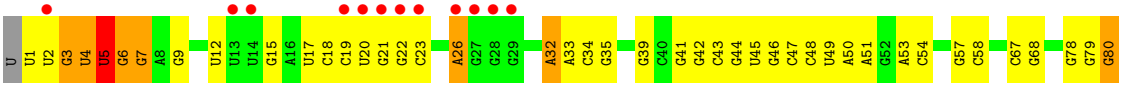
Chain 13:

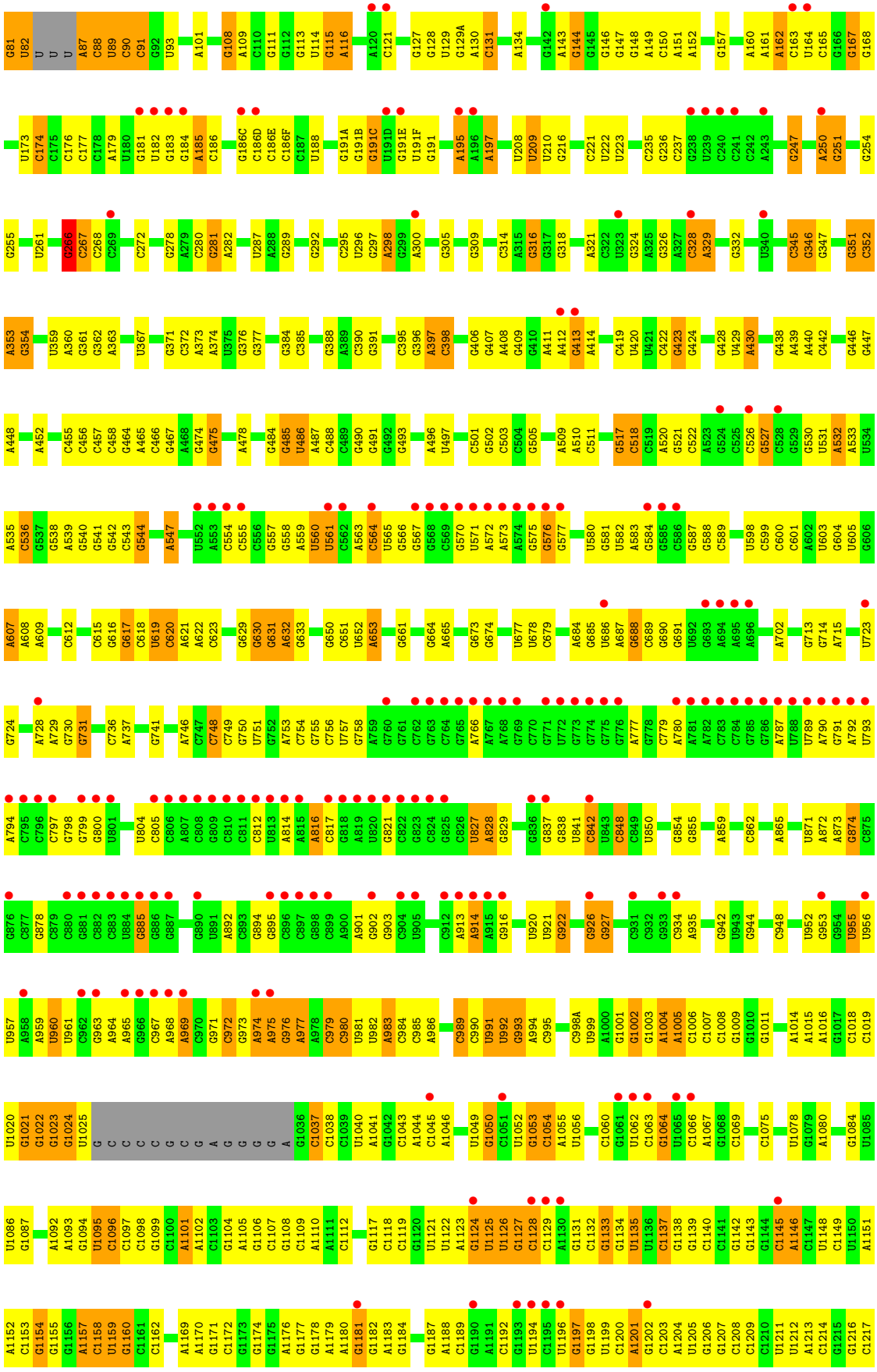


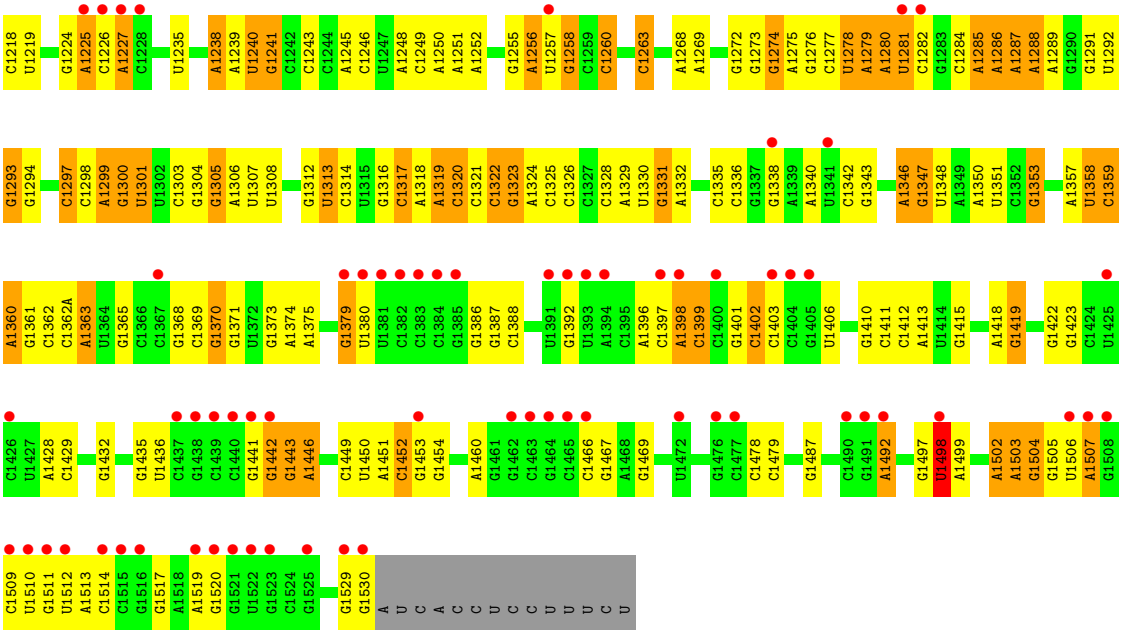


• Molecule 1: 16S ribosomal RNA

Chain 1G:

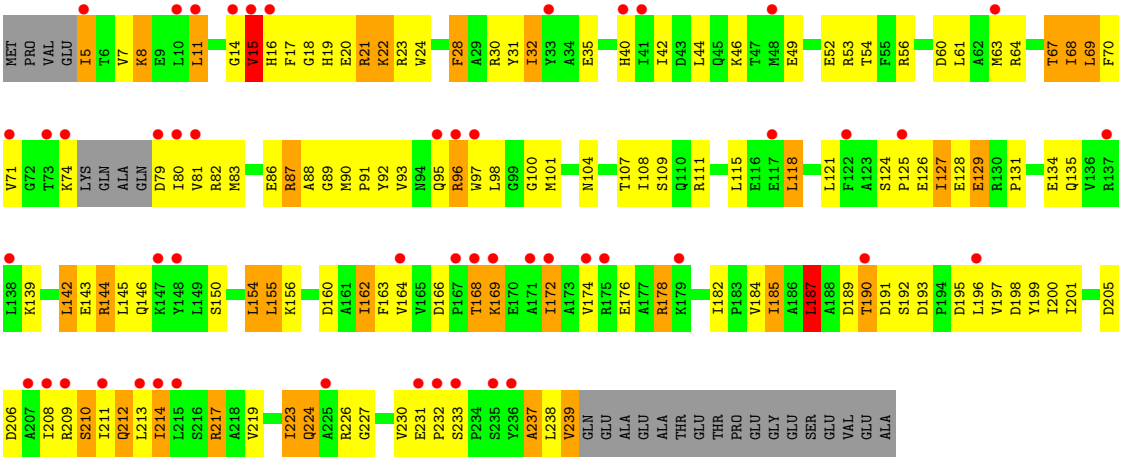






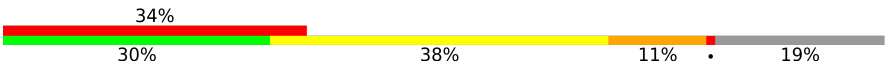
• Molecule 2: 30S ribosomal protein S2

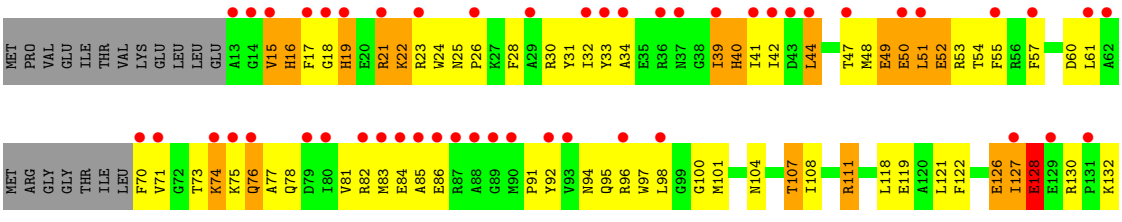
Chain 1E:

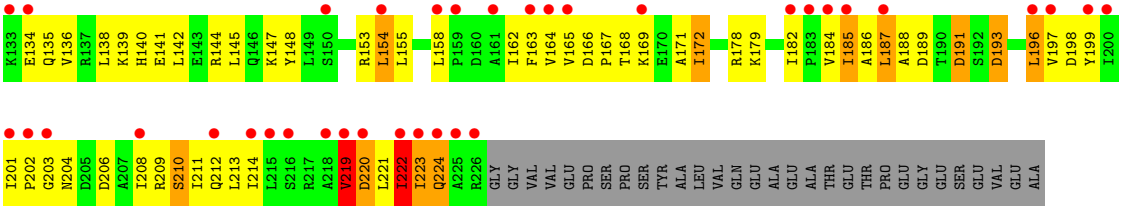


• Molecule 2: 30S ribosomal protein S2

Chain 12:

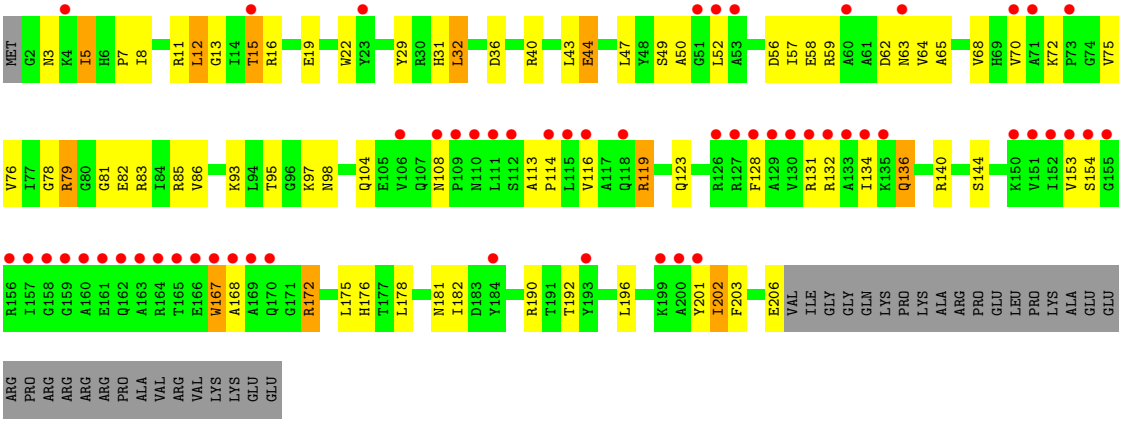






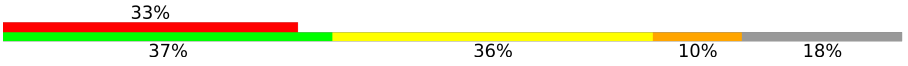
• Molecule 3: 30S ribosomal protein S3

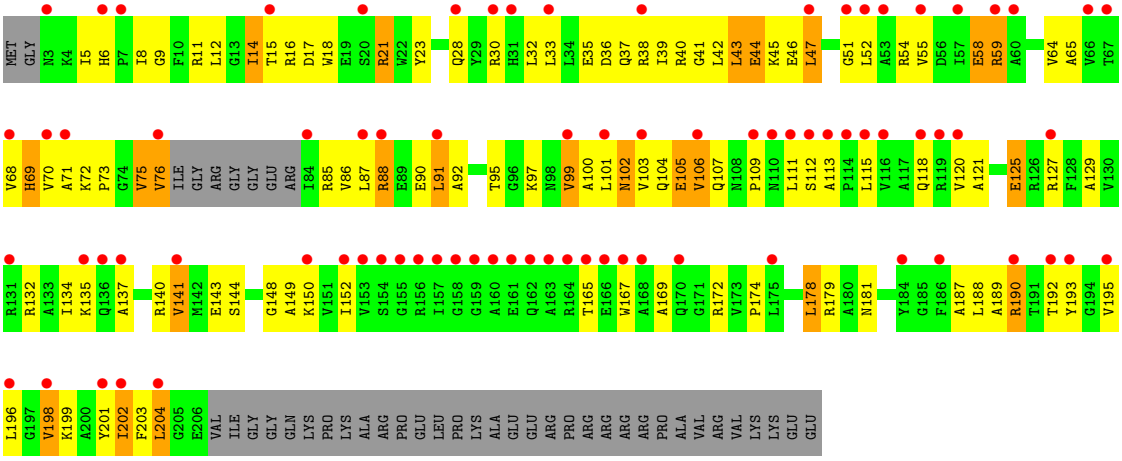
Chain 2E:



• Molecule 3: 30S ribosomal protein S3

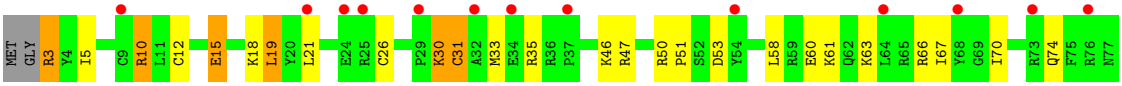
Chain 22:

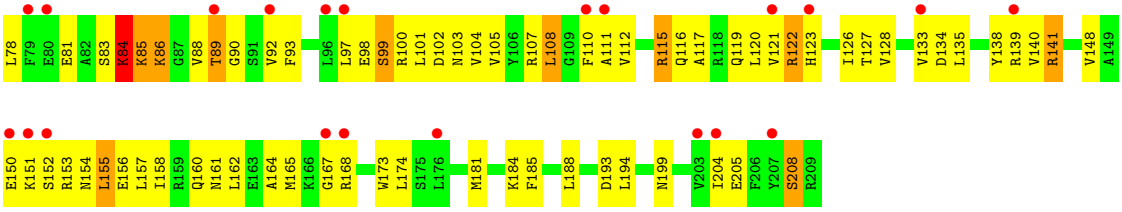




• Molecule 4: 30S ribosomal protein S4

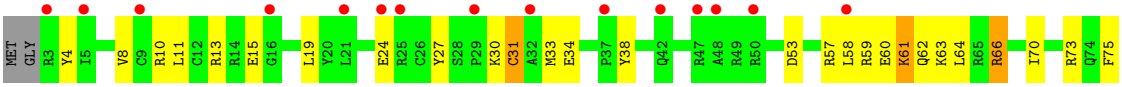
Chain 3E:

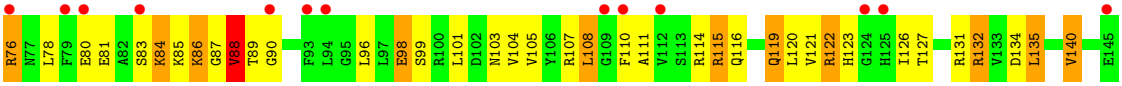


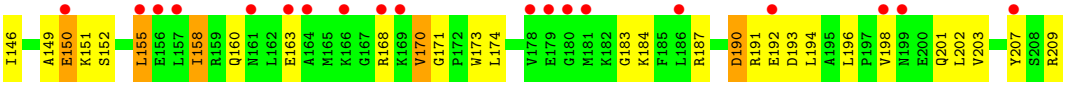


• Molecule 4: 30S ribosomal protein S4

Chain 32:

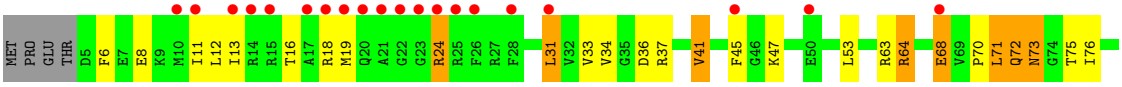


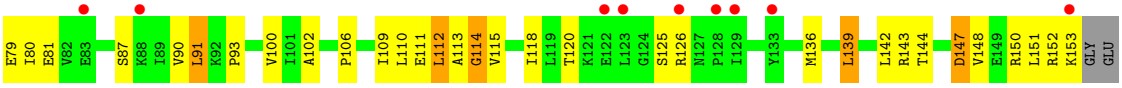


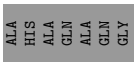


• Molecule 5: 30S ribosomal protein S5

Chain 4E:

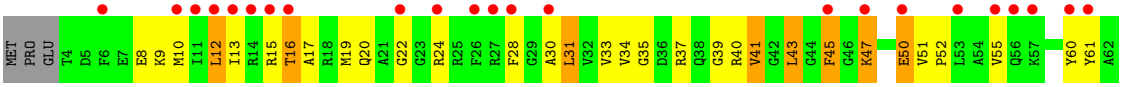


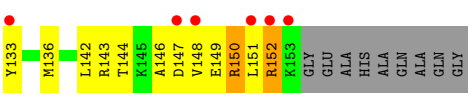




• Molecule 5: 30S ribosomal protein S5

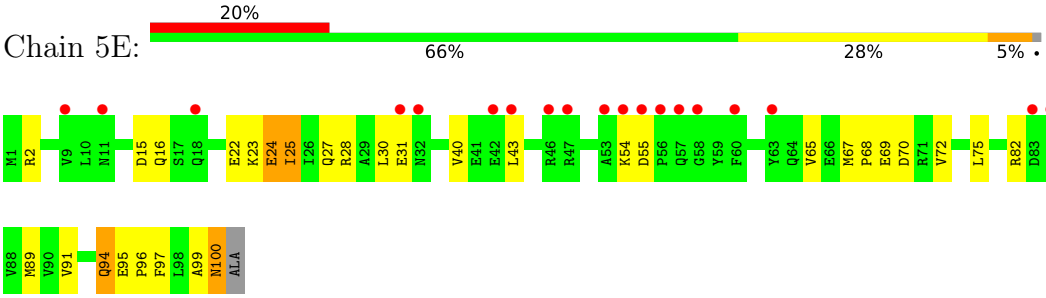
Chain 42:





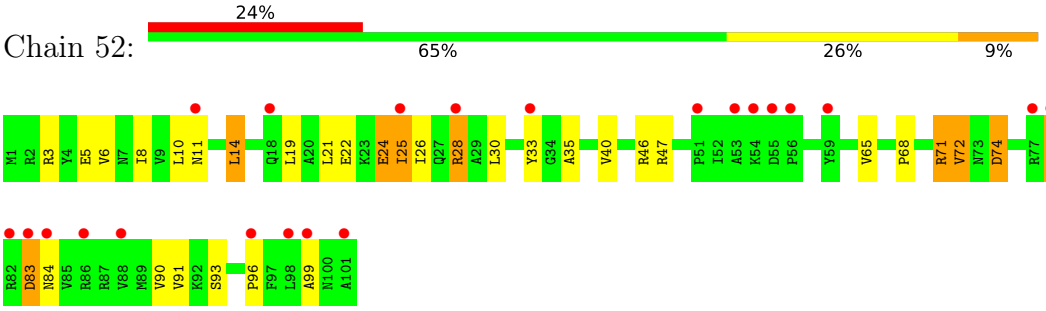
• Molecule 6: 30S ribosomal protein S6

Chain 5E:



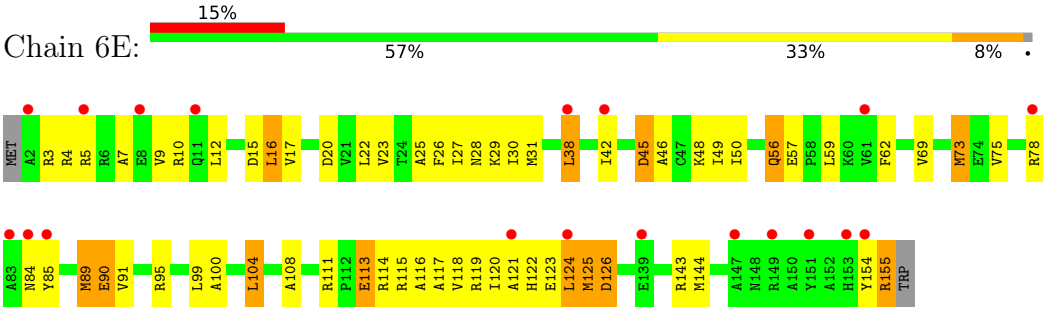
• Molecule 6: 30S ribosomal protein S6

Chain 52:



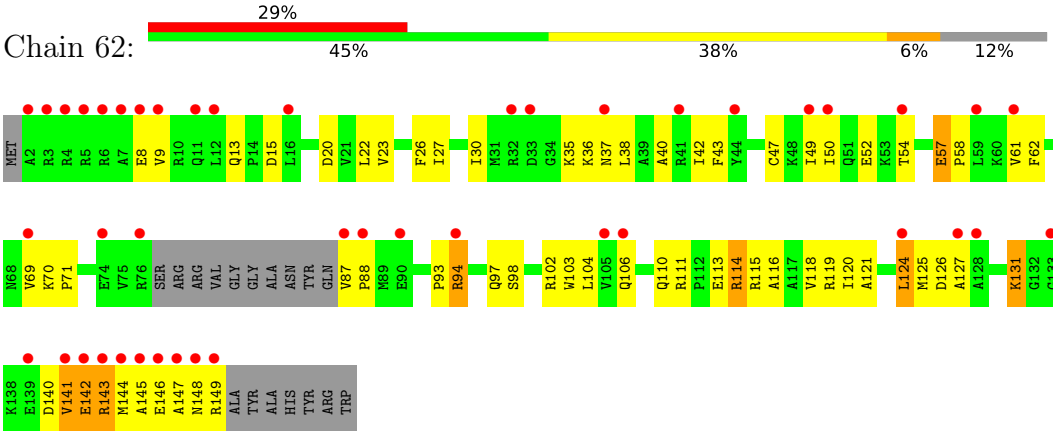
• Molecule 7: 30S ribosomal protein S7

Chain 6E:



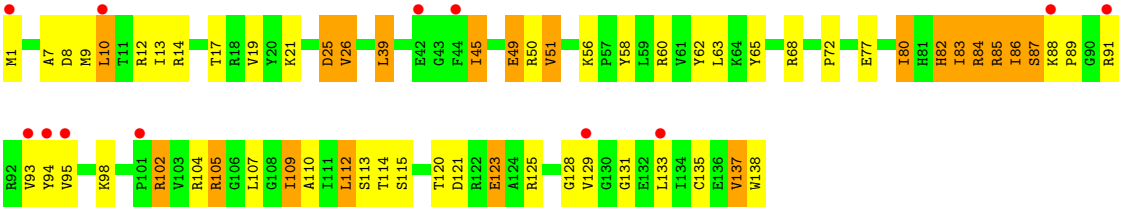
• Molecule 7: 30S ribosomal protein S7

Chain 62:



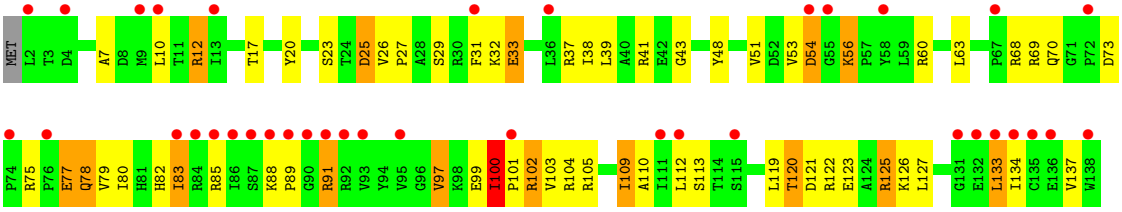
• Molecule 8: 30S ribosomal protein S8

Chain 7E:



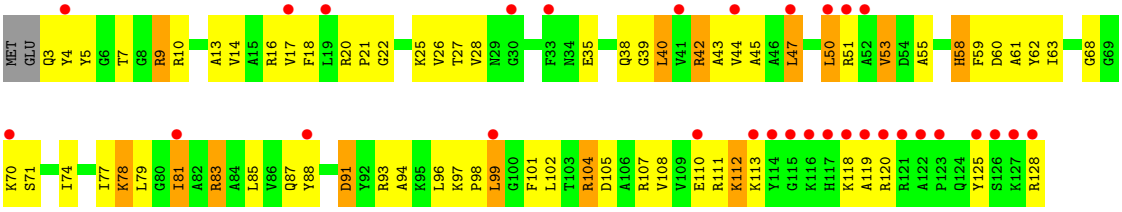
• Molecule 8: 30S ribosomal protein S8

Chain 72:



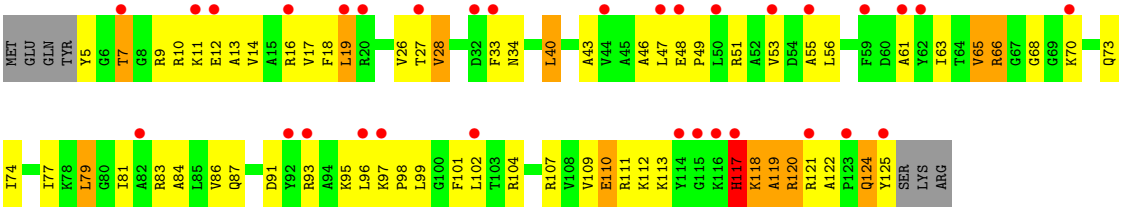
• Molecule 9: 30S ribosomal protein S9

Chain 8E:



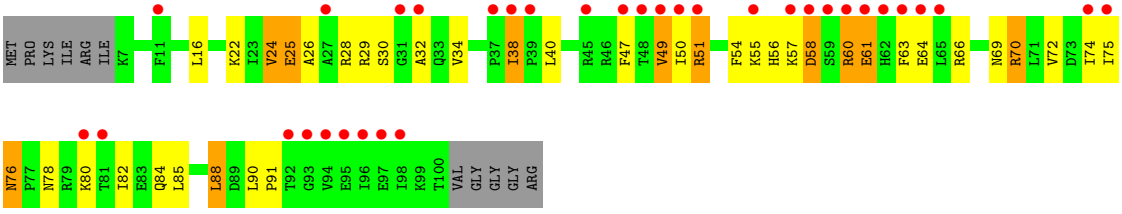
• Molecule 9: 30S ribosomal protein S9

Chain 82:



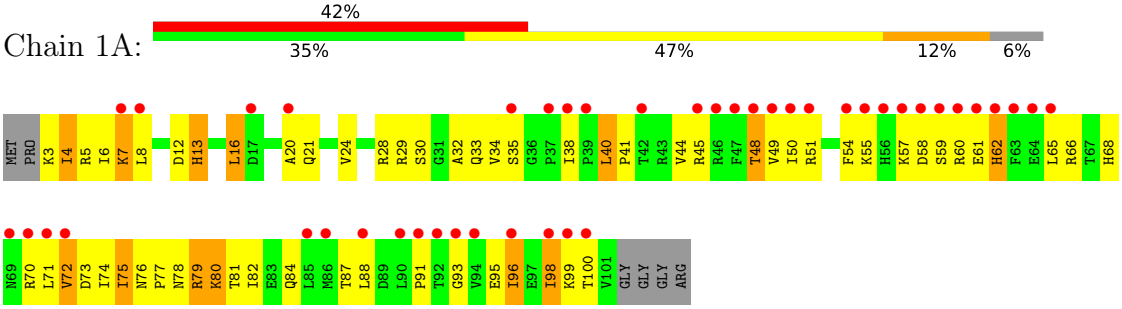
• Molecule 10: 30S ribosomal protein S10

Chain 1I:



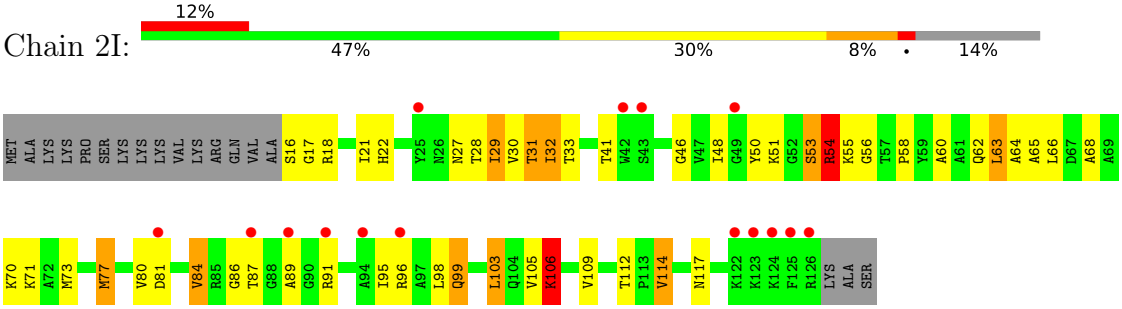
• Molecule 10: 30S ribosomal protein S10

Chain 1A:



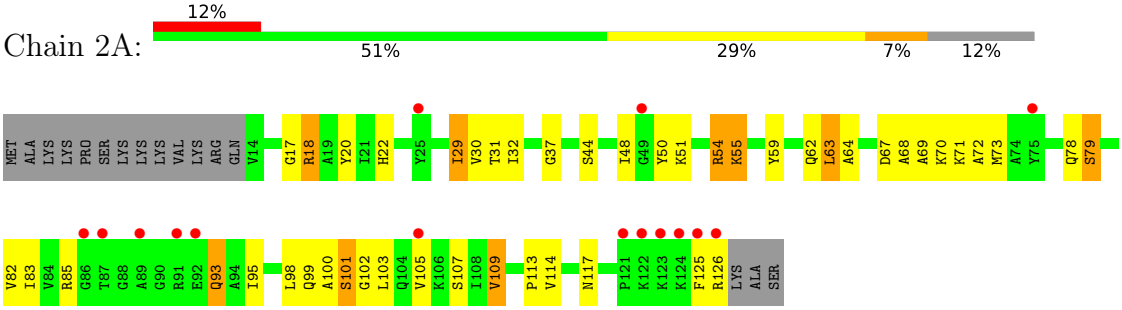
• Molecule 11: 30S ribosomal protein S11

Chain 2I:



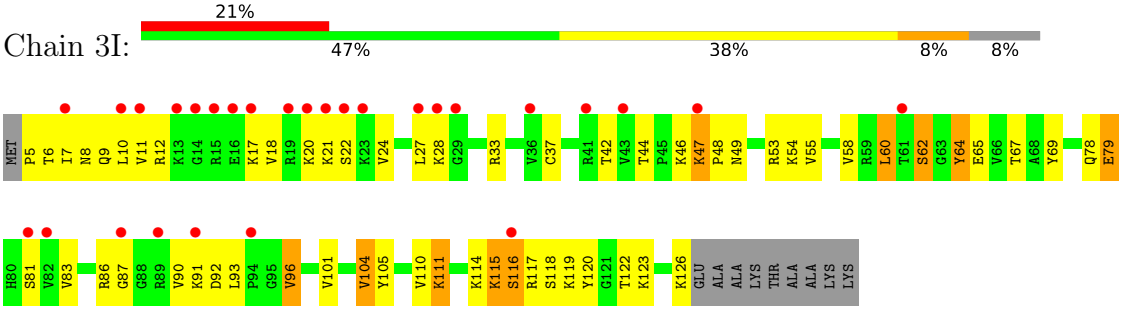
• Molecule 11: 30S ribosomal protein S11

Chain 2A:



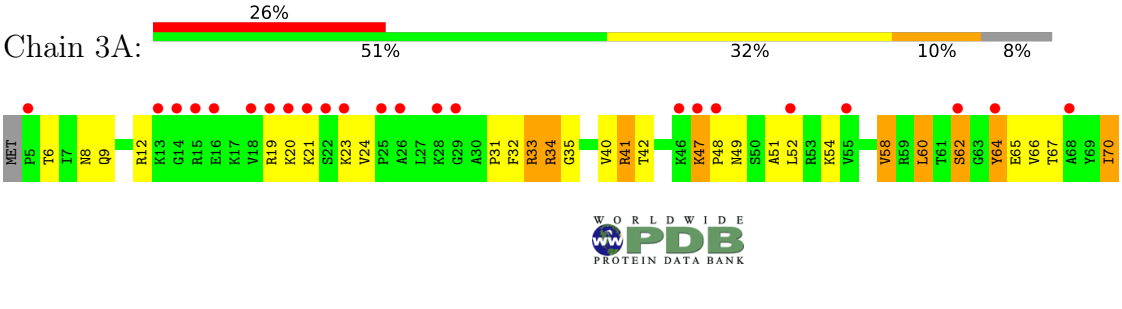
• Molecule 12: 30S ribosomal protein S12

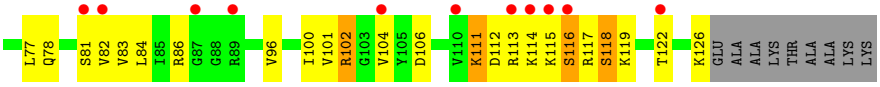
Chain 3I:



• Molecule 12: 30S ribosomal protein S12

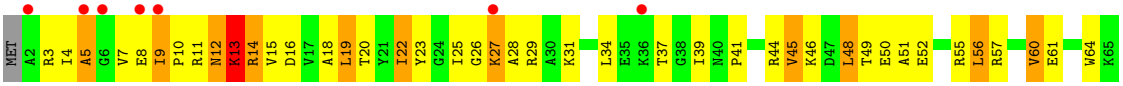
Chain 3A:





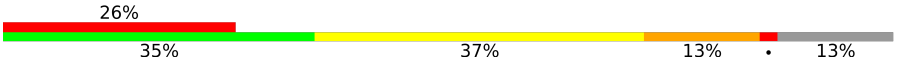
• Molecule 13: 30S ribosomal protein S13

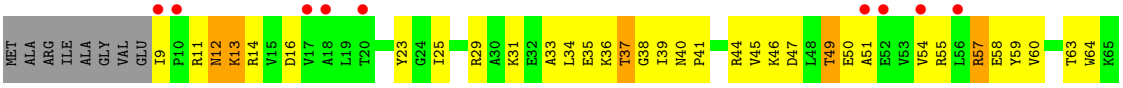
Chain 4I:

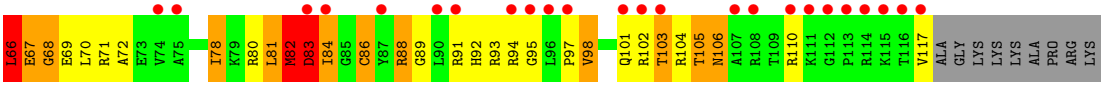


• Molecule 13: 30S ribosomal protein S13

Chain 4A:

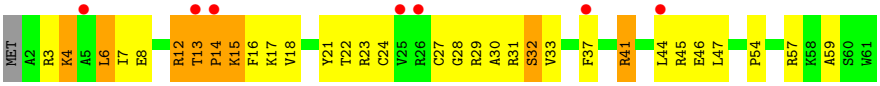






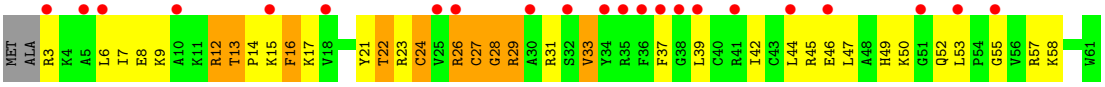
• Molecule 14: 30S ribosomal protein S14 type Z

Chain 5I:



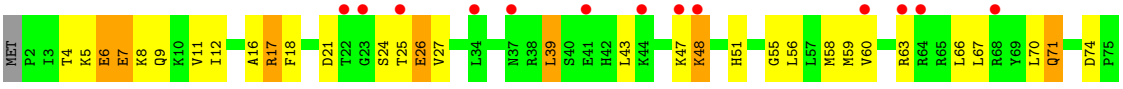
• Molecule 14: 30S ribosomal protein S14 type Z

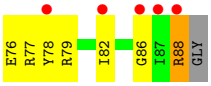
Chain 5A:



• Molecule 15: 30S ribosomal protein S15

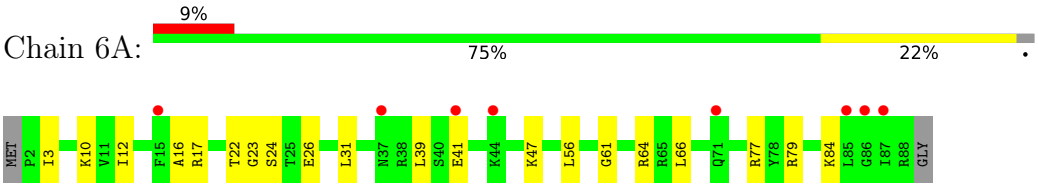
Chain 6I:





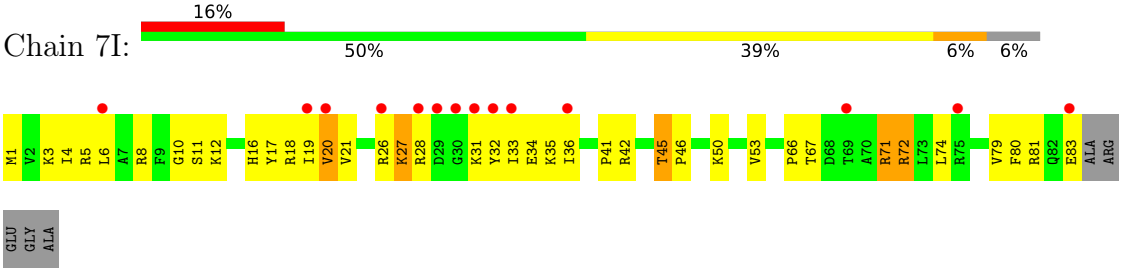
• Molecule 15: 30S ribosomal protein S15

Chain 6A:



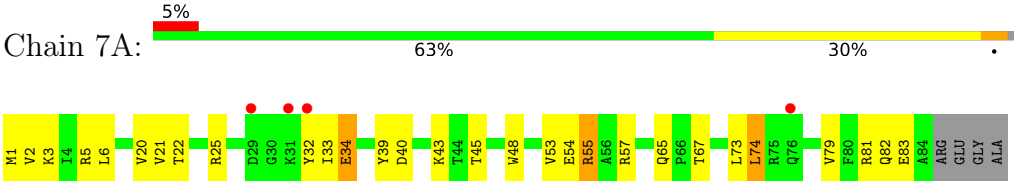
• Molecule 16: 30S ribosomal protein S16

Chain 7I:



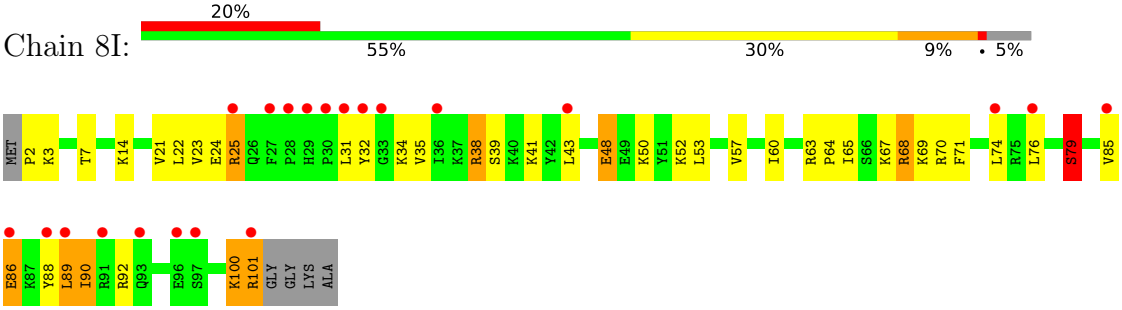
• Molecule 16: 30S ribosomal protein S16

Chain 7A:



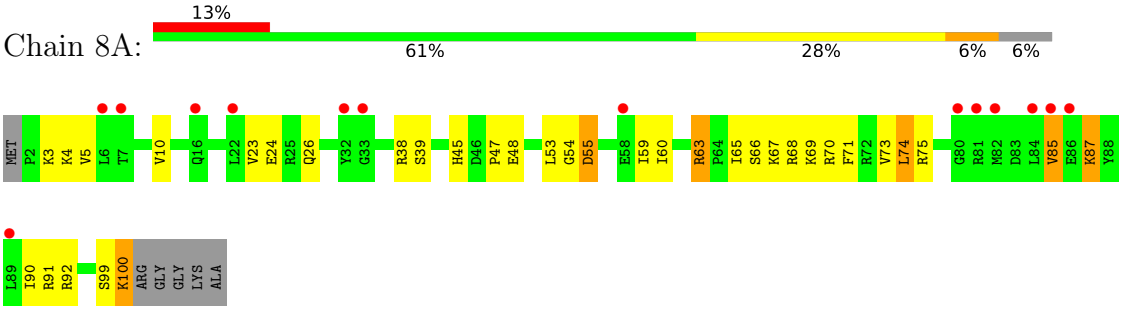
• Molecule 17: 30S ribosomal protein S17

Chain 8I:



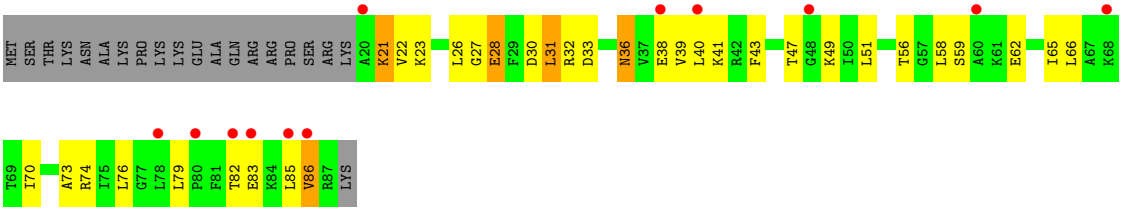
• Molecule 17: 30S ribosomal protein S17

Chain 8A:



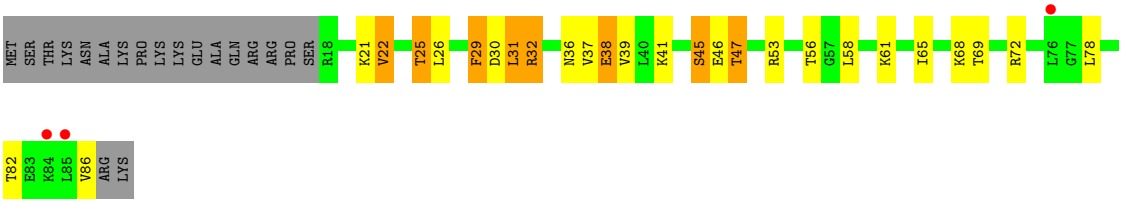
• Molecule 18: 30S ribosomal protein S18

Chain 9I:



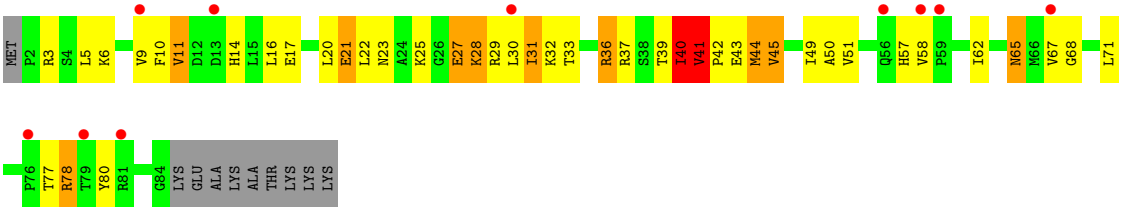
• Molecule 18: 30S ribosomal protein S18

Chain 9A:



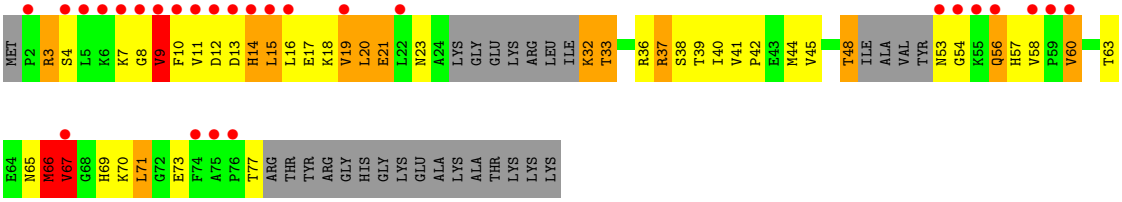
• Molecule 19: 30S ribosomal protein S19

Chain AI:



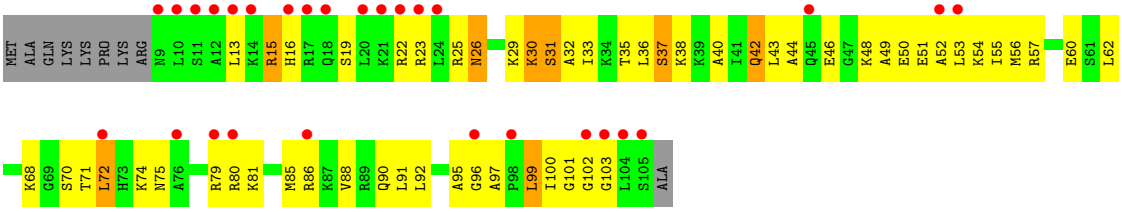
• Molecule 19: 30S ribosomal protein S19

Chain AA:



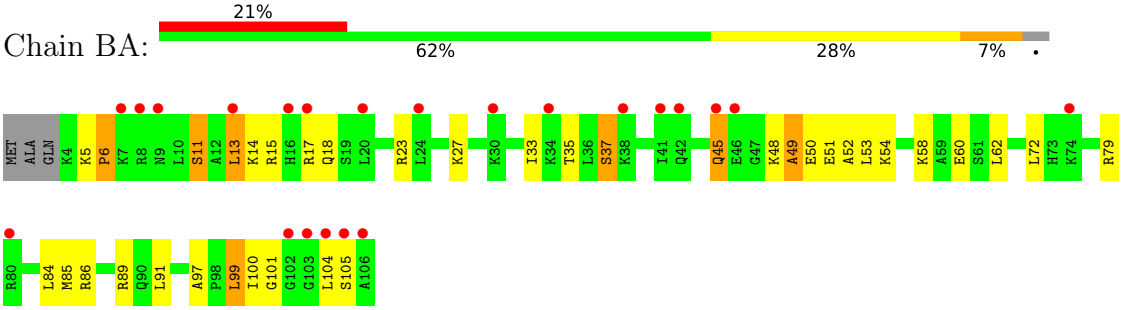
• Molecule 20: 30S ribosomal protein S20

Chain BI:



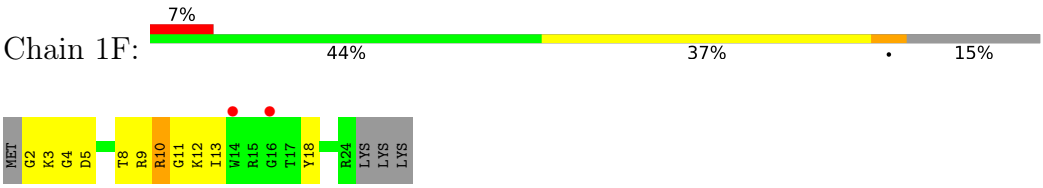
• Molecule 20: 30S ribosomal protein S20

Chain BA:



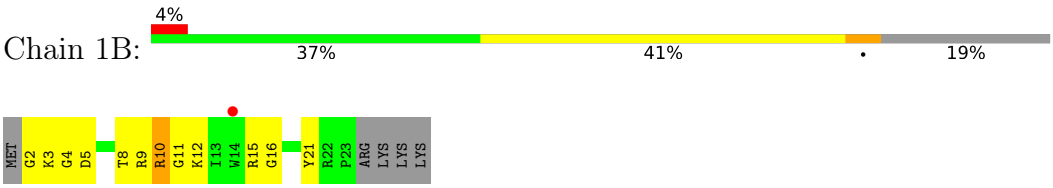
• Molecule 21: 30S ribosomal protein Thx

Chain 1F:



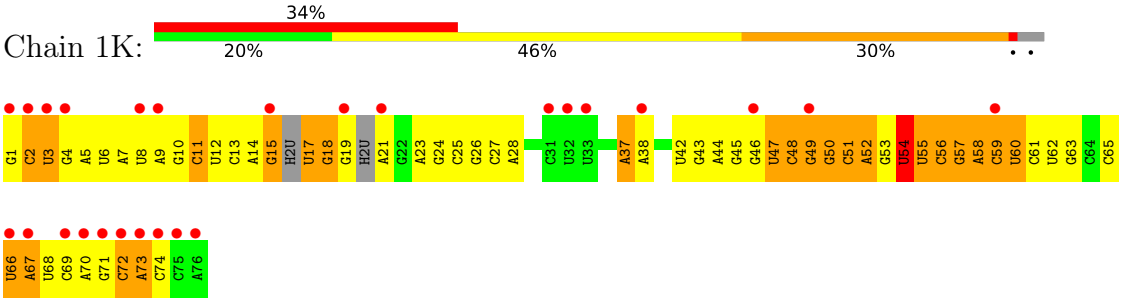
• Molecule 21: 30S ribosomal protein Thx

Chain 1B:



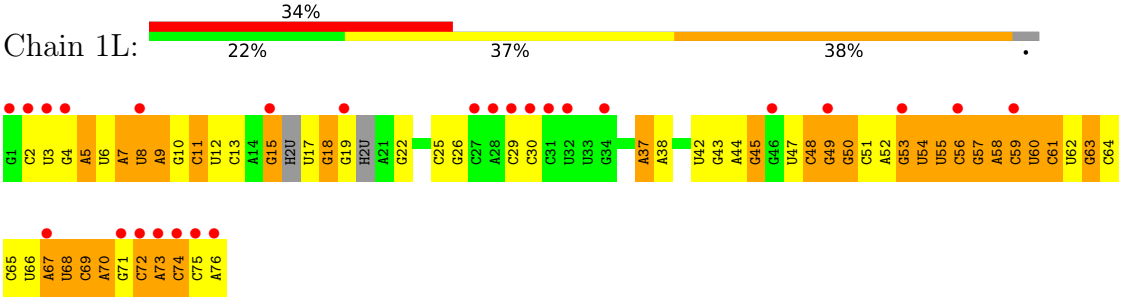
• Molecule 22: tRNAThr

Chain 1K:



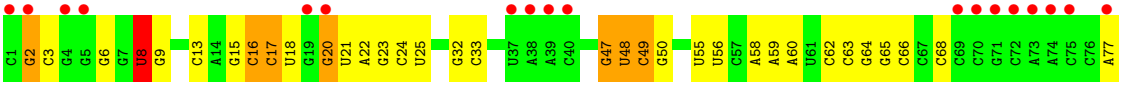
• Molecule 22: tRNAThr

Chain 1L:



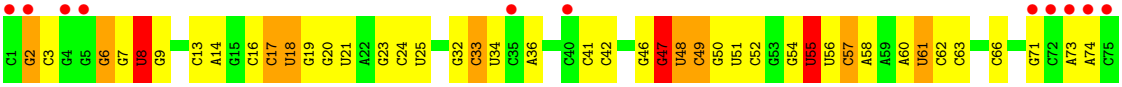
• Molecule 23: tRNAfMet

Chain 2K:



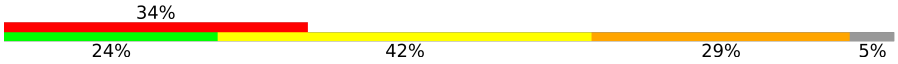
• Molecule 23: tRNAfMet

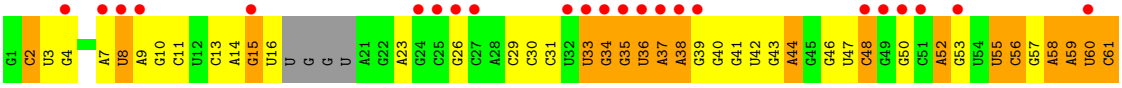
Chain 2L:

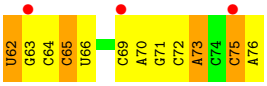


• Molecule 24: tRNAThr

Chain 3K:

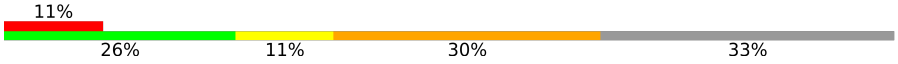


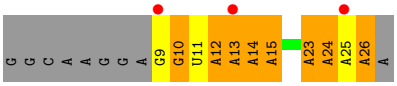




• Molecule 25: RNA (27-MER)

Chain 4K:



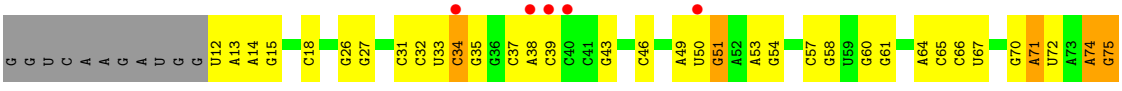


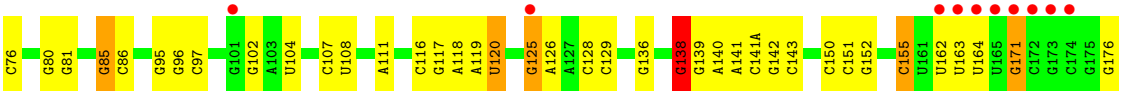
• Molecule 25: RNA (27-MER)

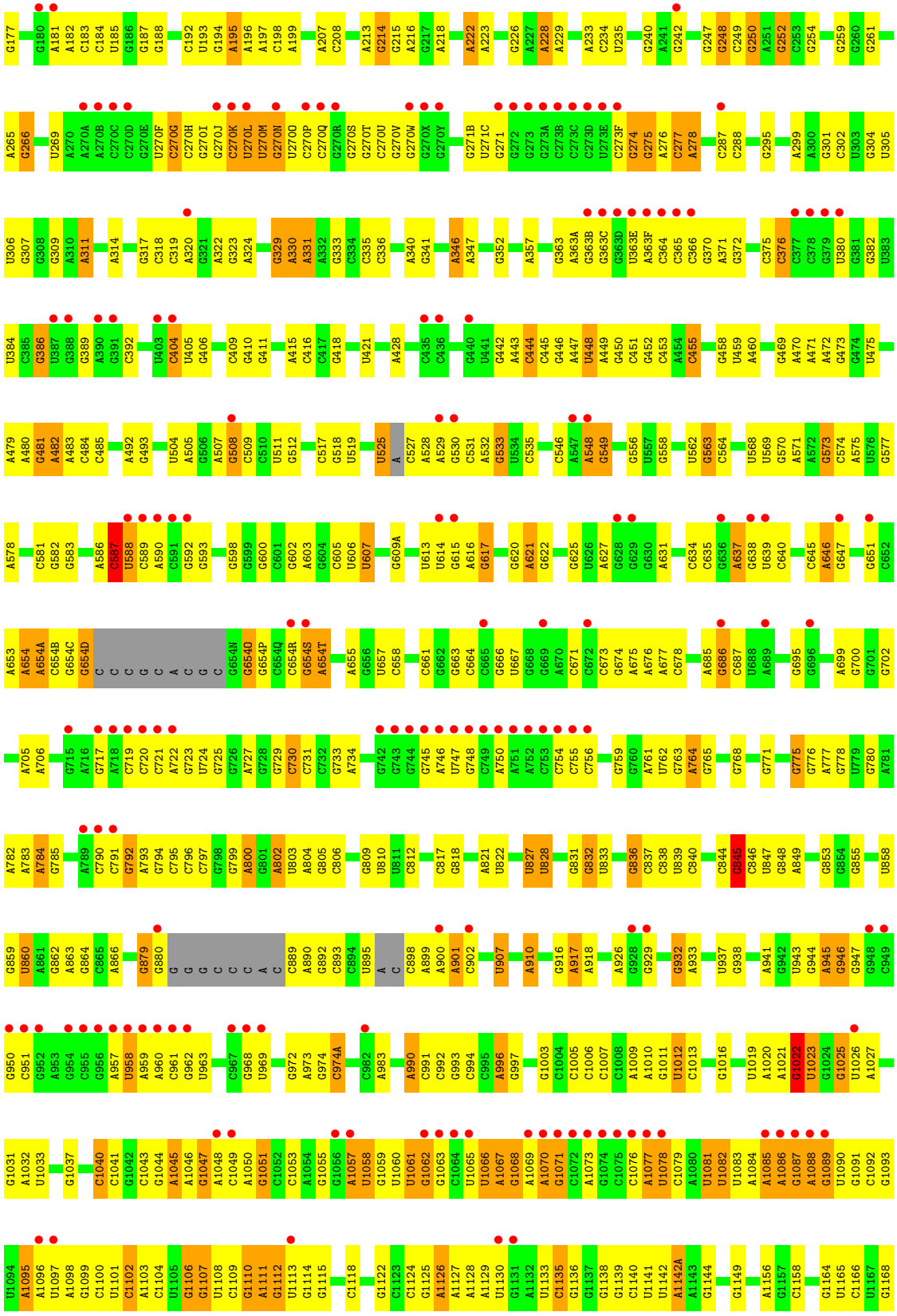
Chain 4L:

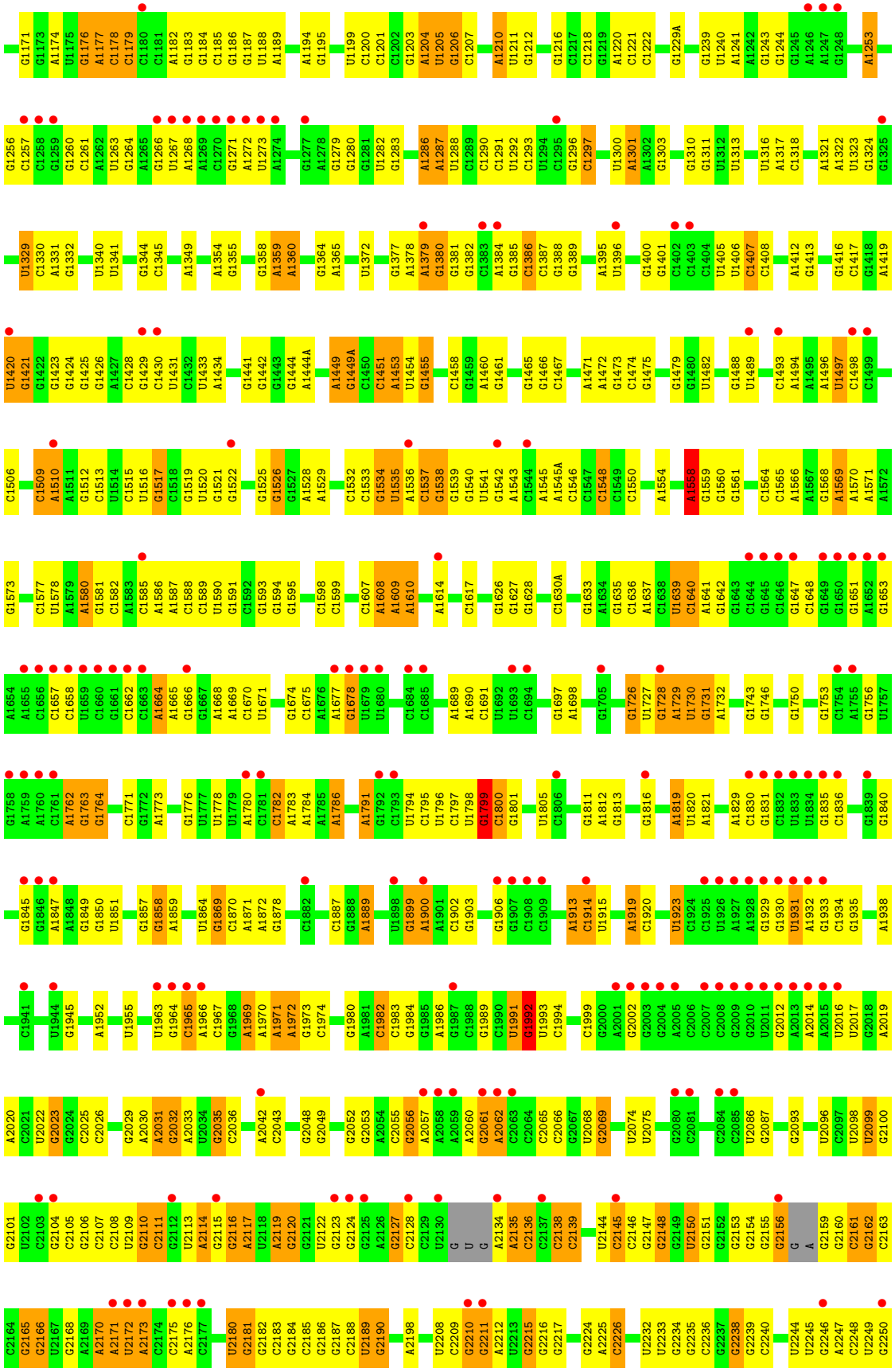
• Molecule 26: 23S ribosomal RNA

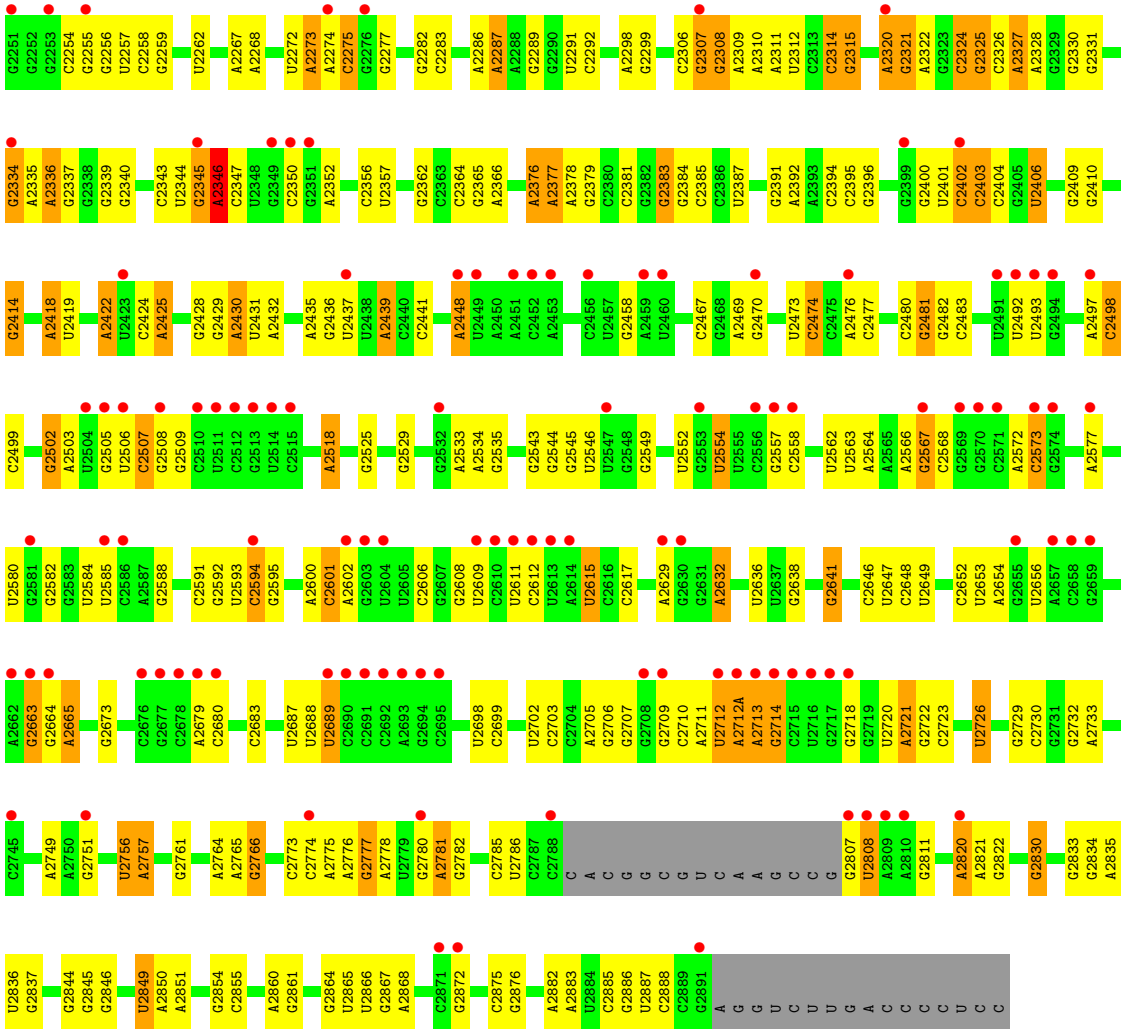
Chain 1H:





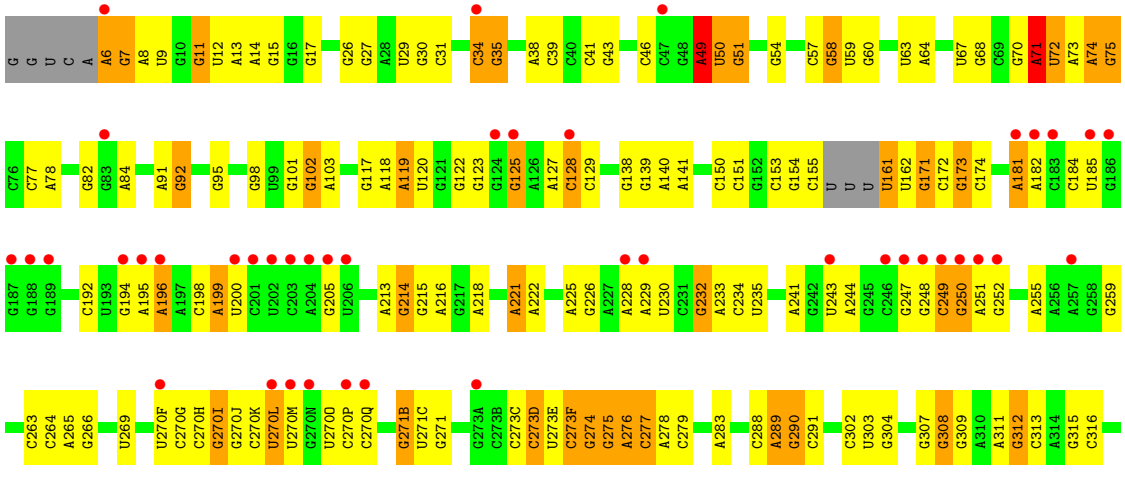


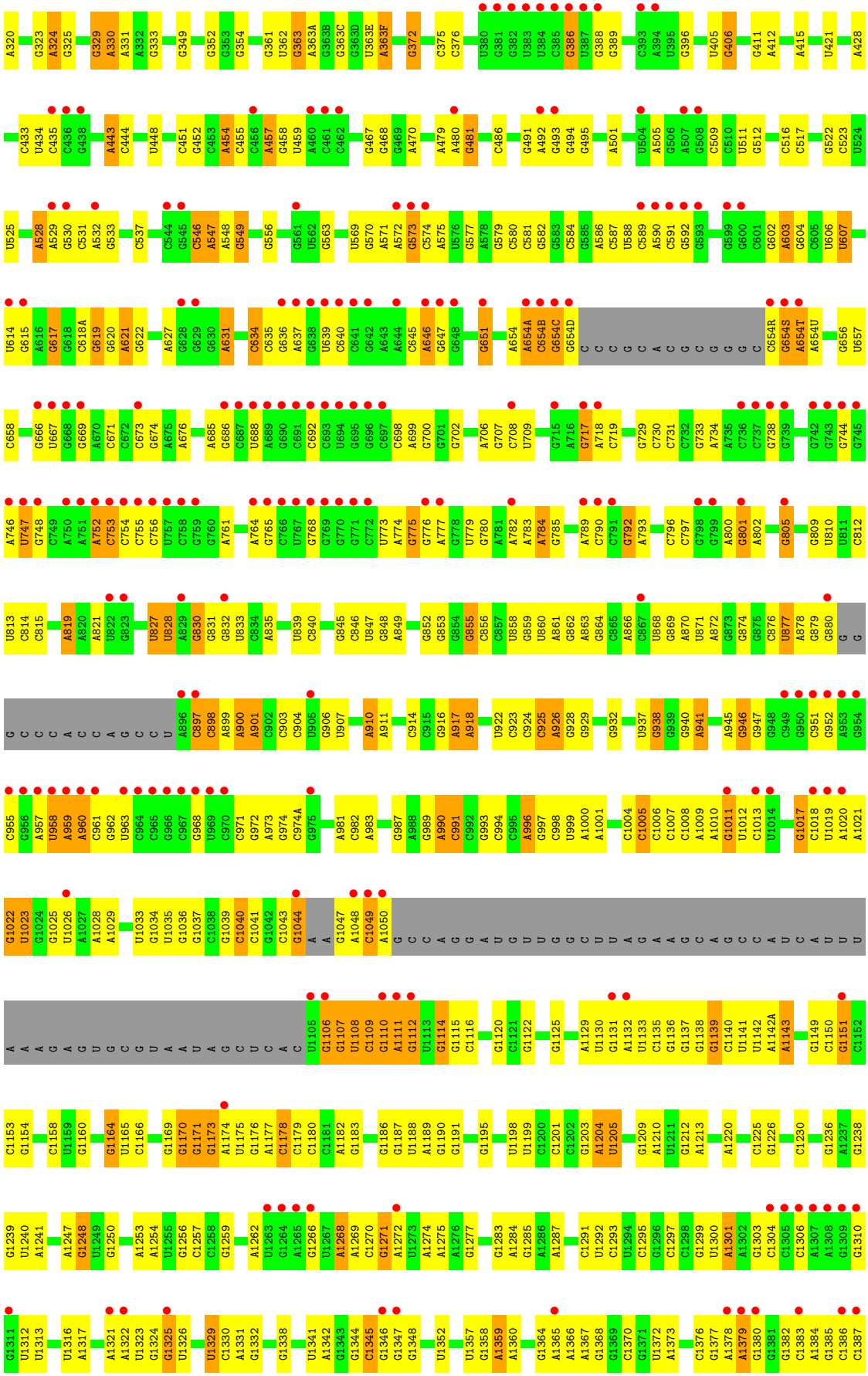


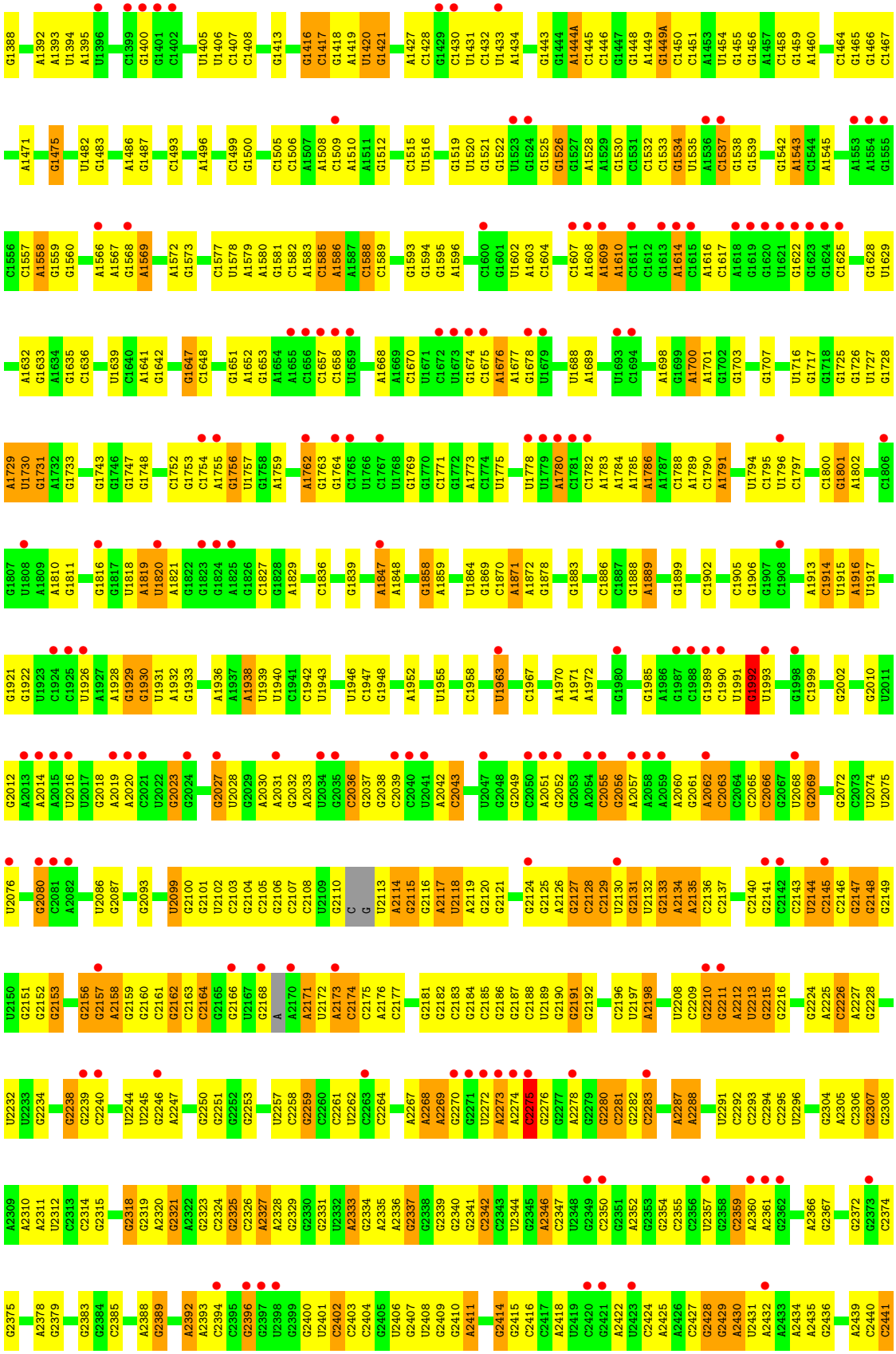


• Molecule 26: 23S ribosomal RNA

Chain 14:



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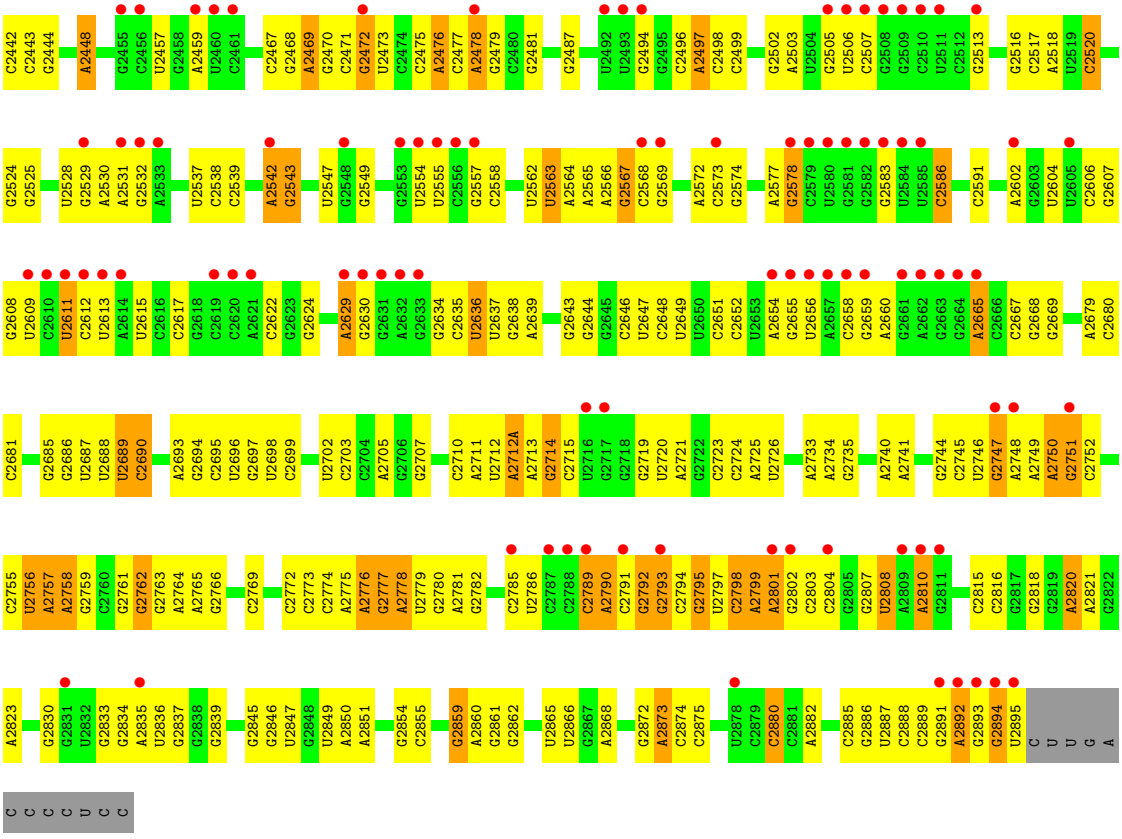
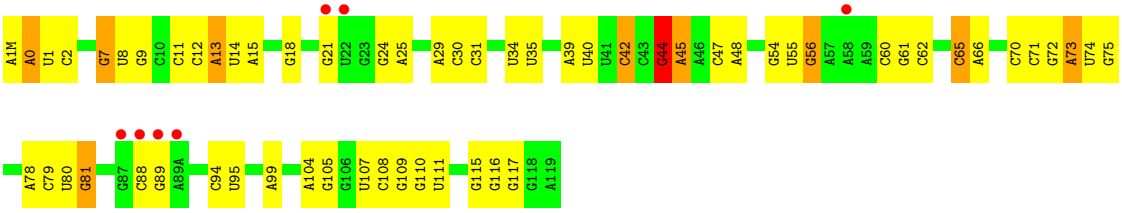


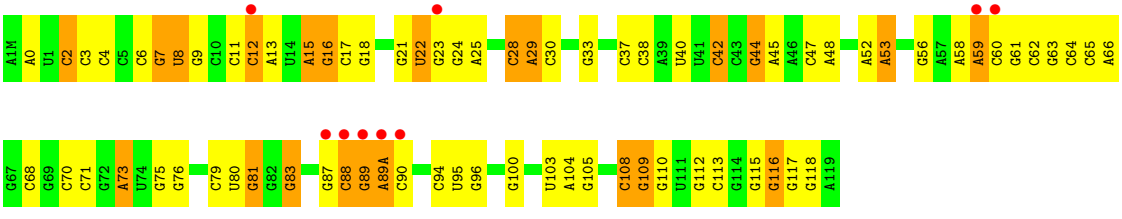
• Molecule 27: 5S ribosomal RNA

Chain 16:



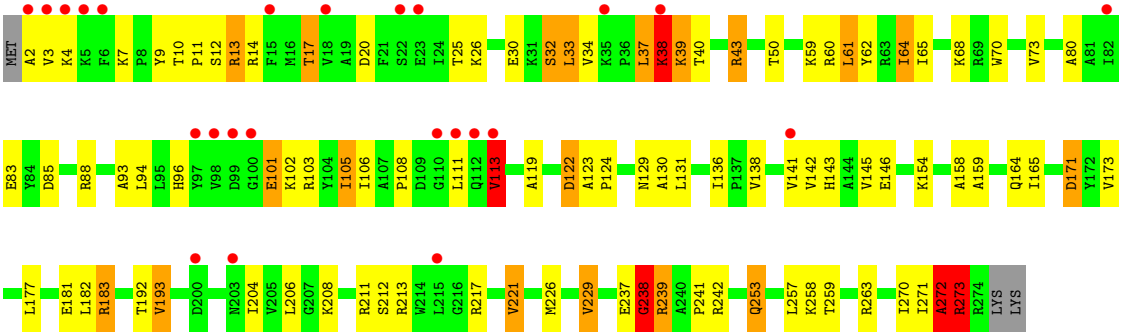
• Molecule 27: 5S ribosomal RNA

Chain 1J:



• Molecule 28: 50S ribosomal protein L2

Chain 11:



• Molecule 28: 50S ribosomal protein L2

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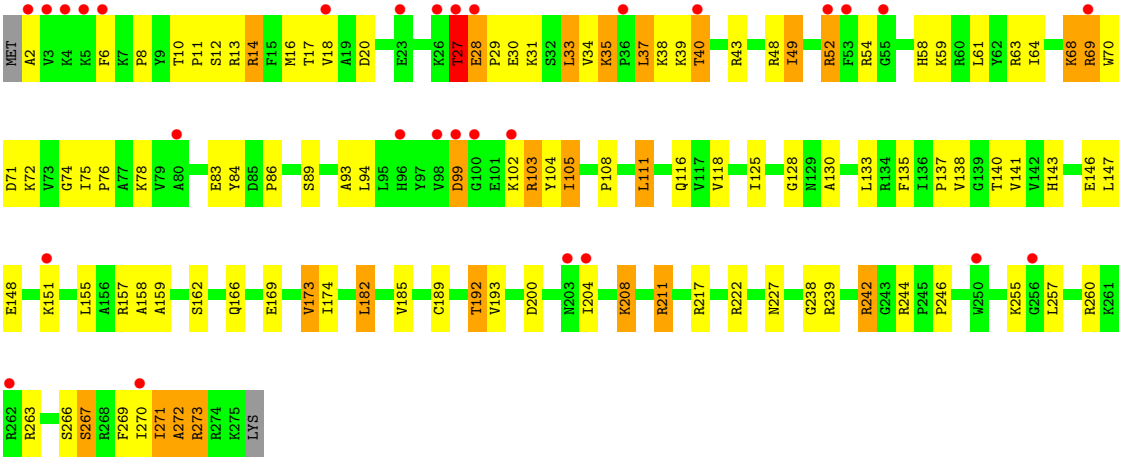

• Molecule 29: 50S ribosomal protein L3

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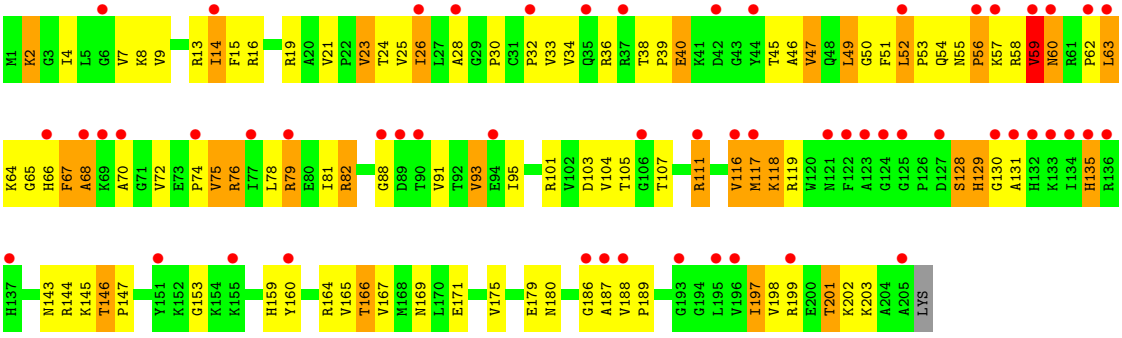
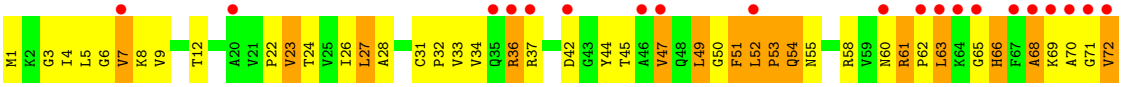
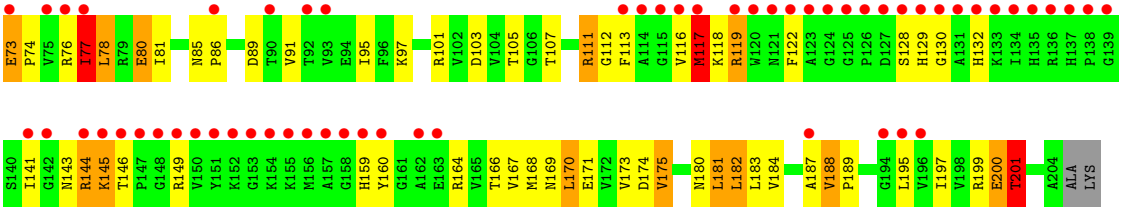


• Molecule 29: 50S ribosomal protein L3

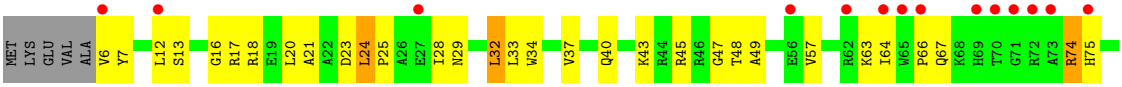
Chain 29:

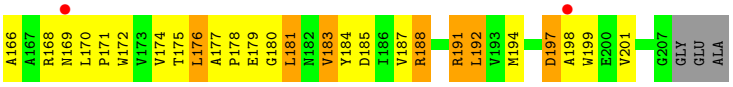




• Molecule 30: 50S ribosomal protein L4

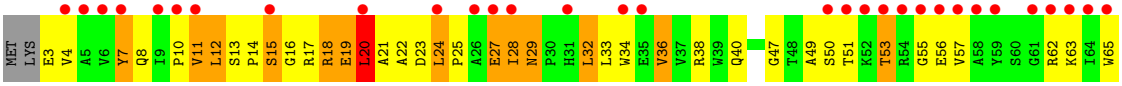
Chain 31:

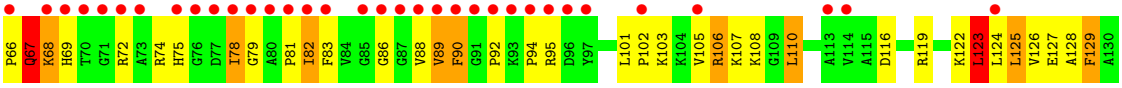


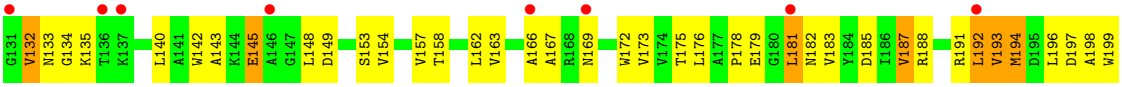


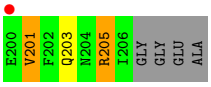
• Molecule 30: 50S ribosomal protein L4

Chain 39:



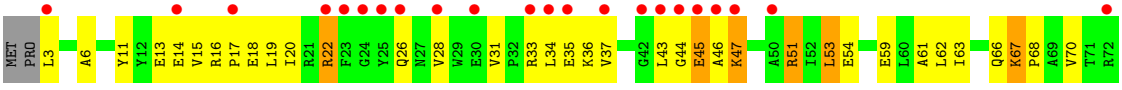


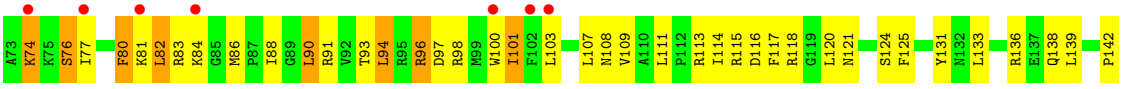


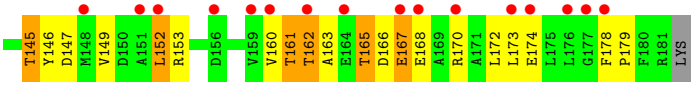


• Molecule 31: 50S ribosomal protein L5

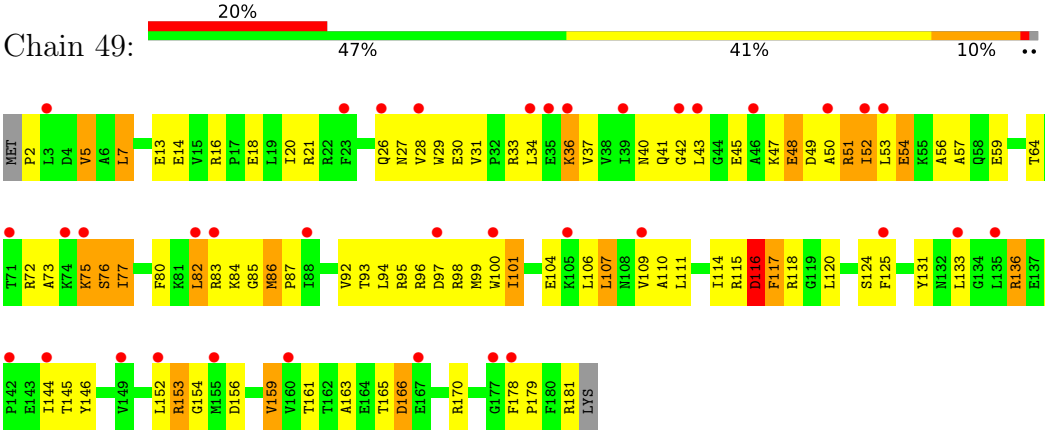
Chain 41:



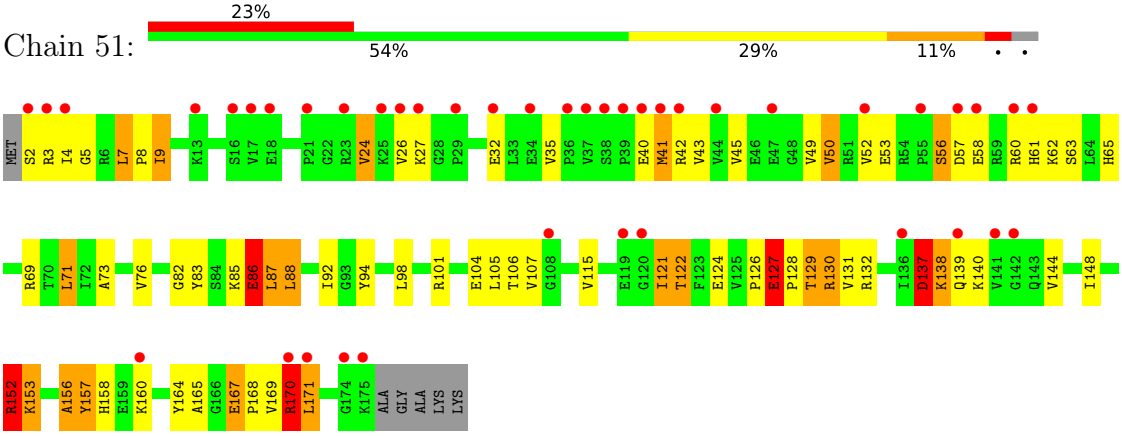




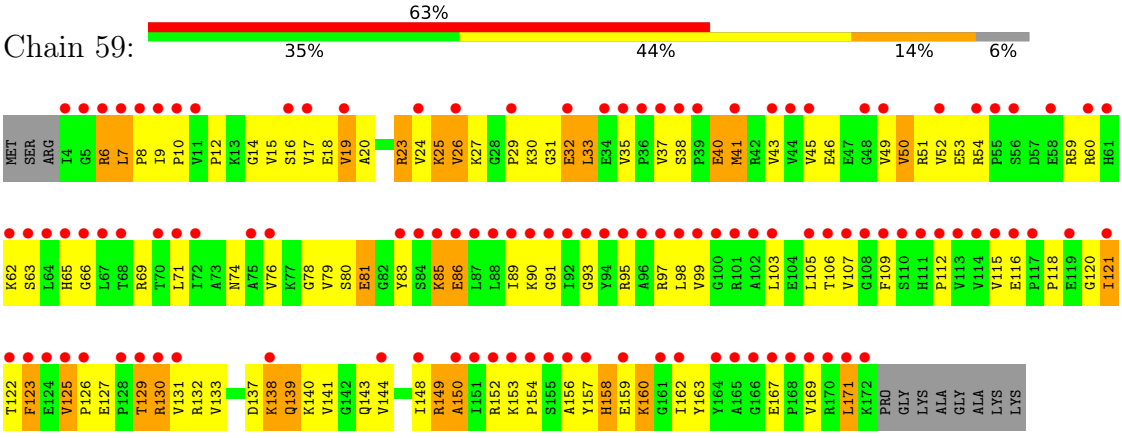
• Molecule 31: 50S ribosomal protein L5



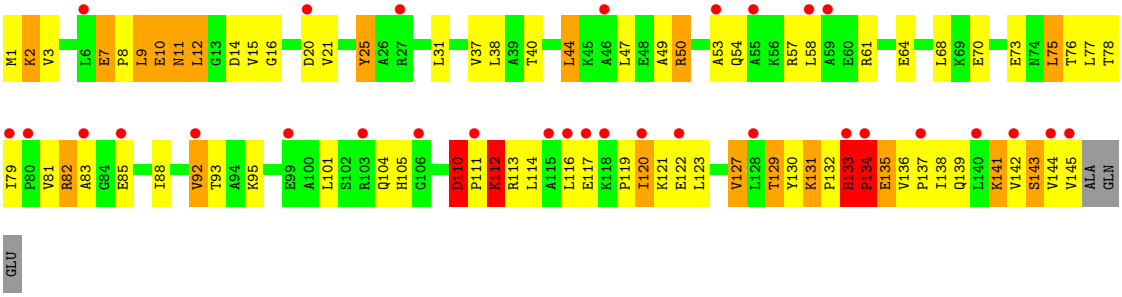
• Molecule 32: 50S ribosomal protein L6



• Molecule 32: 50S ribosomal protein L6

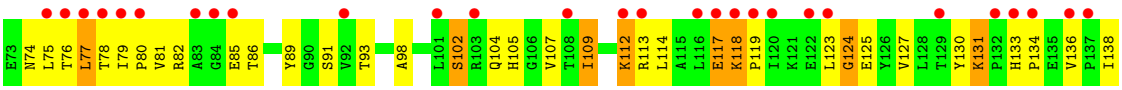


• Molecule 33: 50S ribosomal protein L9



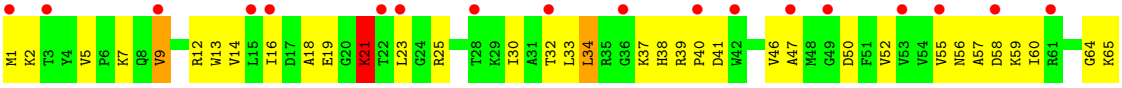
• Molecule 33: 50S ribosomal protein L9

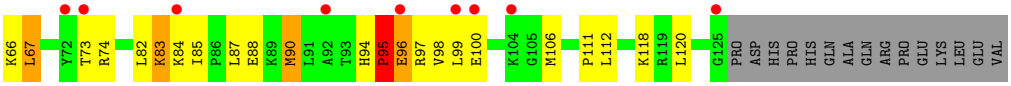
Chain 69:



• Molecule 34: 50S ribosomal protein L13

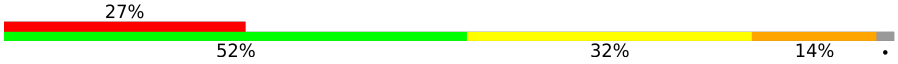
Chain 58:

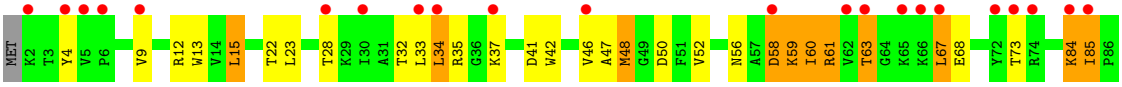


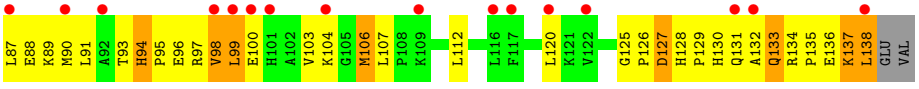


• Molecule 34: 50S ribosomal protein L13

Chain 15:

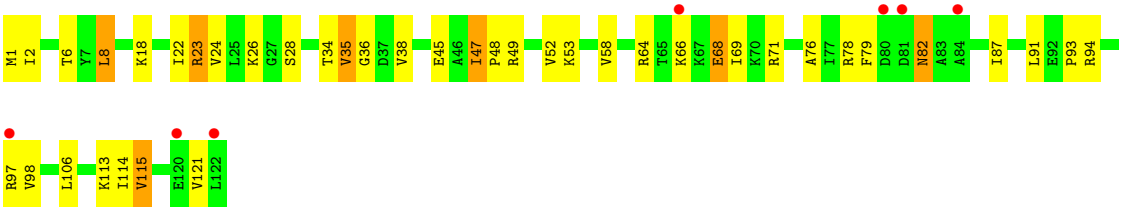






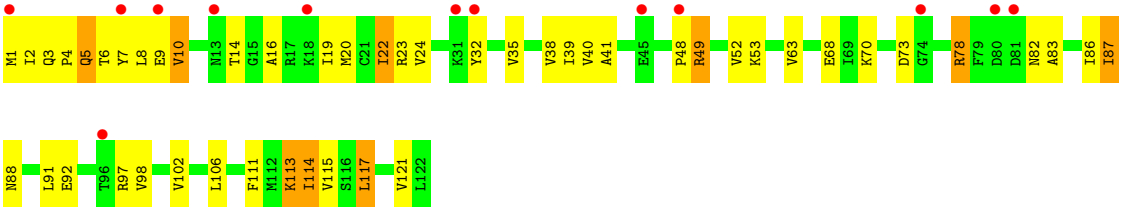
• Molecule 35: 50S ribosomal protein L14

Chain 68:



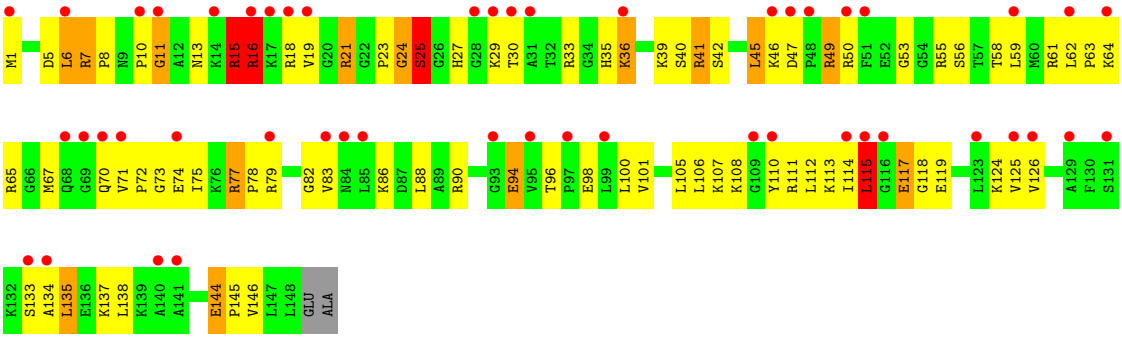
• Molecule 35: 50S ribosomal protein L14

Chain 25:



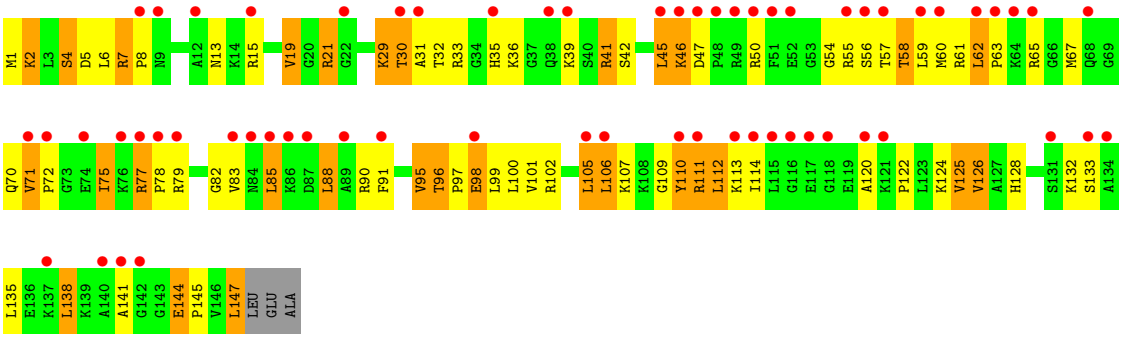
• Molecule 36: 50S ribosomal protein L15

Chain 78:



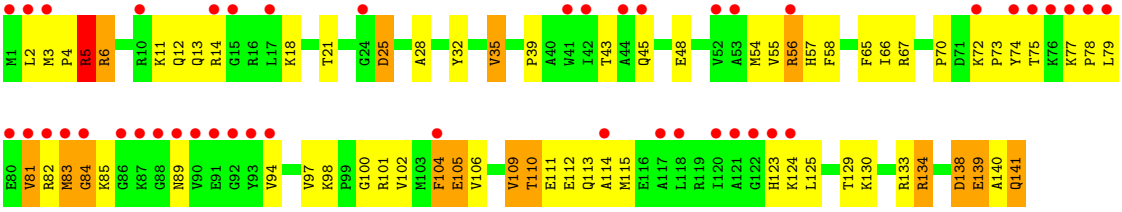
• Molecule 36: 50S ribosomal protein L15

Chain 35:

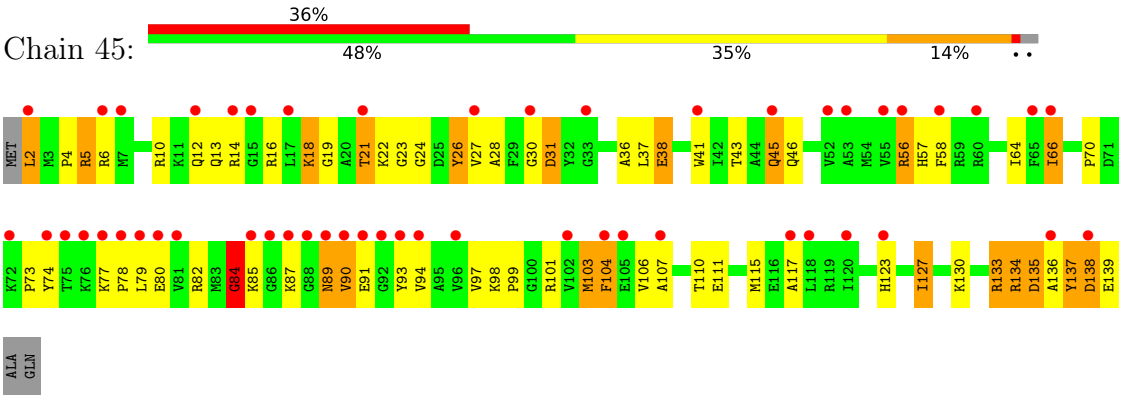


• Molecule 37: 50S ribosomal protein L16

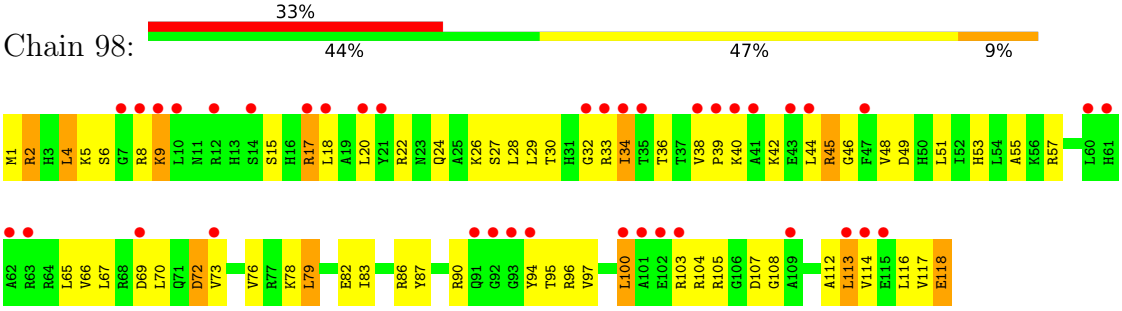
Chain 88:



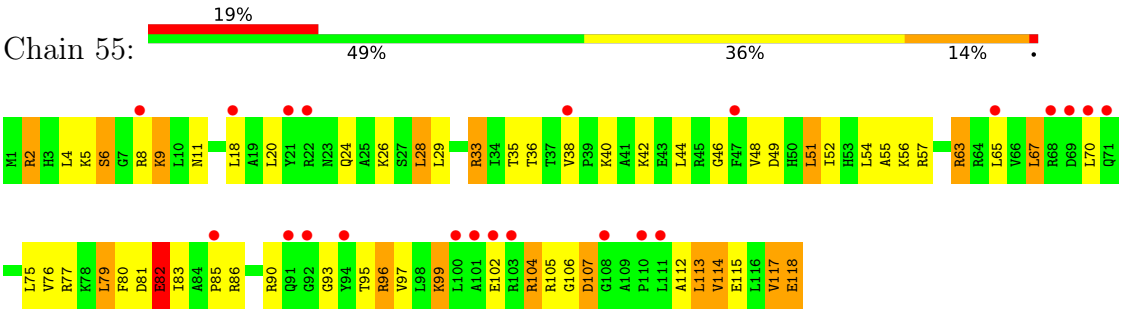
• Molecule 37: 50S ribosomal protein L16



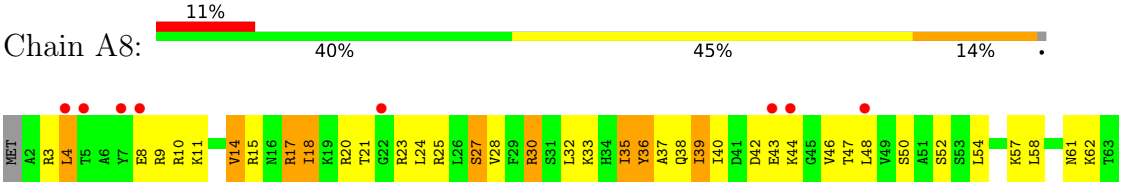
• Molecule 38: 50S ribosomal protein L17

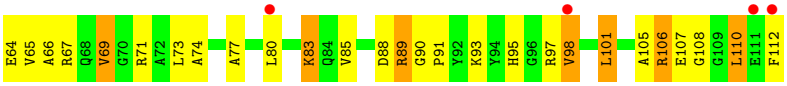


• Molecule 38: 50S ribosomal protein L17



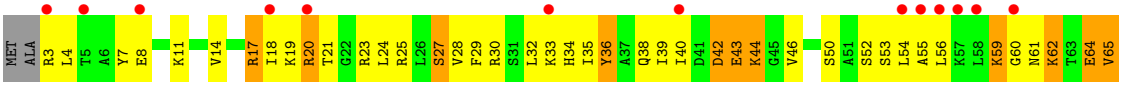
• Molecule 39: 50S ribosomal protein L18

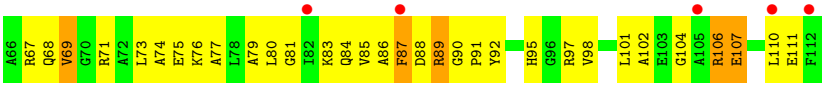




• Molecule 39: 50S ribosomal protein L18

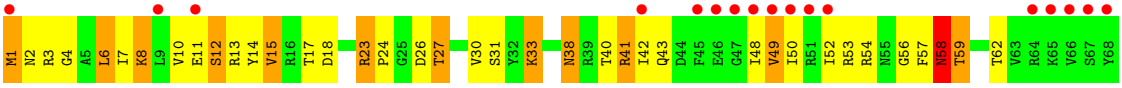
Chain 65:

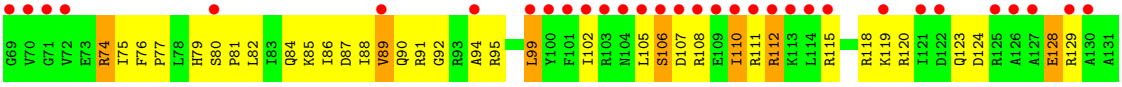


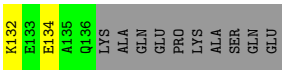


• Molecule 40: 50S ribosomal protein L19

Chain B8:

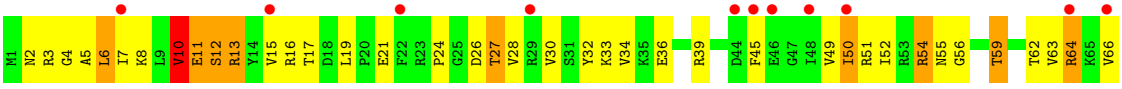


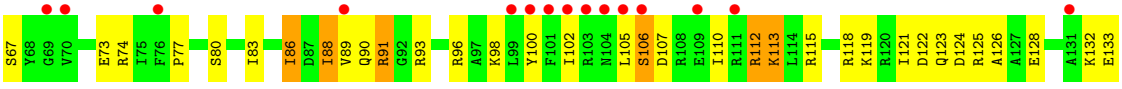


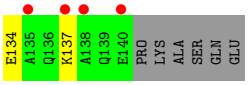


• Molecule 40: 50S ribosomal protein L19

Chain 75:

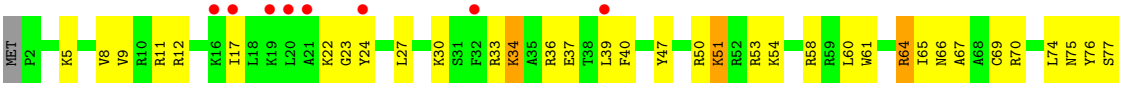


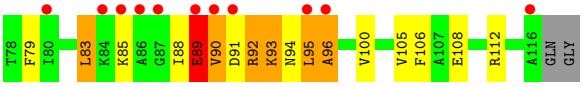




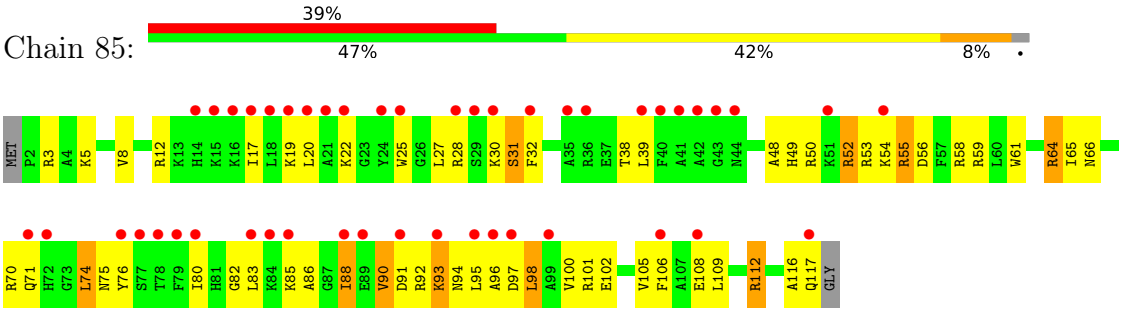
• Molecule 41: 50S ribosomal protein L20

Chain C8:

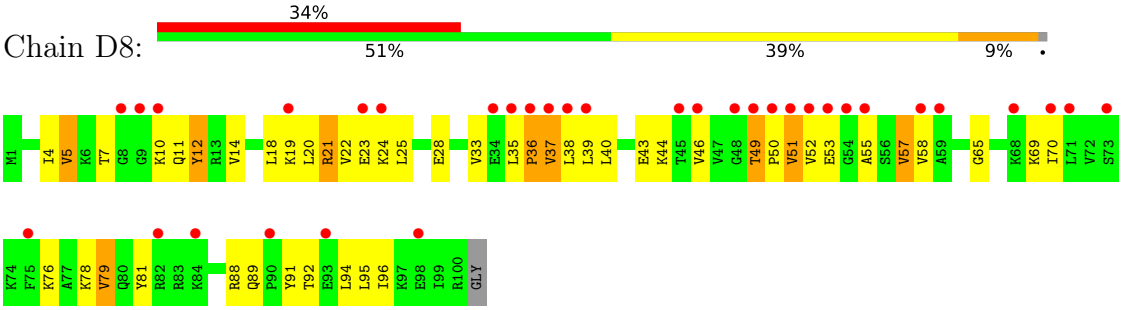




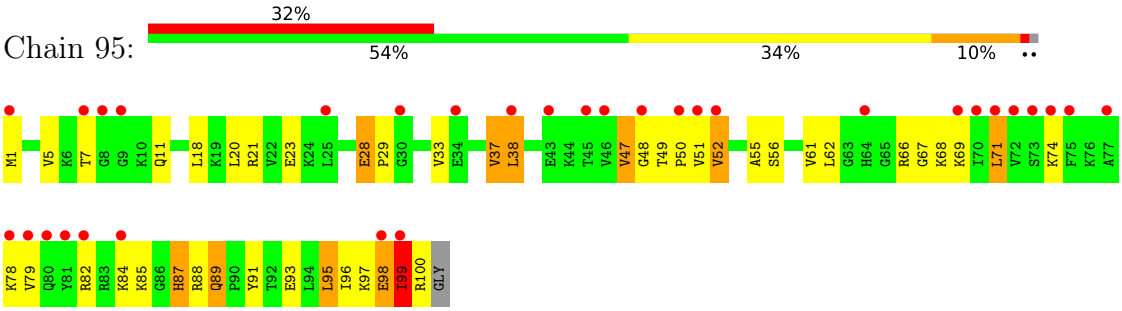
• Molecule 41: 50S ribosomal protein L20



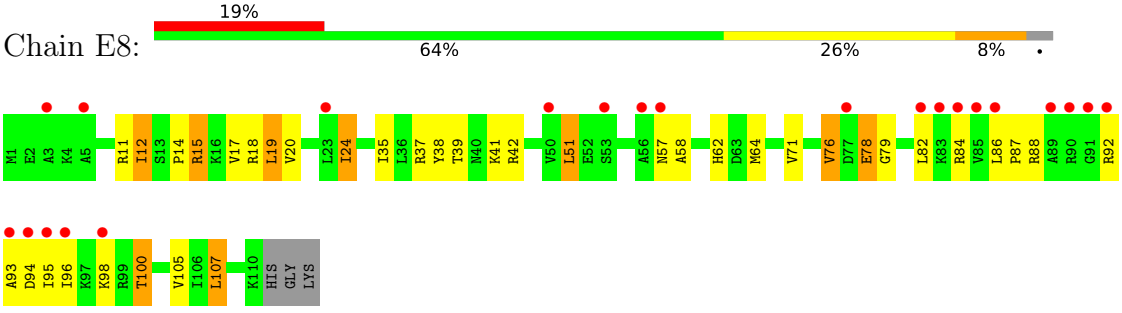
• Molecule 42: 50S ribosomal protein L21



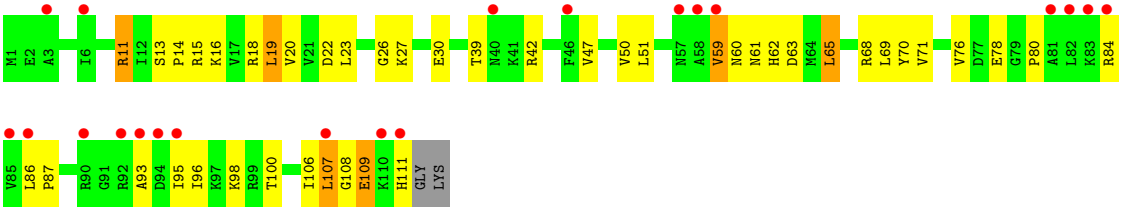
• Molecule 42: 50S ribosomal protein L21



• Molecule 43: 50S ribosomal protein L22

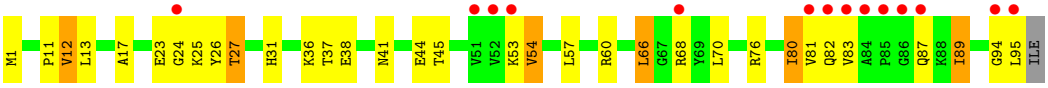


• Molecule 43: 50S ribosomal protein L22



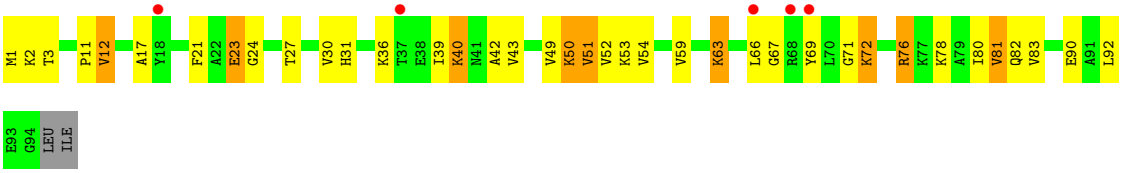
• Molecule 44: 50S ribosomal protein L23

Chain F8:



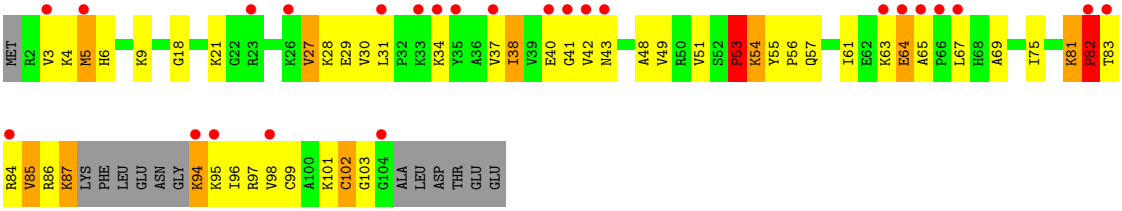
• Molecule 44: 50S ribosomal protein L23

Chain B5:



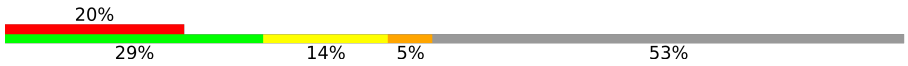
• Molecule 45: 50S ribosomal protein L24

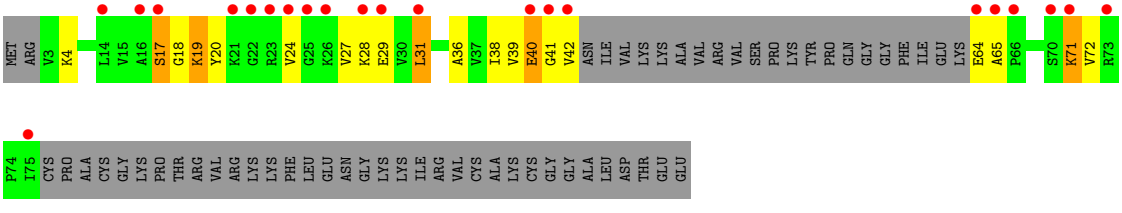
Chain G8:



• Molecule 45: 50S ribosomal protein L24

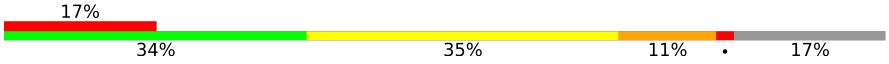
Chain C5:

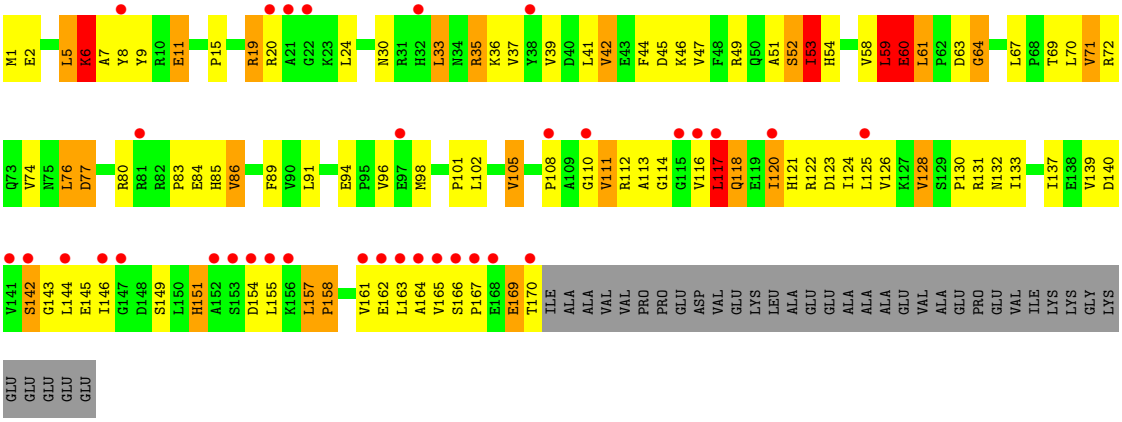


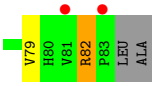


• Molecule 46: 50S ribosomal protein L25

Chain H8:

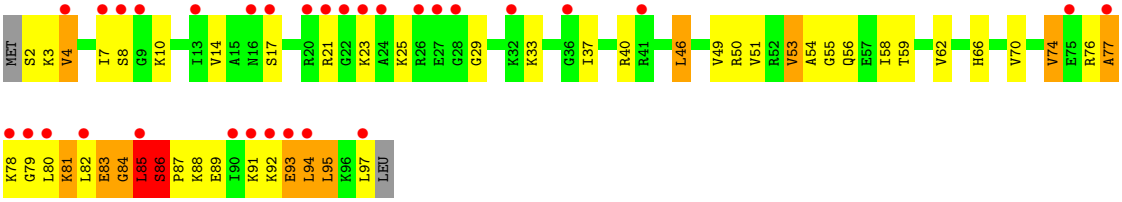






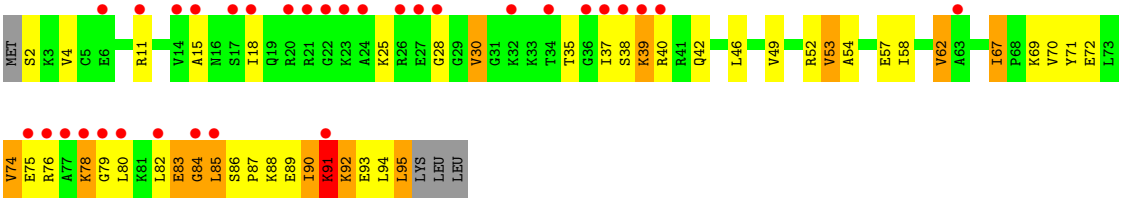
• Molecule 48: 50S ribosomal protein L28

Chain J8:



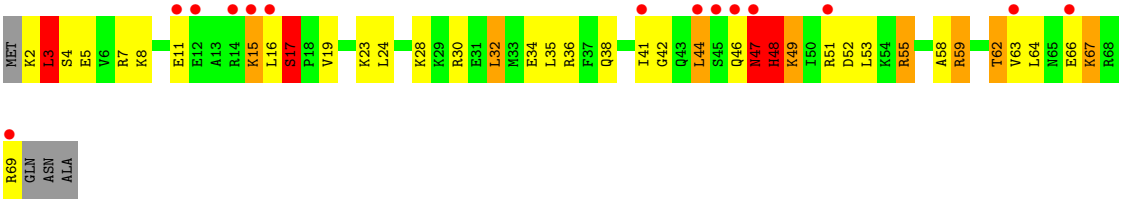
• Molecule 48: 50S ribosomal protein L28

Chain F5:



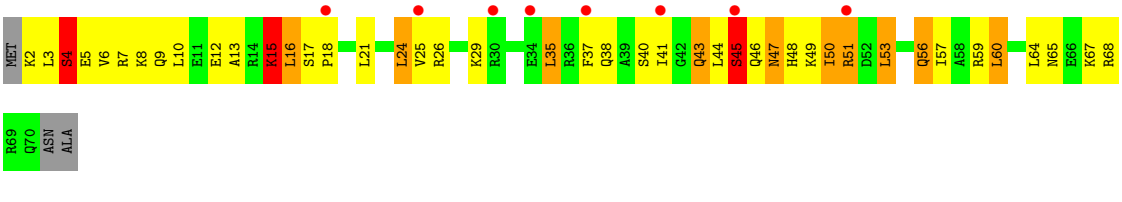
• Molecule 49: 50S ribosomal protein L29

Chain K8:



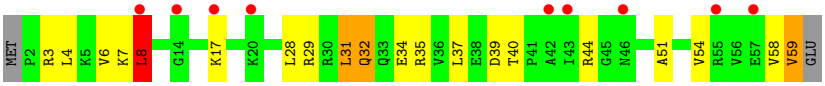
• Molecule 49: 50S ribosomal protein L29

Chain G5:



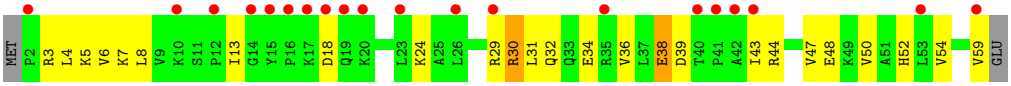
• Molecule 50: 50S ribosomal protein L30

Chain L8:



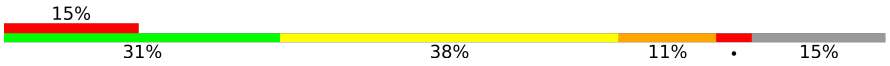
• Molecule 50: 50S ribosomal protein L30

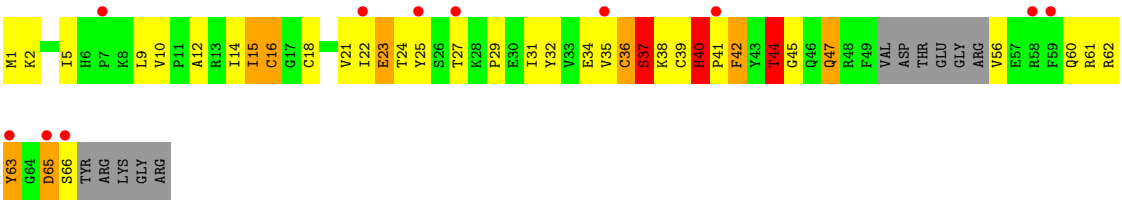
Chain H5:



• Molecule 51: 50S ribosomal protein L31

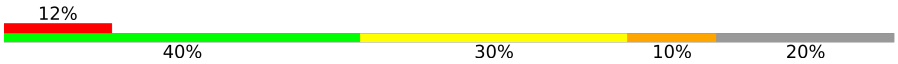
Chain M8:

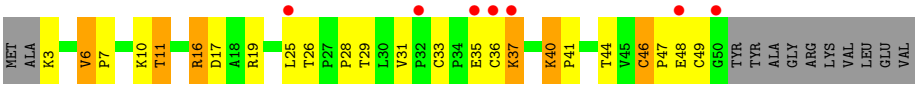




• Molecule 52: 50S ribosomal protein L32

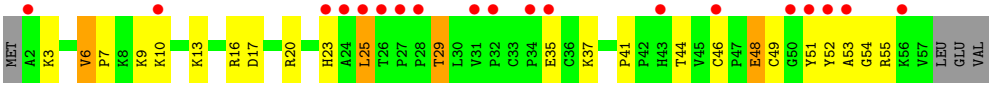
Chain N8:





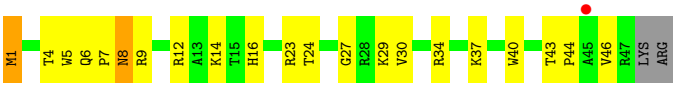
• Molecule 52: 50S ribosomal protein L32

Chain J5:



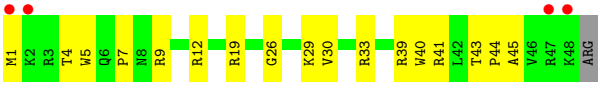
• Molecule 53: 50S ribosomal protein L34

Chain P8:



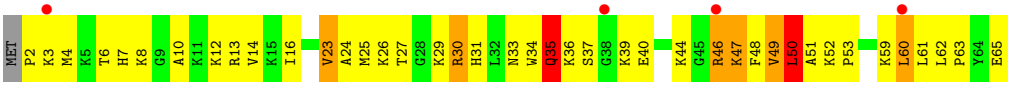
• Molecule 53: 50S ribosomal protein L34

Chain L5:



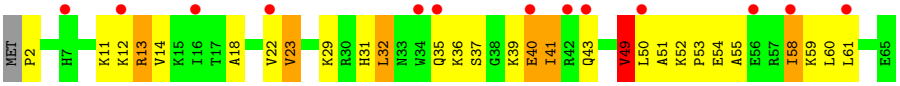
• Molecule 54: 50S ribosomal protein L35

Chain Q8:



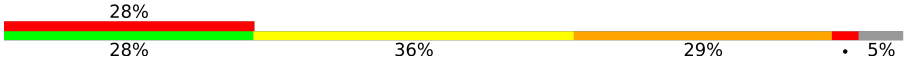
• Molecule 54: 50S ribosomal protein L35

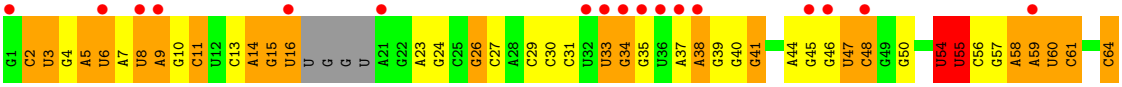
Chain M5:

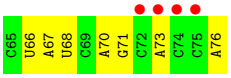


• Molecule 55: tRNAThr

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	209.41Å 449.24Å 618.40Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	224.62 – 2.96 224.62 – 2.96	Depositor EDS
% Data completeness (in resolution range)	100.0 (224.62-2.96) 94.4 (224.62-2.96)	Depositor EDS
R_{merge}	0.29	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	0.76 (at 2.96Å)	Xtriage
Refinement program	PHENIX 1.12_2829	Depositor
R, R_{free}	0.196 , 0.252 0.198 , 0.248	Depositor DCC
R_{free} test set	2000 reflections (0.17%)	wwPDB-VP
Wilson B-factor (Å^2)	82.0	Xtriage
Anisotropy	0.292	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 142.3	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.90	EDS
Total number of atoms	294252	wwPDB-VP
Average B, all atoms (Å^2)	97.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.41% 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 (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: MG, 4SU, H2U, 7MG, OMC, 5MU, ZN, PSU, SF4, AET

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	0.40	0/36095	0.65	7/56332 (0.0%)
1	1G	0.37	0/35850	0.60	4/55949 (0.0%)
2	12	0.41	0/1727	0.69	2/2326 (0.1%)
2	1E	0.38	0/1908	0.66	1/2573 (0.0%)
3	22	0.36	0/1569	0.63	0/2116
3	2E	0.38	0/1629	0.59	0/2195
4	32	0.40	1/1728 (0.1%)	0.62	0/2313
4	3E	0.42	0/1728	0.66	0/2313
5	42	0.37	0/1156	0.58	0/1557
5	4E	0.39	0/1158	0.61	0/1559
6	52	0.36	0/855	0.55	0/1154
6	5E	0.39	0/850	0.61	0/1147
7	62	0.35	0/1122	0.64	2/1500 (0.1%)
7	6E	0.38	0/1259	0.59	0/1686
8	72	0.33	0/1127	0.59	0/1517
8	7E	0.36	0/1135	0.66	0/1527
9	82	0.36	0/971	0.68	1/1304 (0.1%)
9	8E	0.38	0/1019	0.70	0/1367
10	1A	0.38	0/814	0.60	0/1095
10	1I	0.46	0/762	0.73	0/1027
11	2A	0.33	0/850	0.60	1/1150 (0.1%)
11	2I	0.41	0/838	0.71	1/1133 (0.1%)
12	3A	0.43	0/972	0.76	2/1301 (0.2%)
12	3I	0.55	0/972	0.86	0/1301
13	4A	0.41	0/889	0.73	0/1192
13	4I	0.46	0/952	0.75	0/1277
14	5A	0.37	0/495	0.70	0/657
14	5I	0.41	0/500	0.77	2/664 (0.3%)
15	6A	0.33	0/740	0.54	0/987
15	6I	0.42	0/740	0.59	0/987
16	7A	0.38	0/721	0.66	0/970
16	7I	0.40	0/716	0.67	0/963

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
17	8A	0.38	0/836	0.60	0/1117
17	8I	0.39	0/847	0.70	1/1131 (0.1%)
18	9A	0.39	0/559	0.59	0/746
18	9I	0.38	0/554	0.61	0/739
19	AA	0.51	0/520	0.86	1/700 (0.1%)
19	AI	0.39	0/680	0.81	2/915 (0.2%)
20	BA	0.36	0/781	0.59	0/1033
20	BI	0.35	0/748	0.61	0/986
21	1B	0.30	0/192	0.60	0/252
21	1F	0.36	0/203	0.61	0/266
22	1K	0.45	0/1675	0.65	0/2608
22	1L	0.40	0/1675	0.56	0/2608
23	2K	0.45	1/1721 (0.1%)	0.64	0/2682
23	2L	0.41	1/1721 (0.1%)	0.62	0/2682
24	3K	0.40	0/1716	0.59	0/2668
25	4K	0.49	0/440	0.67	0/684
25	4L	0.52	0/341	0.99	1/529 (0.2%)
26	14	0.47	0/67828	0.71	11/105880 (0.0%)
26	1H	0.54	0/68741	0.76	16/107295 (0.0%)
27	16	0.43	0/2928	0.74	1/4568 (0.0%)
27	1J	0.41	0/2928	0.68	0/4568
28	11	0.60	0/2170	0.92	5/2926 (0.2%)
28	19	0.58	0/2175	0.90	4/2933 (0.1%)
29	21	0.56	2/1589 (0.1%)	0.97	3/2145 (0.1%)
29	29	0.48	0/1596	0.90	4/2153 (0.2%)
30	31	0.55	0/1620	0.81	0/2194
30	39	0.46	0/1637	0.84	6/2218 (0.3%)
31	41	0.41	0/1481	0.74	0/1994
31	49	0.40	0/1483	0.72	1/1997 (0.1%)
32	51	0.47	0/1354	0.95	10/1833 (0.5%)
32	59	0.50	0/1320	0.77	1/1787 (0.1%)
33	61	0.41	0/1146	0.79	4/1551 (0.3%)
33	69	0.39	0/1146	0.72	1/1551 (0.1%)
34	15	0.52	1/1123 (0.1%)	0.73	0/1515
34	58	0.46	0/1017	0.82	3/1369 (0.2%)
35	25	0.42	0/942	0.67	0/1269
35	68	0.47	0/942	0.72	0/1269
36	35	0.51	0/1139	0.94	4/1514 (0.3%)
36	78	0.57	0/1144	1.10	5/1521 (0.3%)
37	45	0.47	0/1120	0.86	1/1498 (0.1%)
37	88	0.57	0/1138	0.90	3/1523 (0.2%)
38	55	0.49	0/981	0.78	0/1312
38	98	0.47	0/981	0.81	0/1312

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
39	65	0.43	0/886	0.81	2/1180 (0.2%)
39	A8	0.51	0/891	0.84	0/1187
40	75	0.45	0/1178	0.80	2/1573 (0.1%)
40	B8	0.50	0/1142	0.85	2/1526 (0.1%)
41	85	0.45	0/977	0.70	0/1301
41	C8	0.53	0/968	0.75	0/1289
42	95	0.43	0/781	0.85	4/1048 (0.4%)
42	D8	0.45	0/785	0.81	0/1052
43	A5	0.50	0/897	0.75	0/1204
43	E8	0.53	0/886	0.71	0/1189
44	B5	0.51	0/749	0.80	2/1007 (0.2%)
44	F8	0.57	0/764	0.84	0/1025
45	C5	0.49	0/401	0.80	0/535
45	G8	0.55	0/745	1.00	3/993 (0.3%)
46	D5	0.41	0/1443	0.72	0/1960
46	H8	0.42	0/1395	0.82	3/1890 (0.2%)
47	E5	0.50	0/611	0.83	0/814
47	I8	0.58	0/619	0.92	0/825
48	F5	0.52	0/744	0.87	2/989 (0.2%)
48	J8	0.59	0/754	0.95	3/1003 (0.3%)
49	G5	0.51	0/578	0.82	2/766 (0.3%)
49	K8	0.60	0/577	1.04	2/763 (0.3%)
50	H5	0.40	0/464	0.63	0/623
50	L8	0.49	0/464	0.79	2/623 (0.3%)
51	M8	0.49	0/485	0.93	0/652
52	J5	0.55	0/448	0.86	1/606 (0.2%)
52	N8	0.61	0/381	0.88	0/516
53	L5	0.54	0/414	0.81	2/547 (0.4%)
53	P8	0.71	0/409	0.91	0/540
54	M5	0.59	0/524	0.95	2/691 (0.3%)
54	Q8	0.60	0/524	1.09	2/691 (0.3%)
55	3L	0.39	0/1672	0.63	0/2600
All	All	0.47	6/315281 (0.0%)	0.71	147/472388 (0.0%)

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	12	0	6
2	1E	0	3

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Mol	Chain	#Chirality outliers	#Planarity outliers
3	22	0	2
4	32	0	2
5	4E	0	1
9	82	0	1
9	8E	0	2
10	1A	0	1
11	2I	0	3
12	3A	0	1
12	3I	0	3
13	4A	0	4
13	4I	0	2
14	5A	0	3
16	7A	0	1
19	AA	0	7
20	BA	0	3
20	BI	0	1
28	11	0	4
28	19	0	2
29	21	0	6
29	29	0	6
30	31	0	3
30	39	0	5
31	49	0	2
32	51	0	4
32	59	0	2
33	61	0	5
33	69	0	3
34	58	0	2
36	35	0	3
36	78	0	5
37	45	0	5
37	88	0	2
38	98	0	1
39	65	0	1
39	A8	0	1
40	75	0	2
40	B8	0	3
41	85	0	2
41	C8	0	4
42	95	0	2
42	D8	0	2
44	B5	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
45	G8	0	3
46	D5	0	6
46	H8	0	5
48	F5	0	4
48	J8	0	3
49	G5	0	4
49	K8	0	4
51	M8	0	4
54	M5	0	3
54	Q8	0	3
All	All	0	163

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	15	94	HIS	C-O	-11.07	1.18	1.23
23	2K	8	4SU	O3'-P	5.84	1.62	1.56
23	2L	8	4SU	O3'-P	5.38	1.61	1.56
29	21	135	HIS	CE1-NE2	5.36	1.38	1.32
4	32	87	GLY	C-N	5.14	1.36	1.33
29	21	135	HIS	ND1-CE1	5.10	1.37	1.32

All (147) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
36	78	15	ARG	CA-C-N	9.49	139.66	121.54
36	78	15	ARG	C-N-CA	9.49	139.66	121.54
45	G8	81	LYS	CA-C-N	9.27	149.26	127.00
45	G8	81	LYS	C-N-CA	9.27	149.26	127.00
29	29	23	VAL	N-CA-C	9.26	119.90	112.12
37	45	104	PHE	N-CA-C	8.50	120.86	110.91
36	35	65	ARG	CA-C-N	-8.28	110.55	122.64
36	35	65	ARG	C-N-CA	-8.28	110.55	122.64
49	K8	3	LEU	CA-C-N	8.21	136.48	121.70
49	K8	3	LEU	C-N-CA	8.21	136.48	121.70
26	14	1992	G	C2'-C3'-O3'	8.04	121.56	109.50
30	39	68	LYS	CA-C-N	-8.04	111.19	123.17
30	39	68	LYS	C-N-CA	-8.04	111.19	123.17
45	G8	81	LYS	C-N-CD	-7.84	103.34	120.60
32	51	153	LYS	CA-C-N	7.73	145.56	127.00
32	51	153	LYS	C-N-CA	7.73	145.56	127.00
26	1H	1992	G	C2'-C3'-O3'	7.48	120.71	109.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
33	61	110	ASP	CA-C-N	7.26	144.42	127.00
33	61	110	ASP	C-N-CA	7.26	144.42	127.00
32	59	93	GLY	N-CA-C	7.14	130.10	113.18
46	H8	59	LEU	CA-CB-CG	7.11	141.19	116.30
32	51	82	GLY	N-CA-C	7.11	130.02	113.18
17	8I	79	SER	N-CA-C	7.05	119.83	111.02
2	12	219	VAL	CA-C-N	7.02	134.34	121.70
2	12	219	VAL	C-N-CA	7.02	134.34	121.70
1	13	1498	U	C2'-C3'-O3'	7.01	120.02	109.50
28	11	272	ALA	CA-C-N	6.92	134.75	121.54
28	11	272	ALA	C-N-CA	6.92	134.75	121.54
46	H8	60	GLU	N-CA-C	-6.73	96.47	110.80
7	62	141	VAL	CA-C-N	6.62	133.61	121.70
7	62	141	VAL	C-N-CA	6.62	133.61	121.70
32	51	153	LYS	C-N-CD	-6.60	106.09	120.60
54	Q8	46	ARG	CA-C-N	6.57	133.52	121.70
54	Q8	46	ARG	C-N-CA	6.57	133.52	121.70
28	19	40	THR	N-CA-C	6.49	124.63	110.80
33	61	110	ASP	C-N-CD	-6.48	106.34	120.60
36	78	16	ARG	N-CA-C	6.48	124.60	110.80
49	G5	4	SER	CA-C-N	6.39	133.20	121.70
49	G5	4	SER	C-N-CA	6.39	133.20	121.70
9	82	119	ALA	N-CA-C	6.34	118.33	110.91
26	1H	587	C	C4'-C3'-O3'	6.34	118.91	109.40
54	M5	49	VAL	CA-C-N	6.29	133.02	121.70
54	M5	49	VAL	C-N-CA	6.29	133.02	121.70
26	14	49	A	P-O3'-C3'	6.24	129.56	120.20
36	35	46	LYS	CA-C-N	-6.24	106.59	121.80
36	35	46	LYS	C-N-CA	-6.24	106.59	121.80
26	1H	1297	C	OP2-P-O3'	-6.21	89.36	108.00
26	14	752	A	C2'-C3'-O3'	6.21	118.81	109.50
36	78	23	PRO	CA-C-N	-6.19	109.27	121.41
36	78	23	PRO	C-N-CA	-6.19	109.27	121.41
11	2I	54	ARG	N-CA-C	-6.16	97.67	110.80
28	19	272	ALA	CA-C-N	6.16	133.30	121.54
28	19	272	ALA	C-N-CA	6.16	133.30	121.54
32	51	156	ALA	CA-C-N	6.15	133.28	121.54
32	51	156	ALA	C-N-CA	6.15	133.28	121.54
19	AA	67	VAL	N-CA-C	-6.14	101.25	109.30
26	14	1786	A	N9-C1'-C2'	6.07	123.11	114.00
29	21	117	MET	CA-C-N	5.98	132.96	121.54
29	21	117	MET	C-N-CA	5.98	132.96	121.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	13	49	U	C2'-C3'-O3'	5.95	118.42	109.50
32	51	87	LEU	N-CA-C	5.93	123.43	110.80
48	J8	77	ALA	CA-C-N	5.93	132.37	121.70
48	J8	77	ALA	C-N-CA	5.93	132.37	121.70
40	B8	13	ARG	N-CA-C	5.91	127.54	111.00
1	13	49	U	P-O3'-C3'	5.89	129.04	120.20
26	14	2275	C	C4'-C3'-O3'	5.88	118.22	109.40
26	1H	138	G	N9-C1'-C2'	5.88	120.81	112.00
26	1H	222	A	P-O3'-C3'	5.88	129.01	120.20
44	B5	40	LYS	CA-C-N	-5.87	113.27	122.08
44	B5	40	LYS	C-N-CA	-5.87	113.27	122.08
37	88	104	PHE	N-CA-C	5.83	123.22	110.80
48	F5	84	GLY	CA-C-N	5.76	132.07	121.70
48	F5	84	GLY	C-N-CA	5.76	132.07	121.70
52	J5	53	ALA	CA-C-O	5.75	128.09	119.23
25	4L	12	A	O4'-C1'-N9	5.72	116.78	108.20
37	88	84	GLY	CA-C-N	5.71	131.97	121.70
37	88	84	GLY	C-N-CA	5.71	131.97	121.70
26	1H	2346	A	O4'-C1'-N9	5.71	116.76	108.20
29	29	187	ALA	N-CA-C	5.69	117.57	110.91
1	1G	1498	U	C2'-C3'-O3'	5.68	118.02	109.50
14	5I	12	ARG	CA-C-N	5.66	135.61	121.80
14	5I	12	ARG	C-N-CA	5.66	135.61	121.80
1	1G	266	G	C2'-C3'-O3'	5.66	117.98	109.50
28	11	272	ALA	N-CA-C	5.65	122.84	110.80
40	B8	38	ASN	N-CA-CB	-5.64	107.73	114.17
26	1H	1022	G	C2'-C3'-O3'	5.64	117.96	109.50
31	49	2	PRO	N-CA-CB	5.62	109.18	103.00
40	75	13	ARG	N-CA-C	-5.62	107.43	114.56
26	14	752	A	P-O3'-C3'	5.59	128.59	120.20
26	1H	1786	A	N9-C1'-C2'	5.56	122.34	114.00
30	39	67	GLN	CA-C-N	-5.54	114.91	121.90
30	39	67	GLN	C-N-CA	-5.54	114.91	121.90
26	1H	1899	G	O3'-P-O5'	-5.51	95.73	104.00
30	39	78	ILE	CA-C-N	-5.50	114.09	122.28
30	39	78	ILE	C-N-CA	-5.50	114.09	122.28
28	19	271	ILE	N-CA-C	5.48	120.73	109.34
40	75	6	LEU	N-CA-C	-5.46	95.70	111.00
12	3A	104	VAL	CA-C-N	5.46	131.97	121.54
12	3A	104	VAL	C-N-CA	5.46	131.97	121.54
46	H8	6	LYS	N-CA-C	-5.42	99.25	110.80
26	1H	845	G	P-O3'-C3'	5.38	128.27	120.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
26	1H	1573	G	OP1-P-O3'	-5.36	91.91	108.00
1	1G	266	G	P-O3'-C3'	5.35	128.23	120.20
26	14	71	A	C4'-C3'-O3'	5.35	117.42	109.40
26	1H	1799	G	C2'-C3'-O3'	5.31	117.47	109.50
29	21	79	ARG	N-CA-C	5.29	122.08	110.80
27	16	44	G	P-O3'-C3'	5.28	128.12	120.20
26	1H	195	A	P-O3'-C3'	5.28	128.12	120.20
33	69	124	GLY	N-CA-C	5.27	117.54	110.43
26	14	2275	C	P-O3'-C3'	5.26	128.09	120.20
26	1H	2712	U	O4'-C1'-N1	5.22	116.04	108.20
28	11	38	LYS	CA-C-N	5.22	131.10	121.70
28	11	38	LYS	C-N-CA	5.22	131.10	121.70
50	L8	8	LEU	CA-C-N	-5.22	116.31	122.36
50	L8	8	LEU	C-N-CA	-5.22	116.31	122.36
42	95	79	VAL	CA-C-N	-5.21	114.63	122.24
42	95	79	VAL	C-N-CA	-5.21	114.63	122.24
1	13	1	U	P-O3'-C3'	5.21	128.02	120.20
26	1H	1558	A	P-O3'-C3'	5.20	127.99	120.20
26	14	2357	U	O5'-P-OP2	-5.19	92.42	108.00
53	L5	45	ALA	CA-C-N	-5.18	117.33	122.77
53	L5	45	ALA	C-N-CA	-5.18	117.33	122.77
11	2A	117	ASN	N-CA-C	5.18	116.97	110.91
26	14	1819	A	C4'-C3'-O3'	5.16	117.14	109.40
32	51	86	GLU	N-CA-C	5.16	121.78	110.80
1	13	687	A	P-O3'-C3'	5.14	127.92	120.20
33	61	134	PRO	N-CA-C	5.13	123.05	112.47
34	58	21	LYS	CA-C-N	-5.13	111.74	121.54
34	58	21	LYS	C-N-CA	-5.13	111.74	121.54
1	1G	5	U	C2'-C3'-O3'	5.12	117.17	109.50
34	58	95	PRO	N-CA-C	-5.12	101.93	112.47
19	AI	40	ILE	CA-C-N	5.11	131.59	122.13
19	AI	40	ILE	C-N-CA	5.11	131.59	122.13
48	J8	85	LEU	CA-CB-CG	5.11	134.19	116.30
26	14	752	A	C4'-C3'-O3'	5.08	117.02	109.40
39	65	85	VAL	CA-C-N	-5.07	111.85	121.54
39	65	85	VAL	C-N-CA	-5.07	111.85	121.54
32	51	85	LYS	CA-C-N	5.04	131.17	121.54
32	51	85	LYS	C-N-CA	5.04	131.17	121.54
42	95	97	LYS	CA-C-N	-5.04	113.43	121.44
42	95	97	LYS	C-N-CA	-5.04	113.43	121.44
1	13	1157	A	P-O3'-C3'	5.03	127.75	120.20
1	13	687	A	C2'-C3'-O3'	5.03	117.05	109.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	1E	187	LEU	CA-CB-CG	5.03	133.91	116.30
26	1H	750	A	OP1-P-O3'	-5.03	92.92	108.00
29	29	22	PRO	CA-C-N	-5.01	117.51	122.77
29	29	22	PRO	C-N-CA	-5.01	117.51	122.77

There are no chirality outliers.

All (163) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
28	11	113	VAL	Peptide
28	11	122	ASP	Peptide
28	11	237	GLU	Peptide
28	11	238	GLY	Peptide
2	12	128	GLU	Peptide
2	12	15	VAL	Peptide
2	12	19	HIS	Peptide
2	12	219	VAL	Peptide
2	12	22	LYS	Peptide
2	12	222	ILE	Peptide
28	19	27	THR	Peptide
28	19	28	GLU	Peptide
10	1A	87	THR	Peptide
2	1E	11	LEU	Peptide
2	1E	15	VAL	Peptide
2	1E	237	ALA	Peptide
29	21	128	SER	Peptide
29	21	153	GLY	Peptide
29	21	186	GLY	Peptide
29	21	203	LYS	Peptide
29	21	56	PRO	Peptide
29	21	68	ALA	Peptide
3	22	14	ILE	Peptide
3	22	86	VAL	Peptide
29	29	117	MET	Peptide
29	29	130	GLY	Peptide
29	29	201	THR	Peptide
29	29	53	PRO	Peptide
29	29	61	ARG	Peptide
29	29	77	ILE	Peptide
11	2I	106	LYS	Peptide
11	2I	53	SER	Peptide
11	2I	54	ARG	Peptide

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Mol	Chain	Res	Type	Group
30	31	127	GLU	Peptide
30	31	132	VAL	Peptide
30	31	47	GLY	Peptide
4	32	88	VAL	Peptide
4	32	90	GLY	Peptide
36	35	35	HIS	Peptide
36	35	54	GLY	Peptide
36	35	70	GLN	Peptide
30	39	12	LEU	Peptide
30	39	123	LEU	Peptide
30	39	14	PRO	Peptide
30	39	20	LEU	Peptide
30	39	89	VAL	Peptide
12	3A	47	LYS	Peptide
12	3I	104	VAL	Peptide
12	3I	47	LYS	Peptide
12	3I	87	GLY	Peptide
37	45	26	TYR	Peptide
37	45	58	PHE	Peptide
37	45	78	PRO	Peptide
37	45	84	GLY	Peptide
37	45	89	ASN	Peptide
31	49	116	ASP	Peptide
31	49	36	LYS	Peptide
13	4A	105	THR	Peptide
13	4A	66	LEU	Peptide
13	4A	82	MET	Peptide
13	4A	83	ASP	Peptide
5	4E	114	GLY	Peptide
13	4I	100	GLY	Peptide
13	4I	11	ARG	Peptide
32	51	137	ASP	Peptide
32	51	152	ARG	Peptide
32	51	156	ALA	Peptide
32	51	170	ARG	Peptide
34	58	56	ASN	Peptide
34	58	95	PRO	Peptide
32	59	150	ALA	Peptide
32	59	91	GLY	Peptide
14	5A	26	ARG	Peptide
14	5A	27	CYS	Peptide
14	5A	28	GLY	Peptide

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Mol	Chain	Res	Type	Group
33	61	11	ASN	Peptide
33	61	112	LYS	Peptide
33	61	133	HIS	Peptide
33	61	134	PRO	Peptide
33	61	82	ARG	Peptide
39	65	53	SER	Peptide
33	69	112	LYS	Peptide
33	69	142	VAL	Peptide
33	69	143	SER	Peptide
40	75	10	VAL	Peptide
40	75	12	SER	Peptide
36	78	11	GLY	Peptide
36	78	115	LEU	Peptide
36	78	24	GLY	Peptide
36	78	35	HIS	Peptide
36	78	70	GLN	Peptide
16	7A	82	GLN	Peptide
9	82	117	HIS	Peptide
41	85	90	VAL	Peptide
41	85	98	LEU	Peptide
37	88	139	GLU	Peptide
37	88	58	PHE	Peptide
9	8E	110	GLU	Peptide
9	8E	4	TYR	Peptide
42	95	87	HIS	Peptide
42	95	98	GLU	Peptide
38	98	8	ARG	Peptide
39	A8	106	ARG	Peptide
19	AA	11	VAL	Peptide
19	AA	13	ASP	Peptide
19	AA	3	ARG	Peptide
19	AA	32	LYS	Peptide
19	AA	66	MET	Peptide
19	AA	8	GLY	Peptide
19	AA	9	VAL	Peptide
44	B5	50	LYS	Peptide
40	B8	112	ARG	Peptide
40	B8	12	SER	Peptide
40	B8	58	ASN	Peptide
20	BA	101	GLY	Peptide
20	BA	11	SER	Peptide
20	BA	6	PRO	Peptide

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Mol	Chain	Res	Type	Group
20	BI	95	ALA	Peptide
41	C8	90	VAL	Peptide
41	C8	92	ARG	Peptide
41	C8	95	LEU	Peptide
41	C8	96	ALA	Peptide
46	D5	115	GLY	Peptide
46	D5	140	ASP	Peptide
46	D5	170	THR	Peptide
46	D5	51	ALA	Peptide
46	D5	52	SER	Peptide
46	D5	60	GLU	Peptide
42	D8	36	PRO	Peptide
42	D8	43	GLU	Peptide
48	F5	28	GLY	Peptide
48	F5	53	VAL	Peptide
48	F5	89	GLU	Peptide
48	F5	91	LYS	Peptide
49	G5	15	LYS	Peptide
49	G5	4	SER	Peptide
49	G5	43	GLN	Peptide
49	G5	45	SER	Peptide
45	G8	53	PRO	Peptide
45	G8	54	LYS	Peptide
45	G8	99	CYS	Peptide
46	H8	117	LEU	Peptide
46	H8	143	GLY	Peptide
46	H8	158	PRO	Peptide
46	H8	60	GLU	Peptide
46	H8	63	ASP	Peptide
48	J8	53	VAL	Peptide
48	J8	84	GLY	Peptide
48	J8	86	SER	Peptide
49	K8	17	SER	Peptide
49	K8	3	LEU	Peptide
49	K8	46	GLN	Peptide
49	K8	47	ASN	Peptide
54	M5	40	GLU	Peptide
54	M5	49	VAL	Peptide
54	M5	51	ALA	Peptide
51	M8	37	SER	Peptide
51	M8	40	HIS	Peptide
51	M8	42	PHE	Peptide

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Mol	Chain	Res	Type	Group
51	M8	44	THR	Peptide
54	Q8	30	ARG	Peptide
54	Q8	49	VAL	Peptide
54	Q8	51	ALA	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	32246	0	16276	651	0
1	1G	32028	0	16165	612	0
2	12	1696	0	1730	106	0
2	1E	1874	0	1926	86	0
3	22	1546	0	1608	82	0
3	2E	1605	0	1668	41	0
4	32	1698	0	1761	88	1
4	3E	1698	0	1760	70	0
5	42	1141	0	1199	61	0
5	4E	1142	0	1204	36	0
6	52	842	0	857	19	0
6	5E	837	0	852	20	1
7	62	1110	0	1163	52	0
7	6E	1242	0	1286	45	0
8	72	1107	0	1165	37	0
8	7E	1115	0	1177	46	0
9	82	953	0	983	55	0
9	8E	1000	0	1031	60	0
10	1A	801	0	849	53	0
10	1I	749	0	767	42	0
11	2A	835	0	847	30	0
11	2I	823	0	832	32	0
12	3A	956	0	1046	32	0
12	3I	956	0	1046	36	0
13	4A	879	0	935	49	0
13	4I	942	0	997	58	0
14	5A	486	0	526	23	0
14	5I	491	0	529	27	0
15	6A	729	0	768	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
15	6I	729	0	768	30	0
16	7A	705	0	725	19	0
16	7I	700	0	720	28	0
17	8A	823	0	891	33	0
17	8I	834	0	904	33	0
18	9A	554	0	609	16	0
18	9I	549	0	607	26	0
19	AA	510	0	507	33	0
19	AI	665	0	686	37	0
20	BA	778	0	863	27	0
20	BI	746	0	843	47	0
21	1B	188	0	195	16	0
21	1F	199	0	208	10	0
22	1K	1593	0	813	49	0
22	1L	1593	0	813	48	0
23	2K	1646	0	844	19	0
23	2L	1646	0	842	32	0
24	3K	1537	0	779	46	0
25	4K	391	0	197	7	0
25	4L	303	0	154	15	0
26	14	60561	0	30527	995	0
26	1H	61381	0	30944	1095	0
27	16	2617	0	1328	45	0
27	1J	2617	0	1328	70	0
28	11	2120	0	2197	61	0
28	19	2125	0	2199	73	0
29	21	1556	0	1612	76	0
29	29	1563	0	1629	85	0
30	31	1585	0	1632	76	0
30	39	1602	0	1649	88	0
31	41	1457	0	1514	71	0
31	49	1459	0	1507	62	0
32	51	1328	0	1396	47	0
32	59	1295	0	1366	82	0
33	61	1131	0	1218	49	0
33	69	1131	0	1218	47	0
34	15	1096	0	1168	55	0
34	58	995	0	1077	39	0
35	25	932	0	996	34	0
35	68	932	0	996	22	0
36	35	1122	0	1206	73	0
36	78	1127	0	1208	67	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
37	45	1099	0	1154	70	0
37	88	1117	0	1168	55	0
38	55	967	0	1033	45	0
38	98	967	0	1033	40	0
39	65	876	0	938	72	0
39	A8	881	0	943	46	0
40	75	1164	0	1221	61	0
40	B8	1128	0	1183	60	0
41	85	959	0	1019	62	0
41	C8	950	0	1011	49	0
42	95	770	0	838	34	0
42	D8	774	0	849	30	0
43	A5	886	0	948	25	0
43	E8	876	0	941	26	0
44	B5	735	0	785	21	0
44	F8	750	0	814	20	0
45	C5	396	0	444	18	0
45	G8	734	0	821	38	0
46	D5	1411	0	1436	73	0
46	H8	1365	0	1391	64	0
47	E5	603	0	620	23	0
47	I8	611	0	631	28	0
48	F5	737	0	813	34	0
48	J8	747	0	817	37	0
49	G5	576	0	625	33	0
49	K8	575	0	634	34	0
50	H5	459	0	512	19	0
50	L8	459	0	512	10	0
51	M8	475	0	465	33	0
52	J5	434	0	454	22	0
52	N8	369	0	388	23	0
53	L5	406	0	438	10	0
53	P8	401	0	436	12	0
54	M5	516	0	582	22	0
54	Q8	516	0	582	40	0
55	3L	1538	0	781	38	0
56	11	1	0	0	0	0
56	13	205	0	0	0	0
56	14	435	0	0	0	0
56	16	15	0	0	0	0
56	19	1	0	0	0	0
56	1B	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
56	1G	155	0	0	0	0
56	1H	622	0	0	0	0
56	1J	6	0	0	0	0
56	1K	1	0	0	0	0
56	21	4	0	0	0	0
56	25	1	0	0	0	0
56	29	3	0	0	0	0
56	2A	1	0	0	0	0
56	2I	1	0	0	0	0
56	2K	2	0	0	0	0
56	2L	2	0	0	0	0
56	31	2	0	0	0	0
56	35	3	0	0	0	0
56	39	1	0	0	0	0
56	3E	1	0	0	0	0
56	41	1	0	0	0	0
56	42	1	0	0	0	0
56	45	2	0	0	0	0
56	4A	1	0	0	0	0
56	4L	1	0	0	0	0
56	55	1	0	0	0	0
56	5E	1	0	0	0	0
56	5I	2	0	0	0	0
56	68	2	0	0	0	0
56	78	2	0	0	0	0
56	85	1	0	0	0	0
56	88	3	0	0	0	0
56	8I	1	0	0	0	0
56	98	1	0	0	0	0
56	9A	1	0	0	0	0
56	BA	2	0	0	0	0
56	BI	2	0	0	0	0
56	D8	1	0	0	0	0
56	E5	1	0	0	0	0
56	I8	2	0	0	0	0
56	P8	1	0	0	0	0
56	Q8	1	0	0	0	0
57	32	8	0	0	1	0
57	3E	8	0	0	1	0
58	5A	1	0	0	0	0
58	5I	1	0	0	0	0
59	11	11	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
59	13	339	0	0	42	0
59	14	730	0	0	89	0
59	15	1	0	0	0	0
59	16	19	0	0	0	0
59	19	10	0	0	1	0
59	1A	1	0	0	0	0
59	1E	1	0	0	1	0
59	1F	2	0	0	2	0
59	1G	289	0	0	25	0
59	1H	1047	0	0	184	0
59	1I	3	0	0	1	0
59	1K	1	0	0	0	0
59	21	8	0	0	0	0
59	25	6	0	0	0	0
59	29	2	0	0	0	0
59	2L	6	0	0	0	0
59	31	7	0	0	0	0
59	32	2	0	0	0	0
59	35	6	0	0	0	0
59	39	5	0	0	0	0
59	3E	2	0	0	0	0
59	3I	1	0	0	0	0
59	42	1	0	0	0	0
59	45	4	0	0	0	0
59	4E	2	0	0	0	0
59	4I	2	0	0	1	0
59	4K	2	0	0	0	0
59	4L	3	0	0	1	0
59	52	4	0	0	0	0
59	58	3	0	0	0	0
59	5I	1	0	0	0	0
59	6E	1	0	0	0	0
59	6I	1	0	0	0	0
59	75	1	0	0	0	0
59	78	6	0	0	0	0
59	7A	4	0	0	1	0
59	7I	3	0	0	0	0
59	8E	2	0	0	0	0
59	95	1	0	0	0	0
59	9A	2	0	0	1	0
59	B5	3	0	0	0	0
59	BA	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
59	D8	1	0	0	0	0
59	E8	1	0	0	0	0
59	G8	1	0	0	0	0
59	H5	3	0	0	1	0
59	I8	2	0	0	1	0
59	J8	1	0	0	0	0
59	L8	4	0	0	0	0
59	M5	2	0	0	0	0
59	P8	1	0	0	0	0
59	Q8	2	0	0	1	0
All	All	294252	0	195096	6898	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 15.

All (6898) 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)
26:1H:810:U:OP1	59:1H:3720:HOH:O	1.68	1.09
29:29:54:GLN:HA	29:29:74:PRO:HA	1.35	1.08
26:14:1604:C:OP2	59:14:3509:HOH:O	1.71	1.07
37:45:27:VAL:HB	37:45:28:ALA:HA	1.32	1.07
26:14:2113:U:H3'	26:14:2114:A:H4'	1.34	1.06
26:1H:862:G:OP2	59:1H:3723:HOH:O	1.75	1.04
26:1H:730:C:OP2	59:1H:3721:HOH:O	1.74	1.03
37:45:135:ASP:H	37:45:136:ALA:HA	1.19	1.03
26:1H:1665:A:OP2	59:1H:3722:HOH:O	1.74	1.02
26:1H:2248:C:OP2	59:1H:3724:HOH:O	1.77	1.01
26:1H:763:G:OP1	59:1H:3725:HOH:O	1.78	1.00
45:G8:87:LYS:H	45:G8:94:LYS:HG2	1.23	1.00
26:1H:1764:G:OP2	59:1H:3727:HOH:O	1.80	0.99
26:1H:2308:G:H1	26:1H:2311:A:H2	1.01	0.99
26:14:330:A:H2	26:14:1210:A:HO2'	1.00	0.99
26:1H:1496:A:H8	26:1H:1577:C:HO2'	0.99	0.98
26:1H:2711:A:OP2	59:1H:3726:HOH:O	1.79	0.98
26:1H:1771:C:HO2'	26:1H:1786:A:H8	1.02	0.98
26:1H:2712(A):A:OP2	59:1H:3728:HOH:O	1.82	0.97
26:14:2414:G:H21	36:35:67:MET:HE1	1.30	0.97
2:12:16:HIS:HB3	2:12:209:ARG:HE	1.30	0.97
26:1H:733:G:OP2	59:1H:3730:HOH:O	1.84	0.96
26:14:2210:G:H3'	26:14:2211:G:C8	2.01	0.96

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1H:2712(A):A:OP1	59:1H:3729:HOH:O	1.84	0.95
26:1H:2867:G:OP2	40:B8:119:LYS:NZ	1.99	0.95
26:14:2712(A):A:OP1	59:14:3511:HOH:O	1.83	0.95
49:G5:4:SER:HA	49:G5:6:VAL:H	1.30	0.95
1:13:1197:G:OP1	59:13:1906:HOH:O	1.84	0.94
1:13:1502:A:H2	1:13:1505:G:H1	1.12	0.94
26:1H:1204:A:H62	26:1H:1241:A:H2	1.13	0.94
26:1H:1658:C:OP1	59:1H:3731:HOH:O	1.85	0.94
33:61:112:LYS:HB2	33:61:113:ARG:HG3	1.48	0.94
26:1H:2498:C:OP2	59:1H:3733:HOH:O	1.86	0.93
24:3K:76:A:H8	26:1H:2394:C:H42	1.16	0.92
26:1H:2577:A:OP1	59:1H:3732:HOH:O	1.85	0.92
26:1H:270(I):G:H1	26:1H:270(Q):C:H42	1.06	0.92
26:1H:138:G:N2	44:F8:44:GLU:OE2	2.03	0.92
1:13:970:C:OP2	59:13:1907:HOH:O	1.85	0.92
1:13:346:G:OP1	40:B8:41:ARG:NH2	2.03	0.91
26:1H:990:A:OP2	59:1H:3734:HOH:O	1.86	0.91
26:14:1689:A:H62	26:14:1698:A:H2	1.15	0.91
26:1H:731:C:OP2	59:1H:3721:HOH:O	1.86	0.91
26:1H:453:C:OP1	59:1H:3735:HOH:O	1.87	0.91
26:1H:1689:A:H62	26:1H:1698:A:H2	1.12	0.91
32:59:98:LEU:HB2	32:59:126:PRO:HB3	1.52	0.91
1:13:1054:C:OP2	59:13:1908:HOH:O	1.89	0.91
26:1H:1671:U:OP2	59:1H:3737:HOH:O	1.88	0.91
22:1L:7:A:O2'	22:1L:50:G:OP1	1.87	0.91
22:1L:56:C:H3'	22:1L:57:G:H5"	1.51	0.91
26:1H:607:U:H3	26:1H:621:A:H2	1.18	0.91
26:14:67:U:H3	26:14:74:A:H2	1.18	0.91
8:7E:87:SER:HB2	8:7E:93:VAL:HB	1.52	0.90
26:1H:574:C:OP1	59:1H:3738:HOH:O	1.88	0.90
46:H8:52:SER:O	46:H8:54:HIS:N	2.03	0.90
49:K8:47:ASN:O	49:K8:49:LYS:N	2.04	0.90
1:1G:1305:G:H22	1:1G:1331:G:H2'	1.34	0.90
26:14:2227:A:OP2	59:14:3513:HOH:O	1.88	0.90
26:14:1603:A:OP1	59:14:3509:HOH:O	1.87	0.90
26:14:1899:G:H21	26:14:1902:C:N4	1.69	0.90
1:13:664:G:H22	1:13:741:G:H1	1.11	0.90
48:F5:91:LYS:O	48:F5:93:GLU:N	2.04	0.90
26:1H:1627:G:OP1	59:1H:3740:HOH:O	1.90	0.90
30:31:29:ASN:H	30:31:112:MET:HE1	1.36	0.90
26:1H:800:A:OP1	59:1H:3739:HOH:O	1.89	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1H:847:U:OP2	59:1H:3736:HOH:O	1.87	0.89
32:59:59:ARG:HG2	32:59:62:LYS:HE3	1.55	0.89
1:13:964:A:OP1	59:13:1909:HOH:O	1.90	0.89
26:14:801:G:OP2	59:14:3512:HOH:O	1.88	0.89
29:29:60:ASN:HB2	29:29:62:PRO:HD2	1.54	0.89
1:1G:975:A:H4'	1:1G:976:G:H5"	1.55	0.88
27:1J:80:U:H2'	27:1J:81:G:H21	1.38	0.88
32:59:6:ARG:HB3	32:59:66:GLY:HA2	1.55	0.88
26:1H:2287:A:H62	26:1H:2344:U:H3	1.19	0.88
22:1L:51:C:N4	22:1L:63:G:O6	2.06	0.88
26:14:1771:C:HO2'	26:14:1786:A:H8	0.92	0.88
26:1H:592:G:H21	54:Q8:4:MET:HE1	1.38	0.88
26:14:84:A:N6	26:14:102:G:O2'	2.06	0.88
26:1H:860:U:H5	26:1H:917:A:C2	1.91	0.88
26:1H:450:G:O6	59:1H:3735:HOH:O	1.92	0.87
26:1H:748:G:OP2	59:1H:3742:HOH:O	1.91	0.87
26:1H:1520:U:OP2	59:1H:3743:HOH:O	1.92	0.87
1:1G:1502:A:H2	1:1G:1505:G:H1	1.20	0.87
1:13:394:G:O6	59:13:1910:HOH:O	1.93	0.87
36:78:63:PRO:HB2	54:Q8:30:ARG:HH21	1.38	0.87
26:1H:1138:G:H21	34:58:106:MET:HE3	1.39	0.87
37:45:135:ASP:N	37:45:136:ALA:HA	1.87	0.87
26:1H:409:C:OP1	59:1H:3744:HOH:O	1.92	0.87
26:1H:734:A:OP2	59:1H:3741:HOH:O	1.91	0.87
1:1G:963:G:H21	10:1A:55:LYS:HD3	1.39	0.87
26:14:1395:A:OP1	59:14:3509:HOH:O	1.93	0.86
26:1H:1009:A:OP2	34:58:37:LYS:NZ	2.08	0.86
26:1H:1041:C:H42	26:1H:1114:G:H1	1.24	0.86
26:1H:1189:A:OP2	59:1H:3746:HOH:O	1.92	0.86
26:14:1899:G:H21	26:14:1902:C:H42	1.22	0.86
9:82:28:VAL:HG22	9:82:63:ILE:HB	1.54	0.86
26:1H:452:G:OP2	59:1H:3747:HOH:O	1.94	0.86
26:1H:945:A:OP1	59:1H:3745:HOH:O	1.92	0.86
26:1H:1653:G:H3'	38:98:2:ARG:HG3	1.57	0.86
34:15:56:ASN:H	34:15:125:GLY:HA3	1.39	0.86
26:14:1106:G:H3'	26:14:1107:G:H8	1.40	0.86
26:14:1209:G:OP2	59:14:3514:HOH:O	1.92	0.86
26:14:1313:U:OP1	59:14:3516:HOH:O	1.94	0.86
26:14:2705:A:OP2	59:14:3515:HOH:O	1.93	0.86
28:19:69:ARG:NH2	28:19:128:GLY:O	2.09	0.86
26:1H:2714:G:OP2	59:1H:3728:HOH:O	1.94	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:88:35:VAL:HG13	37:88:130:LYS:HB3	1.58	0.85
26:1H:270(L):U:C2	33:61:50:ARG:HG2	2.11	0.85
26:1H:1678:G:H22	26:1H:1989:G:H22	1.23	0.85
26:14:2210:G:H3'	26:14:2211:G:H8	1.40	0.85
1:13:1352:C:OP1	59:13:1911:HOH:O	1.94	0.85
26:1H:1055:G:H1	26:1H:1104:C:H42	1.21	0.85
26:14:1689:A:N3	59:14:3542:HOH:O	2.10	0.85
26:14:1757:U:H3	26:14:1762:A:H2	1.22	0.85
26:1H:759:G:OP1	59:1H:3751:HOH:O	1.95	0.85
28:11:182:LEU:H	28:11:272:ALA:HB3	1.41	0.85
26:1H:1899:G:H22	26:1H:1902:C:H5	1.21	0.85
26:1H:2656:U:H3	26:1H:2665:A:H2	1.25	0.85
1:1G:278:G:OP2	17:8A:92:ARG:NH2	2.08	0.85
31:49:161:THR:HG22	31:49:163:ALA:H	1.42	0.85
26:1H:1633:G:O6	59:1H:3749:HOH:O	1.94	0.85
26:14:654(B):C:O2'	26:14:654(S):G:N1	2.09	0.85
26:1H:49:A:N7	26:1H:120:U:H5	1.75	0.84
26:14:792:G:O6	59:14:3517:HOH:O	1.95	0.84
26:14:676:A:H8	26:14:2069:G:H21	1.21	0.84
2:12:91:PRO:HG3	2:12:154:LEU:HB2	1.60	0.84
1:13:953:G:OP2	59:13:1912:HOH:O	1.95	0.84
26:1H:392:C:OP1	59:1H:3744:HOH:O	1.94	0.84
26:14:141:A:H8	26:14:1595:G:H21	1.24	0.84
55:3L:50:G:H1	55:3L:64:C:H42	1.25	0.84
26:1H:571:A:OP2	59:1H:3753:HOH:O	1.96	0.84
1:1G:1204:A:OP1	14:5A:3:ARG:NH1	2.10	0.83
26:14:1952:A:C6	35:25:22:ILE:HD11	2.12	0.83
32:59:137:ASP:HB2	32:59:140:LYS:HB2	1.59	0.83
41:85:90:VAL:HG22	42:95:38:LEU:HD11	1.58	0.83
1:13:1034:G:N2	1:13:1035:A:N7	2.24	0.83
1:13:963:G:H1	1:13:972:C:H42	1.24	0.83
26:1H:574:C:OP2	59:1H:3752:HOH:O	1.95	0.83
29:21:55:ASN:HD21	29:21:76:ARG:HB3	1.43	0.83
26:14:1330:C:OP1	59:14:3522:HOH:O	1.96	0.83
1:13:153:C:H42	1:13:168:G:H1	1.26	0.83
2:1E:87:ARG:HH21	2:1E:232:PRO:HB3	1.41	0.83
26:1H:1651:G:O6	59:1H:3748:HOH:O	1.94	0.83
26:1H:2069:G:O3'	59:1H:3756:HOH:O	1.97	0.83
26:14:1990:C:OP2	59:14:3519:HOH:O	1.96	0.83
13:4I:3:ARG:HD3	13:4I:7:VAL:HG13	1.60	0.83
26:1H:676:A:H8	26:1H:2069:G:H21	1.26	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1G:1248:A:N3	9:82:70:LYS:NZ	2.26	0.83
1:13:1198:G:N7	59:13:1929:HOH:O	2.12	0.83
26:1H:2136:C:N4	26:1H:2155:G:O6	2.10	0.83
28:19:182:LEU:H	28:19:272:ALA:HB3	1.42	0.83
26:1H:1664:A:OP1	59:1H:3755:HOH:O	1.97	0.83
21:1F:5:ASP:OD2	59:1F:101:HOH:O	1.96	0.83
26:1H:1007:C:OP2	59:1H:3757:HOH:O	1.97	0.83
1:1G:448:A:OP2	1:1G:485:G:N2	2.09	0.83
1:13:1198:G:OP2	59:13:1906:HOH:O	1.94	0.83
26:14:733:G:OP2	59:14:3520:HOH:O	1.96	0.82
26:1H:778:G:O6	59:1H:3750:HOH:O	1.95	0.82
8:72:120:THR:HG22	8:72:123:GLU:H	1.44	0.82
1:13:1304:G:OP2	59:13:1913:HOH:O	1.97	0.82
26:14:1301:A:OP1	59:14:3518:HOH:O	1.95	0.82
23:2K:47:7MG:H81	23:2K:48:U:H5	1.45	0.82
4:3E:50:ARG:HD2	4:3E:51:PRO:HD2	1.61	0.82
46:H8:128:VAL:HB	46:H8:161:VAL:HG12	1.60	0.82
4:3E:15:GLU:OE1	4:3E:66:ARG:NH1	2.13	0.82
9:82:112:LYS:HA	9:82:119:ALA:HB2	1.62	0.82
26:1H:1641:A:OP2	59:1H:3761:HOH:O	1.98	0.81
2:12:219:VAL:HA	2:12:220:ASP:HB3	1.62	0.81
46:D5:52:SER:O	46:D5:54:HIS:N	2.12	0.81
26:1H:1061:U:H4'	26:1H:1070:A:H1'	1.62	0.81
26:1H:1102:C:H2'	26:1H:1103:A:H8	1.45	0.81
26:1H:1728:G:H8	26:1H:1732:A:H62	1.27	0.81
35:25:7:TYR:HE1	35:25:20:MET:HE3	1.45	0.81
1:13:262:A:H2'	1:13:263:A:C8	2.15	0.81
1:13:1133:G:H2'	1:13:1134:G:H8	1.45	0.81
26:1H:2502:G:OP2	59:1H:3759:HOH:O	1.98	0.81
26:14:517:C:OP1	52:J5:16:ARG:NH2	2.13	0.81
26:14:2292:C:OP1	39:65:17:ARG:NH2	2.13	0.81
1:13:601:C:H2'	1:13:602:A:H8	1.45	0.81
45:G8:28:LYS:HE3	45:G8:40:GLU:HB2	1.61	0.81
29:29:36:ARG:HH21	29:29:89:ASP:HB3	1.44	0.81
26:1H:404:C:OP1	59:1H:3754:HOH:O	1.96	0.81
26:1H:761:A:N7	59:1H:3793:HOH:O	2.11	0.81
26:1H:762:U:OP1	59:1H:3762:HOH:O	1.98	0.81
29:29:37:ARG:NH1	29:29:80:GLU:OE2	2.14	0.81
26:1H:963:U:OP1	59:1H:3766:HOH:O	1.99	0.81
26:1H:1186:G:OP2	59:1H:3760:HOH:O	1.98	0.81
47:I8:53:MET:HG3	47:I8:59:LEU:HD23	1.63	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:M8:14:ILE:HG22	51:M8:24:THR:HG22	1.63	0.81
1:13:1126:U:O2'	1:13:1281:U:O4'	1.99	0.80
26:1H:1022:G:N2	26:1H:1023:U:O4	2.13	0.80
32:59:59:ARG:HA	32:59:62:LYS:HG2	1.63	0.80
20:BI:22:ARG:O	20:BI:26:ASN:ND2	2.14	0.80
22:1L:74:C:H1'	26:14:2555:U:H3	1.46	0.80
26:1H:879:G:N2	26:1H:898:C:O2	2.14	0.80
40:B8:77:PRO:HG2	40:B8:80:SER:HB2	1.64	0.80
13:4I:45:VAL:HA	13:4I:48:LEU:HD22	1.61	0.80
26:1H:929:G:O6	59:1H:3736:HOH:O	1.98	0.80
26:14:947:G:O6	59:14:3525:HOH:O	1.99	0.80
26:1H:1349:A:OP1	59:1H:3764:HOH:O	1.99	0.80
46:D5:19:ARG:NH1	46:D5:84:GLU:O	2.14	0.80
9:8E:7:THR:O	9:8E:83:ARG:NH1	2.14	0.80
26:1H:270(K):C:O2	26:1H:270(N):G:N1	2.15	0.80
26:14:2499:C:OP2	59:14:3523:HOH:O	1.98	0.80
26:1H:780:G:H21	26:1H:783:A:H62	1.27	0.80
1:13:968:A:OP2	59:13:1914:HOH:O	1.99	0.79
10:1I:40:LEU:HB2	10:1I:69:ASN:HB2	1.62	0.79
37:45:36:ALA:HB2	37:45:103:MET:HE3	1.65	0.79
26:1H:1525:G:H2'	26:1H:1526:G:H8	1.47	0.79
28:19:30:GLU:HG3	28:19:63:ARG:NH2	1.98	0.79
26:1H:2588:G:OP1	59:1H:3763:HOH:O	1.99	0.79
46:H8:165:VAL:HB	46:H8:166:SER:HA	1.62	0.79
7:62:93:PRO:HD2	7:62:94:ARG:HH21	1.48	0.79
1:13:830:G:O6	59:13:1916:HOH:O	2.01	0.79
11:2I:22:HIS:HB3	11:2I:29:ILE:HG23	1.64	0.79
26:1H:1899:G:N2	26:1H:1902:C:H5	1.80	0.79
26:14:1633:G:O6	59:14:3526:HOH:O	2.00	0.79
26:14:1729:A:H2'	26:14:1731:G:H22	1.48	0.79
33:69:81:VAL:HG12	33:69:143:SER:HB3	1.64	0.79
26:14:161:U:H5"	26:14:171:G:H22	1.48	0.79
26:14:1383:C:O2	59:14:3527:HOH:O	2.00	0.79
26:1H:2706:G:O6	59:1H:3758:HOH:O	1.97	0.79
19:AA:3:ARG:HB2	19:AA:4:SER:HA	1.62	0.79
26:1H:2061:G:OP2	59:1H:3765:HOH:O	1.99	0.79
41:C8:92:ARG:O	41:C8:94:ASN:N	2.15	0.79
26:14:1359:A:H62	26:14:1372:U:H3	1.31	0.79
26:14:900:A:H3'	26:14:901:A:H8	1.47	0.79
30:39:116:ASP:OD2	36:35:1:MET:N	2.15	0.79
1:13:1303:C:OP1	59:13:1915:HOH:O	2.00	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:21:105:THR:OG1	29:21:199:ARG:NH2	2.16	0.78
1:1G:617:G:OP2	59:1G:1807:HOH:O	2.02	0.78
26:14:847:U:OP2	59:14:3521:HOH:O	2.01	0.78
26:14:1653:G:H3'	38:55:2:ARG:HG2	1.63	0.78
26:1H:1521:G:N7	59:1H:3811:HOH:O	2.16	0.78
26:1H:2249:U:O4	59:1H:3724:HOH:O	2.01	0.78
26:14:929:G:O6	59:14:3521:HOH:O	1.96	0.78
54:M5:40:GLU:H	54:M5:43:GLN:HG3	1.47	0.78
26:14:1022:G:H22	26:14:1142(A):A:H2	1.31	0.78
26:1H:311:A:OP2	59:1H:3767:HOH:O	2.00	0.78
26:1H:792:G:H5"	26:1H:793:A:H5'	1.66	0.78
29:21:38:THR:HB	29:21:40:GLU:HG2	1.65	0.78
5:42:102:ALA:HB1	5:42:106:PRO:HG2	1.64	0.78
26:14:1022:G:O2'	26:14:1023:U:OP2	2.00	0.78
1:13:1348:U:H3	1:13:1374:A:H2	1.29	0.78
32:51:157:TYR:H	32:51:171:LEU:HA	1.47	0.78
26:1H:1381:G:N7	59:1H:3814:HOH:O	2.16	0.78
26:14:54:G:O6	59:14:3528:HOH:O	2.01	0.78
1:1G:261:U:OP2	20:BA:79:ARG:NH2	2.17	0.78
30:31:66:PRO:O	30:31:67:GLN:HB3	1.82	0.78
1:13:158:G:H2'	1:13:159:G:H8	1.49	0.78
26:1H:1037:G:N2	26:1H:1118:C:O2	2.16	0.78
26:14:2270:G:OP2	59:14:3529:HOH:O	2.01	0.78
26:1H:946:G:OP2	59:1H:3769:HOH:O	2.01	0.77
36:78:39:LYS:HG3	36:78:45:LEU:HD22	1.65	0.77
45:G8:82:PRO:HG3	45:G8:97:ARG:HB3	1.65	0.77
26:14:2830:G:O6	59:14:3524:HOH:O	1.98	0.77
5:4E:142:LEU:O	5:4E:143:ARG:NH1	2.17	0.77
26:1H:1670:C:OP1	59:1H:3770:HOH:O	2.02	0.77
46:H8:111:VAL:HG11	46:H8:146:ILE:HG13	1.66	0.77
26:14:2378:A:H4'	39:65:23:ARG:HH11	1.49	0.77
1:1G:1023:G:H5"	1:1G:1024:G:H21	1.49	0.77
33:69:77:LEU:HA	33:69:141:LYS:HB3	1.65	0.77
26:1H:2002:G:N7	59:1H:3819:HOH:O	2.17	0.77
26:1H:2334:G:H5'	39:A8:9:ARG:HG2	1.67	0.77
7:6E:111:ARG:NH1	7:6E:113:GLU:OE2	2.18	0.77
22:1K:66:U:H5"	22:1K:67:A:H8	1.49	0.77
40:B8:12:SER:HA	40:B8:14:TYR:H	1.50	0.77
3:2E:13:GLY:HA2	14:5I:57:ARG:HH21	1.49	0.77
26:1H:860:U:H5	26:1H:917:A:H2	1.32	0.77
41:C8:65:ILE:HG13	41:C8:96:ALA:HB2	1.67	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:H8:6:LYS:N	46:H8:59:LEU:O	2.18	0.77
26:14:2227:A:N7	59:14:3556:HOH:O	2.16	0.77
28:19:68:LYS:HB3	28:19:70:TRP:CH2	2.20	0.77
7:6E:15:ASP:HB3	7:6E:20:ASP:H	1.50	0.76
26:1H:450:G:OP2	59:1H:3768:HOH:O	2.01	0.76
4:32:53:ASP:OD2	5:42:107:ARG:NH2	2.18	0.76
6:5E:100:ASN:ND2	18:9I:27:GLY:O	2.18	0.76
26:1H:2588:G:OP1	59:1H:3771:HOH:O	2.03	0.76
26:14:275:G:N2	26:14:276:A:N7	2.33	0.76
26:1H:2469:A:H2	26:1H:2481:G:H21	1.32	0.76
1:1G:993:G:O6	1:1G:1045:C:N4	2.18	0.76
1:13:1348:U:H4'	9:8E:120:ARG:HD2	1.67	0.76
2:1E:174:VAL:HG13	2:1E:184:VAL:HG11	1.66	0.76
26:1H:1900:A:H5'	26:1H:1900:A:H8	1.50	0.76
26:14:2656:U:H3	26:14:2665:A:H2	1.33	0.76
20:BA:33:ILE:O	20:BA:37:SER:OG	2.04	0.76
22:1L:52:A:H61	22:1L:62:U:H3	1.34	0.76
26:14:958:U:OP2	37:45:14:ARG:NH1	2.18	0.76
26:1H:702:G:N7	59:1H:3822:HOH:O	2.18	0.76
26:14:1413:G:O6	59:14:3530:HOH:O	2.02	0.76
12:3I:42:THR:HG22	12:3I:54:LYS:HD2	1.67	0.76
24:3K:35:G:O6	25:4K:14:A:N6	2.16	0.76
26:14:2471:C:OP2	59:14:3531:HOH:O	2.02	0.76
26:1H:2183:C:H2'	26:1H:2184:G:H8	1.51	0.76
1:1G:957:U:H1'	1:1G:960:U:H5	1.49	0.76
19:AA:9:VAL:CB	19:AA:10:PHE:HA	2.16	0.76
1:13:926:G:O2'	25:4K:12:A:N7	2.18	0.76
26:1H:2016:U:OP1	59:1H:3773:HOH:O	2.04	0.76
26:1H:2101:G:H1	26:1H:2188:C:H42	1.34	0.76
1:1G:1281:U:OP2	1:1G:1282:C:N4	2.18	0.76
49:K8:4:SER:H	49:K8:7:ARG:H	1.32	0.75
26:1H:832:G:H5'	36:78:45:LEU:HD11	1.68	0.75
26:1H:1382:G:O6	59:1H:3772:HOH:O	2.03	0.75
26:1H:2392:A:H2	26:1H:2424:C:H42	1.34	0.75
1:1G:974:A:H5'	14:5A:31:ARG:HD3	1.67	0.75
26:14:123:G:O6	59:14:3532:HOH:O	2.04	0.75
30:39:167:ALA:HB1	30:39:173:VAL:HG11	1.68	0.75
32:59:121:ILE:HD13	32:59:133:VAL:HG11	1.68	0.75
2:1E:185:ILE:HB	2:1E:199:TYR:HB2	1.67	0.75
1:1G:664:G:H22	1:1G:741:G:H1	1.33	0.75
1:13:576:G:OP1	59:13:1918:HOH:O	2.04	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:4I:23:TYR:HD2	13:4I:67:GLU:HA	1.51	0.75
5:42:43:LEU:HD22	5:42:136:MET:HG3	1.66	0.75
26:14:910:A:H62	37:45:12:GLN:HA	1.50	0.75
26:14:2032:G:H21	29:29:146:THR:HG23	1.51	0.75
1:13:1355:G:OP1	59:13:1920:HOH:O	2.05	0.75
16:7I:53:VAL:HG13	16:7I:79:VAL:HG22	1.66	0.75
2:1E:16:HIS:CE1	2:1E:213:LEU:HD12	2.21	0.75
26:1H:363(F):A:O3'	59:1H:3777:HOH:O	2.05	0.75
1:13:145:G:H1	1:13:177:C:H42	1.32	0.75
34:58:39:ARG:NH2	34:58:41:ASP:OD2	2.19	0.75
45:G8:83:THR:HG22	45:G8:84:ARG:HG2	1.68	0.75
7:62:148:ASN:ND2	7:62:148:ASN:O	2.20	0.75
26:14:2267:A:OP2	59:14:3533:HOH:O	2.05	0.75
36:35:29:LYS:HG2	36:35:30:THR:N	2.02	0.75
3:2E:58:GLU:HB2	3:2E:65:ALA:HB3	1.67	0.75
12:3I:117:ARG:HB3	12:3I:122:THR:HB	1.69	0.75
26:1H:2287:A:N6	26:1H:2344:U:H3	1.84	0.75
26:1H:2379:G:O2'	39:A8:17:ARG:NH1	2.20	0.75
40:75:91:ARG:NH1	40:75:124:ASP:OD2	2.17	0.75
51:M8:14:ILE:HG23	51:M8:21:VAL:HB	1.67	0.75
8:72:51:VAL:HG11	8:72:60:ARG:HE	1.49	0.75
22:1L:18:G:H2'	22:1L:57:G:C6	2.22	0.75
26:14:780:G:H21	26:14:783:A:H62	1.34	0.75
33:69:98:ALA:HA	33:69:109:ILE:HD11	1.69	0.75
34:15:128:HIS:ND1	34:15:129:PRO:O	2.20	0.75
50:H5:7:LYS:HG3	50:H5:34:GLU:HG2	1.68	0.75
12:3I:62:SER:HB2	12:3I:64:TYR:HD2	1.52	0.74
26:1H:818:G:OP2	59:1H:3775:HOH:O	2.04	0.74
1:1G:5:U:O2'	1:1G:6:G:OP2	2.05	0.74
26:14:990:A:H5'	26:14:990:A:H8	1.51	0.74
26:14:2681:C:H5	26:14:2725:A:H62	1.34	0.74
1:13:1224:G:OP1	59:13:1917:HOH:O	2.04	0.74
30:39:101:LEU:O	30:39:106:ARG:NH1	2.19	0.74
35:25:115:VAL:HG13	35:25:121:VAL:HG21	1.70	0.74
26:1H:1313:U:OP1	59:1H:3778:HOH:O	2.05	0.74
19:AA:12:ASP:OD1	19:AA:37:ARG:NH1	2.20	0.74
55:3L:54:5MU:O2'	55:3L:55:PSU:OP1	2.05	0.74
26:14:1678:G:N2	26:14:1989:G:H22	1.85	0.74
1:13:1347:G:H5"	9:8E:107:ARG:HB3	1.70	0.74
2:1E:16:HIS:HE1	2:1E:213:LEU:HD12	1.50	0.74
26:1H:2714:G:OP2	59:1H:3726:HOH:O	2.06	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1G:1263:C:N4	1:1G:1272:G:O6	2.17	0.74
13:4A:68:GLY:HA2	13:4A:71:ARG:HB2	1.70	0.74
26:14:2080:G:H5'	48:F5:35:THR:O	1.87	0.74
1:1G:991:U:H4'	1:1G:992:U:H5"	1.69	0.74
26:14:848:G:H2'	26:14:849:A:C8	2.22	0.74
26:14:1533:C:H3'	26:14:1534:G:H4'	1.70	0.74
7:6E:62:PHE:HA	7:6E:124:LEU:HD21	1.69	0.74
26:1H:1434:A:H61	26:1H:1558:A:N6	1.85	0.74
26:1H:2306:C:H3'	26:1H:2307:G:H5"	1.68	0.74
27:1J:7:G:H4'	39:65:29:PHE:HD2	1.52	0.74
32:59:9:ILE:HG21	32:59:51:ARG:HE	1.51	0.74
10:1I:49:VAL:HG23	14:5I:41:ARG:HB2	1.68	0.74
1:13:141:A:O2'	1:13:182:U:O2	2.05	0.74
1:13:937:A:OP2	59:13:1919:HOH:O	2.05	0.74
26:1H:1210:A:H5'	26:1H:1210:A:H8	1.52	0.74
13:4A:54:VAL:HA	13:4A:57:ARG:HB3	1.68	0.74
55:3L:76:A:H8	26:14:2394:C:H42	1.34	0.74
2:12:42:ILE:HG21	2:12:202:PRO:HB2	1.70	0.74
3:22:6:HIS:HD2	3:22:9:GLY:H	1.33	0.74
41:85:86:ALA:HB2	41:85:116:ALA:HB2	1.70	0.74
46:D5:5:LEU:HD11	46:D5:47:VAL:HG11	1.69	0.74
46:D5:169:GLU:HB3	46:D5:171:ILE:HD13	1.70	0.74
1:13:972:C:OP1	59:13:1921:HOH:O	2.06	0.73
24:3K:8:U:O2	24:3K:13:C:N4	2.22	0.73
24:3K:29:C:N4	24:3K:41:G:O6	2.19	0.73
26:1H:1186:G:OP1	59:1H:3774:HOH:O	2.04	0.73
27:16:66:A:H61	27:16:107:U:H2'	1.53	0.73
26:14:654(B):C:HO2'	26:14:654(S):G:H1	1.30	0.73
46:D5:59:LEU:O	46:D5:61:LEU:N	2.21	0.73
26:1H:240:G:O6	59:1H:3776:HOH:O	2.05	0.73
4:3E:88:VAL:HG12	4:3E:89:THR:HG22	1.70	0.73
30:31:6:VAL:N	30:31:24:LEU:O	2.20	0.73
39:A8:83:LYS:O	39:A8:110:LEU:HA	1.88	0.73
26:14:981:A:OP1	59:14:3535:HOH:O	2.06	0.73
26:14:2392:A:H2	26:14:2424:C:H42	1.35	0.73
26:14:1762:A:N6	59:14:3566:HOH:O	2.21	0.73
27:1J:7:G:H4'	39:65:29:PHE:CD2	2.23	0.73
24:3K:15:G:N1	24:3K:59:A:N7	2.37	0.73
30:31:6:VAL:HG21	30:31:119:ARG:HB2	1.69	0.73
38:55:67:LEU:HD23	38:55:76:VAL:HG21	1.71	0.73
26:1H:314:A:N7	59:1H:3842:HOH:O	2.22	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1H:2396:G:H5"	48:J8:25:LYS:HE2	1.70	0.73
2:12:16:HIS:HB3	2:12:209:ARG:NE	2.02	0.73
26:14:2002:G:N7	59:14:3565:HOH:O	2.21	0.73
11:2I:54:ARG:O	11:2I:56:GLY:N	2.21	0.73
20:BI:43:LEU:HD13	20:BI:51:GLU:HB3	1.69	0.73
26:1H:625:G:N7	36:78:107:LYS:NZ	2.36	0.73
26:1H:1006:C:OP2	59:1H:3779:HOH:O	2.05	0.73
26:1H:1164:G:H2'	26:1H:1165:U:C6	2.23	0.73
30:31:198:ALA:HA	30:31:201:VAL:HG12	1.69	0.73
26:14:486:C:O2'	43:A5:60:ASN:ND2	2.21	0.73
26:14:2287:A:N6	26:14:2344:U:H3	1.86	0.73
1:13:1256:A:N6	1:13:1278:U:OP2	2.22	0.73
26:1H:2315:G:OP1	31:41:36:LYS:NZ	2.21	0.73
1:13:659:U:H2'	1:13:660:G:C8	2.24	0.73
33:61:110:ASP:N	33:61:110:ASP:OD1	2.16	0.73
26:14:273(F):C:H3'	26:14:274:G:H5"	1.71	0.73
26:14:993:G:OP1	41:85:50:ARG:NH2	2.22	0.73
50:H5:13:ILE:O	59:H5:101:HOH:O	2.05	0.73
17:8I:67:LYS:HA	17:8I:70:ARG:HH12	1.53	0.73
32:51:107:VAL:HB	32:51:152:ARG:HG2	1.71	0.73
34:58:47:ALA:HB2	34:58:112:LEU:HD11	1.71	0.73
3:22:35:GLU:HA	3:22:38:ARG:HE	1.54	0.73
8:72:29:SER:HB3	8:72:32:LYS:HG3	1.70	0.73
26:1H:259:G:H21	26:1H:621:A:H8	1.33	0.72
12:3A:47:LYS:HA	12:3A:49:ASN:H	1.54	0.72
29:29:68:ALA:O	29:29:70:ALA:N	2.19	0.72
26:1H:31:C:OP1	59:1H:3783:HOH:O	2.07	0.72
26:1H:71:A:H2	44:F8:31:HIS:HE2	1.35	0.72
26:14:2306:C:H3'	26:14:2307:G:H5"	1.71	0.72
30:39:66:PRO:O	30:39:67:GLN:HB3	1.89	0.72
1:13:964:A:N3	1:13:969:A:O2'	2.21	0.72
26:1H:761:A:OP1	59:1H:3782:HOH:O	2.06	0.72
28:11:171:ASP:OD1	28:11:171:ASP:N	2.22	0.72
42:D8:24:LYS:HA	42:D8:92:THR:HG23	1.70	0.72
14:5A:45:ARG:O	14:5A:49:HIS:ND1	2.22	0.72
26:14:2128:C:H42	26:14:2160:G:H1	1.37	0.72
26:14:2148:G:H2'	26:14:2149:G:H8	1.54	0.72
1:13:588:G:OP1	59:13:1922:HOH:O	2.06	0.72
20:BI:57:ARG:HH11	20:BI:102:GLY:HA2	1.54	0.72
26:1H:1388:G:H2'	26:1H:1389:G:H8	1.53	0.72
26:1H:1778:U:H2'	26:1H:1784:A:N6	2.03	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1H:2210:G:H5'	26:1H:2211:G:N7	2.04	0.72
1:1G:827:U:H3	1:1G:872:A:H62	1.35	0.72
2:12:83:MET:SD	2:12:212:GLN:NE2	2.63	0.72
26:14:259:G:H21	26:14:621:A:H8	1.35	0.72
26:14:2448:A:OP2	59:14:3536:HOH:O	2.07	0.72
30:39:192:LEU:HD22	30:39:194:MET:HE2	1.71	0.72
52:N8:40:LYS:HG3	52:N8:47:PRO:HD2	1.71	0.72
55:3L:15:G:H2'	55:3L:59:A:H61	1.53	0.72
1:13:974:A:OP2	14:5I:41:ARG:NH1	2.22	0.72
1:13:1126:U:C5	1:13:1127:G:C8	2.78	0.72
26:1H:1021:A:H8	26:1H:1022:G:H5"	1.53	0.72
26:1H:2615:U:OP1	59:1H:3780:HOH:O	2.06	0.72
3:22:8:ILE:HG23	3:22:16:ARG:HG2	1.71	0.72
26:14:2710:C:O3'	59:14:3539:HOH:O	2.08	0.72
30:39:4:VAL:HA	30:39:19:GLU:HB3	1.72	0.72
1:1G:973:G:OP2	1:1G:974:A:O2'	2.06	0.72
26:14:1187:G:O6	59:14:3537:HOH:O	2.07	0.72
1:13:346:G:N2	1:13:347:G:N3	2.37	0.72
1:13:659:U:H2'	1:13:660:G:H8	1.55	0.72
26:1H:1102:C:H2'	26:1H:1103:A:C8	2.25	0.72
26:1H:1670:C:OP1	59:1H:3784:HOH:O	2.07	0.72
1:1G:411:A:H62	1:1G:413:G:H21	1.37	0.72
1:1G:609:A:N7	59:1G:1825:HOH:O	2.23	0.72
26:14:815:C:OP1	42:95:85:LYS:NZ	2.21	0.72
15:6I:25:THR:HG21	15:6I:70:LEU:HB2	1.71	0.72
1:1G:547:A:OP1	59:1G:1808:HOH:O	2.05	0.72
26:14:6:A:C8	34:15:129:PRO:HB2	2.25	0.72
42:D8:65:GLY:HA3	42:D8:91:TYR:CZ	2.26	0.71
26:14:2379:G:O2'	39:65:17:ARG:NH1	2.22	0.71
1:13:1223:C:P	19:AI:78:ARG:HH12	2.13	0.71
1:1G:542:G:OP1	4:32:10:ARG:NH2	2.21	0.71
26:14:2400:G:H2'	26:14:2401:U:C6	2.25	0.71
20:BI:33:ILE:O	20:BI:37:SER:OG	2.06	0.71
21:1F:8:THR:HG23	21:1F:11:GLY:H	1.54	0.71
32:59:10:PRO:HG2	32:59:50:VAL:HG13	1.72	0.71
26:1H:70:G:H21	26:1H:71:A:N6	1.87	0.71
26:1H:226:G:H21	26:1H:228:A:H2	1.37	0.71
26:1H:1776:G:OP2	59:1H:3781:HOH:O	2.06	0.71
29:29:54:GLN:NE2	29:29:72:VAL:O	2.23	0.71
33:69:117:GLU:HB2	33:69:118:LYS:HE2	1.72	0.71
1:13:468:A:H5"	16:7I:80:PHE:HB3	1.71	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:6E:122:HIS:HA	7:6E:125:MET:HE2	1.73	0.71
20:BI:26:ASN:HD22	20:BI:26:ASN:H	1.38	0.71
8:72:121:ASP:OD1	8:72:125:ARG:NH2	2.23	0.71
40:B8:11:GLU:HG2	40:B8:57:PHE:CD2	2.26	0.71
13:4A:67:GLU:O	13:4A:69:GLU:N	2.23	0.71
26:14:617:G:OP1	30:39:40:GLN:NE2	2.22	0.71
26:1H:674:G:O2'	30:31:74:ARG:HG3	1.89	0.71
26:1H:761:A:OP1	59:1H:3721:HOH:O	2.08	0.71
16:7A:74:LEU:HD12	16:7A:79:VAL:HG21	1.72	0.71
26:14:2293:C:H5"	39:65:89:ARG:HH21	1.55	0.71
26:14:2400:G:H2'	26:14:2401:U:H6	1.56	0.71
13:4I:23:TYR:HB3	13:4I:67:GLU:HB2	1.72	0.71
22:1K:37:AET:HM62	22:1K:38:A:C6	2.25	0.71
26:1H:1784:A:OP1	59:1H:3786:HOH:O	2.08	0.71
26:1H:2448:A:OP2	59:1H:3733:HOH:O	2.07	0.71
1:1G:1238:A:H62	1:1G:1301:U:H3	1.37	0.71
39:65:30:ARG:HG3	39:65:35:ILE:HD12	1.73	0.71
40:75:55:ASN:H	40:75:59:THR:HG22	1.55	0.71
1:1G:1435:G:H2'	1:1G:1436:U:C6	2.25	0.71
30:39:157:VAL:HB	30:39:194:MET:HG3	1.73	0.71
1:13:1124:G:N7	1:13:1145:C:O2'	2.22	0.71
26:1H:248:G:OP1	59:1H:3785:HOH:O	2.08	0.71
54:Q8:33:ASN:HA	54:Q8:36:LYS:HD2	1.71	0.71
34:15:128:HIS:H	34:15:128:HIS:CD2	2.08	0.71
46:D5:149:SER:HA	46:D5:170:THR:HB	1.73	0.71
43:E8:12:ILE:HG13	43:E8:42:ARG:HH11	1.56	0.70
5:42:122:GLU:O	5:42:126:ARG:NH1	2.24	0.70
26:14:1345:C:OP2	59:14:3540:HOH:O	2.09	0.70
40:75:64:ARG:HB2	40:75:73:GLU:HG2	1.71	0.70
1:13:21:G:OP1	59:13:1924:HOH:O	2.08	0.70
1:13:972:C:OP1	59:13:1925:HOH:O	2.09	0.70
1:13:1423:G:OP1	35:68:49:ARG:NH2	2.23	0.70
9:8E:45:ALA:O	9:8E:78:LYS:NZ	2.24	0.70
26:1H:661:C:O2'	36:78:13:ASN:O	2.08	0.70
26:1H:1016:G:O6	59:1H:3787:HOH:O	2.08	0.70
26:14:862:G:OP2	59:14:3538:HOH:O	2.07	0.70
36:35:75:ILE:HD13	36:35:75:ILE:H	1.54	0.70
42:95:52:VAL:HG11	42:95:55:ALA:HB3	1.72	0.70
1:13:486:U:OP2	59:13:1927:HOH:O	2.10	0.70
1:13:1502:A:H2	1:13:1505:G:N1	1.88	0.70
2:1E:80:ILE:HG21	2:1E:212:GLN:HA	1.74	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1H:1184:G:O6	59:1H:3788:HOH:O	2.09	0.70
10:1A:29:ARG:HD3	10:1A:84:GLN:HE22	1.56	0.70
26:14:761:A:N7	59:14:3574:HOH:O	2.24	0.70
26:14:2685:G:O6	59:14:3541:HOH:O	2.09	0.70
41:85:66:ASN:HB2	41:85:76:TYR:HB2	1.72	0.70
22:1K:50:G:N2	22:1K:51:C:N3	2.39	0.70
31:41:97:ASP:O	31:41:101:ILE:HG23	1.91	0.70
32:51:5:GLY:H	32:51:69:ARG:HG2	1.56	0.70
1:1G:1127:G:O2'	1:1G:1148:U:O2	2.08	0.70
3:22:36:ASP:HA	3:22:39:ILE:HD12	1.73	0.70
10:1A:49:VAL:O	10:1A:60:ARG:HB2	1.90	0.70
26:14:2272:U:O4	59:14:3534:HOH:O	2.06	0.70
1:13:1335:C:O2	59:13:1923:HOH:O	2.07	0.70
8:7E:51:VAL:HG11	8:7E:60:ARG:HD2	1.73	0.70
11:2I:65:ALA:HB1	11:2I:98:LEU:HD21	1.74	0.70
37:88:138:ASP:OD1	37:88:138:ASP:N	2.23	0.70
52:N8:36:CYS:HB2	52:N8:49:CYS:SG	2.32	0.70
1:1G:812:C:N3	59:1G:1827:HOH:O	2.24	0.70
1:1G:1286:A:C8	1:1G:1287:A:H4'	2.26	0.70
9:82:112:LYS:HE2	9:82:118:LYS:H	1.57	0.70
10:1A:33:GLN:HB2	10:1A:75:ILE:HG12	1.72	0.70
27:1J:83:G:H5'	50:H5:52:HIS:CE1	2.26	0.70
26:14:1041:C:H42	26:14:1114:G:H1	1.39	0.70
38:55:33:ARG:HD3	38:55:115:GLU:HB3	1.72	0.70
1:13:975:A:H4'	1:13:976:G:H5"	1.73	0.70
15:6I:82:ILE:O	15:6I:86:GLY:N	2.24	0.70
26:14:71:A:H2	44:B5:31:HIS:HE2	1.38	0.70
26:14:733:G:N7	59:14:3579:HOH:O	2.25	0.70
26:1H:860:U:C5	26:1H:917:A:H2	2.10	0.70
26:1H:2414:G:H21	36:78:67:MET:HE3	1.57	0.70
1:1G:353:A:H5'	1:1G:353:A:H8	1.57	0.70
1:1G:920:U:H2'	1:1G:921:U:C6	2.27	0.70
5:42:16:THR:OG1	5:42:17:ALA:N	2.23	0.70
11:2A:29:ILE:HG22	11:2A:44:SER:HB2	1.72	0.70
32:59:97:ARG:HG2	32:59:98:LEU:H	1.57	0.70
45:C5:31:LEU:HD12	45:C5:36:ALA:HB3	1.71	0.70
10:1I:61:GLU:OE2	14:5I:45:ARG:NH1	2.25	0.70
26:1H:674:G:H1'	30:31:74:ARG:HD3	1.72	0.70
8:72:110:ALA:H	8:72:121:ASP:HB2	1.57	0.70
13:4A:84:ILE:H	13:4A:84:ILE:HD12	1.57	0.70
13:4A:91:ARG:NH1	13:4A:97:PRO:O	2.24	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:13:812:C:N3	59:13:1942:HOH:O	2.24	0.70
26:1H:2314:C:H2'	26:1H:2315:G:H8	1.55	0.70
3:22:70:VAL:HG12	3:22:72:LYS:H	1.55	0.70
10:1A:54:PHE:CZ	10:1A:55:LYS:HD2	2.26	0.70
37:45:133:ARG:O	37:45:134:ARG:HD2	1.91	0.70
39:65:59:LYS:HD3	39:65:60:GLY:H	1.57	0.70
1:13:524:G:H2'	1:13:525:C:C6	2.27	0.69
26:1H:1187:G:O6	59:1H:3775:HOH:O	2.08	0.69
26:1H:1607:C:H4'	26:1H:1608:A:O5'	1.92	0.69
26:1H:1664:A:OP1	59:1H:3722:HOH:O	2.10	0.69
33:61:110:ASP:HB2	33:61:112:LYS:H	1.57	0.69
51:M8:45:GLY:O	51:M8:47:GLN:NE2	2.25	0.69
2:1E:126:GLU:HG3	2:1E:129:GLU:HG3	1.73	0.69
45:G8:38:ILE:HD11	45:G8:64:GLU:HG3	1.73	0.69
9:82:13:ALA:HB2	9:82:68:GLY:HA3	1.74	0.69
27:1J:44:G:H1'	27:1J:47:C:H42	1.56	0.69
1:13:598:U:H4'	8:7E:94:TYR:CD2	2.28	0.69
5:42:34:VAL:HG13	5:42:66:MET:HE1	1.74	0.69
12:3A:113:ARG:HH21	12:3A:116:SER:HB2	1.56	0.69
54:M5:40:GLU:HA	54:M5:43:GLN:HB2	1.73	0.69
40:B8:58:ASN:C	40:B8:58:ASN:HD22	1.99	0.69
43:E8:88:ARG:HB2	43:E8:92:ARG:HB3	1.72	0.69
26:14:122:G:N7	59:14:3576:HOH:O	2.24	0.69
40:75:24:PRO:HA	40:75:49:VAL:HG23	1.74	0.69
26:1H:563:G:OP2	59:1H:3789:HOH:O	2.10	0.69
26:1H:2327:A:H2'	26:1H:2328:A:C8	2.27	0.69
35:68:2:ILE:HD12	35:68:6:THR:HG21	1.74	0.69
50:L8:3:ARG:HB2	50:L8:59:VAL:HG22	1.74	0.69
1:1G:1452:C:H4'	1:1G:1453:G:H5'	1.74	0.69
16:7A:53:VAL:HG13	16:7A:79:VAL:HG22	1.75	0.69
26:14:2444:G:OP2	30:39:68:LYS:HE2	1.92	0.69
30:31:29:ASN:H	30:31:112:MET:CE	2.05	0.69
33:61:92:VAL:HG13	33:61:120:ILE:HG23	1.74	0.69
40:B8:105:LEU:O	40:B8:107:ASP:N	2.25	0.69
26:14:2113:U:H3'	26:14:2114:A:C4'	2.20	0.69
26:14:2269:A:OP1	59:14:3543:HOH:O	2.10	0.69
46:D5:51:ALA:HB1	46:D5:57:ILE:HD11	1.75	0.69
8:7E:83:ILE:HB	8:7E:137:VAL:HG13	1.74	0.69
13:4I:12:ASN:O	13:4I:14:ARG:N	2.23	0.69
36:78:114:ILE:HD13	36:78:125:VAL:HG11	1.75	0.69
49:K8:3:LEU:H	49:K8:4:SER:C	2.01	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:14:198:C:H5'	26:14:2244:U:OP1	1.91	0.69
26:14:528:A:O2'	26:14:529:A:H5'	1.92	0.69
26:14:1346:G:OP2	59:14:3546:HOH:O	2.11	0.69
26:14:2068:U:H3	26:14:2430:A:H2	1.40	0.69
34:15:47:ALA:HB2	34:15:112:LEU:HD21	1.75	0.69
1:13:221:C:H2'	1:13:222:U:H6	1.58	0.69
1:13:346:G:H21	1:13:347:G:H1'	1.58	0.69
1:13:963:G:H21	10:1I:55:LYS:NZ	1.91	0.69
1:13:1189:C:OP1	10:1I:51:ARG:NH2	2.25	0.69
26:1H:67:U:H3	26:1H:74:A:H2	1.38	0.69
1:1G:490:G:OP2	4:32:132:ARG:NH2	2.26	0.69
5:42:33:VAL:HG21	5:42:109:ILE:HG12	1.74	0.69
7:62:147:ALA:O	7:62:149:ARG:NH1	2.26	0.69
22:1L:69:C:H1'	22:1L:70:A:C8	2.28	0.69
26:14:1325:G:OP1	59:14:3545:HOH:O	2.10	0.69
26:14:2418:A:OP2	54:M5:29:LYS:NZ	2.25	0.69
26:14:2720:U:H3	26:14:2873:A:H2	1.38	0.69
33:69:75:LEU:HD21	33:69:77:LEU:HB2	1.75	0.69
36:35:138:LEU:HD12	36:35:144:GLU:HG3	1.72	0.69
46:D5:10:ARG:NH2	46:D5:26:GLY:O	2.25	0.69
26:1H:2786:U:O2'	29:21:62:PRO:O	2.10	0.69
1:1G:413:G:O2'	1:1G:428:G:N2	2.26	0.69
26:14:2836:U:H2'	26:14:2837:G:C8	2.26	0.69
32:59:121:ILE:HG23	32:59:133:VAL:HG21	1.74	0.69
36:35:39:LYS:HD2	36:35:45:LEU:HD21	1.73	0.69
1:13:1303:C:O5'	59:13:1913:HOH:O	2.10	0.69
26:1H:620:G:H4'	26:1H:621:A:H5"	1.75	0.69
1:1G:4:U:O4	8:72:105:ARG:HA	1.93	0.69
1:1G:491:G:N7	59:1G:1830:HOH:O	2.26	0.69
1:1G:1279:A:O2'	1:1G:1281:U:OP2	2.09	0.69
32:59:7:LEU:HD12	32:59:8:PRO:HD3	1.74	0.69
2:1E:93:VAL:HG11	2:1E:97:TRP:HD1	1.57	0.68
13:4I:49:THR:HG22	13:4I:51:ALA:H	1.58	0.68
21:1F:3:LYS:NZ	59:1F:102:HOH:O	2.26	0.68
1:1G:235:C:H5'	17:8A:70:ARG:HG2	1.75	0.68
9:82:48:GLU:HB3	9:82:101:PHE:HE2	1.59	0.68
13:4A:23:TYR:HB3	13:4A:67:GLU:HA	1.74	0.68
26:14:1871:A:H2'	26:14:1872:A:C8	2.28	0.68
26:14:2268:A:OP1	59:14:3547:HOH:O	2.11	0.68
36:35:71:VAL:HG13	36:35:72:PRO:HD3	1.75	0.68
24:3K:2:C:H42	24:3K:71:G:H1	1.41	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1H:389:G:H1	36:78:71:VAL:HG12	1.58	0.68
26:1H:958:U:OP2	37:88:14:ARG:NH1	2.27	0.68
26:1H:2836:U:H2'	26:1H:2837:G:C8	2.27	0.68
28:11:17:THR:HG22	28:11:204:ILE:HA	1.73	0.68
46:H8:169:GLU:OE1	46:H8:170:THR:N	2.25	0.68
26:14:1678:G:H22	26:14:1989:G:H22	1.41	0.68
23:2K:17:C:OP2	23:2K:18:U:O2'	2.09	0.68
26:1H:943:U:OP2	59:1H:3790:HOH:O	2.11	0.68
26:1H:1535:U:OP2	26:1H:1538:G:N2	2.26	0.68
26:1H:2781:A:H5"	26:1H:2782:G:H5'	1.76	0.68
26:1H:2846:G:N7	59:1H:3855:HOH:O	2.25	0.68
26:14:1614:A:OP2	59:14:3544:HOH:O	2.10	0.68
26:14:1992:G:N7	59:14:3584:HOH:O	2.26	0.68
26:1H:1525:G:H2'	26:1H:1526:G:C8	2.27	0.68
38:98:34:ILE:HG22	38:98:114:VAL:HB	1.74	0.68
44:F8:27:THR:HB	44:F8:80:ILE:HB	1.76	0.68
10:1A:61:GLU:HG3	14:5A:58:LYS:HE2	1.76	0.68
40:75:77:PRO:HG2	40:75:80:SER:HB2	1.74	0.68
1:13:963:G:N3	10:1I:55:LYS:NZ	2.42	0.68
3:22:106:VAL:HB	3:22:109:PRO:HB3	1.75	0.68
26:14:907:U:O2'	37:45:101:ARG:NH2	2.25	0.68
30:39:129:PHE:HA	30:39:142:TRP:NE1	2.08	0.68
1:13:664:G:N2	1:13:741:G:H1	1.89	0.68
1:13:780:A:OP2	59:13:1926:HOH:O	2.09	0.68
19:AI:40:ILE:HG12	19:AI:41:VAL:HG13	1.76	0.68
26:1H:1332:G:N2	26:1H:1610:A:C8	2.62	0.68
26:1H:2705:A:OP2	59:1H:3792:HOH:O	2.11	0.68
1:1G:328:C:OP1	59:1G:1810:HOH:O	2.11	0.68
1:1G:977:A:O2'	1:1G:981:U:N3	2.26	0.68
26:14:2162:G:O2'	26:14:2173:A:OP1	2.09	0.68
33:69:14:ASP:OD1	33:69:15:VAL:N	2.26	0.68
35:25:92:GLU:OE1	35:25:113:LYS:NZ	2.25	0.68
41:85:88:ILE:HD11	42:95:47:VAL:HG21	1.76	0.68
46:D5:130:PRO:HA	46:D5:133:ILE:HD11	1.74	0.68
26:1H:1107:G:H2'	26:1H:1108:U:H6	1.59	0.68
26:1H:2017:U:P	59:1H:3826:HOH:O	2.52	0.68
26:1H:2849:U:H4'	26:1H:2868:A:C2	2.29	0.68
33:61:110:ASP:HB2	33:61:112:LYS:HG2	1.75	0.68
42:D8:37:VAL:HG23	42:D8:51:VAL:HG21	1.76	0.68
26:14:2115:G:O2'	26:14:2171:A:N6	2.26	0.68
30:39:10:PRO:HA	30:39:127:GLU:HG2	1.73	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:4I:12:ASN:HB3	13:4I:46:LYS:HB2	1.76	0.68
24:3K:31:C:H42	24:3K:39:G:H1	1.41	0.68
26:1H:1678:G:N2	26:1H:1989:G:H22	1.91	0.68
5:42:143:ARG:NH2	8:72:77:GLU:OE1	2.27	0.68
7:62:15:ASP:HB3	7:62:20:ASP:H	1.59	0.68
26:14:2294:C:P	39:65:89:ARG:HH22	2.17	0.68
31:49:50:ALA:HA	31:49:53:LEU:HB3	1.74	0.68
47:E5:36:ILE:HD11	47:E5:39:ARG:HG2	1.76	0.68
1:1G:972:C:OP1	59:1G:1815:HOH:O	2.12	0.68
50:H5:39:ASP:OD1	50:H5:44:ARG:NH1	2.27	0.68
26:1H:1021:A:H62	26:1H:1141:U:H3	1.41	0.68
26:1H:1849:G:OP2	59:1H:3797:HOH:O	2.12	0.68
54:Q8:37:SER:O	54:Q8:40:GLU:N	2.26	0.68
1:1G:576:G:OP1	59:1G:1811:HOH:O	2.11	0.68
3:22:92:ALA:HB2	3:22:99:VAL:HG13	1.76	0.68
11:2A:98:LEU:O	11:2A:101:SER:OG	2.10	0.68
26:14:588:U:H2'	26:14:589:C:C6	2.28	0.68
34:15:13:TRP:O	34:15:135:PRO:HD2	1.94	0.68
37:45:27:VAL:CG1	37:45:134:ARG:HE	2.06	0.68
26:1H:1332:G:N2	26:1H:1609:A:O2'	2.26	0.67
21:1B:2:GLY:O	21:1B:4:GLY:N	2.27	0.67
47:E5:38:VAL:HG13	47:E5:59:LEU:HB2	1.75	0.67
48:F5:92:LYS:O	48:F5:95:LEU:N	2.25	0.67
28:11:38:LYS:HB3	28:11:39:LYS:HA	1.76	0.67
52:N8:40:LYS:HG2	52:N8:46:CYS:HA	1.77	0.67
12:3A:82:VAL:O	12:3A:106:ASP:HB2	1.94	0.67
49:G5:35:LEU:HD23	49:G5:53:LEU:HD12	1.76	0.67
1:13:864:A:OP1	59:13:1930:HOH:O	2.12	0.67
26:1H:1534:G:H21	26:1H:1538:G:N2	1.93	0.67
26:1H:2321:G:H5"	26:1H:2322:A:OP2	1.94	0.67
31:41:161:THR:HG22	31:41:163:ALA:H	1.58	0.67
46:D5:27:VAL:HG12	46:D5:87:ASP:HB3	1.75	0.67
1:13:1367:C:H5'	10:1I:60:ARG:HH11	1.57	0.67
26:1H:1006:C:OP1	59:1H:3795:HOH:O	2.12	0.67
31:41:152:LEU:H	31:41:152:LEU:HD12	1.58	0.67
46:H8:19:ARG:NH1	46:H8:84:GLU:O	2.28	0.67
26:14:1017:G:N7	59:14:3593:HOH:O	2.27	0.67
41:85:92:ARG:HG3	41:85:94:ASN:HB3	1.75	0.67
1:13:645:C:OP2	59:13:1928:HOH:O	2.12	0.67
26:1H:646:A:H2'	26:1H:647:G:O4'	1.95	0.67
26:1H:974(A):C:O2'	59:1H:3800:HOH:O	2.13	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1H:1986:A:OP1	59:1H:3799:HOH:O	2.12	0.67
1:1G:557:G:OP1	59:1G:1814:HOH:O	2.12	0.67
4:32:105:VAL:HG13	4:32:110:PHE:HB2	1.75	0.67
12:3A:60:LEU:HB2	12:3A:64:TYR:HB2	1.75	0.67
26:14:2016:U:O2	52:J5:7:PRO:HG2	1.95	0.67
37:45:138:ASP:N	37:45:138:ASP:OD1	2.27	0.67
1:13:1296:C:OP1	13:4I:44:ARG:NH2	2.28	0.67
4:3E:108:LEU:HD23	4:3E:110:PHE:HE1	1.60	0.67
26:1H:1594:G:OP1	59:1H:3791:HOH:O	2.11	0.67
52:N8:33:CYS:HB2	52:N8:40:LYS:HD3	1.77	0.67
1:1G:247:G:OP2	17:8A:100:LYS:N	2.28	0.67
2:12:118:LEU:HB3	2:12:142:LEU:HD12	1.76	0.67
4:32:89:THR:HA	5:42:97:GLY:HA3	1.76	0.67
46:D5:8:TYR:CD1	46:D5:62:PRO:HG3	2.29	0.67
1:13:619:U:H3	4:3E:134:ASP:HB2	1.60	0.67
1:13:881:G:OP2	12:3I:12:ARG:NH2	2.28	0.67
26:1H:563:G:OP2	59:1H:3794:HOH:O	2.12	0.67
26:1H:1899:G:H1	26:1H:1902:C:H41	1.40	0.67
26:1H:2308:G:N1	26:1H:2311:A:H2	1.85	0.67
26:1H:2400:G:H2'	26:1H:2401:U:H6	1.60	0.67
1:1G:316:G:OP2	1:1G:351:G:O2'	2.13	0.67
2:12:71:VAL:HB	2:12:165:VAL:HG22	1.75	0.67
20:BA:97:ALA:HB1	20:BA:99:LEU:HG	1.77	0.67
26:14:1729:A:H2'	26:14:1731:G:N2	2.08	0.67
27:1J:88:C:H5"	27:1J:89:G:C5	2.29	0.67
26:1H:459:U:H5"	53:P8:40:TRP:CD2	2.29	0.67
26:1H:617:G:OP2	30:31:43:LYS:NZ	2.28	0.67
26:1H:974(A):C:OP1	59:1H:3798:HOH:O	2.12	0.67
1:1G:278:G:N7	17:8A:92:ARG:NH1	2.43	0.67
4:32:107:ARG:HH22	4:32:194:LEU:HD22	1.60	0.67
8:72:7:ALA:HB2	8:72:85:ARG:HD3	1.76	0.67
26:1H:1900:A:H5'	26:1H:1900:A:C8	2.29	0.67
36:78:47:ASP:OD2	36:78:50:ARG:NH2	2.27	0.67
1:1G:1110:A:OP2	59:1G:1812:HOH:O	2.11	0.67
3:22:150:LYS:HG3	3:22:169:ALA:HB2	1.76	0.67
26:14:6:A:H3'	26:14:7:G:H5'	1.76	0.67
26:14:963:U:OP1	59:14:3548:HOH:O	2.12	0.67
28:19:148:GLU:HB2	28:19:151:LYS:HD2	1.77	0.67
50:H5:39:ASP:O	50:H5:44:ARG:NH1	2.27	0.67
1:13:737:A:H2'	1:13:738:C:C6	2.30	0.67
4:3E:141:ARG:HB2	4:3E:141:ARG:CZ	2.25	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:2I:73:MET:HE2	11:2I:103:LEU:HB2	1.76	0.67
26:1H:270(I):G:H1	26:1H:270(Q):C:N4	1.85	0.67
51:M8:39:CYS:HB3	51:M8:41:PRO:HD2	1.75	0.67
14:5A:13:THR:O	14:5A:13:THR:OG1	2.07	0.67
40:75:54:ARG:HA	40:75:59:THR:HB	1.77	0.67
17:8I:65:ILE:HG21	17:8I:69:LYS:HE2	1.77	0.66
33:61:144:VAL:HG12	33:61:145:VAL:HG23	1.77	0.66
22:1L:43:G:H2'	22:1L:44:A:C8	2.30	0.66
27:1J:88:C:H1'	27:1J:89:G:OP2	1.94	0.66
36:35:47:ASP:OD2	36:35:50:ARG:NH1	2.28	0.66
40:75:50:ILE:HD11	40:75:102:ILE:HD11	1.78	0.66
1:13:453:A:H4'	16:7I:72:ARG:HB2	1.76	0.66
33:61:7:GLU:HA	33:61:15:VAL:HG22	1.75	0.66
26:14:1183:G:O3'	50:H5:29:ARG:NH2	2.27	0.66
26:14:1636:C:OP2	59:14:3551:HOH:O	2.14	0.66
26:14:2749:A:N1	26:14:2750:A:N6	2.44	0.66
1:13:608:A:OP2	59:13:1931:HOH:O	2.13	0.66
7:6E:16:LEU:HD11	9:8E:45:ALA:HB2	1.77	0.66
18:9I:22:VAL:HG22	18:9I:56:THR:HA	1.77	0.66
26:1H:142:G:H1'	44:F8:37:THR:HG21	1.77	0.66
6:52:22:GLU:OE1	6:52:84:ASN:ND2	2.28	0.66
6:52:24:GLU:OE1	6:52:28:ARG:NH1	2.28	0.66
9:8E:91:ASP:N	9:8E:91:ASP:OD1	2.27	0.66
26:1H:2402:C:H1'	26:1H:2403:C:H5	1.60	0.66
26:1H:2751:G:C8	32:51:3:ARG:HD3	2.30	0.66
1:1G:324:G:O6	59:1G:1813:HOH:O	2.12	0.66
19:AA:20:LEU:HA	19:AA:23:ASN:HB2	1.77	0.66
26:14:2655:G:N2	26:14:2665:A:OP2	2.28	0.66
26:14:2882:A:H5'	38:55:96:ARG:HB2	1.77	0.66
47:E5:53:MET:HG3	47:E5:59:LEU:HD23	1.78	0.66
1:13:881:G:P	12:3I:12:ARG:HH22	2.18	0.66
6:5E:24:GLU:HG2	6:5E:28:ARG:CZ	2.26	0.66
26:1H:592:G:N2	54:Q8:4:MET:HE1	2.08	0.66
29:29:76:ARG:HD3	29:29:77:ILE:H	1.61	0.66
36:35:122:PRO:HB3	36:35:141:ALA:HB1	1.77	0.66
46:D5:94:GLU:HB3	46:D5:96:VAL:HG23	1.77	0.66
1:13:345:C:H4'	1:13:346:G:N7	2.11	0.66
23:2K:62:C:H2'	23:2K:63:C:H6	1.60	0.66
26:1H:2292:C:OP1	39:A8:17:ARG:NH2	2.28	0.66
1:1G:584:G:H5'	17:8A:91:ARG:HH22	1.61	0.66
23:2L:47:7MG:H3'	23:2L:48:U:C2	2.31	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:14:2074:U:OP1	59:14:3552:HOH:O	2.14	0.66
27:1J:11:C:OP2	27:1J:12:C:N4	2.22	0.66
27:1J:80:U:H2'	27:1J:81:G:N2	2.10	0.66
1:13:1345:U:OP1	59:13:1932:HOH:O	2.14	0.66
13:4I:37:THR:HB	13:4I:55:ARG:HD2	1.78	0.66
22:1K:65:C:H5	22:1K:67:A:H62	1.44	0.66
3:22:40:ARG:HG2	3:22:55:VAL:HG11	1.78	0.66
9:82:5:TYR:N	9:82:87:GLN:OE1	2.29	0.66
6:5E:22:GLU:OE1	6:5E:82:ARG:NH2	2.24	0.66
26:1H:136:G:N7	59:1H:3871:HOH:O	2.29	0.66
26:1H:1635:G:OP1	59:1H:3804:HOH:O	2.13	0.66
30:31:13:SER:HB3	30:31:16:GLY:H	1.59	0.66
35:68:93:PRO:HG3	35:68:114:ILE:HG12	1.78	0.66
2:12:71:VAL:HG11	2:12:164:VAL:HA	1.77	0.66
2:12:71:VAL:HG11	2:12:164:VAL:HG13	1.77	0.66
8:72:54:ASP:N	8:72:54:ASP:OD1	2.28	0.66
16:7A:43:LYS:HG2	16:7A:48:TRP:CD2	2.30	0.66
26:14:1342:A:H2	26:14:1602:U:H3	1.43	0.66
1:13:501:C:H2'	1:13:502:G:C8	2.30	0.66
15:6I:24:SER:HB3	15:6I:27:VAL:HG23	1.77	0.66
26:1H:2864:G:OP1	40:B8:119:LYS:HD2	1.96	0.66
27:16:18:G:H1	27:16:65:C:H42	1.43	0.66
47:I8:23:VAL:HG22	47:I8:38:VAL:HG22	1.78	0.66
26:14:2062:A:O2'	26:14:2063:C:OP1	2.14	0.66
26:14:2624:G:N7	59:14:3599:HOH:O	2.28	0.66
31:49:49:ASP:HB3	31:49:52:ILE:HB	1.78	0.66
49:G5:4:SER:CA	49:G5:6:VAL:H	2.08	0.66
7:6E:80:VAL:HG22	7:6E:85:TYR:HE2	1.61	0.66
26:1H:2431:U:OP2	59:1H:3801:HOH:O	2.13	0.66
33:61:113:ARG:HH21	33:61:132:PRO:HB3	1.60	0.66
36:78:71:VAL:HG13	36:78:72:PRO:HD3	1.78	0.66
37:88:109:VAL:HG13	37:88:113:GLN:HB3	1.78	0.66
45:G8:85:VAL:HG23	45:G8:96:ILE:HB	1.76	0.66
29:29:105:THR:HG21	29:29:164:ARG:HE	1.59	0.66
26:1H:309:G:N3	26:1H:329:G:O2'	2.28	0.65
26:1H:376:C:OP1	59:1H:3809:HOH:O	2.14	0.65
6:52:68:PRO:HG2	6:52:71:ARG:HG3	1.77	0.65
22:1L:53:G:H1	22:1L:61:C:H42	1.43	0.65
27:1J:88:C:H5"	27:1J:89:G:C6	2.31	0.65
39:65:29:PHE:HD1	39:65:30:ARG:N	1.94	0.65
46:D5:60:GLU:HA	46:D5:66:SER:HA	1.79	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:13:310:G:OP2	16:7I:27:LYS:NZ	2.28	0.65
25:4K:9:G:N7	25:4K:10:G:N2	2.44	0.65
26:1H:330:A:HO2'	26:1H:331:A:H8	1.44	0.65
26:1H:2711:A:OP1	59:1H:3803:HOH:O	2.13	0.65
1:1G:3:G:H1	4:32:88:VAL:HG13	1.61	0.65
1:13:1348:U:H2'	1:13:1349:A:H8	1.61	0.65
15:6I:39:LEU:HD13	15:6I:56:LEU:HB2	1.77	0.65
20:BI:40:ALA:HB2	20:BI:55:ILE:HG22	1.78	0.65
37:88:66:ILE:HA	37:88:104:PHE:HA	1.78	0.65
1:1G:1095:U:OP2	1:1G:1108:G:N1	2.24	0.65
26:14:6:A:H62	34:15:131:GLN:H	1.42	0.65
26:14:2074:U:OP1	59:14:3549:HOH:O	2.13	0.65
31:49:95:ARG:O	31:49:99:MET:HG2	1.96	0.65
39:65:61:ASN:O	39:65:65:VAL:HB	1.95	0.65
1:13:1133:G:H2'	1:13:1134:G:C8	2.28	0.65
26:1H:81:G:O6	59:1H:3805:HOH:O	2.14	0.65
26:1H:187:G:OP2	59:1H:3807:HOH:O	2.14	0.65
1:1G:1043:C:H2'	1:1G:1044:A:H8	1.61	0.65
1:1G:1300:G:O2'	1:1G:1301:U:O5'	2.12	0.65
15:6A:39:LEU:HD12	15:6A:56:LEU:HD13	1.78	0.65
26:14:491:G:H2'	26:14:492:A:C8	2.31	0.65
1:13:179:A:H2'	1:13:180:U:H6	1.60	0.65
1:13:455:C:H42	1:13:477:G:H22	1.43	0.65
1:13:1165:C:O2	1:13:1171:G:N2	2.29	0.65
26:1H:1156:A:C8	41:C8:51:LYS:HG2	2.32	0.65
26:1H:2048:G:N7	59:1H:3872:HOH:O	2.29	0.65
1:1G:1224:G:C6	1:1G:1322:C:H1'	2.32	0.65
10:1A:51:ARG:HB2	10:1A:60:ARG:HA	1.79	0.65
1:13:75:C:HO2'	1:13:76:G:H8	1.44	0.65
15:6I:17:ARG:HD3	15:6I:77:ARG:NH2	2.10	0.65
35:68:47:ILE:HG13	35:68:48:PRO:HD2	1.78	0.65
1:1G:1132:C:H2'	1:1G:1133:G:C8	2.31	0.65
26:14:2162:G:H3'	26:14:2164:C:H5	1.62	0.65
1:13:1104:G:OP1	2:1E:144:ARG:NH1	2.28	0.65
26:1H:80:G:N7	59:1H:3878:HOH:O	2.30	0.65
39:A8:89:ARG:HG2	39:A8:89:ARG:O	1.97	0.65
43:E8:86:LEU:HD12	43:E8:87:PRO:HD2	1.77	0.65
2:12:15:VAL:HB	2:12:16:HIS:CE1	2.32	0.65
9:82:40:LEU:HB3	9:82:43:ALA:HB2	1.79	0.65
26:14:1617:C:N3	59:14:3601:HOH:O	2.29	0.65
26:14:2873:A:H8	38:55:6:SER:N	1.95	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:39:21:ALA:C	30:39:23:ASP:H	2.05	0.65
14:5I:6:LEU:HB3	14:5I:23:ARG:NH2	2.12	0.65
26:1H:530:G:O2'	59:1H:3806:HOH:O	2.14	0.65
39:A8:93:LYS:HG2	39:A8:95:HIS:HB2	1.79	0.65
18:9A:31:LEU:HD23	18:9A:31:LEU:H	1.62	0.65
30:39:123:LEU:O	30:39:125:LEU:N	2.29	0.65
45:C5:42:VAL:HG13	45:C5:65:ALA:HB3	1.78	0.65
1:13:1368:G:H5"	9:8E:112:LYS:HB3	1.77	0.65
36:78:115:LEU:HA	36:78:134:ALA:HB2	1.79	0.65
40:B8:56:GLY:O	40:B8:59:THR:HG22	1.97	0.65
1:1G:564:C:O2'	8:72:91:ARG:NH2	2.29	0.65
1:1G:677:U:H3	1:1G:713:G:H22	1.43	0.65
26:14:529:A:H4'	26:14:530:G:H5'	1.77	0.65
26:14:1581:G:H2'	26:14:1582:C:O4'	1.97	0.65
26:14:2531:A:H4'	32:59:157:TYR:HE2	1.62	0.65
33:69:76:THR:HG21	33:69:140:LEU:HD12	1.77	0.65
1:13:737:A:H2'	1:13:738:C:H6	1.61	0.65
26:1H:2256:G:N7	59:1H:3873:HOH:O	2.29	0.65
27:16:66:A:N6	27:16:107:U:H2'	2.10	0.65
48:J8:3:LYS:HG3	48:J8:46:LEU:HD22	1.78	0.65
26:14:1110:G:H2'	26:14:1111:A:C8	2.32	0.65
26:14:2378:A:O2'	39:65:21:THR:HG21	1.97	0.65
27:1J:52:A:H62	39:65:33:LYS:HG3	1.62	0.65
28:19:71:ASP:CG	28:19:103:ARG:HH22	2.05	0.65
26:1H:2134:A:N7	26:1H:2156:G:O2'	2.30	0.64
26:1H:2409:G:N7	59:1H:3875:HOH:O	2.30	0.64
29:21:24:THR:HG21	29:21:188:VAL:HG22	1.79	0.64
32:51:56:SER:OG	32:51:57:ASP:N	2.27	0.64
26:14:1178:C:H2'	26:14:1179:C:C6	2.32	0.64
26:14:1364:G:OP2	48:F5:2:SER:N	2.30	0.64
26:14:2037:G:H2'	26:14:2038:G:C8	2.32	0.64
26:14:2196:C:OP2	59:14:3554:HOH:O	2.14	0.64
30:39:133:ASN:HA	30:39:162:LEU:HD23	1.80	0.64
45:C5:39:VAL:HG23	45:C5:41:GLY:H	1.62	0.64
29:21:111:ARG:HG3	29:21:160:TYR:CD2	2.32	0.64
46:H8:9:TYR:HE1	46:H8:35:ARG:HG2	1.62	0.64
1:1G:474:G:H2'	1:1G:475:G:H8	1.62	0.64
1:1G:1095:U:P	1:1G:1108:G:H1	2.19	0.64
27:1J:44:G:H1'	27:1J:47:C:N4	2.13	0.64
1:1G:957:U:O2'	1:1G:959:A:N7	2.23	0.64
26:14:1756:G:OP2	59:14:3553:HOH:O	2.14	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:14:2268:A:OP1	59:14:3550:HOH:O	2.13	0.64
2:1E:166:ASP:HB3	2:1E:169:LYS:HB2	1.80	0.64
26:1H:1780:A:OP1	59:1H:3808:HOH:O	2.14	0.64
26:1H:2849:U:O4	40:B8:23:ARG:NH2	2.30	0.64
29:21:116:VAL:O	29:21:117:MET:HB3	1.96	0.64
1:1G:1443:G:O2'	40:75:122:ASP:OD2	2.15	0.64
13:4A:81:LEU:HD11	13:4A:86:CYS:SG	2.38	0.64
26:14:389:G:H1	36:35:71:VAL:HG12	1.61	0.64
26:14:1778:U:H2'	26:14:1784:A:N6	2.11	0.64
32:59:152:ARG:HG2	32:59:153:LYS:HG3	1.78	0.64
37:45:21:THR:HG22	37:45:23:GLY:HA3	1.80	0.64
1:13:657:G:N2	1:13:749:C:O2	2.23	0.64
5:4E:11:ILE:HD11	5:4E:31:LEU:HD13	1.79	0.64
36:78:63:PRO:HD3	54:Q8:27:THR:HG22	1.79	0.64
40:B8:26:ASP:HB3	40:B8:92:GLY:H	1.62	0.64
1:1G:79:G:H1	1:1G:90:C:H42	1.45	0.64
1:1G:652:U:H1'	1:1G:653:A:H2	1.63	0.64
26:14:2250:G:OP1	37:45:85:LYS:NZ	2.24	0.64
26:14:2415:G:H4'	36:35:67:MET:N	2.13	0.64
37:45:27:VAL:HG13	37:45:136:ALA:HB1	1.80	0.64
40:75:2:ASN:HB3	40:75:4:GLY:O	1.96	0.64
49:G5:43:GLN:HG3	49:G5:46:GLN:HE22	1.62	0.64
1:13:1122:U:O4	1:13:1123:A:N6	2.31	0.64
26:1H:761:A:C8	59:1H:3831:HOH:O	2.50	0.64
26:1H:1332:G:H21	26:1H:1610:A:H8	1.43	0.64
29:21:129:HIS:H	29:21:129:HIS:CD2	2.15	0.64
39:A8:74:ALA:HB1	39:A8:108:GLY:HA3	1.80	0.64
5:42:28:PHE:HZ	25:4L:25:A:H8	1.44	0.64
8:72:113:SER:HB2	8:72:134:ILE:HD11	1.79	0.64
25:4L:24:A:H2'	25:4L:25:A:H2	1.62	0.64
26:14:1106:G:H3'	26:14:1107:G:C8	2.30	0.64
26:14:2304:G:H22	26:14:2312:U:H3	1.45	0.64
27:1J:48:A:H4'	39:65:95:HIS:HD2	1.63	0.64
26:1H:607:U:OP1	30:31:102:PRO:HA	1.98	0.64
29:21:67:PHE:HD1	29:21:67:PHE:H	1.45	0.64
41:85:92:ARG:HD2	42:95:11:GLN:HB2	1.79	0.64
26:1H:1991:U:H2'	26:1H:1992:G:H5"	1.80	0.64
26:1H:2469:A:H61	26:1H:2481:G:H1'	1.61	0.64
37:88:2:LEU:H	37:88:2:LEU:HD12	1.63	0.64
38:98:42:LYS:HA	38:98:45:ARG:HD2	1.80	0.64
49:K8:42:GLY:O	49:K8:44:LEU:N	2.31	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:12:210:SER:O	2:12:214:ILE:HG12	1.98	0.64
4:32:31:CYS:SG	4:32:33:MET:HB2	2.37	0.64
14:5A:12:ARG:HB2	14:5A:14:PRO:HD3	1.80	0.64
26:14:2839:G:H5'	38:55:46:GLY:HA2	1.78	0.64
32:59:8:PRO:HB2	32:59:69:ARG:CZ	2.28	0.64
1:13:601:C:H2'	1:13:602:A:C8	2.29	0.64
1:13:1422:G:H5"	35:68:48:PRO:HB3	1.79	0.64
7:6E:111:ARG:HD2	7:6E:123:GLU:HB2	1.80	0.64
26:1H:780:G:H21	26:1H:783:A:N6	1.96	0.64
26:14:607:U:H3	26:14:621:A:H2	1.42	0.64
26:14:870:A:H5"	37:45:6:ARG:HB3	1.80	0.64
28:19:35:LYS:O	28:19:35:LYS:HG2	1.97	0.64
30:39:79:GLY:HA2	30:39:86:GLY:HA2	1.79	0.64
32:59:144:VAL:HG12	32:59:148:ILE:HG12	1.78	0.64
1:13:1031:G:H2'	1:13:1032:A:H5'	1.80	0.64
17:8I:67:LYS:HA	17:8I:70:ARG:NH1	2.12	0.64
26:1H:1253:A:C8	59:1H:3720:HOH:O	2.51	0.64
26:1H:1405:U:H2'	26:1H:1406:U:C6	2.32	0.64
26:1H:1697:G:OP2	26:1H:1698:A:O2'	2.14	0.64
1:1G:1154:G:H2'	1:1G:1155:G:H8	1.63	0.64
35:25:73:ASP:OD2	40:75:32:TYR:OH	2.13	0.64
47:E5:27:GLU:HG3	47:E5:68:GLU:HA	1.79	0.64
1:13:396:G:O2'	1:13:398:C:OP1	2.12	0.63
26:1H:1430:C:H2'	26:1H:1431:U:C6	2.34	0.63
40:B8:12:SER:HA	40:B8:14:TYR:N	2.12	0.63
26:14:275:G:O2'	26:14:276:A:O4'	2.15	0.63
26:14:1332:G:C8	26:14:1332:G:H5'	2.32	0.63
44:B5:51:VAL:HG13	44:B5:81:VAL:HG23	1.79	0.63
1:13:1:U:C6	1:13:630:G:H2'	2.32	0.63
1:13:939:G:H2'	1:13:940:C:C6	2.32	0.63
1:13:1497:G:H2'	1:13:1498:U:H5'	1.80	0.63
20:BI:50:GLU:HB2	20:BI:99:LEU:HB3	1.80	0.63
31:41:47:LYS:HE3	31:41:81:LYS:HB2	1.80	0.63
1:1G:1189:C:O2	59:1G:1816:HOH:O	2.13	0.63
6:52:81:ILE:HD11	28:19:125:ILE:HB	1.78	0.63
12:3A:52:LEU:O	12:3A:54:LYS:NZ	2.30	0.63
38:55:38:VAL:HG12	38:55:42:LYS:HD2	1.81	0.63
44:B5:63:LYS:HA	44:B5:72:LYS:HA	1.78	0.63
1:13:266:G:H5"	1:13:267:C:C5	2.34	0.63
3:2E:78:GLY:HA3	3:2E:83:ARG:HB3	1.80	0.63
8:7E:85:ARG:HD3	8:7E:88:LYS:HG2	1.79	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1H:2154:G:H2'	26:1H:2155:G:C8	2.33	0.63
1:1G:345:C:OP2	40:75:39:ARG:NH2	2.31	0.63
13:4A:35:GLU:O	13:4A:38:GLY:N	2.31	0.63
17:8A:66:SER:OG	17:8A:69:LYS:HB2	1.98	0.63
19:AA:39:THR:OG1	19:AA:70:LYS:NZ	2.27	0.63
26:14:1633:G:O6	59:14:3555:HOH:O	2.14	0.63
26:14:2173:A:O2'	26:14:2174:C:OP1	2.15	0.63
26:14:2629:A:H2'	26:14:2629:A:N3	2.14	0.63
28:19:93:ALA:HB3	28:19:105:ILE:HG22	1.80	0.63
46:D5:61:LEU:HG	46:D5:67:LEU:HD12	1.81	0.63
1:13:1435:G:H2'	1:13:1436:U:C6	2.33	0.63
7:6E:20:ASP:OD2	7:6E:23:VAL:N	2.31	0.63
15:6I:17:ARG:HH11	15:6I:77:ARG:NH2	1.97	0.63
26:1H:2154:G:H2'	26:1H:2155:G:H8	1.64	0.63
47:I8:14:ARG:NH1	59:I8:201:HOH:O	2.24	0.63
7:62:111:ARG:NH1	7:62:126:ASP:OD2	2.31	0.63
26:14:864:G:H1'	26:14:914:C:H42	1.63	0.63
26:14:1169:G:H1	26:14:1180:C:H42	1.44	0.63
49:G5:24:LEU:HD12	49:G5:60:LEU:HD21	1.80	0.63
5:4E:102:ALA:HB1	5:4E:106:PRO:HG2	1.78	0.63
39:A8:10:ARG:O	39:A8:14:VAL:HG13	1.98	0.63
1:1G:297:G:N2	1:1G:300:A:OP2	2.31	0.63
3:22:9:GLY:HA3	14:5A:49:HIS:HA	1.81	0.63
3:22:121:ALA:HB1	3:22:189:ALA:HB2	1.79	0.63
26:14:1049:C:N4	26:14:2751:G:O6	2.31	0.63
26:14:1203:G:H3'	26:14:1204:A:H5"	1.80	0.63
31:49:166:ASP:O	31:49:170:ARG:N	2.31	0.63
35:25:111:PHE:HB3	35:25:114:ILE:HG13	1.79	0.63
45:C5:39:VAL:O	45:C5:40:GLU:HB2	1.98	0.63
20:BI:30:LYS:HE3	20:BI:80:ARG:HH22	1.63	0.63
26:14:581:C:H2'	26:14:582:G:H8	1.64	0.63
26:14:2816:C:O3'	38:55:99:LYS:NZ	2.32	0.63
12:3I:58:VAL:O	12:3I:65:GLU:HA	1.98	0.63
46:H8:61:LEU:O	46:H8:64:GLY:HA2	1.99	0.63
12:3A:62:SER:HB2	12:3A:64:TYR:CD1	2.34	0.63
26:14:2611:U:C4	52:J5:3:LYS:HG3	2.34	0.63
26:1H:364:C:H3'	59:1H:3867:HOH:O	1.98	0.63
26:1H:1980:G:O2'	26:1H:1982:C:OP2	2.16	0.63
26:1H:2257:U:O2'	26:1H:2258:C:H5'	1.99	0.63
2:12:220:ASP:H	2:12:222:ILE:HD11	1.64	0.63
3:22:6:HIS:NE2	3:22:8:ILE:HB	2.14	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:42:151:LEU:O	5:42:152:ARG:NH1	2.32	0.63
30:39:134:GLY:HA2	30:39:166:ALA:HB2	1.80	0.63
2:1E:88:ALA:HB2	2:1E:219:VAL:HG13	1.81	0.63
1:1G:167:G:OP2	59:1G:1817:HOH:O	2.15	0.63
1:1G:407:G:OP1	4:32:115:ARG:NH2	2.32	0.63
1:1G:922:G:N3	1:1G:1398:A:H2	1.96	0.63
1:1G:957:U:H1'	1:1G:960:U:C5	2.30	0.63
4:32:122:ARG:NH2	4:32:134:ASP:HB3	2.14	0.63
7:62:62:PHE:HA	7:62:124:LEU:HD13	1.80	0.63
19:AA:42:PRO:HA	19:AA:45:VAL:HG13	1.81	0.63
20:BA:51:GLU:HA	20:BA:54:LYS:HE3	1.81	0.63
26:14:1482:U:H3	26:14:1512:G:H1	1.47	0.63
26:14:1754:C:OP1	40:75:96:ARG:NH1	2.32	0.63
29:29:50:GLY:O	29:29:74:PRO:HG2	1.98	0.63
5:4E:110:LEU:HD13	5:4E:118:ILE:HG21	1.81	0.62
26:1H:270(L):U:H5	26:1H:270(N):G:H21	1.47	0.62
26:1H:1019:U:HO2'	26:1H:1021:A:H2	1.46	0.62
1:1G:438:G:H4'	4:32:123:HIS:CD2	2.34	0.62
55:3L:2:C:H42	55:3L:71:G:H1	1.45	0.62
26:14:226:G:H21	26:14:228:A:H62	1.47	0.62
26:14:2143:C:H42	26:14:2148:G:H1	1.46	0.62
26:1H:1078:U:H1'	26:1H:1088:A:C2	2.35	0.62
26:1H:1786:A:H2	26:1H:2606:C:H1'	1.64	0.62
26:1H:2776:A:H4'	26:1H:2777:G:H5"	1.81	0.62
31:41:77:ILE:HG22	31:41:82:LEU:HD12	1.81	0.62
33:61:50:ARG:HD2	33:61:53:ALA:HB3	1.79	0.62
36:78:49:ARG:HD2	54:Q8:60:LEU:HB3	1.81	0.62
41:85:88:ILE:HG23	41:85:90:VAL:HB	1.80	0.62
24:3K:38:A:H3'	24:3K:39:G:H8	1.63	0.62
26:1H:102:G:OP1	49:K8:7:ARG:NH2	2.32	0.62
26:1H:193:U:H5	59:1H:4020:HOH:O	1.81	0.62
26:1H:991:C:OP2	59:1H:3760:HOH:O	2.16	0.62
1:1G:80:G:H1	1:1G:89:U:H3	1.48	0.62
8:72:109:ILE:HG22	8:72:137:VAL:HB	1.81	0.62
16:7A:34:GLU:OE1	16:7A:55:ARG:NH1	2.30	0.62
26:14:2873:A:H8	38:55:6:SER:H	1.46	0.62
27:1J:87:G:C2	27:1J:89:G:H5'	2.35	0.62
31:49:166:ASP:N	31:49:166:ASP:OD1	2.31	0.62
1:13:661:G:H1	1:13:744:C:H42	1.48	0.62
1:13:1305:G:H22	1:13:1331:G:C2'	2.13	0.62
1:1G:1513:A:H2'	1:1G:1514:C:C6	2.34	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:22:37:GLN:O	3:22:41:GLY:N	2.28	0.62
26:14:71:A:OP2	26:14:71:A:H3'	1.98	0.62
26:14:1537:C:H2'	26:14:1538:G:C8	2.35	0.62
40:75:80:SER:HB3	40:75:83:ILE:HG13	1.81	0.62
1:13:963:G:H21	10:1I:55:LYS:CE	2.12	0.62
3:22:59:ARG:O	10:1A:93:GLY:HA2	1.99	0.62
26:14:102:G:OP1	49:G5:7:ARG:NH2	2.32	0.62
26:14:1186:G:N7	59:14:3604:HOH:O	2.31	0.62
32:59:10:PRO:HD2	32:59:50:VAL:O	2.00	0.62
37:45:136:ALA:N	37:45:137:TYR:HA	2.14	0.62
1:13:501:C:H2'	1:13:502:G:H8	1.62	0.62
10:1I:58:ASP:OD1	59:1I:201:HOH:O	2.16	0.62
22:1K:18:G:H5'	22:1K:57:G:O6	2.00	0.62
26:1H:252:G:OP2	36:78:50:ARG:NH1	2.33	0.62
47:I8:72:ARG:HH11	47:I8:75:LEU:HD12	1.65	0.62
23:2L:24:C:H2'	23:2L:25:U:C6	2.33	0.62
26:14:2238:G:H2'	26:14:2238:G:N3	2.14	0.62
26:1H:33:U:H4'	26:1H:34:C:OP1	1.97	0.62
43:E8:58:ALA:HB1	43:E8:64:MET:HE2	1.82	0.62
49:K8:58:ALA:O	49:K8:62:THR:HG22	1.99	0.62
26:14:2789:C:H2'	26:14:2790:A:C8	2.34	0.62
26:14:2889:C:H3'	26:14:2891:G:C8	2.35	0.62
28:19:10:THR:OG1	28:19:13:ARG:HB2	1.98	0.62
28:19:12:SER:HB2	28:19:208:LYS:HB3	1.80	0.62
1:13:1366:C:H2'	1:13:1367:C:H6	1.64	0.62
2:1E:98:LEU:HB2	2:1E:101:MET:HE3	1.80	0.62
12:3I:11:VAL:HG21	17:8I:34:LYS:HD3	1.79	0.62
40:B8:102:ILE:HG23	40:B8:110:ILE:HD12	1.82	0.62
26:14:389:G:N1	36:35:71:VAL:HG12	2.14	0.62
34:15:56:ASN:N	34:15:125:GLY:HA3	2.14	0.62
1:13:1132:C:H2'	1:13:1133:G:C8	2.34	0.62
4:3E:107:ARG:HH22	4:3E:194:LEU:HD22	1.65	0.62
26:1H:2016:U:O2	52:N8:7:PRO:HG2	1.99	0.62
29:21:25:VAL:HG11	40:B8:7:ILE:HG22	1.82	0.62
40:B8:26:ASP:HB2	40:B8:91:ARG:HA	1.80	0.62
23:2L:8:4SU:H6	23:2L:8:4SU:H5"	1.80	0.62
26:14:833:U:O2	36:35:55:ARG:NH1	2.30	0.62
2:1E:223:ILE:O	2:1E:227:GLY:N	2.32	0.62
18:9I:47:THR:O	18:9I:83:GLU:N	2.29	0.62
26:1H:34:C:O2'	26:1H:35:G:OP2	2.15	0.62
26:1H:86:C:H4'	26:1H:104:U:H1'	1.80	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1H:2183:C:H2'	26:1H:2184:G:C8	2.33	0.62
26:1H:2845:G:H2'	26:1H:2846:G:C8	2.35	0.62
33:61:21:VAL:HG21	33:61:25:TYR:HD2	1.65	0.62
46:H8:105:VAL:HG22	46:H8:140:ASP:HA	1.81	0.62
47:I8:53:MET:HG3	47:I8:59:LEU:CD2	2.30	0.62
22:1L:15:G:H22	22:1L:48:C:H41	1.48	0.62
25:4L:24:A:H2'	25:4L:25:A:C2	2.35	0.62
26:14:855:G:H5'	26:14:856:C:OP2	2.00	0.62
27:1J:22:U:H3	27:1J:61:G:H1	1.47	0.62
37:45:139:GLU:N	37:45:139:GLU:OE2	2.33	0.62
1:13:187:C:O2	1:13:191(A):G:N1	2.33	0.61
1:13:474:G:H2'	1:13:475:G:C8	2.35	0.61
1:13:1129:C:H1'	1:13:1146:A:H61	1.63	0.61
2:1E:21:ARG:O	2:1E:23:ARG:N	2.33	0.61
5:4E:45:PHE:CE2	5:4E:47:LYS:HD2	2.35	0.61
26:1H:71:A:C8	26:1H:71:A:H5'	2.35	0.61
26:1H:1329:U:H5"	26:1H:1330:C:H5	1.63	0.61
1:1G:1460:A:OP2	20:BA:27:LYS:NZ	2.32	0.61
26:14:1021:A:H62	26:14:1141:U:H3	1.47	0.61
26:14:1525:G:H2'	26:14:1526:G:H8	1.64	0.61
33:69:93:THR:HG22	33:69:119:PRO:HG3	1.82	0.61
38:55:38:VAL:HG22	38:55:112:ALA:HB2	1.81	0.61
41:85:98:LEU:HB2	41:85:102:GLU:HB2	1.80	0.61
41:85:100:VAL:O	41:85:101:ARG:HG2	2.00	0.61
1:13:1182:G:H4'	1:13:1183:A:H5"	1.80	0.61
39:A8:28:VAL:HG11	39:A8:98:VAL:HG13	1.82	0.61
51:M8:56:VAL:O	51:M8:60:GLN:NE2	2.33	0.61
1:1G:1023:G:H5"	1:1G:1024:G:N2	2.15	0.61
1:1G:1256:A:N6	1:1G:1278:U:OP2	2.32	0.61
18:9A:22:VAL:HG13	18:9A:56:THR:HA	1.81	0.61
26:14:2232:U:P	48:F5:40:ARG:HH22	2.24	0.61
49:G5:4:SER:HB3	49:G5:7:ARG:HD2	1.81	0.61
1:13:390:C:O3'	16:7I:28:ARG:NH2	2.33	0.61
19:AI:50:ALA:HB1	19:AI:57:HIS:HB3	1.81	0.61
26:1H:176:G:O2'	26:1H:177:G:H5'	2.00	0.61
26:1H:1257:C:H4'	30:31:83:PHE:CD1	2.35	0.61
26:1H:2646:C:OP2	26:1H:2732:G:O2'	2.15	0.61
48:J8:77:ALA:N	48:J8:78:LYS:HB2	2.16	0.61
49:K8:42:GLY:C	49:K8:44:LEU:H	2.08	0.61
1:1G:129(A):G:C6	1:1G:188:U:H4'	2.35	0.61
1:1G:208:U:O2'	1:1G:209:U:H5"	2.00	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:12:33:TYR:HB3	2:12:41:ILE:HG23	1.81	0.61
3:22:28:GLN:HB3	3:22:32:LEU:HD12	1.82	0.61
4:32:15:GLU:OE1	4:32:66:ARG:NH1	2.34	0.61
14:5A:24:CYS:HB3	14:5A:29:ARG:HH21	1.65	0.61
34:15:137:LYS:HB3	34:15:137:LYS:HZ2	1.64	0.61
1:13:1129:C:H42	1:13:1143:G:H1	1.48	0.61
26:1H:577:G:O6	59:1H:3796:HOH:O	2.12	0.61
39:A8:30:ARG:HG3	39:A8:30:ARG:O	2.00	0.61
26:14:1204:A:N1	26:14:1241:A:H2	1.98	0.61
26:14:2212:A:O2'	26:14:2215:G:N7	2.30	0.61
27:1J:9:G:P	39:65:25:ARG:HH22	2.23	0.61
29:29:65:GLY:O	29:29:68:ALA:HB2	2.00	0.61
2:1E:178:ARG:HG3	8:7E:72:PRO:HA	1.81	0.61
26:1H:49:A:N7	26:1H:120:U:C5	2.64	0.61
26:1H:2210:G:H4'	26:1H:2211:G:OP2	2.00	0.61
28:11:177:LEU:HD11	28:11:183:ARG:HG2	1.82	0.61
51:M8:16:CYS:HB3	51:M8:36:CYS:HB3	1.83	0.61
1:1G:1124:G:O2'	1:1G:1145:C:N4	2.33	0.61
1:1G:1322:C:O2'	1:1G:1323:G:H5'	2.00	0.61
19:AA:18:LYS:HA	19:AA:21:GLU:HG2	1.81	0.61
26:14:897:C:N3	26:14:898:C:N4	2.47	0.61
26:14:1332:G:N2	26:14:1609:A:O2'	2.34	0.61
46:D5:48:PHE:HE1	46:D5:71:VAL:HG21	1.64	0.61
8:7E:87:SER:HB2	8:7E:93:VAL:CB	2.27	0.61
1:13:642:A:N3	8:7E:113:SER:OG	2.33	0.61
18:9I:66:LEU:O	18:9I:70:ILE:HG13	2.01	0.61
50:L8:8:LEU:HB2	50:L8:28:LEU:HD22	1.83	0.61
1:1G:222:U:H2'	1:1G:223:U:C6	2.35	0.61
1:1G:1347:G:O2'	1:1G:1373:G:O6	2.10	0.61
4:32:173:TRP:CD1	4:32:174:LEU:HG	2.35	0.61
20:BA:99:LEU:HD12	20:BA:100:ILE:HD12	1.80	0.61
27:1J:103:U:O2'	46:D5:72:ARG:HG2	2.00	0.61
46:D5:69:THR:HB	46:D5:88:PHE:HB3	1.82	0.61
1:13:1349:A:H2'	1:13:1350:A:H8	1.66	0.61
17:8I:22:LEU:HD11	17:8I:39:SER:HB3	1.82	0.61
26:1H:273(F):C:H3'	26:1H:274:G:H5"	1.82	0.61
26:1H:1078:U:H1'	26:1H:1088:A:H2	1.65	0.61
49:K8:3:LEU:H	49:K8:5:GLU:N	1.98	0.61
26:14:479:A:N3	26:14:481:G:H5"	2.16	0.61
26:14:2019:A:OP2	52:J5:9:LYS:NZ	2.32	0.61
27:1J:17:C:H2'	27:1J:18:G:O4'	2.00	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:19:8:PRO:HB3	28:19:14:ARG:HB2	1.83	0.61
1:13:757:U:H2'	1:13:758:G:O4'	1.99	0.61
38:98:87:TYR:HD1	38:98:90:ARG:HD2	1.64	0.61
1:1G:34:C:H2'	1:1G:35:G:C8	2.36	0.61
1:1G:411:A:H62	1:1G:413:G:N2	1.98	0.61
3:22:58:GLU:HB2	3:22:65:ALA:HB3	1.81	0.61
1:13:837:G:OP2	1:13:842:C:N4	2.34	0.61
1:13:1020:U:H2'	1:13:1021:G:C8	2.36	0.61
2:1E:19:HIS:NE2	2:1E:206:ASP:HB2	2.15	0.61
5:4E:76:ILE:HG13	5:4E:93:PRO:HG3	1.82	0.61
26:1H:1022:G:N7	34:58:66:LYS:NZ	2.49	0.61
38:98:48:VAL:O	38:98:51:LEU:N	2.34	0.61
43:E8:14:PRO:HG2	43:E8:78:GLU:HB2	1.83	0.61
47:I8:27:GLU:HG3	47:I8:68:GLU:HA	1.82	0.61
19:AA:41:VAL:HG22	19:AA:44:MET:HG3	1.82	0.61
55:3L:16:U:C2	55:3L:61:C:H5"	2.36	0.61
26:14:2228:G:OP2	28:19:263:ARG:NH2	2.34	0.61
26:14:2275:C:C6	26:14:2275:C:H5'	2.35	0.61
28:19:238:GLY:O	59:19:401:HOH:O	2.16	0.61
30:39:15:SER:OG	30:39:16:GLY:N	2.32	0.61
1:13:153:C:N4	1:13:168:G:H1	1.97	0.60
1:13:170:U:H2'	1:13:171:A:H8	1.66	0.60
4:3E:30:LYS:HA	4:3E:35:ARG:HE	1.65	0.60
13:4I:4:ILE:HG22	13:4I:5:ALA:H	1.66	0.60
26:1H:973:A:OP2	59:1H:3813:HOH:O	2.16	0.60
26:1H:1210:A:H5'	26:1H:1210:A:C8	2.35	0.60
45:C5:27:VAL:HG12	45:C5:28:LYS:O	2.01	0.60
1:13:677:U:H3	1:13:713:G:H22	1.49	0.60
1:13:838:G:H1	1:13:848:C:H42	1.49	0.60
1:13:1007:C:H42	1:13:1022:G:H1	1.48	0.60
1:13:1194:U:H2'	1:13:1195:C:C6	2.36	0.60
22:1K:65:C:H5	22:1K:67:A:N6	1.99	0.60
26:1H:2217:G:N7	59:1H:3882:HOH:O	2.31	0.60
48:J8:93:GLU:C	48:J8:95:LEU:H	2.08	0.60
1:1G:963:G:H21	10:1A:55:LYS:CD	2.11	0.60
5:42:15:ARG:HD3	25:4L:25:A:H2'	1.83	0.60
1:13:13:U:OP1	59:13:1933:HOH:O	2.16	0.60
1:13:74:C:N3	1:13:75:C:N4	2.49	0.60
26:1H:76:C:O2'	49:K8:62:THR:HG21	2.00	0.60
29:21:39:PRO:HD3	29:21:45:THR:HG23	1.81	0.60
29:21:131:ALA:HB1	29:21:135:HIS:HE1	1.66	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:B8:4:GLY:HA2	40:B8:7:ILE:HG12	1.82	0.60
14:5A:21:TYR:HE1	14:5A:23:ARG:HE	1.49	0.60
26:14:2264:C:N4	47:E5:15:ASP:OD2	2.31	0.60
26:14:2327:A:H2'	26:14:2328:A:C8	2.35	0.60
33:69:45:LYS:HA	33:69:48:GLU:HB3	1.83	0.60
41:85:92:ARG:C	41:85:94:ASN:H	2.09	0.60
1:13:1349:A:H2'	1:13:1350:A:C8	2.35	0.60
2:1E:52:GLU:HB3	2:1E:56:ARG:NH1	2.16	0.60
23:2K:24:C:H2'	23:2K:25:U:C6	2.36	0.60
26:1H:582:G:N7	59:1H:3888:HOH:O	2.32	0.60
26:1H:2099:U:N3	26:1H:2190:G:O6	2.19	0.60
1:1G:673:G:H2'	1:1G:674:G:C8	2.37	0.60
3:22:54:ARG:HB2	3:22:69:HIS:HB2	1.82	0.60
13:4A:67:GLU:O	13:4A:70:LEU:N	2.25	0.60
26:14:6:A:C5	34:15:131:GLN:HB2	2.36	0.60
1:13:1305:G:H22	1:13:1331:G:H2'	1.65	0.60
2:1E:231:GLU:OE1	2:1E:231:GLU:N	2.34	0.60
9:8E:13:ALA:HB2	9:8E:68:GLY:HA3	1.83	0.60
26:1H:1113:U:H2'	26:1H:1114:G:C8	2.36	0.60
26:1H:1243:G:H4'	36:78:7:ARG:HH21	1.66	0.60
30:31:6:VAL:HG11	30:31:119:ARG:HA	1.84	0.60
37:88:110:THR:HG23	37:88:113:GLN:OE1	2.00	0.60
1:1G:457:C:H2'	1:1G:458:C:C6	2.37	0.60
1:1G:1268:A:H2'	1:1G:1269:A:C8	2.37	0.60
2:12:74:LYS:HE2	2:12:166:ASP:HB2	1.84	0.60
28:19:30:GLU:HG3	28:19:63:ARG:CZ	2.30	0.60
1:13:1157:A:H2'	1:13:1157:A:N3	2.16	0.60
26:1H:667:U:O2	54:Q8:2:PRO:HD2	2.01	0.60
26:1H:1729:A:O2'	26:1H:1730:U:O5'	2.18	0.60
50:L8:35:ARG:HB3	50:L8:37:LEU:HD21	1.83	0.60
26:14:1141:U:OP2	34:15:63:THR:OG1	2.18	0.60
30:39:21:ALA:O	30:39:23:ASP:N	2.35	0.60
37:45:111:GLU:HG3	37:45:115:MET:HE3	1.84	0.60
37:45:136:ALA:H	37:45:137:TYR:HA	1.66	0.60
39:65:88:ASP:C	39:65:90:GLY:H	2.08	0.60
1:13:877:C:OP1	8:7E:88:LYS:NZ	2.32	0.60
1:13:973:G:H3'	1:13:974:A:H5"	1.83	0.60
1:13:982:U:H5"	14:5I:6:LEU:HD11	1.83	0.60
13:4I:37:THR:O	13:4I:55:ARG:NH1	2.35	0.60
26:1H:336:C:OP1	45:G8:83:THR:HG23	2.02	0.60
26:1H:1728:G:H2'	26:1H:1731:G:O6	2.02	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1H:2401:U:H2'	26:1H:2402:C:O4'	2.00	0.60
31:41:142:PRO:HB2	51:M8:31:ILE:HG21	1.84	0.60
38:98:100:LEU:HD11	38:98:113:LEU:HD13	1.84	0.60
46:H8:116:VAL:HG22	46:H8:146:ILE:HA	1.82	0.60
1:1G:871:U:OP1	59:1G:1818:HOH:O	2.16	0.60
7:62:113:GLU:HB2	7:62:119:ARG:HG2	1.83	0.60
10:1A:79:ARG:H	10:1A:79:ARG:HD3	1.67	0.60
12:3A:58:VAL:O	12:3A:65:GLU:HA	2.01	0.60
19:AA:48:THR:O	19:AA:48:THR:OG1	2.20	0.60
26:14:1794:U:H2'	26:14:1795:C:H6	1.66	0.60
26:14:2099:U:H3	26:14:2190:G:H1	1.50	0.60
26:14:2273:A:H2'	26:14:2274:A:C8	2.37	0.60
40:75:56:GLY:O	40:75:59:THR:HG23	2.02	0.60
26:1H:442:G:H1'	30:31:48:THR:HG21	1.83	0.60
26:1H:1103:A:H3'	26:1H:1104:C:C6	2.37	0.60
31:41:16:ARG:NH2	31:41:31:VAL:HG21	2.16	0.60
41:C8:34:LYS:NZ	41:C8:37:GLU:OE1	2.34	0.60
9:82:70:LYS:O	9:82:74:ILE:HG13	2.01	0.60
26:14:1332:G:H21	26:14:1610:A:H8	1.47	0.60
36:35:126:VAL:HA	36:35:145:PRO:HD2	1.84	0.60
39:65:106:ARG:HA	39:65:110:LEU:HD11	1.84	0.60
40:75:45:PHE:CE1	40:75:74:ARG:HG3	2.37	0.60
48:F5:92:LYS:O	48:F5:94:LEU:N	2.35	0.60
1:13:1167:A:H2'	1:13:1169:A:C8	2.37	0.60
3:2E:123:GLN:O	3:2E:128:PHE:HB2	2.02	0.60
26:1H:259:G:N2	26:1H:621:A:H8	2.00	0.60
26:1H:761:A:H5"	59:1H:3782:HOH:O	2.02	0.60
26:1H:2400:G:H2'	26:1H:2401:U:C6	2.37	0.60
30:31:185:ASP:HA	30:31:188:ARG:HD3	1.82	0.60
9:82:117:HIS:HB2	9:82:121:ARG:O	2.01	0.60
26:14:1266:G:O5'	43:A5:15:ARG:NH2	2.35	0.60
26:14:2152:G:C6	26:14:2153:G:H1'	2.37	0.60
29:29:31:CYS:SG	29:29:51:PHE:HB3	2.41	0.60
5:4E:41:VAL:HG13	5:4E:113:ALA:HB2	1.84	0.60
9:8E:20:ARG:HB2	9:8E:60:ASP:HB2	1.83	0.60
26:1H:654(C):G:C2	26:1H:654(D):G:H1'	2.37	0.60
26:1H:1107:G:H2'	26:1H:1108:U:C6	2.37	0.60
26:1H:1178:C:H4'	26:1H:1179:C:OP1	2.02	0.60
26:1H:2688:U:H1'	26:1H:2721:A:H61	1.67	0.60
29:21:55:ASN:ND2	29:21:76:ARG:HB3	2.17	0.60
26:14:1028:A:H2'	26:14:1029:A:C8	2.36	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:14:1796:U:H2'	26:14:1797:C:C6	2.37	0.60
31:49:120:LEU:N	31:49:179:PRO:O	2.23	0.60
1:13:612:C:O2	1:13:629:G:N2	2.35	0.59
11:2I:21:ILE:HG12	11:2I:30:VAL:HG12	1.84	0.59
26:1H:85:G:OP2	45:G8:9:LYS:HB2	2.02	0.59
29:21:51:PHE:CE2	29:21:52:LEU:HD23	2.37	0.59
41:C8:8:VAL:HG23	41:C8:11:ARG:HH21	1.67	0.59
1:1G:842:C:O2'	1:1G:848:C:N3	2.33	0.59
4:32:150:GLU:CD	4:32:150:GLU:H	2.09	0.59
27:1J:16:G:H1	27:1J:68:C:H42	1.50	0.59
40:75:2:ASN:OD1	40:75:4:GLY:HA3	2.01	0.59
15:6I:39:LEU:HB3	15:6I:56:LEU:HD12	1.84	0.59
26:1H:1058:U:H2'	26:1H:1059:G:H8	1.66	0.59
29:21:57:LYS:HG3	29:21:59:VAL:HG12	1.84	0.59
39:A8:25:ARG:NH1	39:A8:42:ASP:OD2	2.34	0.59
40:75:10:VAL:O	40:75:12:SER:N	2.33	0.59
1:13:645:C:H2'	1:13:646:U:O4'	2.03	0.59
1:13:1062:U:H2'	1:13:1063:C:C6	2.37	0.59
6:5E:96:PRO:HB3	18:9I:30:ASP:CG	2.28	0.59
22:1K:47:U:O2'	22:1K:49:G:OP2	2.20	0.59
49:K8:4:SER:O	49:K8:4:SER:OG	2.15	0.59
1:1G:1018:C:H2'	1:1G:1019:C:O4'	2.01	0.59
1:1G:1208:C:H2'	1:1G:1209:C:H6	1.68	0.59
1:1G:1260:C:H3'	1:1G:1260:C:H6	1.66	0.59
23:2L:62:C:H2'	23:2L:63:C:H6	1.67	0.59
26:14:1019:U:H3	26:14:1142(A):A:H62	1.49	0.59
26:14:1794:U:H2'	26:14:1795:C:C6	2.37	0.59
26:14:1952:A:C5	35:25:22:ILE:HD11	2.37	0.59
32:59:6:ARG:HB2	32:59:65:HIS:CE1	2.38	0.59
32:59:150:ALA:O	32:59:154:PRO:HG3	2.02	0.59
3:2E:32:LEU:HD13	3:2E:59:ARG:HD3	1.85	0.59
26:1H:2052:G:H4'	29:21:143:ASN:O	2.01	0.59
46:H8:19:ARG:HH11	46:H8:84:GLU:HB2	1.67	0.59
51:M8:42:PHE:O	51:M8:44:THR:N	2.36	0.59
1:1G:1392:G:H21	1:1G:1502:A:H8	1.48	0.59
2:12:162:ILE:HG23	2:12:182:ILE:HG21	1.85	0.59
13:4A:23:TYR:CE2	13:4A:71:ARG:HG3	2.37	0.59
55:3L:33:U:H2'	55:3L:34:G:H2'	1.83	0.59
39:65:43:GLU:HB2	47:E5:49:LYS:NZ	2.17	0.59
48:F5:88:LYS:O	48:F5:91:LYS:HB3	2.02	0.59
1:13:826:C:H2'	1:13:827:U:O2	2.01	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:13:1197:G:H5”	59:13:1906:HOH:O	2.02	0.59
10:1I:54:PHE:CZ	10:1I:55:LYS:NZ	2.69	0.59
17:8I:48:GLU:O	17:8I:50:LYS:N	2.36	0.59
26:1H:389:G:N1	36:78:71:VAL:HG12	2.16	0.59
26:1H:1593:G:H2’	26:1H:1594:G:C8	2.36	0.59
26:1H:2255:G:OP2	59:1H:3815:HOH:O	2.17	0.59
26:1H:2499:C:OP2	59:1H:3733:HOH:O	2.17	0.59
32:51:58:GLU:O	32:51:60:ARG:N	2.36	0.59
1:1G:1134:G:C2	1:1G:1135:U:H1’	2.37	0.59
55:3L:47:U:O3’	55:3L:48:C:H4’	2.01	0.59
26:14:6:A:N7	34:15:131:GLN:HB2	2.17	0.59
26:14:918:A:O2’	27:1J:96:G:N2	2.34	0.59
26:14:1226:G:H4’	42:95:84:LYS:HG2	1.84	0.59
7:6E:108:ALA:HA	7:6E:111:ARG:HD2	1.82	0.59
24:3K:38:A:H3’	24:3K:39:G:C8	2.38	0.59
26:1H:833:U:O2	36:78:55:ARG:NH2	2.32	0.59
30:31:136:THR:HG22	30:31:166:ALA:O	2.03	0.59
1:1G:589:C:H42	1:1G:650:G:H1	1.49	0.59
1:1G:1305:G:H22	1:1G:1331:G:C2’	2.11	0.59
1:1G:1423:G:OP1	35:25:49:ARG:NH2	2.35	0.59
8:72:101:PRO:HG3	8:72:133:LEU:HD11	1.85	0.59
32:59:157:TYR:CG	32:59:171:LEU:HD11	2.38	0.59
32:59:158:HIS:O	32:59:158:HIS:ND1	2.30	0.59
1:13:1132:C:H2’	1:13:1133:G:H8	1.67	0.59
19:AI:11:VAL:HG11	19:AI:16:LEU:HD22	1.84	0.59
26:1H:589:C:H2’	26:1H:590:A:C8	2.38	0.59
26:1H:1332:G:H5’	26:1H:1332:G:C8	2.38	0.59
26:1H:1406:U:H2’	26:1H:1407:C:C6	2.37	0.59
26:1H:1516:U:H2’	26:1H:1517:G:H8	1.66	0.59
38:98:55:ALA:HB2	38:98:79:LEU:HD13	1.85	0.59
1:1G:554:C:H2’	1:1G:555:C:H6	1.67	0.59
7:62:26:PHE:O	7:62:30:ILE:HG13	2.03	0.59
39:65:107:GLU:H	39:65:110:LEU:HD11	1.68	0.59
1:13:67:C:H2’	1:13:68:G:C8	2.37	0.59
1:13:67:C:H2’	1:13:68:G:H8	1.67	0.59
1:13:964:A:N6	59:13:1958:HOH:O	2.35	0.59
5:4E:37:ARG:HH12	5:4E:111:GLU:HG2	1.68	0.59
11:2I:84:VAL:HG21	11:2I:91:ARG:HG2	1.84	0.59
22:1K:59:C:O2’	22:1K:60:U:OP2	2.17	0.59
26:1H:270(N):G:N3	33:61:50:ARG:NH2	2.51	0.59
26:1H:2580:U:H4’	29:21:130:GLY:HA3	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1H:2584:U:H2'	26:1H:2585:U:H2'	1.84	0.59
29:21:36:ARG:NH2	29:21:88:GLY:O	2.36	0.59
46:H8:139:VAL:HG22	46:H8:155:LEU:HD22	1.83	0.59
52:N8:41:PRO:O	52:N8:44:THR:OG1	2.20	0.59
1:1G:292:G:OP2	1:1G:305:G:N2	2.27	0.59
1:1G:619:U:H3	4:32:134:ASP:HB2	1.68	0.59
1:1G:1003:G:N2	1:1G:1005:A:OP1	2.34	0.59
1:1G:1110:A:OP2	59:1G:1820:HOH:O	2.17	0.59
26:14:876:C:H2'	26:14:877:U:H5'	1.84	0.59
26:14:2105:C:H2'	26:14:2106:G:O4'	2.03	0.59
31:49:56:ALA:HB2	31:49:153:ARG:CZ	2.33	0.59
32:59:125:VAL:HG22	32:59:126:PRO:HA	1.83	0.59
1:13:323:U:H5'	20:BI:23:ARG:HB2	1.85	0.59
22:1K:21:A:C6	22:1K:48:C:H1'	2.38	0.59
26:1H:1010:A:OP2	59:1H:3812:HOH:O	2.16	0.59
26:1H:2807:G:H3'	26:1H:2808:U:H5"	1.85	0.59
32:51:144:VAL:O	32:51:148:ILE:HG12	2.02	0.59
46:H8:108:PRO:HB2	46:H8:112:ARG:HA	1.85	0.59
2:12:165:VAL:HG23	2:12:166:ASP:H	1.66	0.59
27:1J:15:A:H1'	27:1J:109:G:C8	2.37	0.59
37:45:137:TYR:HD1	37:45:137:TYR:O	1.85	0.59
13:4I:23:TYR:CD2	13:4I:67:GLU:HA	2.37	0.59
26:1H:141:A:C8	26:1H:1408:C:H1'	2.38	0.59
26:1H:2402:C:O2'	26:1H:2403:C:OP2	2.21	0.59
38:98:38:VAL:HG22	38:98:112:ALA:HB2	1.83	0.59
38:98:117:VAL:O	38:98:118:GLU:HB2	2.01	0.59
1:1G:1492:A:H5"	12:3A:47:LYS:HD3	1.84	0.59
18:9A:32:ARG:O	59:9A:201:HOH:O	2.17	0.59
22:1L:53:G:N2	22:1L:61:C:N3	2.39	0.59
26:14:1864:U:OP1	26:14:2410:G:O2'	2.19	0.59
28:19:69:ARG:HD3	28:19:105:ILE:HD11	1.85	0.59
28:19:182:LEU:N	28:19:272:ALA:HB3	2.15	0.59
41:85:82:GLY:O	41:85:86:ALA:N	2.35	0.59
1:13:266:G:H5'	1:13:268:C:H41	1.68	0.58
22:1K:66:U:H3'	22:1K:67:A:C5'	2.33	0.58
24:3K:76:A:H8	26:1H:2394:C:N4	1.96	0.58
26:1H:111:A:H4'	49:K8:69:ARG:NH2	2.18	0.58
26:1H:1794:U:H2'	26:1H:1795:C:H6	1.67	0.58
26:1H:2362:G:OP1	54:Q8:44:LYS:NZ	2.36	0.58
31:41:83:ARG:H	31:41:86:MET:HE2	1.68	0.58
48:J8:8:SER:HB3	48:J8:66:HIS:CD2	2.37	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:BA:53:LEU:HD12	20:BA:100:ILE:HG22	1.85	0.58
26:14:2208:U:H4'	28:19:151:LYS:HG2	1.84	0.58
27:1J:6:C:H2'	27:1J:7:G:H5"	1.85	0.58
29:29:68:ALA:C	29:29:70:ALA:H	2.09	0.58
1:13:1125:U:C2	1:13:1126:U:C4	2.91	0.58
4:3E:31:CYS:SG	4:3E:33:MET:HB2	2.43	0.58
26:1H:1778:U:OP1	59:1H:3816:HOH:O	2.17	0.58
26:1H:2061:G:P	59:1H:3765:HOH:O	2.60	0.58
30:31:12:LEU:HD13	30:31:124:LEU:HD11	1.84	0.58
39:A8:42:ASP:C	39:A8:44:LYS:H	2.10	0.58
1:1G:1318:A:H4'	19:AA:37:ARG:HH21	1.68	0.58
3:22:148:GLY:HA3	3:22:172:ARG:O	2.03	0.58
20:BA:45:GLN:HB2	20:BA:91:LEU:HD22	1.84	0.58
22:1L:37:AET:HM62	22:1L:38:A:C6	2.38	0.58
26:14:1434:A:H61	26:14:1558:A:H62	1.49	0.58
33:69:79:ILE:O	33:69:143:SER:HA	2.03	0.58
33:69:109:ILE:HB	33:69:130:TYR:CZ	2.38	0.58
1:13:475:G:OP1	16:7I:81:ARG:NH2	2.34	0.58
1:13:749:C:H2'	1:13:750:G:H8	1.68	0.58
16:7I:20:VAL:HG21	16:7I:32:TYR:CD2	2.38	0.58
1:1G:600:C:H2'	1:1G:601:C:C6	2.38	0.58
5:42:31:LEU:HA	5:42:45:PHE:HB2	1.84	0.58
10:1A:54:PHE:CE1	10:1A:55:LYS:HD2	2.37	0.58
26:14:1040:C:H2'	26:14:1041:C:C6	2.37	0.58
26:14:1727:U:H3	26:14:1733:G:H1	1.50	0.58
33:69:9:LEU:HD11	33:69:35:LEU:HB3	1.85	0.58
34:15:132:ALA:C	34:15:133:GLN:HG3	2.28	0.58
1:13:559:A:OP1	5:4E:126:ARG:NH2	2.36	0.58
1:13:649:G:H2'	1:13:650:G:H8	1.68	0.58
1:13:1292:U:H2'	1:13:1293:G:C8	2.38	0.58
13:4I:117:VAL:HG13	13:4I:118:ALA:H	1.67	0.58
15:6I:63:ARG:HG2	15:6I:67:LEU:HD12	1.84	0.58
30:31:63:LYS:NZ	30:31:75:HIS:O	2.31	0.58
38:98:97:VAL:HG22	38:98:114:VAL:HG22	1.85	0.58
2:12:70:PHE:N	2:12:92:TYR:HA	2.18	0.58
19:AA:40:ILE:HG22	19:AA:67:VAL:HA	1.84	0.58
26:14:2807:G:H22	26:14:2892:A:N6	2.01	0.58
1:13:870:U:O2'	59:13:1934:HOH:O	2.17	0.58
22:1K:18:G:H5'	22:1K:57:G:C6	2.38	0.58
26:1H:192:C:P	59:1H:4020:HOH:O	2.61	0.58
26:1H:675:A:OP1	30:31:63:LYS:HE2	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:11:221:VAL:HG22	28:11:226:MET:HE2	1.84	0.58
45:G8:49:VAL:HG21	45:G8:55:TYR:CD2	2.39	0.58
1:1G:17:U:H2'	1:1G:18:C:C6	2.38	0.58
2:12:47:THR:HA	2:12:50:GLU:CD	2.28	0.58
11:2A:100:ALA:O	11:2A:102:GLY:N	2.36	0.58
29:29:37:ARG:HD2	29:29:44:TYR:OH	2.03	0.58
6:5E:97:PHE:HD1	18:9I:31:LEU:HD11	1.67	0.58
26:1H:621:A:OP2	36:78:108:LYS:NZ	2.36	0.58
26:1H:2632:A:O2'	26:1H:2811:G:O2'	2.20	0.58
28:11:142:VAL:HG23	28:11:193:VAL:HA	1.85	0.58
1:1G:328:C:H4'	1:1G:329:A:H5"	1.85	0.58
1:1G:620:C:H2'	1:1G:621:A:O4'	2.04	0.58
1:1G:922:G:H4'	5:42:20:GLN:HA	1.86	0.58
11:2A:70:LYS:HA	11:2A:73:MET:HE2	1.85	0.58
26:14:30:G:H2'	26:14:31:C:C6	2.38	0.58
39:65:11:LYS:HG3	39:65:91:PRO:HD3	1.86	0.58
1:13:560:U:O2'	1:13:561:U:OP2	2.19	0.58
1:1G:87:A:H4'	1:1G:88:C:OP1	2.03	0.58
6:52:6:VAL:HG22	6:52:90:VAL:HG22	1.85	0.58
26:14:847:U:OP2	59:14:3557:HOH:O	2.17	0.58
26:14:872:A:H4'	37:45:66:ILE:HD11	1.84	0.58
26:14:1847:A:H4'	26:14:1848:A:OP2	2.04	0.58
1:13:625:G:H4'	16:7I:16:HIS:ND1	2.18	0.58
8:7E:7:ALA:HB2	8:7E:85:ARG:HD2	1.85	0.58
23:2K:2:G:H2'	23:2K:3:C:H6	1.69	0.58
26:1H:600:G:N2	26:1H:605:C:O3'	2.37	0.58
1:1G:1324:A:H4'	1:1G:1362:C:H4'	1.85	0.58
1:1G:1347:G:C8	9:82:107:ARG:HB3	2.39	0.58
26:14:2712(A):A:P	59:14:3511:HOH:O	2.54	0.58
31:49:76:SER:OG	31:49:82:LEU:O	2.13	0.58
52:J5:41:PRO:O	52:J5:44:THR:OG1	2.22	0.58
52:J5:52:TYR:C	52:J5:54:GLY:H	2.10	0.58
1:13:1:U:C5	1:13:630:G:H2'	2.39	0.58
1:13:449:C:H5	16:7I:42:ARG:HH11	1.52	0.58
29:21:131:ALA:HB1	29:21:135:HIS:CE1	2.38	0.58
35:68:115:VAL:HG23	35:68:121:VAL:HG21	1.86	0.58
40:B8:105:LEU:C	40:B8:107:ASP:H	2.10	0.58
1:1G:395:C:N4	59:1G:1846:HOH:O	2.37	0.58
1:1G:957:U:H2'	1:1G:959:A:OP2	2.04	0.58
1:1G:1249:C:O2'	9:82:73:GLN:OE1	2.21	0.58
1:1G:1387:G:H2'	1:1G:1388:C:C6	2.38	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:1L:15:G:H22	22:1L:48:C:N4	2.02	0.58
22:1L:50:G:N2	22:1L:65:C:N3	2.52	0.58
26:14:634:C:H2'	26:14:635:C:C6	2.38	0.58
26:14:2611:U:H6	26:14:2611:U:H5'	1.69	0.58
26:14:2793:G:H21	26:14:2794:C:H5	1.50	0.58
30:39:24:LEU:HD21	30:39:119:ARG:HB3	1.86	0.58
32:59:158:HIS:HB3	32:59:171:LEU:HG	1.86	0.58
48:F5:62:VAL:HG21	48:F5:70:VAL:HG21	1.85	0.58
1:13:1346:A:H5"	9:8E:120:ARG:NH1	2.18	0.58
2:1E:54:THR:HG21	2:1E:201:ILE:HD11	1.86	0.58
15:6I:9:GLN:HA	15:6I:12:ILE:HD12	1.86	0.58
23:2K:2:G:H2'	23:2K:3:C:C6	2.39	0.58
26:1H:1103:A:H3'	26:1H:1104:C:H6	1.69	0.58
26:1H:2312:U:H5'	31:41:88:ILE:HD11	1.86	0.58
30:31:63:LYS:HE3	30:31:67:GLN:HB2	1.86	0.58
1:1G:581:G:OP1	15:6A:61:GLY:HA3	2.03	0.58
1:1G:690:G:H2'	1:1G:691:G:O4'	2.04	0.58
5:42:148:VAL:O	5:42:152:ARG:NH2	2.37	0.58
9:82:53:VAL:HG23	9:82:55:ALA:H	1.69	0.58
13:4A:13:LYS:HA	13:4A:44:ARG:HH11	1.68	0.58
20:BA:49:ALA:HA	20:BA:52:ALA:HB3	1.85	0.58
25:4L:14:A:O2'	25:4L:15:A:O5'	2.22	0.58
26:14:1006:C:H1'	34:15:106:MET:HG2	1.86	0.58
26:14:2591:C:OP2	28:19:239:ARG:HB3	2.04	0.58
29:29:47:VAL:HG21	29:29:86:PRO:HD2	1.85	0.58
41:85:92:ARG:CZ	42:95:11:GLN:H	2.17	0.58
17:8I:43:LEU:HD12	17:8I:68:ARG:HG2	1.86	0.57
26:1H:969:U:OP1	50:L8:17:LYS:HG2	2.04	0.57
1:1G:176:C:H2'	1:1G:177:C:H6	1.69	0.57
2:12:130:ARG:O	2:12:135:GLN:NE2	2.33	0.57
16:7A:22:THR:HA	16:7A:33:ILE:HD12	1.85	0.57
26:14:1048:A:N6	26:14:1111:A:O2'	2.37	0.57
1:13:963:G:N2	10:1I:55:LYS:HZ1	2.02	0.57
11:2I:48:ILE:HG21	11:2I:63:LEU:HD13	1.85	0.57
15:6I:17:ARG:HD3	15:6I:77:ARG:HH21	1.69	0.57
26:1H:827:U:H2'	26:1H:2430:A:C2	2.39	0.57
26:1H:1062:G:H2'	26:1H:1063:G:C8	2.39	0.57
25:4L:12:A:O2'	25:4L:13:A:OP2	2.20	0.57
26:14:729:G:OP2	28:19:13:ARG:NH1	2.35	0.57
30:39:122:LYS:HD2	30:39:191:ARG:HE	1.68	0.57
49:G5:4:SER:HA	49:G5:7:ARG:H	1.69	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:13:875:C:O2'	8:7E:14:ARG:NH1	2.36	0.57
12:3I:93:LEU:O	12:3I:96:VAL:HG13	2.04	0.57
12:3I:104:VAL:HG12	12:3I:105:TYR:H	1.70	0.57
26:1H:1266:G:O5'	43:E8:15:ARG:NH2	2.37	0.57
26:1H:1429:G:H2'	26:1H:1430:C:C6	2.39	0.57
26:1H:2032:G:H21	29:21:146:THR:CG2	2.17	0.57
45:G8:94:LYS:HZ2	45:G8:95:LYS:H	1.52	0.57
1:1G:195:A:OP2	59:1G:1819:HOH:O	2.16	0.57
1:1G:490:G:P	4:32:132:ARG:HH22	2.26	0.57
26:14:2635:C:H5"	29:29:77:ILE:O	2.03	0.57
27:1J:15:A:H3'	27:1J:16:G:H5'	1.87	0.57
31:49:111:LEU:HD23	31:49:117:PHE:HZ	1.69	0.57
46:D5:76:LEU:HA	46:D5:83:PRO:HA	1.85	0.57
48:F5:86:SER:N	48:F5:87:PRO:HD2	2.19	0.57
1:13:1159:U:O4'	1:13:1182:G:N2	2.38	0.57
5:4E:91:LEU:HD12	5:4E:120:THR:HG22	1.84	0.57
13:4I:39:ILE:HD12	13:4I:56:LEU:HD22	1.87	0.57
22:1K:7:A:H61	22:1K:67:A:H2	1.52	0.57
24:3K:16:U:O2	24:3K:61:C:H5"	2.04	0.57
26:1H:1086:A:H1'	26:1H:1103:A:H61	1.69	0.57
31:41:16:ARG:CZ	31:41:31:VAL:HG21	2.35	0.57
1:1G:280:C:H3'	1:1G:281:G:H5'	1.85	0.57
23:2L:7:G:H8	23:2L:7:G:H5'	1.68	0.57
23:2L:24:C:H2'	23:2L:25:U:H6	1.69	0.57
26:14:192:C:O2'	26:14:802:A:N3	2.38	0.57
26:14:1418:G:H8	26:14:1418:G:O5'	1.87	0.57
26:14:1786:A:C2	26:14:2606:C:H1'	2.39	0.57
26:14:2293:C:H5"	39:65:89:ARG:NH2	2.19	0.57
26:14:2531:A:H4'	32:59:157:TYR:CE2	2.39	0.57
29:29:91:VAL:HB	29:29:95:ILE:HD11	1.86	0.57
1:13:316:G:OP2	1:13:351:G:O2'	2.21	0.57
1:13:1369:C:H2'	1:13:1370:G:C8	2.39	0.57
15:6I:4:THR:OG1	15:6I:7:GLU:OE2	2.20	0.57
21:1F:5:ASP:O	21:1F:11:GLY:HA3	2.04	0.57
26:1H:270(W):G:O6	59:1H:3817:HOH:O	2.17	0.57
37:88:12:GLN:HG2	37:88:73:PRO:HD2	1.87	0.57
39:A8:105:ALA:O	39:A8:110:LEU:HD12	2.05	0.57
51:M8:23:GLU:OE1	51:M8:24:THR:N	2.37	0.57
4:32:149:ALA:HB1	4:32:151:LYS:HB3	1.85	0.57
6:52:33:TYR:OH	6:52:78:GLU:HG3	2.05	0.57
29:29:173:VAL:N	29:29:183:LEU:O	2.27	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:45:37:LEU:HD21	37:45:130:LYS:HD3	1.86	0.57
39:65:88:ASP:O	39:65:90:GLY:N	2.36	0.57
44:B5:53:LYS:HB3	44:B5:82:GLN:HB3	1.85	0.57
49:G5:13:ALA:HA	49:G5:16:LEU:HD23	1.87	0.57
1:13:4:U:C5	8:7E:102:ARG:HG3	2.39	0.57
1:13:1014:A:H2'	1:13:1015:A:C8	2.39	0.57
2:1E:163:PHE:HA	2:1E:185:ILE:O	2.03	0.57
10:1I:80:LYS:O	10:1I:84:GLN:HG2	2.04	0.57
47:I8:72:ARG:HB3	47:I8:75:LEU:HB2	1.85	0.57
1:1G:1043:C:H2'	1:1G:1044:A:C8	2.38	0.57
26:14:140:A:H8	26:14:1408:C:HO2'	1.47	0.57
40:75:123:GLN:HA	40:75:126:ALA:HB3	1.85	0.57
48:F5:53:VAL:HG12	48:F5:54:ALA:H	1.69	0.57
1:13:1450:U:N3	1:13:1452:C:O4'	2.38	0.57
2:1E:237:ALA:O	2:1E:239:VAL:N	2.38	0.57
20:BI:50:GLU:HG2	20:BI:100:ILE:HB	1.87	0.57
26:1H:265:A:C8	26:1H:266:G:H1'	2.40	0.57
26:1H:1496:A:H5'	26:1H:1497:U:OP1	2.04	0.57
26:1H:2688:U:H5	26:1H:2720:U:OP2	1.87	0.57
27:16:11:C:H3'	27:16:12:C:H6	1.69	0.57
31:41:124:SER:HB2	31:41:131:TYR:CE1	2.40	0.57
36:78:59:LEU:O	54:Q8:13:ARG:HD2	2.04	0.57
42:D8:14:VAL:HB	42:D8:96:ILE:HG13	1.85	0.57
7:62:88:PRO:HG3	7:62:145:ALA:HA	1.87	0.57
26:14:880:G:H1'	26:14:898:C:H42	1.70	0.57
26:14:2577:A:O4'	52:J5:3:LYS:HB2	2.05	0.57
26:14:2711:A:OP1	59:14:3511:HOH:O	2.18	0.57
39:65:3:ARG:HD2	39:65:4:LEU:N	2.19	0.57
1:13:222:U:H2'	1:13:223:U:C6	2.39	0.57
1:13:271:C:H2'	1:13:272:C:H6	1.68	0.57
1:13:742:G:H4'	15:6I:58:MET:HE1	1.87	0.57
17:8I:100:LYS:HG2	17:8I:101:ARG:HG3	1.87	0.57
26:1H:548:A:N1	42:D8:21:ARG:NH1	2.53	0.57
26:1H:907:U:O2'	37:88:101:ARG:NH2	2.31	0.57
26:1H:1187:G:N7	59:1H:3891:HOH:O	2.32	0.57
26:1H:2172:U:H4'	26:1H:2173:A:OP1	2.04	0.57
27:16:1:U:H2'	27:16:2:C:C6	2.39	0.57
45:G8:30:VAL:HG22	45:G8:37:VAL:HG12	1.86	0.57
4:32:4:TYR:HE2	4:32:11:LEU:HD11	1.68	0.57
5:42:35:GLY:HA3	5:42:41:VAL:HG23	1.85	0.57
26:14:49:A:H5"	26:14:51:G:O4'	2.04	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:14:646:A:H2'	26:14:647:G:O4'	2.05	0.57
26:14:654(A):A:H2'	26:14:654(T):A:N6	2.19	0.57
26:14:1784:A:H4'	26:14:1785:A:O5'	2.05	0.57
41:85:92:ARG:NH1	41:85:94:ASN:HD22	2.03	0.57
54:M5:22:VAL:O	54:M5:50:LEU:HB3	2.04	0.57
1:13:73:G:H2'	1:13:74:C:C5	2.40	0.57
1:13:600:C:H4'	8:7E:128:GLY:O	2.05	0.57
1:13:618:C:H5"	1:13:619:U:H5"	1.87	0.57
4:3E:85:LYS:HD3	4:3E:88:VAL:O	2.05	0.57
5:4E:136:MET:HA	5:4E:139:LEU:HD12	1.85	0.57
24:3K:14:A:N6	24:3K:15:G:O6	2.37	0.57
26:1H:155:C:H42	26:1H:171:G:H1	1.50	0.57
26:1H:376:C:P	59:1H:3809:HOH:O	2.62	0.57
26:1H:957:A:N1	26:1H:2458:G:H4'	2.19	0.57
26:1H:1678:G:N2	26:1H:1989:G:N2	2.51	0.57
26:1H:2334:G:O6	47:I8:74:ARG:NH2	2.30	0.57
29:21:49:LEU:HD22	29:21:81:ILE:HG13	1.85	0.57
29:21:63:LEU:O	29:21:66:HIS:N	2.37	0.57
30:31:29:ASN:N	30:31:112:MET:HE1	2.14	0.57
31:41:16:ARG:O	31:41:20:ILE:HG13	2.05	0.57
33:61:88:ILE:O	33:61:121:LYS:NZ	2.38	0.57
37:88:35:VAL:CG1	37:88:130:LYS:HB3	2.32	0.57
40:B8:4:GLY:O	40:B8:8:LYS:HG3	2.05	0.57
40:B8:107:ASP:O	40:B8:111:ARG:NH1	2.38	0.57
1:1G:191(E):G:H2'	1:1G:191(F):U:H6	1.70	0.57
1:1G:520:A:N1	1:1G:536:C:H1'	2.20	0.57
1:1G:1387:G:H2'	1:1G:1388:C:H6	1.70	0.57
2:12:73:THR:HG21	2:12:97:TRP:H	1.68	0.57
19:AA:38:SER:O	19:AA:71:LEU:HB2	2.05	0.57
26:14:651:G:H5'	54:M5:18:ALA:HB3	1.86	0.57
26:14:1757:U:N3	26:14:1762:A:H2	1.98	0.57
26:14:2761:G:H1'	32:59:143:GLN:OE1	2.05	0.57
30:39:178:PRO:HG2	30:39:179:GLU:OE1	2.05	0.57
46:D5:11:GLU:O	46:D5:36:LYS:NZ	2.38	0.57
1:13:95:G:H3'	1:13:96:G:H8	1.70	0.57
1:13:127:G:O2'	17:8I:2:PRO:O	2.21	0.57
1:13:160:A:N6	1:13:343:U:O2'	2.36	0.57
1:13:223:U:H2'	1:13:224:C:H6	1.68	0.57
1:13:1391:U:H2'	1:13:1392:G:C8	2.39	0.57
5:4E:64:ARG:HB2	5:4E:64:ARG:HH11	1.70	0.57
9:8E:55:ALA:HA	9:8E:58:HIS:HB2	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1H:993:G:OP1	41:C8:50:ARG:NH2	2.37	0.57
26:1H:1805:U:O2	28:11:50:THR:HB	2.05	0.57
33:61:73:GLU:OE2	33:61:137:PRO:HD2	2.05	0.57
46:H8:52:SER:C	46:H8:54:HIS:H	2.08	0.57
48:J8:93:GLU:C	48:J8:95:LEU:N	2.63	0.57
1:1G:222:U:H2'	1:1G:223:U:H6	1.70	0.57
4:32:160:GLN:HA	4:32:163:GLU:HB3	1.87	0.57
8:72:110:ALA:O	8:72:121:ASP:N	2.37	0.57
26:14:987:G:O2'	26:14:1000:A:N3	2.34	0.57
26:14:1769:G:O2'	26:14:1958:C:OP1	2.19	0.57
29:29:54:GLN:HG3	29:29:73:GLU:O	2.04	0.57
35:25:7:TYR:CE1	35:25:20:MET:HE3	2.33	0.57
46:D5:87:ASP:N	46:D5:87:ASP:OD1	2.38	0.57
1:13:553:A:H5"	12:3I:24:VAL:HG21	1.87	0.56
26:1H:719:C:H2'	26:1H:720:C:H6	1.70	0.56
30:31:7:TYR:O	30:31:21:ALA:HA	2.05	0.56
7:62:146:GLU:HG2	11:2A:50:TYR:OH	2.05	0.56
8:72:25:ASP:OD1	8:72:25:ASP:N	2.38	0.56
26:14:11:G:H2'	26:14:12:U:H5'	1.87	0.56
26:14:1568:G:OP2	28:19:63:ARG:NH2	2.36	0.56
26:14:1579:A:H2'	26:14:1580:A:C8	2.40	0.56
26:14:1786:A:H2	26:14:2606:C:H1'	1.70	0.56
26:14:2324:C:H5"	26:14:2325:G:H5'	1.86	0.56
36:35:82:GLY:HA2	36:35:113:LYS:O	2.05	0.56
40:75:3:ARG:HA	40:75:6:LEU:HB3	1.87	0.56
46:D5:30:ASN:HA	46:D5:89:PHE:HE1	1.70	0.56
50:H5:50:VAL:O	50:H5:54:VAL:HG12	2.04	0.56
1:13:1459:C:OP1	20:BI:31:SER:OG	2.19	0.56
26:1H:1264:G:OP1	52:N8:19:ARG:NH2	2.33	0.56
46:H8:60:GLU:O	46:H8:61:LEU:HB3	2.03	0.56
49:K8:15:LYS:H	49:K8:67:LYS:HE3	1.70	0.56
1:1G:23:C:OP2	1:1G:561:U:N3	2.29	0.56
1:1G:41:G:H2'	1:1G:42:G:C8	2.39	0.56
1:1G:1124:G:HO2'	1:1G:1145:C:N4	2.02	0.56
25:4L:23:A:H4'	25:4L:24:A:OP1	2.05	0.56
26:14:548:A:C6	26:14:549:G:H1'	2.40	0.56
26:14:2786:U:O2	29:29:62:PRO:HB3	2.05	0.56
33:69:75:LEU:HG	33:69:76:THR:N	2.20	0.56
37:45:66:ILE:HG22	37:45:104:PHE:CE1	2.40	0.56
1:13:148:G:H2'	1:13:149:A:H8	1.71	0.56
5:4E:143:ARG:NE	8:7E:77:GLU:OE1	2.29	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:1K:18:G:O6	22:1K:56:C:H5”	2.05	0.56
24:3K:64:C:H3’	24:3K:65:C:O4’	2.05	0.56
26:1H:193:U:OP1	59:1H:3820:HOH:O	2.18	0.56
26:1H:270(S):G:H5”	48:J8:76:ARG:HH21	1.70	0.56
26:1H:1512:G:H2’	26:1H:1513:C:C6	2.41	0.56
26:1H:1538:G:H2’	26:1H:1539:G:C8	2.40	0.56
26:1H:2314:C:H2’	26:1H:2315:G:C8	2.40	0.56
30:31:184:TYR:O	30:31:188:ARG:HG3	2.05	0.56
34:58:1:MET:HE2	42:D8:12:TYR:HA	1.87	0.56
37:88:77:LYS:HE3	37:88:84:GLY:O	2.06	0.56
40:B8:26:ASP:O	40:B8:49:VAL:HG13	2.04	0.56
48:J8:86:SER:HB3	48:J8:89:GLU:H	1.71	0.56
1:1G:1:U:H3’	1:1G:1:U:OP2	2.05	0.56
1:1G:998(A):C:H2’	1:1G:999:U:C6	2.40	0.56
1:1G:1316:G:N2	1:1G:1318:A:H3’	2.20	0.56
1:1G:1342:C:H4’	9:82:125:TYR:HB3	1.86	0.56
4:32:98:GLU:HG3	4:32:103:ASN:HD21	1.71	0.56
10:1A:35:SER:OG	10:1A:73:ASP:HB2	2.05	0.56
14:5A:23:ARG:HG3	14:5A:28:GLY:O	2.04	0.56
26:14:491:G:H2’	26:14:492:A:H8	1.70	0.56
26:14:1287:A:H8	38:55:104:ARG:HD3	1.69	0.56
26:14:1783:A:H5’	26:14:2608:G:H4’	1.86	0.56
26:14:2467:C:H4’	37:45:123:HIS:CE1	2.40	0.56
29:29:52:LEU:O	29:29:74:PRO:HB2	2.04	0.56
31:49:97:ASP:H	31:49:100:TRP:CD1	2.24	0.56
34:15:42:TRP:HA	34:15:48:MET:HE1	1.88	0.56
37:45:97:VAL:HG11	37:45:103:MET:HE3	1.88	0.56
40:75:88:ILE:HD11	40:75:91:ARG:HG2	1.87	0.56
42:95:67:GLY:O	42:95:88:ARG:HD2	2.05	0.56
46:D5:10:ARG:HH21	46:D5:26:GLY:H	1.51	0.56
46:D5:10:ARG:HD2	46:D5:36:LYS:HE2	1.87	0.56
52:J5:6:VAL:HG22	52:J5:7:PRO:HD2	1.87	0.56
1:13:186:C:O4’	20:BI:81:LYS:NZ	2.37	0.56
3:2E:15:THR:HG23	3:2E:181:ASN:HA	1.87	0.56
5:4E:115:VAL:HG11	5:4E:118:ILE:HB	1.87	0.56
26:1H:517:C:OP1	52:N8:16:ARG:NH2	2.34	0.56
26:1H:1310:G:OP2	53:P8:9:ARG:NE	2.32	0.56
39:A8:11:LYS:HD3	39:A8:91:PRO:HD3	1.86	0.56
49:K8:4:SER:N	49:K8:7:ARG:H	1.99	0.56
50:L8:39:ASP:OD2	50:L8:44:ARG:NH2	2.35	0.56
1:1G:804:U:H5”	1:1G:805:C:OP2	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1G:1097:C:O2'	1:1G:1169:A:N3	2.37	0.56
1:1G:1142:G:H3'	1:1G:1143:G:C8	2.41	0.56
7:62:93:PRO:CD	7:62:94:ARG:HH21	2.18	0.56
55:3L:9:A:H8	55:3L:11:C:H41	1.52	0.56
26:14:140:A:C8	26:14:1408:C:O2'	2.58	0.56
26:14:2441:C:OP2	26:14:2586:C:O2'	2.24	0.56
28:19:49:ILE:HD11	28:19:52:ARG:HA	1.88	0.56
34:15:85:ILE:HD13	34:15:90:MET:HE3	1.87	0.56
40:75:55:ASN:N	40:75:59:THR:HG22	2.20	0.56
41:85:8:VAL:O	41:85:12:ARG:HG3	2.04	0.56
1:13:1263:C:H2'	1:13:1264:C:H6	1.69	0.56
18:9I:56:THR:HB	18:9I:58:LEU:HD13	1.88	0.56
26:1H:1055:G:O2'	26:1H:1086:A:N6	2.38	0.56
26:1H:1165:U:H2'	26:1H:1166:C:C6	2.40	0.56
51:M8:15:ILE:HB	51:M8:32:TYR:HD1	1.69	0.56
26:14:1154:G:OP2	41:85:58:ARG:NH1	2.38	0.56
30:39:89:VAL:HG12	30:39:90:PHE:H	1.70	0.56
38:55:24:GLN:OE1	38:55:36:THR:HG21	2.06	0.56
1:13:51:A:OP2	1:13:52:G:H8	1.89	0.56
13:4I:49:THR:HB	13:4I:52:GLU:HG2	1.87	0.56
26:1H:848:G:H2'	26:1H:849:A:C8	2.40	0.56
26:1H:2564:A:C2	26:1H:2647:U:H4'	2.41	0.56
45:G8:5:MET:HE2	45:G8:5:MET:H	1.70	0.56
1:1G:1148:U:H2'	1:1G:1149:C:O4'	2.05	0.56
1:1G:1292:U:H2'	1:1G:1293:G:C8	2.40	0.56
11:2A:67:ASP:OD2	11:2A:71:LYS:NZ	2.37	0.56
26:14:29:U:H2'	26:14:30:G:C8	2.41	0.56
26:14:852:G:H2'	26:14:853:G:H8	1.71	0.56
26:14:1044:G:H4'	26:14:1047:G:H4'	1.87	0.56
26:14:2478:A:H5"	26:14:2479:G:OP2	2.06	0.56
40:75:27:THR:HG23	40:75:90:GLN:HB3	1.88	0.56
1:13:75:C:O2'	1:13:76:G:H8	1.89	0.56
1:13:843:U:H3'	1:13:848:C:C6	2.40	0.56
13:4I:26:GLY:C	13:4I:28:ALA:H	2.13	0.56
13:4I:90:LEU:HA	13:4I:93:ARG:HB2	1.87	0.56
26:1H:1101:U:H2'	26:1H:1102:C:C6	2.41	0.56
26:1H:1388:G:H2'	26:1H:1389:G:C8	2.36	0.56
26:1H:2210:G:H3'	26:1H:2211:G:C8	2.40	0.56
33:61:75:LEU:HD21	33:61:105:HIS:HB3	1.88	0.56
40:B8:111:ARG:HD3	40:B8:111:ARG:H	1.71	0.56
54:Q8:49:VAL:HG12	54:Q8:49:VAL:O	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1G:376:G:H5"	16:7A:5:ARG:HB2	1.87	0.56
3:22:73:PRO:O	3:22:76:VAL:HG22	2.05	0.56
15:6A:17:ARG:HD2	15:6A:26:GLU:HG3	1.88	0.56
26:14:2055:C:N3	59:14:3607:HOH:O	2.32	0.56
26:14:2331:G:H4'	47:E5:43:THR:H	1.70	0.56
32:59:15:VAL:HB	32:59:27:LYS:O	2.06	0.56
32:59:26:VAL:HG11	32:59:33:LEU:H	1.69	0.56
36:35:107:LYS:O	36:35:109:GLY:N	2.37	0.56
37:45:74:TYR:O	37:45:90:VAL:O	2.24	0.56
46:D5:121:HIS:ND1	46:D5:123:ASP:O	2.38	0.56
2:1E:118:LEU:HD12	2:1E:142:LEU:HB2	1.88	0.56
2:1E:209:ARG:HD2	2:1E:239:VAL:HA	1.87	0.56
5:4E:33:VAL:HG11	5:4E:109:ILE:HA	1.86	0.56
5:4E:126:ARG:HG3	5:4E:126:ARG:HH11	1.70	0.56
9:8E:5:TYR:HE2	9:8E:16:ARG:HB3	1.71	0.56
9:8E:99:LEU:HD12	9:8E:101:PHE:HE2	1.70	0.56
26:1H:581:C:OP1	41:C8:33:ARG:HG3	2.06	0.56
26:1H:1535:U:O4	26:1H:1538:G:O2'	2.22	0.56
28:11:70:TRP:O	28:11:73:VAL:HG23	2.06	0.56
36:78:71:VAL:CG1	36:78:72:PRO:HD3	2.35	0.56
1:1G:3:G:N1	4:32:88:VAL:HG13	2.20	0.56
26:14:1444(A):A:H2'	26:14:1444(A):A:N3	2.21	0.56
27:1J:7:G:O5'	39:65:29:PHE:HE2	1.88	0.56
28:19:68:LYS:HB3	28:19:70:TRP:CZ3	2.41	0.56
30:39:25:PRO:HB2	30:39:27:GLU:HB2	1.88	0.56
30:39:53:THR:HG22	30:39:56:GLU:HG3	1.88	0.56
1:13:685:G:O2'	1:13:686:U:H5'	2.06	0.56
1:13:1286:A:C8	1:13:1287:A:H4'	2.41	0.56
4:3E:110:PHE:CE2	4:3E:148:VAL:HG23	2.41	0.56
8:7E:82:HIS:CE1	8:7E:84:ARG:HB3	2.40	0.56
26:1H:270(V):G:H2'	26:1H:270(W):G:H8	1.71	0.56
26:1H:589:C:H2'	26:1H:590:A:H8	1.70	0.56
46:H8:11:GLU:OE1	46:H8:36:LYS:NZ	2.31	0.56
1:1G:1095:U:OP1	1:1G:1108:G:N2	2.39	0.56
1:1G:1422:G:H5"	35:25:48:PRO:HB3	1.88	0.56
1:1G:1454:G:H5"	20:BA:35:THR:HG21	1.88	0.56
4:32:111:ALA:HB2	4:32:120:LEU:HD12	1.87	0.56
20:BA:11:SER:HA	20:BA:13:LEU:HD22	1.88	0.56
26:14:2131:G:N2	26:14:2157:G:O2'	2.38	0.56
30:39:18:ARG:HH22	30:39:20:LEU:HD12	1.70	0.56
30:39:18:ARG:HH22	30:39:20:LEU:HB2	1.70	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:69:76:THR:HG22	33:69:139:GLN:O	2.06	0.56
1:13:1:U:H4'	1:13:2:U:O5'	2.06	0.56
26:1H:821:A:H2'	26:1H:946:G:H5"	1.88	0.56
26:1H:1188:U:H4'	42:D8:79:VAL:HG22	1.86	0.56
26:1H:2106:G:C2	26:1H:2107:C:H1'	2.41	0.56
26:1H:2171:A:O2'	26:1H:2172:U:O4'	2.17	0.56
33:61:40:THR:O	33:61:44:LEU:HB2	2.06	0.56
44:F8:26:TYR:O	44:F8:81:VAL:HG12	2.06	0.56
46:H8:19:ARG:NH1	46:H8:84:GLU:HB2	2.20	0.56
1:1G:181:G:O2'	1:1G:183:G:O6	2.24	0.56
1:1G:503:C:OP2	12:3A:116:SER:OG	2.23	0.56
1:1G:518:C:H2'	1:1G:530:G:C8	2.41	0.56
1:1G:1126:U:H4'	1:1G:1127:G:N7	2.21	0.56
2:12:219:VAL:CA	2:12:220:ASP:HB3	2.33	0.56
7:62:144:MET:SD	7:62:145:ALA:N	2.79	0.56
10:1A:54:PHE:O	10:1A:55:LYS:HG3	2.06	0.56
13:4A:81:LEU:HB3	13:4A:89:GLY:HA3	1.87	0.56
26:14:71:A:H2	44:B5:31:HIS:NE2	2.03	0.56
26:14:1341:U:OP2	26:14:1394:U:O2'	2.19	0.56
31:49:125:PHE:HB3	31:49:166:ASP:HB3	1.88	0.56
47:E5:49:LYS:HD2	47:E5:82:ARG:HH22	1.71	0.56
1:13:1301:U:O2'	1:13:1302:U:H3'	2.06	0.55
2:1E:11:LEU:HB3	2:1E:213:LEU:HD13	1.88	0.55
19:AI:41:VAL:HG12	19:AI:44:MET:CB	2.36	0.55
26:1H:363(B):G:H2'	26:1H:363(C):G:H8	1.71	0.55
26:1H:1516:U:H2'	26:1H:1517:G:C8	2.41	0.55
51:M8:12:ALA:O	51:M8:24:THR:OG1	2.21	0.55
1:1G:604:G:H2'	1:1G:605:U:O4'	2.07	0.55
1:1G:837:G:N2	1:1G:850:U:O2	2.38	0.55
26:14:528:A:C2	26:14:2042:A:H2'	2.40	0.55
26:14:1430:C:H2'	26:14:1431:U:C6	2.41	0.55
26:14:2651:C:H42	26:14:2669:G:H1	1.54	0.55
26:14:2711:A:H5'	59:14:3539:HOH:O	2.05	0.55
30:39:172:TRP:CD1	30:39:172:TRP:H	2.23	0.55
32:59:107:VAL:HG23	32:59:109:PHE:H	1.70	0.55
36:35:2:LYS:HG3	36:35:5:ASP:OD2	2.06	0.55
36:35:85:LEU:HA	36:35:88:LEU:HB2	1.88	0.55
1:13:648:A:N6	1:13:649:G:O6	2.40	0.55
1:13:714:G:H2'	1:13:715:A:C8	2.41	0.55
1:13:972:C:OP2	10:1I:57:LYS:HE2	2.06	0.55
1:13:1497:G:C2'	1:13:1498:U:H5'	2.37	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:6E:89:MET:HE1	7:6E:155:ARG:HD2	1.88	0.55
13:4I:12:ASN:CG	13:4I:13:LYS:H	2.10	0.55
26:1H:444:C:H4'	30:31:49:ALA:HB2	1.86	0.55
26:1H:598:G:H5'	36:78:11:GLY:HA3	1.88	0.55
48:J8:2:SER:HB2	48:J8:4:VAL:HG13	1.89	0.55
10:1A:29:ARG:HD3	10:1A:84:GLN:NE2	2.21	0.55
10:1A:99:LYS:HD3	10:1A:100:THR:N	2.21	0.55
26:14:2807:G:H22	26:14:2892:A:H62	1.54	0.55
31:49:72:ARG:HB3	31:49:85:GLY:HA2	1.88	0.55
1:13:406:G:H5'	4:3E:5:ILE:HD13	1.88	0.55
13:4I:13:LYS:O	13:4I:44:ARG:NH1	2.39	0.55
20:BI:100:ILE:HG12	20:BI:101:GLY:H	1.70	0.55
26:1H:945:A:P	59:1H:3825:HOH:O	2.65	0.55
26:1H:1871:A:H2'	26:1H:1872:A:C8	2.41	0.55
26:1H:1935:G:H1'	26:1H:1964:G:N2	2.22	0.55
34:58:9:VAL:HG21	34:58:39:ARG:HH12	1.71	0.55
34:58:12:ARG:HG2	34:58:13:TRP:N	2.20	0.55
36:78:86:LYS:HB3	36:78:118:GLY:HA3	1.87	0.55
53:P8:24:THR:HG23	53:P8:27:GLY:H	1.71	0.55
1:1G:948:C:N4	59:1G:1849:HOH:O	2.38	0.55
1:1G:1328:C:OP1	21:1B:21:TYR:OH	2.19	0.55
2:12:34:ALA:O	2:12:40:HIS:HB3	2.05	0.55
12:3A:6:THR:OG1	12:3A:9:GLN:HG3	2.07	0.55
26:14:754:C:H2'	26:14:755:C:H6	1.71	0.55
27:1J:75:G:O2'	46:D5:85:HIS:NE2	2.36	0.55
46:D5:132:ASN:ND2	46:D5:159:PRO:HG2	2.22	0.55
48:F5:40:ARG:NH2	48:F5:42:GLN:HG2	2.22	0.55
1:13:165:C:H2'	1:13:166:G:H8	1.70	0.55
1:13:963:G:N2	1:13:972:C:N3	2.39	0.55
1:13:1226:C:H4'	19:AI:80:TYR:OH	2.07	0.55
10:1I:24:VAL:O	10:1I:28:ARG:HB2	2.07	0.55
26:1H:214:G:H4'	26:1H:214:G:OP1	2.06	0.55
26:1H:860:U:C5	26:1H:917:A:C2	2.81	0.55
26:1H:2032:G:H21	29:21:146:THR:HG23	1.70	0.55
26:1H:2136:C:N3	26:1H:2155:G:N1	2.38	0.55
41:C8:105:VAL:HG22	42:D8:44:LYS:HG3	1.89	0.55
45:G8:42:VAL:HG23	45:G8:43:ASN:N	2.21	0.55
46:H8:7:ALA:HB2	46:H8:59:LEU:HD22	1.87	0.55
53:P8:12:ARG:NH2	53:P8:44:PRO:HB3	2.22	0.55
1:1G:191(E):G:H2'	1:1G:191(F):U:C6	2.40	0.55
1:1G:1084:G:H5'	1:1G:1102:A:OP2	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:1A:30:SER:OG	10:1A:81:THR:HG22	2.07	0.55
22:1L:18:G:H1'	22:1L:58:A:C2	2.42	0.55
26:14:1019:U:OP1	26:14:1035:U:O2'	2.21	0.55
26:14:2749:A:H4'	32:59:6:ARG:CZ	2.36	0.55
41:85:17:ILE:HD12	41:85:32:PHE:HE1	1.71	0.55
2:1E:7:VAL:HG21	2:1E:217:ARG:HH11	1.71	0.55
14:5I:21:TYR:HE2	14:5I:23:ARG:NE	2.05	0.55
26:1H:724:U:H2'	26:1H:725:G:O4'	2.06	0.55
26:1H:747:U:O2	26:1H:2014:A:H1'	2.07	0.55
26:1H:901:A:H5'	26:1H:902:C:OP2	2.05	0.55
26:1H:1189:A:P	59:1H:3746:HOH:O	2.62	0.55
1:1G:980:C:N3	1:1G:1359:C:N4	2.54	0.55
4:32:84:LYS:H	4:32:84:LYS:HD2	1.71	0.55
13:4A:66:LEU:O	13:4A:67:GLU:O	2.25	0.55
55:3L:8:U:O2'	55:3L:13:C:N4	2.38	0.55
55:3L:76:A:H8	26:14:2394:C:N4	2.04	0.55
40:75:26:ASP:O	40:75:49:VAL:HG22	2.05	0.55
1:13:342:C:H2'	1:13:343:U:H5'	1.89	0.55
1:13:1367:C:H5'	10:1I:60:ARG:NH1	2.21	0.55
4:3E:18:LYS:HD3	4:3E:31:CYS:SG	2.47	0.55
6:5E:89:MET:HE3	18:9I:76:LEU:HD22	1.88	0.55
13:4I:7:VAL:HB	31:41:115:ARG:NH2	2.21	0.55
13:4I:15:VAL:O	13:4I:19:LEU:HD22	2.07	0.55
26:1H:588:U:H2'	26:1H:589:C:C6	2.41	0.55
26:1H:637:A:H2'	36:78:117:GLU:OE1	2.07	0.55
26:1H:2312:U:OP1	31:41:74:LYS:HG2	2.07	0.55
26:1H:2404:C:H1'	36:78:67:MET:HE1	1.89	0.55
30:31:178:PRO:HB3	30:31:198:ALA:CB	2.36	0.55
51:M8:36:CYS:SG	51:M8:37:SER:N	2.80	0.55
1:1G:652:U:O2'	1:1G:653:A:N3	2.37	0.55
1:1G:983:A:H2	1:1G:984:C:C6	2.24	0.55
1:1G:1235:U:O2'	1:1G:1305:G:O5'	2.24	0.55
2:12:82:ARG:NE	2:12:92:TYR:OH	2.36	0.55
4:32:146:ILE:H	4:32:146:ILE:HD12	1.72	0.55
7:62:141:VAL:HA	7:62:142:GLU:HB2	1.89	0.55
10:1A:44:VAL:HG22	10:1A:66:ARG:HG2	1.87	0.55
18:9A:29:PHE:HD2	18:9A:39:VAL:HG11	1.71	0.55
26:14:1047:G:H21	26:14:1111:A:H61	1.54	0.55
26:14:1871:A:H2'	26:14:1872:A:H8	1.71	0.55
34:15:125:GLY:HA2	34:15:126:PRO:O	2.07	0.55
4:3E:161:ASN:O	4:3E:165:MET:HB2	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:2I:27:ASN:OD1	11:2I:28:THR:N	2.39	0.55
15:6I:16:ALA:HB1	15:6I:21:ASP:HB3	1.87	0.55
39:A8:38:GLN:HG2	39:A8:47:THR:HG21	1.89	0.55
30:39:3:GLU:OE1	30:39:3:GLU:N	2.39	0.55
30:39:127:GLU:HG3	30:39:128:ALA:HB2	1.88	0.55
33:69:76:THR:HG23	33:69:77:LEU:H	1.71	0.55
40:75:5:ALA:HB1	40:75:8:LYS:HB2	1.89	0.55
48:F5:92:LYS:O	48:F5:93:GLU:C	2.49	0.55
1:13:1007:C:N4	1:13:1022:G:H1	2.04	0.55
26:1H:1051:G:OP2	26:1H:1051:G:H8	1.90	0.55
26:1H:1858:G:O6	59:1H:3810:HOH:O	2.15	0.55
29:21:15:PHE:HA	29:21:19:ARG:O	2.07	0.55
31:41:161:THR:CG2	31:41:163:ALA:H	2.19	0.55
1:1G:45:U:H2'	1:1G:46:G:C8	2.41	0.55
1:1G:554:C:H2'	1:1G:555:C:C6	2.41	0.55
1:1G:1021:G:H2'	1:1G:1022:G:C8	2.42	0.55
1:1G:1299:A:C8	1:1G:1301:U:H1'	2.42	0.55
6:52:74:ASP:OD1	6:52:74:ASP:N	2.40	0.55
13:4A:12:ASN:O	13:4A:12:ASN:ND2	2.36	0.55
16:7A:40:ASP:HB3	16:7A:48:TRP:HB2	1.89	0.55
22:1L:37:AET:HM62	22:1L:38:A:N6	2.22	0.55
55:3L:23:A:H2'	55:3L:24:G:H8	1.71	0.55
26:14:443:A:H1'	26:14:1201:C:O4'	2.07	0.55
29:29:37:ARG:HD3	29:29:42:ASP:CG	2.32	0.55
29:29:111:ARG:HD2	29:29:160:TYR:CE2	2.41	0.55
37:45:77:LYS:HE3	37:45:84:GLY:HA3	1.89	0.55
39:65:54:LEU:C	39:65:56:LEU:H	2.14	0.55
1:13:265:G:H5'	17:8I:64:PRO:O	2.06	0.55
1:13:1064:G:H4'	1:13:1065:U:OP1	2.07	0.55
8:7E:21:LYS:O	8:7E:65:TYR:OH	2.23	0.55
25:4K:14:A:H4'	25:4K:15:A:H5'	1.89	0.55
26:1H:1331:A:O2'	26:1H:1332:G:H8	1.89	0.55
31:41:33:ARG:O	31:41:162:THR:HG23	2.07	0.55
43:E8:38:TYR:OH	52:N8:47:PRO:HG2	2.07	0.55
46:H8:47:VAL:O	46:H8:51:ALA:N	2.30	0.55
49:K8:32:LEU:HD13	49:K8:36:ARG:HH12	1.72	0.55
1:1G:1075:C:OP1	2:12:179:LYS:NZ	2.39	0.55
26:14:64:A:O3'	44:B5:71:GLY:HA3	2.06	0.55
26:14:796:C:H2'	26:14:797:C:C6	2.42	0.55
26:14:2429:G:O6	36:35:61:ARG:NH2	2.39	0.55
27:1J:2:C:H2'	27:1J:3:C:H6	1.72	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:L5:5:TRP:NE1	53:L5:7:PRO:HG3	2.21	0.55
4:3E:110:PHE:HE2	4:3E:148:VAL:HG23	1.72	0.55
19:AI:39:THR:HG22	19:AI:40:ILE:H	1.71	0.55
32:51:164:TYR:O	32:51:167:GLU:HB3	2.07	0.55
23:2L:3:C:H42	23:2L:71:G:H1	1.54	0.55
26:14:323:G:O2'	26:14:1205:U:N3	2.35	0.55
26:14:2404:C:O3'	36:35:77:ARG:NH2	2.40	0.55
26:14:2745:C:O2	32:59:139:GLN:NE2	2.39	0.55
26:14:2795:G:H4'	26:14:2798:C:H5	1.72	0.55
33:69:57:ARG:O	33:69:61:ARG:HB2	2.07	0.55
35:25:14:THR:HG21	35:25:86:ILE:HG13	1.89	0.55
1:13:407:G:O4'	4:3E:119:GLN:NE2	2.40	0.54
20:BI:86:ARG:O	20:BI:90:GLN:NE2	2.40	0.54
26:1H:1171:G:C5	26:1H:1174:A:N6	2.76	0.54
41:C8:92:ARG:NH1	41:C8:94:ASN:OD1	2.41	0.54
46:H8:151:HIS:HA	46:H8:169:GLU:O	2.07	0.54
1:1G:54:C:N4	1:1G:353:A:OP2	2.35	0.54
1:1G:994:A:C5	1:1G:1216:G:H4'	2.42	0.54
1:1G:1014:A:H2'	1:1G:1015:A:C8	2.42	0.54
1:1G:1126:U:H1'	1:1G:1127:G:OP1	2.06	0.54
1:1G:1363:A:H1'	1:1G:1365:G:N7	2.22	0.54
3:22:121:ALA:HB2	3:22:198:VAL:HG21	1.88	0.54
7:62:116:ALA:HA	7:62:119:ARG:HE	1.71	0.54
55:3L:54:5MU:OP1	55:3L:54:5MU:H4'	2.07	0.54
26:14:127:A:H5"	26:14:128:C:C6	2.42	0.54
26:14:792:G:H5"	26:14:793:A:H5'	1.89	0.54
26:14:1322:A:O3'	43:A5:84:ARG:NH1	2.40	0.54
26:14:2528:U:O2'	26:14:2530:A:OP1	2.15	0.54
29:29:12:THR:HG21	40:75:11:GLU:OE1	2.07	0.54
2:1E:166:ASP:C	2:1E:168:THR:H	2.15	0.54
3:2E:40:ARG:O	3:2E:44:GLU:HG2	2.07	0.54
7:6E:22:LEU:O	7:6E:26:PHE:N	2.36	0.54
26:1H:1057:A:H8	26:1H:1086:A:H2'	1.72	0.54
26:1H:2068:U:H3	26:1H:2430:A:H2	1.53	0.54
46:H8:145:GLU:OE1	46:H8:145:GLU:N	2.39	0.54
4:32:64:LEU:HB2	4:32:198:VAL:HG11	1.89	0.54
16:7A:1:MET:HE1	16:7A:65:GLN:HB2	1.88	0.54
26:14:2147:G:H2'	26:14:2148:G:H4'	1.90	0.54
26:14:2823:A:OP1	29:29:159:HIS:NE2	2.32	0.54
28:19:102:LYS:C	28:19:103:ARG:HG2	2.32	0.54
31:49:97:ASP:H	31:49:100:TRP:HD1	1.55	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:59:6:ARG:HH12	32:59:63:SER:HA	1.72	0.54
34:15:137:LYS:HB3	34:15:137:LYS:NZ	2.21	0.54
36:35:126:VAL:HG12	36:35:147:LEU:HD22	1.89	0.54
1:13:165:C:H2'	1:13:166:G:C8	2.41	0.54
1:13:224:C:H2'	1:13:225:C:C6	2.41	0.54
1:13:1010:G:N2	1:13:1020:U:H1'	2.23	0.54
2:1E:82:ARG:HH12	2:1E:150:SER:HG	1.54	0.54
4:3E:60:GLU:OE2	4:3E:199:ASN:N	2.35	0.54
26:1H:1019:U:O2'	26:1H:1021:A:H2	1.91	0.54
27:16:73:A:C4	27:16:104:A:C2	2.95	0.54
29:21:14:ILE:HG12	29:21:23:VAL:HG21	1.90	0.54
29:21:166:THR:HG21	29:21:199:ARG:HH22	1.73	0.54
45:G8:94:LYS:HG3	45:G8:95:LYS:N	2.22	0.54
54:Q8:8:LYS:O	54:Q8:12:LYS:HB2	2.08	0.54
4:32:61:LYS:HB2	4:32:203:VAL:HG13	1.89	0.54
4:32:107:ARG:HH22	4:32:194:LEU:HD13	1.71	0.54
5:42:60:TYR:HB3	5:42:64:ARG:CZ	2.38	0.54
7:62:20:ASP:HB3	7:62:23:VAL:HB	1.89	0.54
25:4L:18:G:N7	59:4L:501:HOH:O	2.33	0.54
26:14:2158:A:H1'	26:14:2159:G:C8	2.42	0.54
28:19:71:ASP:OD1	28:19:103:ARG:NH2	2.38	0.54
34:15:4:TYR:O	41:85:64:ARG:NH1	2.40	0.54
41:85:70:ARG:HA	41:85:74:LEU:O	2.07	0.54
46:D5:132:ASN:HD22	46:D5:159:PRO:HG2	1.73	0.54
54:M5:52:LYS:N	54:M5:53:PRO:HD2	2.22	0.54
2:1E:80:ILE:HG12	2:1E:212:GLN:HB2	1.90	0.54
2:1E:100:GLY:O	2:1E:104:ASN:N	2.28	0.54
7:6E:42:ILE:HG12	7:6E:116:ALA:HB3	1.90	0.54
15:6I:55:GLY:HA2	15:6I:58:MET:HE3	1.88	0.54
16:7I:4:ILE:HB	16:7I:66:PRO:HB3	1.88	0.54
26:1H:635:C:O2'	26:1H:639:U:OP1	2.23	0.54
26:1H:2849:U:OP2	40:B8:95:ARG:NH1	2.40	0.54
28:11:145:VAL:HG12	28:11:146:GLU:O	2.08	0.54
29:21:13:ARG:NH2	40:B8:77:PRO:HB3	2.23	0.54
1:1G:600:C:H2'	1:1G:601:C:H6	1.71	0.54
1:1G:1272:G:H2'	1:1G:1273:G:O4'	2.07	0.54
1:1G:1291:G:OP1	7:62:37:ASN:ND2	2.41	0.54
5:42:75:THR:OG1	5:42:117:ASP:O	2.20	0.54
17:8A:53:LEU:HD21	17:8A:85:VAL:HG11	1.88	0.54
18:9A:22:VAL:HA	18:9A:25:THR:HG22	1.89	0.54
21:1B:5:ASP:O	21:1B:11:GLY:HA3	2.06	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:3L:50:G:H1	55:3L:64:C:N4	2.01	0.54
26:14:792:G:N3	26:14:2072:G:O2'	2.34	0.54
26:14:1043:C:H42	26:14:1112:G:H1	1.55	0.54
26:14:1198:U:H2'	26:14:1199:U:C6	2.42	0.54
43:A5:47:VAL:HA	43:A5:50:VAL:HG12	1.90	0.54
1:13:221:C:H2'	1:13:222:U:C6	2.42	0.54
1:13:1256:A:O2'	1:13:1257:U:O5'	2.21	0.54
5:4E:73:ASN:OD1	5:4E:73:ASN:N	2.40	0.54
13:4I:68:GLY:HA3	31:41:116:ASP:OD1	2.08	0.54
16:7I:26:ARG:HH21	16:7I:31:LYS:HD2	1.73	0.54
22:1K:18:G:H1'	22:1K:58:A:C4	2.43	0.54
24:3K:33:U:H2'	24:3K:34:G:H2'	1.90	0.54
26:1H:827:U:H2'	26:1H:2430:A:H2	1.72	0.54
26:1H:836:G:H5"	26:1H:837:C:OP2	2.06	0.54
26:1H:1449:A:H5'	26:1H:1449(A):G:OP2	2.07	0.54
26:1H:1786:A:C2	26:1H:2606:C:H1'	2.41	0.54
26:1H:2134:A:O2'	26:1H:2159:G:N2	2.40	0.54
33:61:10:GLU:HG3	33:61:10:GLU:O	2.08	0.54
1:1G:485:G:O2'	1:1G:486:U:O5'	2.25	0.54
5:42:51:VAL:O	5:42:55:VAL:HG23	2.07	0.54
8:72:110:ALA:N	8:72:121:ASP:HB2	2.23	0.54
26:14:2577:A:H5'	52:J5:3:LYS:HD3	1.89	0.54
37:45:27:VAL:CG1	37:45:136:ALA:HB1	2.37	0.54
37:45:57:HIS:ND1	37:45:117:ALA:HB2	2.22	0.54
39:65:18:ILE:C	39:65:20:ARG:H	2.16	0.54
44:B5:50:LYS:O	44:B5:51:VAL:C	2.51	0.54
1:13:407:G:OP1	4:3E:115:ARG:NH2	2.40	0.54
6:5E:100:ASN:HB2	18:9I:28:GLU:HG2	1.90	0.54
20:BI:26:ASN:HD22	20:BI:26:ASN:N	2.05	0.54
20:BI:42:GLN:HG3	20:BI:43:LEU:N	2.22	0.54
22:1K:7:A:N6	22:1K:50:G:O6	2.41	0.54
22:1K:66:U:H5"	22:1K:67:A:C8	2.36	0.54
26:1H:1359:A:H2'	26:1H:1360:A:H5'	1.90	0.54
26:1H:1794:U:H2'	26:1H:1795:C:C6	2.42	0.54
26:1H:1899:G:H1	26:1H:1902:C:N4	2.05	0.54
34:58:30:ILE:HG22	34:58:34:LEU:HD22	1.89	0.54
40:B8:57:PHE:O	40:B8:58:ASN:ND2	2.41	0.54
1:1G:1142:G:H3'	1:1G:1143:G:H8	1.72	0.54
1:1G:1241:G:OP1	7:62:35:LYS:NZ	2.39	0.54
3:22:44:GLU:HA	3:22:52:LEU:HD11	1.88	0.54
13:4A:12:ASN:H	13:4A:45:VAL:HB	1.72	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:AA:63:THR:OG1	19:AA:65:ASN:O	2.25	0.54
26:14:2257:U:O2'	26:14:2258:C:H5'	2.08	0.54
26:14:2557:G:H2'	26:14:2558:C:C6	2.43	0.54
1:13:438:G:H4'	4:3E:123:HIS:CD2	2.42	0.54
1:13:1144:G:N2	1:13:1146:A:H62	2.04	0.54
2:1E:32:ILE:HG21	2:1E:40:HIS:HB3	1.89	0.54
7:6E:73:MET:HE2	7:6E:90:GLU:HB3	1.89	0.54
8:7E:51:VAL:HG21	8:7E:60:ARG:HH11	1.71	0.54
16:7I:17:TYR:HE2	16:7I:41:PRO:HG3	1.73	0.54
24:3K:57:G:H2'	24:3K:58:A:H5'	1.89	0.54
27:16:30:C:H2'	27:16:31:C:H5'	1.90	0.54
28:11:10:THR:OG1	28:11:13:ARG:HB2	2.07	0.54
32:51:5:GLY:HA2	32:51:69:ARG:HB2	1.88	0.54
32:51:101:ARG:NH2	32:51:121:ILE:O	2.41	0.54
32:51:169:VAL:HG22	32:51:170:ARG:H	1.73	0.54
38:98:87:TYR:CD1	38:98:90:ARG:HD2	2.42	0.54
1:1G:1152:A:H5'	10:1A:13:HIS:HD1	1.73	0.54
1:1G:1320:C:H1'	19:AA:73:GLU:HG3	1.90	0.54
1:1G:1392:G:N2	1:1G:1502:A:H8	2.06	0.54
9:82:119:ALA:O	9:82:120:ARG:HB2	2.05	0.54
14:5A:27:CYS:O	14:5A:29:ARG:NH2	2.41	0.54
26:14:2144:U:H1'	26:14:2148:G:N2	2.23	0.54
26:14:2497:A:H5"	59:14:3568:HOH:O	2.08	0.54
45:C5:39:VAL:HG23	45:C5:41:GLY:N	2.22	0.54
49:G5:9:GLN:HE22	49:G5:56:GLN:HG2	1.73	0.54
1:13:179:A:H2'	1:13:180:U:C6	2.41	0.54
1:13:1002:G:H1	1:13:1038:C:H42	1.55	0.54
19:AI:31:ILE:HG22	19:AI:32:LYS:H	1.72	0.54
26:1H:587:C:OP2	36:78:21:ARG:NH2	2.41	0.54
27:16:29:A:H2'	27:16:30:C:C6	2.42	0.54
27:16:75:G:H21	46:H8:85:HIS:CE1	2.26	0.54
34:58:97:ARG:H	34:58:100:GLU:HG3	1.73	0.54
54:Q8:16:ILE:HD13	54:Q8:59:LYS:HG2	1.89	0.54
1:1G:287:U:O4	59:1G:1822:HOH:O	2.18	0.54
1:1G:1238:A:N3	1:1G:1241:G:O2'	2.31	0.54
1:1G:1305:G:HO2'	1:1G:1306:A:H8	1.54	0.54
4:32:173:TRP:CZ3	4:32:193:ASP:HB3	2.43	0.54
4:32:187:ARG:NH2	4:32:193:ASP:OD2	2.40	0.54
20:BA:60:GLU:OE1	20:BA:85:MET:HE1	2.08	0.54
26:14:548:A:H8	26:14:548:A:O5'	1.91	0.54
26:14:918:A:N3	27:1J:80:U:O2'	2.33	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:14:996:A:N6	26:14:1160:G:C6	2.76	0.54
26:14:1607:C:N4	26:14:1622:G:OP2	2.38	0.54
26:14:2295:C:C2	26:14:2296:U:H5	2.26	0.54
26:14:2318:G:H5'	26:14:2319:G:OP2	2.07	0.54
27:1J:18:G:H1	27:1J:65:C:H42	1.54	0.54
29:29:61:ARG:HA	29:29:63:LEU:HD22	1.88	0.54
1:13:1037:C:H2'	1:13:1038:C:H6	1.72	0.54
1:13:1129:C:H3'	1:13:1139:G:N7	2.23	0.54
1:13:1164:G:C6	1:13:1173:G:C6	2.96	0.54
3:2E:136:GLN:OE1	3:2E:140:ARG:NH1	2.41	0.54
8:7E:86:ILE:HG12	8:7E:135:CYS:HA	1.90	0.54
22:1K:1:G:H3'	22:1K:2:C:C6	2.43	0.54
26:1H:96:G:H4'	49:K8:48:HIS:CD2	2.42	0.54
26:1H:729:G:C6	28:11:208:LYS:HB2	2.43	0.54
26:1H:1021:A:C8	26:1H:1021:A:H3'	2.43	0.54
26:1H:1520:U:H2'	26:1H:1521:G:O4'	2.07	0.54
26:1H:2017:U:OP2	59:1H:3826:HOH:O	2.18	0.54
26:1H:2470:G:H5'	37:88:56:ARG:HH22	1.73	0.54
27:16:12:C:O2'	47:I8:74:ARG:HG2	2.08	0.54
28:11:263:ARG:NH1	28:11:263:ARG:HB2	2.23	0.54
41:C8:92:ARG:CZ	42:D8:11:GLN:H	2.21	0.54
47:I8:27:GLU:HA	47:I8:67:VAL:HG22	1.89	0.54
1:1G:1126:U:H2'	1:1G:1281:U:H5'	1.88	0.54
9:82:83:ARG:O	9:82:86:VAL:HG12	2.08	0.54
23:2L:17:C:H3'	23:2L:18:U:H2'	1.89	0.54
26:14:247:G:H4'	26:14:386:G:C5	2.42	0.54
26:14:320:A:OP1	30:39:135:LYS:NZ	2.41	0.54
26:14:1418:G:OP1	26:14:1588:C:O2'	2.25	0.54
26:14:2287:A:H61	26:14:2344:U:H3	1.55	0.54
27:1J:3:C:H2'	27:1J:4:C:C6	2.43	0.54
31:49:97:ASP:O	31:49:101:ILE:HG23	2.08	0.54
37:45:27:VAL:HB	37:45:28:ALA:CA	2.22	0.54
48:F5:83:GLU:O	48:F5:86:SER:OG	2.19	0.54
1:13:35:G:O2'	12:3I:118:SER:O	2.24	0.54
1:13:339:C:OP2	35:68:97:ARG:HD3	2.08	0.54
2:1E:118:LEU:HB3	2:1E:142:LEU:HD12	1.89	0.54
22:1K:52:A:H61	22:1K:62:U:H3	1.55	0.54
26:1H:796:C:H2'	26:1H:797:C:C6	2.43	0.54
26:1H:879:G:N1	26:1H:898:C:N3	2.56	0.54
26:1H:2127:G:H5"	26:1H:2162:G:N2	2.22	0.54
28:11:37:LEU:HD23	28:11:62:TYR:HB2	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:I8:41:ARG:O	47:I8:57:PHE:HD2	1.91	0.54
1:1G:584:G:OP1	17:8A:91:ARG:NH1	2.41	0.54
1:1G:629:G:H2'	1:1G:630:G:O4'	2.08	0.54
1:1G:1256:A:N6	1:1G:1277:C:H3'	2.23	0.54
9:82:43:ALA:HA	9:82:74:ILE:HD13	1.89	0.54
22:1L:8:U:H3'	22:1L:13:C:N4	2.23	0.54
26:14:276:A:N3	26:14:277:C:N4	2.56	0.54
26:14:2762:G:H5'	26:14:2763:G:OP2	2.07	0.54
40:75:10:VAL:C	40:75:12:SER:H	2.15	0.54
1:13:963:G:H21	10:1I:55:LYS:HZ1	1.55	0.53
26:1H:722:A:H2'	26:1H:723:G:C8	2.43	0.53
26:1H:1171:G:N2	26:1H:1178:C:O2	2.38	0.53
26:1H:1420:U:O2'	26:1H:1421:G:OP1	2.24	0.53
26:1H:1678:G:H8	26:1H:1678:G:O5'	1.91	0.53
26:1H:1800:C:OP2	28:11:183:ARG:NH2	2.41	0.53
1:1G:164:U:H2'	1:1G:165:C:C6	2.43	0.53
1:1G:197:A:C6	1:1G:221:C:H4'	2.44	0.53
1:1G:352:C:O2'	1:1G:354:G:OP1	2.24	0.53
1:1G:544:G:OP1	4:32:59:ARG:NH2	2.32	0.53
1:1G:1203:C:H2'	1:1G:1204:A:C8	2.43	0.53
1:1G:1218:C:H2'	1:1G:1219:U:C6	2.43	0.53
1:1G:1492:A:H5"	12:3A:47:LYS:HB3	1.88	0.53
3:22:6:HIS:CD2	3:22:9:GLY:H	2.21	0.53
18:9A:25:THR:O	18:9A:25:THR:OG1	2.26	0.53
26:14:274:G:H2'	26:14:275:G:O4'	2.08	0.53
26:14:2795:G:H2'	26:14:2795:G:N3	2.23	0.53
29:29:7:VAL:HG12	29:29:8:LYS:H	1.73	0.53
30:39:27:GLU:O	30:39:29:ASN:N	2.34	0.53
31:49:104:GLU:C	31:49:106:LEU:H	2.16	0.53
34:15:58:ASP:OD1	34:15:58:ASP:N	2.32	0.53
1:13:730:G:C5	1:13:731:G:H1'	2.42	0.53
1:13:827:U:C5	1:13:872:A:N1	2.76	0.53
3:2E:56:ASP:O	3:2E:57:ILE:HG13	2.09	0.53
4:3E:154:ASN:ND2	4:3E:155:LEU:H	2.06	0.53
12:3I:5:PRO:HG2	12:3I:10:LEU:HD21	1.91	0.53
26:1H:620:G:H4'	26:1H:621:A:C5'	2.38	0.53
26:1H:1061:U:O3'	26:1H:1070:A:H4'	2.08	0.53
31:41:34:LEU:HD23	31:41:172:LEU:HD21	1.90	0.53
41:C8:92:ARG:NH2	42:D8:10:LYS:HB3	2.23	0.53
46:H8:9:TYR:CE1	46:H8:35:ARG:HG2	2.44	0.53
3:22:32:LEU:HD23	3:22:59:ARG:HH22	1.72	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:22:112:SER:HB3	3:22:115:LEU:HB2	1.90	0.53
8:72:17:THR:HG22	8:72:78:GLN:OE1	2.07	0.53
17:8A:59:ILE:HD13	17:8A:73:VAL:HA	1.88	0.53
26:14:67:U:N3	26:14:74:A:H2	1.98	0.53
26:14:1946:U:H2'	26:14:1947:C:C6	2.42	0.53
33:69:5:LEU:HD23	33:69:9:LEU:HD12	1.90	0.53
36:35:95:VAL:O	36:35:126:VAL:HG23	2.08	0.53
1:13:1133:G:H1	1:13:1141:C:H42	1.56	0.53
7:6E:5:ARG:HG3	7:6E:7:ALA:H	1.73	0.53
12:3I:60:LEU:HB2	12:3I:64:TYR:HB2	1.90	0.53
14:5I:23:ARG:NH1	14:5I:30:ALA:HB2	2.23	0.53
22:1K:27:C:H2'	22:1K:28:A:C8	2.43	0.53
26:1H:587:C:N3	36:78:33:ARG:NH1	2.56	0.53
26:1H:2160:G:N7	26:1H:2161:C:H1'	2.24	0.53
26:1H:2209:C:O2	26:1H:2216:G:C2	2.61	0.53
26:1H:2275:C:H5'	26:1H:2275:C:H6	1.72	0.53
43:E8:92:ARG:NH1	43:E8:94:ASP:OD1	2.41	0.53
1:1G:1002:G:H1	1:1G:1038:C:N4	2.06	0.53
1:1G:1093:A:N3	1:1G:1109:C:O2'	2.36	0.53
1:1G:1512:U:H2'	1:1G:1513:A:H8	1.73	0.53
8:72:12:ARG:NH2	8:72:27:PRO:HD3	2.24	0.53
26:14:900:A:OP1	26:14:900:A:H4'	2.07	0.53
29:29:50:GLY:HA3	29:29:78:LEU:HD23	1.89	0.53
1:13:1248:A:N3	9:8E:70:LYS:HE2	2.24	0.53
1:13:1446:A:OP1	1:13:1446:A:H4'	2.08	0.53
1:13:1504:G:OP1	1:13:1507:A:H4'	2.07	0.53
4:3E:152:SER:HB3	4:3E:155:LEU:HG	1.90	0.53
26:1H:185:U:H4'	26:1H:218:A:H4'	1.91	0.53
26:1H:443:A:H1'	26:1H:1201:C:O4'	2.09	0.53
26:1H:1066:U:H2'	26:1H:1068:G:OP2	2.08	0.53
26:1H:2467:C:H4'	37:88:123:HIS:CD2	2.43	0.53
26:1H:2688:U:H1'	26:1H:2721:A:N6	2.23	0.53
26:1H:2698:U:H2'	26:1H:2699:C:C6	2.44	0.53
27:16:14:U:OP2	27:16:70:C:O2'	2.21	0.53
30:31:101:LEU:O	30:31:106:ARG:NH1	2.39	0.53
36:78:59:LEU:HD11	54:Q8:10:ALA:HA	1.89	0.53
1:1G:1316:G:H2'	1:1G:1317:C:H5"	1.90	0.53
1:1G:1368:G:H5"	9:82:112:LYS:HB3	1.90	0.53
5:42:69:VAL:O	5:42:71:LEU:N	2.37	0.53
5:42:80:ILE:HD13	8:72:104:ARG:HH22	1.73	0.53
22:1L:59:C:O2'	22:1L:60:U:OP2	2.24	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:14:271(B):G:N7	26:14:421:U:H2'	2.23	0.53
26:14:1019:U:H2'	26:14:1020:A:H8	1.72	0.53
26:14:2210:G:H5'	26:14:2211:G:N7	2.24	0.53
30:39:110:LEU:HD21	30:39:181:LEU:HD13	1.89	0.53
31:49:56:ALA:HB2	31:49:153:ARG:NE	2.23	0.53
41:85:112:ARG:CZ	42:95:47:VAL:HG13	2.39	0.53
4:3E:165:MET:SD	4:3E:168:ARG:HD3	2.48	0.53
13:4I:84:ILE:HG23	13:4I:86:CYS:H	1.72	0.53
24:3K:39:G:H2'	24:3K:40:G:C8	2.44	0.53
26:1H:1037:G:N1	26:1H:1118:C:N3	2.38	0.53
26:1H:2376:A:H2'	26:1H:2377:A:O4'	2.09	0.53
26:1H:2419:U:O4	59:1H:3827:HOH:O	2.19	0.53
30:31:160:ASN:OD1	30:31:163:VAL:HG23	2.09	0.53
35:68:2:ILE:HG13	35:68:8:LEU:HD11	1.90	0.53
37:88:3:MET:HG3	37:88:4:PRO:O	2.09	0.53
1:1G:250:A:H4'	1:1G:251:G:O5'	2.08	0.53
1:1G:458:C:H2'	1:1G:464:G:H8	1.73	0.53
1:1G:986:A:H1'	19:AA:54:GLY:O	2.08	0.53
1:1G:1316:G:N2	1:1G:1319:A:O5'	2.37	0.53
1:1G:1466:C:H2'	1:1G:1467:G:O4'	2.07	0.53
13:4A:102:ARG:HD3	13:4A:105:THR:OG1	2.08	0.53
26:14:528:A:C2	26:14:2043:C:H4'	2.44	0.53
26:14:1448:G:H1'	26:14:1528:A:H62	1.72	0.53
26:14:2887:U:H2'	26:14:2888:C:C6	2.43	0.53
31:49:42:GLY:O	31:49:43:LEU:HD13	2.09	0.53
34:15:104:LYS:HA	34:15:107:LEU:HD12	1.91	0.53
35:25:5:GLN:HG3	35:25:20:MET:HE2	1.90	0.53
2:1E:143:GLU:HA	2:1E:146:GLN:HB2	1.91	0.53
26:1H:1321:A:H2'	26:1H:1322:A:O4'	2.09	0.53
28:11:70:TRP:CD1	28:11:70:TRP:C	2.86	0.53
30:31:183:VAL:O	30:31:187:VAL:HG23	2.09	0.53
1:1G:1118:C:H1'	1:1G:1179:A:C4	2.44	0.53
1:1G:1226:C:H2'	13:4A:103:THR:HB	1.91	0.53
3:22:73:PRO:HG2	3:22:105:GLU:HB2	1.91	0.53
13:4A:86:CYS:SG	13:4A:88:ARG:HG3	2.49	0.53
19:AA:3:ARG:HH21	19:AA:10:PHE:C	2.17	0.53
26:14:981:A:P	59:14:3577:HOH:O	2.65	0.53
26:14:1582:C:HO2'	26:14:1586:A:H8	1.49	0.53
26:14:2118:U:O2'	26:14:2145:C:N3	2.40	0.53
26:14:2427:C:H5"	26:14:2428:G:OP1	2.09	0.53
35:25:1:MET:HE2	35:25:32:TYR:CE2	2.44	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:45:27:VAL:HG22	37:45:136:ALA:C	2.34	0.53
46:D5:116:VAL:O	46:D5:117:LEU:HD22	2.09	0.53
1:13:244:U:H4'	1:13:245:C:O5'	2.08	0.53
1:13:662:G:H2'	1:13:663:A:C8	2.44	0.53
1:13:673:G:H2'	1:13:674:G:C8	2.44	0.53
1:13:1000:A:H2'	1:13:1001:G:C8	2.44	0.53
1:13:1144:G:H21	1:13:1146:A:H62	1.56	0.53
1:13:1225:A:H2'	1:13:1225:A:N3	2.23	0.53
19:AI:22:LEU:O	19:AI:28:LYS:NZ	2.30	0.53
24:3K:39:G:H2'	24:3K:40:G:H8	1.74	0.53
26:1H:71:A:H5'	26:1H:71:A:H8	1.71	0.53
26:1H:1340:U:H4'	26:1H:1341:U:OP2	2.09	0.53
38:98:104:ARG:NH1	38:98:107:ASP:OD2	2.42	0.53
44:F8:94:GLY:O	44:F8:95:LEU:HB2	2.08	0.53
1:1G:130:A:C8	17:8A:63:ARG:HG3	2.44	0.53
1:1G:1492:A:C5'	12:3A:47:LYS:HB3	2.38	0.53
4:32:4:TYR:CE2	4:32:11:LEU:HD11	2.44	0.53
4:32:11:LEU:O	4:32:15:GLU:HB2	2.09	0.53
8:72:83:ILE:HG13	8:72:137:VAL:HG22	1.91	0.53
26:14:1525:G:H2'	26:14:1526:G:C8	2.42	0.53
27:1J:42:C:O2'	31:49:67:LYS:O	2.21	0.53
36:35:111:ARG:HB3	36:35:128:HIS:CG	2.44	0.53
37:45:43:THR:O	37:45:46:GLN:N	2.42	0.53
40:75:112:ARG:HH21	40:75:113:LYS:HE2	1.72	0.53
1:13:1179:A:H2'	1:13:1180:A:O4'	2.09	0.53
8:7E:25:ASP:OD1	8:7E:60:ARG:HG3	2.09	0.53
10:1I:26:ALA:O	10:1I:30:SER:OG	2.24	0.53
33:61:127:VAL:HA	33:61:138:ILE:O	2.09	0.53
40:B8:24:PRO:HA	40:B8:49:VAL:HG22	1.91	0.53
1:1G:1277:C:O2'	1:1G:1279:A:H8	1.92	0.53
3:22:70:VAL:HG12	3:22:72:LYS:N	2.24	0.53
7:62:146:GLU:HG2	11:2A:50:TYR:CZ	2.44	0.53
26:14:754:C:H2'	26:14:755:C:C6	2.44	0.53
26:14:2012:G:OP1	43:A5:11:ARG:NH2	2.41	0.53
28:19:72:LYS:HB3	28:19:75:ILE:HD12	1.91	0.53
29:29:27:LEU:HA	29:29:180:ASN:O	2.08	0.53
40:75:4:GLY:N	40:75:5:ALA:C	2.67	0.53
41:85:52:ARG:HA	41:85:55:ARG:HG3	1.90	0.53
49:G5:25:VAL:HG12	49:G5:60:LEU:HD23	1.91	0.53
1:13:1286:A:H2	21:1F:18:TYR:HH	1.55	0.53
20:BI:26:ASN:O	20:BI:30:LYS:HB2	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:1K:56:C:O2	22:1K:56:C:H2'	2.07	0.53
26:1H:1189:A:OP2	59:1H:3818:HOH:O	2.17	0.53
26:1H:1614:A:C2	43:E8:93:ALA:HB2	2.43	0.53
26:1H:1731:G:H2'	26:1H:1732:A:C8	2.44	0.53
27:16:54:G:H2'	27:16:55:U:H6	1.74	0.53
38:98:72:ASP:O	38:98:76:VAL:HG23	2.09	0.53
42:D8:44:LYS:O	42:D8:44:LYS:HG2	2.09	0.53
1:1G:67:C:H2'	1:1G:68:G:C8	2.44	0.53
1:1G:1104:G:H4'	2:12:111:ARG:CZ	2.39	0.53
1:1G:1512:U:H2'	1:1G:1513:A:C8	2.44	0.53
4:32:107:ARG:NH2	4:32:194:LEU:HD22	2.24	0.53
26:14:57:C:H2'	26:14:58:G:O4'	2.09	0.53
26:14:309:G:O3'	45:C5:18:GLY:HA3	2.09	0.53
26:14:586:A:N1	26:14:809:G:O2'	2.39	0.53
26:14:631:A:O2'	36:35:67:MET:HB3	2.08	0.53
26:14:1496:A:H8	26:14:1577:C:O2'	1.92	0.53
26:14:1557:C:OP2	26:14:1558:A:O2'	2.26	0.53
27:1J:52:A:N6	39:65:33:LYS:HG3	2.23	0.53
30:39:32:LEU:HD11	30:39:105:VAL:HG13	1.90	0.53
31:49:41:GLN:NE2	31:49:154:GLY:O	2.35	0.53
37:45:138:ASP:N	37:45:139:GLU:OE2	2.42	0.53
44:B5:36:LYS:HA	44:B5:39:ILE:HD12	1.91	0.53
48:F5:15:ALA:O	48:F5:40:ARG:HG3	2.09	0.53
1:13:145:G:H1	1:13:177:C:N4	2.04	0.53
1:13:158:G:H2'	1:13:159:G:C8	2.37	0.53
1:13:814:A:N7	1:13:816:A:C4	2.77	0.53
1:13:963:G:H21	10:1I:55:LYS:HE2	1.72	0.53
19:AI:20:LEU:HA	19:AI:23:ASN:OD1	2.08	0.53
20:BI:30:LYS:NZ	20:BI:80:ARG:HH12	2.06	0.53
26:1H:606:U:H4'	26:1H:658:C:H4'	1.91	0.53
26:1H:1570:A:H2'	26:1H:1571:A:C8	2.43	0.53
26:1H:1675:C:O2	29:21:128:SER:OG	2.27	0.53
31:41:165:THR:OG1	31:41:168:GLU:HG3	2.08	0.53
37:88:48:GLU:HG3	37:88:48:GLU:O	2.08	0.53
1:1G:108:G:C6	20:BA:15:ARG:HD2	2.44	0.53
1:1G:1504:G:OP1	1:1G:1507:A:H4'	2.09	0.53
5:42:144:THR:H	5:42:147:ASP:HB2	1.73	0.53
13:4A:16:ASP:OD1	13:4A:16:ASP:N	2.42	0.53
26:14:1204:A:H2	26:14:1241:A:N1	2.07	0.53
26:14:1292:U:H2'	26:14:1293:C:C6	2.43	0.53
26:14:1932:A:H2'	26:14:1933:G:O4'	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:59:149:ARG:HB2	32:59:149:ARG:HH11	1.73	0.53
39:65:74:ALA:HB1	39:65:107:GLU:HB2	1.90	0.53
50:H5:6:VAL:HB	50:H5:54:VAL:HG21	1.90	0.53
1:13:1129:C:H4'	1:13:1130:A:OP1	2.08	0.52
2:1E:5:ILE:HG22	2:1E:224:GLN:HE22	1.75	0.52
9:8E:53:VAL:HG11	9:8E:85:LEU:HD13	1.90	0.52
26:1H:75:G:H1	26:1H:111:A:H61	1.57	0.52
26:1H:141:A:H8	26:1H:1408:C:H1'	1.73	0.52
26:1H:910:A:N7	37:88:13:GLN:HG3	2.24	0.52
28:11:108:PRO:HD2	28:11:111:LEU:HG	1.92	0.52
1:1G:502:G:OP1	12:3A:118:SER:HB3	2.09	0.52
4:32:194:LEU:HD23	4:32:196:LEU:HG	1.91	0.52
8:72:10:LEU:HD22	8:72:83:ILE:HD11	1.90	0.52
26:14:1614:A:C2	43:A5:93:ALA:HB2	2.44	0.52
26:14:2720:U:N3	26:14:2873:A:H2	2.06	0.52
32:59:150:ALA:O	32:59:152:ARG:N	2.42	0.52
39:65:54:LEU:O	39:65:56:LEU:N	2.40	0.52
40:75:2:ASN:C	40:75:4:GLY:HA3	2.34	0.52
1:13:123:C:OP1	1:13:311:C:O2'	2.25	0.52
1:13:201:C:H42	1:13:216:G:H1	1.57	0.52
1:13:626:U:C2	1:13:627:G:C8	2.97	0.52
27:16:116:G:H2'	27:16:117:G:O4'	2.09	0.52
29:21:16:ARG:HG3	29:21:16:ARG:O	2.08	0.52
38:98:79:LEU:HA	38:98:83:ILE:HD12	1.91	0.52
48:J8:81:LYS:O	48:J8:83:GLU:HG2	2.09	0.52
54:Q8:6:THR:HG22	54:Q8:63:PRO:HD2	1.90	0.52
1:1G:1308:U:OP2	13:4A:101:GLN:NE2	2.41	0.52
1:1G:1478:C:H2'	1:1G:1479:C:H6	1.74	0.52
4:32:187:ARG:HH21	4:32:190:ASP:HB2	1.74	0.52
5:42:146:ALA:O	5:42:150:ARG:N	2.32	0.52
7:62:27:ILE:HD12	7:62:40:ALA:HA	1.92	0.52
55:3L:61:C:O5'	55:3L:61:C:H6	1.90	0.52
26:14:270(L):U:O2	33:69:50:ARG:HD3	2.09	0.52
26:14:871:U:OP1	37:45:5:ARG:HG2	2.08	0.52
26:14:1406:U:H2'	26:14:1407:C:C6	2.44	0.52
35:25:2:ILE:HD12	35:25:6:THR:HG21	1.90	0.52
1:13:188:U:H2'	1:13:189:U:H5"	1.92	0.52
1:13:983:A:H1'	1:13:1049:U:O2	2.09	0.52
1:13:1126:U:O2'	1:13:1281:U:O2	2.15	0.52
1:13:1510:U:H2'	1:13:1511:G:C8	2.44	0.52
9:8E:42:ARG:NH1	9:8E:71:SER:OG	2.38	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:1I:61:GLU:HG2	10:1I:63:PHE:CE2	2.45	0.52
26:1H:274:G:N2	26:1H:276:A:H61	2.06	0.52
26:1H:573:G:O2'	26:1H:574:C:H3'	2.08	0.52
26:1H:944:G:O3'	59:1H:3825:HOH:O	2.18	0.52
1:1G:1502:A:H2	1:1G:1505:G:N1	1.98	0.52
11:2A:20:TYR:CZ	11:2A:83:ILE:HD13	2.45	0.52
13:4A:33:ALA:O	13:4A:37:THR:OG1	2.17	0.52
23:2L:62:C:H2'	23:2L:63:C:C6	2.44	0.52
55:3L:15:G:C2'	55:3L:59:A:H61	2.22	0.52
26:14:2152:G:C5	26:14:2153:G:H1'	2.44	0.52
26:14:2340:G:O2'	26:14:2341:G:H5'	2.09	0.52
30:39:47:GLY:O	30:39:94:PRO:HA	2.09	0.52
31:49:111:LEU:HB3	31:49:117:PHE:CE2	2.44	0.52
35:25:68:GLU:OE2	35:25:78:ARG:NH1	2.42	0.52
40:75:16:ARG:NH2	40:75:19:LEU:HD21	2.25	0.52
47:E5:51:VAL:N	47:E5:62:LEU:HD12	2.24	0.52
49:G5:29:LYS:HE2	49:G5:57:ILE:HG21	1.92	0.52
53:L5:12:ARG:NH2	53:L5:44:PRO:HB3	2.25	0.52
1:13:345:C:H4'	1:13:346:G:C8	2.44	0.52
1:13:727:G:N2	1:13:730:G:OP2	2.39	0.52
1:13:1060:C:O2'	10:1I:56:HIS:ND1	2.35	0.52
1:13:1126:U:H5	1:13:1127:G:C8	2.24	0.52
2:1E:46:LYS:HA	2:1E:49:GLU:OE1	2.10	0.52
3:2E:95:THR:HB	3:2E:97:LYS:HG3	1.91	0.52
20:BI:46:GLU:HB2	20:BI:48:LYS:HG3	1.90	0.52
22:1K:48:C:H2'	22:1K:49:G:C2	2.45	0.52
26:1H:31:C:OP1	59:1H:3824:HOH:O	2.18	0.52
26:1H:1210:A:H5"	26:1H:1212:G:O4'	2.10	0.52
26:1H:2780:G:OP1	34:58:118:LYS:HE2	2.09	0.52
28:11:124:PRO:O	28:11:129:ASN:ND2	2.36	0.52
38:98:32:GLY:HA2	38:98:116:LEU:CD1	2.40	0.52
38:98:67:LEU:HD22	38:98:76:VAL:HG21	1.91	0.52
1:1G:779:C:H2'	1:1G:780:A:O4'	2.10	0.52
5:42:151:LEU:HD21	8:72:77:GLU:OE2	2.09	0.52
26:14:587:C:O2	36:35:33:ARG:NH1	2.42	0.52
26:14:800:A:H8	26:14:800:A:OP1	1.91	0.52
26:14:1189:A:OP2	59:14:3560:HOH:O	2.19	0.52
26:14:2557:G:H2'	26:14:2558:C:H6	1.74	0.52
28:19:70:TRP:CD1	28:19:70:TRP:C	2.87	0.52
34:15:67:LEU:HD23	34:15:88:GLU:HG2	1.92	0.52
47:E5:19:LYS:HG3	47:E5:41:ARG:HH12	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:4I:22:ILE:HB	13:4I:25:ILE:HD12	1.90	0.52
17:8I:70:ARG:C	17:8I:71:PHE:HD1	2.18	0.52
20:BI:92:LEU:HB3	20:BI:96:GLY:HA2	1.90	0.52
26:1H:274:G:H1'	26:1H:276:A:C2	2.45	0.52
26:1H:606:U:OP2	30:31:104:LYS:NZ	2.43	0.52
26:1H:2023:G:H5'	26:1H:2617:C:H4'	1.90	0.52
36:78:29:LYS:HG2	36:78:30:THR:HB	1.92	0.52
40:B8:12:SER:CA	40:B8:14:TYR:H	2.19	0.52
1:1G:1288:A:O3'	21:1B:10:ARG:NH2	2.42	0.52
2:12:98:LEU:HB2	2:12:101:MET:HE3	1.90	0.52
3:22:16:ARG:HH22	3:22:181:ASN:HA	1.75	0.52
26:14:72:U:OP1	59:14:3559:HOH:O	2.19	0.52
26:14:2469:A:H2	26:14:2481:G:H21	1.57	0.52
37:45:26:TYR:HD1	37:45:27:VAL:H	1.56	0.52
41:85:83:LEU:HB3	41:85:88:ILE:HB	1.91	0.52
1:13:163:C:O2'	1:13:164:U:O4'	2.28	0.52
1:13:592:G:H2'	1:13:593:G:H8	1.75	0.52
1:13:1005:A:H1'	1:13:1036:G:N2	2.24	0.52
2:1E:162:ILE:O	2:1E:185:ILE:HG23	2.10	0.52
3:2E:29:TYR:OH	14:5I:54:PRO:O	2.25	0.52
24:3K:15:G:C6	24:3K:59:A:N7	2.77	0.52
30:31:67:GLN:O	30:31:67:GLN:HG3	2.08	0.52
37:88:104:PHE:HE2	37:88:125:LEU:HD11	1.75	0.52
41:C8:92:ARG:HD2	42:D8:11:GLN:HB2	1.91	0.52
43:E8:12:ILE:HD13	43:E8:17:VAL:HB	1.92	0.52
46:H8:161:VAL:HG23	46:H8:161:VAL:O	2.09	0.52
48:J8:77:ALA:HA	48:J8:79:GLY:N	2.25	0.52
1:1G:1:U:H5'	1:1G:630:G:H21	1.73	0.52
1:1G:146:G:H2'	1:1G:147:G:H8	1.74	0.52
1:1G:1357:A:H2'	1:1G:1358:U:H5'	1.92	0.52
2:12:19:HIS:HE2	2:12:206:ASP:HB2	1.75	0.52
17:8A:45:HIS:CD2	17:8A:47:PRO:HD3	2.45	0.52
22:1L:69:C:H4'	22:1L:70:A:OP1	2.09	0.52
26:14:270(F):U:H2'	26:14:270(G):C:C6	2.44	0.52
26:14:839:U:H2'	26:14:840:C:C6	2.44	0.52
26:14:2335:A:C8	26:14:2337:G:C5	2.98	0.52
29:29:68:ALA:C	29:29:70:ALA:N	2.66	0.52
38:55:82:GLU:H	38:55:85:PRO:HG2	1.75	0.52
38:55:106:GLY:O	38:55:107:ASP:HB3	2.09	0.52
41:85:91:ASP:OD2	41:85:96:ALA:HB2	2.10	0.52
1:13:8:A:N7	4:3E:208:SER:HB3	2.25	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1E:11:LEU:HG	2:1E:14:GLY:HA3	1.92	0.52
14:5I:27:CYS:SG	14:5I:29:ARG:HB2	2.50	0.52
26:1H:207:A:H2'	26:1H:208:C:O4'	2.10	0.52
26:1H:1021:A:H8	26:1H:1021:A:H3'	1.75	0.52
26:1H:1359:A:C2	26:1H:1372:U:O4	2.63	0.52
26:1H:1434:A:H61	26:1H:1558:A:H62	1.55	0.52
31:41:107:LEU:HD21	31:41:178:PHE:CE1	2.45	0.52
38:98:32:GLY:HA2	38:98:116:LEU:HD13	1.92	0.52
46:H8:53:ILE:HG22	46:H8:71:VAL:HG22	1.92	0.52
52:N8:33:CYS:SG	52:N8:40:LYS:NZ	2.72	0.52
1:1G:4:U:C4	8:72:105:ARG:HD3	2.45	0.52
1:1G:1169:A:C6	1:1G:1170:A:C6	2.98	0.52
1:1G:1305:G:O2'	1:1G:1306:A:H8	1.93	0.52
7:62:62:PHE:HD1	7:62:124:LEU:HD11	1.74	0.52
7:62:87:VAL:HG23	7:62:148:ASN:HA	1.92	0.52
17:8A:67:LYS:O	17:8A:69:LYS:N	2.43	0.52
26:14:2104:G:N1	26:14:2186:G:C2	2.78	0.52
26:14:2567:G:H2'	26:14:2568:C:C6	2.45	0.52
26:14:2845:G:H5"	40:75:55:ASN:HA	1.91	0.52
29:29:119:ARG:HG2	29:29:160:TYR:HB2	1.92	0.52
50:H5:3:ARG:NH2	50:H5:38:GLU:OE2	2.42	0.52
1:13:693:G:H2'	1:13:694:A:C8	2.45	0.52
4:3E:150:GLU:HA	4:3E:153:ARG:HG3	1.92	0.52
11:2I:58:PRO:HD3	11:2I:89:ALA:HB1	1.91	0.52
19:AI:17:GLU:O	19:AI:21:GLU:HB2	2.09	0.52
26:1H:184:C:H2'	26:1H:185:U:C6	2.45	0.52
26:1H:507:A:H5"	26:1H:508:G:H3'	1.92	0.52
26:1H:1423:G:N7	59:1H:3895:HOH:O	2.34	0.52
26:1H:1639:U:H2'	26:1H:1640:C:H5"	1.92	0.52
26:1H:2053:G:H5'	29:21:144:ARG:O	2.10	0.52
26:1H:2845:G:H2'	26:1H:2846:G:H8	1.74	0.52
40:B8:3:ARG:HA	40:B8:6:LEU:HB2	1.91	0.52
44:F8:36:LYS:HG2	44:F8:54:VAL:HB	1.92	0.52
47:I8:11:ARG:O	47:I8:14:ARG:NH2	2.43	0.52
1:1G:664:G:N2	1:1G:741:G:H1	2.07	0.52
1:1G:1285:A:H8	1:1G:1285:A:OP1	1.93	0.52
9:82:19:LEU:HD11	9:82:84:ALA:HB1	1.91	0.52
22:1L:9:A:H2'	22:1L:11:C:H41	1.75	0.52
26:14:249:C:O2	54:M5:12:LYS:NZ	2.39	0.52
26:14:1858:G:O2'	26:14:1883:G:N2	2.43	0.52
26:14:2275:C:H5'	26:14:2275:C:H6	1.73	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:14:2306:C:H2'	26:14:2307:G:H21	1.75	0.52
26:14:2572:A:OP1	26:14:2574:G:O2'	2.27	0.52
35:25:3:GLN:HB2	35:25:4:PRO:HD2	1.91	0.52
1:13:154:C:H2'	1:13:155:C:C6	2.45	0.52
1:13:963:G:H1	1:13:972:C:N4	1.99	0.52
1:13:963:G:N2	10:1I:55:LYS:NZ	2.57	0.52
7:6E:28:ASN:HA	7:6E:31:MET:HE3	1.91	0.52
23:2K:20:G:C2	23:2K:58:A:N3	2.78	0.52
26:1H:277:C:H3'	26:1H:278:A:O4'	2.09	0.52
26:1H:1313:U:OP1	59:1H:3830:HOH:O	2.19	0.52
26:1H:2109:U:H1'	26:1H:2181:G:N2	2.25	0.52
28:11:38:LYS:HG2	28:11:40:THR:CG2	2.39	0.52
41:C8:88:ILE:C	41:C8:90:VAL:H	2.18	0.52
46:H8:116:VAL:HG22	46:H8:146:ILE:HG12	1.91	0.52
1:1G:296:U:H2'	1:1G:297:G:C8	2.45	0.52
1:1G:501:C:H2'	1:1G:502:G:H8	1.74	0.52
1:1G:1067:A:HO2'	1:1G:1093:A:HO2'	1.45	0.52
3:22:111:LEU:HD11	3:22:144:SER:O	2.09	0.52
6:52:8:ILE:HD11	6:52:79:LEU:HD13	1.92	0.52
10:1A:79:ARG:HA	10:1A:82:ILE:HB	1.91	0.52
26:14:768:G:O2'	26:14:1379:A:N6	2.43	0.52
30:39:7:TYR:CD1	30:39:18:ARG:HB2	2.45	0.52
42:95:37:VAL:HG13	42:95:37:VAL:O	2.10	0.52
1:13:1198:G:OP1	59:13:1935:HOH:O	2.19	0.52
2:1E:15:VAL:HB	2:1E:16:HIS:ND1	2.25	0.52
24:3K:64:C:H5'	24:3K:65:C:OP2	2.10	0.52
26:1H:320:A:H2'	30:31:136:THR:HG21	1.92	0.52
26:1H:818:G:H4'	26:1H:838:C:O3'	2.10	0.52
26:1H:1053:C:H42	26:1H:1106:G:H1	1.58	0.52
26:1H:2062:A:H2'	26:1H:2062:A:N3	2.25	0.52
26:1H:2402:C:H1'	26:1H:2403:C:C5	2.44	0.52
28:11:38:LYS:HG2	28:11:40:THR:HG22	1.92	0.52
6:52:83:ASP:OD1	6:52:83:ASP:N	2.39	0.52
9:82:77:ILE:O	9:82:81:ILE:HG12	2.10	0.52
26:14:1316:U:H2'	26:14:1317:A:C8	2.45	0.52
26:14:1585:C:O2	26:14:1585:C:H2'	2.09	0.52
37:45:10:ARG:NH1	37:45:10:ARG:HA	2.25	0.52
37:45:27:VAL:HG13	37:45:134:ARG:HE	1.75	0.52
45:C5:18:GLY:C	45:C5:20:TYR:H	2.17	0.52
1:13:1197:G:OP2	59:13:1908:HOH:O	2.19	0.51
2:1E:61:LEU:HD23	2:1E:68:ILE:HD11	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:6E:69:VAL:HG12	7:6E:100:ALA:HA	1.92	0.51
11:2I:53:SER:HA	11:2I:54:ARG:O	2.10	0.51
22:1K:47:U:O2'	22:1K:48:C:O5'	2.27	0.51
24:3K:50:G:O2'	24:3K:64:C:N4	2.43	0.51
26:1H:768:G:O2'	26:1H:1379:A:N6	2.43	0.51
26:1H:1124:C:H2'	26:1H:1125:G:O4'	2.10	0.51
26:1H:2679:A:H4'	29:21:165:VAL:HG11	1.91	0.51
37:88:133:ARG:O	37:88:134:ARG:HB2	2.10	0.51
48:J8:93:GLU:O	48:J8:95:LEU:N	2.43	0.51
1:1G:1125:U:O4	10:1A:5:ARG:NH2	2.42	0.51
2:12:75:LYS:H	2:12:78:GLN:HG3	1.74	0.51
7:62:141:VAL:HA	7:62:142:GLU:CB	2.41	0.51
17:8A:10:VAL:HG12	17:8A:55:ASP:O	2.10	0.51
26:14:2272:U:H5"	26:14:2273:A:OP1	2.10	0.51
28:19:84:TYR:HE1	28:19:86:PRO:HB3	1.75	0.51
42:95:51:VAL:HG12	42:95:52:VAL:H	1.76	0.51
1:13:578:C:OP1	59:13:1936:HOH:O	2.19	0.51
26:1H:1678:G:H22	26:1H:1989:G:N2	1.98	0.51
30:31:197:ASP:N	30:31:197:ASP:OD1	2.37	0.51
32:51:24:VAL:HG13	32:51:35:VAL:HB	1.92	0.51
35:68:64:ARG:HB2	35:68:79:PHE:CG	2.45	0.51
1:1G:1062:U:H2'	1:1G:1063:C:C6	2.46	0.51
1:1G:1157:A:N7	1:1G:1181:G:H1'	2.25	0.51
1:1G:1320:C:N3	19:AA:36:ARG:NH2	2.58	0.51
4:32:103:ASN:OD1	4:32:114:ARG:NH2	2.38	0.51
9:82:16:ARG:O	9:82:63:ILE:HG23	2.10	0.51
10:1A:3:LYS:HZ3	10:1A:77:PRO:HD2	1.74	0.51
26:14:1329:U:H5"	26:14:1330:C:H5	1.74	0.51
26:14:2115:G:N1	26:14:2117:A:N7	2.59	0.51
26:14:2152:G:N3	26:14:2152:G:H2'	2.25	0.51
1:13:190:G:H3'	1:13:191(A):G:H5'	1.92	0.51
1:13:710:G:H5"	6:5E:54:LYS:HE2	1.93	0.51
13:4I:23:TYR:CE2	13:4I:71:ARG:HG3	2.45	0.51
20:BI:49:ALA:HA	20:BI:52:ALA:HB3	1.92	0.51
26:1H:617:G:OP1	30:31:40:GLN:NE2	2.43	0.51
26:1H:1593:G:H2'	26:1H:1594:G:H8	1.76	0.51
40:B8:120:ARG:HA	40:B8:123:GLN:HG2	1.93	0.51
2:12:24:TRP:HD1	2:12:25:ASN:C	2.18	0.51
26:14:620:G:H4'	26:14:621:A:H5"	1.92	0.51
26:14:1190:G:H2'	26:14:1191:G:H8	1.74	0.51
36:35:55:ARG:HG2	36:35:56:SER:N	2.24	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:45:4:PRO:HD3	37:45:70:PRO:O	2.09	0.51
37:45:137:TYR:CE2	46:D5:76:LEU:HD22	2.45	0.51
1:13:108:G:C6	20:BI:15:ARG:HD2	2.46	0.51
1:13:455:C:N4	1:13:477:G:H22	2.08	0.51
2:1E:125:PRO:HA	2:1E:127:ILE:HG12	1.92	0.51
8:7E:49:GLU:HG2	8:7E:62:TYR:HE2	1.75	0.51
26:1H:479:A:N3	26:1H:481:G:H5"	2.25	0.51
26:1H:1012:U:O4	34:58:25:ARG:HA	2.09	0.51
26:1H:1425:G:O6	59:1H:3829:HOH:O	2.19	0.51
26:1H:2414:G:H21	36:78:67:MET:CE	2.22	0.51
26:1H:2557:G:H2'	26:1H:2558:C:C6	2.45	0.51
34:58:57:ALA:C	34:58:59:LYS:H	2.18	0.51
48:J8:3:LYS:HG3	48:J8:46:LEU:CD2	2.40	0.51
1:1G:1304:G:N1	1:1G:1332:A:OP2	2.38	0.51
26:14:244:A:C2	26:14:255:A:C4	2.99	0.51
26:14:1515:C:H2'	26:14:1516:U:H6	1.74	0.51
28:19:30:GLU:HG3	28:19:63:ARG:HH21	1.73	0.51
32:59:121:ILE:HA	32:59:133:VAL:HG13	1.92	0.51
36:35:95:VAL:HG13	36:35:100:LEU:HD11	1.92	0.51
36:35:110:TYR:N	36:35:110:TYR:CD1	2.78	0.51
38:55:52:ILE:O	38:55:55:ALA:N	2.42	0.51
1:13:1:U:H6	1:13:630:G:H2'	1.74	0.51
1:13:186:C:H2'	1:13:186(A):C:C6	2.45	0.51
1:13:626:U:N3	1:13:627:G:N7	2.59	0.51
2:1E:128:GLU:OE1	2:1E:135:GLN:NE2	2.44	0.51
3:2E:175:LEU:HD21	3:2E:201:TYR:CE2	2.45	0.51
9:8E:25:LYS:O	9:8E:61:ALA:N	2.43	0.51
10:1I:64:GLU:HG2	14:5I:59:ALA:HB2	1.92	0.51
22:1K:11:C:H2'	22:1K:12:U:C6	2.45	0.51
26:1H:270(L):U:N1	33:61:50:ARG:HG2	2.25	0.51
29:21:9:VAL:HG13	40:B8:3:ARG:HB3	1.93	0.51
38:98:51:LEU:HD22	38:98:66:VAL:HG13	1.91	0.51
43:E8:24:ILE:HD12	43:E8:24:ILE:O	2.11	0.51
1:1G:1112:C:C2	3:22:178:LEU:HB2	2.46	0.51
3:22:95:THR:C	3:22:97:LYS:H	2.18	0.51
22:1L:68:U:H2'	22:1L:69:C:C6	2.45	0.51
26:14:1041:C:H42	26:14:1114:G:H22	1.57	0.51
26:14:1299:G:N7	59:14:3612:HOH:O	2.34	0.51
36:35:47:ASP:HB3	36:35:50:ARG:H	1.76	0.51
46:D5:8:TYR:HD1	46:D5:62:PRO:HG3	1.73	0.51
46:D5:163:LEU:HD12	46:D5:165:VAL:HG22	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:F5:18:ILE:HG12	48:F5:37:ILE:HD12	1.92	0.51
1:13:376:G:H5”	16:7I:5:ARG:HD2	1.92	0.51
1:13:625:G:H4’	16:7I:16:HIS:CG	2.45	0.51
1:13:1126:U:H3’	1:13:1126:U:C6	2.44	0.51
1:13:1176:A:H2’	1:13:1177:G:O4’	2.10	0.51
1:13:1434:A:H2’	1:13:1435:G:O4’	2.10	0.51
8:7E:98:LYS:H	8:7E:98:LYS:HD2	1.75	0.51
9:8E:78:LYS:HE3	9:8E:101:PHE:HE1	1.76	0.51
26:1H:666:G:H1’	54:Q8:4:MET:HE2	1.91	0.51
26:1H:2208:U:O2’	26:1H:2209:C:H5’	2.10	0.51
26:1H:2593:U:O2’	26:1H:2594:C:H5’	2.10	0.51
30:31:178:PRO:HG2	30:31:179:GLU:CD	2.35	0.51
1:1G:952:U:H4’	1:1G:964:A:N1	2.26	0.51
26:14:315:G:H2’	26:14:316:C:C6	2.46	0.51
26:14:2295:C:N3	26:14:2296:U:H5	2.08	0.51
26:14:2850:A:C2	26:14:2851:A:C4	2.98	0.51
38:55:20:LEU:HD21	38:55:40:LYS:HD3	1.92	0.51
38:55:90:ARG:CZ	38:55:117:VAL:HG11	2.41	0.51
46:D5:170:THR:O	46:D5:172:ALA:N	2.44	0.51
1:13:688:G:H2’	1:13:689:C:H6	1.76	0.51
13:4I:60:VAL:HG12	13:4I:66:LEU:HD11	1.93	0.51
22:1K:23:A:H2’	22:1K:24:G:H8	1.75	0.51
22:1K:49:G:O6	22:1K:59:C:H5”	2.11	0.51
26:1H:569:U:C4	26:1H:570:G:C6	2.98	0.51
26:1H:719:C:H2’	26:1H:720:C:C6	2.46	0.51
26:1H:764:A:N3	28:11:213:ARG:NH1	2.58	0.51
26:1H:800:A:P	59:1H:3739:HOH:O	2.61	0.51
36:78:24:GLY:O	36:78:25:SER:HB3	2.09	0.51
45:G8:9:LYS:HA	45:G8:27:VAL:HG22	1.93	0.51
1:1G:736:C:H2’	1:1G:737:A:C8	2.46	0.51
1:1G:1348:U:H3	1:1G:1374:A:H2	1.57	0.51
2:12:127:ILE:HA	2:12:130:ARG:CZ	2.41	0.51
3:22:125:GLU:O	3:22:127:ARG:NH1	2.43	0.51
7:62:111:ARG:NE	7:62:113:GLU:OE2	2.35	0.51
13:4A:78:ILE:O	13:4A:82:MET:N	2.44	0.51
26:14:27:G:N2	26:14:512:G:H1’	2.25	0.51
26:14:1028:A:N6	26:14:1125:G:H2’	2.25	0.51
26:14:1291:C:H2’	26:14:1292:U:C6	2.46	0.51
26:14:1859:A:N6	26:14:1883:G:O2’	2.44	0.51
26:14:2887:U:H2’	26:14:2888:C:H6	1.75	0.51
31:49:7:LEU:HG	31:49:104:GLU:HB2	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:45:97:VAL:HG11	37:45:103:MET:CE	2.41	0.51
1:13:1171:G:H8	1:13:1171:G:O5'	1.94	0.51
26:1H:234:C:H2'	26:1H:235:U:H6	1.76	0.51
26:1H:1453:A:O2'	26:1H:1454:U:H2'	2.10	0.51
26:1H:1509:C:O2'	26:1H:1510:A:O5'	2.28	0.51
26:1H:2287:A:C2	26:1H:2346:A:C2	2.99	0.51
39:A8:35:ILE:HD11	39:A8:101:LEU:HD23	1.91	0.51
40:B8:23:ARG:HG3	40:B8:120:ARG:NH1	2.26	0.51
45:G8:94:LYS:HA	45:G8:94:LYS:HZ3	1.76	0.51
1:1G:20:U:H2'	1:1G:21:G:O4'	2.11	0.51
1:1G:21:G:O2'	1:1G:914:A:N6	2.44	0.51
1:1G:522:C:H42	1:1G:527:G:H1	1.59	0.51
1:1G:1208:C:H2'	1:1G:1209:C:C6	2.46	0.51
22:1L:6:U:H3	22:1L:67:A:H2	1.58	0.51
26:14:673:C:H5"	30:39:81:PRO:HD2	1.92	0.51
26:14:959:A:N3	26:14:2457:U:O2'	2.39	0.51
26:14:2184:G:H2'	26:14:2185:C:C6	2.45	0.51
31:49:66:GLN:NE2	31:49:93:THR:O	2.42	0.51
32:59:6:ARG:HH22	32:59:62:LYS:HG3	1.75	0.51
41:85:91:ASP:O	41:85:92:ARG:HG2	2.11	0.51
11:2I:17:GLY:O	11:2I:80:VAL:HA	2.10	0.51
15:6I:74:ASP:CG	15:6I:77:ARG:HB2	2.36	0.51
26:1H:528:A:N1	26:1H:2042:A:H2'	2.25	0.51
26:1H:860:U:H1'	26:1H:2268:A:H5'	1.93	0.51
26:1H:2233:U:H2'	26:1H:2234:G:C8	2.46	0.51
26:1H:2470:G:H5'	37:88:56:ARG:NH2	2.26	0.51
26:1H:2499:C:P	59:1H:3733:HOH:O	2.68	0.51
26:1H:2688:U:C5	26:1H:2720:U:OP2	2.64	0.51
27:16:9:G:OP1	39:A8:15:ARG:NH1	2.43	0.51
32:51:126:PRO:HG2	32:51:130:ARG:NH2	2.26	0.51
37:88:39:PRO:HA	37:88:97:VAL:O	2.10	0.51
1:1G:1:U:OP1	1:1G:630:G:O2'	2.22	0.51
2:12:163:PHE:HD1	2:12:185:ILE:HB	1.76	0.51
6:52:91:VAL:HG13	18:9A:72:ARG:HH12	1.76	0.51
7:62:22:LEU:HG	7:62:62:PHE:HE2	1.76	0.51
8:72:68:ARG:HD3	8:72:69:ARG:O	2.10	0.51
13:4A:13:LYS:HG2	13:4A:44:ARG:NH1	2.26	0.51
26:14:1434:A:H61	26:14:1558:A:N6	2.08	0.51
26:14:2652:C:H42	26:14:2668:G:H1	1.59	0.51
27:1J:116:G:H5"	39:65:55:ALA:HB2	1.92	0.51
33:69:78:THR:OG1	33:69:104:GLN:NE2	2.44	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:85:28:ARG:NH1	41:85:38:THR:OG1	2.43	0.51
1:13:57:G:H2'	1:13:58:C:C6	2.46	0.51
1:13:652:U:H1'	1:13:653:A:H2	1.75	0.51
19:AI:22:LEU:O	19:AI:25:LYS:N	2.42	0.51
26:1H:323:G:C8	30:31:171:PRO:HG3	2.45	0.51
26:1H:671:C:OP1	36:78:42:SER:O	2.29	0.51
26:1H:1297:C:OP1	26:1H:2710:C:H4'	2.10	0.51
26:1H:1479:G:O2'	26:1H:1558:A:H5'	2.11	0.51
26:1H:2022:U:O2'	26:1H:2617:C:H5'	2.10	0.51
26:1H:2751:G:H4'	32:51:4:ILE:HD11	1.92	0.51
29:21:103:ASP:OD1	29:21:201:THR:HG23	2.10	0.51
29:21:104:VAL:HG13	29:21:198:VAL:HG22	1.92	0.51
49:K8:63:VAL:HA	49:K8:66:GLU:HG2	1.91	0.51
2:12:77:ALA:O	2:12:81:VAL:HG23	2.10	0.51
3:22:172:ARG:HH11	3:22:174:PRO:HG3	1.76	0.51
6:52:26:ILE:O	6:52:30:LEU:HG	2.11	0.51
55:3L:4:G:H2'	55:3L:5:A:C8	2.46	0.51
26:14:900:A:H3'	26:14:901:A:C8	2.37	0.51
26:14:1420:U:O2'	26:14:1421:G:OP1	2.29	0.51
26:14:2542:A:N3	26:14:2542:A:H5"	2.25	0.51
27:1J:104:A:H2'	27:1J:105:G:O4'	2.11	0.51
28:19:108:PRO:HB3	28:19:143:HIS:CE1	2.46	0.51
29:29:199:ARG:HB3	29:29:200:GLU:OE1	2.11	0.51
30:39:53:THR:HG23	30:39:55:GLY:H	1.76	0.51
46:D5:94:GLU:OE1	46:D5:95:PRO:HD2	2.10	0.51
49:G5:15:LYS:H	49:G5:67:LYS:NZ	2.09	0.51
54:M5:22:VAL:HB	54:M5:55:ALA:HB1	1.93	0.51
1:13:8:A:N6	4:3E:205:GLU:O	2.44	0.50
1:13:1097:C:O2'	1:13:1169:A:N3	2.33	0.50
1:13:1372:U:H5"	9:8E:71:SER:HB3	1.93	0.50
26:1H:1919:A:H5"	26:1H:1920:C:OP2	2.11	0.50
33:61:133:HIS:CG	33:61:133:HIS:O	2.64	0.50
46:H8:53:ILE:HA	46:H8:71:VAL:HG13	1.93	0.50
1:1G:371:G:H1	1:1G:390:C:H42	1.58	0.50
1:1G:1023:G:C5	1:1G:1024:G:H1'	2.45	0.50
2:12:71:VAL:HG21	2:12:165:VAL:N	2.26	0.50
12:3A:34:ARG:HG3	12:3A:35:GLY:N	2.26	0.50
19:AA:3:ARG:NH1	19:AA:7:LYS:HZ3	2.09	0.50
26:14:467:G:OP1	53:L5:33:ARG:NH1	2.43	0.50
26:14:2213:U:H2'	26:14:2215:G:H5'	1.93	0.50
27:1J:94:C:H2'	27:1J:95:U:C6	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:59:17:VAL:HG12	32:59:45:VAL:HB	1.92	0.50
32:59:118:PRO:HD2	32:59:121:ILE:HG13	1.93	0.50
36:35:101:VAL:HA	36:35:105:LEU:O	2.10	0.50
36:35:110:TYR:N	36:35:110:TYR:HD1	2.08	0.50
49:G5:18:PRO:HA	49:G5:21:LEU:HD12	1.93	0.50
52:J5:46:CYS:SG	52:J5:48:GLU:HG2	2.51	0.50
1:13:114:U:O2'	1:13:115:G:H5'	2.12	0.50
1:13:877:C:H5"	8:7E:88:LYS:HD3	1.92	0.50
1:13:1202:G:N2	14:5I:46:GLU:OE1	2.38	0.50
19:AI:65:ASN:OD1	19:AI:65:ASN:N	2.45	0.50
24:3K:75:C:H5"	24:3K:76:A:OP1	2.10	0.50
26:1H:607:U:N3	26:1H:621:A:H2	1.98	0.50
26:1H:638:G:C5	26:1H:651:G:C2	2.99	0.50
26:1H:1264:G:H5'	52:N8:11:THR:CG2	2.42	0.50
26:1H:1364:G:C8	48:J8:2:SER:N	2.79	0.50
26:1H:2335:A:C8	26:1H:2337:G:C5	2.98	0.50
35:68:68:GLU:OE2	35:68:78:ARG:NH1	2.45	0.50
38:98:53:HIS:ND1	38:98:94:TYR:OH	2.36	0.50
39:A8:85:VAL:HG22	39:A8:110:LEU:HB3	1.93	0.50
45:G8:87:LYS:N	45:G8:94:LYS:HG2	2.08	0.50
1:1G:45:U:H2'	1:1G:46:G:H8	1.75	0.50
1:1G:588:G:H1	1:1G:651:C:H42	1.58	0.50
1:1G:620:C:C2	4:32:135:LEU:HG	2.46	0.50
1:1G:1189:C:P	10:1A:51:ARG:HH22	2.34	0.50
3:22:18:TRP:CD1	14:5A:55:GLY:H	2.29	0.50
4:32:173:TRP:CE3	4:32:193:ASP:HB3	2.46	0.50
7:62:57:GLU:OE1	7:62:57:GLU:N	2.38	0.50
7:62:93:PRO:HD2	7:62:94:ARG:NH2	2.23	0.50
13:4A:13:LYS:HE2	13:4A:14:ARG:H	1.75	0.50
26:14:1033:U:H3'	26:14:1033:U:H6	1.77	0.50
26:14:1171:G:O2'	26:14:1173:G:OP2	2.29	0.50
26:14:2415:G:H4'	36:35:67:MET:H	1.74	0.50
26:14:2537:U:H2'	26:14:2538:C:C6	2.46	0.50
33:69:123:LEU:HD13	33:69:144:VAL:HG12	1.92	0.50
1:13:401:C:H2'	1:13:402:G:C8	2.46	0.50
1:13:652:U:H1'	1:13:653:A:C2	2.46	0.50
3:2E:136:GLN:HE22	3:2E:140:ARG:HH11	1.60	0.50
22:1K:21:A:N6	22:1K:48:C:H1'	2.26	0.50
26:1H:1021:A:C8	26:1H:1022:G:H5"	2.41	0.50
26:1H:1386:C:H2'	26:1H:1387:C:C6	2.47	0.50
26:1H:2473:U:H2'	26:1H:2474:C:H5'	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:78:50:ARG:HH21	36:78:50:ARG:HG3	1.76	0.50
46:H8:98:MET:O	46:H8:125:LEU:HA	2.12	0.50
1:1G:992:U:O2'	1:1G:1041:A:OP2	2.26	0.50
1:1G:1348:U:H4'	9:82:120:ARG:HD2	1.93	0.50
1:1G:1368:G:OP1	9:82:111:ARG:NH2	2.44	0.50
1:1G:1432:G:OP1	40:75:107:ASP:HB2	2.11	0.50
13:4A:92:HIS:NE2	13:4A:98:VAL:HG11	2.27	0.50
26:14:289:A:H3'	26:14:290:G:H8	1.75	0.50
26:14:1991:U:H2'	26:14:1992:G:H5"	1.93	0.50
26:14:2105:C:N4	26:14:2184:G:H1	2.09	0.50
26:14:2693:A:H2'	26:14:2694:G:H8	1.76	0.50
29:29:12:THR:O	29:29:23:VAL:HG22	2.11	0.50
29:29:60:ASN:OD1	29:29:63:LEU:HD13	2.11	0.50
30:39:20:LEU:HD13	30:39:199:TRP:HH2	1.76	0.50
30:39:107:LYS:HE2	30:39:205:ARG:HD2	1.93	0.50
35:25:49:ARG:HA	35:25:53:LYS:HZ3	1.76	0.50
44:B5:3:THR:HG21	49:G5:26:ARG:HG3	1.93	0.50
46:D5:128:VAL:HG22	46:D5:129:SER:H	1.77	0.50
52:J5:16:ARG:NH1	52:J5:17:ASP:OD1	2.45	0.50
1:13:393:A:OP2	16:7I:12:LYS:NZ	2.35	0.50
1:13:545:C:O2'	1:13:549:C:OP1	2.25	0.50
1:13:1013:G:N2	1:13:1016:A:OP2	2.45	0.50
3:2E:22:TRP:CH2	3:2E:32:LEU:HB3	2.47	0.50
3:2E:131:ARG:HD3	3:2E:131:ARG:H	1.76	0.50
12:3I:7:ILE:O	12:3I:11:VAL:HG23	2.12	0.50
26:1H:578:A:OP2	59:1H:3833:HOH:O	2.19	0.50
26:1H:607:U:N3	26:1H:621:A:C2	2.73	0.50
26:1H:1069:A:H4'	26:1H:1070:A:H5"	1.93	0.50
26:1H:2150:U:H2'	26:1H:2151:G:C8	2.46	0.50
34:58:18:ALA:HA	34:58:21:LYS:HG3	1.92	0.50
34:58:73:THR:HB	34:58:82:LEU:HD11	1.93	0.50
41:C8:65:ILE:CG1	41:C8:96:ALA:HB2	2.41	0.50
46:H8:102:LEU:HG	46:H8:123:ASP:HA	1.94	0.50
46:H8:110:GLY:C	46:H8:112:ARG:H	2.19	0.50
48:J8:83:GLU:HA	48:J8:85:LEU:HD13	1.93	0.50
54:Q8:52:LYS:H	54:Q8:53:PRO:HD2	1.76	0.50
1:1G:42:G:H2'	1:1G:43:C:O4'	2.10	0.50
1:1G:176:C:H2'	1:1G:177:C:C6	2.47	0.50
1:1G:1037:C:H2'	1:1G:1038:C:C6	2.46	0.50
1:1G:1371:G:OP1	9:82:11:LYS:HB3	2.12	0.50
2:12:130:ARG:HB3	2:12:135:GLN:HE21	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:32:15:GLU:HG3	4:32:63:LYS:HE2	1.94	0.50
14:5A:37:PHE:CE1	14:5A:53:LEU:HD13	2.47	0.50
17:8A:66:SER:O	17:8A:70:ARG:NH1	2.44	0.50
22:1L:76:A:H4'	26:14:2506:U:O2'	2.11	0.50
23:2L:48:U:H4'	23:2L:49:C:H5'	1.93	0.50
26:14:635:C:O2'	26:14:639:U:OP1	2.26	0.50
26:14:1366:A:H2'	26:14:1367:A:O4'	2.10	0.50
26:14:1677:A:H8	26:14:1677:A:O5'	1.94	0.50
26:14:2776:A:OP1	26:14:2776:A:H3'	2.12	0.50
33:69:81:VAL:H	33:69:143:SER:CB	2.25	0.50
1:13:45:U:H2'	1:13:46:G:C8	2.46	0.50
1:13:76:G:N2	1:13:93:U:O2	2.30	0.50
1:13:658:G:H2'	1:13:659:U:C6	2.47	0.50
1:13:820:U:H4'	1:13:821:G:OP2	2.12	0.50
1:13:827:U:C5	1:13:870:U:C4	2.99	0.50
1:13:1074:G:O2'	1:13:1101:A:N1	2.41	0.50
1:13:1077:G:N2	1:13:1080:A:OP2	2.41	0.50
1:13:1353:G:C2	1:13:1370:G:C2	3.00	0.50
7:6E:16:LEU:HD23	9:8E:42:ARG:HA	1.93	0.50
7:6E:95:ARG:HH21	7:6E:99:LEU:HD11	1.77	0.50
9:8E:18:PHE:HB2	9:8E:62:TYR:HB3	1.94	0.50
26:1H:192:C:OP1	59:1H:3832:HOH:O	2.19	0.50
26:1H:799:G:H2'	59:1H:3739:HOH:O	2.11	0.50
26:1H:1081:U:O2'	26:1H:1082:U:O5'	2.20	0.50
26:1H:2119:A:H2	26:1H:2171:A:H2	1.58	0.50
1:1G:814:A:H2'	1:1G:816:A:H5"	1.94	0.50
1:1G:1346:A:H5"	9:82:120:ARG:HH12	1.76	0.50
25:4L:12:A:H1'	25:4L:13:A:O5'	2.12	0.50
26:14:2106:G:N2	26:14:2107:C:O2	2.44	0.50
28:19:6:PHE:HE1	28:19:18:VAL:HG23	1.76	0.50
28:19:242:ARG:HG2	28:19:246:PRO:HG3	1.92	0.50
30:39:67:GLN:HG3	30:39:67:GLN:O	2.09	0.50
32:59:50:VAL:HG23	32:59:51:ARG:N	2.26	0.50
44:B5:49:VAL:HB	44:B5:83:VAL:HG23	1.93	0.50
54:M5:22:VAL:HG12	54:M5:50:LEU:HD23	1.94	0.50
1:13:1053:G:N7	1:13:1199:U:H3'	2.27	0.50
1:13:1218:C:H2'	1:13:1219:U:C6	2.46	0.50
1:13:1510:U:H1'	1:13:1526:G:N2	2.26	0.50
4:3E:47:ARG:HH22	25:4K:26:A:N6	2.10	0.50
4:3E:155:LEU:O	4:3E:158:ILE:N	2.39	0.50
13:4I:34:LEU:HD22	13:4I:39:ILE:HB	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1H:142:G:H1'	44:F8:37:THR:CG2	2.42	0.50
26:1H:309:G:H4'	45:G8:18:GLY:HA2	1.94	0.50
26:1H:918:A:N3	27:16:80:U:O2'	2.41	0.50
37:88:35:VAL:HA	37:88:101:ARG:O	2.10	0.50
42:D8:49:THR:O	42:D8:50:PRO:C	2.55	0.50
1:1G:34:C:H2'	1:1G:35:G:H8	1.77	0.50
1:1G:428:G:C5	1:1G:430:A:C6	3.00	0.50
1:1G:750:G:N3	15:6A:23:GLY:HA3	2.27	0.50
1:1G:1326:C:H5"	21:1B:12:LYS:HZ3	1.77	0.50
26:14:516:C:P	52:J5:13:LYS:HZ1	2.35	0.50
26:14:1323:U:H2'	26:14:1324:G:H5'	1.93	0.50
30:39:51:THR:HG23	30:39:92:PRO:HG2	1.93	0.50
1:13:431:A:H2'	1:13:432:A:O4'	2.11	0.50
1:13:691:G:H2'	1:13:692:U:C6	2.46	0.50
1:13:1086:U:H3	1:13:1099:G:H22	1.59	0.50
5:4E:71:LEU:HD22	5:4E:114:GLY:HA3	1.93	0.50
22:1K:5:A:H2'	22:1K:5:A:N3	2.27	0.50
24:3K:8:U:H3	24:3K:14:A:H62	1.59	0.50
26:1H:265:A:H1'	26:1H:266:G:O4'	2.11	0.50
26:1H:2383:G:O2'	26:1H:2384:G:H5'	2.12	0.50
26:1H:2854:G:H2'	26:1H:2855:C:C6	2.47	0.50
29:21:101:ARG:CZ	29:21:171:GLU:HB2	2.42	0.50
37:88:78:PRO:O	37:88:79:LEU:HB3	2.12	0.50
1:1G:266:G:H5"	1:1G:267:C:C5	2.47	0.50
1:1G:713:G:H2'	1:1G:714:G:C8	2.46	0.50
2:12:184:VAL:HG23	2:12:198:ASP:H	1.76	0.50
7:62:26:PHE:CE2	7:62:30:ILE:HD11	2.47	0.50
26:14:1942:C:OP2	26:14:1943:U:O2'	2.16	0.50
26:14:2280:G:C2'	26:14:2281:C:H5'	2.42	0.50
26:14:2865:U:C4	26:14:2866:U:C4	3.00	0.50
27:1J:112:G:H2'	27:1J:113:C:C6	2.46	0.50
36:35:58:THR:HG21	54:M5:54:GLU:HB3	1.94	0.50
1:13:26:A:N6	1:13:558:G:O2'	2.44	0.50
1:13:448:A:P	1:13:485:G:H22	2.35	0.50
1:13:926:G:H5"	1:13:927:G:O5'	2.10	0.50
1:13:953:G:H2'	1:13:954:G:O4'	2.12	0.50
3:2E:119:ARG:O	3:2E:123:GLN:HG3	2.12	0.50
4:3E:101:LEU:HB2	4:3E:138:TYR:HB3	1.94	0.50
5:4E:100:VAL:HG22	5:4E:118:ILE:HG22	1.94	0.50
5:4E:147:ASP:OD1	5:4E:147:ASP:N	2.26	0.50
13:4I:108:ARG:HA	13:4I:108:ARG:HH11	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:1F:9:ARG:HD2	21:1F:13:ILE:HD11	1.92	0.50
23:2K:16:C:H5'	23:2K:17:C:C5	2.46	0.50
30:31:177:ALA:HB1	30:31:178:PRO:HD2	1.93	0.50
32:51:126:PRO:O	32:51:127:GLU:HB3	2.12	0.50
1:1G:892:A:O2'	1:1G:1415:G:H4'	2.12	0.50
1:1G:1207:G:H2'	1:1G:1208:C:C6	2.46	0.50
1:1G:1260:C:H3'	1:1G:1260:C:C6	2.47	0.50
4:32:31:CYS:C	4:32:33:MET:H	2.20	0.50
7:62:38:LEU:O	7:62:42:ILE:HG13	2.12	0.50
9:82:14:VAL:O	9:82:65:VAL:HG23	2.11	0.50
9:82:46:ALA:HB2	9:82:74:ILE:HG23	1.94	0.50
26:14:706:A:H2'	26:14:707:G:O4'	2.12	0.50
28:19:267:SER:C	28:19:269:PHE:H	2.20	0.50
37:45:38:GLU:HG3	37:45:127:ILE:HG22	1.92	0.50
39:65:87:PHE:CE1	39:65:102:ALA:HB2	2.47	0.50
42:95:91:TYR:CD1	42:95:91:TYR:C	2.90	0.50
1:13:456:C:H42	1:13:476:G:H1	1.59	0.50
1:13:456:C:N4	1:13:476:G:H1	2.10	0.50
19:AI:41:VAL:HG12	19:AI:44:MET:HB2	1.93	0.50
26:1H:479:A:H4'	26:1H:480:A:OP1	2.12	0.50
26:1H:784:A:C5	28:11:229:VAL:HG21	2.47	0.50
26:1H:1291:C:OP1	26:1H:1536:A:H4'	2.12	0.50
26:1H:1354:A:H2'	26:1H:1355:G:O4'	2.11	0.50
26:1H:2224:G:H4'	26:1H:2226:C:C2	2.46	0.50
44:F8:12:VAL:HG13	44:F8:27:THR:O	2.12	0.50
1:1G:377:G:OP1	16:7A:3:LYS:NZ	2.44	0.50
1:1G:493:G:H8	1:1G:493:G:O5'	1.93	0.50
1:1G:580:U:H2'	1:1G:581:G:O4'	2.12	0.50
1:1G:1256:A:H62	1:1G:1277:C:H3'	1.76	0.50
22:1L:48:C:O2'	22:1L:49:G:N3	2.40	0.50
26:14:363(F):A:OP2	26:14:363(F):A:H8	1.95	0.50
26:14:2688:U:H5	26:14:2720:U:OP2	1.94	0.50
26:14:2724:C:OP1	29:29:118:LYS:HE3	2.12	0.50
34:15:128:HIS:H	34:15:128:HIS:HD2	1.57	0.50
46:D5:128:VAL:HG23	46:D5:160:GLY:O	2.11	0.50
54:M5:37:SER:OG	54:M5:39:LYS:O	2.29	0.50
1:13:779:C:H2'	1:13:780:A:O4'	2.12	0.49
1:13:1126:U:N3	1:13:1280:A:C8	2.80	0.49
1:13:1396:A:H4'	1:13:1397:C:H5"	1.94	0.49
4:3E:104:VAL:HG21	4:3E:140:VAL:HG21	1.94	0.49
4:3E:173:TRP:CD1	4:3E:174:LEU:HG	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:6E:95:ARG:O	7:6E:99:LEU:HD12	2.12	0.49
9:8E:17:VAL:HG11	9:8E:81:ILE:HD13	1.94	0.49
11:2I:112:THR:O	11:2I:114:VAL:HG12	2.12	0.49
19:AI:3:ARG:NH1	19:AI:10:PHE:HB2	2.27	0.49
26:1H:1313:U:P	59:1H:3830:HOH:O	2.69	0.49
26:1H:2518:A:H5'	26:1H:2518:A:C8	2.46	0.49
26:1H:2712:U:OP1	26:1H:2714:G:H4'	2.12	0.49
29:21:32:PRO:HD2	29:21:50:GLY:O	2.11	0.49
32:51:9:ILE:HD11	32:51:76:VAL:HG21	1.94	0.49
46:H8:61:LEU:HD22	46:H8:67:LEU:HD12	1.94	0.49
53:P8:30:VAL:O	53:P8:34:ARG:HG3	2.12	0.49
1:1G:684:A:N6	59:1G:1860:HOH:O	2.44	0.49
1:1G:1128:C:H5'	9:82:66:ARG:NH2	2.26	0.49
1:1G:1137:C:O2	1:1G:1138:G:N2	2.44	0.49
3:22:149:ALA:HA	3:22:201:TYR:O	2.12	0.49
4:32:13:ARG:HB3	4:32:38:TYR:O	2.11	0.49
7:62:146:GLU:HA	11:2A:59:TYR:HD2	1.77	0.49
10:1A:99:LYS:HD3	10:1A:100:THR:H	1.77	0.49
12:3A:32:PHE:HB3	12:3A:84:LEU:HD11	1.94	0.49
22:1L:9:A:O2'	22:1L:45:G:N2	2.45	0.49
26:14:698:C:O2'	26:14:734:A:N6	2.45	0.49
26:14:2131:G:H5"	26:14:2133:G:C1'	2.42	0.49
26:14:2359:C:H2'	26:14:2360:A:O4'	2.12	0.49
26:14:2773:C:OP1	29:29:166:THR:OG1	2.25	0.49
28:19:39:LYS:O	28:19:40:THR:HG23	2.11	0.49
33:69:125:GLU:OE2	33:69:141:LYS:HB2	2.12	0.49
36:35:97:PRO:HG3	36:35:112:LEU:HD12	1.93	0.49
1:13:247:G:OP2	17:8I:100:LYS:N	2.37	0.49
1:13:255:G:P	17:8I:69:LYS:HZ3	2.34	0.49
1:13:474:G:H2'	1:13:475:G:H8	1.75	0.49
4:3E:19:LEU:HB3	4:3E:21:LEU:HD21	1.94	0.49
12:3I:86:ARG:HG3	12:3I:101:VAL:HG22	1.93	0.49
23:2K:25:U:O2	26:1H:1923:U:H5"	2.12	0.49
26:1H:960:A:C8	26:1H:962:G:C8	2.99	0.49
26:1H:1176:G:H3'	26:1H:1177:A:C8	2.47	0.49
26:1H:1296:G:OP1	26:1H:2709:G:O2'	2.27	0.49
27:16:42:C:O2	31:41:93:THR:N	2.37	0.49
48:J8:55:GLY:HA3	48:J8:85:LEU:HD12	1.94	0.49
49:K8:15:LYS:H	49:K8:67:LYS:CE	2.24	0.49
1:1G:373:A:C2	1:1G:374:A:C8	3.00	0.49
1:1G:540:G:H2'	1:1G:541:G:O4'	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1G:583:A:H2'	1:1G:584:G:O4'	2.12	0.49
1:1G:688:G:H2'	1:1G:689:C:H6	1.77	0.49
1:1G:730:G:C5	1:1G:731:G:H1'	2.48	0.49
1:1G:1015:A:H2'	1:1G:1016:A:O4'	2.12	0.49
2:12:17:PHE:HB2	2:12:44:LEU:HD23	1.94	0.49
7:62:106:GLN:O	7:62:110:GLN:HG2	2.11	0.49
7:62:116:ALA:O	7:62:120:ILE:HG12	2.12	0.49
20:BA:49:ALA:O	20:BA:100:ILE:HG21	2.12	0.49
26:14:6:A:H62	34:15:131:GLN:N	2.09	0.49
26:14:184:C:H2'	26:14:185:U:C6	2.47	0.49
26:14:1628:G:H2'	26:14:1629:U:C6	2.47	0.49
26:14:1676:A:OP2	26:14:1676:A:H8	1.96	0.49
26:14:2010:G:H5"	43:A5:42:ARG:HB2	1.94	0.49
27:1J:83:G:H4'	50:H5:52:HIS:ND1	2.27	0.49
1:13:155:C:H2'	1:13:156:G:O4'	2.12	0.49
1:13:266:G:H5"	1:13:267:C:H5	1.76	0.49
1:13:345:C:H4'	1:13:346:G:C5	2.47	0.49
1:13:1468:A:H8	1:13:1468:A:O5'	1.95	0.49
7:6E:16:LEU:HD21	9:8E:45:ALA:HB2	1.94	0.49
9:8E:47:LEU:HB2	9:8E:50:LEU:HG	1.93	0.49
26:1H:654(B):C:H2'	26:1H:654(C):G:O4'	2.12	0.49
26:1H:1292:U:H2'	26:1H:1293:C:C6	2.47	0.49
26:1H:1442:G:C2	26:1H:1550:C:O2	2.65	0.49
26:1H:1515:C:H2'	26:1H:1516:U:H6	1.76	0.49
26:1H:2364:C:H2'	26:1H:2365:G:O4'	2.12	0.49
31:41:98:ARG:O	31:41:101:ILE:HD13	2.12	0.49
32:51:157:TYR:O	32:51:158:HIS:CG	2.64	0.49
45:G8:102:CYS:SG	45:G8:103:GLY:N	2.85	0.49
1:1G:1307:U:H2'	1:1G:1308:U:C6	2.47	0.49
3:22:43:LEU:O	3:22:47:LEU:HB2	2.12	0.49
6:52:8:ILE:HD12	6:52:26:ILE:HD13	1.94	0.49
11:2A:109:VAL:HG13	18:9A:86:VAL:HG22	1.94	0.49
13:4A:37:THR:O	13:4A:55:ARG:NH2	2.42	0.49
22:1L:65:C:H41	22:1L:67:A:N6	2.10	0.49
26:14:71:A:H5'	26:14:71:A:C8	2.48	0.49
26:14:2611:U:H3'	26:14:2611:U:OP2	2.12	0.49
37:45:2:LEU:O	37:45:70:PRO:HG2	2.12	0.49
41:85:17:ILE:HG23	41:85:39:LEU:HD12	1.93	0.49
45:C5:17:SER:HB2	45:C5:71:LYS:NZ	2.28	0.49
49:G5:15:LYS:H	49:G5:67:LYS:HZ1	1.60	0.49
1:13:254:G:O3'	17:8I:69:LYS:NZ	2.40	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:13:1033:G:H2'	1:13:1034:G:H5'	1.95	0.49
1:13:1220:G:O3'	19:AI:36:ARG:HD3	2.12	0.49
1:13:1274:G:H2'	1:13:1275:A:H8	1.77	0.49
4:3E:128:VAL:HB	4:3E:133:VAL:HG21	1.95	0.49
5:4E:110:LEU:HD13	5:4E:118:ILE:HD13	1.93	0.49
17:8I:41:LYS:NZ	17:8I:88:TYR:OH	2.28	0.49
18:9I:74:ARG:HG3	18:9I:79:LEU:HB2	1.95	0.49
26:1H:699:A:H2'	26:1H:700:G:O4'	2.13	0.49
27:16:14:U:O2	27:16:107:U:H4'	2.12	0.49
31:41:82:LEU:HD21	31:41:88:ILE:HG21	1.93	0.49
46:H8:77:ASP:OD1	46:H8:80:ARG:HD2	2.12	0.49
54:Q8:26:LYS:HE3	54:Q8:48:PHE:CG	2.47	0.49
1:1G:114:U:H2'	1:1G:115:G:C8	2.47	0.49
1:1G:532:A:N6	1:1G:1206:G:O2'	2.45	0.49
15:6A:26:GLU:OE2	15:6A:77:ARG:NH1	2.44	0.49
26:14:30:G:O6	59:14:3561:HOH:O	2.19	0.49
26:14:308:G:H5"	26:14:309:G:OP2	2.13	0.49
26:14:361:G:H2'	26:14:362:U:O2	2.12	0.49
26:14:1115:G:H2'	26:14:1116:C:C6	2.47	0.49
26:14:1331:A:O2'	26:14:1332:G:H8	1.94	0.49
26:14:2711:A:P	59:14:3539:HOH:O	2.71	0.49
32:59:86:GLU:OE1	32:59:86:GLU:N	2.45	0.49
36:35:111:ARG:HG2	36:35:128:HIS:CD2	2.47	0.49
39:65:34:HIS:CE1	39:65:54:LEU:HD12	2.47	0.49
46:D5:105:VAL:HG13	46:D5:106:GLY:H	1.78	0.49
7:6E:95:ARG:NH2	7:6E:99:LEU:HD11	2.27	0.49
7:6E:143:ARG:NH1	24:3K:42:U:H5'	2.27	0.49
16:7I:3:LYS:O	16:7I:21:VAL:HA	2.12	0.49
26:1H:125:G:H5'	26:1H:125:G:C8	2.47	0.49
26:1H:654(A):A:H61	26:1H:654(T):A:H61	1.60	0.49
26:1H:847:U:C5	26:1H:933:A:N1	2.81	0.49
26:1H:910:A:H62	37:88:12:GLN:HA	1.77	0.49
26:1H:972:G:O2'	59:1H:3821:HOH:O	2.18	0.49
26:1H:1359:A:N1	26:1H:1372:U:C4	2.80	0.49
26:1H:1420:U:HO2'	26:1H:1421:G:P	2.34	0.49
30:31:192:LEU:HD21	30:31:194:MET:HE2	1.94	0.49
32:51:94:TYR:HA	32:51:106:THR:O	2.12	0.49
43:E8:35:ILE:HG23	52:N8:28:PRO:HD2	1.93	0.49
46:H8:108:PRO:O	46:H8:144:LEU:HB2	2.11	0.49
26:14:492:A:H2'	26:14:493:G:O4'	2.13	0.49
26:14:495:G:N3	43:A5:61:ASN:ND2	2.59	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:14:1357:U:H2'	26:14:1358:G:O4'	2.13	0.49
27:1J:21:G:H1	27:1J:62:C:H42	1.59	0.49
46:D5:54:HIS:HB3	46:D5:101:PRO:HD3	1.93	0.49
1:13:690:G:H2'	1:13:691:G:O4'	2.12	0.49
1:13:1064:G:H1'	1:13:1190:G:H21	1.77	0.49
2:1E:16:HIS:CD2	2:1E:214:ILE:HD11	2.47	0.49
16:7I:45:THR:HG22	16:7I:46:PRO:HD2	1.94	0.49
26:1H:198:C:H5'	26:1H:2244:U:OP1	2.13	0.49
26:1H:1050:A:N7	26:1H:2751:G:C2	2.80	0.49
26:1H:2567:G:H2'	26:1H:2568:C:C6	2.47	0.49
26:1H:2726:U:H4'	35:68:1:MET:HE1	1.94	0.49
36:78:83:VAL:O	36:78:114:ILE:HA	2.13	0.49
40:B8:74:ARG:HD3	40:B8:76:PHE:CZ	2.48	0.49
46:H8:120:ILE:HG21	46:H8:170:THR:HB	1.93	0.49
47:I8:63:VAL:HG23	47:I8:64:ASP:O	2.12	0.49
52:N8:40:LYS:HE2	52:N8:47:PRO:HD2	1.95	0.49
1:1G:57:G:C6	1:1G:58:C:C4	3.00	0.49
2:12:77:ALA:HB2	2:12:211:ILE:HD13	1.94	0.49
10:1A:61:GLU:OE2	14:5A:45:ARG:NH1	2.45	0.49
26:14:581:C:H2'	26:14:582:G:C8	2.45	0.49
26:14:581:C:H42	26:14:1259:G:H1	1.60	0.49
26:14:1048:A:H5'	26:14:1108:U:O4	2.13	0.49
26:14:2408:U:H2'	26:14:2409:G:C8	2.48	0.49
27:1J:48:A:H4'	39:65:95:HIS:CD2	2.47	0.49
27:1J:65:C:N4	27:1J:108:C:C2	2.81	0.49
29:29:6:GLY:O	29:29:195:LEU:HD12	2.12	0.49
33:69:133:HIS:CG	33:69:134:PRO:HD3	2.48	0.49
36:35:78:PRO:HA	36:35:110:TYR:HD2	1.77	0.49
41:85:27:LEU:HB3	41:85:31:SER:HB3	1.95	0.49
42:95:29:PRO:HA	42:95:61:VAL:HG11	1.93	0.49
43:A5:14:PRO:HG2	43:A5:78:GLU:HB2	1.94	0.49
50:H5:7:LYS:HE2	50:H5:32:GLN:O	2.12	0.49
1:13:1167:A:H8	1:13:1167:A:OP1	1.94	0.49
1:13:1223:C:OP1	19:AI:78:ARG:NH1	2.45	0.49
11:2I:60:ALA:HA	11:2I:63:LEU:HD12	1.94	0.49
13:4I:69:GLU:HG3	31:41:118:ARG:NH2	2.28	0.49
13:4I:107:ALA:HB3	13:4I:111:LYS:HD3	1.95	0.49
26:1H:527:C:N4	26:1H:2777:G:O2'	2.44	0.49
26:1H:863:A:H2'	26:1H:864:G:C8	2.47	0.49
26:1H:1077:A:H5'	26:1H:1078:U:H5"	1.93	0.49
26:1H:1221:C:H2'	26:1H:1222:C:C6	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:78:49:ARG:HG3	36:78:49:ARG:HH11	1.77	0.49
43:E8:57:ASN:O	43:E8:62:HIS:HD2	1.96	0.49
43:E8:79:GLY:HA3	43:E8:100:THR:HG22	1.95	0.49
46:H8:117:LEU:HD12	46:H8:118:GLN:H	1.77	0.49
54:Q8:29:LYS:HG3	54:Q8:44:LYS:HG2	1.93	0.49
1:1G:1443:G:N2	40:75:119:LYS:HB2	2.28	0.49
4:32:119:GLN:HG3	4:32:123:HIS:CE1	2.48	0.49
13:4A:92:HIS:HE2	13:4A:98:VAL:HG11	1.77	0.49
21:1B:2:GLY:C	21:1B:4:GLY:H	2.21	0.49
26:14:1170:G:C2'	26:14:1171:G:H5'	2.42	0.49
26:14:1247:A:OP1	30:39:95:ARG:NH2	2.43	0.49
33:69:72:LEU:HD21	33:69:107:VAL:HG11	1.95	0.49
40:75:51:ARG:HG3	40:75:98:LYS:HD2	1.94	0.49
41:85:49:HIS:HA	41:85:52:ARG:HG2	1.93	0.49
42:95:98:GLU:OE1	42:95:100:ARG:NH2	2.45	0.49
47:E5:53:MET:HG3	47:E5:59:LEU:CD2	2.42	0.49
48:F5:49:VAL:HG21	48:F5:67:ILE:HD12	1.95	0.49
1:13:816:A:OP1	1:13:1526:G:O2'	2.28	0.49
2:1E:131:PRO:HD2	2:1E:134:GLU:HB3	1.95	0.49
11:2I:18:ARG:HB2	11:2I:33:THR:OG1	2.12	0.49
20:BI:25:ARG:O	20:BI:29:LYS:HG3	2.13	0.49
20:BI:49:ALA:HB2	20:BI:92:LEU:HD22	1.94	0.49
26:1H:1614:A:P	26:1H:1614:A:H8	2.35	0.49
26:1H:1639:U:C2'	26:1H:1640:C:H5"	2.42	0.49
26:1H:2483:C:O2	37:88:124:LYS:HE3	2.13	0.49
26:1H:2689:U:H5"	26:1H:2713:A:C2	2.48	0.49
26:1H:2785:C:H2'	26:1H:2786:U:O4'	2.13	0.49
29:21:2:LYS:HD3	29:21:95:ILE:HG13	1.94	0.49
40:B8:12:SER:CB	40:B8:15:VAL:H	2.25	0.49
43:E8:58:ALA:CB	43:E8:64:MET:HE2	2.43	0.49
46:H8:76:LEU:HA	46:H8:83:PRO:HA	1.95	0.49
1:1G:397:A:H5'	1:1G:398:C:OP1	2.12	0.49
1:1G:1134:G:N1	1:1G:1135:U:H1'	2.28	0.49
1:1G:1148:U:O3'	9:82:14:VAL:HG11	2.12	0.49
3:22:47:LEU:HG	3:22:68:VAL:HG11	1.94	0.49
10:1A:6:ILE:HG22	10:1A:98:ILE:HG23	1.94	0.49
26:14:606:U:H4'	26:14:658:C:H4'	1.95	0.49
26:14:813:U:H2'	26:14:814:C:C6	2.48	0.49
26:14:852:G:H2'	26:14:853:G:C8	2.47	0.49
26:14:1275:A:N1	26:14:1295:C:O2'	2.39	0.49
26:14:2275:C:O2	37:45:85:LYS:HD3	2.11	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:14:2520:C:H41	26:14:2542:A:H62	1.61	0.49
32:59:62:LYS:O	32:59:65:HIS:HB3	2.13	0.49
34:15:56:ASN:H	34:15:125:GLY:CA	2.19	0.49
46:D5:98:MET:SD	46:D5:100:VAL:HG23	2.53	0.49
1:13:129(A):G:H4'	1:13:130:A:H5"	1.93	0.49
1:13:286:G:N7	59:13:1960:HOH:O	2.35	0.49
1:13:324:G:N1	1:13:327:A:OP2	2.43	0.49
1:13:484:G:HO2'	1:13:485:G:P	2.36	0.49
1:13:692:U:O4	11:2I:53:SER:HB2	2.12	0.49
8:7E:88:LYS:HB3	8:7E:89:PRO:HD2	1.95	0.49
22:1K:43:G:H2'	22:1K:44:A:C8	2.48	0.49
24:3K:42:U:H2'	24:3K:43:G:C8	2.48	0.49
26:1H:1100:C:C4	26:1H:1101:U:C4	3.01	0.49
26:1H:1614:A:H8	26:1H:1614:A:O5'	1.96	0.49
26:1H:2210:G:H5'	26:1H:2211:G:C8	2.48	0.49
26:1H:2562:U:H1'	35:68:23:ARG:HD3	1.95	0.49
36:78:13:ASN:O	36:78:15:ARG:N	2.45	0.49
47:I8:38:VAL:HG12	47:I8:40:GLN:HG2	1.94	0.49
49:K8:52:ASP:OD1	49:K8:52:ASP:N	2.40	0.49
1:1G:49:U:C2	1:1G:361:G:N2	2.81	0.49
26:14:71:A:C2	44:B5:31:HIS:NE2	2.77	0.49
26:14:916:G:C2'	26:14:917:A:H5"	2.42	0.49
26:14:2151:G:C2	26:14:2152:G:H1'	2.48	0.49
26:14:2158:A:H2'	26:14:2158:A:N3	2.27	0.49
27:1J:116:G:C5'	39:65:55:ALA:HB2	2.43	0.49
29:29:5:LEU:HD13	29:29:49:LEU:HD12	1.95	0.49
29:29:182:LEU:C	29:29:183:LEU:HD12	2.38	0.49
31:49:54:GLU:HA	31:49:57:ALA:HB3	1.95	0.49
46:D5:111:VAL:HG21	46:D5:145:GLU:HB2	1.95	0.49
1:13:10:A:OP2	5:4E:126:ARG:HD3	2.12	0.49
1:13:748:C:H6	1:13:748:C:O5'	1.96	0.49
1:13:1157:A:H8	1:13:1158:C:C4	2.31	0.49
1:13:1174:G:H2'	1:13:1175:G:H8	1.77	0.49
4:3E:102:ASP:OD1	4:3E:103:ASN:N	2.46	0.49
19:AI:42:PRO:HD3	51:M8:63:TYR:OH	2.13	0.49
22:1K:18:G:H2'	22:1K:57:G:C2	2.47	0.49
26:1H:1783:A:H5'	26:1H:2608:G:H4'	1.95	0.49
26:1H:2150:U:O2'	26:1H:2151:G:O4'	2.30	0.49
26:1H:2246:G:H2'	26:1H:2247:A:C8	2.48	0.49
26:1H:2591:C:P	28:11:239:ARG:HG3	2.53	0.49
26:1H:2820:A:O5'	38:98:4:LEU:HD23	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:61:8:PRO:HB3	33:61:14:ASP:HA	1.94	0.49
1:1G:115:G:H1'	1:1G:116:A:N7	2.28	0.49
1:1G:167:G:H2'	1:1G:168:G:H8	1.78	0.49
1:1G:1321:C:C4	1:1G:1322:C:N3	2.81	0.49
2:12:169:LYS:O	2:12:169:LYS:HD3	2.12	0.49
3:22:118:GLN:HG3	3:22:187:ALA:HB2	1.94	0.49
7:62:146:GLU:HG2	11:2A:50:TYR:CE1	2.48	0.49
10:1A:16:LEU:O	10:1A:20:ALA:N	2.45	0.49
17:8A:59:ILE:HG22	17:8A:71:PHE:CD2	2.48	0.49
17:8A:67:LYS:HA	17:8A:70:ARG:HH12	1.78	0.49
26:14:26:G:OP1	43:A5:80:PRO:HB3	2.13	0.49
26:14:590:A:H2'	26:14:591:C:C6	2.48	0.49
26:14:667:U:O2	54:M5:2:PRO:HD2	2.13	0.49
26:14:1926:U:H2'	26:14:1928:A:OP2	2.13	0.49
33:69:133:HIS:CD2	33:69:134:PRO:HD3	2.48	0.49
35:25:4:PRO:O	35:25:5:GLN:HB2	2.12	0.49
36:35:98:GLU:HA	36:35:101:VAL:HG12	1.95	0.49
38:55:97:VAL:HG12	38:55:114:VAL:HG13	1.95	0.49
1:13:1015:A:H2'	1:13:1016:A:C8	2.48	0.48
9:8E:97:LYS:HB2	9:8E:102:LEU:HD12	1.95	0.48
11:2I:95:ILE:HG13	11:2I:96:ARG:N	2.27	0.48
13:4I:3:ARG:HG2	13:4I:9:ILE:HG12	1.95	0.48
26:1H:1280:G:N2	26:1H:1291:C:C2	2.81	0.48
26:1H:1864:U:H2'	26:1H:1869:G:H5"	1.93	0.48
29:21:8:LYS:HA	29:21:26:ILE:HG22	1.94	0.48
29:21:50:GLY:CA	29:21:75:VAL:HG11	2.43	0.48
32:51:9:ILE:O	32:51:9:ILE:HG13	2.12	0.48
51:M8:65:ASP:OD1	51:M8:65:ASP:N	2.46	0.48
1:1G:35:G:O2'	12:3A:118:SER:O	2.26	0.48
1:1G:1022:G:C6	1:1G:1023:G:C8	3.01	0.48
4:32:126:ILE:HG22	4:32:127:THR:H	1.78	0.48
14:5A:15:LYS:C	14:5A:16:PHE:CG	2.91	0.48
19:AA:18:LYS:HA	19:AA:21:GLU:CG	2.43	0.48
23:2L:6:G:H2'	23:2L:7:G:H5"	1.95	0.48
26:14:618(A):C:OP2	30:39:103:LYS:HE2	2.13	0.48
26:14:848:G:H2'	26:14:849:A:H8	1.77	0.48
26:14:1022:G:C6	26:14:1140:C:C4	3.00	0.48
26:14:1593:G:H2'	26:14:1594:G:C8	2.48	0.48
26:14:2689:U:H4'	26:14:2690:C:H5'	1.95	0.48
26:14:2695:C:H2'	26:14:2696:U:H6	1.77	0.48
32:59:106:THR:HG22	32:59:112:PRO:HB3	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:15:95:PRO:O	34:15:98:VAL:HG13	2.12	0.48
37:45:12:GLN:HG2	37:45:73:PRO:HD2	1.94	0.48
43:A5:27:LYS:O	43:A5:71:VAL:HG23	2.13	0.48
45:C5:20:TYR:CE1	45:C5:42:VAL:HB	2.47	0.48
1:13:262:A:H2'	1:13:263:A:H8	1.73	0.48
1:13:452:A:O2'	1:13:453:A:O4'	2.28	0.48
1:13:813:U:OP2	1:13:816:A:N6	2.43	0.48
1:13:838:G:H1	1:13:848:C:N4	2.10	0.48
26:1H:602:G:N2	26:1H:655:A:C8	2.69	0.48
26:1H:1040:C:H42	26:1H:1115:G:H1	1.60	0.48
26:1H:1067:A:N3	26:1H:1067:A:H2'	2.28	0.48
26:1H:1109:C:O2'	26:1H:1110:G:O4'	2.31	0.48
26:1H:1441:G:H2'	26:1H:1442:G:H8	1.78	0.48
26:1H:2235:G:H2'	26:1H:2236:C:C6	2.47	0.48
27:16:13:A:O2'	27:16:14:U:H3'	2.13	0.48
27:16:74:U:H2'	27:16:75:G:O4'	2.13	0.48
34:58:96:GLU:O	34:58:97:ARG:HB2	2.12	0.48
37:88:32:TYR:CE2	37:88:133:ARG:HG3	2.49	0.48
39:A8:27:SER:HA	39:A8:88:ASP:CB	2.43	0.48
40:B8:99:LEU:O	40:B8:102:ILE:HG12	2.12	0.48
1:1G:446:G:H2'	1:1G:447:G:O4'	2.13	0.48
1:1G:1095:U:H2'	1:1G:1096:C:C6	2.48	0.48
1:1G:1402:C:H2'	1:1G:1403:C:O4'	2.13	0.48
4:32:108:LEU:HD21	4:32:183:GLY:HA3	1.93	0.48
10:1A:28:ARG:HH21	10:1A:34:VAL:HB	1.78	0.48
13:4A:59:TYR:O	13:4A:63:THR:OG1	2.29	0.48
19:AA:16:LEU:O	19:AA:19:VAL:HG12	2.14	0.48
26:14:13:A:N1	26:14:525:U:H2'	2.28	0.48
26:14:573:G:O2'	26:14:574:C:H3'	2.13	0.48
26:14:733:G:C8	59:14:3574:HOH:O	2.65	0.48
39:65:28:VAL:HG11	39:65:98:VAL:HG13	1.95	0.48
40:75:91:ARG:HD2	40:75:124:ASP:OD2	2.13	0.48
1:13:128:G:O3'	17:8I:3:LYS:NZ	2.46	0.48
1:13:484:G:O2'	1:13:485:G:OP2	2.25	0.48
1:13:970:C:H42	9:8E:128:ARG:C	2.20	0.48
1:13:1363:A:H1'	1:13:1365:G:N7	2.28	0.48
2:1E:28:PHE:CD2	2:1E:190:THR:HA	2.48	0.48
5:4E:126:ARG:HG3	5:4E:126:ARG:NH1	2.28	0.48
13:4I:16:ASP:OD1	13:4I:16:ASP:N	2.41	0.48
24:3K:43:G:H2'	24:3K:44:A:C8	2.47	0.48
26:1H:654(A):A:N1	26:1H:654(T):A:N1	2.60	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1H:754:C:H2'	26:1H:755:C:C6	2.49	0.48
26:1H:810:U:O5'	26:1H:810:U:H6	1.95	0.48
26:1H:1580:A:H8	26:1H:1580:A:OP2	1.96	0.48
26:1H:1756:G:OP2	59:1H:3834:HOH:O	2.20	0.48
31:41:111:LEU:HD23	31:41:114:ILE:HD12	1.95	0.48
33:61:110:ASP:OD2	33:61:130:TYR:HE1	1.95	0.48
37:88:43:THR:HG22	37:88:94:VAL:HG12	1.95	0.48
38:98:26:LYS:HE3	38:98:70:LEU:O	2.13	0.48
41:C8:8:VAL:HG23	41:C8:11:ARG:NH2	2.28	0.48
42:D8:10:LYS:NZ	42:D8:23:GLU:OE1	2.46	0.48
43:E8:37:ARG:HD3	43:E8:38:TYR:CE2	2.48	0.48
45:G8:49:VAL:HG11	45:G8:61:ILE:HG13	1.94	0.48
1:1G:980:C:H3'	1:1G:981:U:C6	2.49	0.48
1:1G:1179:A:OP2	9:82:93:ARG:NH2	2.45	0.48
1:1G:1369:C:H2'	1:1G:1370:G:C8	2.47	0.48
7:62:65:ALA:HB1	7:62:127:ALA:HB3	1.94	0.48
55:3L:67:A:H2'	55:3L:68:U:C6	2.48	0.48
26:14:375:C:H2'	26:14:376:C:C6	2.48	0.48
26:14:2186:G:C2	26:14:2187:G:N7	2.82	0.48
26:14:2475:C:H3'	26:14:2476:A:H5"	1.95	0.48
26:14:2785:C:H2'	26:14:2786:U:O4'	2.13	0.48
30:39:185:ASP:CG	30:39:188:ARG:HH21	2.21	0.48
32:59:120:GLY:O	32:59:121:ILE:HG12	2.13	0.48
1:13:5:U:C5	4:3E:85:LYS:HB3	2.48	0.48
3:2E:7:PRO:O	3:2E:11:ARG:HG2	2.13	0.48
23:2K:62:C:H2'	23:2K:63:C:C6	2.45	0.48
26:1H:910:A:C5	37:88:13:GLN:HG3	2.48	0.48
26:1H:2062:A:N6	26:1H:2503:A:H62	2.12	0.48
37:88:67:ARG:HD2	37:88:105:GLU:OE1	2.13	0.48
48:J8:51:VAL:HG21	48:J8:74:VAL:HG21	1.94	0.48
1:1G:964:A:N3	1:1G:969:A:O2'	2.44	0.48
1:1G:984:C:H2'	1:1G:985:C:C6	2.48	0.48
1:1G:1205:U:O3'	3:22:190:ARG:NH1	2.46	0.48
1:1G:1274:G:N2	1:1G:1275:A:H62	2.10	0.48
2:12:95:GLN:HB3	2:12:148:TYR:HD1	1.78	0.48
5:42:51:VAL:HB	5:42:52:PRO:HD3	1.96	0.48
26:14:2889:C:H3'	26:14:2891:G:H8	1.75	0.48
32:59:41:MET:N	32:59:41:MET:SD	2.86	0.48
40:75:50:ILE:HD11	40:75:102:ILE:CD1	2.43	0.48
1:13:413:G:N2	1:13:428:G:H1'	2.29	0.48
1:13:652:U:O2'	1:13:653:A:O5'	2.27	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:13:953:G:H5'	1:13:965:A:H61	1.79	0.48
5:4E:72:GLN:O	5:4E:75:THR:HG22	2.14	0.48
9:8E:9:ARG:HB3	9:8E:14:VAL:HG13	1.94	0.48
9:8E:27:THR:HB	9:8E:62:TYR:HD1	1.78	0.48
11:2I:106:LYS:N	11:2I:106:LYS:HD3	2.28	0.48
26:1H:274:G:H21	26:1H:276:A:H61	1.62	0.48
26:1H:2074:U:H2'	26:1H:2075:U:C6	2.48	0.48
26:1H:2170:A:OP2	26:1H:2170:A:H3'	2.13	0.48
26:1H:2552:U:H2'	26:1H:2554:U:H5"	1.96	0.48
28:11:3:VAL:HB	28:11:17:THR:HG23	1.95	0.48
31:41:125:PHE:HB3	31:41:166:ASP:OD2	2.13	0.48
32:51:71:LEU:HD12	32:51:71:LEU:HA	1.76	0.48
35:68:64:ARG:HB2	35:68:79:PHE:CD1	2.49	0.48
42:D8:21:ARG:HG2	42:D8:91:TYR:CD1	2.48	0.48
1:1G:79:G:H1	1:1G:90:C:N4	2.10	0.48
3:22:106:VAL:O	3:22:109:PRO:HD3	2.13	0.48
12:3A:70:ILE:HD13	12:3A:77:LEU:HD12	1.94	0.48
26:14:276:A:H2'	26:14:277:C:C4	2.47	0.48
26:14:468:G:N7	53:L5:39:ARG:NH2	2.57	0.48
26:14:910:A:C5	37:45:13:GLN:HG3	2.48	0.48
26:14:994:C:OP2	41:85:54:LYS:NZ	2.26	0.48
26:14:1262:A:N3	52:J5:10:LYS:HE3	2.28	0.48
26:14:1270:C:H5"	26:14:1271:G:O5'	2.13	0.48
26:14:1689:A:N6	26:14:1698:A:H2	1.98	0.48
26:14:2104:G:H2'	26:14:2105:C:C6	2.48	0.48
26:14:2513:G:N2	29:29:143:ASN:HD21	2.11	0.48
27:1J:73:A:C4	27:1J:104:A:C2	3.02	0.48
30:39:24:LEU:HD11	30:39:119:ARG:HB3	1.95	0.48
49:G5:50:ILE:HD12	49:G5:51:ARG:H	1.77	0.48
54:M5:14:VAL:HG11	54:M5:58:ILE:HD11	1.95	0.48
1:13:610:G:OP2	59:13:1937:HOH:O	2.20	0.48
1:13:613:C:H42	1:13:627:G:H1	1.61	0.48
1:13:920:U:H2'	1:13:921:U:C6	2.49	0.48
1:13:1106:G:H5"	3:2E:172:ARG:HG3	1.96	0.48
7:6E:62:PHE:HA	7:6E:124:LEU:CD2	2.42	0.48
26:1H:492:A:H2'	26:1H:493:G:O4'	2.13	0.48
26:1H:1188:U:C4'	42:D8:79:VAL:HG22	2.44	0.48
26:1H:1538:G:H2'	26:1H:1539:G:H8	1.77	0.48
26:1H:1796:U:H2'	26:1H:1797:C:C6	2.48	0.48
26:1H:2345:G:N3	26:1H:2381:C:H2'	2.29	0.48
40:B8:24:PRO:HD3	40:B8:52:ILE:HG13	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:E8:88:ARG:NH1	43:E8:94:ASP:OD2	2.46	0.48
1:1G:162:A:O5'	1:1G:162:A:H8	1.96	0.48
1:1G:186(C):G:H2'	1:1G:186(D):C:C6	2.48	0.48
1:1G:980:C:H3'	1:1G:981:U:H6	1.78	0.48
1:1G:1132:C:H2'	1:1G:1133:G:H8	1.76	0.48
1:1G:1386:G:C2	1:1G:1387:G:C8	3.00	0.48
5:42:61:TYR:HA	5:42:64:ARG:HG3	1.95	0.48
5:42:76:ILE:HG23	5:42:142:LEU:HD13	1.96	0.48
13:4A:81:LEU:CD2	13:4A:88:ARG:HH21	2.26	0.48
26:14:906:G:OP1	37:45:26:TYR:OH	2.32	0.48
26:14:1532:C:H42	26:14:1539:G:H1	1.61	0.48
26:14:1899:G:N2	26:14:1902:C:N4	2.51	0.48
26:14:2131:G:H5"	26:14:2133:G:O4'	2.14	0.48
26:14:2151:G:H2'	26:14:2152:G:O4'	2.13	0.48
26:14:2262:U:OP2	47:E5:19:LYS:HE2	2.12	0.48
27:1J:112:G:H2'	27:1J:113:C:H6	1.77	0.48
29:29:51:PHE:CG	29:29:52:LEU:N	2.80	0.48
38:55:55:ALA:HB2	38:55:79:LEU:HD13	1.96	0.48
1:13:370:C:C2	1:13:392:G:N2	2.82	0.48
1:13:919:A:O2'	1:13:920:U:H5'	2.14	0.48
2:1E:213:LEU:H	2:1E:213:LEU:HG	1.47	0.48
3:2E:78:GLY:CA	3:2E:83:ARG:HB3	2.42	0.48
8:7E:8:ASP:O	8:7E:12:ARG:HG3	2.13	0.48
9:8E:118:LYS:O	9:8E:119:ALA:HB3	2.13	0.48
23:2K:24:C:H2'	23:2K:25:U:H6	1.79	0.48
26:1H:306:U:H2'	26:1H:307:G:O4'	2.13	0.48
26:1H:831:G:N2	36:78:53:GLY:O	2.46	0.48
26:1H:1569:A:H2'	26:1H:1570:A:O4'	2.14	0.48
26:1H:1641:A:H2'	26:1H:1642:G:O4'	2.13	0.48
26:1H:2254:C:H3'	59:1H:3815:HOH:O	2.13	0.48
28:11:108:PRO:HG3	28:11:143:HIS:CE1	2.48	0.48
33:61:79:ILE:HB	33:61:142:VAL:HG12	1.95	0.48
1:1G:186(D):C:H2'	1:1G:186(E):C:H6	1.79	0.48
1:1G:448:A:P	1:1G:485:G:H22	2.30	0.48
1:1G:1226:C:N4	13:4A:104:ARG:HD2	2.28	0.48
1:1G:1255:G:O2'	1:1G:1258:G:O2'	2.31	0.48
3:22:87:LEU:HB2	3:22:88:ARG:NH2	2.28	0.48
3:22:113:ALA:HB2	3:22:202:ILE:HG13	1.95	0.48
7:62:47:CYS:HB3	7:62:58:PRO:HG2	1.96	0.48
23:2L:60:A:H2'	23:2L:61:U:H5'	1.96	0.48
26:14:784:A:H5"	59:14:3517:HOH:O	2.12	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:14:1405:U:H2'	26:14:1406:U:C6	2.48	0.48
26:14:2392:A:H2	26:14:2424:C:N4	2.09	0.48
26:14:2591:C:OP1	28:19:239:ARG:HG2	2.14	0.48
26:14:2734:A:C8	26:14:2735:G:C8	3.01	0.48
26:14:2793:G:N2	26:14:2794:C:H5	2.11	0.48
30:39:123:LEU:HA	30:39:192:LEU:O	2.14	0.48
32:59:19:VAL:HG13	32:59:43:VAL:HG23	1.95	0.48
40:75:7:ILE:HG13	40:75:8:LYS:N	2.28	0.48
41:85:70:ARG:HG3	41:85:75:ASN:HA	1.95	0.48
1:13:17:U:H2'	1:13:18:C:C6	2.49	0.48
1:13:113:G:H2'	1:13:114:U:C6	2.49	0.48
1:13:1269:A:N1	1:13:1312:G:O2'	2.46	0.48
8:7E:114:THR:HG22	8:7E:131:GLY:HA3	1.96	0.48
22:1K:15:G:N2	22:1K:48:C:H41	2.12	0.48
26:1H:192:C:O2	59:1H:3828:HOH:O	2.19	0.48
26:1H:274:G:H8	26:1H:274:G:H3'	1.79	0.48
26:1H:449:A:N7	59:1H:3899:HOH:O	2.35	0.48
26:1H:639:U:H2'	26:1H:640:C:C6	2.48	0.48
26:1H:654:A:H3'	26:1H:654:A:N3	2.28	0.48
32:51:124:GLU:HB2	32:51:132:ARG:HB2	1.95	0.48
41:C8:79:PHE:HE2	41:C8:106:PHE:CZ	2.32	0.48
1:1G:1162:C:H42	1:1G:1174:G:H1	1.61	0.48
2:12:104:ASN:OD1	2:12:107:THR:OG1	2.31	0.48
2:12:158:LEU:H	2:12:158:LEU:HD12	1.78	0.48
13:4A:92:HIS:CD2	13:4A:98:VAL:HG11	2.49	0.48
20:BA:14:LYS:O	20:BA:18:GLN:HG3	2.13	0.48
26:14:34:C:O2'	26:14:35:G:H5'	2.14	0.48
26:14:603:A:H8	26:14:604:G:H1'	1.77	0.48
26:14:717:G:H2'	26:14:718:A:O4'	2.13	0.48
26:14:1652:A:OP1	38:55:8:ARG:NH1	2.47	0.48
26:14:2121:G:H1	26:14:2177:C:H42	1.62	0.48
26:14:2562:U:H1'	35:25:23:ARG:NE	2.29	0.48
26:14:2772:C:H2'	26:14:2773:C:C6	2.49	0.48
28:19:27:THR:HG22	28:19:29:PRO:O	2.14	0.48
31:49:73:ALA:HB3	31:49:84:LYS:HA	1.95	0.48
1:13:57:G:C5	1:13:58:C:C4	3.01	0.48
1:13:631:G:O2'	1:13:632:A:O5'	2.32	0.48
1:13:722:A:O3'	1:13:723:U:H6	1.97	0.48
1:13:890:G:O2'	1:13:906:G:O6	2.31	0.48
1:13:983:A:O5'	14:5I:3:ARG:NH2	2.47	0.48
1:13:1238:A:N3	1:13:1241:G:O2'	2.45	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:13:1262:C:H2'	1:13:1263:C:C6	2.49	0.48
2:1E:19:HIS:HB3	2:1E:20:GLU:HG2	1.96	0.48
10:1I:32:ALA:HB3	10:1I:76:ASN:O	2.14	0.48
12:3I:20:LYS:HE2	12:3I:20:LYS:HB3	1.79	0.48
18:9I:38:GLU:OE1	18:9I:41:LYS:NZ	2.31	0.48
26:1H:1412:A:H2'	26:1H:1413:G:C8	2.48	0.48
26:1H:1451:C:H2'	26:1H:1458:C:H41	1.79	0.48
26:1H:1454:U:O2'	26:1H:1455:G:N7	2.45	0.48
26:1H:2287:A:H2	26:1H:2346:A:C2	2.32	0.48
27:16:80:U:H2'	27:16:81:G:H21	1.78	0.48
30:31:34:TRP:CH2	36:78:8:PRO:HB3	2.49	0.48
31:41:138:GLN:OE1	31:41:153:ARG:N	2.46	0.48
33:61:16:GLY:O	33:61:47:LEU:HD11	2.13	0.48
33:61:49:ALA:O	33:61:50:ARG:HD3	2.14	0.48
48:J8:53:VAL:O	48:J8:56:GLN:N	2.47	0.48
3:22:6:HIS:HB3	14:5A:49:HIS:CD2	2.49	0.48
3:22:88:ARG:HA	3:22:91:LEU:HD13	1.96	0.48
4:32:107:ARG:HH12	4:32:194:LEU:HD22	1.77	0.48
5:42:110:LEU:O	5:42:115:VAL:HB	2.14	0.48
7:62:50:ILE:HB	7:62:58:PRO:HG3	1.95	0.48
10:1A:7:LYS:HZ3	10:1A:71:LEU:HD13	1.78	0.48
26:14:860:U:O2'	26:14:861:A:H5'	2.13	0.48
26:14:1018:C:H2'	26:14:1019:U:H6	1.79	0.48
26:14:1752:C:P	40:75:115:ARG:HH22	2.37	0.48
26:14:2198:A:OP1	33:69:33:ARG:NH2	2.38	0.48
29:29:105:THR:CG2	29:29:164:ARG:HE	2.26	0.48
29:29:167:VAL:HG11	29:29:189:PRO:HD3	1.96	0.48
30:39:63:LYS:NZ	30:39:67:GLN:HB2	2.28	0.48
35:25:22:ILE:HG22	35:25:40:VAL:HB	1.95	0.48
40:75:91:ARG:HG3	40:75:121:ILE:HG12	1.95	0.48
1:13:191(C):G:H2'	1:13:191(D):U:O4'	2.14	0.48
1:13:261:U:H2'	1:13:263:A:OP2	2.13	0.48
1:13:271:C:H2'	1:13:272:C:C6	2.47	0.48
1:13:977:A:H1'	1:13:982:U:O4	2.14	0.48
1:13:1442:G:H2'	1:13:1443:G:H5'	1.96	0.48
15:6I:6:GLU:H	15:6I:6:GLU:HG2	1.43	0.48
22:1K:72:C:C4	22:1K:73:A:C2	3.01	0.48
26:1H:50:U:H3'	26:1H:51:G:H5'	1.94	0.48
26:1H:150:C:H2'	26:1H:151:C:C6	2.48	0.48
26:1H:247:G:H4'	26:1H:386:G:C5	2.49	0.48
26:1H:270(K):C:H1'	26:1H:270(N):G:H22	1.79	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1H:863:A:H2'	26:1H:864:G:H8	1.79	0.48
26:1H:1187:G:H5"	42:D8:81:TYR:CE1	2.48	0.48
26:1H:1433:U:O2	26:1H:1561:G:C2	2.67	0.48
26:1H:1857:G:C6	26:1H:1858:G:C6	3.02	0.48
26:1H:2029:G:H2'	26:1H:2031:A:OP1	2.14	0.48
29:21:9:VAL:HG13	40:B8:3:ARG:CB	2.44	0.48
29:21:14:ILE:HB	29:21:21:VAL:HG13	1.96	0.48
32:51:9:ILE:HD13	32:51:73:ALA:HA	1.95	0.48
32:51:164:TYR:HB2	32:51:167:GLU:HB2	1.95	0.48
37:88:138:ASP:HA	37:88:139:GLU:HA	1.63	0.48
41:C8:79:PHE:CE1	41:C8:83:LEU:HD21	2.49	0.48
1:1G:1003:G:H21	1:1G:1005:A:P	2.36	0.48
5:42:81:GLU:HA	5:42:89:ILE:O	2.14	0.48
10:1A:28:ARG:NH2	10:1A:34:VAL:HB	2.29	0.48
26:14:249:C:H4'	26:14:250:G:O5'	2.14	0.48
26:14:1007:C:OP1	34:15:35:ARG:NH1	2.47	0.48
26:14:1170:G:H2'	26:14:1171:G:H5'	1.96	0.48
26:14:1342:A:H2	26:14:1602:U:N3	2.08	0.48
26:14:1688:U:O2	26:14:1700:A:H5'	2.14	0.48
26:14:1728:G:N1	26:14:1730:U:OP2	2.47	0.48
26:14:2320:A:H1'	26:14:2321:G:C6	2.48	0.48
29:29:80:GLU:O	29:29:81:ILE:C	2.57	0.48
30:39:65:TRP:CZ3	30:39:72:ARG:HB3	2.49	0.48
39:65:42:ASP:C	39:65:44:LYS:H	2.21	0.48
1:13:1376:U:H2'	1:13:1377:A:C8	2.48	0.47
20:BI:54:LYS:HA	20:BI:57:ARG:NH2	2.29	0.47
24:3K:8:U:O2'	24:3K:13:C:H5	1.96	0.47
26:1H:1101:U:H2'	26:1H:1102:C:H6	1.77	0.47
27:16:44:G:H1'	27:16:47:C:N4	2.29	0.47
29:21:47:VAL:HB	29:21:49:LEU:HD13	1.95	0.47
31:41:96:ARG:HB2	31:41:96:ARG:HH11	1.78	0.47
33:61:11:ASN:O	33:61:12:LEU:HB2	2.13	0.47
36:78:133:SER:O	36:78:137:LYS:HG3	2.13	0.47
1:1G:32:A:C2	1:1G:33:A:C4	3.02	0.47
1:1G:32:A:H2'	1:1G:33:A:C8	2.49	0.47
1:1G:179:A:OP2	59:1G:1823:HOH:O	2.19	0.47
1:1G:584:G:H5'	17:8A:91:ARG:NH2	2.25	0.47
4:32:57:ARG:HH22	5:42:107:ARG:CZ	2.26	0.47
10:1A:48:THR:OG1	10:1A:62:HIS:HB3	2.13	0.47
12:3A:60:LEU:HB3	12:3A:62:SER:H	1.79	0.47
17:8A:23:VAL:O	17:8A:39:SER:HA	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:14:17:G:H4'	41:85:25:TRP:CH2	2.49	0.47
26:14:1678:G:N2	26:14:1989:G:N2	2.58	0.47
26:14:2062:A:HO2'	26:14:2063:C:P	2.36	0.47
28:19:133:LEU:HB3	28:19:173:VAL:HG11	1.96	0.47
29:29:24:THR:HG21	29:29:188:VAL:HG13	1.96	0.47
33:69:50:ARG:HA	33:69:53:ALA:HB3	1.96	0.47
1:13:4:U:O4	8:7E:105:ARG:HG3	2.14	0.47
1:13:883:C:C2'	1:13:884:U:H5'	2.44	0.47
8:7E:9:MET:HG3	8:7E:26:VAL:HG21	1.96	0.47
24:3K:2:C:N4	24:3K:71:G:H1	2.09	0.47
26:1H:49:A:C8	26:1H:120:U:H5	2.31	0.47
26:1H:525:U:O5'	26:1H:525:U:H6	1.97	0.47
26:1H:1025:G:C4	26:1H:1135:C:H1'	2.48	0.47
26:1H:1316:U:H2'	26:1H:1317:A:C8	2.48	0.47
26:1H:1317:A:H2'	26:1H:1318:C:C6	2.49	0.47
26:1H:2031:A:C6	26:1H:2498:C:H1'	2.49	0.47
28:11:124:PRO:HG2	28:11:129:ASN:HD21	1.78	0.47
32:51:27:LYS:HA	32:51:32:GLU:HB3	1.95	0.47
34:58:19:GLU:HG3	34:58:59:LYS:HB3	1.96	0.47
45:G8:85:VAL:O	45:G8:86:ARG:HD2	2.14	0.47
1:1G:563:A:N6	59:1G:1864:HOH:O	2.47	0.47
1:1G:1152:A:H5'	10:1A:13:HIS:ND1	2.29	0.47
1:1G:1243:C:OP1	21:1B:10:ARG:HG3	2.14	0.47
1:1G:1293:G:H2'	1:1G:1294:G:C8	2.48	0.47
1:1G:1369:C:OP2	9:82:112:LYS:N	2.47	0.47
2:12:213:LEU:HG	2:12:214:ILE:HD13	1.96	0.47
5:42:80:ILE:HD13	8:72:104:ARG:NH2	2.29	0.47
11:2A:59:TYR:CE1	11:2A:63:LEU:HD21	2.49	0.47
13:4A:60:VAL:HG13	13:4A:64:TRP:HE1	1.78	0.47
22:1L:18:G:H2'	22:1L:57:G:C5	2.49	0.47
55:3L:48:C:O2	55:3L:59:A:H1'	2.14	0.47
26:14:863:A:H2'	26:14:864:G:C8	2.50	0.47
27:1J:59:A:H3'	27:1J:60:C:C6	2.50	0.47
32:59:37:VAL:HG22	32:59:38:SER:H	1.77	0.47
36:35:138:LEU:HD12	36:35:144:GLU:CG	2.42	0.47
37:45:98:LYS:HB3	37:45:99:PRO:HD2	1.96	0.47
1:13:173:U:C6	1:13:197:A:C2	3.03	0.47
1:13:719:C:O2'	18:9I:49:LYS:HB3	2.14	0.47
1:13:1008:C:H5'	1:13:1009:G:OP2	2.14	0.47
1:13:1016:A:H2'	1:13:1017:G:O4'	2.14	0.47
1:13:1125:U:C4	1:13:1126:U:O4	2.68	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:13:1263:C:H2'	1:13:1264:C:C6	2.48	0.47
3:2E:144:SER:O	3:2E:144:SER:OG	2.32	0.47
4:3E:174:LEU:HD23	4:3E:185:PHE:HA	1.95	0.47
26:1H:451:C:H5'	59:1H:3747:HOH:O	2.13	0.47
26:1H:775:G:C4	26:1H:794:G:C8	3.03	0.47
26:1H:1239:G:H2'	26:1H:1240:U:O4'	2.14	0.47
26:1H:1510:A:H2'	26:1H:1510:A:N3	2.29	0.47
26:1H:1726:G:C6	26:1H:1727:U:C4	3.02	0.47
26:1H:2287:A:N6	26:1H:2344:U:N3	2.59	0.47
27:16:44:G:C2	27:16:48:A:C2	3.02	0.47
31:41:11:TYR:HA	31:41:15:VAL:HB	1.96	0.47
31:41:82:LEU:HD22	31:41:82:LEU:HA	1.73	0.47
40:B8:27:THR:HG23	40:B8:90:GLN:HB3	1.97	0.47
46:H8:5:LEU:HD23	46:H8:47:VAL:HG21	1.95	0.47
52:N8:36:CYS:SG	52:N8:37:LYS:N	2.87	0.47
1:1G:161:A:C6	1:1G:162:A:C6	3.02	0.47
2:12:223:ILE:HG23	2:12:224:GLN:NE2	2.29	0.47
10:1A:4:ILE:HG12	10:1A:100:THR:HG22	1.95	0.47
26:14:363:G:H2'	26:14:363(A):A:H8	1.79	0.47
26:14:813:U:C2	26:14:1195:G:N2	2.82	0.47
26:14:996:A:OP2	41:85:92:ARG:NH1	2.47	0.47
26:14:997:G:OP1	41:85:93:LYS:HB2	2.14	0.47
26:14:1999:C:H5"	26:14:2723:C:O2'	2.13	0.47
26:14:2185:C:H2'	26:14:2186:G:C8	2.49	0.47
31:49:16:ARG:O	31:49:20:ILE:HG13	2.14	0.47
31:49:124:SER:HB2	31:49:131:TYR:CE1	2.48	0.47
37:45:27:VAL:CB	37:45:28:ALA:HA	2.22	0.47
39:65:23:ARG:NH2	39:65:84:GLN:OE1	2.47	0.47
44:B5:23:GLU:H	44:B5:23:GLU:HG2	1.44	0.47
1:13:223:U:H2'	1:13:224:C:C6	2.47	0.47
1:13:1162:C:H2'	1:13:1163:C:C6	2.50	0.47
4:3E:167:GLY:HA2	28:19:135:PHE:CZ	2.49	0.47
8:7E:39:LEU:HB3	8:7E:45:ILE:CG1	2.44	0.47
19:AI:67:VAL:HG23	19:AI:68:GLY:H	1.79	0.47
22:1K:53:G:C2'	22:1K:54:5MU:H5"	2.45	0.47
26:1H:270(V):G:H2'	26:1H:270(W):G:C8	2.49	0.47
26:1H:287:C:H2'	26:1H:288:C:H6	1.79	0.47
26:1H:483:A:O4'	45:G8:48:ALA:HB1	2.14	0.47
26:1H:558:G:OP1	34:58:111:PRO:HD2	2.14	0.47
26:1H:844:C:H3'	26:1H:845:G:H8	1.79	0.47
26:1H:1290:C:H2'	26:1H:1291:C:C6	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1H:1820:U:H4'	26:1H:1821:A:OP2	2.14	0.47
26:1H:2262:U:H4'	26:1H:2328:A:C2	2.49	0.47
26:1H:2615:U:C2	52:N8:7:PRO:HA	2.49	0.47
26:1H:2648:C:H2'	26:1H:2649:U:C6	2.49	0.47
30:31:191:ARG:HB3	30:31:191:ARG:HH11	1.79	0.47
37:88:5:ARG:CZ	37:88:5:ARG:HB2	2.44	0.47
43:E8:18:ARG:NH1	43:E8:76:VAL:O	2.48	0.47
44:F8:24:GLY:H	44:F8:82:GLN:HE22	1.62	0.47
1:1G:1148:U:OP1	9:82:7:THR:HG21	2.14	0.47
1:1G:1151:A:O2'	1:1G:1152:A:O5'	2.31	0.47
2:12:166:ASP:OD2	2:12:169:LYS:HB2	2.14	0.47
10:1A:40:LEU:HG	10:1A:41:PRO:HD2	1.96	0.47
26:14:250:G:OP1	36:35:60:MET:HE1	2.15	0.47
26:14:783:A:H8	26:14:784:A:H4'	1.79	0.47
28:19:267:SER:HA	28:19:270:ILE:HD12	1.97	0.47
31:49:18:GLU:CD	31:49:21:ARG:HH21	2.22	0.47
36:35:79:ARG:HG2	36:35:110:TYR:HB2	1.96	0.47
38:55:33:ARG:HH11	38:55:113:LEU:HD21	1.79	0.47
39:65:106:ARG:NE	39:65:106:ARG:O	2.48	0.47
45:C5:42:VAL:O	45:C5:64:GLU:HA	2.15	0.47
48:F5:91:LYS:O	48:F5:92:LYS:C	2.57	0.47
1:13:200:G:N2	1:13:218:C:O2	2.47	0.47
1:13:279:A:H4'	1:13:280:C:H5"	1.96	0.47
1:13:1492:A:H5"	12:3I:47:LYS:HB3	1.97	0.47
2:1E:67:THR:HG21	2:1E:155:LEU:HG	1.96	0.47
6:5E:100:ASN:C	18:9I:28:GLU:HG2	2.39	0.47
26:1H:18:C:H4'	41:C8:23:GLY:O	2.14	0.47
26:1H:363(B):G:H2'	26:1H:363(C):G:C8	2.49	0.47
26:1H:582:G:H2'	26:1H:583:G:C8	2.49	0.47
26:1H:654(R):C:C2'	26:1H:654(S):G:H5'	2.44	0.47
26:1H:730:C:H3'	59:1H:4230:HOH:O	2.13	0.47
26:1H:1532:C:H42	26:1H:1539:G:H1	1.60	0.47
26:1H:2563:U:H4'	35:68:28:SER:HA	1.96	0.47
26:1H:2572:A:C8	29:21:144:ARG:HD3	2.49	0.47
27:16:80:U:O2'	27:16:81:G:H5"	2.14	0.47
29:21:101:ARG:HG2	29:21:169:ASN:CG	2.39	0.47
30:31:129:PHE:HA	30:31:142:TRP:NE1	2.29	0.47
34:58:94:HIS:C	34:58:95:PRO:O	2.53	0.47
34:58:95:PRO:O	34:58:96:GLU:O	2.32	0.47
35:68:36:GLY:HA2	35:68:106:LEU:HD23	1.95	0.47
37:88:5:ARG:O	37:88:6:ARG:O	2.32	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:98:78:LYS:HE2	38:98:83:ILE:HD11	1.96	0.47
38:98:87:TYR:HB3	38:98:90:ARG:HB3	1.96	0.47
40:B8:58:ASN:ND2	40:B8:58:ASN:O	2.43	0.47
47:I8:10:THR:C	47:I8:12:ASN:H	2.21	0.47
48:J8:81:LYS:C	48:J8:83:GLU:H	2.23	0.47
1:1G:1189:C:O5'	1:1G:1189:C:H6	1.97	0.47
9:82:118:LYS:NZ	9:82:118:LYS:HB3	2.30	0.47
26:14:6:A:C3'	26:14:7:G:H5'	2.44	0.47
26:14:2002:G:C5	59:14:3565:HOH:O	2.67	0.47
26:14:2116:G:H2'	26:14:2117:A:C8	2.49	0.47
26:14:2689:U:OP2	26:14:2719:G:N2	2.46	0.47
26:14:2808:U:H5"	26:14:2891:G:O6	2.15	0.47
28:19:31:LYS:NZ	28:19:33:LEU:HB3	2.28	0.47
31:49:101:ILE:HA	31:49:104:GLU:HB3	1.96	0.47
33:69:81:VAL:N	33:69:143:SER:HB2	2.29	0.47
40:75:112:ARG:NH2	40:75:113:LYS:HE2	2.29	0.47
1:13:150:C:H2'	1:13:151:A:H8	1.80	0.47
1:13:1454:G:H4'	20:BI:36:LEU:HD21	1.96	0.47
2:1E:22:LYS:C	2:1E:24:TRP:H	2.22	0.47
3:2E:81:GLY:O	3:2E:85:ARG:HB2	2.15	0.47
10:1I:25:GLU:O	10:1I:29:ARG:HG2	2.15	0.47
19:AI:9:VAL:HG21	51:M8:63:TYR:CD2	2.49	0.47
26:1H:1952:A:C2	35:68:22:ILE:HG23	2.49	0.47
26:1H:2098:U:H2'	26:1H:2099:U:O4'	2.15	0.47
26:1H:2439:A:H5'	26:1H:2439:A:C8	2.50	0.47
28:11:182:LEU:N	28:11:272:ALA:HB3	2.20	0.47
28:11:221:VAL:HG22	28:11:226:MET:CE	2.45	0.47
30:31:23:ASP:CG	30:31:24:LEU:H	2.22	0.47
30:31:34:TRP:CZ3	36:78:8:PRO:HB3	2.49	0.47
31:41:66:GLN:OE1	31:41:98:ARG:NH1	2.47	0.47
36:78:82:GLY:HA2	36:78:113:LYS:O	2.15	0.47
36:78:94:GLU:HG2	36:78:124:LYS:HD3	1.96	0.47
37:88:106:VAL:HG21	37:88:114:ALA:HB1	1.97	0.47
46:H8:158:PRO:O	46:H8:161:VAL:HG22	2.14	0.47
1:1G:183:G:O5'	1:1G:183:G:H8	1.97	0.47
1:1G:191(B):G:H2'	1:1G:191(C):G:H5"	1.96	0.47
1:1G:1159:U:C5	1:1G:1182:G:C8	3.02	0.47
1:1G:1251:A:H2'	1:1G:1252:A:C8	2.49	0.47
1:1G:1306:A:C6	1:1G:1307:U:C2	3.02	0.47
2:12:81:VAL:O	2:12:85:ALA:N	2.48	0.47
4:32:150:GLU:N	4:32:150:GLU:OE1	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:42:88:LYS:HB3	5:42:123:LEU:HB2	1.96	0.47
12:3A:8:ASN:O	12:3A:12:ARG:HG3	2.15	0.47
12:3A:86:ARG:HB2	12:3A:101:VAL:HG23	1.97	0.47
16:7A:53:VAL:O	16:7A:57:ARG:HG3	2.15	0.47
55:3L:57:G:H2'	55:3L:58:A:H5'	1.96	0.47
26:14:171:G:H2'	26:14:172:C:C6	2.50	0.47
26:14:528:A:N1	26:14:2042:A:H2'	2.30	0.47
26:14:1939:U:OP1	26:14:2604:U:O2'	2.29	0.47
26:14:2745:C:H2'	26:14:2746:U:O4'	2.15	0.47
26:14:2777:G:OP2	26:14:2781:A:O2'	2.24	0.47
32:59:46:GLU:OE1	32:59:51:ARG:NH1	2.41	0.47
41:85:49:HIS:HD2	41:85:52:ARG:HD2	1.80	0.47
41:85:66:ASN:CB	41:85:76:TYR:HB2	2.42	0.47
54:M5:52:LYS:H	54:M5:53:PRO:HD2	1.76	0.47
1:13:169:C:H2'	1:13:170:U:H5'	1.97	0.47
1:13:342:C:C2	1:13:348:G:C2	3.03	0.47
1:13:692:U:O2	1:13:694:A:C8	2.68	0.47
1:13:706:A:N3	11:2I:31:THR:HG21	2.30	0.47
1:13:1026:G:OP2	1:13:1027:C:H5	1.97	0.47
1:13:1054:C:H6	1:13:1054:C:H5"	1.79	0.47
1:13:1118:C:OP1	9:8E:9:ARG:HD3	2.14	0.47
2:1E:100:GLY:N	2:1E:176:GLU:OE2	2.47	0.47
4:3E:112:VAL:HG12	4:3E:116:GLN:OE1	2.14	0.47
7:6E:45:ASP:O	7:6E:49:ILE:HG13	2.13	0.47
7:6E:111:ARG:CD	7:6E:123:GLU:HB2	2.43	0.47
9:8E:112:LYS:HA	9:8E:119:ALA:HB2	1.95	0.47
13:4I:5:ALA:HB2	13:4I:61:GLU:HG2	1.96	0.47
24:3K:35:G:H2'	24:3K:36:U:O4'	2.15	0.47
26:1H:155:C:N4	26:1H:171:G:H1	2.11	0.47
26:1H:273(F):C:N4	26:1H:275:G:H5"	2.28	0.47
26:1H:634:C:H2'	26:1H:635:C:C6	2.48	0.47
26:1H:910:A:N1	26:1H:2277:G:H1'	2.30	0.47
26:1H:1168:G:C2	26:1H:1182:A:C2	3.02	0.47
26:1H:1176:G:N7	26:1H:1177:A:N6	2.62	0.47
26:1H:1545(A):A:H2'	26:1H:1546:C:O4'	2.15	0.47
26:1H:1658:C:P	59:1H:3731:HOH:O	2.63	0.47
26:1H:2432:A:C4	48:J8:33:LYS:HG2	2.49	0.47
26:1H:2600:A:H2'	26:1H:2601:C:C6	2.50	0.47
26:1H:2641:G:H5"	26:1H:2641:G:H8	1.79	0.47
26:1H:2756:U:H1'	26:1H:2757:A:H5"	1.96	0.47
31:41:16:ARG:NH1	31:41:31:VAL:HG21	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:41:108:ASN:HD22	51:M8:21:VAL:HG13	1.79	0.47
37:88:21:THR:HA	37:88:98:LYS:HB2	1.97	0.47
40:B8:57:PHE:HA	40:B8:79:HIS:HD2	1.80	0.47
41:C8:66:ASN:HB2	41:C8:76:TYR:HB2	1.97	0.47
1:1G:828:A:H2'	1:1G:829:G:O4'	2.13	0.47
1:1G:1105:A:H2'	1:1G:1106:G:H8	1.80	0.47
1:1G:1326:C:H5"	21:1B:12:LYS:NZ	2.30	0.47
1:1G:1441:G:H5"	1:1G:1442:G:H5'	1.97	0.47
2:12:187:LEU:HA	2:12:201:ILE:O	2.14	0.47
3:22:37:GLN:NE2	14:5A:52:GLN:OE1	2.47	0.47
5:42:13:ILE:HG13	5:42:13:ILE:O	2.14	0.47
6:52:11:ASN:HB3	6:52:14:LEU:HD22	1.97	0.47
7:62:69:VAL:HG12	7:62:103:TRP:HE3	1.80	0.47
12:3A:102:ARG:HE	12:3A:102:ARG:HB3	1.60	0.47
13:4A:83:ASP:O	13:4A:84:ILE:C	2.58	0.47
18:9A:41:LYS:O	18:9A:41:LYS:HD3	2.15	0.47
26:14:140:A:H8	26:14:1408:C:O2'	1.93	0.47
26:14:234:C:H2'	26:14:235:U:H6	1.79	0.47
26:14:270(H):C:H2'	26:14:270(I):G:C8	2.48	0.47
26:14:579:G:H2'	26:14:580:C:C6	2.50	0.47
26:14:607:U:OP1	30:39:102:PRO:HA	2.15	0.47
26:14:666:G:H5"	36:35:47:ASP:O	2.15	0.47
26:14:773:U:O2'	28:19:48:ARG:HD3	2.15	0.47
26:14:819:A:C4	26:14:1189:A:C2	3.02	0.47
26:14:955:C:OP1	37:45:87:LYS:HE2	2.14	0.47
26:14:997:G:O2'	26:14:998:C:H5'	2.14	0.47
26:14:1310:G:OP2	53:L5:9:ARG:NE	2.36	0.47
26:14:1408:C:C2	26:14:1595:G:N2	2.83	0.47
26:14:1820:U:H4'	26:14:1821:A:OP2	2.14	0.47
26:14:2086:U:H2'	26:14:2087:G:C8	2.49	0.47
26:14:2197:U:H1'	26:14:2198:A:C8	2.49	0.47
26:14:2801:A:H62	26:14:2894:G:H5'	1.80	0.47
27:1J:28:C:H2'	27:1J:29:A:C8	2.50	0.47
27:1J:66:A:N6	27:1J:108:C:O5'	2.48	0.47
27:1J:88:C:H4'	27:1J:89:G:H5"	1.96	0.47
29:29:101:ARG:CZ	29:29:171:GLU:HB2	2.45	0.47
33:69:130:TYR:HB3	33:69:136:VAL:HB	1.97	0.47
34:15:35:ARG:HB3	34:15:42:TRP:CZ3	2.50	0.47
1:13:789:U:O2'	1:13:791:G:N7	2.36	0.47
4:3E:10:ARG:NH1	4:3E:10:ARG:HB2	2.30	0.47
23:2K:8:4SU:H6	23:2K:8:4SU:H5"	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1H:107:C:H2'	26:1H:108:U:H6	1.79	0.47
26:1H:151:C:H2'	26:1H:152:G:H8	1.79	0.47
26:1H:330:A:O2'	26:1H:331:A:H8	1.97	0.47
26:1H:1206:G:C6	26:1H:1207:C:C4	3.02	0.47
26:1H:1441:G:H2'	26:1H:1442:G:C8	2.49	0.47
26:1H:1474:C:H2'	26:1H:1475:G:C8	2.50	0.47
26:1H:1630(A):C:H2'	59:1H:4058:HOH:O	2.14	0.47
26:1H:1729:A:H1'	26:1H:1730:U:C6	2.49	0.47
26:1H:1903:G:OP1	28:11:241:PRO:HB2	2.15	0.47
26:1H:2593:U:H2'	26:1H:2594:C:C6	2.49	0.47
29:21:7:VAL:HG21	40:B8:1:MET:HE1	1.96	0.47
32:51:86:GLU:HB2	32:51:165:ALA:HB3	1.97	0.47
1:1G:474:G:H2'	1:1G:475:G:C8	2.48	0.47
1:1G:1412:C:H2'	1:1G:1413:A:C8	2.50	0.47
2:12:147:LYS:HD2	2:12:148:TYR:CZ	2.49	0.47
11:2A:69:ALA:O	11:2A:73:MET:HG3	2.14	0.47
23:2L:73:A:C6	23:2L:74:A:C6	3.02	0.47
26:14:2378:A:H4'	39:65:23:ARG:NH1	2.24	0.47
27:1J:63:G:H2'	27:1J:64:C:C6	2.49	0.47
39:65:76:LYS:O	39:65:79:ALA:HB3	2.15	0.47
47:E5:19:LYS:C	47:E5:20:ARG:HG2	2.39	0.47
47:E5:50:ASN:O	47:E5:62:LEU:HB2	2.15	0.47
54:M5:36:LYS:HB3	54:M5:41:ILE:HG13	1.97	0.47
1:13:455:C:H42	1:13:477:G:N2	2.12	0.47
3:2E:5:ILE:HG22	10:1I:51:ARG:HH12	1.79	0.47
26:1H:32:C:O2'	26:1H:33:U:H5'	2.14	0.47
26:1H:686:G:H8	53:P8:6:GLN:O	1.97	0.47
26:1H:1932:A:H2'	26:1H:1933:G:O4'	2.15	0.47
26:1H:2688:U:OP2	59:1H:3837:HOH:O	2.20	0.47
26:1H:2721:A:H2'	26:1H:2722:G:O4'	2.14	0.47
30:31:178:PRO:HB3	30:31:198:ALA:HB1	1.97	0.47
35:68:34:THR:OG1	35:68:35:VAL:N	2.47	0.47
38:98:2:ARG:O	38:98:5:LYS:HG3	2.15	0.47
1:1G:26:A:N6	1:1G:558:G:O2'	2.47	0.47
1:1G:57:G:C5	1:1G:58:C:C4	3.03	0.47
1:1G:748:C:H6	1:1G:748:C:O5'	1.98	0.47
1:1G:1217:C:OP1	14:5A:9:LYS:HE3	2.15	0.47
19:AA:14:HIS:NE2	19:AA:15:LEU:HD22	2.30	0.47
23:2L:7:G:H5'	23:2L:7:G:C8	2.49	0.47
26:14:6:A:H2'	26:14:6:A:N3	2.30	0.47
26:14:270(I):G:H2'	26:14:270(J):G:H8	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:14:925:C:H2'	26:14:926:A:H8	1.80	0.47
26:14:1759:A:H4'	26:14:2715:C:O4'	2.15	0.47
26:14:2068:U:N3	26:14:2430:A:H2	2.10	0.47
26:14:2129:C:H5'	26:14:2130:U:OP2	2.15	0.47
26:14:2698:U:H2'	26:14:2699:C:C6	2.50	0.47
29:29:68:ALA:O	29:29:71:GLY:N	2.47	0.47
33:69:76:THR:HG23	33:69:77:LEU:N	2.30	0.47
36:35:147:LEU:HA	36:35:147:LEU:HD13	1.76	0.47
1:13:129(A):G:C2	1:13:188:U:O2'	2.68	0.47
2:1E:96:ARG:HB3	59:1E:301:HOH:O	2.15	0.47
9:8E:43:ALA:HA	9:8E:74:ILE:HD13	1.96	0.47
26:1H:1087:G:C5	26:1H:1089:G:H1'	2.49	0.47
26:1H:1332:G:N2	26:1H:1610:A:H8	2.04	0.47
26:1H:2170:A:OP2	26:1H:2170:A:H8	1.96	0.47
29:21:53:PRO:HA	29:21:75:VAL:HA	1.97	0.47
31:41:163:ALA:HB1	31:41:168:GLU:HB2	1.97	0.47
45:G8:55:TYR:N	45:G8:56:PRO:HD3	2.30	0.47
1:1G:517:G:N2	1:1G:530:G:OP1	2.43	0.47
2:12:49:GLU:HB3	2:12:53:ARG:NH2	2.30	0.47
21:1B:8:THR:HG23	21:1B:11:GLY:H	1.80	0.47
55:3L:44:A:H2'	55:3L:45:G:O4'	2.15	0.47
26:14:309:G:N3	26:14:329:G:O2'	2.48	0.47
26:14:922:U:H2'	26:14:923:C:C6	2.50	0.47
26:14:1213:A:N3	26:14:1238:G:O2'	2.46	0.47
26:14:1430:C:H2'	26:14:1431:U:H6	1.80	0.47
26:14:1636:C:P	59:14:3591:HOH:O	2.73	0.47
26:14:2689:U:P	26:14:2719:G:H22	2.37	0.47
26:14:2712:U:OP1	26:14:2714:G:H4'	2.15	0.47
26:14:2792:G:H2'	26:14:2792:G:N3	2.31	0.47
29:29:23:VAL:HA	29:29:184:VAL:O	2.15	0.47
31:49:27:ASN:HB3	31:49:30:GLU:HG3	1.97	0.47
32:59:158:HIS:HB3	32:59:171:LEU:CG	2.44	0.47
39:65:64:GLU:O	39:65:68:GLN:HG3	2.15	0.47
43:A5:19:LEU:O	43:A5:22:ASP:HB2	2.15	0.47
44:B5:12:VAL:HG22	44:B5:17:ALA:HB2	1.97	0.47
46:D5:58:VAL:O	46:D5:59:LEU:HB2	2.14	0.47
46:D5:110:GLY:HA2	46:D5:143:GLY:H	1.80	0.47
54:M5:14:VAL:CG1	54:M5:22:VAL:HG13	2.45	0.47
1:13:872:A:C5	1:13:874:G:C8	3.03	0.46
1:13:927:G:OP2	1:13:927:G:H4'	2.15	0.46
13:4I:7:VAL:H	31:41:115:ARG:HH12	1.62	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1H:663:G:OP1	36:78:16:ARG:HB2	2.14	0.46
26:1H:674:G:C1'	30:31:74:ARG:HD3	2.44	0.46
26:1H:879:G:N3	26:1H:879:G:H2'	2.31	0.46
26:1H:1889:A:N1	26:1H:2234:G:H1'	2.30	0.46
26:1H:2053:G:OP1	29:21:144:ARG:HG3	2.14	0.46
26:1H:2364:C:H4'	47:I8:56:ASP:OD1	2.15	0.46
28:11:93:ALA:HB3	28:11:105:ILE:HG22	1.96	0.46
28:11:101:GLU:HG3	28:11:102:LYS:N	2.30	0.46
37:88:65:PHE:HB2	37:88:105:GLU:O	2.15	0.46
46:H8:44:PHE:CE2	46:H8:86:VAL:HG11	2.50	0.46
49:K8:15:LYS:HA	49:K8:67:LYS:HZ1	1.80	0.46
1:1G:113:G:O4'	1:1G:354:G:H4'	2.15	0.46
1:1G:167:G:H2'	1:1G:168:G:C8	2.50	0.46
1:1G:362:G:O2'	12:3A:33:ARG:NH2	2.48	0.46
4:32:119:GLN:HG3	4:32:123:HIS:ND1	2.30	0.46
10:1A:6:ILE:HG12	10:1A:72:VAL:O	2.15	0.46
11:2A:82:VAL:HG11	11:2A:95:ILE:HG22	1.96	0.46
12:3A:60:LEU:CB	12:3A:64:TYR:HB2	2.45	0.46
23:2L:2:G:H5'	47:E5:8:GLY:HA2	1.97	0.46
26:14:6:A:N6	34:15:129:PRO:O	2.48	0.46
26:14:172:C:H2'	26:14:173:G:H8	1.79	0.46
26:14:753:C:O2'	26:14:754:C:H5'	2.14	0.46
26:14:1786:A:H1'	26:14:1938:A:N6	2.30	0.46
26:14:2467:C:H4'	37:45:123:HIS:CG	2.50	0.46
26:14:2695:C:H2'	26:14:2696:U:C6	2.50	0.46
32:59:10:PRO:C	32:59:12:PRO:HD3	2.40	0.46
38:55:56:LYS:NZ	38:55:90:ARG:O	2.49	0.46
46:D5:6:LYS:HD3	46:D5:8:TYR:CE2	2.50	0.46
47:E5:69:PHE:CE2	47:E5:79:VAL:HG22	2.50	0.46
1:13:1:U:H1'	1:13:2:U:OP2	2.15	0.46
1:13:645:C:P	59:13:1928:HOH:O	2.73	0.46
4:3E:117:ALA:O	4:3E:121:VAL:HG23	2.15	0.46
7:6E:78:ARG:NH1	7:6E:154:TYR:O	2.48	0.46
14:5I:4:LYS:HE2	14:5I:4:LYS:HB2	1.76	0.46
21:1F:10:ARG:HB3	21:1F:10:ARG:HH11	1.80	0.46
26:1H:822:U:OP1	59:1H:3835:HOH:O	2.20	0.46
26:1H:1405:U:H2'	26:1H:1406:U:H6	1.77	0.46
26:1H:1533:C:H3'	26:1H:1534:G:H5"	1.96	0.46
26:1H:1568:G:H5"	28:11:61:LEU:HD22	1.95	0.46
27:16:11:C:H3'	27:16:12:C:C6	2.50	0.46
27:16:24:G:C2	27:16:56:G:C2	3.03	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:16:94:C:H2'	27:16:95:U:H6	1.80	0.46
1:1G:535:A:H5"	59:1G:1896:HOH:O	2.16	0.46
4:32:107:ARG:NH2	4:32:194:LEU:HD13	2.30	0.46
5:42:37:ARG:HG2	5:42:112:LEU:HA	1.97	0.46
26:14:49:A:H4'	26:14:50:U:H5"	1.97	0.46
26:14:479:A:H1'	26:14:480:A:H5"	1.98	0.46
26:14:1048:A:H62	26:14:1111:A:H1'	1.81	0.46
26:14:1169:G:H1	26:14:1180:C:N4	2.12	0.46
26:14:1338:G:N3	26:14:1393:A:H2	2.13	0.46
26:14:2467:C:H2'	26:14:2468:G:O4'	2.15	0.46
31:49:116:ASP:HB3	31:49:118:ARG:HH12	1.79	0.46
32:59:53:GLU:CD	32:59:54:ARG:H	2.23	0.46
37:45:26:TYR:HD1	37:45:27:VAL:N	2.12	0.46
39:65:88:ASP:C	39:65:90:GLY:N	2.73	0.46
40:75:2:ASN:CB	40:75:4:GLY:HA3	2.45	0.46
41:85:58:ARG:HA	41:85:61:TRP:CE3	2.51	0.46
53:L5:12:ARG:HH21	53:L5:44:PRO:HB3	1.80	0.46
1:13:7:G:H5'	1:13:298:A:O4'	2.15	0.46
1:13:272:C:H2'	1:13:273:A:C8	2.50	0.46
1:13:484:G:O5'	1:13:484:G:H8	1.98	0.46
4:3E:97:LEU:O	4:3E:100:ARG:HG3	2.14	0.46
4:3E:162:LEU:HD12	4:3E:181:MET:CE	2.45	0.46
9:8E:5:TYR:O	9:8E:87:GLN:NE2	2.48	0.46
9:8E:25:LYS:O	9:8E:60:ASP:HA	2.15	0.46
22:1K:72:C:C4	22:1K:73:A:H2	2.34	0.46
26:1H:450:G:P	59:1H:3768:HOH:O	2.71	0.46
26:1H:1057:A:C8	26:1H:1086:A:H2'	2.50	0.46
26:1H:1076:C:H2'	26:1H:1077:A:H5"	1.97	0.46
26:1H:2232:U:P	48:J8:40:ARG:HH12	2.39	0.46
29:21:60:ASN:OD1	29:21:63:LEU:HB2	2.15	0.46
33:61:110:ASP:OD1	33:61:111:PRO:HA	2.15	0.46
37:88:4:PRO:HD3	37:88:70:PRO:O	2.14	0.46
42:D8:35:LEU:HD23	42:D8:35:LEU:HA	1.62	0.46
1:1G:944:G:P	59:1G:1888:HOH:O	2.72	0.46
1:1G:983:A:O2'	1:1G:1050:G:OP2	2.29	0.46
1:1G:1273:G:H3'	1:1G:1274:G:H8	1.81	0.46
1:1G:1306:A:N6	1:1G:1331:G:H1'	2.30	0.46
4:32:85:LYS:O	4:32:86:LYS:C	2.58	0.46
12:3A:111:LYS:HA	12:3A:111:LYS:NZ	2.30	0.46
14:5A:39:LEU:HD13	14:5A:47:LEU:HD12	1.97	0.46
19:AA:56:GLN:CD	19:AA:57:HIS:H	2.23	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:14:1049:C:N4	26:14:1109:C:O2'	2.48	0.46
26:14:2320:A:N6	26:14:2333:A:H2'	2.31	0.46
29:29:101:ARG:O	29:29:201:THR:OG1	2.32	0.46
30:39:18:ARG:NH2	30:39:20:LEU:HB2	2.29	0.46
31:49:49:ASP:O	31:49:53:LEU:N	2.48	0.46
32:59:122:THR:HG22	32:59:123:PHE:H	1.80	0.46
40:75:124:ASP:HB3	40:75:125:ARG:HH11	1.79	0.46
41:85:65:ILE:HD11	41:85:96:ALA:HB3	1.96	0.46
46:D5:94:GLU:O	46:D5:129:SER:HA	2.14	0.46
1:13:8:A:H4'	1:13:9:G:OP1	2.15	0.46
1:13:148:G:H2'	1:13:149:A:C8	2.51	0.46
1:13:692:U:O4	11:2I:53:SER:CB	2.63	0.46
1:13:808:C:OP2	15:6I:48:LYS:NZ	2.49	0.46
2:1E:53:ARG:NH2	2:1E:198:ASP:O	2.48	0.46
2:1E:126:GLU:HA	2:1E:129:GLU:OE2	2.15	0.46
4:3E:138:TYR:CD1	4:3E:138:TYR:C	2.94	0.46
12:3I:111:LYS:HD3	12:3I:111:LYS:HA	1.79	0.46
26:1H:317:G:C2	26:1H:318:C:C2	3.03	0.46
26:1H:1590:U:H2'	26:1H:1591:G:C8	2.50	0.46
27:16:31:C:N4	39:A8:32:LEU:HD22	2.30	0.46
28:11:12:SER:HB2	28:11:208:LYS:HB3	1.98	0.46
28:11:238:GLY:O	28:11:239:ARG:O	2.33	0.46
33:61:130:TYR:C	33:61:131:LYS:HD2	2.40	0.46
45:G8:94:LYS:HA	45:G8:94:LYS:NZ	2.31	0.46
1:1G:300:A:H1'	1:1G:565:U:O2	2.15	0.46
1:1G:397:A:H3'	1:1G:397:A:N3	2.30	0.46
1:1G:714:G:H2'	1:1G:715:A:C8	2.50	0.46
1:1G:1286:A:C8	1:1G:1286:A:H3'	2.51	0.46
2:12:75:LYS:HA	2:12:78:GLN:HB2	1.96	0.46
3:22:18:TRP:HB2	3:22:21:ARG:HG2	1.96	0.46
3:22:42:LEU:O	3:22:46:GLU:HG2	2.15	0.46
3:22:129:ALA:HB3	3:22:132:ARG:NH2	2.30	0.46
3:22:140:ARG:HA	3:22:140:ARG:HD2	1.73	0.46
4:32:152:SER:HB3	4:32:155:LEU:HG	1.96	0.46
9:82:17:VAL:HA	9:82:63:ILE:HG12	1.98	0.46
10:1A:32:ALA:HA	10:1A:76:ASN:HB2	1.98	0.46
11:2A:54:ARG:HH22	55:3L:40:G:P	2.38	0.46
11:2A:62:GLN:HB2	11:2A:93:GLN:NE2	2.31	0.46
22:1L:50:G:O2'	22:1L:51:C:OP2	2.32	0.46
23:2L:76:C:H2'	23:2L:77:A:C8	2.50	0.46
26:14:958:U:O2	27:1J:89(A):A:O2'	2.27	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:14:1775:U:OP1	59:14:3563:HOH:O	2.21	0.46
26:14:2401:U:H2'	26:14:2402:C:C6	2.50	0.46
26:14:2807:G:H1	26:14:2892:A:H62	1.64	0.46
34:15:73:THR:HG22	34:15:84:LYS:HB3	1.97	0.46
35:25:102:VAL:HB	35:25:106:LEU:HD12	1.97	0.46
36:35:144:GLU:OE1	36:35:144:GLU:N	2.49	0.46
37:45:24:GLY:H	37:45:101:ARG:NH1	2.13	0.46
38:55:96:ARG:HD3	38:55:115:GLU:OE1	2.15	0.46
39:65:65:VAL:O	39:65:69:VAL:HG12	2.16	0.46
40:75:134:GLU:HG3	40:75:137:LYS:HD3	1.97	0.46
44:B5:24:GLY:O	44:B5:83:VAL:HG12	2.15	0.46
45:C5:17:SER:OG	45:C5:18:GLY:N	2.47	0.46
46:D5:161:VAL:HG23	46:D5:162:GLU:H	1.80	0.46
48:F5:71:TYR:O	48:F5:74:VAL:HG22	2.15	0.46
1:13:73:G:C2	1:13:74:C:N4	2.84	0.46
1:13:352:C:H6	1:13:352:C:H5"	1.80	0.46
1:13:417:C:H2'	1:13:418:C:H6	1.81	0.46
1:13:542:G:OP1	4:3E:10:ARG:NH2	2.46	0.46
1:13:605:U:H2'	1:13:606:G:O4'	2.16	0.46
1:13:619:U:N3	4:3E:134:ASP:HB2	2.28	0.46
1:13:637:G:H2'	1:13:638:G:H8	1.81	0.46
2:1E:11:LEU:HD12	2:1E:11:LEU:HA	1.68	0.46
7:6E:45:ASP:O	7:6E:48:LYS:HB3	2.15	0.46
19:AI:28:LYS:HE3	19:AI:28:LYS:HB2	1.83	0.46
21:1F:2:GLY:O	21:1F:4:GLY:N	2.49	0.46
26:1H:762:U:H4'	26:1H:763:G:O5'	2.16	0.46
26:1H:1637:A:H4'	26:1H:2711:A:O2'	2.15	0.46
26:1H:2115:G:H2'	26:1H:2116:G:C8	2.51	0.46
26:1H:2262:U:OP1	26:1H:2387:U:O2'	2.25	0.46
27:16:88:C:H2'	27:16:89:G:O4'	2.14	0.46
29:21:67:PHE:CE2	29:21:74:PRO:HA	2.51	0.46
32:51:9:ILE:HG23	32:51:50:VAL:O	2.15	0.46
33:61:143:SER:HB3	33:61:144:VAL:HG23	1.97	0.46
45:G8:40:GLU:HA	45:G8:41:GLY:HA2	1.73	0.46
1:1G:1055:A:C5	1:1G:1206:G:C2	3.03	0.46
1:1G:1095:U:H5"	1:1G:1109:C:O2	2.16	0.46
1:1G:1312:G:H2'	1:1G:1313:U:O4'	2.16	0.46
1:1G:1396:A:H4'	1:1G:1397:C:H5"	1.98	0.46
2:12:48:MET:O	2:12:51:LEU:HG	2.15	0.46
4:32:84:LYS:HE3	4:32:84:LYS:HB3	1.51	0.46
7:62:23:VAL:HG13	7:62:43:PHE:CE2	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:4A:25:ILE:O	13:4A:29:ARG:HB2	2.14	0.46
26:14:70:G:H21	26:14:71:A:H62	1.64	0.46
26:14:406:G:H1	26:14:421:U:H3	1.61	0.46
26:14:493:G:H2'	26:14:494:G:O4'	2.16	0.46
26:14:863:A:H2'	26:14:864:G:H8	1.80	0.46
26:14:1158:C:OP1	50:H5:30:ARG:NH1	2.49	0.46
26:14:2636:U:OP1	29:29:80:GLU:HB2	2.16	0.46
38:55:77:ARG:O	38:55:80:PHE:N	2.49	0.46
42:95:48:GLY:HA3	42:95:51:VAL:C	2.41	0.46
43:A5:86:LEU:HD12	43:A5:87:PRO:HD2	1.96	0.46
1:13:110:C:H2'	1:13:111:G:O4'	2.15	0.46
1:13:129(A):G:N1	1:13:188:U:O2'	2.49	0.46
1:13:476:G:N2	1:13:477:G:H1'	2.31	0.46
1:13:1399:C:H4'	1:13:1400:C:O5'	2.15	0.46
2:1E:17:PHE:CD1	2:1E:44:LEU:HD11	2.51	0.46
4:3E:164:ALA:O	4:3E:168:ARG:NE	2.49	0.46
5:4E:148:VAL:HA	5:4E:151:LEU:HD12	1.97	0.46
10:1I:82:ILE:HA	10:1I:85:LEU:HG	1.97	0.46
13:4I:82:MET:C	13:4I:84:ILE:H	2.22	0.46
23:2K:47:7MG:H81	23:2K:48:U:C5	2.36	0.46
26:1H:535:C:O3'	41:C8:53:ARG:NH1	2.49	0.46
26:1H:1183:G:O2'	50:L8:29:ARG:NH1	2.42	0.46
26:1H:1316:U:H2'	26:1H:1317:A:H8	1.81	0.46
26:1H:1533:C:H6	26:1H:1534:G:H5"	1.81	0.46
26:1H:2053:G:OP2	59:1H:3839:HOH:O	2.21	0.46
26:1H:2062:A:N3	26:1H:2062:A:C2'	2.79	0.46
26:1H:2422:A:N7	54:Q8:31:HIS:HE1	2.13	0.46
31:41:35:GLU:HG3	31:41:36:LYS:HB2	1.96	0.46
37:88:140:ALA:O	37:88:141:GLN:NE2	2.49	0.46
43:E8:79:GLY:CA	43:E8:100:THR:HG22	2.46	0.46
44:F8:26:TYR:CD2	44:F8:89:ILE:HG13	2.51	0.46
49:K8:47:ASN:C	49:K8:49:LYS:H	2.08	0.46
1:1G:108:G:OP1	1:1G:326:G:N2	2.35	0.46
1:1G:501:C:H2'	1:1G:502:G:C8	2.51	0.46
1:1G:862:C:H1'	1:1G:874:G:H5"	1.98	0.46
1:1G:1069:C:O2'	1:1G:1192:C:H1'	2.16	0.46
1:1G:1128:C:H6	1:1G:1128:C:O5'	1.98	0.46
11:2A:32:ILE:HD13	11:2A:72:ALA:HB2	1.97	0.46
26:14:700:G:O2'	26:14:1632:A:N3	2.44	0.46
26:14:860:U:C2	26:14:2268:A:C8	3.03	0.46
26:14:1486:A:H2'	26:14:1487:G:C8	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:14:1520:U:H2'	26:14:1521:G:O4'	2.16	0.46
26:14:1915:U:C2'	26:14:1916:A:H5'	2.46	0.46
26:14:2287:A:C2	26:14:2346:A:H2	2.33	0.46
28:19:146:GLU:HB2	28:19:189:CYS:HB3	1.98	0.46
30:39:178:PRO:HB3	30:39:198:ALA:HA	1.98	0.46
34:15:90:MET:HB3	34:15:98:VAL:HG12	1.97	0.46
1:13:186:C:H2'	1:13:186(A):C:H6	1.81	0.46
1:13:192:U:C1'	20:BI:103:GLY:HA2	2.45	0.46
1:13:1367:C:C5'	10:1I:60:ARG:HH11	2.24	0.46
2:1E:18:GLY:HA2	2:1E:42:ILE:HG13	1.97	0.46
2:1E:231:GLU:H	2:1E:231:GLU:CD	2.23	0.46
4:3E:111:ALA:HB2	4:3E:120:LEU:CD1	2.46	0.46
8:7E:25:ASP:HB3	8:7E:58:TYR:HB3	1.98	0.46
9:8E:78:LYS:HE3	9:8E:101:PHE:CE1	2.50	0.46
11:2I:99:GLN:HE21	11:2I:99:GLN:HB3	1.56	0.46
13:4I:7:VAL:H	31:41:115:ARG:NH1	2.13	0.46
13:4I:107:ALA:O	13:4I:111:LYS:HB2	2.15	0.46
26:1H:958:U:OP1	37:88:74:TYR:OH	2.27	0.46
26:1H:1126:A:H4'	26:1H:1127:A:O5'	2.15	0.46
26:1H:1257:C:OP1	30:31:75:HIS:HE1	1.98	0.46
26:1H:1534:G:H2'	26:1H:1535:U:O4'	2.16	0.46
26:1H:2056:G:C2	26:1H:2057:A:C8	3.04	0.46
26:1H:2086:U:H2'	26:1H:2087:G:C8	2.50	0.46
26:1H:2391:G:O6	26:1H:2425:A:H8	1.99	0.46
26:1H:2436:G:C5	26:1H:2437:U:C5	3.04	0.46
28:11:68:LYS:HB3	28:11:70:TRP:CH2	2.50	0.46
32:51:2:SER:N	32:51:4:ILE:O	2.49	0.46
33:61:77:LEU:HD11	33:61:101:LEU:HB2	1.98	0.46
45:G8:29:GLU:HB3	45:G8:38:ILE:CG2	2.45	0.46
1:1G:1151:A:HO2'	1:1G:1152:A:C5'	2.28	0.46
1:1G:1288:A:H2'	1:1G:1289:A:C8	2.50	0.46
2:12:28:PHE:CE2	2:12:31:TYR:HB2	2.51	0.46
2:12:47:THR:HA	2:12:50:GLU:OE2	2.15	0.46
2:12:71:VAL:HG21	2:12:164:VAL:HA	1.96	0.46
2:12:98:LEU:O	2:12:101:MET:HG2	2.16	0.46
4:32:88:VAL:HB	4:32:89:THR:OG1	2.15	0.46
5:42:50:GLU:OE2	5:42:51:VAL:HG23	2.15	0.46
19:AA:53:ASN:HB2	19:AA:77:THR:HG22	1.97	0.46
26:14:805:G:OP2	36:35:41:ARG:HG2	2.16	0.46
26:14:957:A:N6	26:14:2459:A:C8	2.84	0.46
26:14:993:G:N3	42:95:89:GLN:NE2	2.57	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:14:2051:A:H5'	26:14:2578:G:O4'	2.15	0.46
26:14:2103:C:H2'	26:14:2104:G:C8	2.51	0.46
26:14:2250:G:OP2	26:14:2275:C:H2'	2.15	0.46
26:14:2776:A:H4'	26:14:2777:G:O5'	2.16	0.46
29:29:113:PHE:HA	29:29:159:HIS:HD2	1.81	0.46
46:D5:157:LEU:HG	46:D5:161:VAL:HG21	1.97	0.46
1:13:263:A:H8	1:13:263:A:OP2	1.97	0.46
1:13:267:C:H2'	1:13:268:C:C6	2.50	0.46
1:13:297:G:H4'	1:13:557:G:H4'	1.98	0.46
2:1E:16:HIS:NE2	2:1E:214:ILE:HD11	2.31	0.46
7:6E:104:LEU:HD13	7:6E:104:LEU:HA	1.65	0.46
14:5I:4:LYS:O	14:5I:7:ILE:HG12	2.16	0.46
19:AI:6:LYS:H	51:M8:66:SER:HB3	1.81	0.46
24:3K:16:U:C2	24:3K:61:C:H5"	2.51	0.46
24:3K:34:G:O2'	24:3K:35:G:C8	2.68	0.46
26:1H:192:C:O2'	26:1H:802:A:N3	2.43	0.46
26:1H:654(O):G:H5"	26:1H:654(P):G:C2	2.50	0.46
26:1H:1111:A:N3	26:1H:1112:G:H1'	2.30	0.46
26:1H:2100:G:O6	26:1H:2189:U:N3	2.49	0.46
26:1H:2105:C:H2'	26:1H:2106:G:H8	1.81	0.46
26:1H:2766:G:H2'	26:1H:2766:G:N3	2.31	0.46
26:1H:2887:U:H2'	26:1H:2888:C:C6	2.51	0.46
28:11:96:HIS:CE1	28:11:102:LYS:HE2	2.50	0.46
30:31:117:ARG:HD3	30:31:117:ARG:HA	1.56	0.46
34:58:67:LEU:HD23	34:58:88:GLU:HB3	1.98	0.46
1:1G:1119:C:OP2	9:82:9:ARG:NH2	2.49	0.46
1:1G:1418:A:H2	26:14:1948:G:N3	2.14	0.46
3:22:87:LEU:HB2	3:22:88:ARG:HH21	1.81	0.46
8:72:20:TYR:CE2	8:72:75:ARG:HB3	2.51	0.46
20:BA:50:GLU:HA	20:BA:100:ILE:HG21	1.97	0.46
26:14:26:G:C6	26:14:27:G:N1	2.84	0.46
26:14:51:G:N3	26:14:119:A:C2	2.84	0.46
26:14:270(P):C:H2'	26:14:270(Q):C:C6	2.51	0.46
26:14:302:C:H2'	26:14:303:U:C6	2.50	0.46
26:14:313:C:H5'	59:14:3731:HOH:O	2.16	0.46
26:14:372:G:OP2	48:F5:69:LYS:NZ	2.47	0.46
26:14:937:U:H2'	26:14:938:G:O4'	2.15	0.46
26:14:994:C:OP1	41:85:53:ARG:NH2	2.49	0.46
26:14:1297:C:OP1	26:14:2710:C:H4'	2.15	0.46
26:14:2468:G:H3'	26:14:2476:A:N1	2.30	0.46
32:59:27:LYS:NZ	32:59:32:GLU:HG3	2.31	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:59:85:LYS:N	32:59:85:LYS:HD2	2.31	0.46
33:69:31:LEU:HD21	33:69:38:LEU:HG	1.98	0.46
36:35:125:VAL:HG13	36:35:144:GLU:HB3	1.97	0.46
39:65:106:ARG:NH2	39:65:107:GLU:OE1	2.37	0.46
52:J5:16:ARG:HG3	52:J5:17:ASP:H	1.80	0.46
1:13:49:U:C2	1:13:361:G:N2	2.84	0.46
1:13:353:A:H8	1:13:353:A:H5'	1.81	0.46
1:13:735:C:H2'	1:13:736:C:H6	1.80	0.46
13:4I:12:ASN:HB3	13:4I:46:LYS:HD2	1.96	0.46
20:BI:23:ARG:HA	20:BI:26:ASN:HD21	1.81	0.46
26:1H:568:U:OP1	36:78:36:LYS:HE3	2.16	0.46
26:1H:1053:C:N4	26:1H:1106:G:H1	2.14	0.46
26:1H:1498:C:O4'	26:1H:1577:C:H4'	2.16	0.46
26:1H:1690:A:H2'	26:1H:1691:C:O4'	2.16	0.46
26:1H:1791:A:H5'	28:11:206:LEU:HD12	1.97	0.46
26:1H:2593:U:C2'	26:1H:2594:C:H5'	2.45	0.46
29:21:46:ALA:HB2	29:21:82:ARG:HA	1.98	0.46
34:58:1:MET:HE1	41:C8:95:LEU:HD21	1.98	0.46
39:A8:88:ASP:O	39:A8:89:ARG:HB3	2.15	0.46
43:E8:51:LEU:HD23	43:E8:105:VAL:HG11	1.97	0.46
45:G8:94:LYS:CE	45:G8:95:LYS:H	2.29	0.46
1:1G:359:U:H2'	1:1G:360:A:C8	2.50	0.46
1:1G:751:U:H4'	15:6A:24:SER:HA	1.98	0.46
1:1G:1285:A:H4'	1:1G:1286:A:O5'	2.16	0.46
1:1G:1298:C:H4'	1:1G:1299:A:C4	2.50	0.46
17:8A:59:ILE:HG23	17:8A:71:PHE:HB3	1.98	0.46
26:14:389:G:H22	36:35:72:PRO:HD3	1.81	0.46
26:14:1154:G:OP1	41:85:58:ARG:HD3	2.16	0.46
26:14:1420:U:HO2'	26:14:1421:G:P	2.39	0.46
26:14:2002:G:OP2	38:55:9:LYS:NZ	2.49	0.46
26:14:2328:A:H2'	26:14:2329:G:C8	2.51	0.46
26:14:2686:G:C2	26:14:2724:C:O2	2.69	0.46
26:14:2693:A:H2'	26:14:2694:G:C8	2.51	0.46
30:39:169:ASN:O	30:39:169:ASN:ND2	2.49	0.46
32:59:35:VAL:HG11	32:59:71:LEU:HG	1.96	0.46
33:69:81:VAL:H	33:69:143:SER:HB2	1.81	0.46
38:55:33:ARG:HD2	38:55:113:LEU:HD21	1.98	0.46
41:85:88:ILE:O	41:85:88:ILE:HG22	2.16	0.46
43:A5:65:LEU:HD13	43:A5:68:ARG:CZ	2.46	0.46
50:H5:18:ASP:OD1	50:H5:18:ASP:N	2.44	0.46
1:13:1366:C:H2'	1:13:1367:C:C6	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:13:1490:C:O2'	1:13:1491:G:H5'	2.16	0.46
15:6I:82:ILE:HD13	15:6I:88:ARG:HB2	1.98	0.46
23:2K:48:U:O2'	23:2K:49:C:OP2	2.31	0.46
24:3K:59:A:OP2	24:3K:59:A:H4'	2.16	0.46
26:1H:125:G:H5'	26:1H:125:G:H8	1.81	0.46
26:1H:270(T):G:H2'	26:1H:270(U):C:C6	2.50	0.46
26:1H:674:G:HO2'	30:31:74:ARG:HG3	1.80	0.46
26:1H:2404:C:O3'	36:78:77:ARG:NH2	2.49	0.46
27:16:70:C:H2'	27:16:71:C:H6	1.81	0.46
28:11:25:THR:HG21	28:11:113:VAL:HG11	1.98	0.46
30:31:134:GLY:CA	30:31:166:ALA:HB2	2.45	0.46
31:41:83:ARG:H	31:41:86:MET:CE	2.29	0.46
33:61:31:LEU:HD21	33:61:38:LEU:HD11	1.98	0.46
46:H8:45:ASP:CG	46:H8:49:ARG:HH12	2.22	0.46
1:1G:1152:A:H2'	1:1G:1153:C:O4'	2.16	0.46
2:12:126:GLU:O	2:12:130:ARG:HD3	2.16	0.46
3:22:59:ARG:HG3	3:22:64:VAL:HA	1.97	0.46
3:22:181:ASN:ND2	3:22:204:LEU:HB2	2.31	0.46
4:32:99:SER:O	4:32:140:VAL:HG13	2.15	0.46
8:72:31:PHE:HZ	8:72:134:ILE:HD13	1.80	0.46
8:72:43:GLY:O	8:72:79:VAL:HG11	2.16	0.46
9:82:79:LEU:HD21	9:82:102:LEU:HA	1.98	0.46
11:2A:22:HIS:HB3	11:2A:29:ILE:HG12	1.99	0.46
26:14:635:C:H2'	26:14:636:G:O4'	2.17	0.46
26:14:999:U:H5"	26:14:1154:G:O6	2.16	0.46
26:14:1188:U:O2'	26:14:1189:A:H5'	2.16	0.46
26:14:1771:C:H1'	26:14:1786:A:C8	2.51	0.46
26:14:2473:U:O2	26:14:2473:U:H2'	2.15	0.46
29:29:117:MET:HA	29:29:122:PHE:N	2.30	0.46
30:39:4:VAL:HG13	30:39:19:GLU:CD	2.41	0.46
30:39:27:GLU:C	30:39:29:ASN:H	2.23	0.46
32:59:97:ARG:HG2	32:59:98:LEU:N	2.28	0.46
34:15:136:GLU:OE2	34:15:138:LEU:HD22	2.16	0.46
37:45:10:ARG:HA	37:45:10:ARG:CZ	2.45	0.46
39:65:27:SER:HA	39:65:88:ASP:HB2	1.98	0.46
43:A5:26:GLY:H	43:A5:71:VAL:HB	1.79	0.46
46:D5:27:VAL:CG1	46:D5:87:ASP:HB3	2.43	0.46
49:G5:2:LYS:HA	49:G5:3:LEU:HA	1.76	0.46
1:13:107:G:O6	20:BI:15:ARG:HG3	2.17	0.45
1:13:295:C:H2'	1:13:296:U:O4'	2.16	0.45
1:13:947:G:H2'	1:13:948:C:O4'	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:13:950:U:OP2	13:4I:102:ARG:HD2	2.16	0.45
1:13:1130:A:H5'	9:8E:18:PHE:CE2	2.51	0.45
2:1E:7:VAL:HG22	2:1E:8:LYS:H	1.81	0.45
2:1E:21:ARG:C	2:1E:23:ARG:H	2.24	0.45
19:AI:25:LYS:HD2	19:AI:25:LYS:HA	1.83	0.45
20:BI:48:LYS:HB3	20:BI:51:GLU:HB2	1.99	0.45
26:1H:182:A:H2'	26:1H:183:C:O4'	2.16	0.45
26:1H:195:A:OP1	36:78:46:LYS:HE2	2.15	0.45
26:1H:443:A:N7	30:31:45:ARG:HG2	2.31	0.45
26:1H:511:U:C5	26:1H:512:G:C5	3.04	0.45
26:1H:1141:U:C5	34:58:64:GLY:HA3	2.51	0.45
26:1H:2320:A:H2'	26:1H:2320:A:N3	2.31	0.45
26:1H:2683:C:OP1	40:B8:53:ARG:NH2	2.48	0.45
29:21:143:ASN:HD22	29:21:147:PRO:HD2	1.81	0.45
31:41:11:TYR:O	31:41:16:ARG:HG3	2.16	0.45
38:98:20:LEU:HD21	38:98:40:LYS:HD3	1.98	0.45
40:B8:58:ASN:C	40:B8:58:ASN:ND2	2.71	0.45
41:C8:69:CYS:SG	41:C8:79:PHE:HD2	2.39	0.45
54:Q8:34:TRP:CE2	54:Q8:35:GLN:NE2	2.84	0.45
1:1G:690:G:H22	11:2A:55:LYS:NZ	2.14	0.45
1:1G:983:A:H3'	1:1G:983:A:N3	2.31	0.45
1:1G:1198:G:H2'	1:1G:1199:U:C6	2.51	0.45
2:12:168:THR:HG21	2:12:191:ASP:O	2.15	0.45
13:4A:84:ILE:HG13	19:AA:63:THR:HG21	1.98	0.45
18:9A:36:ASN:HB2	18:9A:38:GLU:OE2	2.16	0.45
22:1L:63:G:H2'	22:1L:64:C:O4'	2.16	0.45
26:14:98:G:OP1	49:G5:3:LEU:HB3	2.17	0.45
26:14:141:A:C8	26:14:1408:C:H1'	2.51	0.45
26:14:572:A:OP2	42:95:78:LYS:HE2	2.15	0.45
26:14:1142:U:O2	26:14:1142:U:H2'	2.16	0.45
26:14:1416:G:O2'	26:14:1417:C:O5'	2.13	0.45
26:14:1534:G:H3'	26:14:1535:U:H5"	1.97	0.45
26:14:1677:A:H2'	26:14:1678:G:C8	2.51	0.45
26:14:2287:A:C2	26:14:2346:A:C2	3.04	0.45
26:14:2335:A:C8	26:14:2337:G:N7	2.84	0.45
26:14:2542:A:H4'	26:14:2542:A:OP1	2.16	0.45
26:14:2572:A:N7	29:29:145:LYS:HB2	2.31	0.45
27:1J:70:C:H2'	27:1J:71:C:H6	1.81	0.45
30:39:194:MET:HE3	30:39:194:MET:HB2	1.63	0.45
33:69:79:ILE:HG13	33:69:140:LEU:HD11	1.97	0.45
40:75:2:ASN:CG	40:75:4:GLY:HA3	2.41	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:75:3:ARG:N	40:75:4:GLY:O	2.49	0.45
46:D5:15:PRO:HA	46:D5:18:LEU:HB2	1.97	0.45
48:F5:91:LYS:HB2	48:F5:91:LYS:HE2	1.53	0.45
50:H5:43:ILE:O	50:H5:47:VAL:HG23	2.16	0.45
1:13:219:C:H2'	1:13:220:G:O4'	2.17	0.45
4:3E:111:ALA:HB2	4:3E:120:LEU:HD12	1.98	0.45
8:7E:112:LEU:HB3	8:7E:133:LEU:HA	1.98	0.45
8:7E:120:THR:OG1	8:7E:123:GLU:OE1	2.30	0.45
10:1I:49:VAL:CG2	14:5I:41:ARG:HB2	2.41	0.45
16:7I:74:LEU:HB3	16:7I:79:VAL:HG21	1.98	0.45
20:BI:16:HIS:O	20:BI:19:SER:HB2	2.16	0.45
22:1K:49:G:H4'	22:1K:50:G:OP2	2.17	0.45
26:1H:140:A:C8	26:1H:1408:C:O2'	2.69	0.45
26:1H:592:G:H21	54:Q8:4:MET:CE	2.18	0.45
26:1H:723:G:H2'	26:1H:724:U:O4'	2.17	0.45
26:1H:944:G:H5"	26:1H:945:A:O5'	2.17	0.45
26:1H:1048:A:H5'	26:1H:1049:C:OP2	2.16	0.45
26:1H:1430:C:H2'	26:1H:1431:U:H6	1.79	0.45
26:1H:1581:G:H2'	26:1H:1582:C:O4'	2.16	0.45
26:1H:1763:G:OP1	26:1H:1763:G:H4'	2.15	0.45
26:1H:2162:G:H2'	26:1H:2163:C:C6	2.51	0.45
26:1H:2508:G:H2'	26:1H:2509:G:H8	1.81	0.45
27:16:94:C:H2'	27:16:95:U:C6	2.51	0.45
31:41:145:THR:O	31:41:146:TYR:HB3	2.16	0.45
32:51:41:MET:HE3	32:51:41:MET:HB2	1.77	0.45
32:51:52:VAL:O	32:51:65:HIS:NE2	2.32	0.45
32:51:101:ARG:HH22	32:51:122:THR:HA	1.81	0.45
42:D8:37:VAL:HG12	42:D8:55:ALA:O	2.15	0.45
45:G8:97:ARG:HH21	45:G8:103:GLY:C	2.24	0.45
1:1G:1322:C:HO2'	1:1G:1323:G:H5'	1.80	0.45
1:1G:1360:A:H2'	1:1G:1361:G:O4'	2.16	0.45
3:22:73:PRO:CG	3:22:105:GLU:HB2	2.46	0.45
7:62:121:ALA:O	7:62:125:MET:HG3	2.16	0.45
16:7A:1:MET:HB2	16:7A:1:MET:HE3	1.55	0.45
26:14:67:U:H2'	26:14:68:G:H8	1.81	0.45
26:14:1287:A:N7	38:55:106:GLY:O	2.49	0.45
26:14:1456:G:OP2	59:14:3564:HOH:O	2.21	0.45
26:14:1728:G:C2	26:14:1730:U:OP2	2.69	0.45
26:14:1869:G:N2	26:14:1872:A:C8	2.84	0.45
26:14:2687:U:C4	26:14:2688:U:C5	3.04	0.45
29:29:66:HIS:C	29:29:68:ALA:H	2.24	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:35:39:LYS:HB2	36:35:45:LEU:HD11	1.97	0.45
41:85:106:PHE:O	41:85:109:LEU:N	2.49	0.45
46:D5:14:LYS:H	46:D5:14:LYS:CD	2.30	0.45
1:13:114:U:H2'	1:13:115:G:C8	2.52	0.45
1:13:313:A:H2'	1:13:314:C:C6	2.50	0.45
1:13:674:G:N2	1:13:717:C:O2	2.50	0.45
1:13:1151:A:O2'	1:13:1152:A:O5'	2.34	0.45
2:1E:79:ASP:N	2:1E:81:VAL:HG22	2.30	0.45
5:4E:81:GLU:HG2	5:4E:90:VAL:HG23	1.98	0.45
26:1H:60:G:H4'	49:K8:51:ARG:HH12	1.82	0.45
26:1H:274:G:H3'	26:1H:274:G:C8	2.51	0.45
26:1H:346:A:H5"	26:1H:347:A:OP2	2.16	0.45
26:1H:783:A:C8	26:1H:783:A:H3'	2.51	0.45
26:1H:1913:A:H8	26:1H:1913:A:OP1	1.98	0.45
26:1H:1971:A:H5'	26:1H:1972:A:H5"	1.97	0.45
26:1H:2104:G:C2	26:1H:2186:G:C2	3.04	0.45
26:1H:2394:C:H1'	59:1H:3930:HOH:O	2.15	0.45
27:16:1(M):A:H8	27:16:0:A:C8	2.34	0.45
28:11:253:GLN:HE21	28:11:253:GLN:HB2	1.58	0.45
38:98:104:ARG:HB3	38:98:107:ASP:HB3	1.98	0.45
41:C8:79:PHE:O	41:C8:79:PHE:HD1	1.99	0.45
44:F8:41:ASN:O	44:F8:45:THR:HG23	2.16	0.45
45:G8:56:PRO:HD2	45:G8:57:GLN:H	1.81	0.45
1:1G:984:C:H2'	1:1G:985:C:H6	1.80	0.45
1:1G:1274:G:H2'	1:1G:1275:A:H8	1.81	0.45
2:12:31:TYR:HB3	2:12:42:ILE:HG23	1.98	0.45
2:12:185:ILE:HG23	2:12:199:TYR:HB2	1.98	0.45
5:42:129:ILE:HG23	5:42:133:TYR:HE2	1.80	0.45
11:2A:48:ILE:HD11	11:2A:64:ALA:HA	1.96	0.45
19:AA:15:LEU:O	19:AA:18:LYS:N	2.46	0.45
26:14:2107:C:H42	26:14:2182:G:H1	1.64	0.45
26:14:2393:A:H4'	36:35:62:LEU:O	2.16	0.45
26:14:2637:U:C4	26:14:2638:G:C6	3.04	0.45
26:14:2799:A:H3'	26:14:2801:A:H4'	1.98	0.45
27:1J:2:C:H2'	27:1J:3:C:C6	2.48	0.45
29:29:3:GLY:HA3	29:29:81:ILE:HG21	1.98	0.45
30:39:7:TYR:HA	30:39:125:LEU:HB3	1.98	0.45
30:39:11:VAL:HG23	30:39:13:SER:HB2	1.98	0.45
32:59:30:LYS:HD3	32:59:80:SER:HA	1.97	0.45
39:65:87:PHE:CZ	39:65:102:ALA:HB2	2.50	0.45
43:A5:19:LEU:HB3	52:J5:25:LEU:HD11	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:F5:90:ILE:C	48:F5:91:LYS:O	2.59	0.45
48:F5:91:LYS:HG3	48:F5:92:LYS:H	1.81	0.45
1:13:722:A:O3'	1:13:723:U:C6	2.70	0.45
15:6I:24:SER:OG	15:6I:26:GLU:HG2	2.17	0.45
22:1K:37:AET:HM62	22:1K:38:A:N6	2.31	0.45
26:1H:1110:G:HO2'	26:1H:1111:A:H8	1.61	0.45
26:1H:1182:A:H2'	26:1H:1183:G:O4'	2.17	0.45
26:1H:1301:A:H2	26:1H:1626:G:N3	2.15	0.45
27:16:21:G:H1	27:16:62:C:H42	1.64	0.45
33:61:134:PRO:HA	33:61:135:GLU:HG3	1.99	0.45
34:58:47:ALA:HB2	34:58:112:LEU:CD1	2.42	0.45
37:88:66:ILE:HD12	37:88:67:ARG:N	2.30	0.45
38:98:22:ARG:HG2	38:98:69:ASP:HB3	1.97	0.45
1:1G:485:G:HO2'	1:1G:486:U:P	2.39	0.45
1:1G:1291:G:P	7:62:37:ASN:HD21	2.39	0.45
1:1G:1347:G:N2	1:1G:1373:G:H2'	2.32	0.45
2:12:74:LYS:HD3	2:12:76:GLN:HG3	1.99	0.45
3:22:120:VAL:HG21	3:22:137:ALA:HB2	1.98	0.45
4:32:85:LYS:HD2	4:32:89:THR:N	2.31	0.45
7:62:115:ARG:O	7:62:118:VAL:HG22	2.16	0.45
16:7A:45:THR:O	16:7A:48:TRP:HD1	1.98	0.45
19:AA:58:VAL:O	19:AA:60:VAL:HG22	2.16	0.45
55:3L:14:A:H2'	55:3L:14:A:N3	2.32	0.45
26:14:729:G:O5'	28:19:208:LYS:NZ	2.46	0.45
26:14:1239:G:H2'	26:14:1240:U:O4'	2.15	0.45
26:14:2056:G:C2	26:14:2057:A:C8	3.04	0.45
26:14:2331:G:O2'	47:E5:43:THR:HG22	2.17	0.45
31:49:111:LEU:HB3	31:49:117:PHE:CZ	2.52	0.45
32:59:98:LEU:HD22	32:59:126:PRO:HB3	1.98	0.45
39:65:7:TYR:CZ	39:65:91:PRO:HG3	2.51	0.45
42:95:37:VAL:HB	42:95:56:SER:HA	1.98	0.45
45:C5:17:SER:HB2	45:C5:71:LYS:HZ3	1.81	0.45
1:13:660:G:OP1	15:6I:5:LYS:HD3	2.16	0.45
1:13:859:A:H2'	1:13:860:A:O4'	2.15	0.45
1:13:1020:U:H2'	1:13:1021:G:H8	1.80	0.45
1:13:1460:A:H2'	1:13:1461:G:O4'	2.16	0.45
14:5I:32:SER:HB3	14:5I:41:ARG:HG2	1.99	0.45
18:9I:40:LEU:HD23	18:9I:40:LEU:HA	1.79	0.45
22:1K:37:AET:N1	22:1K:37:AET:N11	2.52	0.45
26:1H:323:G:HO2'	26:1H:1205:U:H3	1.62	0.45
26:1H:444:C:C4'	30:31:49:ALA:HB2	2.45	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1H:1059:G:O6	26:1H:1088:A:H8	1.99	0.45
26:1H:1140:C:OP1	34:58:23:LEU:HB3	2.17	0.45
26:1H:1141:U:H4'	26:1H:1142(A):A:O4'	2.17	0.45
26:1H:1283:G:N2	26:1H:1286:A:OP2	2.47	0.45
26:1H:2186:G:H2'	26:1H:2187:G:C8	2.52	0.45
26:1H:2309:A:N6	26:1H:2310:A:H62	2.15	0.45
26:1H:2331:G:O3'	47:I8:43:THR:HG22	2.17	0.45
29:21:55:ASN:HB3	29:21:58:ARG:H	1.80	0.45
31:41:107:LEU:HD21	31:41:178:PHE:CD1	2.51	0.45
39:A8:77:ALA:HA	39:A8:80:LEU:HD12	1.98	0.45
49:K8:17:SER:HB3	49:K8:67:LYS:HD3	1.98	0.45
54:Q8:26:LYS:HB2	54:Q8:44:LYS:O	2.16	0.45
1:1G:1003:G:H2'	1:1G:1004:A:H5'	1.99	0.45
1:1G:1239:A:H4'	1:1G:1240:U:C5'	2.47	0.45
3:22:51:GLY:O	3:22:70:VAL:HG13	2.16	0.45
5:42:76:ILE:HG12	5:42:118:ILE:HG13	1.97	0.45
8:72:97:VAL:HA	8:72:100:ILE:HG13	1.98	0.45
15:6A:39:LEU:CD1	15:6A:56:LEU:HB2	2.46	0.45
26:14:1496:A:C8	26:14:1577:C:O2'	2.69	0.45
26:14:2232:U:P	48:F5:40:ARG:NH2	2.89	0.45
26:14:2859:G:C8	26:14:2859:G:H3'	2.52	0.45
28:19:16:MET:HE2	28:19:208:LYS:HG2	1.99	0.45
32:59:132:ARG:O	32:59:133:VAL:HG23	2.17	0.45
39:65:21:THR:HG23	39:65:23:ARG:HG3	1.98	0.45
39:65:86:ALA:O	39:65:87:PHE:HB2	2.17	0.45
42:95:69:LYS:HA	42:95:88:ARG:HG2	1.98	0.45
49:G5:13:ALA:O	49:G5:16:LEU:HB2	2.17	0.45
49:G5:60:LEU:HD12	49:G5:60:LEU:HA	1.79	0.45
54:M5:23:VAL:HG23	54:M5:49:VAL:HG12	1.97	0.45
1:13:177:C:H2'	1:13:178:C:C6	2.51	0.45
1:13:538:G:P	12:3I:115:LYS:HB2	2.57	0.45
1:13:1262:C:H2'	1:13:1263:C:H6	1.79	0.45
1:13:1292:U:H2'	1:13:1293:G:H8	1.79	0.45
2:1E:60:ASP:OD1	2:1E:64:ARG:NH2	2.36	0.45
3:2E:79:ARG:O	3:2E:82:GLU:HG2	2.16	0.45
7:6E:56:GLN:CD	7:6E:57:GLU:H	2.24	0.45
9:8E:40:LEU:HD23	9:8E:74:ILE:HD11	1.99	0.45
10:1I:60:ARG:HE	10:1I:60:ARG:HB3	1.61	0.45
26:1H:533:G:H5'	41:C8:24:TYR:CD1	2.51	0.45
26:1H:795:C:H2'	26:1H:796:C:H6	1.81	0.45
26:1H:1771:C:H1'	26:1H:1786:A:C8	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1H:2392:A:H2	26:1H:2424:C:N4	2.08	0.45
29:21:4:ILE:HD13	29:21:28:ALA:HB1	1.98	0.45
30:31:32:LEU:HD13	30:31:105:VAL:CG1	2.47	0.45
31:41:51:ARG:HA	31:41:54:GLU:HG3	1.99	0.45
45:G8:6:HIS:HE1	45:G8:69:ALA:O	2.00	0.45
45:G8:94:LYS:NZ	45:G8:95:LYS:H	2.13	0.45
46:H8:76:LEU:HD23	46:H8:76:LEU:H	1.82	0.45
1:1G:390:C:H2'	1:1G:391:G:C8	2.51	0.45
1:1G:975:A:H5'	1:1G:975:A:H8	1.81	0.45
1:1G:989:C:H2'	1:1G:990:C:C6	2.52	0.45
1:1G:1435:G:H2'	1:1G:1436:U:C5	2.51	0.45
1:1G:1446:A:OP1	1:1G:1446:A:H4'	2.15	0.45
4:32:119:GLN:HE21	4:32:119:GLN:HB2	1.41	0.45
7:62:144:MET:HB2	7:62:146:GLU:OE1	2.17	0.45
16:7A:43:LYS:HG2	16:7A:48:TRP:CE2	2.51	0.45
26:14:38:A:H2'	26:14:39:C:C6	2.51	0.45
26:14:125:G:H5"	53:L5:19:ARG:HD3	1.98	0.45
26:14:194:G:H2'	26:14:195:A:O4'	2.16	0.45
26:14:631:A:N3	26:14:2415:G:O2'	2.40	0.45
26:14:673:C:H4'	30:39:82:ILE:HG12	1.99	0.45
26:14:674:G:O2'	30:39:74:ARG:HD2	2.16	0.45
26:14:960:A:C8	26:14:962:G:C8	3.05	0.45
26:14:1204:A:N1	26:14:1241:A:C2	2.81	0.45
26:14:2062:A:H2'	26:14:2063:C:O5'	2.17	0.45
26:14:2342:C:O2	26:14:2374:C:H4'	2.16	0.45
26:14:2467:C:H4'	37:45:123:HIS:ND1	2.32	0.45
27:1J:8:U:O3'	39:65:25:ARG:NH2	2.39	0.45
28:19:166:GLN:HB3	28:19:174:ILE:HG22	1.98	0.45
29:29:76:ARG:HD3	29:29:77:ILE:N	2.31	0.45
30:39:7:TYR:CE2	30:39:10:PRO:HD3	2.52	0.45
32:59:167:GLU:HG2	32:59:169:VAL:HG23	1.98	0.45
33:69:71:ILE:HG22	33:69:72:LEU:HD23	1.99	0.45
35:25:22:ILE:HB	35:25:41:ALA:HA	1.99	0.45
36:35:29:LYS:CG	36:35:30:THR:N	2.78	0.45
37:45:19:GLY:O	37:45:99:PRO:HD2	2.16	0.45
48:F5:84:GLY:CA	48:F5:85:LEU:HB3	2.46	0.45
1:13:403:C:O3'	4:3E:122:ARG:HD2	2.16	0.45
1:13:591:U:C2	1:13:592:G:C8	3.04	0.45
1:13:1160:G:C6	1:13:1181:G:O6	2.70	0.45
2:1E:16:HIS:CE1	2:1E:210:SER:O	2.70	0.45
2:1E:192:SER:OG	2:1E:193:ASP:N	2.48	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:4I:7:VAL:O	13:4I:8:GLU:C	2.58	0.45
13:4I:15:VAL:HB	13:4I:41:PRO:O	2.16	0.45
14:5I:29:ARG:NH1	14:5I:31:ARG:HB2	2.32	0.45
17:8I:41:LYS:HZ3	17:8I:92:ARG:HH12	1.64	0.45
26:1H:775:G:C5	26:1H:794:G:C8	3.05	0.45
26:1H:1062:G:H1'	26:1H:1088:A:C5	2.52	0.45
26:1H:1798:U:H5'	28:11:259:THR:OG1	2.15	0.45
26:1H:2025:C:N4	59:1H:3977:HOH:O	2.48	0.45
26:1H:2068:U:N3	26:1H:2430:A:H2	2.14	0.45
29:21:28:ALA:O	29:21:93:VAL:HG22	2.15	0.45
31:41:91:ARG:HD2	31:41:91:ARG:C	2.42	0.45
33:61:10:GLU:O	33:61:11:ASN:HB2	2.17	0.45
38:98:48:VAL:O	38:98:49:ASP:C	2.59	0.45
39:A8:88:ASP:OD1	39:A8:90:GLY:N	2.43	0.45
40:B8:7:ILE:O	40:B8:11:GLU:HB2	2.16	0.45
45:G8:53:PRO:HA	45:G8:56:PRO:HB3	1.98	0.45
51:M8:9:LEU:HD12	51:M8:27:THR:N	2.32	0.45
1:1G:5:U:HO2'	1:1G:6:G:P	2.36	0.45
1:1G:457:C:H2'	1:1G:458:C:H6	1.80	0.45
1:1G:1281:U:H3'	1:1G:1282:C:C5	2.52	0.45
2:12:54:THR:HG23	2:12:57:PHE:HB2	1.99	0.45
3:22:47:LEU:HD12	3:22:52:LEU:HB3	1.99	0.45
9:82:97:LYS:HB3	9:82:98:PRO:HD3	1.98	0.45
9:82:110:GLU:HG3	9:82:111:ARG:N	2.32	0.45
22:1L:37:AET:N1	22:1L:37:AET:N11	2.65	0.45
22:1L:68:U:H2'	22:1L:69:C:C5	2.51	0.45
26:14:1005:C:H2'	26:14:1006:C:C6	2.52	0.45
26:14:1870:C:H2'	26:14:1871:A:C8	2.52	0.45
26:14:2074:U:H2'	26:14:2075:U:C6	2.52	0.45
26:14:2680:C:H5'	29:29:189:PRO:HA	1.98	0.45
32:59:6:ARG:HH11	32:59:66:GLY:HA3	1.81	0.45
32:59:18:GLU:HB2	32:59:25:LYS:HE3	1.98	0.45
32:59:163:TYR:HD1	32:59:167:GLU:CD	2.25	0.45
34:15:23:LEU:HD12	34:15:99:LEU:HD23	1.98	0.45
38:55:26:LYS:HE2	38:55:70:LEU:O	2.16	0.45
1:13:405:U:O2'	1:13:497:U:H5'	2.17	0.45
5:4E:68:GLU:O	5:4E:70:PRO:HD3	2.17	0.45
9:8E:112:LYS:CA	9:8E:119:ALA:HB2	2.47	0.45
10:1I:34:VAL:HG12	10:1I:74:ILE:HG12	1.99	0.45
11:2I:32:ILE:H	11:2I:32:ILE:HG12	1.61	0.45
15:6I:18:PHE:CZ	15:6I:21:ASP:HB2	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:1K:66:U:H3'	22:1K:67:A:H5'	1.98	0.45
26:1H:1424:G:H2'	26:1H:1425:G:O4'	2.17	0.45
26:1H:1590:U:H2'	26:1H:1591:G:H8	1.81	0.45
26:1H:2275:C:O2'	37:88:85:LYS:HA	2.17	0.45
29:21:24:THR:HG21	29:21:188:VAL:CG2	2.45	0.45
31:41:83:ARG:N	31:41:86:MET:HE2	2.32	0.45
37:88:28:ALA:N	37:88:105:GLU:OE2	2.45	0.45
37:88:54:MET:O	37:88:57:HIS:N	2.47	0.45
48:J8:56:GLN:HE21	48:J8:85:LEU:HG	1.82	0.45
1:1G:281:G:H8	1:1G:281:G:OP2	1.99	0.45
1:1G:376:G:O3'	16:7A:5:ARG:HD2	2.16	0.45
1:1G:539:A:H2'	1:1G:540:G:C8	2.51	0.45
1:1G:587:G:N1	1:1G:754:C:OP2	2.49	0.45
2:12:21:ARG:HA	2:12:39:ILE:HA	1.98	0.45
2:12:28:PHE:CZ	2:12:189:ASP:HA	2.52	0.45
4:32:86:LYS:HB2	4:32:86:LYS:HE3	1.47	0.45
12:3A:40:VAL:HG11	12:3A:77:LEU:O	2.17	0.45
13:4A:40:ASN:OD1	13:4A:41:PRO:HD2	2.17	0.45
55:3L:54:5MU:O2'	55:3L:55:PSU:P	2.75	0.45
26:14:196:A:OP2	36:35:46:LYS:NZ	2.50	0.45
26:14:303:U:H2'	26:14:304:G:C8	2.52	0.45
26:14:522:G:H2'	26:14:523:C:C6	2.51	0.45
26:14:631:A:H61	26:14:2402:C:N4	2.14	0.45
26:14:1011:G:C4	26:14:1151:G:N2	2.84	0.45
26:14:1465:G:C4	26:14:1466:G:C8	3.04	0.45
26:14:2823:A:OP1	29:29:113:PHE:HB2	2.17	0.45
28:19:12:SER:O	28:19:16:MET:HE3	2.17	0.45
29:29:76:ARG:NE	29:29:76:ARG:HA	2.24	0.45
30:39:34:TRP:CZ3	36:35:8:PRO:HB3	2.51	0.45
34:15:99:LEU:O	34:15:103:VAL:HG23	2.16	0.45
36:35:29:LYS:HG2	36:35:30:THR:H	1.77	0.45
43:A5:69:LEU:HA	43:A5:108:GLY:O	2.16	0.45
48:F5:39:LYS:HE2	48:F5:39:LYS:HB3	1.71	0.45
52:J5:25:LEU:H	52:J5:25:LEU:HD12	1.80	0.45
1:13:624:C:O3'	16:7I:10:GLY:HA2	2.16	0.45
1:13:939:G:C2	1:13:940:C:C2	3.05	0.45
1:13:942:G:C2	1:13:1342:C:C2	3.05	0.45
1:13:1125:U:C5	1:13:1127:G:C6	3.05	0.45
1:13:1134:G:C2	1:13:1135:U:H1'	2.52	0.45
1:13:1291:G:H4'	9:8E:39:GLY:HA3	1.98	0.45
1:13:1352:C:N4	59:13:1991:HOH:O	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1E:97:TRP:CZ3	2:1E:172:ILE:HB	2.52	0.45
3:2E:62:ASP:OD1	3:2E:97:LYS:HB3	2.17	0.45
3:2E:182:ILE:HA	3:2E:202:ILE:O	2.17	0.45
8:7E:39:LEU:HB3	8:7E:45:ILE:HG12	1.99	0.45
10:1I:50:ILE:CG1	10:1I:60:ARG:HH21	2.30	0.45
12:3I:8:ASN:O	12:3I:12:ARG:HG3	2.16	0.45
16:7I:26:ARG:HE	16:7I:31:LYS:HB3	1.81	0.45
19:AI:31:ILE:HB	19:AI:49:ILE:HG23	1.98	0.45
26:1H:53:A:H2'	26:1H:54:G:O4'	2.17	0.45
26:1H:484:C:OP1	45:G8:51:VAL:HG22	2.17	0.45
26:1H:795:C:H2'	26:1H:796:C:C6	2.52	0.45
26:1H:994:C:OP2	41:C8:54:LYS:NZ	2.50	0.45
26:1H:1329:U:H5"	26:1H:1330:C:C5	2.50	0.45
26:1H:2378:A:O2'	39:A8:21:THR:HG21	2.17	0.45
29:21:57:LYS:HG3	29:21:59:VAL:CG1	2.46	0.45
37:88:66:ILE:HD12	37:88:67:ARG:H	1.81	0.45
39:A8:27:SER:HA	39:A8:88:ASP:HB2	1.98	0.45
52:N8:16:ARG:HG3	52:N8:17:ASP:N	2.31	0.45
1:1G:1178:G:H5"	9:82:93:ARG:NH2	2.31	0.45
2:12:220:ASP:H	2:12:222:ILE:CD1	2.30	0.45
7:62:126:ASP:HB3	7:62:131:LYS:O	2.16	0.45
7:62:141:VAL:C	7:62:143:ARG:H	2.25	0.45
19:AA:17:GLU:O	19:AA:20:LEU:N	2.46	0.45
23:2L:51:U:H2'	23:2L:52:C:C6	2.51	0.45
55:3L:3:U:H2'	55:3L:4:G:O4'	2.17	0.45
26:14:181:A:H1'	26:14:435:C:H5'	1.98	0.45
26:14:923:C:H2'	26:14:924:C:C6	2.52	0.45
26:14:1133:U:O2	26:14:1137:G:H5"	2.16	0.45
26:14:1443:G:O6	59:14:3567:HOH:O	2.21	0.45
26:14:2532:G:O5'	26:14:2532:G:H8	1.99	0.45
29:29:9:VAL:HG23	29:29:26:ILE:O	2.16	0.45
30:39:20:LEU:HB3	30:39:203:GLN:HE22	1.82	0.45
31:49:29:TRP:C	31:49:31:VAL:N	2.74	0.45
31:49:106:LEU:HG	31:49:111:LEU:CD1	2.47	0.45
34:15:37:LYS:HG3	34:15:42:TRP:CE3	2.52	0.45
37:45:30:GLY:HA2	37:45:107:ALA:HB2	1.99	0.45
37:45:43:THR:HG22	37:45:94:VAL:HG12	1.99	0.45
43:A5:71:VAL:HA	43:A5:107:LEU:HD12	1.99	0.45
49:G5:43:GLN:CG	49:G5:46:GLN:HE22	2.28	0.45
50:H5:7:LYS:O	50:H5:54:VAL:HG23	2.17	0.45
1:13:75:C:H42	1:13:96:G:H1	1.65	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:13:454:C:H3'	1:13:455:C:C6	2.52	0.45
1:13:976:G:OP1	14:5I:32:SER:N	2.46	0.45
1:13:1014:A:C2	1:13:1219:U:H1'	2.53	0.45
7:6E:56:GLN:NE2	7:6E:56:GLN:HA	2.31	0.45
20:BI:60:GLU:OE2	20:BI:85:MET:HE2	2.17	0.45
26:1H:445:C:O2'	26:1H:446:G:H5'	2.17	0.45
26:1H:1058:U:H2'	26:1H:1059:G:C8	2.48	0.45
26:1H:1095:A:H2'	26:1H:1095:A:N3	2.32	0.45
26:1H:1264:G:H5'	52:N8:11:THR:HG21	1.99	0.45
26:1H:1359:A:N6	26:1H:1372:U:H3	2.13	0.45
26:1H:1386:C:OP2	26:1H:1396:U:H5	2.00	0.45
30:31:172:TRP:CD1	30:31:172:TRP:H	2.35	0.45
34:58:46:VAL:O	34:58:47:ALA:HB3	2.17	0.45
39:A8:106:ARG:O	39:A8:107:GLU:HB2	2.17	0.45
40:B8:94:ALA:HB1	40:B8:99:LEU:HD21	1.98	0.45
1:1G:157:G:H1	1:1G:164:U:H3	1.64	0.45
1:1G:254:G:OP1	17:8A:67:LYS:O	2.35	0.45
1:1G:1118:C:OP1	9:82:104:ARG:NE	2.40	0.45
1:1G:1157:A:H1'	1:1G:1158:C:OP2	2.17	0.45
1:1G:1278:U:H5'	1:1G:1279:A:C5'	2.47	0.45
1:1G:1359:C:H4'	1:1G:1360:A:OP2	2.16	0.45
3:22:70:VAL:HG12	3:22:71:ALA:N	2.31	0.45
10:1A:78:ASN:HD22	10:1A:80:LYS:HB3	1.82	0.45
22:1L:52:A:N6	22:1L:62:U:H3	2.08	0.45
23:2L:6:G:C2'	23:2L:7:G:H5"	2.47	0.45
26:14:161:U:H5"	26:14:171:G:N2	2.25	0.45
26:14:861:A:N3	27:1J:79:C:O2'	2.50	0.45
26:14:1528:A:C2	26:14:1542:G:C2	3.05	0.45
26:14:2414:G:N2	36:35:67:MET:HE1	2.12	0.45
26:14:2646:C:H2'	26:14:2647:U:O4'	2.17	0.45
26:14:2688:U:C5	26:14:2720:U:OP2	2.69	0.45
29:29:128:SER:OG	29:29:129:HIS:N	2.49	0.45
31:49:29:TRP:C	31:49:31:VAL:H	2.24	0.45
32:59:17:VAL:HG13	32:59:50:VAL:HG12	1.99	0.45
36:35:83:VAL:HG11	36:35:100:LEU:HD23	1.99	0.45
36:35:85:LEU:HA	36:35:88:LEU:HD22	1.99	0.45
37:45:57:HIS:CG	37:45:117:ALA:HB2	2.52	0.45
39:65:80:LEU:HD23	39:65:80:LEU:HA	1.74	0.45
41:85:53:ARG:HA	41:85:56:ASP:HB2	1.99	0.45
41:85:106:PHE:HA	41:85:109:LEU:HD12	1.98	0.45
44:B5:21:PHE:CZ	44:B5:92:LEU:HD23	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:D5:118:GLN:OE1	46:D5:118:GLN:HA	2.17	0.45
54:M5:14:VAL:HG11	54:M5:22:VAL:HG13	1.99	0.45
1:13:113:G:H2'	1:13:114:U:H6	1.82	0.44
1:13:192:U:O4'	20:BI:103:GLY:HA2	2.17	0.44
1:13:540:G:H2'	1:13:541:G:O4'	2.16	0.44
1:13:604:G:H2'	1:13:605:U:O4'	2.17	0.44
8:7E:109:ILE:HG13	8:7E:120:THR:HB	1.98	0.44
11:2I:55:LYS:HG2	11:2I:55:LYS:O	2.17	0.44
13:4I:93:ARG:CZ	26:1H:889:C:H3'	2.48	0.44
14:5I:13:THR:N	14:5I:14:PRO:HD2	2.32	0.44
18:9I:32:ARG:NH1	18:9I:65:ILE:HD12	2.32	0.44
20:BI:56:MET:HG3	20:BI:88:VAL:HG21	1.98	0.44
26:1H:26:G:C6	26:1H:27:G:N1	2.84	0.44
26:1H:483:A:C8	26:1H:484:C:C5	3.05	0.44
28:11:2:ALA:O	28:11:20:ASP:HB2	2.17	0.44
29:21:105:THR:HG21	29:21:164:ARG:CZ	2.47	0.44
30:31:185:ASP:OD1	30:31:188:ARG:NH1	2.44	0.44
31:41:18:GLU:O	31:41:22:ARG:HB2	2.17	0.44
37:88:134:ARG:HH12	46:H8:122:ARG:CD	2.30	0.44
44:F8:11:PRO:HG2	44:F8:13:LEU:HD21	2.00	0.44
46:H8:165:VAL:HB	46:H8:167:PRO:HD3	2.00	0.44
1:1G:87:A:C6	1:1G:88:C:N3	2.85	0.44
1:1G:458:C:H2'	1:1G:464:G:C8	2.52	0.44
1:1G:603:U:H2'	1:1G:604:G:C8	2.52	0.44
1:1G:1324:A:H2'	1:1G:1325:C:C6	2.53	0.44
2:12:128:GLU:O	2:12:130:ARG:HB2	2.18	0.44
2:12:164:VAL:HB	2:12:186:ALA:HB2	1.98	0.44
8:72:29:SER:HB3	8:72:32:LYS:CG	2.45	0.44
13:4A:35:GLU:HG3	13:4A:36:LYS:H	1.82	0.44
17:8A:5:VAL:HA	17:8A:59:ILE:O	2.17	0.44
17:8A:45:HIS:ND1	17:8A:65:ILE:HG21	2.31	0.44
19:AA:3:ARG:HH11	19:AA:7:LYS:HZ3	1.64	0.44
26:14:273(C):C:H5'	26:14:273(D):C:OP2	2.16	0.44
26:14:868:U:C4	26:14:869:G:N7	2.86	0.44
26:14:996:A:O4'	41:85:92:ARG:NH2	2.50	0.44
26:14:1464:C:HO2'	26:14:1528:A:H8	1.56	0.44
26:14:2127:G:H2'	26:14:2128:C:C6	2.52	0.44
26:14:2262:U:H4'	26:14:2328:A:C2	2.52	0.44
26:14:2333:A:H5'	26:14:2333:A:H8	1.82	0.44
26:14:2360:A:H2'	26:14:2361:A:O4'	2.17	0.44
26:14:2416:C:O5'	26:14:2416:C:H6	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:14:2516:G:C6	26:14:2517:C:N4	2.84	0.44
26:14:2688:U:H1'	26:14:2721:A:N6	2.32	0.44
27:1J:116:G:H4'	39:65:54:LEU:HD23	1.99	0.44
31:49:37:VAL:HG23	31:49:99:MET:HE3	1.99	0.44
31:49:145:THR:O	31:49:146:TYR:HB3	2.17	0.44
32:59:46:GLU:CD	32:59:51:ARG:HH12	2.23	0.44
35:25:9:GLU:O	35:25:83:ALA:HA	2.17	0.44
46:D5:63:ASP:OD1	46:D5:65:GLN:HG3	2.17	0.44
1:13:131:C:O2	1:13:131:C:H2'	2.16	0.44
1:13:198:G:H2'	1:13:199:G:H8	1.81	0.44
2:1E:139:LYS:O	2:1E:142:LEU:HB3	2.18	0.44
2:1E:187:LEU:HA	2:1E:201:ILE:O	2.17	0.44
3:2E:134:ILE:HG22	3:2E:168:ALA:HB3	1.99	0.44
12:3I:69:TYR:CG	12:3I:90:VAL:HG21	2.52	0.44
13:4I:10:PRO:HB2	13:4I:18:ALA:HB1	1.99	0.44
14:5I:12:ARG:C	14:5I:14:PRO:HD2	2.42	0.44
15:6I:7:GLU:O	15:6I:11:VAL:HG23	2.17	0.44
26:1H:1142(A):A:C4	26:1H:1144:G:C8	3.05	0.44
26:1H:1210:A:H5"	26:1H:1212:G:H5'	1.99	0.44
26:1H:1216:G:OP2	41:C8:12:ARG:NH2	2.36	0.44
26:1H:1263:U:O2'	52:N8:11:THR:HG23	2.17	0.44
26:1H:2711:A:P	59:1H:3803:HOH:O	2.75	0.44
28:11:17:THR:CG2	28:11:204:ILE:HA	2.44	0.44
29:21:50:GLY:HA2	29:21:75:VAL:HG11	1.98	0.44
29:21:64:LYS:HA	29:21:65:GLY:HA2	1.57	0.44
30:31:24:LEU:HA	30:31:25:PRO:HD2	1.84	0.44
31:41:170:ARG:HE	31:41:174:GLU:HG2	1.82	0.44
32:51:56:SER:HB3	32:51:61:HIS:ND1	2.32	0.44
33:61:123:LEU:HD23	33:61:143:SER:HA	2.00	0.44
34:58:38:HIS:O	41:C8:67:ALA:HB1	2.17	0.44
35:68:76:ALA:HB3	40:B8:75:ILE:HD12	1.99	0.44
41:C8:90:VAL:O	41:C8:92:ARG:N	2.50	0.44
51:M8:14:ILE:HG22	51:M8:24:THR:CG2	2.43	0.44
1:1G:160:A:H2'	1:1G:161:A:O4'	2.17	0.44
1:1G:927:G:OP2	1:1G:1503:A:H8	1.99	0.44
1:1G:1121:U:H2'	1:1G:1122:U:C6	2.52	0.44
1:1G:1297:C:OP1	13:4A:13:LYS:HE3	2.17	0.44
4:32:104:VAL:O	4:32:108:LEU:HB2	2.17	0.44
4:32:155:LEU:HD23	4:32:155:LEU:HA	1.69	0.44
13:4A:81:LEU:HA	13:4A:81:LEU:HD13	1.57	0.44
16:7A:20:VAL:HG11	16:7A:32:TYR:CD2	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:3L:26:G:H2'	55:3L:27:C:H5'	1.99	0.44
26:14:972:G:OP2	26:14:973:A:O2'	2.25	0.44
26:14:2023:G:OP2	26:14:2617:C:H4'	2.18	0.44
26:14:2432:A:C2	48:F5:35:THR:HG22	2.53	0.44
26:14:2648:C:H2'	26:14:2649:U:C6	2.52	0.44
26:14:2873:A:O4'	38:55:6:SER:HB2	2.17	0.44
27:1J:37:C:H2'	27:1J:38:C:H5'	2.00	0.44
34:15:126:PRO:HB2	34:15:127:ASP:H	1.60	0.44
41:85:88:ILE:HG23	41:85:90:VAL:CB	2.46	0.44
1:13:76:G:N3	1:13:76:G:H2'	2.32	0.44
1:13:157:G:H2'	1:13:158:G:H8	1.82	0.44
1:13:580:U:H2'	1:13:581:G:O4'	2.18	0.44
1:13:901:A:C5	1:13:902:G:H1'	2.52	0.44
1:13:1125:U:H5	1:13:1127:G:C6	2.35	0.44
1:13:1129:C:O2'	1:13:1130:A:O5'	2.35	0.44
1:13:1389:C:H2'	1:13:1390:U:O4'	2.17	0.44
4:3E:63:LYS:O	4:3E:67:ILE:HG13	2.18	0.44
15:6I:67:LEU:O	15:6I:71:GLN:HB2	2.17	0.44
26:1H:455:C:N3	26:1H:472:A:H2'	2.32	0.44
26:1H:459:U:H2'	26:1H:460:A:H8	1.83	0.44
26:1H:754:C:H2'	26:1H:755:C:H6	1.82	0.44
26:1H:1093:G:H1'	26:1H:1099:G:H22	1.82	0.44
26:1H:1158:C:H4'	50:L8:32:GLN:HB2	1.99	0.44
26:1H:2114:A:H2'	26:1H:2114:A:N3	2.32	0.44
26:1H:2124:G:O6	26:1H:2173:A:N6	2.51	0.44
26:1H:2756:U:H4'	26:1H:2757:A:OP1	2.18	0.44
30:31:37:VAL:HG21	36:78:6:LEU:HD21	1.99	0.44
32:51:157:TYR:O	32:51:158:HIS:ND1	2.51	0.44
37:88:5:ARG:O	37:88:6:ARG:C	2.59	0.44
47:I8:70:GLN:HB2	47:I8:80:HIS:HE2	1.82	0.44
51:M8:60:GLN:H	51:M8:60:GLN:HG2	1.48	0.44
1:1G:407:G:O2'	4:32:116:GLN:HG3	2.17	0.44
1:1G:420:U:O2'	1:1G:423:G:O6	2.22	0.44
1:1G:979:C:H5"	1:1G:980:C:OP2	2.16	0.44
1:1G:1357:A:C8	1:1G:1358:U:C6	3.06	0.44
2:12:119:GLU:OE2	2:12:153:ARG:NH1	2.50	0.44
4:32:85:LYS:HB3	4:32:88:VAL:HA	1.99	0.44
11:2A:17:GLY:N	11:2A:79:SER:O	2.37	0.44
18:9A:61:LYS:O	18:9A:65:ILE:HD13	2.17	0.44
26:14:270(I):G:H2'	26:14:270(J):G:C8	2.52	0.44
26:14:1250:G:OP2	36:35:21:ARG:NH1	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:14:2036:C:H5'	26:14:2036:C:H6	1.82	0.44
26:14:2283:C:C2	26:14:2389:G:C2	3.05	0.44
28:19:37:LEU:N	28:19:37:LEU:HD12	2.33	0.44
28:19:108:PRO:HB3	28:19:143:HIS:HE1	1.82	0.44
33:69:109:ILE:HB	33:69:130:TYR:OH	2.17	0.44
35:25:10:VAL:HG12	35:25:19:ILE:HG12	1.98	0.44
1:13:5:U:H5	4:3E:85:LYS:HB3	1.83	0.44
1:13:128:G:H5'	17:8I:2:PRO:O	2.18	0.44
1:13:464:G:O6	1:13:466:C:H4'	2.17	0.44
1:13:875:C:C4	1:13:876:G:N7	2.85	0.44
1:13:1012:U:H2'	1:13:1013:G:C8	2.53	0.44
1:13:1064:G:H1'	1:13:1190:G:N2	2.32	0.44
1:13:1320:C:O2	19:AI:36:ARG:NH2	2.50	0.44
1:13:1342:C:H4'	9:8E:125:TYR:HB3	1.99	0.44
2:1E:97:TRP:HZ3	2:1E:172:ILE:HB	1.82	0.44
9:8E:21:PRO:HA	9:8E:59:PHE:HA	1.99	0.44
9:8E:26:VAL:HA	9:8E:61:ALA:HB3	2.00	0.44
9:8E:99:LEU:HD12	9:8E:101:PHE:CE2	2.51	0.44
16:7I:4:ILE:O	16:7I:66:PRO:HA	2.17	0.44
19:AI:41:VAL:O	51:M8:63:TYR:OH	2.35	0.44
26:1H:270(K):C:H6	26:1H:270(K):C:H3'	1.82	0.44
26:1H:722:A:H2'	26:1H:723:G:H8	1.81	0.44
26:1H:916:G:C2'	26:1H:917:A:H5"	2.47	0.44
26:1H:973:A:OP2	59:1H:3823:HOH:O	2.21	0.44
26:1H:1729:A:C8	26:1H:1731:G:C8	3.05	0.44
26:1H:2311:A:H8	31:41:88:ILE:HG21	1.81	0.44
28:11:33:LEU:O	28:11:64:ILE:HG23	2.17	0.44
31:41:6:ALA:H	51:M8:23:GLU:HG3	1.82	0.44
31:41:120:LEU:HG	31:41:179:PRO:O	2.16	0.44
34:58:74:ARG:NH2	34:58:85:ILE:HD11	2.32	0.44
34:58:90:MET:O	34:58:94:HIS:N	2.43	0.44
41:C8:92:ARG:HH21	42:D8:10:LYS:HB3	1.82	0.44
46:H8:116:VAL:H	46:H8:146:ILE:HG12	1.82	0.44
49:K8:55:ARG:O	49:K8:58:ALA:HB3	2.18	0.44
53:P8:1:MET:HE3	53:P8:1:MET:HB2	1.87	0.44
1:1G:1171:G:H2'	1:1G:1172:C:C6	2.52	0.44
1:1G:1288:A:H4'	21:1B:10:ARG:HH22	1.83	0.44
5:42:149:GLU:C	5:42:151:LEU:H	2.25	0.44
7:62:102:ARG:HG2	7:62:106:GLN:NE2	2.32	0.44
13:4A:31:LYS:HA	13:4A:34:LEU:HB2	1.99	0.44
55:3L:2:C:N4	55:3L:71:G:H1	2.12	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:14:619:G:H5"	26:14:620:G:OP2	2.18	0.44
26:14:1141:U:H2'	34:15:63:THR:HB	1.99	0.44
26:14:2273:A:O2'	26:14:2274:A:H5'	2.18	0.44
26:14:2352:A:H2	47:E5:33:ALA:O	1.99	0.44
31:49:27:ASN:OD1	31:49:28:VAL:N	2.49	0.44
31:49:107:LEU:HD11	31:49:178:PHE:CE1	2.52	0.44
32:59:14:GLY:O	32:59:29:PRO:HD3	2.17	0.44
32:59:40:GLU:HB2	32:59:41:MET:SD	2.57	0.44
33:69:91:SER:HB3	33:69:119:PRO:HB3	1.99	0.44
34:15:42:TRP:CA	34:15:48:MET:HE1	2.48	0.44
34:15:97:ARG:HA	34:15:100:GLU:HB2	1.99	0.44
36:35:46:LYS:HB3	36:35:46:LYS:HE2	1.48	0.44
39:65:62:LYS:H	39:65:62:LYS:HG2	1.51	0.44
39:65:77:ALA:O	39:65:80:LEU:N	2.49	0.44
41:85:19:LYS:O	41:85:22:LYS:HG3	2.17	0.44
46:D5:30:ASN:HA	46:D5:89:PHE:CE1	2.51	0.44
46:D5:157:LEU:CG	46:D5:161:VAL:HG21	2.47	0.44
1:13:1125:U:N3	1:13:1126:U:O4	2.50	0.44
4:3E:116:GLN:NE2	4:3E:157:LEU:HD11	2.31	0.44
6:5E:100:ASN:HB2	18:9I:28:GLU:CG	2.47	0.44
10:1I:54:PHE:CE1	10:1I:55:LYS:HE3	2.52	0.44
14:5I:23:ARG:HG3	14:5I:28:GLY:O	2.17	0.44
26:1H:274:G:H1'	26:1H:276:A:N1	2.33	0.44
26:1H:1662:C:O2'	26:1H:2687:U:OP1	2.34	0.44
26:1H:2109:U:C4	26:1H:2110:G:O6	2.71	0.44
26:1H:2135:A:H5'	26:1H:2160:G:C1'	2.48	0.44
26:1H:2182:G:H2'	26:1H:2183:C:O4'	2.18	0.44
26:1H:2646:C:H2'	26:1H:2647:U:O4'	2.18	0.44
30:31:112:MET:HE3	30:31:112:MET:HB3	1.62	0.44
34:58:95:PRO:C	34:58:96:GLU:O	2.60	0.44
38:98:38:VAL:HB	38:98:39:PRO:HD3	1.99	0.44
40:B8:57:PHE:O	40:B8:58:ASN:CG	2.61	0.44
46:H8:113:ALA:N	46:H8:114:GLY:HA2	2.31	0.44
47:I8:19:LYS:HD3	47:I8:19:LYS:HA	1.72	0.44
1:1G:78:G:H1	1:1G:91:C:H42	1.65	0.44
1:1G:197:A:N1	1:1G:221:C:H4'	2.33	0.44
1:1G:295:C:H2'	1:1G:296:U:O4'	2.18	0.44
1:1G:1197:G:C4	1:1G:1198:G:C8	3.06	0.44
2:12:178:ARG:HD2	2:12:196:LEU:O	2.17	0.44
3:22:137:ALA:O	3:22:141:VAL:HG13	2.18	0.44
10:1A:54:PHE:CE2	10:1A:55:LYS:HB2	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:1A:54:PHE:CG	10:1A:55:LYS:N	2.86	0.44
23:2L:54:G:H2'	23:2L:55:5MU:H6	1.83	0.44
26:14:654(A):A:H8	26:14:654(A):A:O5'	2.00	0.44
26:14:671:C:OP1	36:35:42:SER:O	2.34	0.44
26:14:699:A:H2'	26:14:700:G:O4'	2.17	0.44
26:14:996:A:C2	26:14:997:G:C8	3.05	0.44
26:14:1268:A:H2'	26:14:1269:A:O4'	2.17	0.44
28:19:158:ALA:O	28:19:159:ALA:C	2.61	0.44
47:E5:53:MET:HA	47:E5:58:THR:O	2.18	0.44
1:13:170:U:H2'	1:13:171:A:C8	2.49	0.44
3:2E:167:TRP:CD1	3:2E:168:ALA:N	2.85	0.44
6:5E:27:GLN:HA	6:5E:30:LEU:HB2	1.99	0.44
12:3I:21:LYS:HB3	12:3I:21:LYS:HE2	1.69	0.44
13:4I:8:GLU:O	13:4I:10:PRO:HD3	2.17	0.44
26:1H:1482:U:O4	26:1H:1510:A:H1'	2.17	0.44
26:1H:1727:U:H2'	26:1H:1728:G:O4'	2.18	0.44
31:41:76:SER:HB2	31:41:84:LYS:HB2	1.99	0.44
45:G8:43:ASN:OD1	45:G8:65:ALA:HB3	2.18	0.44
45:G8:63:LYS:HA	45:G8:63:LYS:HD2	1.74	0.44
49:K8:42:GLY:C	49:K8:44:LEU:N	2.73	0.44
1:1G:1023:G:C6	1:1G:1024:G:H1'	2.53	0.44
2:12:167:PRO:O	2:12:171:ALA:N	2.51	0.44
20:BA:62:LEU:HD23	20:BA:62:LEU:HA	1.80	0.44
22:1L:44:A:H2'	22:1L:45:G:O4'	2.17	0.44
22:1L:48:C:O2'	22:1L:49:G:H5'	2.18	0.44
22:1L:59:C:HO2'	22:1L:60:U:P	2.38	0.44
23:2L:17:C:H4'	23:2L:18:U:OP2	2.18	0.44
26:14:1034:G:H8	26:14:1034:G:OP1	2.00	0.44
26:14:1225:C:O2	42:95:85:LYS:HD3	2.18	0.44
26:14:2280:G:H2'	26:14:2281:C:H5'	1.99	0.44
26:14:2339:G:H2'	26:14:2340:G:C8	2.53	0.44
26:14:2849:U:H4'	26:14:2868:A:C2	2.53	0.44
31:49:49:ASP:OD1	31:49:51:ARG:HB3	2.18	0.44
32:59:138:LYS:HA	32:59:141:VAL:HG12	1.99	0.44
35:25:7:TYR:CE1	35:25:20:MET:HB2	2.53	0.44
38:55:83:ILE:N	38:55:85:PRO:HD2	2.33	0.44
48:F5:78:LYS:HG2	48:F5:79:GLY:N	2.33	0.44
49:G5:49:LYS:O	49:G5:53:LEU:HB2	2.16	0.44
1:13:182:U:H5	1:13:183:G:C4	2.35	0.44
1:13:1182:G:H4'	1:13:1183:A:C5'	2.46	0.44
1:13:1260:C:O5'	1:13:1284:C:H4'	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:13:1278:U:H5'	1:13:1279:A:O4'	2.17	0.44
10:1I:16:LEU:HD11	10:1I:70:ARG:HB2	1.99	0.44
11:2I:48:ILE:HD11	11:2I:64:ALA:HA	1.99	0.44
12:3I:110:VAL:CG2	12:3I:120:TYR:HB3	2.48	0.44
13:4I:100:GLY:HA3	59:4I:201:HOH:O	2.16	0.44
17:8I:14:LYS:N	17:8I:14:LYS:HD2	2.33	0.44
26:1H:275:G:N7	26:1H:363:G:C2	2.86	0.44
26:1H:389:G:O5'	26:1H:389:G:H8	2.01	0.44
26:1H:817:C:H4'	26:1H:932:G:C5	2.53	0.44
31:41:13:GLU:O	31:41:14:GLU:HG2	2.18	0.44
42:D8:14:VAL:HG21	42:D8:57:VAL:HG21	1.99	0.44
1:1G:41:G:H2'	1:1G:42:G:H8	1.81	0.44
1:1G:143:A:O3'	1:1G:144:G:H8	2.00	0.44
1:1G:408:A:H2'	1:1G:409:G:O4'	2.17	0.44
1:1G:1328:C:H2'	1:1G:1329:A:O4'	2.17	0.44
2:12:134:GLU:O	2:12:138:LEU:HG	2.17	0.44
2:12:178:ARG:HE	2:12:178:ARG:HB3	1.62	0.44
22:1L:5:A:OP2	22:1L:5:A:H8	2.00	0.44
26:14:747:U:O2	26:14:2014:A:H1'	2.17	0.44
26:14:940:G:H2'	26:14:941:A:O4'	2.18	0.44
26:14:2287:A:O2'	26:14:2288:A:H5"	2.18	0.44
31:49:66:GLN:HB3	31:49:92:VAL:HG21	2.00	0.44
33:69:74:ASN:O	33:69:75:LEU:HB2	2.18	0.44
34:15:50:ASP:O	34:15:52:VAL:HG23	2.16	0.44
34:15:59:LYS:HE3	34:15:60:ILE:H	1.83	0.44
42:95:98:GLU:OE2	42:95:100:ARG:HG2	2.17	0.44
1:13:272:C:H2'	1:13:273:A:H8	1.83	0.44
1:13:448:A:OP2	1:13:485:G:N1	2.40	0.44
1:13:768:A:H2'	1:13:769:G:O4'	2.18	0.44
8:7E:13:ILE:O	8:7E:17:THR:HG23	2.18	0.44
9:8E:10:ARG:NE	9:8E:105:ASP:OD2	2.44	0.44
15:6I:17:ARG:HG2	15:6I:21:ASP:OD2	2.18	0.44
20:BI:75:ASN:O	20:BI:79:ARG:HB2	2.17	0.44
26:1H:242:G:C8	54:Q8:3:LYS:HE3	2.53	0.44
26:1H:548:A:H2'	26:1H:549:G:H5'	2.00	0.44
26:1H:721:C:H2'	26:1H:722:A:H8	1.82	0.44
26:1H:1199:U:H2'	26:1H:1200:C:C6	2.53	0.44
26:1H:1364:G:N7	48:J8:2:SER:N	2.66	0.44
26:1H:2180:U:H2'	26:1H:2181:G:C8	2.53	0.44
30:31:181:LEU:HD23	30:31:181:LEU:HA	1.85	0.44
36:78:50:ARG:NH2	36:78:50:ARG:HG3	2.33	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:B8:105:LEU:C	40:B8:107:ASP:N	2.74	0.44
40:B8:124:ASP:O	40:B8:128:GLU:HB3	2.18	0.44
49:K8:59:ARG:O	49:K8:63:VAL:HG23	2.18	0.44
51:M8:34:GLU:HG3	51:M8:35:VAL:H	1.83	0.44
1:1G:266:G:H2'	1:1G:266:G:N3	2.32	0.44
1:1G:1118:C:P	9:82:104:ARG:HE	2.40	0.44
1:1G:1358:U:H2'	1:1G:1359:C:H5'	1.99	0.44
1:1G:1359:C:N4	14:5A:21:TYR:HB3	2.32	0.44
1:1G:1478:C:H2'	1:1G:1479:C:C6	2.51	0.44
2:12:19:HIS:NE2	2:12:206:ASP:HB2	2.33	0.44
4:32:62:GLN:O	4:32:66:ARG:HB2	2.17	0.44
12:3A:34:ARG:HH11	12:3A:82:VAL:HG11	1.83	0.44
26:14:82:G:N1	26:14:103:A:OP2	2.46	0.44
26:14:259:G:N2	26:14:621:A:H8	2.08	0.44
26:14:511:U:C5	26:14:512:G:C5	3.05	0.44
26:14:1312:U:H4'	26:14:1313:U:O5'	2.18	0.44
26:14:1486:A:H2'	26:14:1487:G:H8	1.83	0.44
26:14:2181:G:C6	26:14:2182:G:C5	3.06	0.44
26:14:2622:C:H5'	29:29:159:HIS:ND1	2.32	0.44
26:14:2880:C:O2	38:55:93:GLY:N	2.48	0.44
28:19:49:ILE:CD1	28:19:52:ARG:HA	2.48	0.44
30:39:129:PHE:CD1	30:39:163:VAL:HG21	2.52	0.44
36:35:85:LEU:HG	36:35:120:ALA:HA	1.99	0.44
37:45:22:LYS:N	37:45:23:GLY:HA3	2.32	0.44
1:13:1162:C:H2'	1:13:1163:C:H6	1.83	0.44
3:2E:136:GLN:NE2	3:2E:140:ARG:HH11	2.15	0.44
7:6E:46:ALA:HB2	7:6E:117:ALA:HB1	2.00	0.44
15:6I:56:LEU:O	15:6I:60:VAL:HG23	2.17	0.44
24:3K:61:C:H2'	24:3K:62:U:C6	2.53	0.44
26:1H:448:U:H5'	59:1H:3899:HOH:O	2.18	0.44
26:1H:558:G:P	34:58:111:PRO:HD2	2.58	0.44
26:1H:950:G:H2'	26:1H:951:C:C6	2.53	0.44
26:1H:1221:C:H2'	26:1H:1222:C:H6	1.83	0.44
26:1H:1519:G:H2'	26:1H:1520:U:O4'	2.18	0.44
26:1H:2138:C:H2'	26:1H:2139:C:C6	2.52	0.44
26:1H:2615:U:P	59:1H:3780:HOH:O	2.71	0.44
30:31:6:VAL:HG11	30:31:119:ARG:CA	2.48	0.44
31:41:6:ALA:HB2	51:M8:23:GLU:HB2	2.00	0.44
33:61:2:LYS:NZ	33:61:2:LYS:HB3	2.32	0.44
34:58:38:HIS:CE1	34:58:50:ASP:OD2	2.71	0.44
36:78:39:LYS:CG	36:78:45:LEU:HD22	2.43	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:78:63:PRO:HG2	54:Q8:25:MET:HB2	2.00	0.44
39:A8:36:TYR:N	39:A8:36:TYR:CD1	2.86	0.44
41:C8:58:ARG:HA	41:C8:61:TRP:CE3	2.53	0.44
41:C8:79:PHE:CD1	41:C8:79:PHE:C	2.96	0.44
46:H8:69:THR:HA	46:H8:89:PHE:O	2.18	0.44
48:J8:80:LEU:O	48:J8:81:LYS:C	2.60	0.44
53:P8:5:TRP:NE1	53:P8:7:PRO:HG3	2.33	0.44
1:1G:12:U:O2'	1:1G:526:C:H4'	2.18	0.44
1:1G:15:G:H4'	5:42:24:ARG:NH1	2.32	0.44
1:1G:191:G:H1'	20:BA:104:LEU:O	2.18	0.44
1:1G:542:G:P	4:32:10:ARG:HH22	2.39	0.44
2:12:147:LYS:HD2	2:12:148:TYR:CE1	2.53	0.44
5:42:34:VAL:HG21	5:42:63:ARG:HH11	1.83	0.44
17:8A:99:SER:OG	17:8A:100:LYS:N	2.50	0.44
26:14:91:A:C2'	26:14:92:G:H5'	2.48	0.44
26:14:821:A:O2'	26:14:946:G:OP2	2.29	0.44
26:14:971:C:H2'	26:14:972:G:O4'	2.18	0.44
26:14:993:G:O4'	42:95:87:HIS:NE2	2.51	0.44
26:14:1182:A:H2'	26:14:1183:G:O4'	2.18	0.44
26:14:1283:G:N2	26:14:1285:G:H3'	2.32	0.44
26:14:2815:C:H5'	52:J5:29:THR:HG21	1.99	0.44
30:39:36:VAL:HG11	30:39:183:VAL:HG21	2.00	0.44
31:49:33:ARG:O	31:49:161:THR:HG23	2.17	0.44
46:D5:125:LEU:HD23	46:D5:164:ALA:O	2.18	0.44
1:13:74:C:N3	1:13:75:C:C4	2.86	0.43
1:13:247:G:OP2	17:8I:100:LYS:HB3	2.18	0.43
1:13:1164:G:C6	1:13:1165:C:C4	3.06	0.43
2:1E:87:ARG:HH11	2:1E:223:ILE:HD11	1.83	0.43
10:1I:22:LYS:NZ	10:1I:90:LEU:HB2	2.33	0.43
13:4I:108:ARG:N	13:4I:108:ARG:HD2	2.33	0.43
19:AI:41:VAL:HG23	19:AI:42:PRO:HA	2.00	0.43
22:1K:50:G:C2	22:1K:51:C:N4	2.86	0.43
26:1H:275:G:N7	26:1H:363:G:C4	2.86	0.43
26:1H:322:A:OP1	30:31:168:ARG:NH2	2.40	0.43
26:1H:322:A:P	30:31:168:ARG:HH21	2.39	0.43
26:1H:673:C:H5"	30:31:81:PRO:HD2	1.99	0.43
26:1H:991:C:H2'	26:1H:992:C:H6	1.83	0.43
36:78:144:GLU:HA	36:78:145:PRO:HD3	1.85	0.43
37:88:101:ARG:HG3	37:88:102:VAL:N	2.33	0.43
48:J8:92:LYS:HA	48:J8:95:LEU:HD12	2.00	0.43
51:M8:12:ALA:HA	51:M8:29:PRO:HB3	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:P8:8:ASN:OD1	53:P8:8:ASN:C	2.61	0.43
1:1G:7:G:OP1	4:32:209:ARG:NH1	2.43	0.43
1:1G:15:G:H1'	5:42:19:MET:HE3	2.00	0.43
1:1G:814:A:H2'	1:1G:816:A:C5'	2.48	0.43
1:1G:1313:U:H2'	1:1G:1314:C:C6	2.54	0.43
1:1G:1325:C:OP2	21:1B:15:ARG:NH2	2.51	0.43
1:1G:1342:C:H1'	9:82:124:GLN:NE2	2.33	0.43
1:1G:1359:C:C4	14:5A:21:TYR:HB3	2.52	0.43
2:12:193:ASP:HB2	2:12:196:LEU:HD21	1.99	0.43
12:3A:111:LYS:HD3	12:3A:112:ASP:H	1.83	0.43
17:8A:87:LYS:O	17:8A:91:ARG:HG3	2.17	0.43
23:2L:32:G:C5	23:2L:33:OMC:C5	3.06	0.43
26:14:117:G:C6	26:14:119:A:C6	3.06	0.43
26:14:1043:C:H2'	26:14:1044:G:H5'	1.99	0.43
26:14:1475:G:C4	26:14:1519:G:N2	2.86	0.43
26:14:2245:U:O2'	26:14:2436:G:OP2	2.34	0.43
26:14:2472:G:H8	26:14:2472:G:O5'	2.01	0.43
26:14:2758:A:H2'	26:14:2759:G:O4'	2.18	0.43
32:59:53:GLU:OE2	32:59:54:ARG:HG2	2.17	0.43
36:35:2:LYS:HD2	36:35:4:SER:OG	2.17	0.43
38:55:28:LEU:HD23	38:55:28:LEU:HA	1.85	0.43
39:65:43:GLU:HB2	47:E5:49:LYS:HZ3	1.81	0.43
39:65:67:ARG:HG3	39:65:104:GLY:HA3	1.99	0.43
43:A5:13:SER:HB3	43:A5:16:LYS:HD2	1.99	0.43
1:13:445:G:H1	1:13:489:C:H42	1.66	0.43
1:13:586:C:H2'	1:13:587:G:O4'	2.18	0.43
1:13:738:C:OP1	6:5E:2:ARG:NH1	2.51	0.43
1:13:1455:G:H5'	20:BI:32:ALA:HB2	1.99	0.43
7:6E:73:MET:HG3	7:6E:90:GLU:HA	2.00	0.43
9:8E:111:ARG:HG3	9:8E:112:LYS:H	1.83	0.43
26:1H:1185:C:N4	59:1H:3788:HOH:O	2.51	0.43
26:1H:1379:A:H4'	26:1H:1380:G:OP2	2.19	0.43
26:1H:1914:C:H2'	26:1H:1915:U:O4'	2.18	0.43
26:1H:2119:A:N6	26:1H:2170:A:N1	2.67	0.43
29:21:59:VAL:HG22	29:21:60:ASN:N	2.33	0.43
30:31:106:ARG:H	30:31:106:ARG:HG2	1.65	0.43
31:41:11:TYR:O	31:41:15:VAL:HB	2.18	0.43
41:C8:61:TRP:CE2	41:C8:94:ASN:HA	2.52	0.43
1:1G:134:A:H61	16:7A:25:ARG:NH1	2.15	0.43
1:1G:384:G:H2'	1:1G:385:C:C6	2.53	0.43
1:1G:455:C:O5'	1:1G:455:C:H6	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1G:622:A:C8	1:1G:623:C:C6	3.06	0.43
3:22:6:HIS:CD2	3:22:8:ILE:HB	2.53	0.43
4:32:70:ILE:HG23	4:32:75:PHE:HB2	2.00	0.43
4:32:83:SER:C	4:32:85:LYS:H	2.26	0.43
4:32:107:ARG:HH22	4:32:194:LEU:CD2	2.29	0.43
7:62:67:GLU:HA	7:62:70:LYS:HD2	2.00	0.43
26:14:35:G:H1'	26:14:454:A:C4	2.53	0.43
26:14:172:C:H2'	26:14:173:G:C8	2.53	0.43
26:14:241:A:H5'	26:14:243:U:O4'	2.17	0.43
26:14:388:G:O2'	26:14:389:G:N7	2.45	0.43
26:14:1528:A:H2	26:14:1542:G:C2	2.36	0.43
26:14:1569:A:O2'	28:19:37:LEU:HD23	2.17	0.43
26:14:2115:G:C6	26:14:2117:A:C8	3.06	0.43
26:14:2162:G:H2'	26:14:2163:C:H5'	2.00	0.43
26:14:2292:C:H4'	26:14:2375:G:H4'	2.01	0.43
26:14:2820:A:P	38:55:2:ARG:HH12	2.41	0.43
31:49:48:GLU:H	31:49:48:GLU:HG2	1.57	0.43
39:65:38:GLN:HB2	39:65:40:ILE:HD11	2.00	0.43
41:85:92:ARG:O	41:85:94:ASN:N	2.50	0.43
41:85:95:LEU:HD23	41:85:95:LEU:HA	1.85	0.43
47:E5:49:LYS:HD2	47:E5:82:ARG:NH2	2.33	0.43
48:F5:84:GLY:HA3	48:F5:86:SER:H	1.82	0.43
48:F5:86:SER:H	48:F5:87:PRO:HD2	1.83	0.43
1:13:1053:G:O5'	1:13:1054:C:H3'	2.19	0.43
1:13:1148:U:H2'	1:13:1149:C:O4'	2.18	0.43
1:13:1149:C:H2'	1:13:1150:U:C6	2.53	0.43
1:13:1308:U:OP1	13:4I:98:VAL:HG22	2.19	0.43
2:1E:70:PHE:HB2	2:1E:92:TYR:CB	2.48	0.43
24:3K:48:C:O2	24:3K:59:A:H1'	2.18	0.43
26:1H:686:G:H4'	26:1H:687:C:OP2	2.18	0.43
26:1H:1055:G:H1'	26:1H:1085:A:C2	2.53	0.43
26:1H:2401:U:H3'	26:1H:2402:C:H6	1.83	0.43
29:21:68:ALA:HB1	29:21:70:ALA:O	2.17	0.43
33:61:130:TYR:CG	33:61:131:LYS:N	2.86	0.43
35:68:2:ILE:HD11	35:68:82:ASN:HB3	2.00	0.43
36:78:62:LEU:O	54:Q8:13:ARG:HD3	2.18	0.43
37:88:54:MET:HE1	37:88:104:PHE:HB3	1.98	0.43
39:A8:62:LYS:HA	39:A8:65:VAL:HB	2.00	0.43
48:J8:92:LYS:HE3	48:J8:92:LYS:HB3	1.67	0.43
48:J8:94:LEU:N	48:J8:97:LEU:O	2.52	0.43
49:K8:59:ARG:O	49:K8:62:THR:HG23	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1G:109:A:H2'	1:1G:326:G:N2	2.33	0.43
1:1G:797:C:O2'	1:1G:798:G:H5'	2.19	0.43
1:1G:1080:A:OP1	5:42:47:LYS:HE2	2.18	0.43
1:1G:1286:A:H3'	1:1G:1286:A:H8	1.83	0.43
2:12:54:THR:HA	2:12:57:PHE:CG	2.54	0.43
2:12:91:PRO:HG2	2:12:155:LEU:HG	2.00	0.43
2:12:119:GLU:CD	2:12:153:ARG:HH12	2.25	0.43
5:42:103:GLY:O	5:42:104:ALA:C	2.61	0.43
10:1A:13:HIS:CD2	10:1A:13:HIS:C	2.96	0.43
12:3A:62:SER:HB2	12:3A:64:TYR:HD1	1.81	0.43
15:6A:47:LYS:H	15:6A:47:LYS:HG2	1.57	0.43
18:9A:37:VAL:HG11	18:9A:78:LEU:HB3	2.00	0.43
26:14:1006:C:C2	26:14:1138:G:N2	2.85	0.43
26:14:2135:A:C5	26:14:2156:G:N2	2.85	0.43
26:14:2269:A:P	59:14:3550:HOH:O	2.76	0.43
30:39:34:TRP:CE2	36:35:8:PRO:HD3	2.53	0.43
31:49:106:LEU:HD12	31:49:110:ALA:HB3	2.00	0.43
32:59:129:THR:HG22	32:59:130:ARG:H	1.83	0.43
40:75:19:LEU:HD22	40:75:86:ILE:CG2	2.48	0.43
41:85:8:VAL:HB	41:85:12:ARG:HE	1.82	0.43
52:J5:20:ARG:HG2	52:J5:23:HIS:CD2	2.53	0.43
1:13:192:U:H1'	20:BI:103:GLY:HA2	1.99	0.43
1:13:983:A:H3'	1:13:983:A:N3	2.33	0.43
1:13:1074:G:N3	1:13:1102:A:C2	2.86	0.43
1:13:1157:A:O2'	1:13:1158:C:OP2	2.34	0.43
1:13:1228:C:H2'	1:13:1229:A:H8	1.83	0.43
1:13:1234:C:H2'	1:13:1235:U:C6	2.54	0.43
6:5E:100:ASN:HD22	18:9I:28:GLU:HA	1.83	0.43
9:8E:26:VAL:HG13	9:8E:61:ALA:HB3	2.00	0.43
11:2I:32:ILE:HG12	11:2I:41:THR:O	2.18	0.43
17:8I:76:LEU:HD21	17:8I:79:SER:OG	2.17	0.43
22:1K:53:G:O2'	22:1K:54:5MU:H5"	2.18	0.43
26:1H:997:G:OP1	41:C8:93:LYS:HD2	2.18	0.43
26:1H:1114:G:H2'	26:1H:1115:G:H8	1.82	0.43
26:1H:1931:U:H5	26:1H:1969:A:N7	2.16	0.43
26:1H:2111:C:H41	26:1H:2145:C:H2'	1.83	0.43
26:1H:2256:G:H4'	47:I8:9:SER:HB2	2.00	0.43
31:41:45:GLU:H	31:41:45:GLU:HG2	1.38	0.43
34:58:9:VAL:HG21	34:58:39:ARG:NH1	2.31	0.43
39:A8:37:ALA:HB2	39:A8:101:LEU:HD21	1.99	0.43
39:A8:64:GLU:H	39:A8:64:GLU:HG2	1.56	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:F8:25:LYS:HG3	44:F8:82:GLN:OE1	2.18	0.43
45:G8:34:LYS:O	45:G8:34:LYS:HG2	2.18	0.43
46:H8:59:LEU:O	46:H8:60:GLU:HB2	2.18	0.43
48:J8:23:LYS:HB3	48:J8:29:GLY:HA3	1.99	0.43
54:Q8:30:ARG:NH1	59:Q8:201:HOH:O	2.50	0.43
1:1G:926:G:N2	25:4L:15:A:OP2	2.51	0.43
1:1G:1004:A:H3'	1:1G:1004:A:N3	2.33	0.43
1:1G:1273:G:H3'	1:1G:1274:G:C8	2.53	0.43
3:22:11:ARG:O	3:22:14:ILE:N	2.46	0.43
6:52:99:ALA:HB3	18:9A:29:PHE:CE1	2.53	0.43
12:3A:41:ARG:HE	12:3A:41:ARG:HB2	1.56	0.43
23:2L:20:G:C4	23:2L:58:A:C2	3.07	0.43
55:3L:40:G:H2'	55:3L:41:G:C8	2.53	0.43
26:14:270(P):C:O5'	26:14:270(P):C:H6	2.01	0.43
26:14:1515:C:H2'	26:14:1516:U:C6	2.52	0.43
26:14:2239:G:P	59:14:3594:HOH:O	2.75	0.43
26:14:2524:G:H1	26:14:2539:C:H42	1.66	0.43
27:1J:42:C:O2	31:49:93:THR:N	2.34	0.43
29:29:33:VAL:HB	29:29:89:ASP:HB2	1.99	0.43
30:39:183:VAL:O	30:39:187:VAL:HG23	2.19	0.43
31:49:131:TYR:O	31:49:159:VAL:HG13	2.18	0.43
32:59:43:VAL:HG12	32:59:51:ARG:O	2.18	0.43
36:35:59:LEU:O	36:35:59:LEU:HD22	2.18	0.43
44:B5:59:VAL:N	44:B5:76:ARG:O	2.44	0.43
52:J5:51:TYR:HD1	52:J5:52:TYR:CE1	2.36	0.43
1:13:407:G:H2'	1:13:408:A:C8	2.54	0.43
1:13:486:U:H2'	1:13:487:A:H8	1.83	0.43
1:13:640:A:O2'	8:7E:115:SER:HB2	2.18	0.43
1:13:690:G:H22	11:2I:55:LYS:NZ	2.17	0.43
1:13:1032:A:H2'	1:13:1032(B):G:P	2.59	0.43
9:8E:91:ASP:C	9:8E:93:ARG:H	2.26	0.43
9:8E:112:LYS:HD2	9:8E:113:LYS:N	2.33	0.43
12:3I:53:ARG:HB3	12:3I:69:TYR:HE1	1.83	0.43
17:8I:22:LEU:HD13	17:8I:41:LYS:HG3	2.00	0.43
23:2K:59:A:H4'	23:2K:60:A:OP1	2.19	0.43
24:3K:37:A:C2	25:4K:13:A:H2	2.36	0.43
26:1H:57:C:H2'	26:1H:58:G:O4'	2.18	0.43
26:1H:530:G:N3	26:1H:530:G:O4'	2.52	0.43
26:1H:1021:A:H3'	26:1H:1022:G:H5"	2.00	0.43
26:1H:1203:G:H3'	26:1H:1204:A:H5"	2.01	0.43
26:1H:1444:G:C2	26:1H:1548:C:N3	2.87	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1H:2298:A:H2'	26:1H:2299:G:O4'	2.18	0.43
26:1H:2507:C:H5'	26:1H:2573:C:N4	2.33	0.43
29:21:59:VAL:HG22	29:21:60:ASN:H	1.83	0.43
36:78:15:ARG:HD2	36:78:15:ARG:HA	1.57	0.43
37:88:72:LYS:HB3	37:88:94:VAL:HG23	2.00	0.43
1:1G:4:U:C5	8:72:102:ARG:HG3	2.53	0.43
1:1G:278:G:O4'	1:1G:282:A:H1'	2.19	0.43
1:1G:612:C:O2	1:1G:629:G:N2	2.51	0.43
1:1G:865:A:H5'	1:1G:1078:U:C5	2.54	0.43
1:1G:942:G:C2	1:1G:1342:C:C2	3.06	0.43
1:1G:953:G:H5'	1:1G:965:A:H61	1.84	0.43
1:1G:1300:G:HO2'	1:1G:1301:U:P	2.41	0.43
2:12:15:VAL:HB	2:12:16:HIS:CG	2.54	0.43
3:22:42:LEU:HA	3:22:45:LYS:HE2	1.99	0.43
3:22:47:LEU:HB3	3:22:52:LEU:HD22	2.01	0.43
4:32:207:TYR:C	4:32:209:ARG:N	2.77	0.43
8:72:103:VAL:HG21	8:72:110:ALA:HB2	2.00	0.43
10:1A:50:ILE:HD13	10:1A:60:ARG:HD3	2.00	0.43
26:14:139:G:N2	26:14:1596:A:H4'	2.33	0.43
26:14:1344:G:H4'	26:14:1384:A:C5	2.53	0.43
26:14:1530:G:O6	26:14:1542:G:N2	2.51	0.43
26:14:1567:A:O2'	28:19:63:ARG:NH2	2.51	0.43
26:14:1946:U:H2'	26:14:1947:C:H6	1.84	0.43
26:14:2401:U:H2'	26:14:2402:C:H5"	1.99	0.43
26:14:2543:G:H21	26:14:2646:C:H5"	1.83	0.43
28:19:70:TRP:CZ3	28:19:146:GLU:CD	2.97	0.43
28:19:74:GLY:O	28:19:76:PRO:HD3	2.18	0.43
30:39:192:LEU:O	30:39:193:VAL:HG23	2.18	0.43
37:45:38:GLU:HG3	37:45:127:ILE:CG2	2.49	0.43
37:45:45:GLN:H	37:45:45:GLN:CD	2.24	0.43
41:85:92:ARG:C	41:85:94:ASN:N	2.77	0.43
45:C5:20:TYR:CZ	45:C5:42:VAL:HB	2.53	0.43
46:D5:17:ALA:HA	46:D5:20:ARG:HB2	2.00	0.43
1:13:49:U:O2'	1:13:50:A:H3'	2.18	0.43
1:13:411:A:O2'	1:13:413:G:H5'	2.18	0.43
1:13:1223:C:P	19:AI:78:ARG:NH1	2.88	0.43
1:13:1257:U:H5'	1:13:1258:G:C8	2.53	0.43
1:13:1533:C:H4'	1:13:1534:A:H8	1.84	0.43
2:1E:89:GLY:O	2:1E:90:MET:HE2	2.18	0.43
2:1E:131:PRO:O	2:1E:135:GLN:N	2.51	0.43
5:4E:8:GLU:OE2	5:4E:63:ARG:NH2	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:5E:67:MET:HB2	6:5E:68:PRO:HD2	2.00	0.43
18:9I:59:SER:HB3	18:9I:62:GLU:HG3	2.01	0.43
19:AI:51:VAL:O	19:AI:57:HIS:HA	2.19	0.43
20:BI:26:ASN:HB2	20:BI:71:THR:HG23	1.99	0.43
26:1H:974(A):C:H4'	26:1H:974(A):C:OP2	2.18	0.43
26:1H:2016:U:H1'	52:N8:6:VAL:HG13	1.99	0.43
26:1H:2330:G:H2'	26:1H:2331:G:O4'	2.18	0.43
26:1H:2572:A:N7	29:21:145:LYS:HB2	2.33	0.43
26:1H:2689:U:H5"	26:1H:2713:A:H2	1.83	0.43
31:41:17:PRO:HA	31:41:20:ILE:HD12	2.00	0.43
32:51:5:GLY:N	32:51:69:ARG:HG2	2.30	0.43
32:51:169:VAL:HG13	32:51:170:ARG:N	2.33	0.43
33:61:131:LYS:HA	33:61:131:LYS:NZ	2.33	0.43
34:58:12:ARG:HB3	34:58:50:ASP:OD1	2.19	0.43
36:78:18:ARG:HH21	36:78:18:ARG:HG3	1.82	0.43
44:F8:25:LYS:HA	44:F8:81:VAL:O	2.17	0.43
54:Q8:60:LEU:HA	54:Q8:60:LEU:HD12	1.70	0.43
1:1G:44:G:H2'	1:1G:45:U:O4'	2.17	0.43
1:1G:616:G:H2'	1:1G:617:G:H8	1.84	0.43
1:1G:963:G:N2	10:1A:55:LYS:HD3	2.21	0.43
1:1G:1277:C:H1'	1:1G:1282:C:O2	2.17	0.43
1:1G:1353:G:C2	1:1G:1370:G:C2	3.07	0.43
1:1G:1510:U:H2'	1:1G:1511:G:C8	2.53	0.43
3:22:44:GLU:HG3	3:22:52:LEU:HD11	2.01	0.43
19:AA:32:LYS:N	19:AA:33:THR:HG22	2.34	0.43
23:2L:41:C:H2'	23:2L:42:C:C6	2.53	0.43
55:3L:59:A:O5'	55:3L:60:U:H5"	2.18	0.43
26:14:275:G:N2	26:14:276:A:C5	2.78	0.43
26:14:329:G:H1	45:C5:19:LYS:NZ	2.16	0.43
26:14:639:U:H2'	26:14:640:C:C6	2.53	0.43
26:14:827:U:O2	26:14:2246:G:H4'	2.18	0.43
26:14:1139:G:O2'	26:14:1143:A:N1	2.43	0.43
26:14:1810:A:H2'	26:14:1811:G:O4'	2.18	0.43
26:14:2020:A:P	41:85:27:LEU:HD23	2.58	0.43
26:14:2342:C:O2'	26:14:2374:C:H5"	2.17	0.43
27:1J:83:G:H4'	50:H5:52:HIS:CG	2.53	0.43
32:59:27:LYS:HZ3	32:59:32:GLU:HG3	1.84	0.43
33:69:8:PRO:N	33:69:15:VAL:HG22	2.32	0.43
44:B5:49:VAL:HB	44:B5:83:VAL:CG2	2.48	0.43
1:13:874:G:C6	1:13:875:C:C4	3.07	0.43
1:13:1165:C:H2'	1:13:1166:G:O4'	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:13:1363:A:H4'	1:13:1364:U:H2'	2.00	0.43
4:3E:89:THR:OG1	4:3E:90:GLY:N	2.49	0.43
8:7E:56:LYS:HD2	8:7E:56:LYS:N	2.33	0.43
8:7E:104:ARG:HG3	8:7E:138:TRP:CD1	2.54	0.43
12:3I:24:VAL:HB	12:3I:27:LEU:HD12	1.99	0.43
24:3K:16:U:O4'	24:3K:60:U:O2'	2.19	0.43
24:3K:34:G:O2'	24:3K:35:G:O4'	2.36	0.43
26:1H:340:A:H2'	26:1H:341:G:O4'	2.18	0.43
26:1H:2272:U:H5"	26:1H:2273:A:OP1	2.19	0.43
26:1H:2378:A:H4'	39:A8:23:ARG:NH1	2.34	0.43
26:1H:2492:U:H2'	26:1H:2493:U:C6	2.54	0.43
27:16:66:A:C5	27:16:108:C:C5	3.07	0.43
27:16:110:G:H2'	27:16:111:U:O4'	2.19	0.43
28:11:59:LYS:HG2	28:11:60:ARG:N	2.34	0.43
28:11:272:ALA:HB1	28:11:273:ARG:H	1.43	0.43
29:21:52:LEU:O	29:21:76:ARG:HG3	2.18	0.43
30:31:197:ASP:O	30:31:199:TRP:N	2.48	0.43
31:41:61:ALA:HB2	31:41:67:LYS:HA	2.00	0.43
36:78:144:GLU:CD	36:78:144:GLU:N	2.77	0.43
38:98:113:LEU:HD12	38:98:113:LEU:HA	1.82	0.43
47:I8:41:ARG:HA	47:I8:41:ARG:HE	1.83	0.43
52:N8:46:CYS:HB2	52:N8:48:GLU:O	2.19	0.43
1:1G:19:C:H5"	5:42:86:ALA:HB3	2.01	0.43
1:1G:975:A:C4'	1:1G:976:G:H5"	2.40	0.43
1:1G:1020:U:H2'	1:1G:1021:G:O4'	2.19	0.43
1:1G:1347:G:C5	9:82:107:ARG:NH2	2.87	0.43
2:12:136:VAL:HG13	2:12:139:LYS:HD3	2.01	0.43
3:22:65:ALA:HA	3:22:100:ALA:CB	2.48	0.43
4:32:155:LEU:HB3	4:32:158:ILE:HB	2.01	0.43
5:42:101:ILE:HD11	5:42:119:LEU:HD23	2.00	0.43
5:42:101:ILE:HG13	5:42:119:LEU:HA	2.00	0.43
9:82:17:VAL:HG11	9:82:81:ILE:HD13	2.01	0.43
10:1A:28:ARG:NH2	10:1A:34:VAL:O	2.52	0.43
20:BA:14:LYS:HB2	20:BA:17:ARG:NH2	2.33	0.43
22:1L:11:C:H2'	22:1L:12:U:C6	2.54	0.43
26:14:459:U:H4'	53:L5:40:TRP:CZ3	2.53	0.43
26:14:547:A:C6	26:14:548:A:N6	2.86	0.43
26:14:588:U:H1'	30:39:90:PHE:CG	2.54	0.43
26:14:719:C:H6	26:14:719:C:O5'	2.01	0.43
26:14:1198:U:H2'	26:14:1199:U:H6	1.81	0.43
26:14:2156:G:N7	26:14:2157:G:N2	2.67	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:14:2212:A:H1'	26:14:2215:G:C6	2.54	0.43
59:14:3512:HOH:O	30:39:55:GLY:HA2	2.18	0.43
27:1J:15:A:H1'	27:1J:109:G:C5	2.53	0.43
27:1J:79:C:H2'	27:1J:80:U:O4'	2.18	0.43
27:1J:117:G:O5'	27:1J:117:G:H8	2.01	0.43
29:29:101:ARG:HD2	29:29:169:ASN:ND2	2.34	0.43
30:39:20:LEU:HD13	30:39:199:TRP:CH2	2.53	0.43
30:39:78:ILE:HA	30:39:83:PHE:CD2	2.53	0.43
30:39:143:ALA:O	30:39:148:LEU:HB2	2.18	0.43
36:35:7:ARG:HA	36:35:8:PRO:HD2	1.90	0.43
39:65:27:SER:HA	39:65:88:ASP:CB	2.49	0.43
54:M5:50:LEU:HD12	54:M5:50:LEU:HA	1.49	0.43
1:13:143:A:OP1	1:13:144:G:H5'	2.18	0.43
1:13:143:A:H5"	1:13:144:G:H5'	2.00	0.43
1:13:599:C:H2'	1:13:600:C:H6	1.84	0.43
1:13:986:A:H2'	1:13:987:G:O4'	2.18	0.43
1:13:1298:C:P	7:6E:114:ARG:HH22	2.42	0.43
1:13:1429:C:H2'	1:13:1430:C:C6	2.53	0.43
2:1E:11:LEU:C	2:1E:14:GLY:H	2.26	0.43
2:1E:162:ILE:HD11	2:1E:182:ILE:HG21	2.00	0.43
4:3E:148:VAL:HG21	4:3E:158:ILE:HG21	2.00	0.43
9:8E:21:PRO:HG3	9:8E:88:TYR:OH	2.19	0.43
12:3I:60:LEU:HA	12:3I:60:LEU:HD13	1.73	0.43
13:4I:87:TYR:C	13:4I:89:GLY:N	2.77	0.43
14:5I:21:TYR:CE2	14:5I:23:ARG:NE	2.86	0.43
23:2K:17:C:H5'	23:2K:62:C:OP1	2.18	0.43
26:1H:142:G:H2'	26:1H:143:C:C6	2.54	0.43
26:1H:799:G:C2'	59:1H:3739:HOH:O	2.66	0.43
26:1H:1568:G:H5"	28:11:61:LEU:CD2	2.49	0.43
26:1H:1799:G:H5'	26:1H:1819:A:H61	1.83	0.43
26:1H:2244:U:H2'	26:1H:2245:U:O4'	2.19	0.43
26:1H:2534:A:N7	59:1H:3711:HOH:O	2.51	0.43
28:11:181:GLU:HA	28:11:272:ALA:HB3	2.00	0.43
30:31:7:TYR:HD2	30:31:21:ALA:HB1	1.84	0.43
31:41:68:PRO:HG2	31:41:90:LEU:HG	2.01	0.43
32:51:126:PRO:HG2	32:51:130:ARG:HH22	1.83	0.43
39:A8:106:ARG:HB3	39:A8:112:PHE:CE1	2.54	0.43
40:B8:81:PRO:HG2	40:B8:82:LEU:HD12	2.01	0.43
40:B8:132:LYS:HE3	40:B8:132:LYS:HB3	1.60	0.43
43:E8:64:MET:HE3	43:E8:64:MET:HB3	1.66	0.43
50:L8:31:LEU:O	50:L8:32:GLN:HB2	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1G:1060:C:H5”	10:1A:51:ARG:HG2	2.00	0.43
1:1G:1497:G:C2’	1:1G:1498:U:H5’	2.49	0.43
17:8A:4:LYS:HD2	17:8A:5:VAL:H	1.84	0.43
55:3L:2:C:O2’	55:3L:3:U:OP1	2.31	0.43
55:3L:38:A:H5’	55:3L:39:G:OP2	2.18	0.43
55:3L:59:A:N3	55:3L:59:A:H2’	2.33	0.43
26:14:307:G:N2	26:14:309:G:H3’	2.33	0.43
26:14:2182:G:H2’	26:14:2183:C:C6	2.54	0.43
26:14:2849:U:H1’	26:14:2866:U:O2	2.19	0.43
26:14:2875:C:OP1	40:75:3:ARG:NH2	2.48	0.43
27:1J:6:C:C2	27:1J:115:G:N2	2.87	0.43
31:49:64:THR:HB	31:49:94:LEU:HD21	2.00	0.43
37:45:41:TRP:HZ3	37:45:74:TYR:HE1	1.65	0.43
45:C5:28:LYS:HB3	45:C5:38:ILE:HB	2.01	0.43
1:13:2:U:O2	1:13:612:C:O2’	2.37	0.43
1:13:280:C:C2	17:8I:38:ARG:HG3	2.54	0.43
1:13:1271:G:H2’	1:13:1272:G:H5”	2.00	0.43
1:13:1277:C:O2’	1:13:1279:A:H1’	2.19	0.43
1:13:1306:A:N6	1:13:1331:G:H1’	2.34	0.43
2:1E:91:PRO:HG3	2:1E:155:LEU:HB2	1.99	0.43
4:3E:26:CYS:HA	57:3E:302:SF4:S3	2.59	0.43
4:3E:98:GLU:OE2	4:3E:107:ARG:NH1	2.51	0.43
4:3E:108:LEU:HD13	4:3E:174:LEU:HD13	2.00	0.43
9:8E:22:GLY:HA3	9:8E:60:ASP:OD1	2.18	0.43
14:5I:47:LEU:HA	14:5I:47:LEU:HD23	1.71	0.43
22:1K:52:A:N6	22:1K:62:U:H3	2.17	0.43
26:1H:95:G:O2’	49:K8:48:HIS:HB3	2.18	0.43
26:1H:254:G:O2’	26:1H:384:U:H5’	2.18	0.43
26:1H:783:A:H8	26:1H:784:A:H4’	1.84	0.43
26:1H:818:G:OP2	59:1H:3838:HOH:O	2.21	0.43
26:1H:1331:A:HO2’	26:1H:1332:G:H8	1.65	0.43
26:1H:2822:G:H5”	29:21:159:HIS:NE2	2.34	0.43
31:41:53:LEU:HA	31:41:53:LEU:HD12	1.73	0.43
32:51:88:LEU:HD13	32:51:129:THR:O	2.18	0.43
38:98:9:LYS:HA	38:98:17:ARG:NE	2.34	0.43
41:C8:47:TYR:CD1	41:C8:47:TYR:C	2.97	0.43
43:E8:71:VAL:HA	43:E8:107:LEU:HD12	2.01	0.43
1:1G:111:G:H8	1:1G:111:G:O5’	2.01	0.43
1:1G:789:U:O2’	1:1G:791:G:N7	2.45	0.43
1:1G:1357:A:C2’	1:1G:1358:U:H5’	2.48	0.43
2:12:15:VAL:HB	2:12:16:HIS:ND1	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:32:60:GLU:HG2	4:32:202:LEU:HB2	2.01	0.43
13:4A:37:THR:HG22	13:4A:55:ARG:HB3	2.00	0.43
20:BA:49:ALA:HB3	20:BA:100:ILE:HD13	2.01	0.43
22:1L:74:C:H5	22:1L:75:C:N4	2.17	0.43
22:1L:76:A:H1'	26:14:2583:G:N2	2.34	0.43
55:3L:37:A:H2'	55:3L:38:A:O4'	2.18	0.43
26:14:324:A:H2'	26:14:325:G:O4'	2.19	0.43
26:14:2291:U:H2'	26:14:2292:C:C6	2.54	0.43
26:14:2734:A:H2'	26:14:2735:G:O4'	2.19	0.43
29:29:112:GLY:O	29:29:159:HIS:HA	2.19	0.43
31:49:95:ARG:C	31:49:99:MET:HG2	2.44	0.43
32:59:156:ALA:HB3	32:59:160:LYS:O	2.19	0.43
36:35:57:THR:HG22	36:35:60:MET:H	1.84	0.43
46:D5:152:ALA:HA	46:D5:171:ILE:HD11	2.01	0.43
1:13:73:G:H2'	1:13:74:C:H5	1.82	0.43
1:13:158:G:C4	1:13:159:G:N7	2.87	0.43
1:13:346:G:N2	1:13:347:G:C4	2.86	0.43
1:13:538:G:OP2	12:3I:115:LYS:HB2	2.18	0.43
1:13:639:G:C2	1:13:640:A:C8	3.07	0.43
1:13:652:U:O4	1:13:752:G:O2'	2.30	0.43
1:13:658:G:H2'	1:13:659:U:H6	1.82	0.43
1:13:680:C:H2'	1:13:681:C:C6	2.54	0.43
1:13:972:C:O3'	10:1I:57:LYS:HD3	2.19	0.43
1:13:1113:C:H2'	1:13:1114:C:H6	1.82	0.43
1:13:1118:C:H1'	1:13:1179:A:C4	2.54	0.43
1:13:1253:G:H2'	1:13:1254:C:C6	2.54	0.43
1:13:1286:A:H2'	1:13:1287:A:H4'	2.01	0.43
5:4E:80:ILE:HG12	5:4E:81:GLU:N	2.33	0.43
8:7E:10:LEU:HB3	8:7E:83:ILE:CD1	2.49	0.43
16:7I:21:VAL:HG23	16:7I:34:GLU:H	1.84	0.43
26:1H:141(A):C:H2'	26:1H:142:G:O4'	2.19	0.43
26:1H:415:A:H2'	26:1H:416:C:O4'	2.18	0.43
26:1H:721:C:H2'	26:1H:722:A:C8	2.54	0.43
26:1H:839:U:H2'	26:1H:840:C:C6	2.53	0.43
26:1H:844:C:H3'	26:1H:845:G:C8	2.54	0.43
26:1H:918:A:H8	26:1H:918:A:O5'	2.02	0.43
26:1H:1092:C:H2'	26:1H:1093:G:O4'	2.19	0.43
26:1H:1419:A:C8	26:1H:1421:G:C6	3.07	0.43
26:1H:1465:G:C4	26:1H:1466:G:C8	3.07	0.43
26:1H:1678:G:O5'	26:1H:1678:G:C8	2.72	0.43
27:16:7:G:H5"	27:16:7:G:H8	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:31:102:PRO:O	30:31:106:ARG:HG2	2.19	0.43
32:51:87:LEU:HD23	32:51:87:LEU:HA	1.74	0.43
33:61:68:LEU:HD12	33:61:68:LEU:HA	1.80	0.43
38:98:86:ARG:HH21	38:98:118:GLU:HG2	1.84	0.43
38:98:104:ARG:HD3	38:98:107:ASP:OD2	2.19	0.43
41:C8:36:ARG:HD3	41:C8:40:PHE:CZ	2.53	0.43
41:C8:66:ASN:O	41:C8:70:ARG:HB2	2.19	0.43
41:C8:92:ARG:HH21	42:D8:10:LYS:CB	2.32	0.43
47:I8:51:VAL:N	47:I8:62:LEU:HD12	2.33	0.43
53:P8:16:HIS:HB2	53:P8:44:PRO:HG2	2.01	0.43
1:1G:328:C:O2	1:1G:328:C:H2'	2.19	0.43
1:1G:345:C:H4'	1:1G:346:G:O5'	2.18	0.43
1:1G:1276:G:H2'	1:1G:1277:C:C6	2.54	0.43
3:22:38:ARG:H	3:22:38:ARG:HG2	1.71	0.43
3:22:152:ILE:HB	3:22:199:LYS:HB2	2.01	0.43
4:32:31:CYS:HA	57:32:301:SF4:S2	2.59	0.43
5:42:70:PRO:HD2	5:42:142:LEU:HB2	2.00	0.43
17:8A:69:LYS:C	17:8A:70:ARG:HD2	2.44	0.43
17:8A:90:ILE:HD12	17:8A:90:ILE:HA	1.85	0.43
20:BA:50:GLU:N	20:BA:100:ILE:HG12	2.34	0.43
22:1L:49:G:N3	22:1L:49:G:H2'	2.34	0.43
55:3L:70:A:H2'	55:3L:71:G:C8	2.54	0.43
26:14:218:A:C2	26:14:235:U:H4'	2.54	0.43
26:14:839:U:H2'	26:14:840:C:H6	1.84	0.43
26:14:1277:G:O2'	38:55:24:GLN:HG2	2.19	0.43
26:14:2068:U:N3	26:14:2430:A:C2	2.77	0.43
26:14:2563:U:O2	26:14:2565:A:H8	2.01	0.43
29:29:32:PRO:O	29:29:34:VAL:HG23	2.18	0.43
30:39:149:ASP:N	30:39:149:ASP:OD1	2.51	0.43
31:49:115:ARG:HB2	31:49:136:ARG:NH2	2.34	0.43
33:69:52:ARG:HA	33:69:55:ALA:HB3	2.01	0.43
34:15:61:ARG:HA	34:15:61:ARG:NH1	2.33	0.43
34:15:96:GLU:H	34:15:96:GLU:CD	2.27	0.43
35:25:113:LYS:O	35:25:117:LEU:HD22	2.18	0.43
39:65:36:TYR:CD1	39:65:36:TYR:N	2.87	0.43
46:D5:91:LEU:HD12	46:D5:91:LEU:H	1.84	0.43
1:13:590:C:H2'	1:13:591:U:H6	1.83	0.42
1:13:648:A:C6	1:13:649:G:C6	3.07	0.42
6:5E:25:ILE:HA	6:5E:25:ILE:HD13	1.80	0.42
20:BI:44:ALA:HB3	20:BI:91:LEU:HD12	2.01	0.42
22:1K:3:U:O2	22:1K:3:U:H2'	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1H:139:G:N3	26:1H:141:A:N1	2.67	0.42
26:1H:248:G:H5'	26:1H:250:G:N7	2.33	0.42
26:1H:1425:G:H2'	26:1H:1426:G:O4'	2.19	0.42
26:1H:1677:A:H8	26:1H:1677:A:O5'	2.02	0.42
26:1H:2287:A:C4	26:1H:2289:G:C8	3.07	0.42
26:1H:2680:C:H5'	29:21:189:PRO:HA	2.01	0.42
26:1H:2774:C:H2'	26:1H:2775:A:O4'	2.18	0.42
27:16:79:C:O5'	27:16:79:C:H6	2.01	0.42
32:51:86:GLU:OE2	32:51:165:ALA:N	2.52	0.42
42:D8:49:THR:OG1	42:D8:50:PRO:HD2	2.18	0.42
46:H8:120:ILE:HG21	46:H8:170:THR:CB	2.49	0.42
1:1G:631:G:H1'	1:1G:632:A:H5'	2.01	0.42
1:1G:1142:G:H2'	1:1G:1143:G:O4'	2.19	0.42
3:22:73:PRO:HA	3:22:76:VAL:HG13	2.01	0.42
4:32:170:VAL:HG12	4:32:171:GLY:H	1.84	0.42
7:62:65:ALA:HB3	7:62:124:LEU:HD22	2.00	0.42
10:1A:7:LYS:HZ1	10:1A:40:LEU:HD22	1.83	0.42
55:3L:40:G:H2'	55:3L:41:G:H8	1.84	0.42
26:14:185:U:H4'	26:14:218:A:H4'	2.00	0.42
26:14:486:C:H4'	43:A5:60:ASN:HD22	1.84	0.42
26:14:620:G:N3	26:14:620:G:H5'	2.34	0.42
26:14:688:U:H5'	26:14:1780:A:C2	2.54	0.42
26:14:1153:C:H2'	26:14:1154:G:O4'	2.19	0.42
29:29:37:ARG:HA	29:29:42:ASP:OD2	2.19	0.42
32:59:31:GLY:C	32:59:79:VAL:HB	2.44	0.42
35:25:87:ILE:HG23	35:25:88:ASN:O	2.19	0.42
37:45:73:PRO:HB3	37:45:93:TYR:CE1	2.54	0.42
39:65:35:ILE:HB	39:65:97:ARG:HH21	1.84	0.42
40:75:24:PRO:HD3	40:75:52:ILE:HD12	2.01	0.42
40:75:45:PHE:CD1	40:75:74:ARG:HG3	2.53	0.42
40:75:128:GLU:HB3	40:75:132:LYS:HZ2	1.83	0.42
42:95:29:PRO:HA	42:95:61:VAL:CG1	2.48	0.42
46:D5:6:LYS:HD3	46:D5:8:TYR:HE2	1.83	0.42
46:D5:94:GLU:HB3	46:D5:96:VAL:CG2	2.47	0.42
1:13:444:C:H42	1:13:490:G:H1	1.66	0.42
1:13:603:U:H2'	1:13:604:G:C8	2.54	0.42
1:13:1286:A:C2	21:1F:18:TYR:OH	2.70	0.42
1:13:1329:A:H5'	13:4I:29:ARG:HD2	2.01	0.42
1:13:1429:C:H2'	1:13:1430:C:H6	1.83	0.42
3:2E:50:ALA:HB2	3:2E:75:VAL:HB	2.01	0.42
7:6E:25:ALA:O	7:6E:29:LYS:HG2	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:6E:121:ALA:O	7:6E:125:MET:HG3	2.19	0.42
17:8I:89:LEU:HD22	17:8I:89:LEU:HA	1.88	0.42
20:BI:44:ALA:HB1	20:BI:91:LEU:HB2	2.00	0.42
26:1H:184:C:H2'	26:1H:185:U:H6	1.82	0.42
26:1H:482:A:H5"	26:1H:483:A:OP1	2.20	0.42
26:1H:657:U:H2'	26:1H:658:C:C6	2.54	0.42
26:1H:996:A:H4'	41:C8:92:ARG:NE	2.34	0.42
26:1H:1657:C:H2'	26:1H:1658:C:C6	2.54	0.42
26:1H:2025:C:H2'	26:1H:2026:C:C6	2.54	0.42
26:1H:2065:C:H2'	26:1H:2066:C:C6	2.54	0.42
26:1H:2135:A:H5'	26:1H:2160:G:O4'	2.19	0.42
26:1H:2849:U:H1'	26:1H:2866:U:O2	2.20	0.42
27:16:40:U:H2'	51:M8:2:LYS:HE3	2.01	0.42
28:11:119:ALA:CB	28:11:130:ALA:HB3	2.49	0.42
30:31:7:TYR:CD2	30:31:21:ALA:HB1	2.53	0.42
31:41:97:ASP:HA	31:41:100:TRP:HB2	2.01	0.42
32:51:115:VAL:HG11	32:51:148:ILE:HD11	2.01	0.42
34:58:73:THR:HA	34:58:83:LYS:O	2.18	0.42
46:H8:30:ASN:OD1	46:H8:33:LEU:HD23	2.19	0.42
54:Q8:23:VAL:CG1	54:Q8:47:LYS:HD3	2.49	0.42
1:1G:363:A:C5	12:3A:31:PRO:HD2	2.54	0.42
1:1G:678:U:H2'	1:1G:679:C:C6	2.54	0.42
1:1G:901:A:C5	1:1G:902:G:H1'	2.54	0.42
1:1G:1052:U:O2'	1:1G:1055:A:OP2	2.18	0.42
1:1G:1101:A:N7	2:12:172:ILE:HD11	2.34	0.42
1:1G:1206:G:O2'	3:22:193:TYR:HA	2.19	0.42
1:1G:1289:A:OP1	21:1B:9:ARG:NH2	2.52	0.42
3:22:95:THR:C	3:22:97:LYS:N	2.77	0.42
10:1A:33:GLN:HB2	10:1A:75:ILE:CG1	2.45	0.42
13:4A:23:TYR:CZ	13:4A:71:ARG:HG3	2.54	0.42
17:8A:87:LYS:O	17:8A:90:ILE:HG22	2.19	0.42
22:1L:72:C:O2'	22:1L:73:A:H5'	2.19	0.42
23:2L:14:A:C2	23:2L:23:G:C4	3.07	0.42
23:2L:50:G:H1	23:2L:66:C:H42	1.67	0.42
26:14:546:C:H2'	26:14:547:A:C8	2.55	0.42
26:14:830:G:H5"	59:14:3748:HOH:O	2.19	0.42
26:14:1035:U:H2'	26:14:1036:G:C8	2.55	0.42
26:14:1657:C:H2'	26:14:1658:C:C6	2.54	0.42
26:14:2212:A:H1'	26:14:2215:G:C5	2.54	0.42
26:14:2410:G:C2	26:14:2411:A:H1'	2.54	0.42
29:29:4:ILE:HD13	29:29:28:ALA:HB1	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:29:181:LEU:HD12	29:29:181:LEU:HA	1.85	0.42
32:59:20:ALA:HB3	32:59:23:ARG:C	2.44	0.42
34:15:91:LEU:HA	34:15:91:LEU:HD23	1.65	0.42
36:35:107:LYS:C	36:35:109:GLY:H	2.27	0.42
39:65:23:ARG:NH2	39:65:84:GLN:HB3	2.33	0.42
41:85:48:ALA:O	41:85:52:ARG:HB3	2.20	0.42
42:95:18:LEU:O	42:95:96:ILE:HG12	2.19	0.42
42:95:91:TYR:C	42:95:91:TYR:HD1	2.27	0.42
1:13:933:G:OP2	7:6E:3:ARG:HB2	2.19	0.42
1:13:1240:U:OP2	7:6E:116:ALA:N	2.47	0.42
2:1E:154:LEU:CD1	2:1E:154:LEU:H	2.32	0.42
3:2E:72:LYS:HD3	3:2E:75:VAL:HG21	2.00	0.42
7:6E:115:ARG:HB3	7:6E:118:VAL:HG12	2.02	0.42
12:3I:37:CYS:O	12:3I:79:GLU:O	2.37	0.42
16:7I:4:ILE:HD12	16:7I:66:PRO:HD3	2.01	0.42
26:1H:176:G:C2'	26:1H:177:G:H5'	2.50	0.42
26:1H:508:G:N3	26:1H:508:G:H5"	2.34	0.42
26:1H:937:U:H2'	26:1H:938:G:O4'	2.19	0.42
26:1H:1279:G:N2	26:1H:1292:U:C2	2.87	0.42
26:1H:1311:G:C2	44:F8:60:ARG:NH1	2.87	0.42
26:1H:1381:G:H2'	26:1H:1382:G:H5'	2.01	0.42
26:1H:1528:A:C6	26:1H:1529:A:C6	3.08	0.42
26:1H:1671:U:O5'	26:1H:1671:U:H6	2.02	0.42
26:1H:1782:C:O2	26:1H:2608:G:O2'	2.33	0.42
26:1H:2035:G:H4'	26:1H:2036:C:OP2	2.19	0.42
26:1H:2309:A:C6	26:1H:2310:A:N7	2.87	0.42
26:1H:2418:A:H5"	26:1H:2419:U:OP2	2.20	0.42
26:1H:2687:U:H2'	26:1H:2688:U:O4'	2.19	0.42
29:21:76:ARG:HG3	29:21:76:ARG:H	1.69	0.42
32:51:7:LEU:HD23	32:51:8:PRO:HD2	2.02	0.42
37:88:75:THR:HA	37:88:89:ASN:O	2.19	0.42
38:98:46:GLY:HA2	38:98:49:ASP:HB2	2.01	0.42
42:D8:69:LYS:HA	42:D8:88:ARG:HB3	2.01	0.42
45:G8:64:GLU:H	45:G8:64:GLU:HG2	1.67	0.42
46:H8:5:LEU:HD11	46:H8:39:VAL:HB	2.01	0.42
54:Q8:36:LYS:HA	54:Q8:40:GLU:OE1	2.19	0.42
1:1G:148:G:H1	1:1G:174:C:H42	1.67	0.42
1:1G:652:U:O2'	1:1G:653:A:O5'	2.38	0.42
1:1G:731:G:OP1	1:1G:766:A:H1'	2.18	0.42
1:1G:999:U:H3	1:1G:1041:A:H61	1.67	0.42
1:1G:1011:G:C2	1:1G:1019:C:O2	2.72	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1G:1216:G:H2'	1:1G:1217:C:H6	1.84	0.42
1:1G:1305:G:H8	1:1G:1305:G:OP2	2.02	0.42
1:1G:1305:G:H5"	21:1B:4:GLY:C	2.44	0.42
1:1G:1324:A:C4'	1:1G:1362:C:H4'	2.48	0.42
2:12:189:ASP:OD1	2:12:189:ASP:N	2.53	0.42
4:32:81:GLU:HG2	4:32:96:LEU:HD21	2.01	0.42
5:42:79:GLU:HB3	5:42:92:LYS:HG3	2.00	0.42
6:52:96:PRO:HB3	18:9A:30:ASP:CG	2.44	0.42
15:6A:12:ILE:O	15:6A:16:ALA:N	2.52	0.42
21:1B:2:GLY:C	21:1B:4:GLY:N	2.78	0.42
22:1L:53:G:H2'	22:1L:54:5MU:O4'	2.19	0.42
25:4L:24:A:H3'	25:4L:24:A:H8	1.84	0.42
26:14:6:A:C6	34:15:129:PRO:O	2.72	0.42
26:14:232:G:H8	26:14:232:G:OP2	2.02	0.42
26:14:1316:U:H2'	26:14:1317:A:H8	1.84	0.42
26:14:1505:C:H2'	26:14:1506:C:H6	1.84	0.42
26:14:1754:C:H2'	26:14:1755:A:C8	2.54	0.42
26:14:2810:A:N6	26:14:2891:G:O2'	2.52	0.42
29:29:5:LEU:HD13	29:29:49:LEU:CD1	2.48	0.42
30:39:178:PRO:HB2	30:39:201:VAL:HG11	2.02	0.42
33:69:78:THR:C	33:69:80:PRO:HD3	2.43	0.42
36:35:39:LYS:CD	36:35:45:LEU:HD21	2.47	0.42
39:65:7:TYR:O	39:65:11:LYS:HB2	2.19	0.42
41:85:90:VAL:HA	42:95:38:LEU:HD21	2.01	0.42
46:D5:158:PRO:O	46:D5:161:VAL:HG22	2.19	0.42
1:13:8:A:H62	4:3E:208:SER:HB2	1.85	0.42
1:13:376:G:H5"	16:7I:5:ARG:HB2	2.00	0.42
4:3E:90:GLY:O	4:3E:93:PHE:HB3	2.19	0.42
4:3E:156:GLU:O	4:3E:160:GLN:HG3	2.19	0.42
12:3I:47:LYS:HA	12:3I:49:ASN:H	1.83	0.42
17:8I:48:GLU:H	17:8I:48:GLU:HG3	1.64	0.42
19:AI:40:ILE:CG1	19:AI:41:VAL:HG13	2.48	0.42
20:BI:35:THR:O	20:BI:38:LYS:HB2	2.19	0.42
22:1K:15:G:H22	22:1K:48:C:H41	1.66	0.42
24:3K:52:A:H2'	24:3K:53:G:C8	2.55	0.42
26:1H:365:C:H2'	26:1H:366:C:O4'	2.19	0.42
26:1H:475:U:C4	26:1H:481:G:O6	2.73	0.42
26:1H:574:C:P	59:1H:3752:HOH:O	2.72	0.42
26:1H:705:A:C8	26:1H:727:A:C2	3.08	0.42
26:1H:733:G:O6	59:1H:3831:HOH:O	2.19	0.42
26:1H:806:C:OP2	36:78:41:ARG:HD3	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1H:1185:C:P	59:1H:3939:HOH:O	2.77	0.42
26:1H:1933:G:H2'	26:1H:1934:C:O4'	2.19	0.42
26:1H:1965:C:H3'	26:1H:1966:A:H2'	2.01	0.42
26:1H:2101:G:H1	26:1H:2188:C:N4	2.10	0.42
26:1H:2356:C:O3'	47:I8:20:ARG:HD3	2.19	0.42
26:1H:2533:A:H2'	26:1H:2534:A:O4'	2.19	0.42
26:1H:2761:G:N7	59:1H:3916:HOH:O	2.37	0.42
29:21:49:LEU:HD12	29:21:49:LEU:HA	1.51	0.42
30:31:20:LEU:HD12	30:31:21:ALA:H	1.84	0.42
31:41:80:PHE:O	31:41:82:LEU:HB2	2.18	0.42
34:58:23:LEU:HA	34:58:23:LEU:HD12	1.76	0.42
40:B8:54:ARG:HA	40:B8:59:THR:HB	2.01	0.42
47:I8:14:ARG:HE	47:I8:14:ARG:HB2	1.51	0.42
50:L8:7:LYS:HD2	50:L8:34:GLU:CD	2.44	0.42
54:Q8:50:LEU:HD22	54:Q8:50:LEU:HA	1.67	0.42
1:1G:575:G:H4'	1:1G:576:G:O5'	2.19	0.42
1:1G:652:U:H1'	1:1G:653:A:C2	2.49	0.42
1:1G:1238:A:N7	1:1G:1303:C:H1'	2.35	0.42
2:12:74:LYS:C	2:12:76:GLN:H	2.27	0.42
2:12:111:ARG:HG3	2:12:145:LEU:HD11	2.01	0.42
2:12:189:ASP:HB3	2:12:203:GLY:O	2.18	0.42
3:22:203:PHE:C	3:22:204:LEU:HG	2.44	0.42
16:7A:25:ARG:HB2	59:7A:103:HOH:O	2.18	0.42
22:1L:50:G:N2	22:1L:51:C:N3	2.68	0.42
26:14:198:C:O2'	26:14:199:A:H5'	2.18	0.42
26:14:263:C:H2'	26:14:264:C:O4'	2.20	0.42
26:14:1149:G:H2'	26:14:1150:C:C6	2.54	0.42
26:14:1668:A:OP1	35:25:5:GLN:HG2	2.20	0.42
26:14:1790:C:H2'	26:14:1791:A:C5	2.54	0.42
26:14:1915:U:H2'	26:14:1916:A:O4'	2.19	0.42
26:14:2607:G:H2'	26:14:2608:G:O4'	2.19	0.42
32:59:20:ALA:HB1	32:59:23:ARG:HG3	2.00	0.42
35:25:22:ILE:HA	35:25:22:ILE:HD13	1.39	0.42
36:35:96:THR:HG23	36:35:99:LEU:HB2	2.02	0.42
37:45:43:THR:OG1	37:45:45:GLN:HG2	2.19	0.42
39:65:18:ILE:O	39:65:20:ARG:N	2.51	0.42
40:75:45:PHE:CZ	40:75:74:ARG:HG3	2.55	0.42
44:B5:11:PRO:HD3	49:G5:37:PHE:CD2	2.54	0.42
1:13:31:G:O2'	1:13:48:C:N4	2.53	0.42
5:4E:8:GLU:HG2	5:4E:34:VAL:HG22	2.01	0.42
14:5I:3:ARG:O	14:5I:7:ILE:HG23	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:6I:43:LEU:HD12	15:6I:56:LEU:HD13	2.01	0.42
22:1K:43:G:H2'	22:1K:44:A:H8	1.84	0.42
26:1H:322:A:OP2	30:31:169:ASN:HB2	2.19	0.42
26:1H:455:C:N3	26:1H:473:G:H5'	2.34	0.42
26:1H:459:U:H2'	26:1H:460:A:C8	2.54	0.42
26:1H:1850:G:H2'	26:1H:1851:U:C6	2.54	0.42
59:1H:4095:HOH:O	38:98:15:SER:HB3	2.20	0.42
28:11:32:SER:C	28:11:33:LEU:HD13	2.45	0.42
33:61:70:GLU:HA	33:61:70:GLU:OE2	2.19	0.42
33:61:78:THR:HG22	33:61:141:LYS:HB2	2.01	0.42
39:A8:106:ARG:HB3	39:A8:112:PHE:HE1	1.85	0.42
46:H8:124:ILE:HD12	46:H8:125:LEU:H	1.85	0.42
48:J8:86:SER:HB3	48:J8:89:GLU:HB2	2.02	0.42
49:K8:4:SER:H	49:K8:7:ARG:N	2.06	0.42
51:M8:22:ILE:O	51:M8:24:THR:HG23	2.19	0.42
1:1G:108:G:H5"	1:1G:108:G:N3	2.35	0.42
1:1G:130:A:O2'	1:1G:131:C:O5'	2.32	0.42
1:1G:184:G:O2'	1:1G:185:A:H5'	2.19	0.42
1:1G:1160:G:H1	1:1G:1176:A:H61	1.67	0.42
2:12:49:GLU:HA	2:12:52:GLU:HG3	2.00	0.42
4:32:98:GLU:HG3	4:32:103:ASN:ND2	2.34	0.42
5:42:90:VAL:O	5:42:120:THR:HA	2.20	0.42
13:4A:68:GLY:O	13:4A:72:ALA:N	2.50	0.42
19:AA:37:ARG:H	19:AA:37:ARG:HG3	1.65	0.42
22:1L:50:G:C2	22:1L:51:C:C4	3.08	0.42
23:2L:34:U:O2'	23:2L:36:A:N7	2.46	0.42
26:14:302:C:N4	59:14:3693:HOH:O	2.52	0.42
26:14:1542:G:O5'	26:14:1543:A:H5"	2.19	0.42
26:14:1543:A:H1'	26:14:1545:A:H1'	2.02	0.42
26:14:1670:C:O2	29:29:129:HIS:NE2	2.47	0.42
26:14:1716:U:O2'	26:14:1717:G:H5'	2.20	0.42
26:14:2101:G:H2'	26:14:2102:U:O4'	2.19	0.42
26:14:2261:C:H1'	26:14:2388:A:N3	2.34	0.42
26:14:2396:G:H4'	48:F5:30:VAL:HA	2.02	0.42
26:14:2441:C:O2'	26:14:2442:C:H5'	2.19	0.42
27:1J:23:G:C2	27:1J:24:G:O6	2.73	0.42
27:1J:76:G:H5"	46:D5:15:PRO:HG3	2.00	0.42
28:19:2:ALA:N	28:19:200:ASP:OD2	2.52	0.42
42:95:98:GLU:O	42:95:99:ILE:C	2.62	0.42
46:D5:127:LYS:HB3	46:D5:162:GLU:O	2.20	0.42
52:J5:41:PRO:HG2	52:J5:44:THR:OG1	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:13:7:G:O2'	5:4E:120:THR:O	2.38	0.42
1:13:384:G:H2'	1:13:385:C:C6	2.55	0.42
1:13:721:G:C6	1:13:733:A:C2	3.08	0.42
1:13:1331:G:O2'	1:13:1332:A:O5'	2.34	0.42
2:1E:69:LEU:HB3	2:1E:162:ILE:HG23	2.00	0.42
2:1E:74:LYS:HG3	2:1E:208:ILE:HD13	2.01	0.42
3:2E:58:GLU:O	3:2E:59:ARG:HG3	2.20	0.42
6:5E:99:ALA:HB1	18:9I:23:LYS:HD2	2.01	0.42
12:3I:62:SER:HB2	12:3I:64:TYR:CD2	2.42	0.42
13:4I:87:TYR:C	13:4I:89:GLY:H	2.27	0.42
18:9I:85:LEU:HD12	18:9I:86:VAL:H	1.84	0.42
22:1K:18:G:H2'	22:1K:57:G:C4	2.54	0.42
26:1H:832:G:C5'	36:78:45:LEU:HD11	2.43	0.42
26:1H:1762:A:OP1	26:1H:1762:A:H4'	2.20	0.42
30:31:197:ASP:C	30:31:199:TRP:H	2.27	0.42
33:61:1:MET:O	33:61:21:VAL:N	2.39	0.42
36:78:79:ARG:HB3	36:78:110:TYR:CD1	2.54	0.42
39:A8:61:ASN:OD1	39:A8:64:GLU:HG2	2.18	0.42
41:C8:89:GLU:H	41:C8:89:GLU:HG3	1.51	0.42
42:D8:5:VAL:HG12	42:D8:38:LEU:HB3	2.00	0.42
51:M8:60:GLN:HG3	51:M8:61:ARG:NH1	2.35	0.42
1:1G:1279:A:H5"	1:1G:1280:A:P	2.60	0.42
1:1G:1374:A:H2'	1:1G:1375:A:H5'	2.01	0.42
2:12:18:GLY:O	2:12:204:ASN:ND2	2.53	0.42
2:12:54:THR:HA	2:12:57:PHE:HB2	2.01	0.42
3:22:65:ALA:HA	3:22:100:ALA:HB3	2.02	0.42
3:22:125:GLU:H	3:22:125:GLU:HG3	1.65	0.42
4:32:110:PHE:N	4:32:110:PHE:CD1	2.87	0.42
5:42:31:LEU:HD11	5:42:43:LEU:HD12	2.02	0.42
9:82:5:TYR:HD1	9:82:18:PHE:HD1	1.68	0.42
10:1A:45:ARG:O	10:1A:65:LEU:N	2.52	0.42
13:4A:80:ARG:NE	19:AA:66:MET:HG2	2.35	0.42
22:1L:2:C:H42	22:1L:68:U:H5	1.67	0.42
26:14:991:C:O2	26:14:1164:G:C2	2.73	0.42
26:14:1028:A:H61	26:14:1125:G:H2'	1.83	0.42
26:14:1190:G:OP1	36:35:32:THR:HA	2.19	0.42
26:14:2020:A:OP1	41:85:27:LEU:HD23	2.20	0.42
26:14:2209:C:O2	26:14:2216:G:C2	2.72	0.42
26:14:2494:G:O2'	37:45:80:GLU:HA	2.19	0.42
29:29:8:LYS:HE2	29:29:188:VAL:HG22	2.01	0.42
29:29:174:ASP:OD1	29:29:175:VAL:N	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:39:11:VAL:O	30:39:12:LEU:C	2.62	0.42
30:39:103:LYS:HA	30:39:106:ARG:HG3	2.00	0.42
31:49:34:LEU:HB3	31:49:99:MET:HE1	2.02	0.42
34:15:22:THR:HA	34:15:61:ARG:HB2	2.02	0.42
36:35:105:LEU:O	36:35:106:LEU:HB3	2.18	0.42
1:13:157:G:H2'	1:13:158:G:C8	2.55	0.42
1:13:760:G:H2'	1:13:761:G:H5'	2.01	0.42
1:13:985:C:H2'	1:13:986:A:H8	1.85	0.42
1:13:1174:G:H2'	1:13:1175:G:C8	2.54	0.42
1:13:1179:A:OP2	9:8E:97:LYS:NZ	2.49	0.42
7:6E:113:GLU:HG3	7:6E:119:ARG:HA	2.00	0.42
8:7E:121:ASP:HB2	8:7E:125:ARG:NH2	2.34	0.42
9:8E:42:ARG:HE	9:8E:42:ARG:HB2	1.31	0.42
11:2I:86:GLY:HA2	11:2I:112:THR:HG23	2.02	0.42
14:5I:15:LYS:HG2	14:5I:16:PHE:CE2	2.55	0.42
15:6I:17:ARG:HG2	15:6I:17:ARG:H	1.68	0.42
17:8I:31:LEU:HD22	17:8I:32:TYR:CE1	2.54	0.42
20:BI:72:LEU:HD23	20:BI:72:LEU:HA	1.74	0.42
26:1H:116:C:O2'	26:1H:117:G:H5'	2.19	0.42
26:1H:304:G:H2'	26:1H:305:U:C6	2.55	0.42
26:1H:562:U:O4	26:1H:2036:C:H1'	2.19	0.42
26:1H:1164:G:O6	59:1H:3788:HOH:O	2.22	0.42
26:1H:1317:A:H2'	26:1H:1318:C:H6	1.84	0.42
26:1H:1535:U:H3'	26:1H:1537:C:C4	2.54	0.42
26:1H:1598:C:O2'	26:1H:1599:C:H5'	2.20	0.42
26:1H:2238:G:H2'	26:1H:2238:G:N3	2.34	0.42
26:1H:2860:A:N7	26:1H:2861:G:H1'	2.35	0.42
26:1H:2865:U:C4	26:1H:2866:U:C4	3.08	0.42
26:1H:2876:G:O5'	40:B8:2:ASN:HA	2.20	0.42
27:16:71:C:C2	27:16:72:G:C8	3.08	0.42
38:98:86:ARG:NH2	38:98:118:GLU:HG2	2.34	0.42
38:98:103:ARG:NH1	38:98:108:GLY:O	2.52	0.42
44:F8:12:VAL:HG22	44:F8:17:ALA:HB2	2.02	0.42
44:F8:24:GLY:O	44:F8:83:VAL:HG22	2.20	0.42
48:J8:49:VAL:HG11	48:J8:70:VAL:HG11	2.00	0.42
54:Q8:37:SER:C	54:Q8:39:LYS:N	2.77	0.42
1:1G:396:G:O2'	1:1G:398:C:OP1	2.31	0.42
1:1G:538:G:O3'	12:3A:114:LYS:NZ	2.41	0.42
1:1G:837:G:H2'	1:1G:838:G:C8	2.54	0.42
1:1G:1049:U:H1'	1:1G:1201:A:C8	2.54	0.42
1:1G:1157:A:H61	1:1G:1177:G:H1	1.68	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:72:100:ILE:O	8:72:125:ARG:NH1	2.52	0.42
11:2A:125:PHE:C	11:2A:126:ARG:HG3	2.44	0.42
18:9A:32:ARG:HA	18:9A:69:THR:HG21	2.02	0.42
26:14:878:A:N7	26:14:879:G:H1'	2.34	0.42
26:14:1000:A:C6	26:14:1001:A:N1	2.87	0.42
26:14:1449(A):G:H2'	26:14:1450:C:C6	2.55	0.42
26:14:1999:C:H4'	26:14:2723:C:O2	2.20	0.42
26:14:2062:A:N6	26:14:2503:A:H62	2.16	0.42
26:14:2319:G:N7	39:65:3:ARG:HG3	2.34	0.42
26:14:2643:G:H2'	26:14:2644:G:O4'	2.20	0.42
26:14:2873:A:C8	38:55:5:LYS:HA	2.55	0.42
29:29:47:VAL:HG21	29:29:85:ASN:HA	2.00	0.42
31:49:47:LYS:HA	31:49:87:PRO:HG2	2.01	0.42
34:15:15:LEU:HD23	34:15:134:ARG:HB2	2.01	0.42
46:D5:44:PHE:HE2	46:D5:88:PHE:CZ	2.38	0.42
46:D5:94:GLU:O	46:D5:130:PRO:HD3	2.20	0.42
46:D5:157:LEU:HA	46:D5:161:VAL:HG11	2.02	0.42
49:G5:3:LEU:C	49:G5:5:GLU:HB2	2.45	0.42
1:13:38:G:C2	1:13:397:A:C2	3.08	0.42
1:13:280:C:H4'	1:13:281:G:OP2	2.20	0.42
1:13:309:G:H8	1:13:309:G:O5'	2.03	0.42
1:13:468:A:H3'	1:13:474:G:H8	1.85	0.42
1:13:651:C:N4	1:13:753:A:OP2	2.53	0.42
1:13:909:A:H2'	1:13:910:C:O4'	2.20	0.42
1:13:1145:C:H4'	1:13:1146:A:H5'	2.02	0.42
1:13:1147:C:O2'	9:8E:16:ARG:HD2	2.18	0.42
1:13:1157:A:O2'	1:13:1158:C:P	2.77	0.42
1:13:1306:A:H61	1:13:1331:G:H1'	1.85	0.42
5:4E:112:LEU:HD23	5:4E:112:LEU:HA	1.78	0.42
13:4I:56:LEU:O	13:4I:60:VAL:HG23	2.19	0.42
26:1H:270(F):U:H2'	26:1H:270(G):C:C6	2.55	0.42
26:1H:1069:A:H4'	26:1H:1070:A:C5'	2.50	0.42
26:1H:1541:U:H2'	26:1H:1542:G:O4'	2.19	0.42
26:1H:1845:G:OP1	28:11:258:LYS:NZ	2.46	0.42
26:1H:2844:G:O6	59:1H:3836:HOH:O	2.20	0.42
32:51:129:THR:O	32:51:129:THR:OG1	2.36	0.42
33:61:93:THR:HG22	33:61:119:PRO:HB3	2.02	0.42
35:68:68:GLU:HA	35:68:78:ARG:HB3	2.02	0.42
40:B8:48:ILE:HD12	40:B8:110:ILE:HD11	2.02	0.42
41:C8:75:ASN:HB3	41:C8:77:SER:N	2.34	0.42
42:D8:19:LYS:HG3	42:D8:95:LEU:HD23	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:H8:157:LEU:O	46:H8:158:PRO:C	2.63	0.42
48:J8:53:VAL:HB	48:J8:58:ILE:HD13	2.01	0.42
1:1G:128:G:H4'	17:8A:3:LYS:HG2	2.02	0.42
1:1G:186(D):C:H2'	1:1G:186(E):C:C6	2.54	0.42
1:1G:522:C:N4	1:1G:527:G:H1	2.17	0.42
1:1G:631:G:H8	1:1G:631:G:OP2	2.02	0.42
1:1G:992:U:H5'	1:1G:993:G:O4'	2.20	0.42
1:1G:1049:U:H5'	1:1G:1201:A:OP2	2.19	0.42
1:1G:1418:A:H5"	1:1G:1419:G:OP2	2.20	0.42
3:22:102:ASN:OD1	3:22:102:ASN:N	2.53	0.42
4:32:101:LEU:HD23	4:32:121:VAL:CG1	2.49	0.42
4:32:207:TYR:C	4:32:209:ARG:H	2.28	0.42
5:42:8:GLU:HB3	5:42:34:VAL:HG23	2.02	0.42
6:52:72:VAL:H	6:52:72:VAL:HG12	1.56	0.42
8:72:120:THR:HG23	8:72:122:ARG:H	1.84	0.42
21:1B:12:LYS:O	21:1B:16:GLY:N	2.52	0.42
23:2L:77:A:H2'	23:2L:77:A:N3	2.34	0.42
26:14:656:G:H2'	26:14:657:U:O4'	2.19	0.42
26:14:692:C:H4'	28:19:40:THR:OG1	2.19	0.42
26:14:1313:U:P	59:14:3516:HOH:O	2.73	0.42
26:14:1382:G:O4'	26:14:1572:A:H2	2.02	0.42
26:14:2134:A:H2'	26:14:2134:A:N3	2.35	0.42
26:14:2259:G:C2	26:14:2282:G:N1	2.88	0.42
26:14:2498:C:H3'	59:14:3523:HOH:O	2.20	0.42
26:14:2740:A:C6	26:14:2741:A:C6	3.08	0.42
31:49:104:GLU:C	31:49:106:LEU:N	2.76	0.42
35:25:24:VAL:HA	35:25:39:ILE:HG22	2.01	0.42
38:55:118:GLU:OE1	38:55:118:GLU:HA	2.20	0.42
40:75:12:SER:HA	40:75:15:VAL:HG22	2.00	0.42
43:A5:62:HIS:O	43:A5:63:ASP:C	2.62	0.42
46:D5:45:ASP:O	46:D5:49:ARG:HG2	2.20	0.42
50:H5:3:ARG:HG3	50:H5:59:VAL:C	2.45	0.42
1:13:533:A:C2	1:13:536:C:C5	3.08	0.42
1:13:1007:C:N3	1:13:1022:G:N2	2.63	0.42
1:13:1123:A:O2'	10:1I:38:ILE:HG23	2.20	0.42
1:13:1240:U:O2'	7:6E:38:LEU:HD12	2.20	0.42
1:13:1346:A:OP1	9:8E:120:ARG:NH1	2.41	0.42
1:13:1357:A:N6	1:13:1358:U:O4	2.53	0.42
8:7E:80:ILE:H	8:7E:80:ILE:HG12	1.64	0.42
8:7E:121:ASP:OD2	8:7E:125:ARG:NH2	2.52	0.42
9:8E:10:ARG:HG3	9:8E:105:ASP:HB3	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:2I:32:ILE:HD11	11:2I:68:ALA:O	2.18	0.42
16:7I:71:ARG:HA	16:7I:74:LEU:HD12	2.02	0.42
19:AI:27:GLU:OE1	19:AI:27:GLU:N	2.44	0.42
26:1H:363:G:C2	26:1H:363(A):A:C5	3.08	0.42
26:1H:1204:A:H61	26:1H:1240:U:H2'	1.85	0.42
26:1H:1358:G:N2	26:1H:1372:U:C5	2.88	0.42
26:1H:1628:G:N7	59:1H:3913:HOH:O	2.37	0.42
26:1H:1813:G:H4'	28:11:43:ARG:O	2.20	0.42
39:A8:66:ALA:HA	39:A8:69:VAL:HG13	2.02	0.42
41:C8:85:LYS:HA	41:C8:85:LYS:HD2	1.68	0.42
47:I8:36:ILE:C	47:I8:36:ILE:HD13	2.44	0.42
48:J8:50:ARG:HG2	48:J8:59:THR:OG1	2.19	0.42
1:1G:149:A:H2'	1:1G:150:C:C6	2.54	0.42
1:1G:582:U:OP1	15:6A:64:ARG:NH1	2.53	0.42
1:1G:967:C:O2'	9:82:125:TYR:OH	2.32	0.42
1:1G:1216:G:H2'	1:1G:1217:C:C6	2.55	0.42
1:1G:1260:C:OP1	1:1G:1284:C:H4'	2.20	0.42
3:22:23:TYR:CD1	3:22:23:TYR:C	2.98	0.42
5:42:104:ALA:HA	5:42:107:ARG:NH2	2.35	0.42
11:2A:51:LYS:HE2	11:2A:51:LYS:HB3	1.84	0.42
11:2A:54:ARG:NH2	55:3L:39:G:O3'	2.53	0.42
12:3A:51:ALA:O	12:3A:52:LEU:HD23	2.19	0.42
13:4A:49:THR:C	13:4A:51:ALA:H	2.28	0.42
17:8A:74:LEU:HD23	17:8A:74:LEU:HA	1.90	0.42
26:14:72:U:P	59:14:3559:HOH:O	2.78	0.42
26:14:150:C:H2'	26:14:151:C:C6	2.55	0.42
26:14:273(E):U:H2'	26:14:273(F):C:O4'	2.20	0.42
26:14:452:G:N3	26:14:457:A:H2	2.18	0.42
26:14:458:G:O2'	53:L5:39:ARG:HD3	2.19	0.42
26:14:775:G:O5'	26:14:777:A:H1'	2.19	0.42
26:14:1165:U:H2'	26:14:1166:C:C6	2.55	0.42
26:14:1446:C:H42	26:14:1465:G:H1	1.67	0.42
26:14:1788:C:C2	26:14:1789:A:C8	3.08	0.42
26:14:2065:C:H2'	26:14:2066:C:C6	2.55	0.42
26:14:2104:G:H2'	26:14:2105:C:H6	1.85	0.42
29:29:50:GLY:HA2	29:29:78:LEU:HA	2.01	0.42
29:29:167:VAL:CG1	29:29:189:PRO:HD3	2.49	0.42
30:39:123:LEU:HA	30:39:192:LEU:C	2.44	0.42
34:15:41:ASP:O	41:85:64:ARG:NH2	2.53	0.42
34:15:91:LEU:O	34:15:95:PRO:HB3	2.20	0.42
36:35:79:ARG:HG2	36:35:110:TYR:CB	2.50	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:75:128:GLU:O	40:75:132:LYS:HG3	2.20	0.42
43:A5:13:SER:O	43:A5:14:PRO:C	2.63	0.42
45:C5:17:SER:HB2	45:C5:71:LYS:CE	2.49	0.42
46:D5:39:VAL:HG21	46:D5:44:PHE:HB2	2.01	0.42
49:G5:4:SER:H	49:G5:6:VAL:HG13	1.84	0.42
1:13:191:G:C2	1:13:192:U:C2	3.07	0.42
1:13:405:U:OP2	4:3E:3:ARG:NH1	2.53	0.42
1:13:607:A:C2	16:7I:31:LYS:HG3	2.55	0.42
1:13:1014:A:H4'	19:AI:14:HIS:CE1	2.55	0.42
1:13:1190:G:H5"	3:2E:176:HIS:NE2	2.33	0.42
2:1E:189:ASP:OD1	2:1E:189:ASP:N	2.53	0.42
12:3I:42:THR:HA	12:3I:53:ARG:O	2.20	0.42
13:4I:26:GLY:O	13:4I:28:ALA:N	2.53	0.42
19:AI:40:ILE:HG22	19:AI:68:GLY:HA2	2.00	0.42
22:1K:37:AET:H2'	22:1K:38:A:O4'	2.20	0.42
24:3K:55:U:OP1	24:3K:55:U:H4'	2.20	0.42
26:1H:363:G:H2'	26:1H:363(A):A:H8	1.84	0.42
26:1H:458:G:O2'	26:1H:469:G:O6	2.38	0.42
26:1H:1021:A:C8	26:1H:1021:A:C3'	3.02	0.42
26:1H:1176:G:H5'	26:1H:1177:A:OP2	2.20	0.42
26:1H:1379:A:H1'	26:1H:1380:G:OP1	2.20	0.42
26:1H:2101:G:N2	26:1H:2189:U:O2	2.53	0.42
26:1H:2170:A:H3'	26:1H:2170:A:P	2.60	0.42
26:1H:2215:G:H2'	26:1H:2216:G:H8	1.85	0.42
26:1H:2250:G:C5	37:88:83:MET:HB3	2.55	0.42
26:1H:2652:C:H2'	26:1H:2653:U:O4'	2.20	0.42
35:68:18:LYS:HB2	35:68:45:GLU:HB3	2.01	0.42
37:88:25:ASP:HA	37:88:100:GLY:O	2.19	0.42
46:H8:15:PRO:HB2	46:H8:19:ARG:NH2	2.35	0.42
46:H8:101:PRO:HA	46:H8:123:ASP:HB3	2.02	0.42
49:K8:7:ARG:O	49:K8:11:GLU:HB2	2.20	0.42
1:1G:21:G:OP1	59:1G:1824:HOH:O	2.22	0.42
1:1G:685:G:C2	1:1G:686:U:C4	3.08	0.42
1:1G:1203:C:H2'	1:1G:1204:A:H8	1.82	0.42
2:12:141:GLU:O	2:12:145:LEU:HB2	2.20	0.42
4:32:126:ILE:HG22	4:32:127:THR:N	2.35	0.42
9:82:19:LEU:HD12	9:82:19:LEU:H	1.84	0.42
22:1L:53:G:H5"	37:45:56:ARG:CZ	2.50	0.42
23:2L:32:G:H2'	23:2L:33:OMC:H6	1.85	0.42
26:14:74:A:H4'	26:14:75:G:O5'	2.20	0.42
26:14:200:U:O2	26:14:386:G:N2	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:14:571:A:H5'	26:14:2030:A:N7	2.35	0.42
26:14:1499:C:H2'	26:14:1500:G:C8	2.55	0.42
26:14:2027:G:H2'	26:14:2028:U:O4'	2.20	0.42
26:14:2820:A:O5'	38:55:4:LEU:HD23	2.20	0.42
27:1J:21:G:H2'	27:1J:22:U:O4'	2.20	0.42
27:1J:44:G:O2'	27:1J:47:C:N4	2.47	0.42
28:19:11:PRO:C	28:19:13:ARG:H	2.27	0.42
30:39:33:LEU:O	30:39:36:VAL:HG12	2.19	0.42
34:15:34:LEU:HD21	34:15:120:LEU:HD13	2.02	0.42
35:25:14:THR:HG23	35:25:16:ALA:H	1.84	0.42
35:25:63:VAL:HG12	35:25:106:LEU:HD11	2.01	0.42
41:85:76:TYR:CZ	41:85:80:ILE:HG13	2.54	0.42
42:95:69:LYS:HG2	42:95:71:LEU:HD22	2.02	0.42
48:F5:83:GLU:N	48:F5:83:GLU:OE2	2.52	0.42
1:13:123:C:OP1	1:13:312:C:H5'	2.20	0.41
1:13:447:G:H8	1:13:447:G:O5'	2.03	0.41
1:13:538:G:H5"	12:3I:114:LYS:HB2	2.02	0.41
1:13:660:G:C2	1:13:746:A:C2	3.08	0.41
1:13:1026:G:H2'	1:13:1027:C:H5'	2.02	0.41
2:1E:87:ARG:NH1	2:1E:223:ILE:HD11	2.35	0.41
9:8E:77:ILE:O	9:8E:81:ILE:HG12	2.20	0.41
10:1I:88:LEU:HD12	10:1I:88:LEU:O	2.20	0.41
18:9I:21:LYS:HE3	18:9I:21:LYS:HB2	1.79	0.41
26:1H:518:G:H2'	26:1H:519:U:C6	2.54	0.41
26:1H:1032:A:H2	26:1H:1122:G:H22	1.68	0.41
26:1H:1811:G:H2'	26:1H:1812:A:O4'	2.20	0.41
26:1H:2165:G:N7	26:1H:2166:G:N2	2.68	0.41
31:41:37:VAL:HG21	31:41:103:LEU:HD21	2.02	0.41
33:61:57:ARG:O	33:61:61:ARG:HG2	2.20	0.41
50:L8:51:ALA:HA	50:L8:54:VAL:HG12	2.02	0.41
1:1G:885:G:O2'	1:1G:914:A:N1	2.34	0.41
1:1G:1002:G:H1	1:1G:1038:C:H42	1.67	0.41
1:1G:1154:G:H2'	1:1G:1155:G:C8	2.48	0.41
1:1G:1288:A:H2'	1:1G:1289:A:H8	1.84	0.41
3:22:16:ARG:NH2	3:22:181:ASN:HA	2.35	0.41
5:42:30:ALA:O	5:42:45:PHE:HA	2.20	0.41
7:62:114:ARG:H	7:62:114:ARG:HG2	1.32	0.41
10:1A:91:PRO:HB3	10:1A:96:ILE:HD11	2.02	0.41
11:2A:32:ILE:HD11	11:2A:68:ALA:HB1	2.02	0.41
17:8A:10:VAL:HG13	17:8A:54:GLY:H	1.85	0.41
26:14:221:A:N1	26:14:265:A:O2'	2.45	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:14:288:C:H2'	26:14:289:A:C8	2.55	0.41
26:14:1257:C:H4'	30:39:83:PHE:CD1	2.54	0.41
26:14:1372:U:H2'	26:14:1373:A:O4'	2.20	0.41
26:14:1432:C:H2'	26:14:1433:U:O4'	2.19	0.41
26:14:1827:C:OP2	28:19:222:ARG:HD2	2.19	0.41
26:14:2037:G:H2'	26:14:2038:G:H8	1.80	0.41
27:1J:16:G:H2'	27:1J:17:C:H6	1.85	0.41
29:29:182:LEU:O	29:29:183:LEU:HD12	2.19	0.41
32:59:10:PRO:HG2	32:59:50:VAL:HG22	2.02	0.41
33:69:130:TYR:O	33:69:131:LYS:HD2	2.19	0.41
36:35:19:VAL:CG1	36:35:31:ALA:HB1	2.49	0.41
1:13:232:G:H1'	1:13:262:A:N1	2.36	0.41
1:13:947:G:H4'	13:4I:109:THR:HG23	2.02	0.41
1:13:1133:G:C4	1:13:1134:G:C8	3.08	0.41
4:3E:81:GLU:O	4:3E:84:LYS:HB2	2.20	0.41
6:5E:86:ARG:O	6:5E:87:ARG:HG2	2.20	0.41
11:2I:77:MET:HE2	11:2I:77:MET:HB2	1.70	0.41
12:3I:6:THR:OG1	12:3I:9:GLN:HG3	2.20	0.41
18:9I:73:ALA:HB3	18:9I:79:LEU:HD12	2.02	0.41
22:1K:42:U:H2'	22:1K:43:G:C8	2.55	0.41
23:2K:65:G:C2	23:2K:66:C:C2	3.08	0.41
26:1H:270(T):G:H2'	26:1H:270(U):C:H6	1.85	0.41
26:1H:370:G:H4'	26:1H:371:A:OP2	2.19	0.41
26:1H:484:C:H2'	26:1H:485:C:C6	2.56	0.41
26:1H:654(C):G:N3	26:1H:654(D):G:H1'	2.35	0.41
26:1H:962:G:H2'	26:1H:963:U:C6	2.56	0.41
26:1H:1665:A:H2'	26:1H:1666:G:O4'	2.20	0.41
26:1H:2017:U:O2	52:N8:10:LYS:HB2	2.20	0.41
26:1H:2030:A:H4'	26:1H:2031:A:C8	2.55	0.41
26:1H:2291:U:H2'	26:1H:2292:C:C6	2.56	0.41
29:21:14:ILE:HA	29:21:14:ILE:HD13	1.64	0.41
40:B8:31:SER:HB2	40:B8:84:GLN:HB3	2.01	0.41
46:H8:157:LEU:N	46:H8:158:PRO:HD3	2.35	0.41
47:I8:53:MET:HE2	47:I8:53:MET:HB3	1.84	0.41
1:1G:1:U:H5'	1:1G:630:G:N3	2.35	0.41
1:1G:974:A:H1'	1:1G:975:A:OP2	2.20	0.41
1:1G:1151:A:H5'	10:1A:41:PRO:HA	2.02	0.41
1:1G:1245:A:H2'	1:1G:1246:C:O4'	2.20	0.41
1:1G:1368:G:OP1	10:1A:62:HIS:HE1	2.04	0.41
2:12:71:VAL:HG23	2:12:165:VAL:HG13	2.02	0.41
2:12:182:ILE:H	2:12:182:ILE:HD12	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:32:76:ARG:NH2	4:32:80:GLU:OE2	2.53	0.41
4:32:107:ARG:HA	4:32:107:ARG:HD2	1.94	0.41
5:42:15:ARG:NH1	25:4L:25:A:H5"	2.35	0.41
14:5A:22:THR:HB	14:5A:33:VAL:HG21	2.01	0.41
55:3L:6:U:O4	55:3L:67:A:N6	2.53	0.41
26:14:251:A:C5	26:14:252:G:H1'	2.55	0.41
26:14:602:G:O2'	26:14:604:G:O2'	2.30	0.41
26:14:999:U:O2'	26:14:1000:A:H5'	2.20	0.41
26:14:1041:C:N4	26:14:1114:G:H22	2.16	0.41
26:14:1801:G:H3'	26:14:1802:A:H5'	2.02	0.41
26:14:1929:G:H4'	26:14:1930:G:OP1	2.20	0.41
26:14:2408:U:H2'	26:14:2409:G:H8	1.85	0.41
26:14:2747:G:O6	26:14:2755:C:H5"	2.20	0.41
26:14:2888:C:H2'	26:14:2889:C:C6	2.55	0.41
28:19:83:GLU:OE1	28:19:104:TYR:OH	2.35	0.41
30:39:107:LYS:CE	30:39:205:ARG:HD2	2.49	0.41
31:49:5:VAL:CG1	31:49:101:ILE:HG22	2.50	0.41
31:49:96:ARG:C	31:49:98:ARG:H	2.28	0.41
33:69:133:HIS:H	33:69:133:HIS:HD1	1.67	0.41
34:15:128:HIS:CE1	34:15:134:ARG:HD3	2.55	0.41
41:85:17:ILE:HD12	41:85:32:PHE:CE1	2.53	0.41
45:C5:18:GLY:O	45:C5:20:TYR:N	2.50	0.41
46:D5:4:ARG:HD3	46:D5:60:GLU:OE2	2.20	0.41
49:G5:24:LEU:HA	49:G5:24:LEU:HD22	1.83	0.41
54:M5:31:HIS:O	54:M5:32:LEU:HB2	2.20	0.41
1:13:1240:U:P	7:6E:116:ALA:HB2	2.60	0.41
7:6E:26:PHE:O	7:6E:30:ILE:HG13	2.20	0.41
10:1I:90:LEU:N	10:1I:91:PRO:HD2	2.34	0.41
13:4I:34:LEU:HD23	13:4I:34:LEU:HA	1.83	0.41
17:8I:7:THR:O	17:8I:23:VAL:HG13	2.20	0.41
17:8I:65:ILE:CG2	17:8I:69:LYS:HE2	2.45	0.41
18:9I:36:ASN:HD22	18:9I:39:VAL:HG21	1.83	0.41
22:1K:66:U:C5'	22:1K:67:A:H8	2.28	0.41
23:2K:63:C:O2	23:2K:64:G:C8	2.73	0.41
26:1H:613:U:H5'	26:1H:616:A:N6	2.35	0.41
26:1H:637:A:H2'	36:78:117:GLU:CD	2.46	0.41
26:1H:2331:G:O2'	26:1H:2336:A:N1	2.49	0.41
26:1H:2773:C:OP1	29:21:166:THR:OG1	2.38	0.41
27:16:1(M):A:C8	27:16:0:A:C8	3.09	0.41
27:16:78:A:C2	27:16:99:A:C4	3.07	0.41
28:11:11:PRO:O	28:11:12:SER:OG	2.33	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:11:26:LYS:NZ	28:11:30:GLU:OE2	2.52	0.41
28:11:80:ALA:HB2	28:11:96:HIS:CD2	2.55	0.41
30:31:103:LYS:HA	30:31:106:ARG:HG3	2.03	0.41
30:31:197:ASP:O	30:31:198:ALA:HB3	2.19	0.41
31:41:62:LEU:HD12	51:M8:27:THR:HG21	2.02	0.41
38:98:97:VAL:HA	38:98:113:LEU:O	2.20	0.41
40:B8:87:ASP:O	40:B8:89:VAL:HG12	2.20	0.41
1:1G:543:C:C2'	1:1G:544:G:H5'	2.50	0.41
1:1G:837:G:H2'	1:1G:838:G:H8	1.85	0.41
1:1G:1240:U:OP2	7:62:116:ALA:N	2.53	0.41
1:1G:1286:A:C8	1:1G:1286:A:C3'	3.04	0.41
1:1G:1325:C:P	21:1B:15:ARG:HH21	2.44	0.41
1:1G:1329:A:H2'	1:1G:1330:U:O4'	2.20	0.41
2:12:42:ILE:CG2	2:12:202:PRO:HB2	2.47	0.41
2:12:54:THR:HA	2:12:57:PHE:CD2	2.55	0.41
4:32:84:LYS:HG2	4:32:86:LYS:HG2	2.01	0.41
11:2A:125:PHE:O	11:2A:126:ARG:HG3	2.21	0.41
16:7A:74:LEU:HD13	16:7A:74:LEU:HA	1.88	0.41
26:14:569:U:C4	26:14:570:G:C6	3.09	0.41
26:14:755:C:H2'	26:14:756:C:C6	2.55	0.41
26:14:830:G:H4'	26:14:831:G:OP2	2.21	0.41
26:14:951:C:O2'	26:14:952:G:H5'	2.20	0.41
26:14:1204:A:C2	26:14:1241:A:N1	2.88	0.41
26:14:1359:A:N7	26:14:1372:U:O4	2.53	0.41
26:14:1572:A:H2'	26:14:1573:G:O4'	2.20	0.41
26:14:1818:U:H2'	28:19:157:ARG:HD3	2.02	0.41
26:14:1921:G:H2'	26:14:1922:G:H8	1.86	0.41
26:14:2531:A:C4'	32:59:157:TYR:HE2	2.30	0.41
36:35:19:VAL:HG13	36:35:31:ALA:HB1	2.02	0.41
38:55:49:ASP:OD1	38:55:95:THR:HG22	2.20	0.41
38:55:63:ARG:O	38:55:67:LEU:HB2	2.20	0.41
40:75:51:ARG:HD3	40:75:100:TYR:OH	2.20	0.41
1:13:503:C:OP2	12:3I:116:SER:OG	2.34	0.41
1:13:1116:C:C2'	1:13:1117:G:H5'	2.50	0.41
1:13:1455:G:H5"	20:BI:31:SER:HB2	2.01	0.41
2:1E:178:ARG:NH1	2:1E:196:LEU:O	2.23	0.41
3:2E:172:ARG:HH21	3:2E:203:PHE:HZ	1.68	0.41
10:1I:54:PHE:CD2	10:1I:55:LYS:HG2	2.56	0.41
10:1I:54:PHE:CG	10:1I:55:LYS:HG2	2.55	0.41
11:2I:73:MET:HE2	11:2I:103:LEU:HD22	2.02	0.41
24:3K:56:C:H2'	24:3K:57:G:O4'	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1H:271(B):G:N7	26:1H:421:U:H2'	2.35	0.41
26:1H:581:C:H2'	26:1H:582:G:H8	1.84	0.41
26:1H:803:U:C4	26:1H:804:A:N7	2.88	0.41
26:1H:1400:G:H2'	26:1H:1401:G:C8	2.56	0.41
26:1H:1408:C:C2	26:1H:1595:G:N2	2.89	0.41
26:1H:1488:G:C6	26:1H:1489:U:C4	3.09	0.41
26:1H:1545(A):A:N7	26:1H:1546:C:C2	2.89	0.41
26:1H:2352:A:C4	26:1H:2366:A:C2	3.09	0.41
30:31:129:PHE:O	30:31:142:TRP:CD1	2.73	0.41
36:78:49:ARG:HH11	36:78:49:ARG:CG	2.34	0.41
41:C8:88:ILE:C	41:C8:90:VAL:N	2.78	0.41
1:1G:157:G:C2	1:1G:165:C:C2	3.08	0.41
1:1G:407:G:P	4:32:115:ARG:HH21	2.42	0.41
1:1G:878:G:H5'	8:72:89:PRO:HG2	2.02	0.41
1:1G:1067:A:O2'	1:1G:1093:A:O2'	2.23	0.41
1:1G:1145:C:H4'	1:1G:1146:A:O5'	2.20	0.41
2:12:26:PRO:C	2:12:28:PHE:H	2.29	0.41
2:12:140:HIS:NE2	2:12:144:ARG:HD2	2.36	0.41
3:22:46:GLU:HG2	3:22:46:GLU:H	1.64	0.41
3:22:72:LYS:HG3	3:22:75:VAL:HG23	2.02	0.41
5:42:90:VAL:HG23	5:42:121:LYS:HB3	2.01	0.41
9:82:99:LEU:HB3	9:82:101:PHE:CE1	2.55	0.41
10:1A:78:ASN:HD22	10:1A:80:LYS:CB	2.32	0.41
11:2A:67:ASP:O	11:2A:71:LYS:HG3	2.21	0.41
25:4L:24:A:H3'	25:4L:24:A:C8	2.55	0.41
26:14:451:C:H41	26:14:454:A:H5'	1.84	0.41
26:14:2314:C:H2'	26:14:2315:G:H8	1.85	0.41
26:14:2547:U:O2	35:25:23:ARG:NH2	2.52	0.41
26:14:2639:A:C2	26:14:2778:A:C8	3.08	0.41
26:14:2846:G:H2'	26:14:2847:U:O4'	2.21	0.41
27:1J:109:G:C6	27:1J:110:G:C5	3.08	0.41
28:19:17:THR:O	28:19:211:ARG:NH2	2.52	0.41
28:19:105:ILE:HD12	28:19:105:ILE:HA	1.88	0.41
31:49:75:LYS:O	31:49:75:LYS:HD3	2.20	0.41
32:59:10:PRO:O	32:59:12:PRO:HD3	2.21	0.41
37:45:19:GLY:O	37:45:98:LYS:HB3	2.21	0.41
38:55:51:LEU:HA	38:55:51:LEU:HD23	1.70	0.41
39:65:107:GLU:N	39:65:110:LEU:HD11	2.33	0.41
41:85:66:ASN:O	41:85:70:ARG:HB2	2.21	0.41
1:13:429:U:H1'	1:13:430:A:H5"	2.02	0.41
1:13:1126:U:C6	1:13:1126:U:C3'	3.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:13:1516:G:N1	1:13:1519:A:OP2	2.54	0.41
2:1E:30:ARG:HB3	2:1E:31:TYR:CD1	2.55	0.41
9:8E:5:TYR:CD2	9:8E:18:PHE:CE1	3.09	0.41
19:AI:41:VAL:HG21	19:AI:45:VAL:HB	2.03	0.41
20:BI:13:LEU:C	20:BI:13:LEU:HD12	2.45	0.41
22:1K:49:G:H1	22:1K:59:C:C5'	2.34	0.41
24:3K:70:A:H2'	24:3K:71:G:C8	2.55	0.41
26:1H:58:G:N2	26:1H:70:G:C4	2.89	0.41
26:1H:141:A:H8	26:1H:1595:G:H21	1.68	0.41
26:1H:234:C:H2'	26:1H:235:U:C6	2.54	0.41
26:1H:1359:A:N1	26:1H:1372:U:O4	2.53	0.41
26:1H:1472:A:H2'	26:1H:1473:G:O4'	2.20	0.41
26:1H:1799:G:H5'	26:1H:1819:A:N6	2.35	0.41
26:1H:1999:C:H5"	26:1H:2723:C:O2'	2.20	0.41
26:1H:2830:G:N3	26:1H:2883:A:H2	2.19	0.41
29:21:30:PRO:HD3	29:21:180:ASN:ND2	2.36	0.41
31:41:97:ASP:H	31:41:100:TRP:CD1	2.39	0.41
31:41:109:VAL:O	31:41:113:ARG:HG3	2.20	0.41
31:41:145:THR:C	31:41:147:ASP:H	2.28	0.41
39:A8:32:LEU:O	39:A8:62:LYS:NZ	2.48	0.41
39:A8:67:ARG:O	39:A8:71:ARG:HG3	2.20	0.41
42:D8:76:LYS:O	42:D8:79:VAL:HG12	2.21	0.41
53:P8:37:LYS:O	53:P8:37:LYS:HG2	2.19	0.41
1:1G:309:G:H1'	1:1G:608:A:C2	2.56	0.41
1:1G:566:G:H4'	1:1G:567:G:OP1	2.20	0.41
1:1G:854:G:C2	1:1G:855:G:C8	3.09	0.41
1:1G:1122:U:N3	1:1G:1123:A:N7	2.68	0.41
1:1G:1179:A:OP2	9:82:93:ARG:NH1	2.53	0.41
1:1G:1187:G:H5'	9:82:113:LYS:NZ	2.35	0.41
1:1G:1343:G:H4'	9:82:122:ALA:HB3	2.01	0.41
1:1G:1379:G:C6	1:1G:1380:U:O4	2.74	0.41
1:1G:1399:C:C2	1:1G:1502:A:N6	2.89	0.41
1:1G:1509:C:H2'	1:1G:1510:U:O4'	2.21	0.41
2:12:51:LEU:O	2:12:54:THR:N	2.50	0.41
3:22:88:ARG:CZ	3:22:88:ARG:HB3	2.50	0.41
10:1A:12:ASP:OD1	10:1A:13:HIS:N	2.54	0.41
10:1A:84:GLN:O	10:1A:88:LEU:HB2	2.21	0.41
11:2A:18:ARG:HH21	11:2A:37:GLY:N	2.18	0.41
13:4A:37:THR:CG2	13:4A:55:ARG:HB3	2.51	0.41
17:8A:55:ASP:OD1	17:8A:55:ASP:N	2.52	0.41
20:BA:5:LYS:O	20:BA:6:PRO:C	2.63	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:BA:11:SER:HA	20:BA:13:LEU:CD2	2.49	0.41
20:BA:51:GLU:HG2	20:BA:54:LYS:NZ	2.35	0.41
22:1L:49:G:H22	22:1L:59:C:P	2.43	0.41
23:2L:41:C:H2'	23:2L:42:C:H6	1.85	0.41
55:3L:29:C:H2'	55:3L:30:C:O4'	2.20	0.41
26:14:273(C):C:H42	26:14:363(C):G:H1	1.69	0.41
26:14:654(C):G:C8	26:14:654(C):G:H3'	2.55	0.41
26:14:1019:U:H2'	26:14:1020:A:C8	2.54	0.41
26:14:1109:C:H2'	26:14:1110:G:C1'	2.50	0.41
26:14:1358:G:N2	26:14:1372:U:C5	2.89	0.41
26:14:1635:G:H2'	26:14:1636:C:C6	2.55	0.41
26:14:1707:G:C5	26:14:1756:G:C6	3.09	0.41
27:1J:16:G:H1	27:1J:68:C:N4	2.14	0.41
27:1J:30:C:OP2	39:65:32:LEU:HD11	2.19	0.41
28:19:130:ALA:HA	28:19:192:THR:HA	2.02	0.41
30:39:49:ALA:O	30:39:92:PRO:HB2	2.19	0.41
30:39:68:LYS:HG2	30:39:69:HIS:NE2	2.35	0.41
31:49:170:ARG:HA	31:49:170:ARG:HD2	1.86	0.41
40:75:2:ASN:HB3	40:75:4:GLY:C	2.45	0.41
52:J5:16:ARG:HG3	52:J5:17:ASP:N	2.36	0.41
54:M5:35:GLN:HG3	54:M5:35:GLN:O	2.20	0.41
1:13:243:A:H5"	1:13:244:U:H3'	2.02	0.41
1:13:474:G:H5"	16:7I:81:ARG:CZ	2.50	0.41
1:13:646:U:H2'	1:13:647:C:C6	2.55	0.41
1:13:1037:C:H2'	1:13:1038:C:C6	2.53	0.41
1:13:1070:U:H2'	1:13:1071:C:H6	1.85	0.41
1:13:1342:C:H2'	1:13:1343:G:C8	2.56	0.41
1:13:1442:G:C6	1:13:1446:A:C6	3.08	0.41
2:1E:155:LEU:HD23	2:1E:155:LEU:HA	1.94	0.41
3:2E:11:ARG:O	3:2E:12:LEU:C	2.63	0.41
3:2E:134:ILE:HD11	3:2E:153:VAL:HG23	2.03	0.41
15:6I:70:LEU:HG	15:6I:78:TYR:HB2	2.02	0.41
26:1H:97:C:H5"	49:K8:2:LYS:HB2	2.03	0.41
26:1H:1070:A:H5'	26:1H:1071:G:H5"	2.02	0.41
26:1H:1110:G:O2'	26:1H:1111:A:H8	2.02	0.41
26:1H:1323:U:H2'	26:1H:1324:G:H5'	2.03	0.41
26:1H:1899:G:H22	26:1H:1902:C:H41	1.68	0.41
26:1H:2153:G:H2'	26:1H:2154:G:O4'	2.20	0.41
26:1H:2287:A:C2	26:1H:2346:A:H2	2.38	0.41
26:1H:2356:C:H2'	26:1H:2357:U:O4'	2.20	0.41
36:78:78:PRO:HB3	36:78:111:ARG:NH2	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:A8:3:ARG:O	39:A8:4:LEU:C	2.63	0.41
40:B8:128:GLU:O	40:B8:128:GLU:HG2	2.20	0.41
44:F8:66:LEU:HA	44:F8:66:LEU:HD13	1.77	0.41
54:Q8:7:HIS:HB3	54:Q8:61:LEU:HB3	2.02	0.41
54:Q8:23:VAL:HG22	54:Q8:49:VAL:HG22	2.03	0.41
1:1G:184:G:C2'	1:1G:185:A:H5'	2.51	0.41
1:1G:560:U:H4'	1:1G:561:U:O5'	2.20	0.41
1:1G:564:C:C4	1:1G:565:U:C4	3.09	0.41
1:1G:955:U:H1'	1:1G:1227:A:H61	1.84	0.41
4:32:63:LYS:HE3	4:32:63:LYS:HB2	1.71	0.41
9:82:26:VAL:HG22	9:82:61:ALA:N	2.36	0.41
19:AA:66:MET:HG3	19:AA:69:HIS:NE2	2.35	0.41
20:BA:89:ARG:NH1	20:BA:105:SER:O	2.53	0.41
23:2L:54:G:O2'	23:2L:55:5MU:H5"	2.21	0.41
23:2L:57:C:OP1	23:2L:57:C:H6	2.04	0.41
26:14:291:C:H42	26:14:349:G:H1	1.68	0.41
26:14:784:A:O4'	28:19:227:ASN:ND2	2.53	0.41
30:39:132:VAL:O	30:39:133:ASN:HB2	2.20	0.41
30:39:182:ASN:HD21	30:39:185:ASP:CG	2.29	0.41
34:15:15:LEU:O	34:15:136:GLU:HA	2.20	0.41
39:65:7:TYR:CE1	39:65:91:PRO:HG3	2.55	0.41
40:75:133:GLU:O	40:75:137:LYS:NZ	2.35	0.41
42:95:20:LEU:O	42:95:93:GLU:HA	2.21	0.41
44:B5:67:GLY:C	44:B5:69:TYR:H	2.27	0.41
49:G5:4:SER:HB3	49:G5:7:ARG:CD	2.50	0.41
50:H5:5:LYS:HB3	50:H5:5:LYS:HE3	1.81	0.41
1:13:303:A:H2'	1:13:304:U:O4'	2.20	0.41
1:13:725:G:H2'	1:13:726:C:H6	1.85	0.41
2:1E:163:PHE:CD1	2:1E:185:ILE:HG12	2.55	0.41
6:5E:69:GLU:O	6:5E:72:VAL:HG12	2.19	0.41
6:5E:95:GLU:OE1	6:5E:95:GLU:N	2.44	0.41
12:3I:53:ARG:HH12	12:3I:92:ASP:CG	2.28	0.41
13:4I:93:ARG:O	13:4I:94:ARG:HD3	2.21	0.41
23:2K:47:7MG:O2'	23:2K:48:U:H6	2.04	0.41
24:3K:72:C:H3'	24:3K:73:A:H5"	2.03	0.41
25:4K:23:A:H1'	25:4K:24:A:C8	2.55	0.41
26:1H:346:A:N3	26:1H:346:A:H2'	2.36	0.41
26:1H:810:U:P	59:1H:3720:HOH:O	2.64	0.41
26:1H:973:A:O4'	26:1H:1188:U:C6	2.73	0.41
26:1H:1386:C:H2'	26:1H:1387:C:H6	1.86	0.41
26:1H:1451:C:H2'	26:1H:1458:C:N4	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1H:1664:A:P	59:1H:3722:HOH:O	2.76	0.41
26:1H:1899:G:O2'	26:1H:1900:A:OP2	2.35	0.41
26:1H:2275:C:H5'	26:1H:2275:C:C6	2.55	0.41
28:11:206:LEU:HD22	28:11:211:ARG:HG2	2.02	0.41
31:41:94:LEU:N	31:41:94:LEU:HD23	2.36	0.41
31:41:98:ARG:NH2	51:M8:1:MET:HG3	2.35	0.41
32:51:5:GLY:HA2	32:51:69:ARG:CB	2.50	0.41
36:78:65:ARG:HD3	54:Q8:25:MET:SD	2.60	0.41
37:88:104:PHE:O	37:88:105:GLU:C	2.64	0.41
40:B8:11:GLU:OE1	40:B8:57:PHE:HB3	2.20	0.41
40:B8:33:LYS:H	40:B8:33:LYS:HG2	1.49	0.41
43:E8:82:LEU:HD13	43:E8:84:ARG:NH2	2.36	0.41
46:H8:130:PRO:O	46:H8:133:ILE:HG13	2.20	0.41
1:1G:750:G:H1'	15:6A:22:THR:OG1	2.20	0.41
1:1G:757:U:H2'	1:1G:758:G:O4'	2.20	0.41
1:1G:1401:G:OP1	25:4L:18:G:O2'	2.37	0.41
2:12:100:GLY:O	2:12:104:ASN:N	2.44	0.41
13:4A:84:ILE:H	13:4A:84:ILE:CD1	2.30	0.41
26:14:213:A:H5"	26:14:214:G:OP2	2.21	0.41
26:14:702:G:C2	26:14:731:C:C2	3.08	0.41
26:14:900:A:H5'	26:14:901:A:OP2	2.21	0.41
26:14:997:G:H2'	26:14:998:C:H6	1.86	0.41
26:14:1568:G:P	28:19:63:ARG:HH12	2.40	0.41
26:14:1641:A:H2'	26:14:1642:G:O4'	2.20	0.41
26:14:1747:G:H2'	26:14:1748:G:H8	1.86	0.41
26:14:2319:G:N2	26:14:2334:G:OP1	2.39	0.41
26:14:2366:A:H2'	26:14:2367:G:O4'	2.20	0.41
26:14:2854:G:C2	26:14:2855:C:C2	3.08	0.41
28:19:6:PHE:CE1	28:19:18:VAL:HG23	2.55	0.41
29:29:103:ASP:OD2	29:29:168:MET:HE2	2.21	0.41
31:49:83:ARG:O	31:49:86:MET:HB2	2.21	0.41
33:69:124:GLY:O	33:69:142:VAL:HG23	2.20	0.41
34:15:61:ARG:HA	34:15:61:ARG:HH11	1.85	0.41
36:35:63:PRO:O	54:M5:13:ARG:HG2	2.20	0.41
38:55:86:ARG:HB3	38:55:118:GLU:OE2	2.21	0.41
40:75:51:ARG:HG3	40:75:98:LYS:HE3	2.02	0.41
41:85:85:LYS:HD2	41:85:85:LYS:HA	1.92	0.41
43:A5:68:ARG:O	43:A5:109:GLU:HA	2.20	0.41
46:D5:23:LYS:HD3	46:D5:40:ASP:HA	2.02	0.41
49:G5:8:LYS:HE2	49:G5:8:LYS:HB3	1.89	0.41
50:H5:4:LEU:O	50:H5:36:VAL:HA	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:13:320:C:H42	1:13:333:G:H1	1.69	0.41
1:13:967:C:H5"	1:13:968:A:OP2	2.20	0.41
1:13:1226:C:OP2	13:4I:103:THR:OG1	2.33	0.41
2:1E:28:PHE:CE2	2:1E:190:THR:HA	2.55	0.41
4:3E:126:ILE:HD13	4:3E:126:ILE:HA	1.91	0.41
8:7E:110:ALA:HB3	8:7E:121:ASP:HB3	2.01	0.41
15:6I:71:GLN:O	15:6I:71:GLN:NE2	2.53	0.41
24:3K:29:C:N3	24:3K:41:G:N1	2.55	0.41
24:3K:38:A:H2'	24:3K:39:G:O4'	2.20	0.41
24:3K:59:A:N3	24:3K:59:A:H2'	2.35	0.41
26:1H:270(M):U:O2'	26:1H:270(N):G:C8	2.74	0.41
26:1H:1266:G:O2'	26:1H:2012:G:O6	2.38	0.41
26:1H:1973:G:H2'	26:1H:1974:C:C6	2.55	0.41
26:1H:2259:G:C2	26:1H:2282:G:N1	2.89	0.41
28:11:9:TYR:CZ	28:11:13:ARG:HG2	2.56	0.41
28:11:158:ALA:O	28:11:159:ALA:C	2.62	0.41
29:21:105:THR:HB	29:21:197:ILE:HG23	2.03	0.41
31:41:44:GLY:C	31:41:46:ALA:H	2.28	0.41
31:41:167:GLU:CD	31:41:167:GLU:H	2.27	0.41
36:78:50:ARG:HD3	54:Q8:7:HIS:CD2	2.56	0.41
39:A8:42:ASP:C	39:A8:44:LYS:N	2.77	0.41
41:C8:91:ASP:O	41:C8:92:ARG:C	2.63	0.41
1:1G:790:A:H2'	1:1G:791:G:C8	2.56	0.41
1:1G:1117:G:O3'	9:82:104:ARG:HG2	2.20	0.41
1:1G:1153:C:H2'	1:1G:1154:G:O4'	2.21	0.41
1:1G:1194:U:H4'	5:42:22:GLY:O	2.21	0.41
1:1G:1205:U:O2'	3:22:195:VAL:HG13	2.20	0.41
1:1G:1206:G:C6	1:1G:1207:G:C6	3.09	0.41
1:1G:1321:C:C4	1:1G:1322:C:C4	3.08	0.41
1:1G:1410:G:H2'	1:1G:1411:C:C6	2.56	0.41
2:12:22:LYS:HE2	2:12:24:TRP:HZ3	1.86	0.41
3:22:39:ILE:O	3:22:43:LEU:HB2	2.20	0.41
5:42:99:GLY:O	5:42:117:ASP:HA	2.19	0.41
6:52:5:GLU:HG3	6:52:93:SER:OG	2.20	0.41
11:2A:103:LEU:HD12	11:2A:103:LEU:HA	1.81	0.41
26:14:228:A:H2'	26:14:230:U:O4'	2.19	0.41
26:14:744:G:OP1	29:29:132:HIS:HA	2.21	0.41
26:14:957:A:H4'	37:45:74:TYR:OH	2.21	0.41
28:19:70:TRP:HZ3	28:19:146:GLU:CD	2.29	0.41
29:29:76:ARG:C	29:29:78:LEU:H	2.29	0.41
37:45:64:ILE:HA	37:45:106:VAL:HG12	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:55:117:VAL:O	38:55:118:GLU:HB2	2.21	0.41
39:65:89:ARG:HG3	39:65:92:TYR:O	2.21	0.41
41:85:92:ARG:NH2	42:95:11:GLN:H	2.18	0.41
43:A5:59:VAL:HG12	43:A5:60:ASN:OD1	2.21	0.41
46:D5:5:LEU:HD21	46:D5:44:PHE:HA	2.03	0.41
1:13:20:U:H2'	1:13:21:G:O4'	2.20	0.41
1:13:184:G:H2'	1:13:185:A:H8	1.85	0.41
1:13:322:C:O2'	20:BI:23:ARG:HD2	2.20	0.41
1:13:507:C:OP2	1:13:508:C:O2'	2.34	0.41
1:13:648:A:C6	1:13:649:G:C5	3.09	0.41
1:13:848:C:H6	1:13:848:C:O5'	2.04	0.41
1:13:1226:C:O3'	13:4I:111:LYS:NZ	2.53	0.41
2:1E:118:LEU:CD1	2:1E:142:LEU:HB2	2.51	0.41
4:3E:99:SER:HB3	4:3E:139:ARG:HG3	2.02	0.41
5:4E:6:PHE:CD1	5:4E:36:ASP:HB3	2.55	0.41
6:5E:94:GLN:NE2	18:9I:33:ASP:OD2	2.42	0.41
7:6E:16:LEU:HD12	7:6E:16:LEU:HA	1.80	0.41
10:1I:47:PHE:CE1	14:5I:37:PHE:HE2	2.37	0.41
11:2I:73:MET:HG2	11:2I:103:LEU:HD13	2.03	0.41
17:8I:86:GLU:O	17:8I:90:ILE:HG12	2.21	0.41
19:AI:41:VAL:HA	19:AI:44:MET:HG3	2.03	0.41
20:BI:97:ALA:O	20:BI:99:LEU:HD13	2.20	0.41
22:1K:21:A:C5	22:1K:46:G:C6	3.08	0.41
24:3K:43:G:H2'	24:3K:44:A:H8	1.85	0.41
26:1H:37:C:H2'	26:1H:38:A:C8	2.56	0.41
26:1H:270(G):C:H2'	26:1H:270(H):C:C6	2.56	0.41
26:1H:592:G:C2	54:Q8:4:MET:HE1	2.55	0.41
26:1H:705:A:O3'	28:11:7:LYS:HD2	2.21	0.41
26:1H:1061:U:N3	26:1H:1063:G:OP1	2.54	0.41
26:1H:1931:U:O2	26:1H:1931:U:O4'	2.39	0.41
26:1H:1983:C:O2'	26:1H:1984:G:H5'	2.20	0.41
26:1H:2019:A:C4'	41:C8:34:LYS:HD2	2.51	0.41
26:1H:2114:A:H5"	26:1H:2117:A:OP2	2.21	0.41
26:1H:2543:G:H2'	26:1H:2544:G:C8	2.54	0.41
26:1H:2638:G:OP1	29:21:82:ARG:NH2	2.54	0.41
26:1H:2729:G:H1'	29:21:187:ALA:HB2	2.02	0.41
27:16:8:U:O2'	39:A8:40:ILE:HD13	2.20	0.41
28:11:14:ARG:HH11	28:11:14:ARG:HD2	1.67	0.41
28:11:123:ALA:HB3	28:11:131:LEU:HG	2.02	0.41
29:21:55:ASN:O	29:21:56:PRO:C	2.63	0.41
32:51:137:ASP:OD1	32:51:138:LYS:N	2.49	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:61:44:LEU:HD12	33:61:44:LEU:HA	1.92	0.41
33:61:114:LEU:HA	33:61:129:THR:O	2.21	0.41
34:58:30:ILE:HG23	34:58:52:VAL:HG11	2.03	0.41
34:58:37:LYS:HE2	34:58:37:LYS:HB3	1.75	0.41
37:88:81:VAL:HG23	37:88:82:ARG:O	2.20	0.41
38:98:53:HIS:HB2	38:98:94:TYR:HE2	1.86	0.41
39:A8:14:VAL:O	39:A8:18:ILE:HD13	2.21	0.41
39:A8:89:ARG:O	39:A8:90:GLY:C	2.64	0.41
39:A8:108:GLY:O	39:A8:110:LEU:HG	2.21	0.41
40:B8:24:PRO:O	40:B8:94:ALA:HB2	2.21	0.41
41:C8:75:ASN:HB3	41:C8:77:SER:H	1.86	0.41
47:I8:47:PRO:HG3	47:I8:53:MET:HB2	2.02	0.41
51:M8:41:PRO:HA	51:M8:47:GLN:OE1	2.20	0.41
1:1G:128:G:C6	1:1G:129:U:C4	3.09	0.41
1:1G:236:G:H2'	1:1G:237:C:O4'	2.19	0.41
1:1G:345:C:H5'	1:1G:346:G:C5	2.55	0.41
1:1G:570:G:H2'	1:1G:571:U:C6	2.56	0.41
1:1G:756:C:H2'	1:1G:757:U:O4'	2.21	0.41
1:1G:894:G:C6	1:1G:895:G:C5	3.09	0.41
1:1G:965:A:C2	1:1G:969:A:C2	3.09	0.41
1:1G:1181:G:C2	1:1G:1182:G:H1'	2.56	0.41
1:1G:1300:G:O2'	1:1G:1301:U:P	2.78	0.41
2:12:19:HIS:O	2:12:39:ILE:HG22	2.21	0.41
2:12:25:ASN:HA	2:12:26:PRO:HD3	1.89	0.41
2:12:132:LYS:HA	2:12:135:GLN:HG3	2.03	0.41
2:12:136:VAL:O	2:12:139:LYS:HG2	2.21	0.41
3:22:14:ILE:O	3:22:16:ARG:N	2.54	0.41
4:32:31:CYS:SG	4:32:34:GLU:HG2	2.60	0.41
4:32:107:ARG:HH22	4:32:194:LEU:CD1	2.34	0.41
5:42:12:LEU:O	5:42:30:ALA:HA	2.21	0.41
5:42:39:GLY:O	5:42:69:VAL:N	2.50	0.41
7:62:15:ASP:CB	7:62:20:ASP:H	2.31	0.41
7:62:71:PRO:HD3	7:62:103:TRP:CZ3	2.55	0.41
10:1A:13:HIS:HB3	10:1A:68:HIS:NE2	2.36	0.41
13:4A:97:PRO:HA	13:4A:110:ARG:HD3	2.02	0.41
26:14:577:G:O2'	26:14:1254:A:OP1	2.38	0.41
26:14:1007:C:H5"	34:15:35:ARG:HH11	1.86	0.41
26:14:1033:U:H3'	26:14:1033:U:C6	2.55	0.41
26:14:2032:G:O2'	29:29:145:LYS:HE3	2.21	0.41
26:14:2038:G:H2'	26:14:2039:C:O4'	2.21	0.41
26:14:2052:G:C8	29:29:141:ILE:HD11	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:14:2756:U:H4'	26:14:2757:A:OP1	2.18	0.41
26:14:2781:A:H5"	26:14:2782:G:H5'	2.03	0.41
26:14:2861:G:C2	26:14:2862:G:C4	3.09	0.41
31:49:77:ILE:HD13	31:49:77:ILE:HA	1.81	0.41
31:49:114:ILE:HD13	31:49:140:ILE:HG21	2.03	0.41
32:59:121:ILE:HG23	32:59:133:VAL:CG2	2.47	0.41
33:69:6:LEU:HD13	33:69:37:VAL:HG22	2.03	0.41
33:69:82:ARG:O	33:69:89:TYR:HD2	2.04	0.41
37:45:31:ASP:O	37:45:133:ARG:HG2	2.21	0.41
40:75:10:VAL:C	40:75:12:SER:N	2.79	0.41
40:75:106:SER:HA	40:75:110:ILE:HD11	2.03	0.41
42:95:62:LEU:HD11	42:95:95:LEU:HB2	2.02	0.41
48:F5:80:LEU:CD1	48:F5:82:LEU:HD13	2.51	0.41
1:13:280:C:O2	17:8I:38:ARG:HG3	2.20	0.41
1:13:321:A:H62	1:13:328:C:H1'	1.85	0.41
1:13:392:G:H5"	16:7I:12:LYS:HE3	2.03	0.41
1:13:447:G:C6	1:13:485:G:H1'	2.56	0.41
1:13:465:A:H2'	1:13:467:G:N7	2.35	0.41
1:13:532:A:N6	1:13:1206:G:O2'	2.54	0.41
1:13:631:G:O2'	1:13:632:A:H8	2.04	0.41
1:13:711:G:O2'	1:13:712:A:H5'	2.21	0.41
1:13:868:C:H2'	1:13:869:G:O4'	2.20	0.41
1:13:940:C:H2'	1:13:941:G:C8	2.56	0.41
1:13:985:C:H2'	1:13:986:A:C8	2.56	0.41
1:13:1044:A:C5	1:13:1045:C:H1'	2.56	0.41
1:13:1274:G:H2'	1:13:1275:A:C8	2.56	0.41
4:3E:155:LEU:HD22	4:3E:155:LEU:HA	1.93	0.41
7:6E:122:HIS:O	7:6E:126:ASP:N	2.43	0.41
9:8E:28:VAL:HA	9:8E:63:ILE:O	2.21	0.41
26:1H:12:U:P	26:1H:12:U:H6	2.44	0.41
26:1H:38:A:H2'	26:1H:39:C:C6	2.55	0.41
26:1H:259:G:N2	26:1H:621:A:C8	2.83	0.41
26:1H:705:A:C2	26:1H:706:A:C4	3.09	0.41
26:1H:1059:G:O6	26:1H:1088:A:C8	2.74	0.41
26:1H:2110:G:C6	26:1H:2120:G:C8	3.09	0.41
26:1H:2173:A:P	26:1H:2173:A:H8	2.44	0.41
26:1H:2273:A:H2'	26:1H:2274:A:C8	2.55	0.41
26:1H:2339:G:H2'	26:1H:2340:G:C8	2.55	0.41
26:1H:2483:C:C2	37:88:124:LYS:HE3	2.56	0.41
33:61:38:LEU:O	33:61:40:THR:HG23	2.21	0.41
34:58:40:PRO:O	41:C8:64:ARG:HG2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:88:134:ARG:HH12	46:H8:122:ARG:NE	2.19	0.41
39:A8:62:LYS:H	39:A8:62:LYS:HG2	1.53	0.41
43:E8:51:LEU:HD23	43:E8:51:LEU:HA	1.93	0.41
44:F8:57:LEU:N	44:F8:57:LEU:HD23	2.35	0.41
45:G8:94:LYS:HZ2	45:G8:95:LYS:N	2.17	0.41
49:K8:49:LYS:HA	49:K8:52:ASP:OD1	2.21	0.41
54:Q8:24:ALA:O	54:Q8:48:PHE:N	2.47	0.41
1:1G:598:U:H2'	1:1G:599:C:C6	2.56	0.41
1:1G:1063:C:H3'	1:1G:1064:G:H2'	2.03	0.41
1:1G:1250:A:H4'	9:82:68:GLY:H	1.86	0.41
1:1G:1328:C:O2'	13:4A:29:ARG:NE	2.40	0.41
1:1G:1410:G:H2'	1:1G:1411:C:H6	1.85	0.41
2:12:167:PRO:HG2	2:12:188:ALA:HB2	2.03	0.41
8:72:53:VAL:O	8:72:56:LYS:N	2.49	0.41
9:82:48:GLU:N	9:82:49:PRO:HD2	2.36	0.41
26:14:234:C:H2'	26:14:235:U:C6	2.56	0.41
26:14:685:A:H1'	26:14:688:U:O4	2.21	0.41
26:14:928:G:H2'	26:14:929:G:O4'	2.21	0.41
26:14:1376:C:N4	26:14:1377:G:C6	2.89	0.41
26:14:1914:C:H2'	26:14:1915:U:O4'	2.21	0.41
27:1J:52:A:O2'	27:1J:53:A:N7	2.51	0.41
28:19:75:ILE:HD13	28:19:99:ASP:OD2	2.20	0.41
29:29:101:ARG:HD2	29:29:169:ASN:CG	2.45	0.41
29:29:170:LEU:HD13	29:29:170:LEU:HA	1.91	0.41
30:39:145:GLU:O	30:39:145:GLU:HG2	2.21	0.41
35:25:49:ARG:HA	35:25:53:LYS:NZ	2.36	0.41
38:55:99:LYS:O	52:J5:44:THR:HA	2.21	0.41
1:13:186(C):G:C4	1:13:191(E):G:C2	3.10	0.40
1:13:186(F):C:H5"	1:13:187:C:OP2	2.22	0.40
1:13:237:C:H5"	17:8I:25:ARG:NH1	2.35	0.40
1:13:667:G:H4'	15:6I:51:HIS:CE1	2.56	0.40
1:13:1333:A:H2'	1:13:1334:G:O4'	2.21	0.40
4:3E:105:VAL:HG13	4:3E:110:PHE:HB2	2.03	0.40
8:7E:51:VAL:HG21	8:7E:60:ARG:NH1	2.36	0.40
18:9I:47:THR:HA	18:9I:83:GLU:HB2	2.02	0.40
21:1F:2:GLY:C	21:1F:4:GLY:H	2.27	0.40
24:3K:37:A:C5	24:3K:38:A:C8	3.09	0.40
26:1H:287:C:O2'	26:1H:288:C:H5'	2.20	0.40
26:1H:828:U:H4'	26:1H:831:G:N1	2.36	0.40
26:1H:1045:A:H1'	26:1H:1047:G:C4	2.56	0.40
26:1H:1287:A:H5"	26:1H:1288:U:OP2	2.20	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1H:1564:C:O2'	26:1H:1565:C:H5'	2.21	0.40
26:1H:1668:A:H4'	26:1H:1669:A:O5'	2.20	0.40
26:1H:1728:G:O6	26:1H:1730:U:H5"	2.22	0.40
26:1H:2882:A:OP1	38:98:96:ARG:NH1	2.42	0.40
28:11:85:ASP:OD2	28:11:88:ARG:NH1	2.44	0.40
32:51:92:ILE:HD12	32:51:92:ILE:N	2.37	0.40
36:78:71:VAL:HG13	36:78:72:PRO:CD	2.49	0.40
37:88:111:GLU:O	37:88:115:MET:HG2	2.21	0.40
46:H8:125:LEU:C	46:H8:164:ALA:HB3	2.45	0.40
48:J8:86:SER:O	48:J8:88:LYS:N	2.54	0.40
49:K8:34:GLU:O	49:K8:38:GLN:HG3	2.21	0.40
1:1G:255:G:C2	1:1G:272:C:C2	3.09	0.40
1:1G:728:A:H2'	1:1G:729:A:C8	2.56	0.40
1:1G:1178:G:H2'	1:1G:1180:A:N7	2.37	0.40
1:1G:1428:A:H2'	1:1G:1429:C:C6	2.55	0.40
1:1G:1505:G:H2'	25:4L:15:A:OP2	2.21	0.40
3:22:9:GLY:HA2	3:22:12:LEU:HG	2.03	0.40
3:22:152:ILE:O	3:22:198:VAL:HA	2.21	0.40
17:8A:45:HIS:O	17:8A:73:VAL:HG12	2.20	0.40
19:AA:21:GLU:HG2	19:AA:21:GLU:H	1.69	0.40
20:BA:86:ARG:CZ	20:BA:86:ARG:HB2	2.51	0.40
23:2L:51:U:H2'	23:2L:52:C:H6	1.86	0.40
26:14:77:C:OP1	49:G5:59:ARG:HD3	2.21	0.40
26:14:1568:G:P	28:19:63:ARG:HH22	2.44	0.40
26:14:1651:G:N7	38:55:11:ASN:ND2	2.69	0.40
26:14:2658:C:H2'	26:14:2659:G:O4'	2.21	0.40
28:19:58:HIS:ND1	28:19:59:LYS:N	2.69	0.40
37:45:16:ARG:HB2	37:45:18:LYS:HG3	2.03	0.40
39:65:81:GLY:O	39:65:83:LYS:HG3	2.21	0.40
44:B5:40:LYS:C	44:B5:42:ALA:H	2.30	0.40
46:D5:48:PHE:CE1	46:D5:71:VAL:HG21	2.49	0.40
46:D5:53:ILE:HA	46:D5:71:VAL:HG13	2.02	0.40
48:F5:57:GLU:O	48:F5:58:ILE:HD13	2.21	0.40
49:G5:43:GLN:HA	49:G5:45:SER:H	1.85	0.40
1:13:19:C:OP1	5:4E:125:SER:OG	2.36	0.40
1:13:1331:G:HO2'	1:13:1332:A:P	2.44	0.40
3:2E:19:GLU:O	3:2E:40:ARG:NH2	2.54	0.40
3:2E:47:LEU:HB2	3:2E:52:LEU:HD13	2.04	0.40
4:3E:74:GLN:O	4:3E:78:LEU:HG	2.20	0.40
4:3E:86:LYS:HB2	4:3E:86:LYS:HE3	1.82	0.40
5:4E:142:LEU:HA	5:4E:142:LEU:HD23	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:6E:42:ILE:HG13	7:6E:117:ALA:HB2	2.01	0.40
11:2I:46:GLY:HA2	11:2I:50:TYR:O	2.22	0.40
11:2I:62:GLN:O	11:2I:66:LEU:HG	2.21	0.40
20:BI:55:ILE:HD13	20:BI:55:ILE:HA	1.89	0.40
26:1H:65:C:H2'	26:1H:66:C:H6	1.85	0.40
26:1H:301:G:C4	26:1H:302:C:C5	3.09	0.40
26:1H:319:C:C2	26:1H:333:G:N2	2.89	0.40
26:1H:330:A:H2	26:1H:1210:A:O2'	2.04	0.40
26:1H:363:G:N2	26:1H:363(A):A:C5	2.89	0.40
26:1H:527:C:H4'	26:1H:528:A:H5'	2.03	0.40
26:1H:1043:C:C4	26:1H:1044:G:N7	2.89	0.40
26:1H:1087:G:C4	26:1H:1089:G:H1'	2.56	0.40
26:1H:1185:C:H5"	59:1H:3774:HOH:O	2.21	0.40
26:1H:1636:C:H2'	26:1H:1637:A:C8	2.57	0.40
26:1H:1729:A:H1'	26:1H:1730:U:C5	2.56	0.40
26:1H:1753:G:N1	26:1H:1756:G:C2	2.89	0.40
26:1H:2545:G:H2'	26:1H:2546:U:O4'	2.22	0.40
27:16:1(M):A:H3'	27:16:0:A:C8	2.56	0.40
27:16:30:C:OP2	39:A8:32:LEU:HD11	2.22	0.40
33:61:25:TYR:HD1	33:61:25:TYR:HA	1.79	0.40
33:61:123:LEU:HD23	33:61:142:VAL:O	2.21	0.40
39:A8:25:ARG:O	39:A8:39:ILE:HA	2.21	0.40
41:C8:50:ARG:HG2	41:C8:53:ARG:NH2	2.36	0.40
41:C8:95:LEU:HD22	42:D8:4:ILE:HD13	2.02	0.40
42:D8:19:LYS:HA	42:D8:94:LEU:O	2.21	0.40
42:D8:37:VAL:HG23	42:D8:51:VAL:CG2	2.50	0.40
46:H8:116:VAL:CG2	46:H8:146:ILE:HA	2.47	0.40
48:J8:53:VAL:HG12	48:J8:54:ALA:H	1.87	0.40
48:J8:95:LEU:C	48:J8:97:LEU:H	2.29	0.40
49:K8:32:LEU:HD13	49:K8:36:ARG:NH1	2.34	0.40
51:M8:16:CYS:CB	51:M8:36:CYS:HB3	2.49	0.40
52:N8:40:LYS:NZ	52:N8:46:CYS:HB3	2.36	0.40
1:1G:607:A:H2'	1:1G:608:A:O4'	2.22	0.40
1:1G:956:U:H1'	1:1G:1225:A:H2	1.85	0.40
1:1G:1287:A:H2'	1:1G:1288:A:C8	2.56	0.40
5:42:60:TYR:HB3	5:42:64:ARG:NH2	2.36	0.40
6:52:25:ILE:H	6:52:25:ILE:HG12	1.58	0.40
8:72:33:GLU:HG3	8:72:48:TYR:CE2	2.57	0.40
18:9A:45:SER:HG	18:9A:47:THR:HG1	1.66	0.40
26:14:41:C:H2'	26:14:43:G:H8	1.86	0.40
26:14:59:U:O2'	26:14:73:A:H2'	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:14:492:A:H8	26:14:492:A:O5'	2.05	0.40
26:14:858:U:OP1	47:E5:44:ARG:NH2	2.54	0.40
26:14:1005:C:H2'	26:14:1006:C:H6	1.85	0.40
26:14:1007:C:H5"	34:15:35:ARG:NH1	2.36	0.40
26:14:1248:G:C5	41:85:3:ARG:HB2	2.56	0.40
26:14:1257:C:OP1	30:39:75:HIS:HE1	2.04	0.40
26:14:1266:G:O2'	26:14:2012:G:O6	2.37	0.40
26:14:1647:G:P	26:14:1647:G:H3'	2.61	0.40
26:14:1889:A:N1	26:14:2234:G:H1'	2.36	0.40
26:14:2697:G:H2'	26:14:2698:U:O4'	2.22	0.40
28:19:108:PRO:HG2	28:19:111:LEU:HG	2.03	0.40
30:39:4:VAL:HG12	30:39:17:ARG:HG2	2.03	0.40
31:49:43:LEU:HD12	31:49:45:GLU:CD	2.46	0.40
32:59:149:ARG:O	32:59:154:PRO:HB3	2.21	0.40
32:59:149:ARG:HA	32:59:162:ILE:HD12	2.03	0.40
46:D5:4:ARG:HD3	46:D5:60:GLU:CD	2.46	0.40
1:13:160:A:N3	1:13:160:A:H2'	2.35	0.40
1:13:454:C:H3'	1:13:455:C:H6	1.85	0.40
1:13:626:U:C4	1:13:627:G:N7	2.89	0.40
1:13:827:U:H5	1:13:872:A:N1	2.20	0.40
1:13:955:U:H1'	1:13:1227:A:N6	2.37	0.40
1:13:1118:C:P	9:8E:104:ARG:HH11	2.44	0.40
2:1E:5:ILE:HG22	2:1E:224:GLN:NE2	2.34	0.40
3:2E:36:ASP:O	3:2E:40:ARG:HG3	2.21	0.40
3:2E:113:ALA:O	3:2E:114:PRO:C	2.62	0.40
3:2E:167:TRP:CD1	3:2E:167:TRP:C	2.99	0.40
4:3E:107:ARG:HA	4:3E:107:ARG:HD2	1.74	0.40
4:3E:122:ARG:HH11	4:3E:122:ARG:HG2	1.86	0.40
8:7E:7:ALA:HB2	8:7E:85:ARG:HH11	1.86	0.40
8:7E:12:ARG:HD3	8:7E:26:VAL:HB	2.03	0.40
9:8E:94:ALA:O	9:8E:98:PRO:HD2	2.21	0.40
12:3I:117:ARG:C	12:3I:119:LYS:O	2.64	0.40
17:8I:67:LYS:O	17:8I:68:ARG:HB3	2.21	0.40
19:AI:10:PHE:CD1	19:AI:10:PHE:C	3.00	0.40
26:1H:128:C:H2'	26:1H:129:C:H6	1.85	0.40
26:1H:453:C:H5"	59:1H:4145:HOH:O	2.21	0.40
26:1H:654(A):A:C2	26:1H:654(T):A:N1	2.89	0.40
26:1H:755:C:H2'	26:1H:756:C:C6	2.56	0.40
26:1H:2145:C:H5	26:1H:2148:G:H21	1.69	0.40
26:1H:2235:G:H2'	26:1H:2236:C:H6	1.86	0.40
26:1H:2406:U:N3	36:78:73:GLY:O	2.33	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1H:2592:G:N7	59:1H:3915:HOH:O	2.37	0.40
26:1H:2729:G:H2'	26:1H:2730:C:C6	2.55	0.40
27:16:40:U:H1'	27:16:45:A:N6	2.37	0.40
30:31:151:SER:C	30:31:152:GLU:HG3	2.44	0.40
30:31:178:PRO:HB2	30:31:201:VAL:HG11	2.03	0.40
31:41:59:GLU:OE1	31:41:138:GLN:NE2	2.54	0.40
32:51:132:ARG:HE	32:51:132:ARG:HB3	1.73	0.40
35:68:71:ARG:HH11	40:B8:74:ARG:HH21	1.69	0.40
36:78:79:ARG:HD2	36:78:110:TYR:CE1	2.57	0.40
43:E8:12:ILE:HG13	43:E8:42:ARG:NH1	2.31	0.40
46:H8:7:ALA:O	46:H8:8:TYR:CG	2.74	0.40
46:H8:142:SER:C	46:H8:144:LEU:HG	2.46	0.40
48:J8:8:SER:OG	48:J8:10:LYS:HG3	2.22	0.40
51:M8:39:CYS:HB3	51:M8:41:PRO:CD	2.48	0.40
53:P8:5:TRP:HA	53:P8:5:TRP:CE3	2.55	0.40
1:1G:799:G:O6	1:1G:800:G:C2	2.74	0.40
1:1G:957:U:C1'	1:1G:960:U:H5	2.27	0.40
1:1G:1086:U:H2'	1:1G:1087:G:H8	1.86	0.40
1:1G:1131:G:N7	1:1G:1132:C:C5	2.89	0.40
1:1G:1240:U:H5'	1:1G:1241:G:C8	2.57	0.40
1:1G:1350:A:C6	1:1G:1351:U:C4	3.10	0.40
2:12:144:ARG:HE	2:12:144:ARG:HB2	1.64	0.40
5:42:70:PRO:HB3	5:42:144:THR:CG2	2.52	0.40
15:6A:39:LEU:HD12	15:6A:56:LEU:HB2	2.02	0.40
16:7A:39:TYR:CD2	16:7A:73:LEU:HD11	2.57	0.40
22:1L:18:G:N2	22:1L:57:G:H5'	2.37	0.40
26:14:312:G:H4'	26:14:331:A:N3	2.36	0.40
26:14:315:G:H2'	26:14:316:C:H6	1.86	0.40
26:14:780:G:H21	26:14:783:A:N6	2.09	0.40
26:14:828:U:C5	26:14:2247:A:H4'	2.56	0.40
26:14:1131:G:C2	26:14:1132:A:C4	3.10	0.40
26:14:1387:C:C2	26:14:1388:G:C8	3.09	0.40
26:14:1392:A:N6	26:14:1393:A:N6	2.69	0.40
26:14:1499:C:H2'	26:14:1500:G:H8	1.86	0.40
26:14:1614:A:N1	43:A5:93:ALA:HB2	2.36	0.40
26:14:1628:G:H2'	26:14:1629:U:H6	1.84	0.40
26:14:1753:G:N1	26:14:1756:G:C2	2.89	0.40
26:14:1963:U:O2	26:14:1963:U:H2'	2.21	0.40
26:14:2224:G:H4'	26:14:2226:C:C2	2.57	0.40
26:14:2688:U:H3'	26:14:2688:U:O2	2.21	0.40
27:1J:11:C:H3'	27:1J:12:C:C6	2.57	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:19:35:LYS:HB3	28:19:35:LYS:HE2	1.12	0.40
29:29:103:ASP:OD1	29:29:201:THR:HG23	2.22	0.40
31:49:51:ARG:O	31:49:51:ARG:HG3	2.20	0.40
32:59:103:LEU:HD11	32:59:115:VAL:O	2.22	0.40
32:59:157:TYR:CD2	32:59:171:LEU:HD11	2.56	0.40
33:69:102:SER:HA	33:69:107:VAL:O	2.21	0.40
33:69:125:GLU:OE1	33:69:141:LYS:HD3	2.21	0.40
42:95:28:GLU:O	42:95:61:VAL:HG11	2.21	0.40
44:B5:1:MET:HA	44:B5:2:LYS:HA	1.74	0.40
1:13:560:U:H4'	1:13:561:U:H5"	2.04	0.40
1:13:878:G:H5'	8:7E:89:PRO:HG2	2.04	0.40
1:13:1533:C:H4'	1:13:1534:A:C8	2.56	0.40
59:13:2055:HOH:O	10:1I:57:LYS:HG2	2.22	0.40
3:2E:43:LEU:O	3:2E:47:LEU:HB2	2.20	0.40
4:3E:99:SER:O	4:3E:140:VAL:HG22	2.21	0.40
18:9I:43:PHE:O	18:9I:51:LEU:HG	2.21	0.40
19:AI:33:THR:HG22	19:AI:49:ILE:HG22	2.02	0.40
26:1H:65:C:H2'	26:1H:66:C:C6	2.56	0.40
26:1H:107:C:H2'	26:1H:108:U:C6	2.56	0.40
26:1H:1515:C:H2'	26:1H:1516:U:C6	2.55	0.40
26:1H:1588:C:H2'	26:1H:1589:C:C6	2.57	0.40
26:1H:1830:C:O2'	26:1H:1831:G:H5'	2.22	0.40
26:1H:2184:G:C6	26:1H:2185:C:C4	3.09	0.40
26:1H:2324:C:H5"	26:1H:2325:G:H5'	2.02	0.40
30:31:176:LEU:HD21	30:31:180:GLY:O	2.21	0.40
32:51:83:TYR:CE2	32:51:138:LYS:HB2	2.56	0.40
33:61:9:LEU:HD13	33:61:9:LEU:HA	1.95	0.40
36:78:64:LYS:HD2	54:Q8:12:LYS:HG2	2.02	0.40
46:H8:7:ALA:HB3	46:H8:61:LEU:HB2	2.03	0.40
46:H8:42:VAL:H	46:H8:42:VAL:HG23	1.61	0.40
49:K8:3:LEU:HA	49:K8:3:LEU:HD23	1.66	0.40
1:1G:81:G:HO2'	1:1G:82:U:P	2.44	0.40
1:1G:151:A:H2'	1:1G:152:A:O4'	2.22	0.40
1:1G:1239:A:H4'	1:1G:1240:U:H5"	2.03	0.40
1:1G:1285:A:OP1	1:1G:1285:A:C8	2.73	0.40
6:52:35:ALA:HB1	6:52:65:VAL:HG11	2.04	0.40
7:62:93:PRO:HG2	7:62:94:ARG:HE	1.87	0.40
11:2A:85:ARG:HD3	11:2A:113:PRO:HD3	2.03	0.40
20:BA:54:LYS:HE3	20:BA:54:LYS:HB3	1.81	0.40
26:14:265:A:H1'	26:14:266:G:O4'	2.22	0.40
26:14:389:G:O5'	26:14:389:G:H8	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:14:654(C):G:N1	26:14:654(R):C:O2'	2.54	0.40
26:14:810:U:H6	26:14:810:U:O5'	2.04	0.40
26:14:1153:C:OP1	41:85:93:LYS:NZ	2.54	0.40
26:14:2323:G:H2'	26:14:2324:C:O4'	2.22	0.40
26:14:2478:A:H3'	26:14:2479:G:H8	1.86	0.40
26:14:2563:U:O2	26:14:2565:A:C8	2.74	0.40
26:14:2774:C:H2'	26:14:2775:A:O4'	2.21	0.40
28:19:137:PRO:HG2	28:19:140:THR:OG1	2.22	0.40
30:39:74:ARG:HH11	30:39:74:ARG:HD3	1.72	0.40
32:59:78:GLY:HA2	32:59:81:GLU:O	2.21	0.40
38:55:52:ILE:O	38:55:54:LEU:N	2.55	0.40
39:65:29:PHE:CD1	39:65:30:ARG:N	2.82	0.40
39:65:35:ILE:HG12	39:65:101:LEU:HD22	2.04	0.40
40:75:4:GLY:O	40:75:6:LEU:HB2	2.21	0.40
42:95:20:LEU:HA	42:95:20:LEU:HD12	1.81	0.40
42:95:99:ILE:H	42:95:99:ILE:HG13	1.62	0.40
46:D5:23:LYS:HB3	46:D5:38:TYR:CD1	2.56	0.40
48:F5:85:LEU:O	48:F5:85:LEU:HG	2.21	0.40
49:G5:4:SER:N	49:G5:5:GLU:HB2	2.36	0.40
1:13:848:C:H2'	1:13:849:C:O4'	2.20	0.40
1:13:949:A:OP1	13:4I:101:GLN:HB3	2.22	0.40
1:13:1024:G:N2	1:13:1025:U:H3	2.20	0.40
1:13:1319:A:O2'	1:13:1323:G:N7	2.42	0.40
2:1E:115:LEU:HD13	2:1E:145:LEU:HB2	2.02	0.40
5:4E:19:MET:HE1	5:4E:24:ARG:HH21	1.85	0.40
17:8I:70:ARG:O	17:8I:71:PHE:HD1	2.05	0.40
26:1H:194:G:H2'	26:1H:195:A:O4'	2.20	0.40
26:1H:586:A:N1	26:1H:809:G:O2'	2.43	0.40
26:1H:860:U:H5	26:1H:917:A:N1	2.17	0.40
26:1H:1063:G:N2	26:1H:1076:C:H1'	2.36	0.40
26:1H:1110:G:O2'	26:1H:1111:A:O5'	2.39	0.40
26:1H:1165:U:H2'	26:1H:1166:C:H6	1.86	0.40
26:1H:1260:G:C6	26:1H:1261:C:C4	3.09	0.40
26:1H:1386:C:OP2	26:1H:1396:U:C5	2.75	0.40
26:1H:2331:G:N3	26:1H:2336:A:C2	2.90	0.40
26:1H:2663:G:C6	26:1H:2664:G:C4	3.09	0.40
26:1H:2749:A:H4'	32:51:62:LYS:HB3	2.04	0.40
27:16:60:C:C2	27:16:61:G:C8	3.10	0.40
29:21:64:LYS:HD2	29:21:65:GLY:HA2	2.04	0.40
30:31:66:PRO:O	30:31:67:GLN:CB	2.62	0.40
36:78:135:LEU:HD23	36:78:135:LEU:HA	1.92	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:B8:26:ASP:CB	40:B8:91:ARG:HA	2.51	0.40
41:C8:39:LEU:O	41:C8:40:PHE:C	2.65	0.40
43:E8:19:LEU:O	52:N8:25:LEU:HD12	2.21	0.40
47:I8:23:VAL:HB	47:I8:26:TYR:HE1	1.86	0.40
48:J8:84:GLY:H	48:J8:85:LEU:HD22	1.86	0.40
54:Q8:62:LEU:HB3	54:Q8:65:GLU:HG2	2.04	0.40
1:1G:7:G:H5'	1:1G:298:A:O4'	2.21	0.40
1:1G:266:G:H5'	1:1G:268:C:H41	1.86	0.40
1:1G:487:A:H2'	1:1G:488:C:O4'	2.22	0.40
1:1G:1053:G:H4'	1:1G:1054:C:H3'	2.03	0.40
2:12:22:LYS:HB2	2:12:24:TRP:CE3	2.55	0.40
2:12:126:GLU:HB3	2:12:130:ARG:HH11	1.87	0.40
4:32:64:LEU:HB2	4:32:198:VAL:HG21	2.02	0.40
4:32:78:LEU:HD22	4:32:96:LEU:HB3	2.03	0.40
4:32:191:ARG:O	4:32:191:ARG:NH1	2.48	0.40
7:62:148:ASN:O	7:62:149:ARG:HD3	2.21	0.40
14:5A:47:LEU:HD23	14:5A:47:LEU:HA	1.74	0.40
26:14:433:C:C4	26:14:434:U:O4	2.75	0.40
26:14:676:A:H1'	26:14:2443:C:H1'	2.03	0.40
26:14:761:A:OP2	59:14:3569:HOH:O	2.22	0.40
26:14:1416:G:HO2'	26:14:1417:C:P	2.38	0.40
26:14:2190:G:H2'	26:14:2191:G:O4'	2.22	0.40
26:14:2801:A:N6	26:14:2894:G:H5'	2.36	0.40
39:65:18:ILE:HD13	39:65:87:PHE:O	2.20	0.40
40:75:5:ALA:N	40:75:6:LEU:CA	2.84	0.40
47:E5:50:ASN:C	47:E5:62:LEU:HB2	2.47	0.40
49:G5:46:GLN:N	49:G5:46:GLN:CD	2.80	0.40
53:L5:26:GLY:O	53:L5:30:VAL:HG23	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)
6:5E:15:ASP:OD2	4:32:27:TYR:OH[4_555]	2.19	0.01

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	203/256 (79%)	161 (79%)	41 (20%)	1 (0%)	24 49
2	1E	227/256 (89%)	175 (77%)	49 (22%)	3 (1%)	9 26
3	22	193/239 (81%)	161 (83%)	31 (16%)	1 (0%)	24 49
3	2E	203/239 (85%)	181 (89%)	21 (10%)	1 (0%)	24 49
4	32	205/209 (98%)	186 (91%)	19 (9%)	0	100 100
4	3E	205/209 (98%)	175 (85%)	29 (14%)	1 (0%)	24 49
5	42	148/162 (91%)	136 (92%)	12 (8%)	0	100 100
5	4E	147/162 (91%)	140 (95%)	7 (5%)	0	100 100
6	52	99/101 (98%)	93 (94%)	6 (6%)	0	100 100
6	5E	98/101 (97%)	91 (93%)	7 (7%)	0	100 100
7	62	134/156 (86%)	127 (95%)	7 (5%)	0	100 100
7	6E	152/156 (97%)	142 (93%)	10 (7%)	0	100 100
8	72	135/138 (98%)	118 (87%)	16 (12%)	1 (1%)	18 40
8	7E	136/138 (99%)	123 (90%)	11 (8%)	2 (2%)	8 23
9	82	119/128 (93%)	103 (87%)	14 (12%)	2 (2%)	7 20
9	8E	124/128 (97%)	102 (82%)	22 (18%)	0	100 100
10	1A	97/105 (92%)	83 (86%)	14 (14%)	0	100 100
10	1I	92/105 (88%)	80 (87%)	12 (13%)	0	100 100
11	2A	111/129 (86%)	96 (86%)	14 (13%)	1 (1%)	14 34
11	2I	109/129 (84%)	94 (86%)	14 (13%)	1 (1%)	14 34
12	3A	120/132 (91%)	100 (83%)	19 (16%)	1 (1%)	16 37
12	3I	120/132 (91%)	104 (87%)	15 (12%)	1 (1%)	16 37
13	4A	107/126 (85%)	84 (78%)	17 (16%)	6 (6%)	1 2
13	4I	117/126 (93%)	86 (74%)	26 (22%)	5 (4%)	2 4
14	5A	57/61 (93%)	46 (81%)	10 (18%)	1 (2%)	6 19

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
14	5I	58/61 (95%)	50 (86%)	5 (9%)	3 (5%)	1 3
15	6A	85/89 (96%)	82 (96%)	3 (4%)	0	100 100
15	6I	85/89 (96%)	71 (84%)	14 (16%)	0	100 100
16	7A	82/88 (93%)	74 (90%)	7 (8%)	1 (1%)	10 28
16	7I	81/88 (92%)	72 (89%)	9 (11%)	0	100 100
17	8A	97/105 (92%)	91 (94%)	6 (6%)	0	100 100
17	8I	98/105 (93%)	87 (89%)	11 (11%)	0	100 100
18	9A	67/88 (76%)	65 (97%)	2 (3%)	0	100 100
18	9I	66/88 (75%)	62 (94%)	4 (6%)	0	100 100
19	AA	59/93 (63%)	43 (73%)	15 (25%)	1 (2%)	7 20
19	AI	81/93 (87%)	67 (83%)	13 (16%)	1 (1%)	10 28
20	BA	101/106 (95%)	83 (82%)	17 (17%)	1 (1%)	12 32
20	BI	95/106 (90%)	84 (88%)	11 (12%)	0	100 100
21	1B	20/27 (74%)	17 (85%)	2 (10%)	1 (5%)	1 3
21	1F	21/27 (78%)	19 (90%)	2 (10%)	0	100 100
28	11	271/276 (98%)	249 (92%)	17 (6%)	5 (2%)	6 19
28	19	272/276 (99%)	235 (86%)	36 (13%)	1 (0%)	30 53
29	21	203/206 (98%)	159 (78%)	39 (19%)	5 (2%)	4 13
29	29	202/206 (98%)	146 (72%)	48 (24%)	8 (4%)	2 5
30	31	200/210 (95%)	178 (89%)	22 (11%)	0	100 100
30	39	202/210 (96%)	163 (81%)	35 (17%)	4 (2%)	6 16
31	41	177/182 (97%)	153 (86%)	23 (13%)	1 (1%)	21 45
31	49	178/182 (98%)	149 (84%)	27 (15%)	2 (1%)	11 29
32	51	172/180 (96%)	132 (77%)	31 (18%)	9 (5%)	1 3
32	59	167/180 (93%)	125 (75%)	42 (25%)	0	100 100
33	61	143/148 (97%)	111 (78%)	28 (20%)	4 (3%)	4 11
33	69	143/148 (97%)	107 (75%)	34 (24%)	2 (1%)	9 24
34	15	135/140 (96%)	118 (87%)	16 (12%)	1 (1%)	18 40
34	58	123/140 (88%)	109 (89%)	13 (11%)	1 (1%)	16 37
35	25	120/122 (98%)	110 (92%)	10 (8%)	0	100 100
35	68	120/122 (98%)	112 (93%)	8 (7%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
36	35	145/150 (97%)	117 (81%)	26 (18%)	2 (1%)	9 24
36	78	146/150 (97%)	111 (76%)	30 (20%)	5 (3%)	3 7
37	45	136/141 (96%)	106 (78%)	29 (21%)	1 (1%)	18 40
37	88	139/141 (99%)	120 (86%)	15 (11%)	4 (3%)	3 10
38	55	116/118 (98%)	104 (90%)	10 (9%)	2 (2%)	7 20
38	98	116/118 (98%)	102 (88%)	14 (12%)	0	100 100
39	65	108/112 (96%)	84 (78%)	23 (21%)	1 (1%)	14 34
39	A8	109/112 (97%)	85 (78%)	24 (22%)	0	100 100
40	75	138/146 (94%)	120 (87%)	16 (12%)	2 (1%)	9 24
40	B8	134/146 (92%)	112 (84%)	21 (16%)	1 (1%)	18 40
41	85	114/118 (97%)	99 (87%)	15 (13%)	0	100 100
41	C8	113/118 (96%)	97 (86%)	14 (12%)	2 (2%)	6 19
42	95	98/101 (97%)	79 (81%)	16 (16%)	3 (3%)	3 8
42	D8	98/101 (97%)	85 (87%)	13 (13%)	0	100 100
43	A5	109/113 (96%)	102 (94%)	7 (6%)	0	100 100
43	E8	108/113 (96%)	100 (93%)	8 (7%)	0	100 100
44	B5	92/96 (96%)	77 (84%)	14 (15%)	1 (1%)	11 29
44	F8	93/96 (97%)	88 (95%)	5 (5%)	0	100 100
45	C5	48/110 (44%)	39 (81%)	8 (17%)	1 (2%)	5 16
45	G8	93/110 (84%)	64 (69%)	25 (27%)	4 (4%)	2 4
46	D5	175/206 (85%)	123 (70%)	45 (26%)	7 (4%)	2 5
46	H8	168/206 (82%)	127 (76%)	35 (21%)	6 (4%)	2 6
47	E5	74/85 (87%)	64 (86%)	8 (11%)	2 (3%)	4 11
47	I8	75/85 (88%)	66 (88%)	9 (12%)	0	100 100
48	F5	92/98 (94%)	78 (85%)	12 (13%)	2 (2%)	5 15
48	J8	94/98 (96%)	79 (84%)	13 (14%)	2 (2%)	5 16
49	G5	67/72 (93%)	60 (90%)	6 (9%)	1 (2%)	8 23
49	K8	66/72 (92%)	58 (88%)	7 (11%)	1 (2%)	8 23
50	H5	56/60 (93%)	52 (93%)	4 (7%)	0	100 100
50	L8	56/60 (93%)	50 (89%)	6 (11%)	0	100 100
51	M8	56/71 (79%)	35 (62%)	19 (34%)	2 (4%)	2 6

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
52	J5	54/60 (90%)	45 (83%)	9 (17%)	0	100 100
52	N8	46/60 (77%)	37 (80%)	9 (20%)	0	100 100
53	L5	46/49 (94%)	44 (96%)	2 (4%)	0	100 100
53	P8	45/49 (92%)	42 (93%)	2 (4%)	1 (2%)	5 15
54	M5	62/65 (95%)	54 (87%)	8 (13%)	0	100 100
54	Q8	62/65 (95%)	47 (76%)	12 (19%)	3 (5%)	2 3
All	All	10929/11875 (92%)	9262 (85%)	1532 (14%)	135 (1%)	10 28

All (135) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
13	4I	12	ASN
28	11	239	ARG
33	61	134	PRO
34	58	96	GLU
36	78	36	LYS
37	88	6	ARG
40	B8	106	SER
41	C8	93	LYS
46	H8	53	ILE
46	H8	60	GLU
48	J8	87	PRO
49	K8	48	HIS
9	82	118	LYS
13	4A	67	GLU
13	4A	68	GLY
16	7A	83	GLU
36	35	36	LYS
38	55	107	ASP
40	75	11	GLU
46	D5	53	ILE
46	D5	60	GLU
48	F5	92	LYS
8	7E	87	SER
11	2I	54	ARG
19	AI	41	VAL
28	11	238	GLY
29	21	60	ASN
29	21	129	HIS
32	51	157	TYR

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Mol	Chain	Res	Type
32	51	171	LEU
33	61	12	LEU
36	78	15	ARG
36	78	16	ARG
36	78	25	SER
37	88	134	ARG
45	G8	54	LYS
45	G8	81	LYS
46	H8	6	LYS
46	H8	64	GLY
48	J8	86	SER
11	2A	101	SER
13	4A	84	ILE
21	1B	3	LYS
29	29	54	GLN
29	29	69	LYS
30	39	22	ALA
30	39	28	ILE
33	69	113	ARG
33	69	144	VAL
34	15	127	ASP
40	75	10	VAL
42	95	99	ILE
2	1E	238	LEU
13	4I	13	LYS
13	4I	14	ARG
14	5I	17	LYS
29	21	118	LYS
31	41	117	PHE
32	51	138	LYS
32	51	170	ARG
41	C8	89	GLU
51	M8	25	TYR
54	Q8	35	GLN
54	Q8	50	LEU
2	12	223	ILE
3	22	15	THR
14	5A	17	LYS
20	BA	49	ALA
28	19	273	ARG
30	39	124	LEU
37	45	84	GLY

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Mol	Chain	Res	Type
39	65	87	PHE
42	95	38	LEU
46	D5	93	ASP
46	D5	112	ARG
47	E5	33	ALA
48	F5	91	LYS
2	1E	156	LYS
3	2E	12	LEU
8	7E	86	ILE
13	4I	5	ALA
13	4I	27	LYS
14	5I	14	PRO
28	11	272	ALA
28	11	273	ARG
29	21	72	VAL
32	51	153	LYS
33	61	133	HIS
37	88	105	GLU
46	H8	52	SER
46	H8	111	VAL
54	Q8	47	LYS
12	3A	48	PRO
13	4A	83	ASP
13	4A	106	ASN
38	55	82	GLU
49	G5	47	ASN
2	1E	22	LYS
4	3E	84	LYS
32	51	137	ASP
36	78	7	ARG
37	88	5	ARG
51	M8	40	HIS
9	82	120	ARG
29	29	53	PRO
29	29	68	ALA
29	29	144	ARG
30	39	90	PHE
31	49	117	PHE
45	C5	17	SER
47	E5	34	GLY
28	11	122	ASP
33	61	83	ALA

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Mol	Chain	Res	Type
13	4A	95	GLY
19	AA	9	VAL
29	29	55	ASN
42	95	50	PRO
46	D5	52	SER
14	5I	13	THR
8	72	100	ILE
31	49	5	VAL
29	21	59	VAL
32	51	128	PRO
32	51	168	PRO
45	G8	53	PRO
29	29	77	ILE
44	B5	51	VAL
32	51	127	GLU
29	29	52	LEU
36	35	7	ARG
53	P8	46	VAL
46	D5	171	ILE
12	3I	48	PRO
46	D5	116	VAL
45	G8	82	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	179/220 (81%)	136 (76%)	43 (24%)	1 1
2	1E	200/220 (91%)	144 (72%)	56 (28%)	0 0
3	22	154/188 (82%)	113 (73%)	41 (27%)	0 1
3	2E	159/188 (85%)	126 (79%)	33 (21%)	1 3
4	32	180/181 (99%)	149 (83%)	31 (17%)	2 5
4	3E	180/181 (99%)	148 (82%)	32 (18%)	2 4
5	42	114/123 (93%)	88 (77%)	26 (23%)	1 2

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
5	4E	115/123 (94%)	92 (80%)	23 (20%)	1 3
6	52	90/90 (100%)	74 (82%)	16 (18%)	2 4
6	5E	90/90 (100%)	75 (83%)	15 (17%)	2 6
7	62	114/127 (90%)	92 (81%)	22 (19%)	1 3
7	6E	125/127 (98%)	99 (79%)	26 (21%)	1 3
8	72	118/119 (99%)	85 (72%)	33 (28%)	0 0
8	7E	119/119 (100%)	92 (77%)	27 (23%)	1 2
9	82	92/99 (93%)	70 (76%)	22 (24%)	1 1
9	8E	97/99 (98%)	75 (77%)	22 (23%)	1 2
10	1A	89/92 (97%)	66 (74%)	23 (26%)	0 1
10	1I	81/92 (88%)	66 (82%)	15 (18%)	1 4
11	2A	85/99 (86%)	70 (82%)	15 (18%)	2 5
11	2I	84/99 (85%)	64 (76%)	20 (24%)	1 1
12	3A	103/109 (94%)	73 (71%)	30 (29%)	0 0
12	3I	103/109 (94%)	80 (78%)	23 (22%)	1 2
13	4A	90/101 (89%)	66 (73%)	24 (27%)	0 0
13	4I	94/101 (93%)	72 (77%)	22 (23%)	1 2
14	5A	49/50 (98%)	33 (67%)	16 (33%)	0 0
14	5I	49/50 (98%)	38 (78%)	11 (22%)	1 2
15	6A	79/80 (99%)	72 (91%)	7 (9%)	9 24
15	6I	79/80 (99%)	65 (82%)	14 (18%)	2 4
16	7A	72/74 (97%)	63 (88%)	9 (12%)	4 13
16	7I	72/74 (97%)	55 (76%)	17 (24%)	1 1
17	8A	94/97 (97%)	81 (86%)	13 (14%)	3 10
17	8I	95/97 (98%)	75 (79%)	20 (21%)	1 2
18	9A	58/77 (75%)	43 (74%)	15 (26%)	0 1
18	9I	58/77 (75%)	51 (88%)	7 (12%)	5 14
19	AA	56/80 (70%)	43 (77%)	13 (23%)	1 2
19	AI	72/80 (90%)	51 (71%)	21 (29%)	0 0
20	BA	76/82 (93%)	67 (88%)	9 (12%)	5 15
20	BI	75/82 (92%)	62 (83%)	13 (17%)	2 5

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
21	1B	17/22 (77%)	16 (94%)	1 (6%)	18 41
21	1F	18/22 (82%)	16 (89%)	2 (11%)	6 17
28	11	214/218 (98%)	173 (81%)	41 (19%)	1 3
28	19	214/218 (98%)	164 (77%)	50 (23%)	1 2
29	21	162/166 (98%)	128 (79%)	34 (21%)	1 2
29	29	165/166 (99%)	132 (80%)	33 (20%)	1 3
30	31	161/166 (97%)	131 (81%)	30 (19%)	1 4
30	39	163/166 (98%)	118 (72%)	45 (28%)	0 0
31	41	153/156 (98%)	119 (78%)	34 (22%)	1 2
31	49	152/156 (97%)	120 (79%)	32 (21%)	1 2
32	51	143/148 (97%)	112 (78%)	31 (22%)	1 2
32	59	140/148 (95%)	98 (70%)	42 (30%)	0 0
33	61	122/124 (98%)	86 (70%)	36 (30%)	0 0
33	69	122/124 (98%)	93 (76%)	29 (24%)	1 1
34	15	116/119 (98%)	87 (75%)	29 (25%)	0 1
34	58	105/119 (88%)	83 (79%)	22 (21%)	1 2
35	25	100/100 (100%)	82 (82%)	18 (18%)	2 4
35	68	100/100 (100%)	80 (80%)	20 (20%)	1 3
36	35	114/116 (98%)	75 (66%)	39 (34%)	0 0
36	78	114/116 (98%)	77 (68%)	37 (32%)	0 0
37	45	109/111 (98%)	87 (80%)	22 (20%)	1 3
37	88	110/111 (99%)	94 (86%)	16 (14%)	3 9
38	55	101/101 (100%)	73 (72%)	28 (28%)	0 0
38	98	101/101 (100%)	73 (72%)	28 (28%)	0 0
39	65	87/88 (99%)	60 (69%)	27 (31%)	0 0
39	A8	87/88 (99%)	58 (67%)	29 (33%)	0 0
40	75	122/127 (96%)	95 (78%)	27 (22%)	1 2
40	B8	118/127 (93%)	82 (70%)	36 (30%)	0 0
41	85	93/94 (99%)	76 (82%)	17 (18%)	2 4
41	C8	92/94 (98%)	76 (83%)	16 (17%)	2 5
42	95	81/82 (99%)	62 (76%)	19 (24%)	1 1

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
42	D8	82/82 (100%)	57 (70%)	25 (30%)	0 0
43	A5	91/92 (99%)	71 (78%)	20 (22%)	1 2
43	E8	90/92 (98%)	74 (82%)	16 (18%)	2 4
44	B5	74/78 (95%)	59 (80%)	15 (20%)	1 3
44	F8	77/78 (99%)	63 (82%)	14 (18%)	2 4
45	C5	43/91 (47%)	35 (81%)	8 (19%)	1 4
45	G8	79/91 (87%)	62 (78%)	17 (22%)	1 2
46	D5	156/179 (87%)	125 (80%)	31 (20%)	1 3
46	H8	151/179 (84%)	104 (69%)	47 (31%)	0 0
47	E5	61/67 (91%)	48 (79%)	13 (21%)	1 2
47	I8	62/67 (92%)	53 (86%)	9 (14%)	3 9
48	F5	79/83 (95%)	59 (75%)	20 (25%)	0 1
48	J8	79/83 (95%)	62 (78%)	17 (22%)	1 2
49	G5	63/67 (94%)	41 (65%)	22 (35%)	0 0
49	K8	64/67 (96%)	41 (64%)	23 (36%)	0 0
50	H5	50/52 (96%)	44 (88%)	6 (12%)	5 14
50	L8	50/52 (96%)	42 (84%)	8 (16%)	2 8
51	M8	52/63 (82%)	37 (71%)	15 (29%)	0 0
52	J5	48/52 (92%)	40 (83%)	8 (17%)	2 6
52	N8	43/52 (83%)	32 (74%)	11 (26%)	0 1
53	L5	38/42 (90%)	33 (87%)	5 (13%)	4 12
53	P8	38/42 (90%)	31 (82%)	7 (18%)	1 4
54	M5	54/55 (98%)	44 (82%)	10 (18%)	1 4
54	Q8	54/55 (98%)	48 (89%)	6 (11%)	6 17
All	All	9213/9831 (94%)	7145 (78%)	2068 (22%)	1 2

All (2068) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	1E	5	ILE
2	1E	8	LYS
2	1E	15	VAL
2	1E	21	ARG
2	1E	28	PHE

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Mol	Chain	Res	Type
2	1E	32	ILE
2	1E	35	GLU
2	1E	63	MET
2	1E	67	THR
2	1E	68	ILE
2	1E	69	LEU
2	1E	71	VAL
2	1E	83	MET
2	1E	86	GLU
2	1E	87	ARG
2	1E	95	GLN
2	1E	96	ARG
2	1E	107	THR
2	1E	108	ILE
2	1E	109	SER
2	1E	111	ARG
2	1E	118	LEU
2	1E	121	LEU
2	1E	124	SER
2	1E	127	ILE
2	1E	129	GLU
2	1E	142	LEU
2	1E	144	ARG
2	1E	154	LEU
2	1E	155	LEU
2	1E	160	ASP
2	1E	162	ILE
2	1E	164	VAL
2	1E	168	THR
2	1E	169	LYS
2	1E	172	ILE
2	1E	178	ARG
2	1E	185	ILE
2	1E	187	LEU
2	1E	190	THR
2	1E	191	ASP
2	1E	195	ASP
2	1E	197	VAL
2	1E	200	ILE
2	1E	205	ASP
2	1E	210	SER
2	1E	211	ILE

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Mol	Chain	Res	Type
2	1E	212	GLN
2	1E	214	ILE
2	1E	217	ARG
2	1E	223	ILE
2	1E	224	GLN
2	1E	226	ARG
2	1E	230	VAL
2	1E	233	SER
2	1E	239	VAL
3	2E	3	ASN
3	2E	5	ILE
3	2E	8	ILE
3	2E	15	THR
3	2E	16	ARG
3	2E	31	HIS
3	2E	32	LEU
3	2E	44	GLU
3	2E	49	SER
3	2E	63	ASN
3	2E	64	VAL
3	2E	68	VAL
3	2E	70	VAL
3	2E	76	VAL
3	2E	79	ARG
3	2E	86	VAL
3	2E	93	LYS
3	2E	98	ASN
3	2E	104	GLN
3	2E	108	ASN
3	2E	116	VAL
3	2E	119	ARG
3	2E	132	ARG
3	2E	136	GLN
3	2E	154	SER
3	2E	167	TRP
3	2E	172	ARG
3	2E	178	LEU
3	2E	190	ARG
3	2E	192	THR
3	2E	196	LEU
3	2E	202	ILE
3	2E	206	GLU

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Mol	Chain	Res	Type
4	3E	3	ARG
4	3E	10	ARG
4	3E	12	CYS
4	3E	15	GLU
4	3E	19	LEU
4	3E	30	LYS
4	3E	31	CYS
4	3E	46	LYS
4	3E	53	ASP
4	3E	58	LEU
4	3E	61	LYS
4	3E	70	ILE
4	3E	83	SER
4	3E	84	LYS
4	3E	85	LYS
4	3E	86	LYS
4	3E	89	THR
4	3E	92	VAL
4	3E	99	SER
4	3E	108	LEU
4	3E	115	ARG
4	3E	122	ARG
4	3E	127	THR
4	3E	135	LEU
4	3E	141	ARG
4	3E	151	LYS
4	3E	155	LEU
4	3E	184	LYS
4	3E	188	LEU
4	3E	193	ASP
4	3E	204	ILE
4	3E	208	SER
5	4E	12	LEU
5	4E	13	ILE
5	4E	16	THR
5	4E	18	ARG
5	4E	24	ARG
5	4E	31	LEU
5	4E	41	VAL
5	4E	53	LEU
5	4E	64	ARG
5	4E	68	GLU

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Mol	Chain	Res	Type
5	4E	71	LEU
5	4E	72	GLN
5	4E	73	ASN
5	4E	79	GLU
5	4E	87	SER
5	4E	91	LEU
5	4E	112	LEU
5	4E	139	LEU
5	4E	144	THR
5	4E	147	ASP
5	4E	150	ARG
5	4E	152	ARG
5	4E	153	LYS
6	5E	16	GLN
6	5E	23	LYS
6	5E	24	GLU
6	5E	25	ILE
6	5E	31	GLU
6	5E	40	VAL
6	5E	43	LEU
6	5E	55	ASP
6	5E	65	VAL
6	5E	70	ASP
6	5E	75	LEU
6	5E	86	ARG
6	5E	91	VAL
6	5E	94	GLN
6	5E	100	ASN
7	6E	4	ARG
7	6E	9	VAL
7	6E	10	ARG
7	6E	12	LEU
7	6E	16	LEU
7	6E	17	VAL
7	6E	27	ILE
7	6E	38	LEU
7	6E	45	ASP
7	6E	50	ILE
7	6E	56	GLN
7	6E	59	LEU
7	6E	73	MET
7	6E	75	VAL

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Mol	Chain	Res	Type
7	6E	84	ASN
7	6E	89	MET
7	6E	90	GLU
7	6E	91	VAL
7	6E	104	LEU
7	6E	113	GLU
7	6E	120	ILE
7	6E	124	LEU
7	6E	125	MET
7	6E	126	ASP
7	6E	144	MET
7	6E	155	ARG
8	7E	1	MET
8	7E	10	LEU
8	7E	19	VAL
8	7E	25	ASP
8	7E	26	VAL
8	7E	39	LEU
8	7E	45	ILE
8	7E	49	GLU
8	7E	50	ARG
8	7E	51	VAL
8	7E	63	LEU
8	7E	68	ARG
8	7E	80	ILE
8	7E	82	HIS
8	7E	83	ILE
8	7E	84	ARG
8	7E	85	ARG
8	7E	91	ARG
8	7E	95	VAL
8	7E	102	ARG
8	7E	105	ARG
8	7E	107	LEU
8	7E	109	ILE
8	7E	112	LEU
8	7E	123	GLU
8	7E	129	VAL
8	7E	137	VAL
9	8E	3	GLN
9	8E	9	ARG
9	8E	35	GLU

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Mol	Chain	Res	Type
9	8E	38	GLN
9	8E	40	LEU
9	8E	42	ARG
9	8E	44	VAL
9	8E	47	LEU
9	8E	50	LEU
9	8E	51	ARG
9	8E	53	VAL
9	8E	58	HIS
9	8E	78	LYS
9	8E	79	LEU
9	8E	81	ILE
9	8E	83	ARG
9	8E	91	ASP
9	8E	96	LEU
9	8E	99	LEU
9	8E	104	ARG
9	8E	108	VAL
9	8E	112	LYS
10	1I	24	VAL
10	1I	25	GLU
10	1I	38	ILE
10	1I	49	VAL
10	1I	51	ARG
10	1I	58	ASP
10	1I	60	ARG
10	1I	61	GLU
10	1I	66	ARG
10	1I	70	ARG
10	1I	72	VAL
10	1I	75	ILE
10	1I	76	ASN
10	1I	78	ASN
10	1I	88	LEU
11	2I	16	SER
11	2I	29	ILE
11	2I	31	THR
11	2I	32	ILE
11	2I	51	LYS
11	2I	54	ARG
11	2I	63	LEU
11	2I	70	LYS

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Mol	Chain	Res	Type
11	2I	71	LYS
11	2I	77	MET
11	2I	81	ASP
11	2I	84	VAL
11	2I	87	THR
11	2I	99	GLN
11	2I	103	LEU
11	2I	105	VAL
11	2I	106	LYS
11	2I	109	VAL
11	2I	114	VAL
11	2I	117	ASN
12	3I	17	LYS
12	3I	18	VAL
12	3I	22	SER
12	3I	28	LYS
12	3I	33	ARG
12	3I	44	THR
12	3I	46	LYS
12	3I	55	VAL
12	3I	60	LEU
12	3I	62	SER
12	3I	64	TYR
12	3I	67	THR
12	3I	78	GLN
12	3I	79	GLU
12	3I	81	SER
12	3I	83	VAL
12	3I	91	LYS
12	3I	96	VAL
12	3I	111	LYS
12	3I	115	LYS
12	3I	116	SER
12	3I	123	LYS
12	3I	126	LYS
13	4I	9	ILE
13	4I	13	LYS
13	4I	19	LEU
13	4I	20	THR
13	4I	22	ILE
13	4I	27	LYS
13	4I	31	LYS

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Mol	Chain	Res	Type
13	4I	45	VAL
13	4I	48	LEU
13	4I	50	GLU
13	4I	56	LEU
13	4I	57	ARG
13	4I	60	VAL
13	4I	64	TRP
13	4I	67	GLU
13	4I	70	LEU
13	4I	82	MET
13	4I	106	ASN
13	4I	108	ARG
13	4I	109	THR
13	4I	111	LYS
13	4I	114	ARG
14	5I	4	LYS
14	5I	6	LEU
14	5I	8	GLU
14	5I	15	LYS
14	5I	18	VAL
14	5I	22	THR
14	5I	24	CYS
14	5I	32	SER
14	5I	33	VAL
14	5I	41	ARG
14	5I	44	LEU
15	6I	6	GLU
15	6I	7	GLU
15	6I	8	LYS
15	6I	17	ARG
15	6I	26	GLU
15	6I	39	LEU
15	6I	47	LYS
15	6I	48	LYS
15	6I	59	MET
15	6I	66	LEU
15	6I	71	GLN
15	6I	76	GLU
15	6I	79	ARG
15	6I	88	ARG
16	7I	1	MET
16	7I	6	LEU

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Mol	Chain	Res	Type
16	7I	8	ARG
16	7I	11	SER
16	7I	18	ARG
16	7I	19	ILE
16	7I	20	VAL
16	7I	27	LYS
16	7I	33	ILE
16	7I	35	LYS
16	7I	36	ILE
16	7I	45	THR
16	7I	50	LYS
16	7I	67	THR
16	7I	71	ARG
16	7I	72	ARG
16	7I	83	GLU
17	8I	21	VAL
17	8I	24	GLU
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	63	ARG
17	8I	68	ARG
17	8I	74	LEU
17	8I	79	SER
17	8I	85	VAL
17	8I	86	GLU
17	8I	89	LEU
17	8I	90	ILE
17	8I	100	LYS
17	8I	101	ARG
18	9I	21	LYS
18	9I	26	LEU
18	9I	28	GLU
18	9I	31	LEU
18	9I	36	ASN
18	9I	82	THR
18	9I	86	VAL

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Mol	Chain	Res	Type
19	AI	5	LEU
19	AI	11	VAL
19	AI	21	GLU
19	AI	27	GLU
19	AI	28	LYS
19	AI	29	ARG
19	AI	30	LEU
19	AI	31	ILE
19	AI	36	ARG
19	AI	37	ARG
19	AI	40	ILE
19	AI	41	VAL
19	AI	43	GLU
19	AI	44	MET
19	AI	45	VAL
19	AI	58	VAL
19	AI	62	ILE
19	AI	65	ASN
19	AI	71	LEU
19	AI	77	THR
19	AI	78	ARG
20	BI	15	ARG
20	BI	26	ASN
20	BI	30	LYS
20	BI	31	SER
20	BI	37	SER
20	BI	42	GLN
20	BI	53	LEU
20	BI	62	LEU
20	BI	68	LYS
20	BI	70	SER
20	BI	72	LEU
20	BI	74	LYS
20	BI	99	LEU
21	1F	10	ARG
21	1F	12	LYS
28	11	4	LYS
28	11	13	ARG
28	11	17	THR
28	11	32	SER
28	11	33	LEU
28	11	34	VAL

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Mol	Chain	Res	Type
28	11	37	LEU
28	11	38	LYS
28	11	39	LYS
28	11	43	ARG
28	11	61	LEU
28	11	64	ILE
28	11	65	ILE
28	11	83	GLU
28	11	94	LEU
28	11	101	GLU
28	11	103	ARG
28	11	105	ILE
28	11	106	ILE
28	11	113	VAL
28	11	136	ILE
28	11	138	VAL
28	11	141	VAL
28	11	154	LYS
28	11	164	GLN
28	11	165	ILE
28	11	171	ASP
28	11	173	VAL
28	11	183	ARG
28	11	192	THR
28	11	193	VAL
28	11	212	SER
28	11	217	ARG
28	11	221	VAL
28	11	229	VAL
28	11	242	ARG
28	11	253	GLN
28	11	257	LEU
28	11	270	ILE
28	11	271	ILE
28	11	273	ARG
29	21	2	LYS
29	21	14	ILE
29	21	23	VAL
29	21	26	ILE
29	21	33	VAL
29	21	34	VAL
29	21	40	GLU

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Mol	Chain	Res	Type
29	21	47	VAL
29	21	49	LEU
29	21	52	LEU
29	21	54	GLN
29	21	59	VAL
29	21	63	LEU
29	21	67	PHE
29	21	75	VAL
29	21	76	ARG
29	21	78	LEU
29	21	79	ARG
29	21	82	ARG
29	21	91	VAL
29	21	93	VAL
29	21	107	THR
29	21	111	ARG
29	21	116	VAL
29	21	118	LYS
29	21	119	ARG
29	21	146	THR
29	21	166	THR
29	21	167	VAL
29	21	175	VAL
29	21	179	GLU
29	21	197	ILE
29	21	201	THR
29	21	202	LYS
30	31	17	ARG
30	31	18	ARG
30	31	24	LEU
30	31	28	ILE
30	31	32	LEU
30	31	33	LEU
30	31	57	VAL
30	31	64	ILE
30	31	74	ARG
30	31	88	VAL
30	31	106	ARG
30	31	107	LYS
30	31	112	MET
30	31	117	ARG
30	31	137	LYS

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Mol	Chain	Res	Type
30	31	140	LEU
30	31	145	GLU
30	31	153	SER
30	31	158	THR
30	31	161	GLU
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	188	ARG
30	31	191	ARG
30	31	192	LEU
30	31	197	ASP
31	41	3	LEU
31	41	19	LEU
31	41	22	ARG
31	41	26	GLN
31	41	28	VAL
31	41	43	LEU
31	41	45	GLU
31	41	47	LYS
31	41	51	ARG
31	41	53	LEU
31	41	63	ILE
31	41	67	LYS
31	41	70	VAL
31	41	74	LYS
31	41	76	SER
31	41	80	PHE
31	41	82	LEU
31	41	90	LEU
31	41	94	LEU
31	41	96	ARG
31	41	101	ILE
31	41	121	ASN
31	41	133	LEU
31	41	136	ARG
31	41	139	LEU
31	41	145	THR
31	41	149	VAL

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Mol	Chain	Res	Type
31	41	152	LEU
31	41	160	VAL
31	41	161	THR
31	41	162	THR
31	41	165	THR
31	41	167	GLU
31	41	173	LEU
32	51	7	LEU
32	51	9	ILE
32	51	24	VAL
32	51	26	VAL
32	51	40	GLU
32	51	41	MET
32	51	42	ARG
32	51	43	VAL
32	51	45	VAL
32	51	49	VAL
32	51	50	VAL
32	51	53	GLU
32	51	56	SER
32	51	63	SER
32	51	71	LEU
32	51	86	GLU
32	51	88	LEU
32	51	98	LEU
32	51	104	GLU
32	51	105	LEU
32	51	121	ILE
32	51	122	THR
32	51	127	GLU
32	51	129	THR
32	51	130	ARG
32	51	131	VAL
32	51	139	GLN
32	51	140	LYS
32	51	152	ARG
32	51	160	LYS
32	51	167	GLU
33	61	2	LYS
33	61	3	VAL
33	61	7	GLU
33	61	9	LEU

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Mol	Chain	Res	Type
33	61	10	GLU
33	61	20	ASP
33	61	25	TYR
33	61	37	VAL
33	61	44	LEU
33	61	50	ARG
33	61	54	GLN
33	61	58	LEU
33	61	64	GLU
33	61	75	LEU
33	61	76	THR
33	61	81	VAL
33	61	82	ARG
33	61	85	GLU
33	61	92	VAL
33	61	95	LYS
33	61	104	GLN
33	61	110	ASP
33	61	112	LYS
33	61	116	LEU
33	61	117	GLU
33	61	120	ILE
33	61	122	GLU
33	61	127	VAL
33	61	129	THR
33	61	131	LYS
33	61	133	HIS
33	61	135	GLU
33	61	136	VAL
33	61	139	GLN
33	61	141	LYS
33	61	143	SER
34	58	2	LYS
34	58	5	VAL
34	58	7	LYS
34	58	9	VAL
34	58	14	VAL
34	58	16	ILE
34	58	21	LYS
34	58	32	THR
34	58	33	LEU
34	58	34	LEU

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Mol	Chain	Res	Type
34	58	55	VAL
34	58	58	ASP
34	58	60	ILE
34	58	65	LYS
34	58	67	LEU
34	58	83	LYS
34	58	84	LYS
34	58	87	LEU
34	58	90	MET
34	58	98	VAL
34	58	99	LEU
34	58	120	LEU
35	68	8	LEU
35	68	23	ARG
35	68	24	VAL
35	68	26	LYS
35	68	35	VAL
35	68	38	VAL
35	68	47	ILE
35	68	52	VAL
35	68	53	LYS
35	68	58	VAL
35	68	66	LYS
35	68	68	GLU
35	68	69	ILE
35	68	82	ASN
35	68	87	ILE
35	68	91	LEU
35	68	94	ARG
35	68	98	VAL
35	68	113	LYS
35	68	115	VAL
36	78	1	MET
36	78	5	ASP
36	78	6	LEU
36	78	10	PRO
36	78	15	ARG
36	78	19	VAL
36	78	21	ARG
36	78	25	SER
36	78	27	HIS
36	78	40	SER

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Mol	Chain	Res	Type
36	78	41	ARG
36	78	45	LEU
36	78	49	ARG
36	78	56	SER
36	78	58	THR
36	78	61	ARG
36	78	74	GLU
36	78	75	ILE
36	78	77	ARG
36	78	88	LEU
36	78	90	ARG
36	78	94	GLU
36	78	96	THR
36	78	98	GLU
36	78	100	LEU
36	78	101	VAL
36	78	105	LEU
36	78	106	LEU
36	78	112	LEU
36	78	115	LEU
36	78	117	GLU
36	78	119	GLU
36	78	126	VAL
36	78	135	LEU
36	78	138	LEU
36	78	144	GLU
36	78	146	VAL
37	88	5	ARG
37	88	11	LYS
37	88	18	LYS
37	88	25	ASP
37	88	35	VAL
37	88	45	GLN
37	88	55	VAL
37	88	56	ARG
37	88	81	VAL
37	88	83	MET
37	88	109	VAL
37	88	110	THR
37	88	112	GLU
37	88	129	THR
37	88	138	ASP

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Mol	Chain	Res	Type
37	88	141	GLN
38	98	1	MET
38	98	2	ARG
38	98	4	LEU
38	98	6	SER
38	98	9	LYS
38	98	17	ARG
38	98	18	LEU
38	98	24	GLN
38	98	27	SER
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	45	ARG
38	98	57	ARG
38	98	65	LEU
38	98	72	ASP
38	98	73	VAL
38	98	79	LEU
38	98	82	GLU
38	98	95	THR
38	98	100	LEU
38	98	105	ARG
38	98	113	LEU
38	98	118	GLU
39	A8	4	LEU
39	A8	8	GLU
39	A8	14	VAL
39	A8	17	ARG
39	A8	18	ILE
39	A8	20	ARG
39	A8	24	LEU
39	A8	27	SER
39	A8	30	ARG
39	A8	33	LYS
39	A8	35	ILE
39	A8	36	TYR
39	A8	39	ILE

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Mol	Chain	Res	Type
39	A8	43	GLU
39	A8	46	VAL
39	A8	48	LEU
39	A8	50	SER
39	A8	52	SER
39	A8	54	LEU
39	A8	57	LYS
39	A8	58	LEU
39	A8	69	VAL
39	A8	73	LEU
39	A8	83	LYS
39	A8	89	ARG
39	A8	97	ARG
39	A8	98	VAL
39	A8	101	LEU
39	A8	110	LEU
40	B8	1	MET
40	B8	6	LEU
40	B8	8	LYS
40	B8	10	VAL
40	B8	15	VAL
40	B8	17	THR
40	B8	18	ASP
40	B8	23	ARG
40	B8	27	THR
40	B8	30	VAL
40	B8	33	LYS
40	B8	38	ASN
40	B8	40	THR
40	B8	41	ARG
40	B8	42	ILE
40	B8	43	GLN
40	B8	49	VAL
40	B8	50	ILE
40	B8	58	ASN
40	B8	59	THR
40	B8	62	THR
40	B8	74	ARG
40	B8	85	LYS
40	B8	86	ILE
40	B8	88	ILE
40	B8	89	VAL

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Mol	Chain	Res	Type
40	B8	99	LEU
40	B8	106	SER
40	B8	108	ARG
40	B8	110	ILE
40	B8	112	ARG
40	B8	115	ARG
40	B8	118	ARG
40	B8	128	GLU
40	B8	129	ARG
40	B8	134	GLU
41	C8	5	LYS
41	C8	9	VAL
41	C8	17	ILE
41	C8	22	LYS
41	C8	27	LEU
41	C8	30	LYS
41	C8	34	LYS
41	C8	51	LYS
41	C8	60	LEU
41	C8	64	ARG
41	C8	74	LEU
41	C8	83	LEU
41	C8	89	GLU
41	C8	100	VAL
41	C8	108	GLU
41	C8	112	ARG
42	D8	5	VAL
42	D8	7	THR
42	D8	12	TYR
42	D8	18	LEU
42	D8	20	LEU
42	D8	21	ARG
42	D8	22	VAL
42	D8	25	LEU
42	D8	28	GLU
42	D8	33	VAL
42	D8	36	PRO
42	D8	37	VAL
42	D8	39	LEU
42	D8	40	LEU
42	D8	46	VAL
42	D8	49	THR

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Mol	Chain	Res	Type
42	D8	51	VAL
42	D8	52	VAL
42	D8	53	GLU
42	D8	57	VAL
42	D8	58	VAL
42	D8	70	ILE
42	D8	78	LYS
42	D8	79	VAL
42	D8	89	GLN
43	E8	11	ARG
43	E8	12	ILE
43	E8	15	ARG
43	E8	19	LEU
43	E8	20	VAL
43	E8	24	ILE
43	E8	39	THR
43	E8	41	LYS
43	E8	51	LEU
43	E8	76	VAL
43	E8	78	GLU
43	E8	95	ILE
43	E8	96	ILE
43	E8	98	LYS
43	E8	100	THR
43	E8	107	LEU
44	F8	1	MET
44	F8	12	VAL
44	F8	23	GLU
44	F8	27	THR
44	F8	38	GLU
44	F8	53	LYS
44	F8	54	VAL
44	F8	66	LEU
44	F8	68	ARG
44	F8	70	LEU
44	F8	76	ARG
44	F8	80	ILE
44	F8	87	GLN
44	F8	89	ILE
45	G8	3	VAL
45	G8	4	LYS
45	G8	5	MET

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Mol	Chain	Res	Type
45	G8	21	LYS
45	G8	27	VAL
45	G8	31	LEU
45	G8	38	ILE
45	G8	64	GLU
45	G8	67	LEU
45	G8	75	ILE
45	G8	82	PRO
45	G8	85	VAL
45	G8	87	LYS
45	G8	94	LYS
45	G8	98	VAL
45	G8	101	LYS
45	G8	102	CYS
46	H8	1	MET
46	H8	2	GLU
46	H8	5	LEU
46	H8	6	LYS
46	H8	11	GLU
46	H8	19	ARG
46	H8	20	ARG
46	H8	24	LEU
46	H8	33	LEU
46	H8	35	ARG
46	H8	37	VAL
46	H8	41	LEU
46	H8	42	VAL
46	H8	46	LYS
46	H8	53	ILE
46	H8	58	VAL
46	H8	59	LEU
46	H8	60	GLU
46	H8	61	LEU
46	H8	70	LEU
46	H8	71	VAL
46	H8	72	ARG
46	H8	74	VAL
46	H8	76	LEU
46	H8	77	ASP
46	H8	86	VAL
46	H8	91	LEU
46	H8	94	GLU

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Mol	Chain	Res	Type
46	H8	96	VAL
46	H8	105	VAL
46	H8	117	LEU
46	H8	118	GLN
46	H8	120	ILE
46	H8	121	HIS
46	H8	126	VAL
46	H8	128	VAL
46	H8	131	ARG
46	H8	132	ASN
46	H8	137	ILE
46	H8	142	SER
46	H8	149	SER
46	H8	151	HIS
46	H8	154	ASP
46	H8	157	LEU
46	H8	162	GLU
46	H8	163	LEU
46	H8	169	GLU
47	I8	10	THR
47	I8	31	VAL
47	I8	36	ILE
47	I8	41	ARG
47	I8	66	VAL
47	I8	67	VAL
47	I8	70	GLN
47	I8	82	ARG
47	I8	84	LEU
48	J8	4	VAL
48	J8	7	ILE
48	J8	14	VAL
48	J8	17	SER
48	J8	21	ARG
48	J8	37	ILE
48	J8	46	LEU
48	J8	62	VAL
48	J8	74	VAL
48	J8	81	LYS
48	J8	82	LEU
48	J8	83	GLU
48	J8	85	LEU
48	J8	91	LYS

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Mol	Chain	Res	Type
48	J8	93	GLU
48	J8	94	LEU
48	J8	95	LEU
49	K8	3	LEU
49	K8	8	LYS
49	K8	15	LYS
49	K8	16	LEU
49	K8	17	SER
49	K8	19	VAL
49	K8	23	LYS
49	K8	24	LEU
49	K8	28	LYS
49	K8	30	ARG
49	K8	32	LEU
49	K8	35	LEU
49	K8	41	ILE
49	K8	44	LEU
49	K8	47	ASN
49	K8	48	HIS
49	K8	49	LYS
49	K8	53	LEU
49	K8	55	ARG
49	K8	59	ARG
49	K8	62	THR
49	K8	64	LEU
49	K8	67	LYS
50	L8	4	LEU
50	L8	6	VAL
50	L8	8	LEU
50	L8	31	LEU
50	L8	32	GLN
50	L8	40	THR
50	L8	58	VAL
50	L8	59	VAL
51	M8	5	ILE
51	M8	10	VAL
51	M8	15	ILE
51	M8	16	CYS
51	M8	18	CYS
51	M8	23	GLU
51	M8	36	CYS
51	M8	37	SER

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Mol	Chain	Res	Type
51	M8	38	LYS
51	M8	40	HIS
51	M8	44	THR
51	M8	47	GLN
51	M8	62	ARG
51	M8	63	TYR
51	M8	65	ASP
52	N8	3	LYS
52	N8	6	VAL
52	N8	11	THR
52	N8	16	ARG
52	N8	26	THR
52	N8	29	THR
52	N8	31	VAL
52	N8	35	GLU
52	N8	37	LYS
52	N8	40	LYS
52	N8	46	CYS
53	P8	1	MET
53	P8	4	THR
53	P8	8	ASN
53	P8	14	LYS
53	P8	23	ARG
53	P8	29	LYS
53	P8	43	THR
54	Q8	14	VAL
54	Q8	23	VAL
54	Q8	35	GLN
54	Q8	46	ARG
54	Q8	50	LEU
54	Q8	60	LEU
2	12	16	HIS
2	12	21	ARG
2	12	23	ARG
2	12	30	ARG
2	12	32	ILE
2	12	39	ILE
2	12	40	HIS
2	12	44	LEU
2	12	49	GLU
2	12	50	GLU
2	12	51	LEU

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Mol	Chain	Res	Type
2	12	52	GLU
2	12	55	PHE
2	12	60	ASP
2	12	61	LEU
2	12	74	LYS
2	12	76	GLN
2	12	84	GLU
2	12	86	GLU
2	12	94	ASN
2	12	96	ARG
2	12	107	THR
2	12	108	ILE
2	12	111	ARG
2	12	121	LEU
2	12	122	PHE
2	12	126	GLU
2	12	127	ILE
2	12	128	GLU
2	12	154	LEU
2	12	172	ILE
2	12	185	ILE
2	12	187	LEU
2	12	191	ASP
2	12	193	ASP
2	12	196	LEU
2	12	197	VAL
2	12	208	ILE
2	12	210	SER
2	12	220	ASP
2	12	221	LEU
2	12	222	ILE
2	12	224	GLN
3	22	5	ILE
3	22	17	ASP
3	22	21	ARG
3	22	30	ARG
3	22	33	LEU
3	22	43	LEU
3	22	44	GLU
3	22	47	LEU
3	22	58	GLU
3	22	59	ARG

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Mol	Chain	Res	Type
3	22	69	HIS
3	22	75	VAL
3	22	76	VAL
3	22	85	ARG
3	22	88	ARG
3	22	90	GLU
3	22	91	LEU
3	22	99	VAL
3	22	101	LEU
3	22	102	ASN
3	22	103	VAL
3	22	104	GLN
3	22	105	GLU
3	22	106	VAL
3	22	107	GLN
3	22	125	GLU
3	22	134	ILE
3	22	135	LYS
3	22	141	VAL
3	22	143	GLU
3	22	165	THR
3	22	167	TRP
3	22	178	LEU
3	22	179	ARG
3	22	188	LEU
3	22	190	ARG
3	22	192	THR
3	22	196	LEU
3	22	198	VAL
3	22	202	ILE
3	22	204	LEU
4	32	8	VAL
4	32	19	LEU
4	32	24	GLU
4	32	30	LYS
4	32	31	CYS
4	32	58	LEU
4	32	61	LYS
4	32	66	ARG
4	32	73	ARG
4	32	76	ARG
4	32	84	LYS

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Mol	Chain	Res	Type
4	32	86	LYS
4	32	88	VAL
4	32	98	GLU
4	32	108	LEU
4	32	115	ARG
4	32	119	GLN
4	32	122	ARG
4	32	131	ARG
4	32	132	ARG
4	32	135	LEU
4	32	140	VAL
4	32	150	GLU
4	32	155	LEU
4	32	158	ILE
4	32	168	ARG
4	32	170	VAL
4	32	184	LYS
4	32	190	ASP
4	32	192	GLU
4	32	201	GLN
5	42	9	LYS
5	42	10	MET
5	42	12	LEU
5	42	16	THR
5	42	31	LEU
5	42	40	ARG
5	42	41	VAL
5	42	43	LEU
5	42	45	PHE
5	42	47	LYS
5	42	50	GLU
5	42	63	ARG
5	42	64	ARG
5	42	66	MET
5	42	75	THR
5	42	78	HIS
5	42	79	GLU
5	42	81	GLU
5	42	90	VAL
5	42	101	ILE
5	42	110	LEU
5	42	118	ILE

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Mol	Chain	Res	Type
5	42	119	LEU
5	42	131	ILE
5	42	150	ARG
5	42	152	ARG
6	52	3	ARG
6	52	10	LEU
6	52	14	LEU
6	52	19	LEU
6	52	21	LEU
6	52	24	GLU
6	52	25	ILE
6	52	28	ARG
6	52	40	VAL
6	52	46	ARG
6	52	47	ARG
6	52	71	ARG
6	52	72	VAL
6	52	74	ASP
6	52	78	GLU
6	52	83	ASP
7	62	8	GLU
7	62	9	VAL
7	62	13	GLN
7	62	36	LYS
7	62	49	ILE
7	62	52	GLU
7	62	54	THR
7	62	57	GLU
7	62	61	VAL
7	62	66	VAL
7	62	67	GLU
7	62	94	ARG
7	62	97	GLN
7	62	98	SER
7	62	104	LEU
7	62	114	ARG
7	62	124	LEU
7	62	131	LYS
7	62	137	LYS
7	62	140	ASP
7	62	142	GLU
7	62	143	ARG

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Mol	Chain	Res	Type
8	72	12	ARG
8	72	23	SER
8	72	25	ASP
8	72	26	VAL
8	72	33	GLU
8	72	37	ARG
8	72	38	ILE
8	72	39	LEU
8	72	41	ARG
8	72	54	ASP
8	72	56	LYS
8	72	63	LEU
8	72	70	GLN
8	72	73	ASP
8	72	77	GLU
8	72	78	GLN
8	72	80	ILE
8	72	82	HIS
8	72	83	ILE
8	72	88	LYS
8	72	91	ARG
8	72	97	VAL
8	72	99	GLU
8	72	100	ILE
8	72	102	ARG
8	72	109	ILE
8	72	112	LEU
8	72	119	LEU
8	72	120	THR
8	72	125	ARG
8	72	126	LYS
8	72	127	LEU
8	72	133	LEU
9	82	7	THR
9	82	10	ARG
9	82	12	GLU
9	82	19	LEU
9	82	27	THR
9	82	28	VAL
9	82	33	PHE
9	82	34	ASN
9	82	40	LEU

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Mol	Chain	Res	Type
9	82	47	LEU
9	82	51	ARG
9	82	56	LEU
9	82	65	VAL
9	82	66	ARG
9	82	79	LEU
9	82	91	ASP
9	82	95	LYS
9	82	96	LEU
9	82	109	VAL
9	82	110	GLU
9	82	117	HIS
9	82	124	GLN
10	1A	4	ILE
10	1A	7	LYS
10	1A	8	LEU
10	1A	13	HIS
10	1A	16	LEU
10	1A	21	GLN
10	1A	24	VAL
10	1A	38	ILE
10	1A	40	LEU
10	1A	48	THR
10	1A	57	LYS
10	1A	58	ASP
10	1A	59	SER
10	1A	62	HIS
10	1A	70	ARG
10	1A	72	VAL
10	1A	74	ILE
10	1A	75	ILE
10	1A	79	ARG
10	1A	80	LYS
10	1A	95	GLU
10	1A	96	ILE
10	1A	98	ILE
11	2A	18	ARG
11	2A	29	ILE
11	2A	30	VAL
11	2A	31	THR
11	2A	54	ARG
11	2A	55	LYS

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Mol	Chain	Res	Type
11	2A	63	LEU
11	2A	78	GLN
11	2A	79	SER
11	2A	93	GLN
11	2A	99	GLN
11	2A	105	VAL
11	2A	107	SER
11	2A	109	VAL
11	2A	114	VAL
12	3A	19	ARG
12	3A	20	LYS
12	3A	21	LYS
12	3A	23	LYS
12	3A	24	VAL
12	3A	33	ARG
12	3A	34	ARG
12	3A	41	ARG
12	3A	42	THR
12	3A	58	VAL
12	3A	60	LEU
12	3A	62	SER
12	3A	64	TYR
12	3A	66	VAL
12	3A	67	THR
12	3A	70	ILE
12	3A	78	GLN
12	3A	81	SER
12	3A	83	VAL
12	3A	96	VAL
12	3A	100	ILE
12	3A	102	ARG
12	3A	111	LYS
12	3A	115	LYS
12	3A	116	SER
12	3A	117	ARG
12	3A	118	SER
12	3A	119	LYS
12	3A	122	THR
12	3A	126	LYS
13	4A	9	ILE
13	4A	11	ARG
13	4A	12	ASN

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Mol	Chain	Res	Type
13	4A	13	LYS
13	4A	37	THR
13	4A	39	ILE
13	4A	46	LYS
13	4A	47	ASP
13	4A	49	THR
13	4A	50	GLU
13	4A	57	ARG
13	4A	58	GLU
13	4A	66	LEU
13	4A	78	ILE
13	4A	81	LEU
13	4A	82	MET
13	4A	86	CYS
13	4A	88	ARG
13	4A	93	ARG
13	4A	94	ARG
13	4A	98	VAL
13	4A	103	THR
13	4A	106	ASN
13	4A	117	VAL
14	5A	6	LEU
14	5A	7	ILE
14	5A	8	GLU
14	5A	12	ARG
14	5A	13	THR
14	5A	16	PHE
14	5A	22	THR
14	5A	24	CYS
14	5A	26	ARG
14	5A	29	ARG
14	5A	33	VAL
14	5A	42	ILE
14	5A	44	LEU
14	5A	46	GLU
14	5A	50	LYS
14	5A	57	ARG
15	6A	3	ILE
15	6A	10	LYS
15	6A	31	LEU
15	6A	41	GLU
15	6A	66	LEU

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Mol	Chain	Res	Type
15	6A	79	ARG
15	6A	84	LYS
16	7A	2	VAL
16	7A	6	LEU
16	7A	21	VAL
16	7A	34	GLU
16	7A	54	GLU
16	7A	55	ARG
16	7A	67	THR
16	7A	74	LEU
16	7A	81	ARG
17	8A	24	GLU
17	8A	26	GLN
17	8A	38	ARG
17	8A	48	GLU
17	8A	55	ASP
17	8A	60	ILE
17	8A	63	ARG
17	8A	68	ARG
17	8A	74	LEU
17	8A	75	ARG
17	8A	85	VAL
17	8A	87	LYS
17	8A	100	LYS
18	9A	21	LYS
18	9A	22	VAL
18	9A	25	THR
18	9A	26	LEU
18	9A	29	PHE
18	9A	31	LEU
18	9A	32	ARG
18	9A	38	GLU
18	9A	45	SER
18	9A	46	GLU
18	9A	47	THR
18	9A	53	ARG
18	9A	58	LEU
18	9A	68	LYS
18	9A	82	THR
19	AA	14	HIS
19	AA	15	LEU
19	AA	19	VAL

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Mol	Chain	Res	Type
19	AA	20	LEU
19	AA	21	GLU
19	AA	33	THR
19	AA	37	ARG
19	AA	48	THR
19	AA	56	GLN
19	AA	60	VAL
19	AA	66	MET
19	AA	67	VAL
19	AA	71	LEU
20	BA	13	LEU
20	BA	23	ARG
20	BA	37	SER
20	BA	45	GLN
20	BA	48	LYS
20	BA	58	LYS
20	BA	72	LEU
20	BA	84	LEU
20	BA	99	LEU
21	1B	10	ARG
28	19	14	ARG
28	19	20	ASP
28	19	27	THR
28	19	28	GLU
28	19	33	LEU
28	19	34	VAL
28	19	35	LYS
28	19	37	LEU
28	19	38	LYS
28	19	43	ARG
28	19	49	ILE
28	19	52	ARG
28	19	54	ARG
28	19	61	LEU
28	19	64	ILE
28	19	68	LYS
28	19	69	ARG
28	19	78	LYS
28	19	89	SER
28	19	94	LEU
28	19	99	ASP
28	19	103	ARG

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Mol	Chain	Res	Type
28	19	105	ILE
28	19	111	LEU
28	19	116	GLN
28	19	118	VAL
28	19	138	VAL
28	19	141	VAL
28	19	147	LEU
28	19	155	LEU
28	19	162	SER
28	19	169	GLU
28	19	173	VAL
28	19	182	LEU
28	19	185	VAL
28	19	192	THR
28	19	193	VAL
28	19	204	ILE
28	19	208	LYS
28	19	211	ARG
28	19	217	ARG
28	19	242	ARG
28	19	244	ARG
28	19	255	LYS
28	19	257	LEU
28	19	260	ARG
28	19	266	SER
28	19	267	SER
28	19	271	ILE
28	19	273	ARG
29	29	1	MET
29	29	7	VAL
29	29	27	LEU
29	29	36	ARG
29	29	45	THR
29	29	47	VAL
29	29	49	LEU
29	29	51	PHE
29	29	58	ARG
29	29	63	LEU
29	29	66	HIS
29	29	72	VAL
29	29	73	GLU
29	29	77	ILE

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Mol	Chain	Res	Type
29	29	78	LEU
29	29	80	GLU
29	29	97	LYS
29	29	107	THR
29	29	111	ARG
29	29	116	VAL
29	29	117	MET
29	29	119	ARG
29	29	144	ARG
29	29	145	LYS
29	29	149	ARG
29	29	170	LEU
29	29	175	VAL
29	29	181	LEU
29	29	182	LEU
29	29	188	VAL
29	29	197	ILE
29	29	200	GLU
29	29	201	THR
30	39	7	TYR
30	39	8	GLN
30	39	11	VAL
30	39	15	SER
30	39	18	ARG
30	39	19	GLU
30	39	20	LEU
30	39	24	LEU
30	39	27	GLU
30	39	28	ILE
30	39	29	ASN
30	39	32	LEU
30	39	36	VAL
30	39	38	ARG
30	39	50	SER
30	39	53	THR
30	39	57	VAL
30	39	62	ARG
30	39	67	GLN
30	39	82	ILE
30	39	88	VAL
30	39	106	ARG
30	39	108	LYS

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Mol	Chain	Res	Type
30	39	110	LEU
30	39	123	LEU
30	39	125	LEU
30	39	126	VAL
30	39	129	PHE
30	39	132	VAL
30	39	140	LEU
30	39	145	GLU
30	39	153	SER
30	39	154	VAL
30	39	158	THR
30	39	175	THR
30	39	176	LEU
30	39	181	LEU
30	39	187	VAL
30	39	192	LEU
30	39	193	VAL
30	39	194	MET
30	39	196	LEU
30	39	197	ASP
30	39	201	VAL
30	39	205	ARG
31	49	7	LEU
31	49	13	GLU
31	49	14	GLU
31	49	26	GLN
31	49	36	LYS
31	49	40	ASN
31	49	48	GLU
31	49	51	ARG
31	49	52	ILE
31	49	54	GLU
31	49	59	GLU
31	49	75	LYS
31	49	76	SER
31	49	77	ILE
31	49	80	PHE
31	49	82	LEU
31	49	86	MET
31	49	101	ILE
31	49	107	LEU
31	49	109	VAL

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Mol	Chain	Res	Type
31	49	116	ASP
31	49	133	LEU
31	49	136	ARG
31	49	138	GLN
31	49	144	ILE
31	49	152	LEU
31	49	153	ARG
31	49	156	ASP
31	49	159	VAL
31	49	165	THR
31	49	166	ASP
31	49	181	ARG
32	59	6	ARG
32	59	7	LEU
32	59	16	SER
32	59	19	VAL
32	59	23	ARG
32	59	24	VAL
32	59	25	LYS
32	59	26	VAL
32	59	32	GLU
32	59	33	LEU
32	59	40	GLU
32	59	41	MET
32	59	49	VAL
32	59	50	VAL
32	59	52	VAL
32	59	60	ARG
32	59	74	ASN
32	59	76	VAL
32	59	81	GLU
32	59	83	TYR
32	59	85	LYS
32	59	86	GLU
32	59	89	ILE
32	59	90	LYS
32	59	95	ARG
32	59	99	VAL
32	59	105	LEU
32	59	116	GLU
32	59	121	ILE
32	59	123	PHE

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Mol	Chain	Res	Type
32	59	125	VAL
32	59	127	GLU
32	59	129	THR
32	59	130	ARG
32	59	131	VAL
32	59	138	LYS
32	59	139	GLN
32	59	149	ARG
32	59	158	HIS
32	59	159	GLU
32	59	160	LYS
32	59	171	LEU
33	69	1	MET
33	69	4	ILE
33	69	6	LEU
33	69	7	GLU
33	69	15	VAL
33	69	19	VAL
33	69	27	ARG
33	69	37	VAL
33	69	40	THR
33	69	47	LEU
33	69	58	LEU
33	69	61	ARG
33	69	68	LEU
33	69	69	LYS
33	69	77	LEU
33	69	85	GLU
33	69	86	THR
33	69	102	SER
33	69	105	HIS
33	69	109	ILE
33	69	112	LYS
33	69	114	LEU
33	69	117	GLU
33	69	118	LYS
33	69	127	VAL
33	69	131	LYS
33	69	138	ILE
33	69	141	LYS
33	69	142	VAL
34	15	9	VAL

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Mol	Chain	Res	Type
34	15	12	ARG
34	15	15	LEU
34	15	28	THR
34	15	32	THR
34	15	33	LEU
34	15	34	LEU
34	15	46	VAL
34	15	48	MET
34	15	58	ASP
34	15	59	LYS
34	15	60	ILE
34	15	61	ARG
34	15	63	THR
34	15	67	LEU
34	15	68	GLU
34	15	84	LYS
34	15	85	ILE
34	15	87	LEU
34	15	89	LYS
34	15	93	THR
34	15	94	HIS
34	15	98	VAL
34	15	99	LEU
34	15	106	MET
34	15	130	HIS
34	15	133	GLN
34	15	137	LYS
34	15	138	LEU
35	25	5	GLN
35	25	8	LEU
35	25	10	VAL
35	25	22	ILE
35	25	35	VAL
35	25	38	VAL
35	25	49	ARG
35	25	52	VAL
35	25	70	LYS
35	25	78	ARG
35	25	82	ASN
35	25	87	ILE
35	25	91	LEU
35	25	97	ARG

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Mol	Chain	Res	Type
35	25	98	VAL
35	25	113	LYS
35	25	114	ILE
35	25	117	LEU
36	35	2	LYS
36	35	4	SER
36	35	6	LEU
36	35	13	ASN
36	35	15	ARG
36	35	19	VAL
36	35	21	ARG
36	35	29	LYS
36	35	30	THR
36	35	41	ARG
36	35	45	LEU
36	35	58	THR
36	35	62	LEU
36	35	71	VAL
36	35	75	ILE
36	35	77	ARG
36	35	85	LEU
36	35	88	LEU
36	35	90	ARG
36	35	91	PHE
36	35	95	VAL
36	35	96	THR
36	35	98	GLU
36	35	102	ARG
36	35	105	LEU
36	35	106	LEU
36	35	110	TYR
36	35	111	ARG
36	35	112	LEU
36	35	114	ILE
36	35	124	LYS
36	35	125	VAL
36	35	126	VAL
36	35	132	LYS
36	35	133	SER
36	35	135	LEU
36	35	138	LEU
36	35	144	GLU

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Mol	Chain	Res	Type
36	35	147	LEU
37	45	2	LEU
37	45	5	ARG
37	45	18	LYS
37	45	21	THR
37	45	31	ASP
37	45	38	GLU
37	45	45	GLN
37	45	56	ARG
37	45	66	ILE
37	45	79	LEU
37	45	82	ARG
37	45	89	ASN
37	45	90	VAL
37	45	91	GLU
37	45	103	MET
37	45	110	THR
37	45	127	ILE
37	45	133	ARG
37	45	134	ARG
37	45	135	ASP
37	45	137	TYR
37	45	138	ASP
38	55	2	ARG
38	55	6	SER
38	55	9	LYS
38	55	18	LEU
38	55	28	LEU
38	55	29	LEU
38	55	33	ARG
38	55	35	THR
38	55	44	LEU
38	55	48	VAL
38	55	51	LEU
38	55	57	ARG
38	55	63	ARG
38	55	65	LEU
38	55	67	LEU
38	55	75	LEU
38	55	79	LEU
38	55	81	ASP
38	55	82	GLU

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Mol	Chain	Res	Type
38	55	96	ARG
38	55	99	LYS
38	55	102	GLU
38	55	104	ARG
38	55	105	ARG
38	55	113	LEU
38	55	114	VAL
38	55	117	VAL
38	55	118	GLU
39	65	8	GLU
39	65	14	VAL
39	65	17	ARG
39	65	19	LYS
39	65	20	ARG
39	65	24	LEU
39	65	27	SER
39	65	36	TYR
39	65	39	ILE
39	65	42	ASP
39	65	43	GLU
39	65	44	LYS
39	65	46	VAL
39	65	50	SER
39	65	52	SER
39	65	59	LYS
39	65	62	LYS
39	65	64	GLU
39	65	65	VAL
39	65	69	VAL
39	65	71	ARG
39	65	73	LEU
39	65	75	GLU
39	65	89	ARG
39	65	106	ARG
39	65	107	GLU
39	65	111	GLU
40	75	13	ARG
40	75	17	THR
40	75	21	GLU
40	75	27	THR
40	75	28	VAL
40	75	30	VAL

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Mol	Chain	Res	Type
40	75	33	LYS
40	75	34	VAL
40	75	36	GLU
40	75	50	ILE
40	75	54	ARG
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	86	ILE
40	75	88	ILE
40	75	89	VAL
40	75	91	ARG
40	75	93	ARG
40	75	105	LEU
40	75	106	SER
40	75	112	ARG
40	75	113	LYS
40	75	118	ARG
41	85	5	LYS
41	85	20	LEU
41	85	30	LYS
41	85	31	SER
41	85	52	ARG
41	85	55	ARG
41	85	59	ARG
41	85	64	ARG
41	85	71	GLN
41	85	74	LEU
41	85	88	ILE
41	85	93	LYS
41	85	97	ASP
41	85	105	VAL
41	85	108	GLU
41	85	112	ARG
41	85	117	GLN
42	95	1	MET
42	95	5	VAL
42	95	7	THR
42	95	21	ARG

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Mol	Chain	Res	Type
42	95	23	GLU
42	95	28	GLU
42	95	33	VAL
42	95	37	VAL
42	95	47	VAL
42	95	49	THR
42	95	52	VAL
42	95	66	ARG
42	95	68	LYS
42	95	71	LEU
42	95	74	LYS
42	95	82	ARG
42	95	89	GLN
42	95	95	LEU
42	95	99	ILE
43	A5	11	ARG
43	A5	18	ARG
43	A5	19	LEU
43	A5	20	VAL
43	A5	23	LEU
43	A5	30	GLU
43	A5	39	THR
43	A5	51	LEU
43	A5	59	VAL
43	A5	65	LEU
43	A5	70	TYR
43	A5	76	VAL
43	A5	95	ILE
43	A5	96	ILE
43	A5	98	LYS
43	A5	100	THR
43	A5	106	ILE
43	A5	107	LEU
43	A5	109	GLU
43	A5	111	HIS
44	B5	12	VAL
44	B5	23	GLU
44	B5	27	THR
44	B5	30	VAL
44	B5	43	VAL
44	B5	52	VAL
44	B5	54	VAL

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Mol	Chain	Res	Type
44	B5	63	LYS
44	B5	66	LEU
44	B5	72	LYS
44	B5	76	ARG
44	B5	78	LYS
44	B5	80	ILE
44	B5	81	VAL
44	B5	90	GLU
45	C5	4	LYS
45	C5	19	LYS
45	C5	24	VAL
45	C5	29	GLU
45	C5	31	LEU
45	C5	40	GLU
45	C5	71	LYS
45	C5	72	VAL
46	D5	14	LYS
46	D5	18	LEU
46	D5	19	ARG
46	D5	24	LEU
46	D5	36	LYS
46	D5	41	LEU
46	D5	63	ASP
46	D5	70	LEU
46	D5	71	VAL
46	D5	73	GLN
46	D5	87	ASP
46	D5	90	VAL
46	D5	91	LEU
46	D5	93	ASP
46	D5	100	VAL
46	D5	105	VAL
46	D5	117	LEU
46	D5	123	ASP
46	D5	129	SER
46	D5	137	ILE
46	D5	140	ASP
46	D5	146	ILE
46	D5	151	HIS
46	D5	155	LEU
46	D5	161	VAL
46	D5	162	GLU

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Mol	Chain	Res	Type
46	D5	168	GLU
46	D5	169	GLU
46	D5	171	ILE
46	D5	174	VAL
46	D5	178	GLU
47	E5	12	ASN
47	E5	16	SER
47	E5	20	ARG
47	E5	32	ARG
47	E5	36	ILE
47	E5	38	VAL
47	E5	43	THR
47	E5	46	LYS
47	E5	62	LEU
47	E5	68	GLU
47	E5	70	GLN
47	E5	74	ARG
47	E5	82	ARG
48	F5	4	VAL
48	F5	11	ARG
48	F5	25	LYS
48	F5	30	VAL
48	F5	38	SER
48	F5	39	LYS
48	F5	46	LEU
48	F5	52	ARG
48	F5	62	VAL
48	F5	67	ILE
48	F5	72	GLU
48	F5	74	VAL
48	F5	75	GLU
48	F5	76	ARG
48	F5	78	LYS
48	F5	83	GLU
48	F5	85	LEU
48	F5	90	ILE
48	F5	91	LYS
48	F5	95	LEU
49	G5	10	LEU
49	G5	12	GLU
49	G5	15	LYS
49	G5	16	LEU

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Mol	Chain	Res	Type
49	G5	17	SER
49	G5	24	LEU
49	G5	35	LEU
49	G5	38	GLN
49	G5	40	SER
49	G5	41	ILE
49	G5	44	LEU
49	G5	45	SER
49	G5	47	ASN
49	G5	48	HIS
49	G5	50	ILE
49	G5	51	ARG
49	G5	53	LEU
49	G5	56	GLN
49	G5	60	LEU
49	G5	64	LEU
49	G5	65	ASN
49	G5	68	ARG
50	H5	8	LEU
50	H5	24	LYS
50	H5	30	ARG
50	H5	31	LEU
50	H5	38	GLU
50	H5	48	GLU
52	J5	6	VAL
52	J5	25	LEU
52	J5	29	THR
52	J5	35	GLU
52	J5	37	LYS
52	J5	48	GLU
52	J5	49	CYS
52	J5	55	ARG
53	L5	1	MET
53	L5	4	THR
53	L5	29	LYS
53	L5	41	ARG
53	L5	43	THR
54	M5	11	LYS
54	M5	13	ARG
54	M5	23	VAL
54	M5	32	LEU
54	M5	41	ILE

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Mol	Chain	Res	Type
54	M5	49	VAL
54	M5	58	ILE
54	M5	59	LYS
54	M5	60	LEU
54	M5	61	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (54) such sidechains are listed below:

Mol	Chain	Res	Type
2	1E	135	GLN
6	5E	27	GLN
6	5E	64	GLN
6	5E	100	ASN
7	6E	84	ASN
8	7E	70	GLN
9	8E	87	GLN
11	2I	38	ASN
13	4I	62	ASN
15	6I	62	GLN
20	BI	26	ASN
28	11	87	ASN
28	11	166	GLN
29	21	135	HIS
30	31	29	ASN
30	31	204	ASN
31	41	41	GLN
33	61	11	ASN
38	98	31	HIS
40	B8	58	ASN
40	B8	79	HIS
42	D8	80	GLN
46	H8	132	ASN
49	K8	56	GLN
49	K8	65	ASN
51	M8	60	GLN
54	Q8	35	GLN
2	12	212	GLN
3	22	3	ASN
3	22	6	HIS
3	22	104	GLN
3	22	181	ASN
4	32	45	GLN

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Mol	Chain	Res	Type
4	32	119	GLN
4	32	123	HIS
6	52	100	ASN
7	62	106	GLN
9	82	29	ASN
15	6A	37	ASN
20	BA	16	HIS
28	19	203	ASN
33	69	104	GLN
35	25	90	GLN
38	55	31	HIS
40	75	136	GLN
41	85	94	ASN
41	85	104	GLN
42	95	80	GLN
43	A5	60	ASN
44	B5	41	ASN
49	G5	9	GLN
49	G5	46	GLN
49	G5	56	GLN
50	H5	32	GLN

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	13	1499/1522 (98%)	328 (21%)	36 (2%)
1	1G	1488/1522 (97%)	315 (21%)	31 (2%)
22	1K	72/76 (94%)	39 (54%)	5 (6%)
22	1L	71/76 (93%)	40 (56%)	1 (1%)
23	2K	76/77 (98%)	18 (23%)	1 (1%)
23	2L	76/77 (98%)	18 (23%)	3 (3%)
24	3K	69/76 (90%)	36 (52%)	2 (2%)
25	4K	17/27 (62%)	10 (58%)	3 (17%)
25	4L	14/27 (51%)	6 (42%)	3 (21%)
26	14	2805/2917 (96%)	635 (22%)	35 (1%)
26	1H	2841/2917 (97%)	582 (20%)	45 (1%)
27	16	121/122 (99%)	17 (14%)	1 (0%)
27	1J	121/122 (99%)	33 (27%)	1 (0%)
55	3L	69/76 (90%)	31 (44%)	3 (4%)
All	All	9339/9634 (96%)	2108 (22%)	170 (1%)

All (2108) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	13	2	U
1	13	4	U
1	13	5	U
1	13	6	G
1	13	7	G
1	13	9	G
1	13	21	G
1	13	26	A
1	13	32	A
1	13	39	G
1	13	48	C
1	13	49	U
1	13	50	A
1	13	51	A
1	13	54	C
1	13	61	G
1	13	65	U
1	13	66	G
1	13	69	G
1	13	73	G
1	13	74	C
1	13	76	G
1	13	77	C
1	13	78	G
1	13	92	G
1	13	93	U
1	13	96	G
1	13	97	U
1	13	99	C
1	13	101	A
1	13	108	G
1	13	115	G
1	13	116	A
1	13	121	C
1	13	122	G
1	13	131	C
1	13	142	G
1	13	144	G
1	13	151	A
1	13	158	G
1	13	160	A
1	13	162	A
1	13	163	C

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Mol	Chain	Res	Type
1	13	169	C
1	13	172	A
1	13	173	U
1	13	174	C
1	13	182	U
1	13	186(F)	C
1	13	187	C
1	13	188	U
1	13	189	U
1	13	190	G
1	13	191(A)	G
1	13	191(E)	G
1	13	195	A
1	13	197	A
1	13	199	G
1	13	201	C
1	13	208	U
1	13	209	U
1	13	210	U
1	13	217	C
1	13	220	G
1	13	222	U
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	263	A
1	13	266	G
1	13	267	C
1	13	289	G
1	13	316	G
1	13	317	G
1	13	321	A
1	13	328	C
1	13	329	A
1	13	330	C
1	13	332	G
1	13	343	U
1	13	344	A
1	13	345	C

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Mol	Chain	Res	Type
1	13	346	G
1	13	347	G
1	13	348	G
1	13	352	C
1	13	353	A
1	13	354	G
1	13	356	A
1	13	363	A
1	13	365	U
1	13	367	U
1	13	372	C
1	13	373	A
1	13	384	G
1	13	388	G
1	13	390	C
1	13	392	G
1	13	397	A
1	13	398	C
1	13	406	G
1	13	412	A
1	13	413	G
1	13	414	A
1	13	423	G
1	13	424	G
1	13	429	U
1	13	430	A
1	13	439	A
1	13	458	C
1	13	465	A
1	13	466	C
1	13	467	G
1	13	482	A
1	13	484	G
1	13	485	G
1	13	487	A
1	13	496	A
1	13	497	U
1	13	498	A
1	13	504	C
1	13	505	G
1	13	511	C
1	13	518	C

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Mol	Chain	Res	Type
1	13	521	G
1	13	524	G
1	13	527	G
1	13	531	U
1	13	532	A
1	13	533	A
1	13	536	C
1	13	547	A
1	13	559	A
1	13	561	U
1	13	572	A
1	13	573	A
1	13	576	G
1	13	577	G
1	13	607	A
1	13	630	G
1	13	631	G
1	13	632	A
1	13	633	G
1	13	639	G
1	13	654	G
1	13	665	A
1	13	666	G
1	13	687	A
1	13	688	G
1	13	723	U
1	13	749	C
1	13	755	G
1	13	759	A
1	13	774	G
1	13	777	A
1	13	787	A
1	13	792	A
1	13	793	U
1	13	794	A
1	13	802	A
1	13	813	U
1	13	815	A
1	13	817	C
1	13	828	A
1	13	836	G
1	13	842	C

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Mol	Chain	Res	Type
1	13	843	U
1	13	848	C
1	13	859	A
1	13	864	A
1	13	870	U
1	13	871	U
1	13	872	A
1	13	874	G
1	13	884	U
1	13	885	G
1	13	902	G
1	13	914	A
1	13	921	U
1	13	922	G
1	13	926	G
1	13	927	G
1	13	933	G
1	13	934	C
1	13	936	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	991	U
1	13	992	U
1	13	993	G
1	13	997	U
1	13	999	U
1	13	1004	A
1	13	1006	C
1	13	1007	C
1	13	1008	C
1	13	1009	G
1	13	1012	U
1	13	1016	A
1	13	1024	G
1	13	1025	U

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Mol	Chain	Res	Type
1	13	1026	G
1	13	1028	C
1	13	1028(A)	C
1	13	1028(B)	C
1	13	1029	G
1	13	1031	G
1	13	1032	A
1	13	1032(A)	G
1	13	1032(B)	G
1	13	1035	A
1	13	1039	C
1	13	1042	G
1	13	1046	A
1	13	1054	C
1	13	1055	A
1	13	1065	U
1	13	1066	C
1	13	1094	G
1	13	1095	U
1	13	1101	A
1	13	1117	G
1	13	1125	U
1	13	1127	G
1	13	1129	C
1	13	1130	A
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	1146	A
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	1176	A
1	13	1177	G
1	13	1178	G
1	13	1181	G

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Mol	Chain	Res	Type
1	13	1182	G
1	13	1184	G
1	13	1189	C
1	13	1190	G
1	13	1196	U
1	13	1197	G
1	13	1212	U
1	13	1213	A
1	13	1227	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	1262	C
1	13	1270	C
1	13	1272	G
1	13	1278	U
1	13	1279	A
1	13	1280	A
1	13	1281	U
1	13	1286	A
1	13	1287	A
1	13	1292	U
1	13	1299	A
1	13	1300	G
1	13	1301	U
1	13	1302	U
1	13	1303	C
1	13	1312	G
1	13	1320	C
1	13	1331	G
1	13	1332	A
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

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Mol	Chain	Res	Type
1	13	1350	A
1	13	1353	G
1	13	1363	A
1	13	1364	U
1	13	1381	U
1	13	1397	C
1	13	1398	A
1	13	1401	G
1	13	1419	G
1	13	1442	G
1	13	1443	G
1	13	1446	A
1	13	1449	C
1	13	1450	U
1	13	1451	A
1	13	1452	C
1	13	1453	G
1	13	1454	G
1	13	1487	G
1	13	1492	A
1	13	1497	G
1	13	1498	U
1	13	1499	A
1	13	1503	A
1	13	1504	G
1	13	1506	U
1	13	1507	A
1	13	1517	G
1	13	1525	G
1	13	1529	G
1	13	1530	G
1	13	1534	A
1	13	1535	C
22	1K	3	U
22	1K	4	G
22	1K	6	U
22	1K	8	U
22	1K	9	A
22	1K	10	G
22	1K	11	C
22	1K	13	C
22	1K	14	A

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Mol	Chain	Res	Type
22	1K	15	G
22	1K	18	G
22	1K	19	G
22	1K	25	C
22	1K	26	G
22	1K	45	G
22	1K	47	U
22	1K	48	C
22	1K	49	G
22	1K	50	G
22	1K	51	C
22	1K	52	A
22	1K	54	5MU
22	1K	55	PSU
22	1K	56	C
22	1K	57	G
22	1K	58	A
22	1K	59	C
22	1K	60	U
22	1K	61	C
22	1K	63	G
22	1K	66	U
22	1K	67	A
22	1K	68	U
22	1K	69	C
22	1K	70	A
22	1K	71	G
22	1K	72	C
22	1K	73	A
22	1K	74	C
23	2K	2	G
23	2K	6	G
23	2K	8	4SU
23	2K	9	G
23	2K	13	C
23	2K	15	G
23	2K	16	C
23	2K	17	C
23	2K	20	G
23	2K	21	U
23	2K	22	A
23	2K	23	G

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Mol	Chain	Res	Type
23	2K	32	G
23	2K	48	U
23	2K	49	C
23	2K	50	G
23	2K	68	C
23	2K	77	A
24	3K	2	C
24	3K	3	U
24	3K	4	G
24	3K	7	A
24	3K	8	U
24	3K	9	A
24	3K	10	G
24	3K	11	C
24	3K	15	G
24	3K	23	A
24	3K	26	G
24	3K	30	C
24	3K	33	U
24	3K	34	G
24	3K	35	G
24	3K	36	U
24	3K	37	A
24	3K	38	A
24	3K	44	A
24	3K	46	G
24	3K	47	U
24	3K	48	C
24	3K	52	A
24	3K	55	U
24	3K	56	C
24	3K	58	A
24	3K	59	A
24	3K	60	U
24	3K	61	C
24	3K	62	U
24	3K	63	G
24	3K	65	C
24	3K	66	U
24	3K	69	C
24	3K	73	A
24	3K	75	C

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Mol	Chain	Res	Type
25	4K	10	G
25	4K	11	U
25	4K	12	A
25	4K	13	A
25	4K	14	A
25	4K	15	A
25	4K	23	A
25	4K	24	A
25	4K	25	A
25	4K	26	A
26	1H	13	A
26	1H	14	A
26	1H	15	G
26	1H	34	C
26	1H	43	G
26	1H	46	C
26	1H	51	G
26	1H	61	G
26	1H	64	A
26	1H	71	A
26	1H	72	U
26	1H	74	A
26	1H	75	G
26	1H	85	G
26	1H	118	A
26	1H	119	A
26	1H	120	U
26	1H	125	G
26	1H	126	A
26	1H	138	G
26	1H	155	C
26	1H	162	U
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	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	228	A
26	1H	229	A
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	269	U
26	1H	270(G)	C
26	1H	270(J)	G
26	1H	270(K)	C
26	1H	270(L)	U
26	1H	270(M)	U
26	1H	270(N)	G
26	1H	270(O)	U
26	1H	270(P)	C
26	1H	271(C)	U
26	1H	271	G
26	1H	274	G
26	1H	275	G
26	1H	277	C
26	1H	278	A
26	1H	295	G
26	1H	299	A
26	1H	311	A
26	1H	324	A
26	1H	329	G
26	1H	330	A
26	1H	331	A
26	1H	335	C
26	1H	346	A
26	1H	352	G
26	1H	357	A
26	1H	363(E)	U
26	1H	372	G
26	1H	375	C

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Mol	Chain	Res	Type
26	1H	376	C
26	1H	380	U
26	1H	382	G
26	1H	386	G
26	1H	405	U
26	1H	406	G
26	1H	410	G
26	1H	411	G
26	1H	418	G
26	1H	428	A
26	1H	444	C
26	1H	447	A
26	1H	448	U
26	1H	455	C
26	1H	470	A
26	1H	471	A
26	1H	481	G
26	1H	482	A
26	1H	504	U
26	1H	505	A
26	1H	508	G
26	1H	509	C
26	1H	525	U
26	1H	529	A
26	1H	531	C
26	1H	532	A
26	1H	533	G
26	1H	546	C
26	1H	548	A
26	1H	549	G
26	1H	556	G
26	1H	563	G
26	1H	564	C
26	1H	573	G
26	1H	575	A
26	1H	588	U
26	1H	593	G
26	1H	603	A
26	1H	607	U
26	1H	609(A)	G
26	1H	614	U
26	1H	615	G

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Mol	Chain	Res	Type
26	1H	617	G
26	1H	621	A
26	1H	622	G
26	1H	627	A
26	1H	631	A
26	1H	637	A
26	1H	645	C
26	1H	646	A
26	1H	653	A
26	1H	654	A
26	1H	654(A)	A
26	1H	654(D)	G
26	1H	654(O)	G
26	1H	654(S)	G
26	1H	654(T)	A
26	1H	664	C
26	1H	677	A
26	1H	678	C
26	1H	686	G
26	1H	695	G
26	1H	717	G
26	1H	730	C
26	1H	745	G
26	1H	765	G
26	1H	771	G
26	1H	775	G
26	1H	776	G
26	1H	777	A
26	1H	782	A
26	1H	784	A
26	1H	785	G
26	1H	790	C
26	1H	791	C
26	1H	792	G
26	1H	800	A
26	1H	802	A
26	1H	805	G
26	1H	812	C
26	1H	827	U
26	1H	828	U
26	1H	832	G
26	1H	836	G

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Mol	Chain	Res	Type
26	1H	845	G
26	1H	846	C
26	1H	853	G
26	1H	855	G
26	1H	859	G
26	1H	860	U
26	1H	866	A
26	1H	879	G
26	1H	880	G
26	1H	890	A
26	1H	892	G
26	1H	893	C
26	1H	895	U
26	1H	899	A
26	1H	900	A
26	1H	901	A
26	1H	907	U
26	1H	910	A
26	1H	917	A
26	1H	926	A
26	1H	932	G
26	1H	941	A
26	1H	945	A
26	1H	946	G
26	1H	947	G
26	1H	958	U
26	1H	959	A
26	1H	961	C
26	1H	968	G
26	1H	974	G
26	1H	974(A)	C
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	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	1031	G
26	1H	1033	U
26	1H	1040	C
26	1H	1045	A
26	1H	1046	A
26	1H	1047	G
26	1H	1051	G
26	1H	1057	A
26	1H	1058	U
26	1H	1060	U
26	1H	1061	U
26	1H	1062	G
26	1H	1065	U
26	1H	1066	U
26	1H	1067	A
26	1H	1068	G
26	1H	1070	A
26	1H	1071	G
26	1H	1073	A
26	1H	1077	A
26	1H	1078	U
26	1H	1079	C
26	1H	1081	U
26	1H	1082	U
26	1H	1083	U
26	1H	1084	A
26	1H	1085	A
26	1H	1086	A
26	1H	1087	G
26	1H	1088	A
26	1H	1089	G
26	1H	1090	U
26	1H	1091	G
26	1H	1095	A
26	1H	1096	A
26	1H	1097	U
26	1H	1098	A
26	1H	1102	C
26	1H	1106	G

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Mol	Chain	Res	Type
26	1H	1107	G
26	1H	1111	A
26	1H	1112	G
26	1H	1126	A
26	1H	1128	A
26	1H	1129	A
26	1H	1130	U
26	1H	1133	U
26	1H	1135	C
26	1H	1136	G
26	1H	1139	G
26	1H	1142	U
26	1H	1142(A)	A
26	1H	1149	G
26	1H	1177	A
26	1H	1178	C
26	1H	1179	C
26	1H	1194	A
26	1H	1195	G
26	1H	1204	A
26	1H	1205	U
26	1H	1206	G
26	1H	1210	A
26	1H	1211	U
26	1H	1218	C
26	1H	1220	A
26	1H	1229(A)	G
26	1H	1244	G
26	1H	1253	A
26	1H	1256	G
26	1H	1267	U
26	1H	1268	A
26	1H	1271	G
26	1H	1272	A
26	1H	1273	U
26	1H	1282	U
26	1H	1286	A
26	1H	1287	A
26	1H	1300	U
26	1H	1301	A
26	1H	1303	G
26	1H	1329	U

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Mol	Chain	Res	Type
26	1H	1344	G
26	1H	1345	C
26	1H	1359	A
26	1H	1360	A
26	1H	1365	A
26	1H	1377	G
26	1H	1379	A
26	1H	1380	G
26	1H	1384	A
26	1H	1385	G
26	1H	1386	C
26	1H	1395	A
26	1H	1407	C
26	1H	1416	G
26	1H	1417	C
26	1H	1420	U
26	1H	1421	G
26	1H	1428	C
26	1H	1444(A)	A
26	1H	1449	A
26	1H	1449(A)	G
26	1H	1453	A
26	1H	1455	G
26	1H	1460	A
26	1H	1461	G
26	1H	1467	C
26	1H	1471	A
26	1H	1493	C
26	1H	1494	A
26	1H	1497	U
26	1H	1506	C
26	1H	1509	C
26	1H	1510	A
26	1H	1517	G
26	1H	1522	G
26	1H	1526	G
26	1H	1534	G
26	1H	1535	U
26	1H	1537	C
26	1H	1538	G
26	1H	1540	G
26	1H	1543	A

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Mol	Chain	Res	Type
26	1H	1545	A
26	1H	1548	C
26	1H	1554	A
26	1H	1558	A
26	1H	1559	G
26	1H	1560	G
26	1H	1566	A
26	1H	1569	A
26	1H	1578	U
26	1H	1580	A
26	1H	1585	C
26	1H	1586	A
26	1H	1587	A
26	1H	1608	A
26	1H	1609	A
26	1H	1610	A
26	1H	1617	C
26	1H	1639	U
26	1H	1640	C
26	1H	1647	G
26	1H	1648	C
26	1H	1664	A
26	1H	1674	G
26	1H	1678	G
26	1H	1726	G
26	1H	1728	G
26	1H	1729	A
26	1H	1730	U
26	1H	1731	G
26	1H	1743	G
26	1H	1746	G
26	1H	1750	G
26	1H	1762	A
26	1H	1763	G
26	1H	1764	G
26	1H	1773	A
26	1H	1782	C
26	1H	1791	A
26	1H	1799	G
26	1H	1800	C
26	1H	1801	G
26	1H	1816	G

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Mol	Chain	Res	Type
26	1H	1819	A
26	1H	1829	A
26	1H	1835	G
26	1H	1836	C
26	1H	1840	G
26	1H	1847	A
26	1H	1859	A
26	1H	1869	G
26	1H	1870	C
26	1H	1878	G
26	1H	1887	C
26	1H	1889	A
26	1H	1900	A
26	1H	1906	G
26	1H	1913	A
26	1H	1914	C
26	1H	1919	A
26	1H	1923	U
26	1H	1929	G
26	1H	1930	G
26	1H	1931	U
26	1H	1938	A
26	1H	1945	G
26	1H	1955	U
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	1982	C
26	1H	1991	U
26	1H	1992	G
26	1H	1993	U
26	1H	1994	C
26	1H	2020	A
26	1H	2023	G
26	1H	2031	A
26	1H	2032	G
26	1H	2033	A
26	1H	2035	G

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Mol	Chain	Res	Type
26	1H	2043	C
26	1H	2049	G
26	1H	2055	C
26	1H	2056	G
26	1H	2060	A
26	1H	2061	G
26	1H	2062	A
26	1H	2069	G
26	1H	2093	G
26	1H	2096	U
26	1H	2099	U
26	1H	2108	C
26	1H	2110	G
26	1H	2111	C
26	1H	2113	U
26	1H	2114	A
26	1H	2116	G
26	1H	2117	A
26	1H	2119	A
26	1H	2120	G
26	1H	2122	U
26	1H	2123	G
26	1H	2127	G
26	1H	2128	C
26	1H	2135	A
26	1H	2136	C
26	1H	2138	C
26	1H	2139	C
26	1H	2144	U
26	1H	2145	C
26	1H	2146	C
26	1H	2147	G
26	1H	2148	G
26	1H	2150	U
26	1H	2156	G
26	1H	2161	C
26	1H	2162	G
26	1H	2165	G
26	1H	2166	G
26	1H	2168	G
26	1H	2170	A
26	1H	2171	A

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Mol	Chain	Res	Type
26	1H	2173	A
26	1H	2175	C
26	1H	2176	A
26	1H	2180	U
26	1H	2181	G
26	1H	2189	U
26	1H	2190	G
26	1H	2198	A
26	1H	2210	G
26	1H	2211	G
26	1H	2212	A
26	1H	2215	G
26	1H	2225	A
26	1H	2226	C
26	1H	2238	G
26	1H	2239	G
26	1H	2240	C
26	1H	2267	A
26	1H	2273	A
26	1H	2275	C
26	1H	2283	C
26	1H	2286	A
26	1H	2287	A
26	1H	2307	G
26	1H	2308	G
26	1H	2314	C
26	1H	2315	G
26	1H	2320	A
26	1H	2321	G
26	1H	2324	C
26	1H	2325	G
26	1H	2326	C
26	1H	2327	A
26	1H	2334	G
26	1H	2336	A
26	1H	2343	C
26	1H	2345	G
26	1H	2346	A
26	1H	2347	C
26	1H	2350	C
26	1H	2376	A
26	1H	2377	A

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Mol	Chain	Res	Type
26	1H	2383	G
26	1H	2385	C
26	1H	2395	C
26	1H	2402	C
26	1H	2403	C
26	1H	2406	U
26	1H	2410	G
26	1H	2414	G
26	1H	2418	A
26	1H	2422	A
26	1H	2425	A
26	1H	2428	G
26	1H	2429	G
26	1H	2430	A
26	1H	2435	A
26	1H	2439	A
26	1H	2441	C
26	1H	2448	A
26	1H	2474	C
26	1H	2476	A
26	1H	2477	C
26	1H	2480	C
26	1H	2482	G
26	1H	2497	A
26	1H	2498	C
26	1H	2502	G
26	1H	2505	G
26	1H	2506	U
26	1H	2507	C
26	1H	2518	A
26	1H	2525	G
26	1H	2529	G
26	1H	2535	G
26	1H	2549	G
26	1H	2554	U
26	1H	2566	A
26	1H	2567	G
26	1H	2573	C
26	1H	2582	G
26	1H	2594	C
26	1H	2595	G
26	1H	2601	C

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Mol	Chain	Res	Type
26	1H	2602	A
26	1H	2609	U
26	1H	2611	U
26	1H	2612	C
26	1H	2615	U
26	1H	2629	A
26	1H	2632	A
26	1H	2636	U
26	1H	2641	G
26	1H	2654	A
26	1H	2663	G
26	1H	2665	A
26	1H	2673	G
26	1H	2689	U
26	1H	2702	U
26	1H	2703	C
26	1H	2707	G
26	1H	2712(A)	A
26	1H	2713	A
26	1H	2714	G
26	1H	2718	G
26	1H	2721	A
26	1H	2726	U
26	1H	2733	A
26	1H	2756	U
26	1H	2757	A
26	1H	2764	A
26	1H	2765	A
26	1H	2766	G
26	1H	2777	G
26	1H	2778	A
26	1H	2781	A
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	2849	U
26	1H	2850	A
26	1H	2851	A

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Mol	Chain	Res	Type
26	1H	2872	G
26	1H	2875	C
26	1H	2885	C
26	1H	2886	G
27	16	0	A
27	16	7	G
27	16	13	A
27	16	15	A
27	16	25	A
27	16	34	U
27	16	35	U
27	16	39	A
27	16	42	C
27	16	45	A
27	16	56	G
27	16	65	C
27	16	73	A
27	16	81	G
27	16	105	G
27	16	109	G
27	16	115	G
1	1G	2	U
1	1G	3	G
1	1G	4	U
1	1G	5	U
1	1G	6	G
1	1G	7	G
1	1G	9	G
1	1G	22	G
1	1G	26	A
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	53	A
1	1G	81	G
1	1G	82	U
1	1G	88	C
1	1G	89	U
1	1G	90	C

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Mol	Chain	Res	Type
1	1G	91	C
1	1G	93	U
1	1G	101	A
1	1G	108	G
1	1G	115	G
1	1G	116	A
1	1G	121	C
1	1G	127	G
1	1G	131	C
1	1G	144	G
1	1G	162	A
1	1G	163	C
1	1G	167	G
1	1G	173	U
1	1G	174	C
1	1G	182	U
1	1G	185	A
1	1G	186	C
1	1G	186(F)	C
1	1G	191(A)	G
1	1G	191(C)	G
1	1G	195	A
1	1G	197	A
1	1G	209	U
1	1G	210	U
1	1G	216	G
1	1G	247	G
1	1G	251	G
1	1G	266	G
1	1G	267	C
1	1G	281	G
1	1G	289	G
1	1G	298	A
1	1G	314	C
1	1G	316	G
1	1G	318	G
1	1G	321	A
1	1G	328	C
1	1G	329	A
1	1G	332	G
1	1G	346	G
1	1G	347	G

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Mol	Chain	Res	Type
1	1G	351	G
1	1G	352	C
1	1G	353	A
1	1G	354	G
1	1G	367	U
1	1G	372	C
1	1G	388	G
1	1G	397	A
1	1G	398	C
1	1G	406	G
1	1G	412	A
1	1G	413	G
1	1G	414	A
1	1G	419	C
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	440	A
1	1G	442	C
1	1G	452	A
1	1G	456	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
1	1G	497	U
1	1G	505	G
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	531	U

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Mol	Chain	Res	Type
1	1G	532	A
1	1G	533	A
1	1G	536	C
1	1G	544	G
1	1G	547	A
1	1G	559	A
1	1G	561	U
1	1G	564	C
1	1G	572	A
1	1G	573	A
1	1G	576	G
1	1G	577	G
1	1G	607	A
1	1G	615	C
1	1G	617	G
1	1G	618	C
1	1G	619	U
1	1G	620	C
1	1G	630	G
1	1G	631	G
1	1G	632	A
1	1G	633	G
1	1G	653	A
1	1G	661	G
1	1G	665	A
1	1G	687	A
1	1G	688	G
1	1G	702	A
1	1G	723	U
1	1G	724	G
1	1G	731	G
1	1G	746	A
1	1G	749	C
1	1G	753	A
1	1G	755	G
1	1G	777	A
1	1G	787	A
1	1G	792	A
1	1G	793	U
1	1G	794	A
1	1G	816	A
1	1G	817	C

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Mol	Chain	Res	Type
1	1G	821	G
1	1G	827	U
1	1G	828	A
1	1G	841	U
1	1G	842	C
1	1G	848	C
1	1G	859	A
1	1G	873	A
1	1G	874	G
1	1G	885	G
1	1G	903	G
1	1G	914	A
1	1G	916	G
1	1G	922	G
1	1G	926	G
1	1G	927	G
1	1G	934	C
1	1G	935	A
1	1G	955	U
1	1G	960	U
1	1G	961	U
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	979	C
1	1G	980	C
1	1G	982	U
1	1G	983	A
1	1G	989	C
1	1G	991	U
1	1G	992	U
1	1G	993	G
1	1G	995	C
1	1G	1001	G
1	1G	1002	G
1	1G	1004	A
1	1G	1005	A

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Mol	Chain	Res	Type
1	1G	1006	C
1	1G	1007	C
1	1G	1008	C
1	1G	1009	G
1	1G	1021	G
1	1G	1022	G
1	1G	1023	G
1	1G	1024	G
1	1G	1025	U
1	1G	1037	C
1	1G	1040	U
1	1G	1046	A
1	1G	1050	G
1	1G	1054	C
1	1G	1056	U
1	1G	1064	G
1	1G	1066	C
1	1G	1092	A
1	1G	1094	G
1	1G	1095	U
1	1G	1096	C
1	1G	1098	C
1	1G	1099	G
1	1G	1101	A
1	1G	1107	C
1	1G	1124	G
1	1G	1125	U
1	1G	1126	U
1	1G	1127	G
1	1G	1128	C
1	1G	1129	C
1	1G	1133	G
1	1G	1135	U
1	1G	1137	C
1	1G	1139	G
1	1G	1140	C
1	1G	1146	A
1	1G	1154	G
1	1G	1157	A
1	1G	1158	C
1	1G	1159	U
1	1G	1160	G

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Mol	Chain	Res	Type
1	1G	1181	G
1	1G	1183	A
1	1G	1184	G
1	1G	1188	A
1	1G	1196	U
1	1G	1197	G
1	1G	1200	C
1	1G	1201	A
1	1G	1202	G
1	1G	1211	U
1	1G	1212	U
1	1G	1213	A
1	1G	1214	C
1	1G	1225	A
1	1G	1227	A
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	1274	G
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	1299	A
1	1G	1300	G
1	1G	1301	U
1	1G	1305	G
1	1G	1313	U
1	1G	1317	C
1	1G	1319	A
1	1G	1320	C
1	1G	1322	C

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Mol	Chain	Res	Type
1	1G	1323	G
1	1G	1331	G
1	1G	1335	C
1	1G	1336	C
1	1G	1338	G
1	1G	1340	A
1	1G	1346	A
1	1G	1347	G
1	1G	1353	G
1	1G	1358	U
1	1G	1359	C
1	1G	1360	A
1	1G	1362(A)	C
1	1G	1363	A
1	1G	1370	G
1	1G	1379	G
1	1G	1398	A
1	1G	1399	C
1	1G	1402	C
1	1G	1406	U
1	1G	1419	G
1	1G	1443	G
1	1G	1446	A
1	1G	1449	C
1	1G	1450	U
1	1G	1451	A
1	1G	1452	C
1	1G	1469	G
1	1G	1487	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	1529	G
1	1G	1530	G

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Mol	Chain	Res	Type
22	1L	3	U
22	1L	4	G
22	1L	5	A
22	1L	7	A
22	1L	8	U
22	1L	9	A
22	1L	10	G
22	1L	11	C
22	1L	15	G
22	1L	18	G
22	1L	19	G
22	1L	22	G
22	1L	25	C
22	1L	26	G
22	1L	29	C
22	1L	30	C
22	1L	42	U
22	1L	45	G
22	1L	47	U
22	1L	48	C
22	1L	49	G
22	1L	50	G
22	1L	53	G
22	1L	55	PSU
22	1L	56	C
22	1L	57	G
22	1L	58	A
22	1L	59	C
22	1L	60	U
22	1L	61	C
22	1L	63	G
22	1L	66	U
22	1L	67	A
22	1L	68	U
22	1L	69	C
22	1L	70	A
22	1L	71	G
22	1L	72	C
22	1L	73	A
22	1L	74	C
23	2L	2	G
23	2L	6	G

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Mol	Chain	Res	Type
23	2L	8	4SU
23	2L	9	G
23	2L	13	C
23	2L	16	C
23	2L	17	C
23	2L	18	U
23	2L	19	G
23	2L	21	U
23	2L	46	G
23	2L	47	7MG
23	2L	48	U
23	2L	49	C
23	2L	55	5MU
23	2L	57	C
23	2L	61	U
23	2L	77	A
55	3L	2	C
55	3L	3	U
55	3L	6	U
55	3L	7	A
55	3L	8	U
55	3L	9	A
55	3L	10	G
55	3L	11	C
55	3L	14	A
55	3L	15	G
55	3L	16	U
55	3L	26	G
55	3L	31	C
55	3L	33	U
55	3L	34	G
55	3L	35	G
55	3L	38	A
55	3L	41	G
55	3L	46	G
55	3L	47	U
55	3L	48	C
55	3L	54	5MU
55	3L	55	PSU
55	3L	56	C
55	3L	58	A
55	3L	59	A

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Mol	Chain	Res	Type
55	3L	60	U
55	3L	61	C
55	3L	64	C
55	3L	66	U
55	3L	73	A
25	4L	13	A
25	4L	14	A
25	4L	15	A
25	4L	23	A
25	4L	24	A
25	4L	25	A
26	14	7	G
26	14	8	A
26	14	9	U
26	14	11	G
26	14	14	A
26	14	15	G
26	14	34	C
26	14	35	G
26	14	46	C
26	14	49	A
26	14	50	U
26	14	51	G
26	14	58	G
26	14	60	G
26	14	63	U
26	14	71	A
26	14	72	U
26	14	74	A
26	14	75	G
26	14	78	A
26	14	92	G
26	14	95	G
26	14	101	G
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	138	G
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	171	G
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	205	G
26	14	214	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	232	G
26	14	233	A
26	14	248	G
26	14	249	C
26	14	250	G
26	14	269	U
26	14	270(I)	G
26	14	270(K)	C
26	14	270(L)	U
26	14	270(M)	U
26	14	270(O)	U
26	14	271(B)	G
26	14	271(C)	U
26	14	271	G
26	14	273(D)	C
26	14	273(F)	C
26	14	274	G
26	14	275	G
26	14	276	A
26	14	277	C
26	14	278	A
26	14	279	C
26	14	283	A

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Mol	Chain	Res	Type
26	14	289	A
26	14	290	G
26	14	308	G
26	14	311	A
26	14	312	G
26	14	324	A
26	14	329	G
26	14	330	A
26	14	333	G
26	14	352	G
26	14	354	G
26	14	363	G
26	14	363(E)	U
26	14	363(F)	A
26	14	372	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	415	A
26	14	428	A
26	14	443	A
26	14	444	C
26	14	448	U
26	14	454	A
26	14	455	C
26	14	457	A
26	14	470	A
26	14	481	G
26	14	501	A
26	14	505	A
26	14	509	C
26	14	528	A
26	14	531	C
26	14	532	A
26	14	533	G
26	14	537	C
26	14	546	C
26	14	547	A
26	14	549	G

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Mol	Chain	Res	Type
26	14	556	G
26	14	563	G
26	14	573	G
26	14	575	A
26	14	584	C
26	14	592	G
26	14	603	A
26	14	607	U
26	14	614	U
26	14	615	G
26	14	617	G
26	14	619	G
26	14	621	A
26	14	622	G
26	14	627	A
26	14	631	A
26	14	634	C
26	14	637	A
26	14	645	C
26	14	646	A
26	14	651	G
26	14	654	A
26	14	654(A)	A
26	14	654(B)	C
26	14	654(C)	G
26	14	654(D)	G
26	14	654(S)	G
26	14	654(T)	A
26	14	654(U)	A
26	14	669	G
26	14	686	G
26	14	708	C
26	14	709	U
26	14	717	G
26	14	730	C
26	14	738	G
26	14	747	U
26	14	748	G
26	14	752	A
26	14	753	C
26	14	765	G
26	14	775	G

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Mol	Chain	Res	Type
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	790	C
26	14	792	G
26	14	801	G
26	14	805	G
26	14	812	C
26	14	819	A
26	14	827	U
26	14	828	U
26	14	830	G
26	14	832	G
26	14	835	A
26	14	845	G
26	14	846	C
26	14	855	G
26	14	859	G
26	14	866	A
26	14	874	G
26	14	877	U
26	14	897	C
26	14	898	C
26	14	899	A
26	14	900	A
26	14	901	A
26	14	903	C
26	14	904	C
26	14	910	A
26	14	911	A
26	14	917	A
26	14	918	A
26	14	925	C
26	14	926	A
26	14	932	G
26	14	938	G
26	14	941	A
26	14	945	A
26	14	946	G

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Mol	Chain	Res	Type
26	14	958	U
26	14	959	A
26	14	960	A
26	14	961	C
26	14	968	G
26	14	974	G
26	14	974(A)	C
26	14	982	C
26	14	983	A
26	14	989	G
26	14	990	A
26	14	991	C
26	14	996	A
26	14	1004	C
26	14	1005	C
26	14	1008	C
26	14	1009	A
26	14	1010	A
26	14	1011	G
26	14	1012	U
26	14	1013	C
26	14	1017	G
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	1040	C
26	14	1044	G
26	14	1049	C
26	14	1050	A
26	14	1106	G
26	14	1107	G
26	14	1108	U
26	14	1109	C
26	14	1110	G
26	14	1111	A
26	14	1112	G
26	14	1114	G
26	14	1120	G
26	14	1122	G

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Mol	Chain	Res	Type
26	14	1129	A
26	14	1130	U
26	14	1135	C
26	14	1136	G
26	14	1139	G
26	14	1143	A
26	14	1151	G
26	14	1164	G
26	14	1170	G
26	14	1171	G
26	14	1173	G
26	14	1174	A
26	14	1175	U
26	14	1176	G
26	14	1177	A
26	14	1178	C
26	14	1204	A
26	14	1205	U
26	14	1212	G
26	14	1220	A
26	14	1230	C
26	14	1236	G
26	14	1248	G
26	14	1253	A
26	14	1256	G
26	14	1268	A
26	14	1271	G
26	14	1272	A
26	14	1274	A
26	14	1284	A
26	14	1300	U
26	14	1301	A
26	14	1303	G
26	14	1304	C
26	14	1306	C
26	14	1321	A
26	14	1325	G
26	14	1326	U
26	14	1329	U
26	14	1345	C
26	14	1347	G
26	14	1348	G

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Mol	Chain	Res	Type
26	14	1352	U
26	14	1359	A
26	14	1360	A
26	14	1365	A
26	14	1368	G
26	14	1370	C
26	14	1380	G
26	14	1385	G
26	14	1386	C
26	14	1400	G
26	14	1416	G
26	14	1417	C
26	14	1419	A
26	14	1421	G
26	14	1427	A
26	14	1428	C
26	14	1444(A)	A
26	14	1445	C
26	14	1449	A
26	14	1449(A)	G
26	14	1451	C
26	14	1454	U
26	14	1455	G
26	14	1458	C
26	14	1459	G
26	14	1460	A
26	14	1467	C
26	14	1471	A
26	14	1475	G
26	14	1483	G
26	14	1493	C
26	14	1508	A
26	14	1509	C
26	14	1510	A
26	14	1522	G
26	14	1526	G
26	14	1534	G
26	14	1537	C
26	14	1543	A
26	14	1558	A
26	14	1559	G
26	14	1560	G

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Mol	Chain	Res	Type
26	14	1566	A
26	14	1569	A
26	14	1578	U
26	14	1583	A
26	14	1585	C
26	14	1586	A
26	14	1588	C
26	14	1589	C
26	14	1608	A
26	14	1609	A
26	14	1610	A
26	14	1614	A
26	14	1616	A
26	14	1625	C
26	14	1639	U
26	14	1647	G
26	14	1648	C
26	14	1674	G
26	14	1675	C
26	14	1676	A
26	14	1700	A
26	14	1701	A
26	14	1703	G
26	14	1725	G
26	14	1726	G
26	14	1729	A
26	14	1730	U
26	14	1731	G
26	14	1743	G
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
26	14	1801	G
26	14	1816	G
26	14	1819	A
26	14	1820	U

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Mol	Chain	Res	Type
26	14	1829	A
26	14	1836	C
26	14	1839	G
26	14	1847	A
26	14	1858	G
26	14	1871	A
26	14	1878	G
26	14	1886	C
26	14	1888	G
26	14	1889	A
26	14	1905	C
26	14	1906	G
26	14	1913	A
26	14	1914	C
26	14	1916	A
26	14	1917	U
26	14	1929	G
26	14	1930	G
26	14	1931	U
26	14	1936	A
26	14	1938	A
26	14	1940	U
26	14	1955	U
26	14	1963	U
26	14	1967	C
26	14	1970	A
26	14	1971	A
26	14	1972	A
26	14	1985	G
26	14	1992	G
26	14	1993	U
26	14	2018	G
26	14	2023	G
26	14	2027	G
26	14	2031	A
26	14	2033	A
26	14	2036	C
26	14	2043	C
26	14	2049	G
26	14	2055	C
26	14	2056	G
26	14	2060	A

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Mol	Chain	Res	Type
26	14	2061	G
26	14	2062	A
26	14	2063	C
26	14	2066	C
26	14	2069	G
26	14	2076	U
26	14	2080	G
26	14	2093	G
26	14	2099	U
26	14	2100	G
26	14	2108	C
26	14	2110	G
26	14	2114	A
26	14	2115	G
26	14	2117	A
26	14	2118	U
26	14	2119	A
26	14	2120	G
26	14	2124	G
26	14	2125	G
26	14	2126	A
26	14	2127	G
26	14	2128	C
26	14	2129	C
26	14	2131	G
26	14	2132	U
26	14	2133	G
26	14	2134	A
26	14	2135	A
26	14	2136	C
26	14	2137	C
26	14	2140	C
26	14	2141	G
26	14	2144	U
26	14	2145	C
26	14	2146	C
26	14	2147	G
26	14	2148	G
26	14	2153	G
26	14	2156	G
26	14	2157	G
26	14	2158	A

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Mol	Chain	Res	Type
26	14	2161	C
26	14	2162	G
26	14	2164	C
26	14	2166	G
26	14	2168	G
26	14	2171	A
26	14	2172	U
26	14	2173	A
26	14	2174	C
26	14	2175	C
26	14	2176	A
26	14	2188	C
26	14	2189	U
26	14	2191	G
26	14	2192	G
26	14	2198	A
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	2238	G
26	14	2240	C
26	14	2251	G
26	14	2253	G
26	14	2259	G
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	2287	A
26	14	2288	A
26	14	2305	A
26	14	2307	G
26	14	2308	G

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Mol	Chain	Res	Type
26	14	2310	A
26	14	2311	A
26	14	2318	G
26	14	2321	G
26	14	2325	G
26	14	2326	C
26	14	2327	A
26	14	2333	A
26	14	2336	A
26	14	2337	G
26	14	2342	C
26	14	2346	A
26	14	2347	C
26	14	2350	C
26	14	2354	G
26	14	2355	C
26	14	2359	C
26	14	2372	G
26	14	2383	G
26	14	2385	C
26	14	2389	G
26	14	2392	A
26	14	2396	G
26	14	2402	C
26	14	2403	C
26	14	2406	U
26	14	2407	G
26	14	2411	A
26	14	2414	G
26	14	2422	A
26	14	2425	A
26	14	2428	G
26	14	2429	G
26	14	2430	A
26	14	2431	U
26	14	2434	A
26	14	2435	A
26	14	2439	A
26	14	2440	C
26	14	2441	C
26	14	2448	A
26	14	2469	A

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Mol	Chain	Res	Type
26	14	2470	G
26	14	2472	G
26	14	2476	A
26	14	2477	C
26	14	2478	A
26	14	2487	G
26	14	2496	C
26	14	2497	A
26	14	2502	G
26	14	2505	G
26	14	2507	C
26	14	2518	A
26	14	2520	C
26	14	2525	G
26	14	2529	G
26	14	2542	A
26	14	2543	G
26	14	2549	G
26	14	2554	U
26	14	2563	U
26	14	2564	A
26	14	2566	A
26	14	2567	G
26	14	2569	G
26	14	2573	C
26	14	2578	G
26	14	2586	C
26	14	2602	A
26	14	2609	U
26	14	2611	U
26	14	2612	C
26	14	2613	U
26	14	2615	U
26	14	2630	G
26	14	2634	G
26	14	2636	U
26	14	2654	A
26	14	2660	A
26	14	2665	A
26	14	2667	C
26	14	2679	A
26	14	2689	U

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Mol	Chain	Res	Type
26	14	2690	C
26	14	2702	U
26	14	2703	C
26	14	2707	G
26	14	2712(A)	A
26	14	2713	A
26	14	2714	G
26	14	2726	U
26	14	2733	A
26	14	2744	G
26	14	2747	G
26	14	2748	A
26	14	2750	A
26	14	2751	G
26	14	2752	C
26	14	2757	A
26	14	2758	A
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	2780	G
26	14	2789	C
26	14	2790	A
26	14	2791	C
26	14	2792	G
26	14	2793	G
26	14	2795	G
26	14	2797	U
26	14	2798	C
26	14	2799	A
26	14	2801	A
26	14	2802	G
26	14	2803	C
26	14	2804	C
26	14	2808	U
26	14	2810	A
26	14	2818	G

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Mol	Chain	Res	Type
26	14	2820	A
26	14	2821	A
26	14	2833	G
26	14	2834	G
26	14	2835	A
26	14	2860	A
26	14	2872	G
26	14	2873	A
26	14	2874	C
26	14	2880	C
26	14	2885	C
26	14	2886	G
26	14	2892	A
26	14	2893	G
26	14	2894	G
26	14	2895	U
27	1J	0	A
27	1J	2	C
27	1J	7	G
27	1J	8	U
27	1J	12	C
27	1J	13	A
27	1J	15	A
27	1J	16	G
27	1J	22	U
27	1J	25	A
27	1J	28	C
27	1J	29	A
27	1J	33	G
27	1J	40	U
27	1J	42	C
27	1J	44	G
27	1J	45	A
27	1J	53	A
27	1J	56	G
27	1J	58	A
27	1J	59	A
27	1J	73	A
27	1J	81	G
27	1J	83	G
27	1J	88	C
27	1J	89	G

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Mol	Chain	Res	Type
27	1J	89(A)	A
27	1J	90	C
27	1J	100	G
27	1J	108	C
27	1J	109	G
27	1J	116	G
27	1J	118	G

All (170) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	13	1	U
1	13	5	U
1	13	31	G
1	13	49	U
1	13	50	A
1	13	108	G
1	13	115	G
1	13	181	G
1	13	244	U
1	13	266	G
1	13	429	U
1	13	484	G
1	13	560	U
1	13	687	A
1	13	748	C
1	13	793	U
1	13	871	U
1	13	913	A
1	13	1023	G
1	13	1054	C
1	13	1064	G
1	13	1065	U
1	13	1128	C
1	13	1129	C
1	13	1157	A
1	13	1182	G
1	13	1256	A
1	13	1285	A
1	13	1301	U
1	13	1331	G
1	13	1336	C

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Mol	Chain	Res	Type
1	13	1397	C
1	13	1453	G
1	13	1498	U
1	13	1503	A
1	13	1533	C
22	1K	2	C
22	1K	17	H2U
22	1K	48	C
22	1K	68	U
22	1K	69	C
23	2K	48	U
24	3K	2	C
24	3K	8	U
25	4K	11	U
25	4K	12	A
25	4K	24	A
26	1H	125	G
26	1H	196	A
26	1H	222	A
26	1H	249	C
26	1H	404	C
26	1H	508	G
26	1H	587	C
26	1H	685	A
26	1H	746	A
26	1H	764	A
26	1H	776	G
26	1H	827	U
26	1H	845	G
26	1H	858	U
26	1H	859	G
26	1H	1022	G
26	1H	1026	U
26	1H	1060	U
26	1H	1085	A
26	1H	1110	G
26	1H	1176	G
26	1H	1178	C
26	1H	1210	A
26	1H	1378	A
26	1H	1379	A
26	1H	1420	U

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Mol	Chain	Res	Type
26	1H	1451	C
26	1H	1509	C
26	1H	1558	A
26	1H	1608	A
26	1H	1609	A
26	1H	1799	G
26	1H	1858	G
26	1H	1900	A
26	1H	1992	G
26	1H	2035	G
26	1H	2062	A
26	1H	2172	U
26	1H	2210	G
26	1H	2422	A
26	1H	2439	A
26	1H	2481	G
26	1H	2566	A
26	1H	2611	U
26	1H	2756	U
27	16	44	G
1	1G	2	U
1	1G	5	U
1	1G	80	G
1	1G	87	A
1	1G	89	U
1	1G	115	G
1	1G	250	A
1	1G	266	G
1	1G	345	C
1	1G	412	A
1	1G	429	U
1	1G	465	A
1	1G	485	G
1	1G	509	A
1	1G	560	U
1	1G	687	A
1	1G	748	C
1	1G	793	U
1	1G	913	A
1	1G	974	A
1	1G	1053	G
1	1G	1126	U

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Mol	Chain	Res	Type
1	1G	1145	C
1	1G	1157	A
1	1G	1285	A
1	1G	1300	G
1	1G	1359	C
1	1G	1442	G
1	1G	1449	C
1	1G	1450	U
1	1G	1498	U
22	1L	69	C
23	2L	21	U
23	2L	47	7MG
23	2L	48	U
55	3L	2	C
55	3L	5	A
55	3L	58	A
25	4L	12	A
25	4L	22	A
25	4L	23	A
26	14	6	A
26	14	49	A
26	14	71	A
26	14	128	C
26	14	278	A
26	14	746	A
26	14	752	A
26	14	764	A
26	14	774	A
26	14	960	A
26	14	974	G
26	14	1022	G
26	14	1325	G
26	14	1378	A
26	14	1379	A
26	14	1420	U
26	14	1534	G
26	14	1558	A
26	14	1608	A
26	14	1819	A
26	14	1992	G
26	14	2062	A
26	14	2173	A

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Mol	Chain	Res	Type
26	14	2174	C
26	14	2275	C
26	14	2406	U
26	14	2439	A
26	14	2477	C
26	14	2611	U
26	14	2629	A
26	14	2689	U
26	14	2756	U
26	14	2776	A
26	14	2791	C
26	14	2859	G
27	1J	88	C

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

20 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	$\#\|Z\| > 2$
22	5MU	1K	54	22	19,22,23	4.30	5 (26%)	27,32,35	3.49	13 (48%)
22	AET	1K	37	22	32,35,36	2.55	6 (18%)	43,51,54	2.23	12 (27%)
23	5MU	2K	55	23	19,22,23	3.92	5 (26%)	27,32,35	3.26	9 (33%)
22	PSU	1L	55	22	18,21,22	1.39	1 (5%)	21,30,33	1.87	5 (23%)
23	7MG	2K	47	23	23,26,27	3.02	9 (39%)	27,39,42	2.75	9 (33%)
22	H2U	1K	17	22	18,21,22	2.33	4 (22%)	19,30,33	1.57	3 (15%)
22	H2U	1L	17	22	18,21,22	2.52	4 (22%)	19,30,33	1.62	4 (21%)
23	4SU	2L	8	23	18,21,22	1.86	3 (16%)	25,30,33	2.44	7 (28%)
22	AET	1L	37	22	32,35,36	2.51	6 (18%)	43,51,54	2.19	18 (41%)
23	4SU	2K	8	23	18,21,22	1.90	4 (22%)	25,30,33	3.01	8 (32%)
23	OMC	2L	33	23	19,22,23	1.70	3 (15%)	25,31,34	0.83	0
23	PSU	2L	56	23	18,21,22	1.23	2 (11%)	21,30,33	1.58	2 (9%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
55	PSU	3L	55	55	18,21,22	1.27	2 (11%)	21,30,33	1.92	5 (23%)
23	7MG	2L	47	23	23,26,27	3.01	7 (30%)	27,39,42	2.88	9 (33%)
22	PSU	1K	55	22	18,21,22	1.37	2 (11%)	21,30,33	1.92	3 (14%)
23	5MU	2L	55	23	19,22,23	4.00	5 (26%)	27,32,35	3.40	10 (37%)
23	OMC	2K	33	23	19,22,23	1.80	3 (15%)	25,31,34	1.26	4 (16%)
23	PSU	2K	56	23	18,21,22	1.29	2 (11%)	21,30,33	2.12	4 (19%)
55	5MU	3L	54	55	19,22,23	3.97	5 (26%)	27,32,35	3.29	9 (33%)
22	5MU	1L	54	22	19,22,23	4.18	5 (26%)	27,32,35	3.25	10 (37%)

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
22	5MU	1K	54	22	-	0/7/25/26	0/2/2/2
22	AET	1K	37	22	-	10/27/45/46	0/3/3/3
23	5MU	2K	55	23	-	0/7/25/26	0/2/2/2
22	PSU	1L	55	22	-	2/7/25/26	0/2/2/2
23	7MG	2K	47	23	-	2/7/37/38	0/3/3/3
22	H2U	1K	17	22	-	4/7/38/39	0/2/2/2
22	H2U	1L	17	22	-	5/7/38/39	0/2/2/2
23	4SU	2L	8	23	-	2/7/25/26	0/2/2/2
22	AET	1L	37	22	-	5/27/45/46	0/3/3/3
23	4SU	2K	8	23	-	2/7/25/26	0/2/2/2
23	OMC	2L	33	23	-	0/9/27/28	0/2/2/2
23	PSU	2L	56	23	-	0/7/25/26	0/2/2/2
55	PSU	3L	55	55	-	2/7/25/26	0/2/2/2
23	7MG	2L	47	23	-	0/7/37/38	0/3/3/3
22	PSU	1K	55	22	-	2/7/25/26	0/2/2/2
23	5MU	2L	55	23	-	2/7/25/26	0/2/2/2
23	OMC	2K	33	23	-	1/9/27/28	0/2/2/2
23	PSU	2K	56	23	-	0/7/25/26	0/2/2/2
55	5MU	3L	54	55	-	2/7/25/26	0/2/2/2
22	5MU	1L	54	22	-	0/7/25/26	0/2/2/2

All (83) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
22	1K	54	5MU	C2-N1	14.60	1.61	1.38
22	1L	54	5MU	C2-N1	13.77	1.60	1.38
23	2L	55	5MU	C2-N1	13.02	1.58	1.38
23	2K	55	5MU	C2-N1	12.72	1.58	1.38
55	3L	54	5MU	C2-N1	12.47	1.58	1.38
22	1K	37	AET	C10-N6	10.58	1.51	1.37
22	1L	37	AET	C10-N6	10.33	1.51	1.37
23	2K	47	7MG	C5-N7	8.01	1.45	1.35
22	1L	17	H2U	C2-N1	7.87	1.46	1.35
23	2L	47	7MG	C5-N7	7.59	1.45	1.35
22	1K	17	H2U	C2-N1	7.29	1.45	1.35
23	2K	47	7MG	C4-N9	-6.67	1.29	1.37
22	1L	37	AET	C10-N11	6.61	1.49	1.35
23	2L	47	7MG	C4-N9	-6.59	1.29	1.37
22	1K	37	AET	C10-N11	6.39	1.49	1.35
22	1K	54	5MU	C4-C5	6.38	1.55	1.44
23	2L	47	7MG	C4-N3	6.19	1.48	1.34
55	3L	54	5MU	C6-N1	6.14	1.48	1.38
23	2K	55	5MU	C2-N3	6.14	1.48	1.38
23	2L	55	5MU	C2-N3	6.09	1.48	1.38
55	3L	54	5MU	C2-N3	6.02	1.48	1.38
23	2K	47	7MG	C4-N3	5.99	1.48	1.34
55	3L	54	5MU	C4-N3	-5.96	1.27	1.38
22	1L	54	5MU	C4-C5	5.95	1.54	1.44
22	1L	54	5MU	C2-N3	5.92	1.48	1.38
23	2L	55	5MU	C4-N3	-5.92	1.27	1.38
22	1L	54	5MU	C4-N3	-5.92	1.27	1.38
22	1K	54	5MU	C4-N3	-5.82	1.28	1.38
22	1L	54	5MU	C6-N1	5.67	1.47	1.38
23	2L	55	5MU	C6-N1	5.62	1.47	1.38
23	2K	55	5MU	C6-N1	5.51	1.47	1.38
22	1K	54	5MU	C2-N3	5.47	1.47	1.38
23	2K	8	4SU	C5-C4	5.47	1.49	1.42
23	2K	55	5MU	C4-N3	-5.46	1.28	1.38
22	1K	54	5MU	C6-N1	5.44	1.47	1.38
23	2K	55	5MU	C4-C5	5.43	1.53	1.44
23	2L	8	4SU	C5-C4	5.33	1.48	1.42
23	2L	55	5MU	C4-C5	5.22	1.53	1.44
22	1L	55	PSU	C6-C5	5.14	1.41	1.35
55	3L	54	5MU	C4-C5	5.13	1.53	1.44
23	2K	33	OMC	C2-N3	5.05	1.46	1.36
22	1L	17	H2U	C2-N3	5.03	1.46	1.38
23	2L	47	7MG	C8-N7	4.69	1.65	1.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
22	1K	55	PSU	C6-C5	4.65	1.40	1.35
23	2L	33	OMC	C2-N3	4.59	1.45	1.36
23	2K	47	7MG	C8-N7	4.58	1.64	1.42
22	1K	17	H2U	C2-N3	4.54	1.45	1.38
23	2L	47	7MG	C5-C4	-4.48	1.24	1.37
23	2K	33	OMC	C4-N4	4.36	1.44	1.33
23	2K	56	PSU	C6-C5	4.27	1.40	1.35
23	2L	8	4SU	C2-N1	4.16	1.45	1.38
55	3L	55	PSU	C6-C5	4.14	1.39	1.35
23	2L	56	PSU	C6-C5	4.14	1.39	1.35
23	2K	47	7MG	C5-C4	-4.12	1.25	1.37
23	2K	8	4SU	C2-N1	4.10	1.44	1.38
22	1L	37	AET	C6-N6	4.09	1.48	1.39
22	1K	37	AET	C6-N6	3.95	1.47	1.39
22	1L	17	H2U	C4-N3	3.94	1.44	1.37
23	2L	33	OMC	C4-N4	3.89	1.43	1.33
22	1K	17	H2U	C4-N3	3.63	1.43	1.37
23	2K	33	OMC	C5-C4	3.44	1.50	1.42
23	2L	33	OMC	C5-C4	3.35	1.50	1.42
23	2L	47	7MG	C2-N2	3.09	1.41	1.34
23	2K	47	7MG	C2-N2	2.98	1.41	1.34
23	2K	8	4SU	C6-N1	2.90	1.45	1.38
23	2L	8	4SU	C6-N1	2.84	1.44	1.38
22	1K	37	AET	C5-N7	-2.80	1.34	1.39
22	1K	37	AET	C5-C4	-2.77	1.34	1.39
22	1L	37	AET	C5-N7	-2.72	1.34	1.39
22	1L	37	AET	C5-C4	-2.52	1.34	1.39
22	1K	37	AET	C4-N9	-2.45	1.32	1.37
22	1K	55	PSU	C2-N1	2.39	1.39	1.36
23	2L	47	7MG	C5-C6	2.35	1.49	1.43
22	1K	17	H2U	C6-N1	-2.32	1.43	1.47
23	2K	47	7MG	C8-N9	2.30	1.47	1.45
23	2K	8	4SU	C4-S4	-2.25	1.64	1.68
22	1L	17	H2U	C6-N1	-2.21	1.43	1.47
55	3L	55	PSU	C2-N1	2.19	1.39	1.36
23	2K	47	7MG	C6-N1	-2.18	1.34	1.38
23	2K	47	7MG	C5-C6	2.14	1.48	1.43
23	2L	56	PSU	C2-N1	2.13	1.39	1.36
22	1L	37	AET	C8-N9	-2.13	1.33	1.37
23	2K	56	PSU	C4-C5	-2.04	1.38	1.44

All (144) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
23	2L	55	5MU	C5-C4-N3	10.91	124.81	115.32
55	3L	54	5MU	C5-C4-N3	10.61	124.55	115.32
22	1K	54	5MU	C5-C4-N3	10.52	124.46	115.32
22	1L	54	5MU	C5-C4-N3	10.46	124.41	115.32
23	2K	55	5MU	C5-C4-N3	9.57	123.64	115.32
23	2K	8	4SU	C4-N3-C2	-8.91	118.77	127.31
23	2K	8	4SU	C5-C4-N3	8.88	123.01	114.75
23	2K	47	7MG	C4-C5-N7	7.91	114.72	105.38
23	2L	47	7MG	C4-C5-N7	7.69	114.47	105.38
22	1K	37	AET	N3-C2-N1	-7.17	117.73	128.58
23	2L	8	4SU	C5-C4-N3	7.15	121.40	114.75
23	2L	55	5MU	C4-N3-C2	-6.81	118.42	127.34
23	2L	8	4SU	C4-N3-C2	-6.55	121.03	127.31
23	2K	55	5MU	C6-C5-C4	6.32	123.23	118.02
22	1K	54	5MU	C5M-C5-C6	-6.30	114.32	122.85
22	1L	37	AET	N3-C2-N1	-6.28	119.07	128.58
22	1L	54	5MU	C4-N3-C2	-6.25	119.15	127.34
23	2L	47	7MG	C5-C4-N9	6.24	114.32	106.33
55	3L	54	5MU	C4-N3-C2	-6.20	119.21	127.34
23	2K	55	5MU	C4-N3-C2	-6.16	119.26	127.34
23	2L	55	5MU	C5-C6-N1	-6.04	116.75	123.31
22	1K	54	5MU	C4-N3-C2	-6.04	119.42	127.34
23	2K	55	5MU	C5-C6-N1	-5.95	116.86	123.31
23	2K	47	7MG	C5-C4-N9	5.94	113.95	106.33
23	2L	55	5MU	C6-C5-C4	5.87	122.86	118.02
22	1L	54	5MU	C5-C6-N1	-5.80	117.01	123.31
22	1K	54	5MU	C5-C6-N1	-5.71	117.11	123.31
22	1L	54	5MU	C6-C5-C4	5.60	122.64	118.02
22	1K	54	5MU	C6-C5-C4	5.41	122.48	118.02
55	3L	54	5MU	O4-C4-C5	-5.40	118.74	124.92
23	2K	56	PSU	N1-C2-N3	5.34	120.80	115.17
23	2L	55	5MU	O4-C4-C5	-5.30	118.85	124.92
55	3L	54	5MU	C5-C6-N1	-5.27	117.59	123.31
23	2K	55	5MU	O4-C4-C5	-5.16	119.01	124.92
23	2K	55	5MU	C5M-C5-C6	-5.10	115.94	122.85
22	1K	37	AET	C2-N1-C6	5.05	124.16	111.83
23	2K	47	7MG	C6-C5-N7	-4.98	124.21	131.93
55	3L	54	5MU	C6-C5-C4	4.94	122.09	118.02
23	2L	47	7MG	C5-C6-N1	4.90	119.56	110.94
22	1L	54	5MU	C5M-C5-C6	-4.82	116.32	122.85
23	2K	56	PSU	C4-N3-C2	-4.82	119.73	126.37
22	1K	55	PSU	N1-C2-N3	4.81	120.24	115.17
55	3L	55	PSU	C4-N3-C2	-4.80	119.76	126.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
22	1K	55	PSU	C4-N3-C2	-4.67	119.93	126.37
23	2L	47	7MG	C6-C5-N7	-4.59	124.82	131.93
23	2K	8	4SU	C5-C4-S4	-4.56	119.10	124.31
22	1L	55	PSU	N1-C2-N3	4.56	119.97	115.17
23	2K	47	7MG	C5-C6-N1	4.51	118.88	110.94
23	2L	8	4SU	C5-C4-S4	-4.48	119.19	124.31
55	3L	55	PSU	N1-C2-N3	4.46	119.87	115.17
22	1K	37	AET	C12-N11-C10	4.46	134.01	122.64
23	2L	47	7MG	C5-C4-N3	-4.44	119.79	128.13
22	1L	37	AET	C13-C12-N11	-4.42	100.46	110.17
23	2L	47	7MG	C2-N3-C4	4.40	119.88	112.30
22	1K	37	AET	C14-C12-C13	4.33	117.59	110.03
23	2L	55	5MU	C5M-C5-C6	-4.31	117.01	122.85
23	2K	47	7MG	C5-C4-N3	-4.24	120.17	128.13
23	2L	56	PSU	C4-N3-C2	-4.24	120.54	126.37
22	1L	37	AET	C5-C4-N3	-4.22	120.90	126.72
22	1L	37	AET	C2-N1-C6	4.21	122.10	111.83
22	1K	54	5MU	C5M-C5-C4	4.14	123.20	118.78
22	1K	37	AET	N9-C8-N7	-4.13	108.08	113.94
22	1K	17	H2U	N3-C2-N1	4.05	120.72	116.65
55	3L	54	5MU	C5M-C5-C6	-4.04	117.38	122.85
22	1L	37	AET	N9-C8-N7	-3.99	108.28	113.94
22	1L	54	5MU	O4-C4-C5	-3.97	120.38	124.92
22	1L	55	PSU	C4-N3-C2	-3.95	120.93	126.37
23	2K	8	4SU	N3-C2-N1	3.89	119.96	114.89
23	2K	56	PSU	C6-N1-C2	-3.86	119.11	122.69
22	1L	17	H2U	C5-C6-N1	3.84	123.14	111.52
23	2K	47	7MG	C2-N3-C4	3.75	118.76	112.30
22	1L	37	AET	C12-N11-C10	3.56	131.72	122.64
23	2L	56	PSU	N1-C2-N3	3.50	118.86	115.17
22	1K	54	5MU	O4-C4-C5	-3.42	121.00	124.92
22	1L	55	PSU	C6-N1-C2	-3.40	119.53	122.69
22	1L	17	H2U	N3-C2-N1	3.31	119.98	116.65
22	1K	17	H2U	C5-C6-N1	3.31	121.54	111.52
22	1L	37	AET	C2-N3-C4	3.29	119.87	111.83
23	2K	56	PSU	O2-C2-N1	-3.28	119.40	122.79
22	1K	54	5MU	C1'-N1-C2	3.26	123.45	117.59
55	3L	54	5MU	C6-N1-C2	-3.24	118.08	121.30
22	1L	37	AET	C4-C5-C6	3.21	119.23	115.91
22	1K	37	AET	C5-C4-N9	3.18	109.28	105.81
23	2L	47	7MG	C2-N1-C6	-3.16	119.38	125.11
22	1K	37	AET	C2-N3-C4	3.09	119.39	111.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
55	3L	55	PSU	C6-C5-C4	3.08	120.25	118.17
22	1L	17	H2U	C5-C4-N3	3.06	119.94	116.69
22	1K	37	AET	C4-C5-N7	-3.06	107.09	110.58
23	2L	8	4SU	C1'-N1-C2	3.05	123.07	117.59
23	2K	47	7MG	C2-N1-C6	-3.02	119.63	125.11
22	1K	55	PSU	C6-N1-C2	-3.01	119.90	122.69
22	1K	37	AET	C5-C4-N3	-2.98	122.61	126.72
22	1K	37	AET	C5-N7-C8	2.98	108.13	103.45
22	1K	54	5MU	O4-C4-N3	-2.97	114.53	120.11
22	1L	37	AET	C5-N7-C8	2.92	108.04	103.45
23	2L	47	7MG	N9-C8-N7	-2.89	99.28	103.37
23	2K	8	4SU	C6-C5-C4	-2.85	117.49	119.95
22	1K	17	H2U	C5-C4-N3	2.84	119.71	116.69
23	2L	47	7MG	O6-C6-C5	-2.84	120.64	127.62
23	2K	47	7MG	O6-C6-C5	-2.80	120.75	127.62
23	2K	33	OMC	C1'-N1-C6	-2.77	114.86	120.78
55	3L	54	5MU	N3-C2-N1	2.75	118.48	114.89
22	1L	37	AET	O10-C10-N6	-2.73	119.19	122.19
23	2L	8	4SU	C6-C5-C4	-2.71	117.60	119.95
23	2L	55	5MU	N3-C2-N1	2.71	118.42	114.89
23	2K	8	4SU	O2-C2-N3	-2.66	116.59	121.49
22	1L	54	5MU	C6-N1-C2	-2.65	118.66	121.30
23	2K	33	OMC	N4-C4-N3	2.62	122.59	117.91
22	1L	54	5MU	O4-C4-N3	-2.61	115.21	120.11
23	2L	55	5MU	C6-N1-C2	-2.59	118.72	121.30
55	3L	54	5MU	O2-C2-N1	-2.56	119.47	122.80
22	1L	54	5MU	N3-C2-N1	2.49	118.13	114.89
22	1L	37	AET	C4-C5-N7	-2.47	107.76	110.58
22	1L	37	AET	C14-C12-C13	2.43	114.27	110.03
23	2K	47	7MG	N9-C8-N7	-2.36	100.02	103.37
22	1K	54	5MU	O2-C2-N3	-2.36	117.13	121.49
23	2K	8	4SU	C1'-N1-C2	2.36	121.83	117.59
22	1K	54	5MU	C6-N1-C2	-2.35	118.96	121.30
23	2K	55	5MU	O2-C2-N1	-2.35	119.74	122.80
23	2K	55	5MU	N3-C2-N1	2.34	117.93	114.89
55	3L	55	PSU	O2-C2-N1	-2.32	120.40	122.79
22	1L	55	PSU	O3'-C3'-C4'	2.28	117.64	111.08
23	2K	33	OMC	C1'-N1-C2	2.28	123.47	118.44
22	1K	37	AET	C4-C5-C6	2.28	118.27	115.91
22	1L	37	AET	N3-C4-N9	2.26	131.00	127.17
23	2K	55	5MU	C6-N1-C2	-2.25	119.06	121.30
23	2K	8	4SU	S4-C4-N3	-2.21	117.89	120.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
22	1L	55	PSU	O2-C2-N1	-2.19	120.53	122.79
22	1K	54	5MU	C1'-N1-C6	-2.16	117.59	121.15
22	1L	54	5MU	C5M-C5-C4	2.12	121.04	118.78
23	2K	33	OMC	CM2-O2'-C2'	2.11	119.90	114.47
22	1L	37	AET	N1-C6-N6	2.11	118.65	116.36
23	2L	55	5MU	O2-C2-N1	-2.10	120.06	122.80
23	2L	8	4SU	C1'-N1-C6	-2.09	116.32	120.78
22	1L	37	AET	C5-C4-N9	2.08	108.07	105.81
22	1L	37	AET	CM6-N6-C6	2.06	122.18	118.22
22	1K	54	5MU	N3-C2-N1	2.05	117.56	114.89
23	2L	8	4SU	N3-C2-N1	2.04	117.55	114.89
22	1K	37	AET	ODB-C13-C12	2.04	121.22	114.15
55	3L	55	PSU	O4'-C1'-C2'	2.03	107.96	105.15
22	1L	17	H2U	O2-C2-N3	-2.02	117.76	121.49
23	2L	55	5MU	O4-C4-N3	-2.01	116.33	120.11
22	1L	37	AET	C14-C12-N11	2.00	117.02	111.70
22	1L	37	AET	C4-N9-C8	2.00	107.84	105.74

There are no chirality outliers.

All (41) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
55	3L	54	5MU	C4'-C5'-O5'-P
22	1K	17	H2U	O4'-C1'-N1-C2
22	1K	17	H2U	O4'-C1'-N1-C6
22	1K	17	H2U	C2'-C1'-N1-C6
22	1L	17	H2U	O4'-C1'-N1-C2
22	1L	17	H2U	O4'-C1'-N1-C6
22	1K	37	AET	C5-C6-N6-CM6
22	1K	37	AET	N1-C6-N6-CM6
22	1K	37	AET	C14-C12-N11-C10
22	1K	37	AET	C13-C12-C14-O14
22	1K	37	AET	C13-C12-C14-C15
22	1L	37	AET	C14-C12-N11-C10
22	1K	55	PSU	O4'-C4'-C5'-O5'
23	2K	47	7MG	C2'-C1'-N9-C8
22	1K	17	H2U	C2'-C1'-N1-C2
22	1K	55	PSU	C3'-C4'-C5'-O5'
22	1L	55	PSU	C3'-C4'-C5'-O5'
22	1L	55	PSU	O4'-C4'-C5'-O5'
22	1L	17	H2U	O4'-C4'-C5'-O5'
22	1L	17	H2U	C3'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
23	2K	8	4SU	O4'-C4'-C5'-O5'
23	2L	55	5MU	C3'-C4'-C5'-O5'
23	2L	55	5MU	O4'-C4'-C5'-O5'
22	1K	37	AET	N11-C12-C14-O14
22	1K	37	AET	N11-C12-C14-C15
23	2L	8	4SU	O4'-C4'-C5'-O5'
55	3L	54	5MU	C3'-C4'-C5'-O5'
22	1L	37	AET	C13-C12-C14-C15
23	2K	8	4SU	C3'-C4'-C5'-O5'
22	1L	37	AET	N1-C6-N6-CM6
22	1K	37	AET	N11-C12-C13-ODA
55	3L	55	PSU	O4'-C1'-C5-C4
22	1L	17	H2U	C4'-C5'-O5'-P
23	2K	47	7MG	C4'-C5'-O5'-P
23	2L	8	4SU	C4'-C5'-O5'-P
55	3L	55	PSU	O4'-C1'-C5-C6
22	1L	37	AET	C5-C6-N6-CM6
22	1K	37	AET	N1-C6-N6-C10
23	2K	33	OMC	C2'-C1'-N1-C2
22	1K	37	AET	C5-C6-N6-C10
22	1L	37	AET	C5-C6-N6-C10

There are no ring outliers.

12 monomers are involved in 23 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
22	1K	54	5MU	2	0
22	1K	37	AET	4	0
23	2K	47	7MG	3	0
23	2L	8	4SU	1	0
22	1L	37	AET	3	0
23	2K	8	4SU	1	0
23	2L	33	OMC	2	0
55	3L	55	PSU	2	0
23	2L	47	7MG	1	0
23	2L	55	5MU	2	0
55	3L	54	5MU	3	0
22	1L	54	5MU	1	0

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 1498 ligands modelled in this entry, 1496 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	$\#\|Z\| > 2$
57	SF4	3E	302	4	0,12,12	-	-	-		
57	SF4	32	301	4	0,12,12	-	-	-		

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	SF4	3E	302	4	-	-	0/6/5/5
57	SF4	32	301	4	-	-	0/6/5/5

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
57	3E	302	SF4	1	0
57	32	301	SF4	1	0

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
55	3L	1
24	3K	1
26	1H	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	3L	48:C	O3'	49:G	P	5.87
1	3K	48:C	O3'	49:G	P	5.53
1	1H	1053:C	O3'	1054:A	P	3.55

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	1500/1522 (98%)	1.00	303 (20%)	3	2	60, 99, 150, 173	0
1	1G	1490/1522 (97%)	0.89	254 (17%)	4	3	69, 111, 148, 171	0
2	12	207/256 (80%)	2.04	86 (41%)	0	0	116, 138, 149, 156	0
2	1E	231/256 (90%)	1.40	51 (22%)	2	2	107, 131, 148, 156	0
3	22	197/239 (82%)	2.26	80 (40%)	0	0	114, 131, 144, 153	0
3	2E	205/239 (85%)	1.68	57 (27%)	1	1	82, 106, 127, 136	0
4	32	207/209 (99%)	1.34	47 (22%)	2	2	91, 110, 129, 137	0
4	3E	207/209 (99%)	1.06	34 (16%)	4	4	82, 105, 125, 132	0
5	42	150/162 (92%)	1.70	46 (30%)	1	1	99, 117, 132, 142	0
5	4E	149/162 (91%)	1.29	29 (19%)	3	3	83, 100, 118, 125	0
6	52	101/101 (100%)	1.38	24 (23%)	2	2	87, 104, 119, 131	0
6	5E	100/101 (99%)	1.22	20 (20%)	3	3	88, 105, 119, 128	0
7	62	138/156 (88%)	1.74	46 (33%)	1	1	110, 120, 130, 136	0
7	6E	154/156 (98%)	1.75	23 (14%)	5	5	101, 116, 137, 150	0
8	72	137/138 (99%)	1.42	37 (27%)	1	1	97, 119, 130, 138	0
8	7E	138/138 (100%)	0.73	12 (8%)	16	14	91, 108, 122, 128	0
9	82	121/128 (94%)	1.48	32 (26%)	1	1	105, 135, 143, 150	0
9	8E	126/128 (98%)	1.64	31 (24%)	2	1	86, 127, 142, 150	0
10	1A	99/105 (94%)	2.15	44 (44%)	0	0	112, 135, 147, 153	0
10	1I	94/105 (89%)	1.68	34 (36%)	1	1	77, 120, 141, 143	0
11	2A	113/129 (87%)	1.15	15 (13%)	7	7	83, 108, 122, 131	0
11	2I	111/129 (86%)	1.32	15 (13%)	7	6	76, 105, 125, 137	0
12	3A	122/132 (92%)	1.78	34 (27%)	1	1	81, 99, 118, 132	0
12	3I	122/132 (92%)	1.37	28 (22%)	2	2	64, 77, 108, 126	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
13	4A	109/126 (86%)	1.73	33 (30%) 1 1	111, 131, 145, 152	0
13	4I	119/126 (94%)	1.10	21 (17%) 4 3	87, 116, 130, 141	0
14	5A	59/61 (96%)	2.21	22 (37%) 1 1	120, 129, 138, 142	0
14	5I	60/61 (98%)	0.79	7 (11%) 9 8	82, 95, 116, 123	0
15	6A	87/89 (97%)	0.74	8 (9%) 14 13	86, 108, 123, 126	0
15	6I	87/89 (97%)	1.10	18 (20%) 2 2	81, 100, 119, 128	0
16	7A	84/88 (95%)	0.86	4 (4%) 35 30	91, 101, 125, 143	0
16	7I	83/88 (94%)	1.23	14 (16%) 4 4	96, 110, 130, 143	0
17	8A	99/105 (94%)	0.95	14 (14%) 6 6	93, 107, 122, 127	0
17	8I	100/105 (95%)	1.26	21 (21%) 2 2	89, 105, 116, 119	0
18	9A	69/88 (78%)	0.62	3 (4%) 40 32	94, 110, 130, 139	0
18	9I	68/88 (77%)	1.05	12 (17%) 4 3	88, 106, 123, 131	0
19	AA	65/93 (69%)	1.98	27 (41%) 0 0	122, 140, 150, 156	0
19	AI	83/93 (89%)	0.99	10 (12%) 9 8	93, 112, 138, 145	0
20	BA	103/106 (97%)	1.22	22 (21%) 2 2	89, 110, 132, 136	0
20	BI	97/106 (91%)	1.48	28 (28%) 1 1	105, 116, 134, 137	0
21	1B	22/27 (81%)	0.48	1 (4%) 38 31	109, 122, 128, 128	0
21	1F	23/27 (85%)	0.36	2 (8%) 16 14	94, 102, 111, 117	0
22	1K	70/76 (92%)	2.60	26 (37%) 1 1	79, 151, 170, 173	0
22	1L	70/76 (92%)	2.40	26 (37%) 1 1	111, 158, 174, 179	0
23	2K	72/77 (93%)	1.58	18 (25%) 2 1	67, 93, 126, 137	0
23	2L	72/77 (93%)	0.92	12 (16%) 4 4	75, 104, 139, 145	0
24	3K	72/76 (94%)	2.06	26 (36%) 1 1	70, 157, 167, 169	0
25	4K	18/27 (66%)	0.72	3 (16%) 4 4	69, 124, 164, 170	0
25	4L	14/27 (51%)	0.42	0 100 100	87, 122, 152, 154	0
26	14	2811/2917 (96%)	0.79	483 (17%) 4 3	52, 85, 154, 176	0
26	1H	2850/2917 (97%)	0.64	443 (15%) 5 5	41, 73, 157, 180	0
27	16	122/122 (100%)	0.35	7 (5%) 29 24	67, 90, 108, 164	0
27	1J	122/122 (100%)	0.48	9 (7%) 20 18	85, 110, 127, 162	0
28	11	273/276 (98%)	0.44	24 (8%) 15 14	45, 67, 87, 99	0
28	19	274/276 (99%)	0.66	29 (10%) 11 10	50, 73, 91, 110	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å^2)	Q<0.9
29	21	205/206 (99%)	1.27	56 (27%)	1	1	51, 88, 122, 131	0
29	29	204/206 (99%)	2.26	79 (38%)	1	0	58, 97, 127, 140	0
30	31	202/210 (96%)	1.21	33 (16%)	4	4	47, 80, 115, 131	0
30	39	204/210 (97%)	1.96	74 (36%)	1	1	57, 102, 138, 149	0
31	41	179/182 (98%)	1.58	45 (25%)	1	1	84, 104, 132, 151	0
31	49	180/182 (98%)	1.21	36 (20%)	3	3	103, 122, 144, 154	0
32	51	174/180 (96%)	1.33	42 (24%)	2	2	83, 101, 117, 136	0
32	59	169/180 (93%)	3.44	114 (67%)	0	0	129, 156, 164, 168	0
33	61	145/148 (97%)	1.30	31 (21%)	2	2	79, 121, 132, 139	0
33	69	145/148 (97%)	1.83	54 (37%)	1	1	84, 117, 137, 143	0
34	15	137/140 (97%)	1.58	38 (27%)	1	1	80, 106, 131, 138	0
34	58	125/140 (89%)	1.29	27 (21%)	2	2	69, 89, 105, 131	0
35	25	122/122 (100%)	0.85	13 (10%)	11	10	68, 89, 105, 119	0
35	68	122/122 (100%)	0.41	7 (5%)	29	24	60, 78, 97, 105	0
36	35	147/150 (98%)	2.21	62 (42%)	0	0	59, 99, 130, 139	0
36	78	148/150 (98%)	1.55	49 (33%)	1	1	52, 83, 109, 121	0
37	45	138/141 (97%)	1.95	51 (36%)	1	1	72, 100, 121, 133	0
37	88	141/141 (100%)	2.30	45 (31%)	1	1	56, 80, 102, 129	0
38	55	118/118 (100%)	1.00	22 (18%)	3	3	64, 84, 99, 110	0
38	98	118/118 (100%)	1.57	39 (33%)	1	1	63, 83, 102, 115	0
39	65	110/112 (98%)	1.00	18 (16%)	4	4	86, 106, 125, 130	0
39	A8	111/112 (99%)	0.87	12 (10%)	11	10	77, 88, 106, 113	0
40	75	140/146 (95%)	1.34	30 (21%)	2	2	82, 98, 145, 155	0
40	B8	136/146 (93%)	2.04	49 (36%)	1	1	73, 92, 131, 146	0
41	85	116/118 (98%)	1.76	46 (39%)	1	0	68, 93, 128, 140	0
41	C8	115/118 (97%)	0.88	19 (16%)	4	4	56, 79, 108, 116	0
42	95	100/101 (99%)	1.72	32 (32%)	1	1	66, 114, 131, 136	0
42	D8	100/101 (99%)	1.60	34 (34%)	1	1	55, 101, 120, 127	0
43	A5	111/113 (98%)	1.16	21 (18%)	3	3	66, 78, 103, 131	0
43	E8	110/113 (97%)	1.57	22 (20%)	3	3	59, 74, 98, 108	0
44	B5	94/96 (97%)	0.51	5 (5%)	32	27	72, 84, 105, 116	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
44	F8	95/96 (98%)	0.66	14 (14%) 6 5	57, 70, 101, 112	0
45	C5	52/110 (47%)	2.02	22 (42%) 0 0	93, 103, 119, 123	0
45	G8	97/110 (88%)	1.35	25 (25%) 1 1	76, 96, 127, 133	0
46	D5	177/206 (85%)	1.72	57 (32%) 1 1	106, 131, 162, 166	0
46	H8	170/206 (82%)	1.33	34 (20%) 3 3	81, 116, 154, 162	0
47	E5	76/85 (89%)	1.49	25 (32%) 1 1	66, 87, 102, 110	0
47	I8	77/85 (90%)	0.60	6 (7%) 19 17	57, 72, 96, 104	0
48	F5	94/98 (95%)	1.80	32 (34%) 1 1	63, 83, 121, 129	0
48	J8	96/98 (97%)	1.48	31 (32%) 1 1	53, 75, 123, 138	0
49	G5	69/72 (95%)	0.94	8 (11%) 9 8	85, 106, 126, 142	0
49	K8	68/72 (94%)	1.06	14 (20%) 2 2	63, 84, 103, 121	0
50	H5	58/60 (96%)	1.68	20 (34%) 1 1	77, 98, 120, 127	0
50	L8	58/60 (96%)	1.19	9 (15%) 5 5	60, 81, 108, 113	0
51	M8	60/71 (84%)	1.37	11 (18%) 3 3	105, 135, 148, 152	0
52	J5	56/60 (93%)	1.71	19 (33%) 1 1	60, 85, 127, 136	0
52	N8	48/60 (80%)	0.84	7 (14%) 6 5	51, 87, 121, 128	0
53	L5	48/49 (97%)	0.12	4 (8%) 17 15	52, 61, 95, 104	0
53	P8	47/49 (95%)	-0.10	1 (2%) 63 55	47, 52, 71, 89	0
54	M5	64/65 (98%)	1.05	13 (20%) 3 2	68, 81, 95, 115	0
54	Q8	64/65 (98%)	0.41	4 (6%) 26 22	56, 69, 83, 95	0
55	3L	70/76 (92%)	1.67	21 (30%) 1 1	80, 150, 162, 164	0
All	All	20486/21509 (95%)	1.14	4337 (21%) 2 2	41, 98, 147, 180	0

All (4337) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
22	1L	76	A	19.5
32	59	151	ILE	19.2
7	6E	81	GLY	19.1
3	22	158	GLY	16.8
37	88	80	GLU	16.2
22	1K	76	A	15.5
32	51	39	PRO	15.2
40	B8	104	ASN	14.8
23	2K	1	C	14.5

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Mol	Chain	Res	Type	RSRZ
40	75	104	ASN	13.9
26	1H	790	C	13.9
22	1L	75	C	13.9
43	E8	92	ARG	13.8
42	D8	37	VAL	13.5
13	4I	120	LYS	13.4
12	3A	19	ARG	13.2
22	1K	72	C	13.2
3	2E	166	GLU	13.0
37	88	79	LEU	13.0
7	6E	80	VAL	13.0
40	B8	106	SER	12.9
3	22	159	GLY	12.8
29	29	116	VAL	12.5
7	6E	84	ASN	12.2
7	6E	83	ALA	12.2
32	59	169	VAL	12.1
3	2E	165	THR	12.1
7	6E	82	GLY	12.0
5	4E	21	ALA	11.9
37	88	91	GLU	11.6
9	82	115	GLY	11.5
3	2E	167	TRP	11.5
28	19	5	LYS	11.2
36	35	110	TYR	11.2
30	31	72	ARG	11.1
37	88	78	PRO	11.1
3	2E	164	ARG	11.1
1	13	1531	A	11.1
30	39	72	ARG	10.8
5	4E	24	ARG	10.7
1	13	1516	G	10.6
26	1H	2612	C	10.6
43	E8	93	ALA	10.5
30	39	56	GLU	10.5
3	22	157	ILE	10.4
7	6E	85	TYR	10.4
32	59	87	LEU	10.4
30	31	66	PRO	10.4
7	6E	79	ARG	10.3
26	14	125	G	10.3
26	1H	2062	A	10.2

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Mol	Chain	Res	Type	RSRZ
26	1H	2690	C	10.2
1	13	1394	A	10.2
3	22	160	ALA	10.2
43	E8	85	VAL	10.1
22	1K	75	C	10.1
22	1K	73	A	10.0
37	45	79	LEU	9.9
30	39	55	GLY	9.8
32	59	111	HIS	9.8
11	2I	124	LYS	9.8
9	8E	115	GLY	9.8
26	14	1379	A	9.7
37	45	80	GLU	9.7
24	3K	35	G	9.7
32	59	112	PRO	9.6
13	4A	94	ARG	9.6
8	72	86	ILE	9.6
32	59	92	ILE	9.6
13	4A	95	GLY	9.6
12	3A	21	LYS	9.5
46	H8	166	SER	9.5
32	59	122	THR	9.4
36	35	46	LYS	9.4
31	41	26	GLN	9.3
1	13	1196	U	9.3
14	5A	38	GLY	9.3
20	BA	9	ASN	9.3
1	13	1397	C	9.2
1	13	1515	C	9.2
7	62	146	GLU	9.1
26	1H	746	A	9.1
22	1K	74	C	9.1
28	11	2	ALA	9.1
26	14	508	G	9.1
36	35	50	ARG	9.1
43	E8	90	ARG	9.1
30	39	62	ARG	9.1
3	22	155	GLY	9.1
43	E8	91	GLY	9.1
32	59	91	GLY	9.0
7	6E	78	ARG	9.0
33	69	11	ASN	9.0

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Mol	Chain	Res	Type	RSRZ
5	4E	23	GLY	9.0
7	62	6	ARG	8.9
37	88	77	LYS	8.9
43	E8	94	ASP	8.9
1	1G	966	G	8.9
29	29	134	ILE	8.9
37	88	76	LYS	8.9
47	I8	8	GLY	8.8
29	29	131	ALA	8.8
26	14	229	A	8.8
37	45	91	GLU	8.8
29	29	125	GLY	8.8
32	59	148	ILE	8.8
7	62	5	ARG	8.7
32	59	93	GLY	8.7
3	2E	168	ALA	8.7
27	1J	88	C	8.7
6	52	83	ASP	8.7
37	88	81	VAL	8.7
32	51	42	ARG	8.7
28	19	2	ALA	8.6
26	1H	2602	A	8.6
37	88	41	TRP	8.6
26	14	790	C	8.5
11	2I	125	PHE	8.5
24	3K	34	G	8.5
37	45	74	TYR	8.4
26	14	958	U	8.4
30	39	65	TRP	8.4
43	A5	93	ALA	8.4
5	4E	22	GLY	8.4
26	14	2611	U	8.4
4	32	24	GLU	8.4
30	31	70	THR	8.4
29	29	126	PRO	8.4
30	31	65	TRP	8.3
12	3A	64	TYR	8.3
28	11	5	LYS	8.3
46	H8	165	VAL	8.3
32	59	117	PRO	8.3
31	41	25	TYR	8.2
36	35	47	ASP	8.2

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Mol	Chain	Res	Type	RSRZ
1	13	793	U	8.2
1	13	796	C	8.2
36	35	51	PHE	8.1
1	1G	913	A	8.1
1	13	1195	C	8.1
40	75	106	SER	8.1
10	1A	58	ASP	8.1
29	29	122	PHE	8.1
37	88	89	ASN	8.1
10	1A	59	SER	8.1
34	15	84	LYS	8.1
1	13	1514	C	8.1
9	8E	125	TYR	8.0
22	1K	1	G	8.0
55	3L	34	G	8.0
10	1I	60	ARG	8.0
24	3K	37	A	8.0
23	2L	1	C	7.9
32	59	94	TYR	7.9
29	29	128	SER	7.9
46	D5	153	SER	7.9
1	13	1193	G	7.9
11	2I	123	LYS	7.9
12	3A	28	LYS	7.9
29	29	150	VAL	7.9
29	29	135	HIS	7.9
1	13	1437	C	7.9
1	13	1509	C	7.9
26	1H	958	U	7.9
50	H5	17	LYS	7.9
32	59	89	ILE	7.8
31	41	164	GLU	7.8
26	1H	2611	U	7.8
2	12	86	GLU	7.8
22	1L	73	A	7.8
26	1H	747	U	7.7
29	29	115	GLY	7.7
29	29	127	ASP	7.7
46	H8	153	SER	7.7
9	8E	127	LYS	7.7
1	1G	915	A	7.7
6	5E	47	ARG	7.7

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Mol	Chain	Res	Type	RSRZ
20	BI	20	LEU	7.7
3	2E	160	ALA	7.7
41	85	40	PHE	7.6
30	39	64	ILE	7.6
29	29	133	LYS	7.5
19	AA	76	PRO	7.5
32	51	34	GLU	7.5
38	98	69	ASP	7.5
52	J5	26	THR	7.5
1	1G	693	G	7.5
40	B8	105	LEU	7.5
29	29	136	ARG	7.4
32	51	40	GLU	7.4
29	29	151	TYR	7.4
31	41	24	GLY	7.4
7	62	2	ALA	7.4
7	62	148	ASN	7.4
14	5A	39	LEU	7.4
2	12	79	ASP	7.4
9	8E	116	LYS	7.4
37	45	77	LYS	7.4
1	1G	1202	G	7.4
30	39	79	GLY	7.4
10	1A	47	PHE	7.4
3	22	162	GLN	7.4
40	B8	109	GLU	7.4
32	59	63	SER	7.3
41	C8	86	ALA	7.3
8	72	91	ARG	7.3
23	2K	74	A	7.3
1	13	1465	C	7.3
1	13	1510	U	7.3
13	4A	111	LYS	7.3
37	88	88	GLY	7.3
23	2K	71	G	7.2
32	51	21	PRO	7.2
22	1K	3	U	7.2
41	85	20	LEU	7.2
29	29	114	ALA	7.2
37	45	81	VAL	7.2
1	13	1511	G	7.2
1	13	1529	G	7.2

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Mol	Chain	Res	Type	RSRZ
5	42	12	LEU	7.2
26	1H	2613	U	7.2
14	5A	37	PHE	7.2
22	1L	74	C	7.1
10	1A	49	VAL	7.1
6	52	81	ILE	7.1
22	1L	1	G	7.1
32	59	114	VAL	7.1
36	35	71	VAL	7.1
41	85	17	ILE	7.1
29	21	195	LEU	7.1
8	7E	91	ARG	7.1
37	88	90	VAL	7.1
51	M8	66	SER	7.1
30	31	131	GLY	7.1
43	A5	85	VAL	7.1
22	1L	72	C	7.1
26	1H	1658	C	7.1
1	13	926	G	7.1
1	13	1194	U	7.0
11	2A	125	PHE	7.0
37	45	76	LYS	7.0
9	8E	126	SER	7.0
26	1H	2014	A	7.0
26	14	1306	C	7.0
46	H8	167	PRO	7.0
30	39	78	ILE	7.0
48	F5	37	ILE	7.0
29	29	155	LYS	7.0
1	13	1385	G	7.0
29	29	124	GLY	7.0
43	E8	96	ILE	7.0
29	29	64	LYS	7.0
37	88	92	GLY	6.9
26	1H	165	U	6.9
26	1H	2506	U	6.9
7	6E	154	TYR	6.9
26	1H	748	G	6.9
48	F5	77	ALA	6.9
30	31	64	ILE	6.9
1	13	693	G	6.9
38	55	103	ARG	6.9

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Mol	Chain	Res	Type	RSRZ
26	14	1554	A	6.9
1	13	1384	C	6.9
38	55	101	ALA	6.9
7	62	8	GLU	6.9
12	3A	16	GLU	6.8
37	88	74	TYR	6.8
9	8E	117	HIS	6.8
3	2E	169	ALA	6.8
29	29	123	ALA	6.8
5	4E	25	ARG	6.8
26	14	751	A	6.8
1	1G	883	C	6.8
3	22	131	ARG	6.8
9	8E	114	TYR	6.8
12	3A	20	LYS	6.8
32	59	152	ARG	6.8
24	3K	36	U	6.8
1	13	815	A	6.7
1	13	1508	G	6.7
3	22	161	GLU	6.7
1	1G	912	C	6.7
1	13	1398	A	6.7
31	49	35	GLU	6.7
22	1K	71	G	6.7
26	1H	1678	G	6.7
1	1G	1195	C	6.7
26	1H	2610	C	6.7
26	14	2612	C	6.7
8	72	133	LEU	6.7
30	39	69	HIS	6.7
36	35	59	LEU	6.7
26	1H	752	A	6.7
37	45	92	GLY	6.7
17	8I	89	LEU	6.6
26	14	2609	U	6.6
1	13	269	C	6.6
55	3L	74	C	6.6
42	95	75	PHE	6.6
10	1I	58	ASP	6.6
31	41	23	PHE	6.6
1	13	924	C	6.6
11	2A	25	TYR	6.6

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Mol	Chain	Res	Type	RSRZ
1	13	771	G	6.6
26	1H	745	G	6.6
26	1H	751	A	6.6
20	BA	38	LYS	6.6
2	1E	232	PRO	6.6
19	AI	13	ASP	6.6
1	13	1383	C	6.6
2	1E	208	ILE	6.5
48	J8	27	GLU	6.5
2	1E	96	ARG	6.5
30	39	57	VAL	6.5
11	2I	25	TYR	6.5
42	95	71	LEU	6.5
2	12	163	PHE	6.5
10	1I	47	PHE	6.5
9	8E	121	ARG	6.5
12	3I	19	ARG	6.5
45	C5	29	GLU	6.5
13	4I	119	GLY	6.5
44	F8	52	VAL	6.5
5	4E	18	ARG	6.5
13	4A	114	ARG	6.5
33	69	20	ASP	6.5
55	3L	37	A	6.5
1	13	1520	G	6.4
1	13	311	C	6.4
30	31	69	HIS	6.4
43	E8	95	ILE	6.4
43	A5	90	ARG	6.4
26	1H	1963	U	6.4
26	14	387	U	6.4
5	42	88	LYS	6.4
19	AI	56	GLN	6.4
26	1H	2015	A	6.4
26	14	1307	A	6.4
36	35	74	GLU	6.4
1	13	965	A	6.4
10	1A	54	PHE	6.4
3	22	109	PRO	6.4
26	1H	1660	C	6.3
1	13	1513	A	6.3
26	14	752	A	6.3

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Mol	Chain	Res	Type	RSRZ
42	D8	36	PRO	6.3
51	M8	65	ASP	6.3
55	3L	35	G	6.3
5	42	15	ARG	6.3
26	14	967	C	6.3
30	39	93	LYS	6.3
30	39	96	ASP	6.3
26	1H	1930	G	6.3
6	5E	56	PRO	6.3
26	14	2602	A	6.3
3	2E	158	GLY	6.3
33	69	1	MET	6.3
26	14	2506	U	6.3
1	1G	886	G	6.3
26	14	382	G	6.3
34	15	98	VAL	6.3
37	88	1	MET	6.3
26	1H	2712(A)	A	6.2
37	88	82	ARG	6.2
33	61	80	PRO	6.2
20	BI	23	ARG	6.2
3	22	193	TYR	6.2
3	22	106	VAL	6.2
5	4E	19	MET	6.2
40	B8	66	VAL	6.2
1	1G	796	C	6.2
13	4A	113	PRO	6.2
1	13	809	G	6.2
3	22	167	TRP	6.2
2	12	225	ALA	6.1
3	2E	128	PHE	6.1
32	59	106	THR	6.1
26	1H	1657	C	6.1
26	14	1305	C	6.1
26	1H	789	A	6.1
1	13	769	G	6.1
2	12	154	LEU	6.1
30	39	63	LYS	6.1
43	E8	84	ARG	6.1
1	13	1466	C	6.1
43	E8	86	LEU	6.1
40	75	101	PHE	6.1

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Mol	Chain	Res	Type	RSRZ
33	69	85	GLU	6.1
26	14	747	U	6.1
26	14	2015	A	6.1
32	59	113	VAL	6.1
1	1G	887	G	6.1
26	14	767	U	6.1
1	13	1382	C	6.0
26	14	951	C	6.0
40	B8	68	TYR	6.0
3	22	70	VAL	6.0
26	1H	2013	A	6.0
40	B8	70	VAL	6.0
40	B8	67	SER	6.0
5	4E	20	GLN	6.0
29	29	76	ARG	6.0
29	29	149	ARG	6.0
1	13	1381	U	6.0
37	45	93	TYR	6.0
9	8E	123	PRO	6.0
37	45	78	PRO	6.0
23	2K	72	C	6.0
26	1H	756	C	6.0
29	29	145	LYS	6.0
26	14	2532	G	6.0
1	13	1393	U	6.0
1	1G	569	C	6.0
1	1G	787	A	6.0
50	L8	17	LYS	6.0
11	2A	126	ARG	6.0
43	A5	92	ARG	6.0
34	58	72	TYR	6.0
42	95	81	TYR	6.0
26	1H	1420	U	6.0
6	52	77	ARG	6.0
1	13	1533	C	6.0
26	1H	2693	A	6.0
26	14	1614	A	6.0
32	59	123	PHE	6.0
2	12	92	TYR	5.9
3	22	184	TYR	5.9
40	75	69	GLY	5.9
20	BI	17	ARG	5.9

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Mol	Chain	Res	Type	RSRZ
26	14	952	G	5.9
2	1E	231	GLU	5.9
3	22	71	ALA	5.9
30	31	96	ASP	5.9
12	3I	11	VAL	5.9
26	1H	1906	G	5.9
1	1G	1227	A	5.9
26	1H	591	C	5.9
13	4A	102	ARG	5.9
26	1H	1659	U	5.9
33	69	83	ALA	5.9
29	29	152	LYS	5.9
40	75	105	LEU	5.9
26	1H	2872	G	5.9
1	1G	1397	C	5.9
17	8A	7	THR	5.9
20	BA	42	GLN	5.9
30	39	83	PHE	5.9
1	13	884	U	5.9
1	1G	965	A	5.8
30	39	80	ALA	5.8
26	14	1963	U	5.8
26	14	2584	U	5.8
3	22	115	LEU	5.8
45	C5	64	GLU	5.8
30	39	61	GLY	5.8
1	13	890	G	5.8
26	14	668	G	5.8
26	14	2659	G	5.8
3	22	164	ARG	5.8
10	1A	61	GLU	5.8
48	J8	32	LYS	5.8
1	13	1396	A	5.8
1	13	562	C	5.8
32	59	86	GLU	5.8
30	39	82	ILE	5.8
30	39	90	PHE	5.8
33	69	144	VAL	5.8
32	51	23	ARG	5.8
37	88	14	ARG	5.8
47	E5	9	SER	5.8
48	F5	38	SER	5.8

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Mol	Chain	Res	Type	RSRZ
41	C8	89	GLU	5.8
40	B8	69	GLY	5.8
1	13	310	G	5.7
26	1H	1816	G	5.7
27	1J	89	G	5.7
32	59	102	ALA	5.7
3	22	165	THR	5.7
7	6E	153	HIS	5.7
12	3A	23	LYS	5.7
30	39	52	LYS	5.7
12	3I	16	GLU	5.7
26	14	1026	U	5.7
1	13	784	C	5.7
42	D8	38	LEU	5.7
5	42	14	ARG	5.7
1	13	785	G	5.7
1	13	1386	G	5.7
26	14	769	G	5.7
12	3I	91	LYS	5.7
36	35	76	LYS	5.7
50	H5	20	LYS	5.7
38	98	14	SER	5.7
1	13	1391	U	5.7
9	82	50	LEU	5.7
1	13	334	C	5.7
1	1G	1400	C	5.7
2	1E	168	THR	5.7
9	82	123	PRO	5.7
26	14	201	C	5.7
4	3E	24	GLU	5.7
46	D5	162	GLU	5.7
29	29	153	GLY	5.7
1	13	789	U	5.7
5	42	24	ARG	5.7
26	1H	273(A)	G	5.6
26	1H	2004	G	5.6
3	2E	193	TYR	5.6
10	1A	64	GLU	5.6
28	11	23	GLU	5.6
3	22	112	SER	5.6
48	F5	32	LYS	5.6
1	13	1392	G	5.6

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Mol	Chain	Res	Type	RSRZ
1	13	1405	G	5.6
26	14	1816	G	5.6
26	14	2664	G	5.6
1	1G	574	A	5.6
32	59	52	VAL	5.6
9	8E	119	ALA	5.6
26	1H	2712	U	5.6
38	98	21	TYR	5.6
38	55	102	GLU	5.6
5	42	123	LEU	5.6
7	62	32	ARG	5.6
38	98	7	GLY	5.6
26	14	696	G	5.6
26	1H	1932	A	5.6
19	AA	53	ASN	5.6
19	AA	56	GLN	5.6
26	14	436	C	5.6
1	1G	788	U	5.6
24	3K	33	U	5.6
26	1H	387	U	5.6
32	51	18	GLU	5.6
52	J5	25	LEU	5.6
2	12	88	ALA	5.6
1	1G	882	C	5.5
29	29	130	GLY	5.5
8	72	93	VAL	5.5
32	59	17	VAL	5.5
10	1A	37	PRO	5.5
10	1A	62	HIS	5.5
26	1H	2003	G	5.5
4	32	179	GLU	5.5
26	1H	2691	C	5.5
30	39	6	VAL	5.5
6	5E	83	ASP	5.5
26	14	196	A	5.5
42	95	73	SER	5.5
36	35	45	LEU	5.5
1	13	799	G	5.5
1	13	1403	C	5.5
1	1G	1509	C	5.5
13	4I	118	ALA	5.5
36	78	141	ALA	5.5

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Mol	Chain	Res	Type	RSRZ
18	9A	84	LYS	5.5
1	13	968	A	5.5
32	59	99	VAL	5.5
14	5A	34	TYR	5.5
36	78	31	ALA	5.5
1	13	1438	G	5.5
26	14	1623	G	5.5
26	14	2610	C	5.5
26	1H	1269	A	5.4
31	41	34	LEU	5.4
1	13	328	C	5.4
26	1H	273	G	5.4
26	14	654(D)	G	5.4
5	4E	28	PHE	5.4
34	15	72	TYR	5.4
50	H5	15	TYR	5.4
43	E8	83	LYS	5.4
1	13	790	A	5.4
1	13	923	A	5.4
4	3E	96	LEU	5.4
2	12	70	PHE	5.4
23	2K	40	C	5.4
45	C5	24	VAL	5.4
1	13	760	G	5.4
26	1H	2505	G	5.4
26	14	968	G	5.4
26	14	2893	G	5.4
33	61	118	LYS	5.4
2	12	87	ARG	5.4
2	1E	81	VAL	5.4
2	12	89	GLY	5.4
5	42	22	GLY	5.4
42	95	74	LYS	5.4
6	5E	55	ASP	5.4
1	1G	810	C	5.4
40	75	103	ARG	5.4
32	59	168	PRO	5.4
26	14	1620	G	5.4
33	61	116	LEU	5.4
48	F5	27	GLU	5.3
2	12	61	LEU	5.3
20	BI	104	LEU	5.3

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Mol	Chain	Res	Type	RSRZ
3	2E	4	LYS	5.3
4	32	178	VAL	5.3
9	82	116	LYS	5.3
26	1H	1273	U	5.3
26	1H	1072	C	5.3
13	4I	117	VAL	5.3
32	59	107	VAL	5.3
48	F5	22	GLY	5.3
1	1G	809	G	5.3
7	62	4	ARG	5.3
8	72	84	ARG	5.3
26	14	954	G	5.3
26	14	2505	G	5.3
36	78	10	PRO	5.3
20	BI	105	SER	5.3
1	13	1400	C	5.3
40	B8	111	ARG	5.3
1	13	238	G	5.3
1	13	698	G	5.3
1	1G	916	G	5.3
26	1H	1929	G	5.3
29	29	132	HIS	5.3
3	2E	170	GLN	5.3
48	J8	22	GLY	5.3
1	13	1389	C	5.2
46	D5	125	LEU	5.2
36	35	57	THR	5.2
26	1H	1931	U	5.2
6	5E	54	LYS	5.2
1	1G	568	G	5.2
26	14	669	G	5.2
26	14	748	G	5.2
2	12	200	ILE	5.2
30	39	81	PRO	5.2
37	45	89	ASN	5.2
1	13	788	U	5.2
26	1H	2512	C	5.2
1	1G	1394	A	5.2
26	1H	2513	G	5.2
29	29	157	ALA	5.2
2	12	133	LYS	5.2
26	14	2272	U	5.2

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Mol	Chain	Res	Type	RSRZ
26	1H	961	C	5.2
26	1H	1925	C	5.2
36	35	116	GLY	5.2
4	32	32	ALA	5.2
26	14	739	G	5.2
1	1G	1381	U	5.2
26	14	200	U	5.2
26	14	614	U	5.2
1	13	810	C	5.2
1	13	912	C	5.2
1	13	1192	C	5.2
1	1G	896	C	5.2
15	6I	41	GLU	5.2
26	1H	1694	C	5.2
41	C8	84	LYS	5.2
45	C5	65	ALA	5.2
1	13	787	A	5.1
1	13	792	A	5.1
26	1H	1070	A	5.1
36	78	16	ARG	5.1
1	13	1517	G	5.1
40	B8	101	PHE	5.1
33	69	12	LEU	5.1
48	F5	79	GLY	5.1
37	45	66	ILE	5.1
49	K8	15	LYS	5.1
1	1G	1226	C	5.1
12	3I	23	LYS	5.1
29	29	63	LEU	5.1
50	L8	43	ILE	5.1
52	J5	50	GLY	5.1
4	3E	207	TYR	5.1
50	H5	12	PRO	5.1
26	1H	1754	C	5.1
20	BI	16	HIS	5.1
24	3K	38	A	5.1
26	14	1308	A	5.1
28	19	6	PHE	5.1
32	51	27	LYS	5.1
2	1E	10	LEU	5.1
32	59	64	LEU	5.1
3	22	166	GLU	5.1

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Mol	Chain	Res	Type	RSRZ
15	6I	87	ILE	5.1
1	13	773	G	5.1
26	14	252	G	5.1
3	22	68	VAL	5.1
12	3A	18	VAL	5.1
1	1G	1437	C	5.1
28	11	112	GLN	5.1
47	E5	12	ASN	5.1
12	3I	14	GLY	5.1
42	D8	53	GLU	5.1
26	1H	1272	A	5.1
30	39	77	ASP	5.1
1	13	1390	U	5.1
13	4A	115	LYS	5.0
48	F5	78	LYS	5.0
42	D8	49	THR	5.0
9	82	47	LEU	5.0
47	E5	21	LEU	5.0
26	1H	744	G	5.0
26	14	1347	G	5.0
7	6E	139	GLU	5.0
26	1H	273(B)	C	5.0
26	14	961	C	5.0
48	F5	36	GLY	5.0
32	59	128	PRO	5.0
8	72	92	ARG	5.0
41	85	36	ARG	5.0
1	1G	789	U	5.0
1	1G	1257	U	5.0
26	1H	614	U	5.0
37	88	87	LYS	5.0
3	2E	153	VAL	5.0
8	7E	93	VAL	5.0
34	15	85	ILE	5.0
5	4E	50	GLU	5.0
46	H8	162	GLU	5.0
26	1H	615	G	5.0
26	14	2631	G	5.0
26	14	2663	G	5.0
37	45	41	TRP	5.0
1	13	921	U	5.0
20	BA	20	LEU	5.0

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Mol	Chain	Res	Type	RSRZ
4	32	166	LYS	5.0
7	6E	151	TYR	5.0
26	14	1429	G	5.0
1	1G	553	A	5.0
26	14	667	U	5.0
5	4E	26	PHE	5.0
46	H8	168	GLU	5.0
17	8I	101	ARG	5.0
33	61	111	PRO	5.0
45	G8	34	LYS	5.0
17	8I	32	TYR	5.0
38	98	18	LEU	5.0
46	D5	155	LEU	5.0
55	3L	75	C	4.9
1	13	772	U	4.9
1	13	1506	U	4.9
8	72	9	MET	4.9
29	29	117	MET	4.9
26	1H	1062	G	4.9
26	14	1847	A	4.9
37	88	75	THR	4.9
48	F5	39	LYS	4.9
33	61	144	VAL	4.9
28	11	22	SER	4.9
1	13	692	U	4.9
1	13	1436	U	4.9
1	1G	1196	U	4.9
26	1H	34	C	4.9
1	13	922	G	4.9
26	1H	2694	G	4.9
26	14	1619	G	4.9
26	14	2271	G	4.9
36	35	115	LEU	4.9
41	85	25	TRP	4.9
2	1E	80	ILE	4.9
5	42	81	GLU	4.9
9	8E	122	ALA	4.9
55	3L	33	U	4.9
1	13	883	C	4.9
32	59	98	LEU	4.9
26	1H	1651	G	4.9
26	14	745	G	4.9

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Mol	Chain	Res	Type	RSRZ
26	14	2581	G	4.9
3	2E	159	GLY	4.9
17	8I	31	LEU	4.9
29	29	195	LEU	4.9
1	1G	562	C	4.9
1	1G	811	C	4.9
26	14	955	C	4.9
26	14	2556	C	4.9
36	35	64	LYS	4.9
1	1G	890	G	4.8
26	14	654(C)	G	4.8
12	3A	29	GLY	4.8
11	2A	87	THR	4.8
5	42	126	ARG	4.8
6	5E	46	ARG	4.8
23	2L	72	C	4.8
41	85	32	PHE	4.8
3	2E	201	TYR	4.8
40	B8	100	TYR	4.8
1	1G	570	G	4.8
14	5A	44	LEU	4.8
28	11	35	LYS	4.8
39	65	20	ARG	4.8
1	13	1063	C	4.8
26	14	1509	C	4.8
1	1G	914	A	4.8
29	29	65	GLY	4.8
31	41	30	GLU	4.8
46	D5	152	ALA	4.8
10	1A	60	ARG	4.8
38	98	47	PHE	4.8
1	13	338	A	4.8
1	13	967	C	4.8
37	45	75	THR	4.8
32	59	85	LYS	4.8
17	8A	85	VAL	4.8
32	59	155	SER	4.8
29	29	137	HIS	4.8
12	3I	20	LYS	4.7
20	BI	21	LYS	4.7
33	69	22	LYS	4.7
39	65	33	LYS	4.7

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Mol	Chain	Res	Type	RSRZ
29	29	129	HIS	4.7
1	1G	884	U	4.7
30	31	71	GLY	4.7
41	85	71	GLN	4.7
7	62	88	PRO	4.7
32	59	105	LEU	4.7
16	7I	32	TYR	4.7
33	69	2	LYS	4.7
3	22	152	ILE	4.7
48	J8	21	ARG	4.7
1	1G	328	C	4.7
3	2E	163	ALA	4.7
31	49	142	PRO	4.7
44	F8	85	PRO	4.7
48	F5	18	ILE	4.7
19	AA	11	VAL	4.7
1	13	786	G	4.7
1	13	800	G	4.7
1	1G	786	G	4.7
26	1H	1650	G	4.7
26	1H	1907	G	4.7
26	1H	2603	G	4.7
26	14	1309	G	4.7
1	13	795	C	4.7
32	59	7	LEU	4.7
30	31	94	PRO	4.7
7	62	41	ARG	4.7
40	B8	112	ARG	4.7
5	42	90	VAL	4.7
32	59	45	VAL	4.7
15	6I	44	LYS	4.7
1	13	1491	G	4.7
1	13	1505	G	4.7
1	1G	1438	G	4.7
26	1H	173	G	4.7
40	B8	47	GLY	4.7
11	2A	91	ARG	4.7
26	1H	1755	A	4.7
26	14	181	A	4.7
1	1G	808	C	4.7
19	AA	6	LYS	4.6
3	2E	129	ALA	4.6

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Mol	Chain	Res	Type	RSRZ
32	59	29	PRO	4.6
52	J5	2	ALA	4.6
2	12	80	ILE	4.6
4	32	168	ARG	4.6
37	88	10	ARG	4.6
15	6I	37	ASN	4.6
26	1H	1089	G	4.6
1	13	1501	C	4.6
26	1H	1656	C	4.6
36	35	35	HIS	4.6
37	88	2	LEU	4.6
4	32	29	PRO	4.6
6	52	78	GLU	4.6
10	1I	95	GLU	4.6
12	3I	29	GLY	4.6
19	AA	2	PRO	4.6
28	19	100	GLY	4.6
29	29	138	PRO	4.6
32	51	60	ARG	4.6
38	98	17	ARG	4.6
29	29	141	ILE	4.6
32	59	172	LYS	4.6
1	13	1523	G	4.6
22	1L	31	C	4.6
26	1H	272	G	4.6
26	14	654(S)	G	4.6
4	32	164	ALA	4.6
30	39	66	PRO	4.6
37	88	15	GLY	4.6
6	5E	57	GLN	4.6
30	39	51	THR	4.6
39	A8	112	PHE	4.6
1	1G	815	A	4.6
35	68	80	ASP	4.6
26	1H	1781	C	4.6
26	14	34	C	4.6
26	14	754	C	4.6
1	1G	1516	G	4.6
26	1H	1933	G	4.6
26	14	956	G	4.6
3	22	116	VAL	4.6
5	42	105	VAL	4.6

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Mol	Chain	Res	Type	RSRZ
10	1I	59	SER	4.6
1	13	802	A	4.5
26	1H	1966	A	4.5
40	B8	50	ILE	4.5
32	59	5	GLY	4.5
3	2E	161	GLU	4.5
26	1H	436	C	4.5
26	14	753	C	4.5
31	41	160	VAL	4.5
33	69	21	VAL	4.5
26	14	738	G	4.5
26	14	1311	G	4.5
29	21	90	THR	4.5
10	1I	98	ILE	4.5
2	12	29	ALA	4.5
11	2A	89	ALA	4.5
4	32	109	GLY	4.5
26	14	2585	U	4.5
38	55	69	ASP	4.5
17	8I	96	GLU	4.5
8	72	88	LYS	4.5
14	5A	18	VAL	4.5
28	19	4	LYS	4.5
1	13	1500	A	4.5
1	13	1404	C	4.5
1	1G	1404	C	4.5
32	59	88	LEU	4.5
33	69	68	LEU	4.5
6	52	82	ARG	4.5
26	1H	669	G	4.5
26	14	250	G	4.5
26	14	1678	G	4.5
48	J8	26	ARG	4.5
5	4E	128	PRO	4.5
32	59	39	PRO	4.5
32	51	25	LYS	4.5
36	78	29	LYS	4.5
41	C8	85	LYS	4.5
43	A5	94	ASP	4.5
49	K8	12	GLU	4.5
1	1G	968	A	4.5
29	21	135	HIS	4.5

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Mol	Chain	Res	Type	RSRZ
33	61	27	ARG	4.5
34	58	61	ARG	4.5
1	13	1463	C	4.5
8	72	134	ILE	4.5
9	82	125	TYR	4.5
37	45	120	ILE	4.5
5	42	128	PRO	4.5
50	L8	42	ALA	4.5
1	13	1464	G	4.5
1	1G	1529	G	4.5
15	6A	86	GLY	4.5
26	1H	1071	G	4.5
26	1H	2494	G	4.5
1	13	239	U	4.5
46	D5	163	LEU	4.5
2	1E	209	ARG	4.5
3	2E	131	ARG	4.5
32	59	101	ARG	4.5
36	35	79	ARG	4.5
15	6A	37	ASN	4.5
20	BA	41	ILE	4.4
50	L8	20	LYS	4.4
29	29	62	PRO	4.4
19	AI	9	VAL	4.4
19	AI	67	VAL	4.4
19	AA	58	VAL	4.4
29	29	148	GLY	4.4
32	59	66	GLY	4.4
2	12	76	GLN	4.4
1	13	966	G	4.4
1	1G	1530	G	4.4
26	1H	1325	G	4.4
26	14	383	U	4.4
26	14	770	G	4.4
26	14	1989	G	4.4
3	2E	52	LEU	4.4
43	A5	86	LEU	4.4
5	4E	15	ARG	4.4
31	41	178	PHE	4.4
37	88	104	PHE	4.4
30	31	78	ILE	4.4
1	13	782	A	4.4

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Mol	Chain	Res	Type	RSRZ
1	1G	412	A	4.4
26	1H	2058	A	4.4
32	59	126	PRO	4.4
34	58	92	ALA	4.4
5	42	124	GLY	4.4
11	2A	86	GLY	4.4
28	11	3	VAL	4.4
33	69	136	VAL	4.4
42	95	9	GLY	4.4
31	41	35	GLU	4.4
26	1H	753	C	4.4
26	1H	949	C	4.4
26	14	737	C	4.4
54	M5	61	LEU	4.4
12	3I	17	LYS	4.4
10	1A	98	ILE	4.4
26	14	743	G	4.4
6	52	84	ASN	4.4
29	29	120	TRP	4.4
34	15	9	VAL	4.4
37	45	55	VAL	4.4
1	1G	250	A	4.4
26	14	746	A	4.4
26	14	2892	A	4.4
39	A8	7	TYR	4.4
40	75	100	TYR	4.4
7	6E	5	ARG	4.4
1	1G	163	C	4.4
22	1K	31	C	4.4
26	14	2568	C	4.4
5	4E	10	MET	4.4
14	5A	25	VAL	4.4
30	39	89	VAL	4.4
32	51	41	MET	4.4
32	59	115	VAL	4.4
1	13	1530	G	4.4
23	2K	2	G	4.4
26	1H	2659	G	4.4
26	14	1555	G	4.4
31	49	82	LEU	4.4
41	85	39	LEU	4.4
48	F5	20	ARG	4.4

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Mol	Chain	Res	Type	RSRZ
10	1A	63	PHE	4.4
40	B8	102	ILE	4.4
1	1G	806	C	4.4
26	1H	1926	U	4.4
7	62	7	ALA	4.3
41	C8	21	ALA	4.3
33	69	92	VAL	4.3
2	12	36	ARG	4.3
36	35	62	LEU	4.3
46	H8	163	LEU	4.3
2	1E	74	LYS	4.3
9	8E	118	LYS	4.3
36	35	121	LYS	4.3
45	G8	33	LYS	4.3
1	13	1521	G	4.3
1	13	913	A	4.3
55	3L	73	A	4.3
1	1G	897	C	4.3
2	12	62	ALA	4.3
26	14	766	C	4.3
32	59	26	VAL	4.3
36	78	71	VAL	4.3
45	C5	42	VAL	4.3
6	52	86	ARG	4.3
36	35	49	ARG	4.3
40	B8	103	ARG	4.3
20	BI	18	GLN	4.3
2	1E	211	ILE	4.3
2	12	208	ILE	4.3
48	J8	90	ILE	4.3
1	13	791	G	4.3
23	2K	77	A	4.3
26	14	205	G	4.3
26	14	2655	G	4.3
34	15	90	MET	4.3
3	2E	109	PRO	4.3
41	85	24	TYR	4.3
45	G8	35	TYR	4.3
17	8I	29	HIS	4.3
19	AA	9	VAL	4.3
26	14	789	A	4.3
26	14	1762	A	4.3

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Mol	Chain	Res	Type	RSRZ
26	14	2014	A	4.3
32	51	44	VAL	4.3
52	J5	28	PRO	4.3
1	13	576	G	4.3
1	13	763	G	4.3
1	13	1469	G	4.3
5	42	151	LEU	4.3
13	4I	96	LEU	4.3
35	25	18	LYS	4.3
42	95	8	GLY	4.3
48	F5	91	LYS	4.3
26	1H	1026	U	4.3
32	59	110	SER	4.3
1	13	336	C	4.3
1	1G	795	C	4.3
26	1H	2788	C	4.3
3	2E	60	ALA	4.3
2	1E	196	LEU	4.3
31	41	167	GLU	4.3
10	1I	48	THR	4.2
26	1H	2713	A	4.2
22	1L	32	U	4.2
26	14	202	U	4.2
26	1H	1063	G	4.2
1	13	797	C	4.2
1	13	882	C	4.2
26	1H	1830	C	4.2
26	1H	2556	C	4.2
34	58	55	VAL	4.2
36	35	48	PRO	4.2
40	75	138	ALA	4.2
46	D5	175	VAL	4.2
30	39	76	GLY	4.2
38	98	43	GLU	4.2
3	22	136	GLN	4.2
36	35	68	GLN	4.2
26	14	2533	A	4.2
26	14	2555	U	4.2
3	22	6	HIS	4.2
1	13	333	G	4.2
1	13	1467	G	4.2
1	1G	885	G	4.2

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Mol	Chain	Res	Type	RSRZ
1	1G	1453	G	4.2
26	1H	956	G	4.2
42	95	82	ARG	4.2
10	1I	49	VAL	4.2
1	13	934	C	4.2
9	82	102	LEU	4.2
26	1H	2715	C	4.2
26	14	687	C	4.2
26	14	1657	C	4.2
46	D5	154	ASP	4.2
5	42	131	ILE	4.2
13	4A	103	THR	4.2
29	29	35	GLN	4.2
30	39	53	THR	4.2
40	B8	110	ILE	4.2
2	12	90	MET	4.2
1	1G	1398	A	4.2
12	3I	13	LYS	4.2
22	1L	3	U	4.2
26	1H	163	U	4.2
26	1H	1614	A	4.2
26	14	2058	A	4.2
37	88	93	TYR	4.2
40	B8	65	LYS	4.2
31	41	22	ARG	4.2
31	41	33	ARG	4.2
20	BA	13	LEU	4.2
29	21	32	PRO	4.2
33	69	123	LEU	4.2
46	D5	111	VAL	4.2
32	59	156	ALA	4.2
34	15	92	ALA	4.2
3	2E	51	GLY	4.2
28	11	100	GLY	4.2
1	1G	818	G	4.2
26	14	768	G	4.2
26	14	1622	G	4.2
26	14	2569	G	4.2
33	61	117	GLU	4.2
32	59	121	ILE	4.2
53	L5	1	MET	4.2
16	7I	31	LYS	4.2

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Mol	Chain	Res	Type	RSRZ
2	12	199	TYR	4.2
22	1K	32	U	4.2
26	1H	1679	U	4.2
32	59	83	TYR	4.2
1	13	901	A	4.2
2	12	44	LEU	4.2
13	4A	117	VAL	4.2
38	98	10	LEU	4.2
13	4A	107	ALA	4.2
37	45	117	ALA	4.2
46	H8	97	GLU	4.2
17	8I	36	ILE	4.2
5	42	28	PHE	4.2
1	13	564	C	4.1
51	M8	27	THR	4.1
1	1G	1392	G	4.1
1	1G	1511	G	4.1
32	59	97	ARG	4.1
13	4A	90	LEU	4.1
36	78	115	LEU	4.1
45	G8	67	LEU	4.1
29	29	147	PRO	4.1
45	G8	66	PRO	4.1
26	1H	2609	U	4.1
26	14	2460	U	4.1
44	F8	86	GLY	4.1
55	3L	9	A	4.1
32	59	162	ILE	4.1
15	6I	88	ARG	4.1
30	31	95	ARG	4.1
22	1L	2	C	4.1
26	14	2081	C	4.1
19	AA	5	LEU	4.1
32	59	67	LEU	4.1
3	22	201	TYR	4.1
24	3K	49	G	4.1
26	1H	743	G	4.1
26	1H	1074	G	4.1
26	14	686	G	4.1
26	14	2630	G	4.1
40	B8	126	ALA	4.1
32	59	84	SER	4.1

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Mol	Chain	Res	Type	RSRZ
36	35	52	GLU	4.1
26	14	394	A	4.1
46	H8	154	ASP	4.1
3	22	163	ALA	4.1
26	1H	174	C	4.1
30	31	97	TYR	4.1
48	J8	79	GLY	4.1
12	3I	7	ILE	4.1
1	13	898	G	4.1
1	1G	28	G	4.1
22	1K	4	G	4.1
23	2K	4	G	4.1
23	2L	71	G	4.1
26	1H	2717	G	4.1
26	14	530	G	4.1
31	41	14	GLU	4.1
36	35	98	GLU	4.1
46	H8	20	ARG	4.1
1	13	1503	A	4.1
1	1G	807	A	4.1
26	1H	1088	A	4.1
26	1H	1268	A	4.1
3	22	52	LEU	4.1
32	59	171	LEU	4.1
38	98	113	LEU	4.1
41	C8	20	LEU	4.1
48	F5	80	LEU	4.1
7	62	9	VAL	4.1
9	8E	44	VAL	4.1
45	G8	42	VAL	4.1
34	58	40	PRO	4.1
29	21	131	ALA	4.1
42	95	77	ALA	4.1
52	J5	51	TYR	4.1
36	35	60	MET	4.1
37	45	87	LYS	4.1
26	14	461	C	4.1
3	22	30	ARG	4.1
38	98	103	ARG	4.1
36	35	38	GLN	4.1
26	14	695	G	4.1
26	14	950	G	4.1

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Mol	Chain	Res	Type	RSRZ
26	14	966	G	4.1
17	8A	89	LEU	4.0
30	39	24	LEU	4.0
35	68	81	ASP	4.0
30	39	75	HIS	4.0
2	12	219	VAL	4.0
32	59	11	VAL	4.0
46	D5	159	PRO	4.0
31	41	50	ALA	4.0
32	59	4	ILE	4.0
35	25	45	GLU	4.0
36	35	77	ARG	4.0
1	13	697	U	4.0
26	1H	589	C	4.0
26	1H	2011	U	4.0
26	14	2493	U	4.0
10	1A	48	THR	4.0
1	1G	765	G	4.0
26	1H	270(X)	G	4.0
43	E8	98	LYS	4.0
26	1H	2001	A	4.0
2	12	42	ILE	4.0
2	12	23	ARG	4.0
48	J8	20	ARG	4.0
32	51	16	SER	4.0
16	7A	76	GLN	4.0
31	49	26	GLN	4.0
36	78	68	GLN	4.0
41	C8	95	LEU	4.0
1	1G	554	C	4.0
22	1L	59	C	4.0
26	1H	270(C)	C	4.0
28	19	27	THR	4.0
28	19	40	THR	4.0
30	39	70	THR	4.0
32	59	125	VAL	4.0
48	J8	78	LYS	4.0
50	H5	2	PRO	4.0
41	85	43	GLY	4.0
42	D8	54	GLY	4.0
1	13	1518	A	4.0
7	62	149	ARG	4.0

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Mol	Chain	Res	Type	RSRZ
26	1H	957	A	4.0
26	14	1780	A	4.0
46	D5	149	SER	4.0
13	4A	101	GLN	4.0
32	59	24	VAL	4.0
37	88	94	VAL	4.0
46	D5	121	HIS	4.0
3	22	7	PRO	4.0
1	13	770	C	4.0
1	13	896	C	4.0
1	13	1535	C	4.0
26	1H	1761	C	4.0
26	1H	2573	C	4.0
26	14	574	C	4.0
26	14	654(B)	C	4.0
26	14	654(R)	C	4.0
26	14	1675	C	4.0
32	59	95	ARG	4.0
48	J8	93	GLU	4.0
1	1G	792	A	4.0
10	1A	8	LEU	4.0
26	1H	1077	A	4.0
12	3I	81	SER	4.0
26	1H	2012	G	4.0
26	14	1624	G	4.0
26	14	2508	G	4.0
32	59	90	LYS	4.0
32	59	153	LYS	4.0
3	2E	70	VAL	4.0
41	85	72	HIS	4.0
33	69	76	THR	4.0
52	J5	32	PRO	4.0
26	14	694	U	3.9
11	2I	81	ASP	3.9
14	5A	3	ARG	3.9
14	5A	35	ARG	3.9
29	21	6	GLY	3.9
26	1H	366	C	3.9
26	1H	2695	C	3.9
26	14	249	C	3.9
15	6A	15	PHE	3.9
37	45	2	LEU	3.9

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Mol	Chain	Res	Type	RSRZ
40	B8	99	LEU	3.9
1	13	915	A	3.9
26	1H	1069	A	3.9
26	14	182	A	3.9
39	65	5	THR	3.9
3	2E	71	ALA	3.9
13	4I	2	ALA	3.9
43	A5	3	ALA	3.9
1	13	230	G	3.9
1	13	906	G	3.9
1	13	933	G	3.9
26	14	270(N)	G	3.9
1	1G	793	U	3.9
32	59	60	ARG	3.9
38	55	92	GLY	3.9
33	69	10	GLU	3.9
49	K8	11	GLU	3.9
44	F8	95	LEU	3.9
26	1H	2063	C	3.9
26	14	756	C	3.9
26	14	1656	C	3.9
42	95	80	GLN	3.9
32	59	56	SER	3.9
1	13	1499	A	3.9
4	32	48	ALA	3.9
26	1H	590	A	3.9
26	1H	1652	A	3.9
42	95	70	ILE	3.9
32	59	68	THR	3.9
41	85	41	ALA	3.9
30	31	56	GLU	3.9
1	13	761	G	3.9
1	1G	1124	G	3.9
1	1G	1464	G	3.9
26	1H	125	G	3.9
26	1H	2010	G	3.9
33	69	75	LEU	3.9
34	58	15	LEU	3.9
43	A5	46	PHE	3.9
32	59	164	TYR	3.9
20	BI	45	GLN	3.9
29	29	7	VAL	3.9

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Mol	Chain	Res	Type	RSRZ
1	13	121	C	3.9
1	13	1527	C	3.9
22	1K	2	C	3.9
26	14	1537	C	3.9
36	78	140	ALA	3.9
43	E8	53	SER	3.9
26	14	2082	A	3.9
1	13	1512	U	3.9
1	1G	820	U	3.9
26	1H	2585	U	3.9
26	1H	2689	U	3.9
34	15	100	GLU	3.9
40	B8	46	GLU	3.9
1	13	1497	G	3.9
22	1K	49	G	3.9
26	14	2509	G	3.9
9	8E	128	ARG	3.9
36	35	111	ARG	3.9
9	82	55	ALA	3.9
29	29	70	ALA	3.9
1	13	699	C	3.9
26	1H	1646	C	3.9
26	1H	2571	C	3.9
30	31	93	LYS	3.8
40	B8	71	GLY	3.8
31	41	43	LEU	3.8
17	8I	86	GLU	3.8
1	13	935	A	3.8
1	1G	1492	A	3.8
23	2K	73	A	3.8
26	1H	2059	A	3.8
26	14	204	A	3.8
1	13	1528	U	3.8
29	21	59	VAL	3.8
48	F5	14	VAL	3.8
13	4I	114	ARG	3.8
13	4A	97	PRO	3.8
40	B8	64	ARG	3.8
46	D5	49	ARG	3.8
7	62	147	ALA	3.8
1	1G	800	G	3.8
1	1G	821	G	3.8

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Mol	Chain	Res	Type	RSRZ
22	1L	71	G	3.8
26	14	1824	G	3.8
10	1A	71	LEU	3.8
11	2I	49	GLY	3.8
20	BI	103	GLY	3.8
31	49	34	LEU	3.8
31	49	133	LEU	3.8
46	H8	117	LEU	3.8
1	1G	783	C	3.8
26	14	203	C	3.8
34	15	117	PHE	3.8
48	J8	75	GLU	3.8
2	1E	79	ASP	3.8
29	21	127	ASP	3.8
1	13	780	A	3.8
23	2K	39	A	3.8
26	1H	1086	A	3.8
3	2E	134	ILE	3.8
19	AI	81	ARG	3.8
54	M5	34	TRP	3.8
2	12	33	TYR	3.8
12	3I	47	LYS	3.8
20	BA	7	LYS	3.8
29	29	194	GLY	3.8
39	65	60	GLY	3.8
45	C5	41	GLY	3.8
1	1G	181	G	3.8
17	8A	82	MET	3.8
26	14	388	G	3.8
1	13	337	C	3.8
1	13	783	C	3.8
1	1G	1382	C	3.8
6	52	55	ASP	3.8
9	8E	120	ARG	3.8
10	1A	51	ARG	3.8
30	39	54	ARG	3.8
1	13	14	U	3.8
26	14	688	U	3.8
26	14	2357	U	3.8
55	3L	36	U	3.8
26	14	2273	A	3.8
26	14	2662	A	3.8

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Mol	Chain	Res	Type	RSRZ
12	3I	28	LYS	3.8
19	AA	7	LYS	3.8
12	3A	26	ALA	3.8
41	85	96	ALA	3.8
3	2E	115	LEU	3.8
42	95	1	MET	3.8
7	62	90	GLU	3.8
10	1I	61	GLU	3.8
32	51	58	GLU	3.8
5	4E	13	ILE	3.8
16	7I	29	ASP	3.8
40	75	50	ILE	3.8
47	E5	71	ASP	3.8
54	M5	58	ILE	3.8
23	2K	75	C	3.8
26	1H	755	C	3.8
26	1H	2007	C	3.8
26	14	591	C	3.8
26	14	801	G	3.8
26	14	2080	G	3.8
26	14	2507	C	3.8
29	21	133	LYS	3.8
26	14	2613	U	3.8
3	22	137	ALA	3.8
2	1E	14	GLY	3.8
2	12	83	MET	3.8
2	12	17	PHE	3.8
38	98	102	GLU	3.7
12	3A	22	SER	3.7
46	D5	166	SER	3.7
30	39	114	VAL	3.7
32	59	19	VAL	3.7
36	78	95	VAL	3.7
6	52	54	LYS	3.7
12	3I	21	LYS	3.7
19	AI	59	PRO	3.7
43	E8	56	ALA	3.7
1	13	320	C	3.7
3	22	110	ASN	3.7
26	14	270(P)	C	3.7
26	14	755	C	3.7
26	14	1672	C	3.7

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Mol	Chain	Res	Type	RSRZ
28	11	111	LEU	3.7
26	1H	1653	G	3.7
26	1H	2124	G	3.7
26	14	2583	G	3.7
1	13	807	A	3.7
1	13	1507	A	3.7
26	1H	270(B)	A	3.7
26	1H	529	A	3.7
26	1H	2497	A	3.7
32	59	109	PHE	3.7
29	21	136	ARG	3.7
36	78	18	ARG	3.7
40	B8	125	ARG	3.7
46	H8	108	PRO	3.7
50	H5	42	ALA	3.7
1	1G	813	U	3.7
1	1G	1380	U	3.7
31	49	177	GLY	3.7
1	13	808	C	3.7
1	13	1367	C	3.7
1	13	1395	C	3.7
1	1G	805	C	3.7
26	14	693	C	3.7
26	14	2788	C	3.7
5	42	122	GLU	3.7
31	49	167	GLU	3.7
41	85	78	THR	3.7
1	1G	576	G	3.7
26	1H	440	G	3.7
26	14	1380	G	3.7
47	I8	82	ARG	3.7
1	13	607	A	3.7
26	1H	2451	A	3.7
26	14	2632	A	3.7
28	19	3	VAL	3.7
40	75	70	VAL	3.7
30	39	10	PRO	3.7
2	1E	225	ALA	3.7
19	AA	10	PHE	3.7
30	39	86	GLY	3.7
31	41	42	GLY	3.7
32	59	100	GLY	3.7

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Mol	Chain	Res	Type	RSRZ
36	78	28	GLY	3.7
26	1H	50	U	3.7
26	14	1621	U	3.7
38	98	33	ARG	3.7
9	82	27	THR	3.7
12	3A	46	LYS	3.7
5	42	11	ILE	3.7
1	13	1434	A	3.7
24	3K	7	A	3.7
26	14	1048	A	3.7
55	3L	38	A	3.7
26	1H	1645	G	3.7
26	14	248	G	3.7
26	14	880	G	3.7
46	D5	52	SER	3.7
46	D5	68	PRO	3.7
2	12	212	GLN	3.7
6	5E	11	ASN	3.7
11	2A	75	TYR	3.7
16	7I	28	ARG	3.7
37	45	88	GLY	3.7
44	F8	24	GLY	3.7
11	2I	122	LYS	3.7
42	95	43	GLU	3.7
9	8E	81	ILE	3.7
9	82	44	VAL	3.7
15	6A	87	ILE	3.7
34	58	73	THR	3.7
1	13	1490	C	3.6
1	1G	240	C	3.6
20	BA	24	LEU	3.6
26	1H	1836	C	3.6
26	14	691	C	3.6
26	14	1782	C	3.6
37	88	45	GLN	3.6
26	1H	1677	A	3.6
26	14	1378	A	3.6
26	14	194	G	3.6
26	14	247	G	3.6
27	16	89	G	3.6
33	69	118	LYS	3.6
41	85	19	LYS	3.6

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Mol	Chain	Res	Type	RSRZ
47	E5	13	GLY	3.6
47	E5	20	ARG	3.6
2	12	93	VAL	3.6
3	2E	106	VAL	3.6
3	22	198	VAL	3.6
10	1I	96	ILE	3.6
34	15	5	VAL	3.6
37	88	120	ILE	3.6
12	3I	22	SER	3.6
1	13	1342	C	3.6
26	1H	2692	C	3.6
2	12	226	ARG	3.6
12	3A	89	ARG	3.6
26	1H	750	A	3.6
26	1H	2809	A	3.6
26	14	2274	A	3.6
33	69	69	LYS	3.6
45	G8	41	GLY	3.6
4	32	207	TYR	3.6
32	59	157	TYR	3.6
46	H8	146	ILE	3.6
1	1G	575	G	3.6
1	1G	1520	G	3.6
26	1H	271	G	3.6
26	1H	388	G	3.6
33	61	134	PRO	3.6
20	BA	106	ALA	3.6
12	3A	116	SER	3.6
32	59	62	LYS	3.6
15	6I	64	ARG	3.6
1	13	23	C	3.6
1	13	811	C	3.6
26	1H	1258	C	3.6
26	14	692	C	3.6
26	14	1430	C	3.6
1	13	1519	A	3.6
2	1E	41	ILE	3.6
49	K8	66	GLU	3.6
10	1A	100	THR	3.6
1	13	691	G	3.6
24	3K	26	G	3.6
26	1H	2716	U	3.6

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Mol	Chain	Res	Type	RSRZ
26	14	1310	G	3.6
26	14	1764	G	3.6
26	14	1778	U	3.6
37	45	72	LYS	3.6
39	65	57	LYS	3.6
41	C8	16	LYS	3.6
48	J8	24	ALA	3.6
11	2I	126	ARG	3.6
15	6I	63	ARG	3.6
32	51	2	SER	3.6
31	49	42	GLY	3.6
45	C5	25	GLY	3.6
50	L8	14	GLY	3.6
31	41	77	ILE	3.6
38	98	34	ILE	3.6
10	1I	97	GLU	3.6
14	5I	25	VAL	3.6
31	41	45	GLU	3.6
40	75	66	VAL	3.6
1	1G	526	C	3.6
24	3K	75	C	3.6
26	1H	2008	C	3.6
20	BI	9	ASN	3.6
26	14	1050	A	3.6
26	14	2531	A	3.6
30	31	169	ASN	3.6
17	8I	30	PRO	3.6
2	1E	207	ALA	3.5
1	13	1425	U	3.5
14	5A	26	ARG	3.5
37	45	53	ALA	3.5
1	13	15	G	3.5
1	13	319	G	3.5
1	1G	1061	G	3.5
26	1H	379	G	3.5
26	1H	2581	G	3.5
26	14	1131	G	3.5
26	14	1264	G	3.5
42	D8	8	GLY	3.5
3	22	141	VAL	3.5
17	8A	86	GLU	3.5
32	59	58	GLU	3.5

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Mol	Chain	Res	Type	RSRZ
32	59	124	GLU	3.5
37	45	90	VAL	3.5
3	2E	150	LYS	3.5
13	4A	116	THR	3.5
26	1H	1847	A	3.5
26	14	1658	C	3.5
26	14	2461	C	3.5
2	12	161	ALA	3.5
29	21	79	ARG	3.5
29	21	187	ALA	3.5
32	59	165	ALA	3.5
38	98	41	ALA	3.5
40	B8	115	ARG	3.5
1	1G	182	U	3.5
22	1K	8	U	3.5
31	41	44	GLY	3.5
45	C5	70	SER	3.5
4	3E	150	GLU	3.5
1	1G	881	G	3.5
14	5A	6	LEU	3.5
26	1H	363(D)	G	3.5
26	1H	1831	G	3.5
26	1H	2211	G	3.5
26	14	561	G	3.5
26	14	1987	G	3.5
37	88	118	LEU	3.5
48	J8	97	LEU	3.5
19	AA	13	ASP	3.5
52	J5	27	PRO	3.5
3	2E	132	ARG	3.5
4	3E	168	ARG	3.5
4	32	3	ARG	3.5
8	72	85	ARG	3.5
40	75	64	ARG	3.5
46	D5	81	ARG	3.5
40	B8	130	ALA	3.5
17	8I	93	GLN	3.5
1	13	268	C	3.5
1	13	335	C	3.5
1	1G	1403	C	3.5
24	3K	27	C	3.5
26	1H	273(C)	C	3.5

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Mol	Chain	Res	Type	RSRZ
26	1H	1048	A	3.5
26	14	970	C	3.5
26	14	1049	C	3.5
26	14	2350	C	3.5
3	22	202	ILE	3.5
29	21	134	ILE	3.5
1	13	920	U	3.5
26	14	1396	U	3.5
28	11	113	VAL	3.5
9	82	48	GLU	3.5
18	9A	85	LEU	3.5
38	55	65	LEU	3.5
3	22	114	PRO	3.5
37	45	14	ARG	3.5
1	13	122	G	3.5
1	13	347	G	3.5
1	13	351	G	3.5
1	13	1343	G	3.5
1	13	1525	G	3.5
1	1G	791	G	3.5
1	1G	825	G	3.5
2	12	34	ALA	3.5
14	5A	10	ALA	3.5
22	1K	15	G	3.5
24	3K	39	G	3.5
26	1H	742	G	3.5
26	1H	1087	G	3.5
26	1H	2709	G	3.5
26	14	823	G	3.5
26	14	2396	G	3.5
55	3L	46	G	3.5
49	G5	37	PHE	3.5
1	13	291	C	3.5
22	1K	70	A	3.5
26	14	251	A	3.5
26	14	2510	C	3.5
26	14	2658	C	3.5
37	88	122	GLY	3.5
45	G8	104	GLY	3.5
48	F5	28	GLY	3.5
8	7E	10	LEU	3.5
28	19	26	LYS	3.5

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Mol	Chain	Res	Type	RSRZ
33	69	35	LEU	3.5
38	55	100	LEU	3.5
46	D5	156	LYS	3.5
3	22	154	SER	3.5
8	72	89	PRO	3.5
7	62	145	ALA	3.5
29	29	159	HIS	3.5
34	15	132	ALA	3.5
36	78	84	ASN	3.5
31	41	102	PHE	3.4
1	1G	183	G	3.4
26	14	638	G	3.4
4	32	16	GLY	3.4
11	2A	105	VAL	3.4
36	78	93	GLY	3.4
7	6E	38	LEU	3.4
11	2A	124	LYS	3.4
1	13	412	A	3.4
1	13	694	A	3.4
1	1G	573	A	3.4
1	13	312	C	3.4
26	14	2619	C	3.4
6	52	28	ARG	3.4
7	62	33	ASP	3.4
2	1E	73	THR	3.4
19	AA	14	HIS	3.4
30	39	73	ALA	3.4
34	58	22	THR	3.4
37	88	117	ALA	3.4
37	45	123	HIS	3.4
3	2E	23	TYR	3.4
46	D5	164	ALA	3.4
43	A5	57	ASN	3.4
2	12	223	ILE	3.4
40	75	102	ILE	3.4
14	5A	36	PHE	3.4
36	35	86	LYS	3.4
10	1I	94	VAL	3.4
36	35	117	GLU	3.4
1	13	78	G	3.4
1	1G	763	G	3.4
1	1G	775	G	3.4

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Mol	Chain	Res	Type	RSRZ
1	1G	926	G	3.4
3	2E	156	ARG	3.4
4	3E	76	ARG	3.4
26	1H	2002	G	3.4
26	14	1112	G	3.4
26	14	2397	G	3.4
34	15	74	ARG	3.4
49	K8	69	ARG	3.4
26	14	969	U	3.4
1	1G	958	A	3.4
26	1H	2171	A	3.4
26	1H	951	C	3.4
26	1H	982	C	3.4
26	1H	2658	C	3.4
26	14	393	C	3.4
26	14	1383	C	3.4
4	3E	32	ALA	3.4
38	98	61	HIS	3.4
13	4A	87	TYR	3.4
17	8I	88	TYR	3.4
30	39	59	TYR	3.4
31	41	162	THR	3.4
51	M8	25	TYR	3.4
13	4I	9	ILE	3.4
2	1E	122	PHE	3.4
28	11	203	ASN	3.4
47	E5	19	LYS	3.4
4	3E	21	LEU	3.4
28	11	98	VAL	3.4
35	25	74	GLY	3.4
41	85	18	LEU	3.4
13	4I	8	GLU	3.4
30	39	35	GLU	3.4
32	59	116	GLU	3.4
28	19	52	ARG	3.4
30	31	62	ARG	3.4
4	32	37	PRO	3.4
6	52	56	PRO	3.4
1	13	1406	U	3.4
26	1H	2016	U	3.4
26	14	2034	U	3.4
1	13	124	G	3.4

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Mol	Chain	Res	Type	RSRZ
1	13	1036	G	3.4
1	1G	1508	G	3.4
1	1G	1521	G	3.4
26	1H	2253	G	3.4
26	14	1566	A	3.4
26	14	2270	G	3.4
29	21	66	HIS	3.4
8	72	83	ILE	3.4
30	31	136	THR	3.4
40	B8	48	ILE	3.4
12	3A	13	LYS	3.4
26	1H	172	C	3.4
26	1H	435	C	3.4
26	1H	1383	C	3.4
26	1H	1585	C	3.4
46	H8	38	TYR	3.4
5	42	55	VAL	3.4
12	3A	14	GLY	3.4
15	6I	60	VAL	3.4
29	21	63	LEU	3.4
34	58	49	GLY	3.4
31	41	174	GLU	3.4
37	45	60	ARG	3.4
45	C5	23	ARG	3.4
45	C5	40	GLU	3.4
17	8I	28	PRO	3.4
6	52	53	ALA	3.4
1	1G	772	U	3.4
3	2E	112	SER	3.4
3	2E	157	ILE	3.4
10	1A	38	ILE	3.4
12	3A	115	LYS	3.4
31	49	144	ILE	3.4
41	85	84	LYS	3.4
48	F5	17	SER	3.4
5	42	26	PHE	3.4
1	1G	1225	A	3.4
9	82	114	TYR	3.4
19	AA	15	LEU	3.3
32	59	71	LEU	3.3
34	15	116	LEU	3.3
39	65	110	LEU	3.3

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Mol	Chain	Res	Type	RSRZ
1	13	925	G	3.3
26	1H	2751	G	3.3
26	14	386	G	3.3
26	14	615	G	3.3
26	14	642	G	3.3
26	14	2661	G	3.3
32	59	37	VAL	3.3
34	58	125	GLY	3.3
39	65	3	ARG	3.3
5	42	50	GLU	3.3
33	69	117	GLU	3.3
49	G5	34	GLU	3.3
29	21	62	PRO	3.3
45	C5	21	LYS	3.3
45	C5	28	LYS	3.3
26	1H	2511	U	3.3
26	14	2041	U	3.3
47	I8	9	SER	3.3
49	K8	45	SER	3.3
2	12	165	VAL	3.3
12	3A	15	ARG	3.3
20	BI	80	ARG	3.3
29	29	121	ASN	3.3
36	78	11	GLY	3.3
40	75	29	ARG	3.3
26	1H	2173	A	3.3
26	14	2459	A	3.3
8	72	136	GLU	3.3
46	D5	11	GLU	3.3
1	1G	762	C	3.3
1	13	579	G	3.3
1	1G	584	G	3.3
1	1G	1442	G	3.3
26	1H	880	G	3.3
26	1H	2345	G	3.3
26	14	1401	G	3.3
26	14	2747	G	3.3
11	2A	123	LYS	3.3
15	6I	47	LYS	3.3
34	15	2	LYS	3.3
35	25	1	MET	3.3
43	A5	111	HIS	3.3

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Mol	Chain	Res	Type	RSRZ
46	D5	51	ALA	3.3
48	J8	80	LEU	3.3
1	13	801	U	3.3
4	3E	25	ARG	3.3
37	45	94	VAL	3.3
50	H5	59	VAL	3.3
7	62	74	GLU	3.3
32	59	167	GLU	3.3
54	M5	40	GLU	3.3
1	13	768	A	3.3
26	1H	2176	A	3.3
26	14	2665	A	3.3
9	82	97	LYS	3.3
11	2A	122	LYS	3.3
46	D5	176	PRO	3.3
50	H5	16	PRO	3.3
1	1G	1514	C	3.3
2	12	214	ILE	3.3
5	4E	11	ILE	3.3
10	1A	96	ILE	3.3
23	2L	35	C	3.3
26	1H	273(D)	C	3.3
26	1H	955	C	3.3
26	14	1625	C	3.3
26	14	1694	C	3.3
36	35	12	ALA	3.3
36	35	134	ALA	3.3
1	13	798	G	3.3
1	1G	773	G	3.3
26	1H	950	G	3.3
26	1H	1705	G	3.3
26	1H	2532	G	3.3
26	14	744	G	3.3
26	14	2362	G	3.3
2	1E	11	LEU	3.3
3	22	175	LEU	3.3
4	32	9	CYS	3.3
10	1A	94	VAL	3.3
11	2I	87	THR	3.3
37	88	52	VAL	3.3
44	B5	68	ARG	3.3
54	M5	42	ARG	3.3

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Mol	Chain	Res	Type	RSRZ
17	8I	97	SER	3.3
37	45	33	GLY	3.3
17	8A	32	TYR	3.3
36	78	46	LYS	3.3
2	12	159	PRO	3.3
1	13	270	A	3.3
1	13	1227	A	3.3
1	1G	782	A	3.3
1	1G	794	A	3.3
26	1H	390	A	3.3
42	D8	70	ILE	3.3
5	4E	123	LEU	3.3
33	61	140	LEU	3.3
38	98	44	LEU	3.3
10	1I	63	PHE	3.3
26	1H	365	C	3.3
26	1H	2452	C	3.3
30	31	83	PHE	3.3
33	61	103	ARG	3.3
30	39	105	VAL	3.3
37	45	52	VAL	3.3
38	98	38	VAL	3.3
46	D5	174	VAL	3.3
51	M8	35	VAL	3.3
4	3E	9	CYS	3.3
1	13	902	G	3.3
1	1G	567	G	3.3
1	1G	785	G	3.3
26	1H	1259	G	3.3
26	1H	2156	G	3.3
26	1H	2708	G	3.3
26	14	647	G	3.3
36	78	116	GLY	3.3
32	59	16	SER	3.3
1	1G	801	U	3.2
2	1E	169	LYS	3.2
10	1A	7	LYS	3.2
16	7A	29	ASP	3.2
19	AA	55	LYS	3.2
29	29	42	ASP	3.2
34	58	100	GLU	3.2
35	68	66	LYS	3.2

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Mol	Chain	Res	Type	RSRZ
39	A8	111	GLU	3.2
43	E8	57	ASN	3.2
29	21	205	ALA	3.2
30	31	75	HIS	3.2
34	15	33	LEU	3.2
38	55	111	LEU	3.2
39	65	58	LEU	3.2
1	13	1005	A	3.2
26	1H	38	A	3.2
26	1H	1073	A	3.2
26	1H	2042	A	3.2
26	14	764	A	3.2
33	69	50	ARG	3.2
38	55	8	ARG	3.2
2	1E	95	GLN	3.2
2	12	224	GLN	3.2
3	22	99	VAL	3.2
28	19	18	VAL	3.2
42	D8	46	VAL	3.2
1	13	554	C	3.2
1	1G	23	C	3.2
26	14	964	C	3.2
26	14	1990	C	3.2
26	14	2050	C	3.2
27	16	88	C	3.2
32	59	70	THR	3.2
31	49	75	LYS	3.2
42	D8	84	LYS	3.2
2	12	216	SER	3.2
36	35	56	SER	3.2
29	21	42	ASP	3.2
1	13	1470	G	3.2
1	1G	771	G	3.2
1	1G	1194	U	3.2
12	3A	25	PRO	3.2
22	1L	4	G	3.2
26	1H	968	G	3.2
26	14	742	G	3.2
9	8E	47	LEU	3.2
13	4A	96	LEU	3.2
36	35	85	LEU	3.2
41	C8	96	ALA	3.2

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Mol	Chain	Res	Type	RSRZ
48	F5	24	ALA	3.2
30	39	95	ARG	3.2
32	59	170	ARG	3.2
37	45	56	ARG	3.2
28	11	15	PHE	3.2
45	G8	98	VAL	3.2
8	72	90	GLY	3.2
31	49	74	LYS	3.2
34	15	63	THR	3.2
38	98	93	GLY	3.2
7	6E	8	GLU	3.2
52	N8	35	GLU	3.2
1	1G	1045	C	3.2
3	22	20	SER	3.2
23	2K	70	C	3.2
26	14	949	C	3.2
26	14	2055	C	3.2
29	21	117	MET	3.2
35	25	81	ASP	3.2
4	32	161	ASN	3.2
2	12	215	LEU	3.2
40	B8	114	LEU	3.2
32	59	6	ARG	3.2
41	85	42	ALA	3.2
23	2K	20	G	3.2
25	4K	9	G	3.2
26	1H	2557	G	3.2
38	55	47	PHE	3.2
46	D5	105	VAL	3.2
9	8E	70	LYS	3.2
34	15	104	LYS	3.2
3	2E	155	GLY	3.2
29	21	88	GLY	3.2
1	13	696	A	3.2
26	1H	718	A	3.2
26	1H	2476	A	3.2
40	75	109	GLU	3.2
12	3A	81	SER	3.2
30	39	9	ILE	3.2
40	B8	107	ASP	3.2
41	85	91	ASP	3.2
1	1G	1515	C	3.2

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Mol	Chain	Res	Type	RSRZ
7	62	143	ARG	3.2
26	1H	2678	C	3.2
26	14	708	C	3.2
1	1G	1522	U	3.2
26	1H	1065	U	3.2
32	59	96	ALA	3.2
55	3L	32	U	3.2
31	49	178	PHE	3.2
5	42	148	VAL	3.2
10	1A	72	VAL	3.2
36	78	14	LYS	3.2
38	55	38	VAL	3.2
42	D8	51	VAL	3.2
45	C5	71	LYS	3.2
46	H8	116	VAL	3.2
46	D5	71	VAL	3.2
48	J8	23	LYS	3.2
3	22	28	GLN	3.2
6	5E	18	GLN	3.2
1	13	260	G	3.2
1	1G	933	G	3.2
15	6I	86	GLY	3.2
26	14	2553	G	3.2
28	19	55	GLY	3.2
32	59	108	GLY	3.2
47	E5	34	GLY	3.2
55	3L	1	G	3.2
10	1I	64	GLU	3.2
42	95	50	PRO	3.2
52	J5	34	PRO	3.2
1	13	262	A	3.1
1	1G	767	A	3.1
26	1H	960	A	3.1
26	14	896	A	3.1
9	82	16	ARG	3.1
12	3I	89	ARG	3.1
36	35	65	ARG	3.1
38	55	70	LEU	3.1
50	L8	55	ARG	3.1
18	9I	20	ALA	3.1
29	29	60	ASN	3.1
30	39	5	ALA	3.1

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Mol	Chain	Res	Type	RSRZ
33	69	65	ALA	3.1
36	35	140	ALA	3.1
41	85	21	ALA	3.1
13	4I	111	LYS	3.1
39	A8	44	LYS	3.1
42	D8	19	LYS	3.1
1	13	91	C	3.1
1	13	806	C	3.1
1	1G	239	U	3.1
1	1G	1477	C	3.1
7	62	141	VAL	3.1
26	1H	364	C	3.1
26	1H	720	C	3.1
26	1H	1908	C	3.1
26	14	758	C	3.1
4	32	180	GLY	3.1
34	58	1	MET	3.1
37	88	84	GLY	3.1
4	32	150	GLU	3.1
1	13	524	G	3.1
8	72	112	LEU	3.1
9	82	96	LEU	3.1
10	1A	65	LEU	3.1
26	1H	962	G	3.1
26	1H	2664	G	3.1
26	1H	2714	G	3.1
26	14	381	G	3.1
26	14	438	G	3.1
26	14	765	G	3.1
26	14	2557	G	3.1
7	62	127	ALA	3.1
41	85	77	SER	3.1
2	12	220	ASP	3.1
26	14	2062	A	3.1
33	61	20	ASP	3.1
2	12	184	VAL	3.1
31	49	28	VAL	3.1
32	59	49	VAL	3.1
1	1G	905	U	3.1
22	1L	8	U	3.1
23	2K	37	U	3.1
26	1H	1130	U	3.1

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Mol	Chain	Res	Type	RSRZ
26	1H	2460	U	3.1
1	1G	1465	C	3.1
10	1A	93	GLY	3.1
26	1H	270(K)	C	3.1
26	1H	377	C	3.1
26	1H	1544	C	3.1
26	1H	2402	C	3.1
12	3A	122	THR	3.1
31	49	52	ILE	3.1
32	59	159	GLU	3.1
34	15	6	PRO	3.1
37	88	17	LEU	3.1
39	A8	4	LEU	3.1
40	75	99	LEU	3.1
46	D5	79	ARG	3.1
36	35	137	LYS	3.1
40	B8	119	LYS	3.1
41	85	16	LYS	3.1
2	1E	148	TYR	3.1
2	12	13	ALA	3.1
6	5E	53	ALA	3.1
9	8E	52	ALA	3.1
52	J5	24	ALA	3.1
2	1E	16	HIS	3.1
3	22	153	VAL	3.1
4	32	112	VAL	3.1
5	4E	45	PHE	3.1
8	72	135	CYS	3.1
32	59	131	VAL	3.1
32	59	144	VAL	3.1
40	75	44	ASP	3.1
40	75	89	VAL	3.1
46	D5	56	VAL	3.1
51	M8	59	PHE	3.1
1	13	775	G	3.1
1	13	776	G	3.1
1	1G	876	G	3.1
6	5E	84	ASN	3.1
23	2L	2	G	3.1
26	1H	270(J)	G	3.1
1	13	344	A	3.1
23	2L	74	A	3.1

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Mol	Chain	Res	Type	RSRZ
26	14	1132	A	3.1
26	14	2019	A	3.1
17	8A	33	GLY	3.1
4	32	192	GLU	3.1
29	29	73	GLU	3.1
1	13	314	C	3.1
2	12	47	THR	3.1
3	22	119	ARG	3.1
11	2A	121	PRO	3.1
22	1K	59	C	3.1
24	3K	25	C	3.1
26	1H	721	C	3.1
26	1H	2676	C	3.1
26	14	965	C	3.1
26	14	1611	C	3.1
32	51	55	PRO	3.1
35	68	97	ARG	3.1
44	B5	37	THR	3.1
48	F5	40	ARG	3.1
37	88	72	LYS	3.1
37	88	124	LYS	3.1
2	12	218	ALA	3.1
31	49	50	ALA	3.1
9	8E	4	TYR	3.1
30	31	6	VAL	3.1
31	49	23	PHE	3.1
36	35	133	SER	3.1
37	45	45	GLN	3.1
42	D8	48	GLY	3.1
47	E5	22	GLY	3.1
1	1G	696	A	3.1
24	3K	50	G	3.1
26	1H	363(C)	G	3.1
26	1H	948	G	3.1
26	1H	1780	A	3.1
26	1H	1835	G	3.1
26	1H	2123	G	3.1
26	1H	2663	G	3.1
26	1H	2679	A	3.1
26	14	1272	A	3.1
26	14	1322	A	3.1
26	14	1524	G	3.1

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Mol	Chain	Res	Type	RSRZ
26	1H	162	U	3.1
26	1H	1267	U	3.1
10	1A	70	ARG	3.1
20	BA	8	ARG	3.1
32	51	3	ARG	3.1
38	98	8	ARG	3.1
40	B8	108	ARG	3.1
48	F5	11	ARG	3.1
2	12	75	LYS	3.1
8	72	2	LEU	3.1
31	49	105	LYS	3.1
32	59	55	PRO	3.1
33	69	9	LEU	3.1
33	69	80	PRO	3.1
36	78	59	LEU	3.1
43	A5	83	LYS	3.1
1	1G	1367	C	3.1
26	1H	270(Q)	C	3.1
26	14	385	C	3.1
26	14	589	C	3.1
55	3L	48	C	3.1
12	3A	55	VAL	3.0
32	59	76	VAL	3.0
35	25	32	TYR	3.0
46	H8	8	TYR	3.0
4	32	83	SER	3.0
5	42	125	SER	3.0
3	22	118	GLN	3.0
7	62	11	GLN	3.0
30	39	131	GLY	3.0
5	42	13	ILE	3.0
7	62	50	ILE	3.0
31	49	39	ILE	3.0
2	12	129	GLU	3.0
5	42	47	LYS	3.0
13	4I	27	LYS	3.0
19	AA	59	PRO	3.0
29	21	56	PRO	3.0
32	59	8	PRO	3.0
33	61	85	GLU	3.0
38	98	60	LEU	3.0
26	1H	2459	A	3.0

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Mol	Chain	Res	Type	RSRZ
26	1H	2493	U	3.0
27	1J	89(A)	A	3.0
3	22	192	THR	3.0
29	29	92	THR	3.0
46	H8	170	THR	3.0
1	13	606	G	3.0
1	1G	413	G	3.0
26	1H	2251	G	3.0
27	16	21	G	3.0
11	2I	89	ALA	3.0
33	69	49	ALA	3.0
3	22	186	PHE	3.0
19	AA	67	VAL	3.0
1	1G	962	C	3.0
22	1L	30	C	3.0
26	1H	2177	C	3.0
26	14	1615	C	3.0
28	11	97	TYR	3.0
51	M8	63	TYR	3.0
12	3I	116	SER	3.0
34	58	58	ASP	3.0
2	1E	5	ILE	3.0
2	12	201	ILE	3.0
3	22	84	ILE	3.0
30	39	91	GLY	3.0
5	4E	88	LYS	3.0
30	31	135	LYS	3.0
31	49	83	ARG	3.0
40	B8	52	ILE	3.0
40	75	137	LYS	3.0
20	BI	24	LEU	3.0
33	69	41	GLU	3.0
33	69	122	GLU	3.0
26	14	1820	U	3.0
1	13	814	A	3.0
26	1H	722	A	3.0
26	1H	1928	A	3.0
26	1H	2614	A	3.0
4	3E	110	PHE	3.0
8	7E	95	VAL	3.0
1	13	309	G	3.0
1	13	346	G	3.0

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Mol	Chain	Res	Type	RSRZ
1	13	837	G	3.0
22	1K	19	G	3.0
23	2K	5	G	3.0
26	1H	508	G	3.0
26	1H	1846	G	3.0
26	14	1823	G	3.0
26	14	2548	G	3.0
2	1E	33	TYR	3.0
7	62	44	TYR	3.0
16	7A	32	TYR	3.0
38	55	21	TYR	3.0
1	1G	817	C	3.0
3	22	170	GLN	3.0
26	1H	404	C	3.0
26	14	128	C	3.0
30	39	68	LYS	3.0
32	51	4	ILE	3.0
33	69	27	ARG	3.0
36	78	64	LYS	3.0
48	F5	21	ARG	3.0
52	N8	50	GLY	3.0
6	5E	43	LEU	3.0
13	4I	90	LEU	3.0
12	3I	94	PRO	3.0
15	6A	41	GLU	3.0
32	59	119	GLU	3.0
35	25	9	GLU	3.0
52	N8	36	CYS	3.0
30	39	136	THR	3.0
1	13	1522	U	3.0
1	1G	20	U	3.0
31	49	155	MET	3.0
33	61	46	ALA	3.0
47	E5	33	ALA	3.0
29	29	72	VAL	3.0
36	78	51	PHE	3.0
40	B8	72	VAL	3.0
27	1J	59	A	3.0
31	41	72	ARG	3.0
36	78	110	TYR	3.0
36	35	114	ILE	3.0
45	C5	73	ARG	3.0

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Mol	Chain	Res	Type	RSRZ
3	22	51	GLY	3.0
29	21	106	GLY	3.0
32	51	142	GLY	3.0
32	59	161	GLY	3.0
36	78	69	GLY	3.0
43	E8	23	LEU	3.0
47	I8	84	LEU	3.0
1	13	293	G	3.0
1	1G	27	G	3.0
1	1G	1476	G	3.0
23	2L	4	G	3.0
26	1H	592	G	3.0
26	1H	1522	G	3.0
26	1H	1758	G	3.0
26	1H	2255	G	3.0
26	14	1613	G	3.0
3	2E	154	SER	3.0
9	82	32	ASP	3.0
20	BA	105	SER	3.0
1	13	240	C	3.0
1	13	805	C	3.0
1	1G	269	C	3.0
1	1G	1440	C	3.0
26	1H	754	C	3.0
26	14	435	C	3.0
30	39	94	PRO	3.0
41	85	89	GLU	3.0
42	95	98	GLU	3.0
2	1E	171	ALA	3.0
37	88	3	MET	3.0
3	22	55	VAL	3.0
31	41	28	VAL	3.0
32	59	35	VAL	3.0
33	61	145	VAL	3.0
10	1I	62	HIS	3.0
20	BA	16	HIS	3.0
26	14	757	U	3.0
8	7E	88	LYS	2.9
32	51	160	LYS	2.9
2	1E	175	ARG	2.9
4	32	25	ARG	2.9
4	32	50	ARG	2.9

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Mol	Chain	Res	Type	RSRZ
11	2I	42	TRP	2.9
11	2I	96	ARG	2.9
49	G5	51	ARG	2.9
5	42	133	TYR	2.9
26	1H	363(F)	A	2.9
26	14	960	A	2.9
26	14	2801	A	2.9
13	4A	112	GLY	2.9
17	8I	33	GLY	2.9
29	29	139	GLY	2.9
30	39	20	LEU	2.9
10	1A	86	MET	2.9
23	2K	19	G	2.9
26	14	2494	G	2.9
26	14	2633	G	2.9
36	78	1	MET	2.9
1	13	578	C	2.9
1	1G	1490	C	2.9
26	1H	1832	C	2.9
26	14	640	C	2.9
36	78	129	ALA	2.9
8	72	31	PHE	2.9
19	AA	19	VAL	2.9
32	51	37	VAL	2.9
44	F8	83	VAL	2.9
46	D5	116	VAL	2.9
32	51	61	HIS	2.9
1	1G	552	U	2.9
14	5A	41	ARG	2.9
26	1H	363(E)	U	2.9
26	1H	1834	U	2.9
26	14	1673	U	2.9
26	14	2895	U	2.9
29	21	199	ARG	2.9
49	K8	14	ARG	2.9
5	4E	129	ILE	2.9
4	32	186	LEU	2.9
33	61	58	LEU	2.9
39	65	56	LEU	2.9
42	D8	35	LEU	2.9
12	3I	87	GLY	2.9
20	BA	103	GLY	2.9

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Mol	Chain	Res	Type	RSRZ
29	29	160	TYR	2.9
37	88	86	GLY	2.9
26	1H	1379	A	2.9
26	1H	2134	A	2.9
26	1H	2274	A	2.9
26	14	507	A	2.9
26	14	957	A	2.9
26	14	2748	A	2.9
45	G8	40	GLU	2.9
19	AA	4	SER	2.9
19	AA	12	ASP	2.9
48	J8	17	SER	2.9
28	19	98	VAL	2.9
32	51	52	VAL	2.9
36	35	141	ALA	2.9
42	D8	55	ALA	2.9
4	32	79	PHE	2.9
42	95	79	VAL	2.9
46	D5	69	THR	2.9
1	13	1132	C	2.9
1	1G	528	C	2.9
5	4E	14	ARG	2.9
26	1H	791	C	2.9
26	1H	2586	C	2.9
26	14	1781	C	2.9
27	1J	60	C	2.9
1	13	1133	G	2.9
1	13	1139	G	2.9
1	1G	585	G	2.9
26	1H	270(W)	G	2.9
26	1H	2250	G	2.9
2	12	187	LEU	2.9
26	1H	1078	U	2.9
26	1H	1833	U	2.9
26	14	2554	U	2.9
29	21	35	GLN	2.9
12	3A	48	PRO	2.9
20	BI	98	PRO	2.9
36	35	8	PRO	2.9
48	F5	75	GLU	2.9
1	13	439	A	2.9
1	1G	766	A	2.9

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Mol	Chain	Res	Type	RSRZ
23	2L	77	A	2.9
26	1H	1247	A	2.9
26	14	1111	A	2.9
26	14	1265	A	2.9
14	5I	5	ALA	2.9
28	11	4	LYS	2.9
36	35	131	SER	2.9
30	31	163	VAL	2.9
46	D5	173	ALA	2.9
6	52	80	ARG	2.9
54	Q8	46	ARG	2.9
18	9I	85	LEU	2.9
40	B8	9	LEU	2.9
1	13	762	C	2.9
1	13	1402	C	2.9
1	1G	812	C	2.9
4	32	124	GLY	2.9
8	72	55	GLY	2.9
26	1H	39	C	2.9
26	1H	665	C	2.9
26	1H	1049	C	2.9
26	1H	2084	C	2.9
26	1H	2350	C	2.9
26	14	2787	C	2.9
26	14	639	U	2.9
26	14	1926	U	2.9
26	14	2492	U	2.9
42	D8	9	GLY	2.9
1	13	251	G	2.9
1	13	1182	G	2.9
1	13	1526	G	2.9
14	5I	14	PRO	2.9
22	1L	19	G	2.9
26	14	771	G	2.9
6	5E	42	GLU	2.9
5	42	153	LYS	2.9
10	1A	55	LYS	2.9
13	4I	36	LYS	2.9
52	J5	10	LYS	2.9
29	21	70	ALA	2.9
32	59	150	ALA	2.9
37	45	27	VAL	2.9

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Mol	Chain	Res	Type	RSRZ
46	D5	93	ASP	2.9
46	D5	113	ALA	2.9
2	1E	235	SER	2.9
9	82	59	PHE	2.9
1	1G	814	A	2.9
1	1G	819	A	2.9
10	1A	46	ARG	2.9
36	78	133	SER	2.9
23	2L	73	A	2.9
26	1H	1274	A	2.9
26	1H	1536	A	2.9
26	1H	2810	A	2.9
7	62	124	LEU	2.9
12	3I	27	LEU	2.9
33	69	140	LEU	2.9
41	85	95	LEU	2.9
46	H8	120	ILE	2.9
46	D5	144	LEU	2.9
18	9I	48	GLY	2.8
36	35	22	GLY	2.8
2	12	202	PRO	2.8
1	13	241	C	2.8
1	13	267	C	2.8
1	13	322	C	2.8
1	1G	1384	C	2.8
1	1G	1393	U	2.8
23	2K	69	C	2.8
3	22	150	LYS	2.8
12	3A	47	LYS	2.8
14	5A	46	GLU	2.8
26	14	2039	C	2.8
26	14	2789	C	2.8
34	15	65	LYS	2.8
41	85	51	LYS	2.8
1	1G	1491	G	2.8
5	42	86	ALA	2.8
20	BI	76	ALA	2.8
22	1K	46	G	2.8
26	14	717	G	2.8
32	51	17	VAL	2.8
7	62	94	ARG	2.8
33	61	115	ALA	2.8

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Mol	Chain	Res	Type	RSRZ
8	72	4	ASP	2.8
28	19	99	ASP	2.8
49	G5	45	SER	2.8
6	52	98	LEU	2.8
7	62	54	THR	2.8
9	8E	19	LEU	2.8
10	1I	81	THR	2.8
42	D8	45	THR	2.8
42	95	45	THR	2.8
1	13	695	A	2.8
1	1G	243	A	2.8
1	1G	969	A	2.8
1	1G	975	A	2.8
26	1H	1760	A	2.8
26	14	777	A	2.8
26	14	2278	A	2.8
26	14	2810	A	2.8
37	88	24	GLY	2.8
38	98	91	GLN	2.8
5	42	121	LYS	2.8
31	41	47	LYS	2.8
32	51	13	LYS	2.8
52	N8	37	LYS	2.8
1	1G	1510	U	2.8
26	14	2423	U	2.8
1	13	701	C	2.8
1	1G	967	C	2.8
1	1G	1439	C	2.8
1	1G	1463	C	2.8
2	12	85	ALA	2.8
26	1H	2456	C	2.8
26	14	2145	C	2.8
26	14	2275	C	2.8
37	45	102	VAL	2.8
48	J8	77	ALA	2.8
29	29	113	PHE	2.8
7	62	59	LEU	2.8
8	72	111	ILE	2.8
30	39	28	ILE	2.8
34	15	101	HIS	2.8
36	78	47	ASP	2.8
41	C8	39	LEU	2.8

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Mol	Chain	Res	Type	RSRZ
41	85	83	LEU	2.8
43	A5	107	LEU	2.8
46	D5	41	LEU	2.8
41	85	29	SER	2.8
1	13	292	G	2.8
1	13	774	G	2.8
1	13	1064	G	2.8
1	1G	22	G	2.8
1	1G	963	G	2.8
26	1H	715	G	2.8
26	14	592	G	2.8
26	14	1266	G	2.8
26	14	2751	G	2.8
1	13	632	A	2.8
1	13	687	A	2.8
43	A5	110	LYS	2.8
45	C5	26	LYS	2.8
30	39	200	GLU	2.8
42	D8	98	GLU	2.8
5	42	61	TYR	2.8
6	52	33	TYR	2.8
33	69	18	VAL	2.8
34	58	53	VAL	2.8
44	F8	68	ARG	2.8
1	13	1341	U	2.8
3	22	53	ALA	2.8
2	1E	40	HIS	2.8
15	6I	34	LEU	2.8
34	15	87	LEU	2.8
39	65	54	LEU	2.8
47	E5	36	ILE	2.8
48	F5	85	LEU	2.8
26	1H	378	C	2.8
26	14	1304	C	2.8
26	14	1754	C	2.8
31	41	81	LYS	2.8
37	45	85	LYS	2.8
9	8E	30	GLY	2.8
16	7I	30	GLY	2.8
48	J8	28	GLY	2.8
4	3E	37	PRO	2.8
3	2E	162	GLN	2.8

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Mol	Chain	Res	Type	RSRZ
26	1H	2009	G	2.8
26	14	690	G	2.8
26	14	759	G	2.8
46	D5	177	PRO	2.8
1	13	349	A	2.8
2	12	84	GLU	2.8
4	32	145	GLU	2.8
26	14	2054	A	2.8
45	G8	64	GLU	2.8
4	32	47	ARG	2.8
16	7I	26	ARG	2.8
29	29	47	VAL	2.8
36	78	19	VAL	2.8
5	42	6	PHE	2.8
14	5A	5	ALA	2.8
29	29	67	PHE	2.8
43	E8	89	ALA	2.8
7	6E	124	LEU	2.8
10	1I	65	LEU	2.8
13	4A	56	LEU	2.8
15	6I	82	ILE	2.8
20	BI	13	LEU	2.8
33	69	77	LEU	2.8
31	49	97	ASP	2.8
41	85	30	LYS	2.8
1	13	308	C	2.8
1	1G	1228	C	2.8
23	2L	75	C	2.8
26	1H	1402	C	2.8
26	1H	2175	C	2.8
26	14	697	C	2.8
26	14	897	C	2.8
26	14	2620	C	2.8
32	59	38	SER	2.8
30	39	71	GLY	2.8
32	59	48	GLY	2.8
38	98	39	PRO	2.8
45	G8	82	PRO	2.8
20	BI	86	ARG	2.7
40	75	46	GLU	2.7
50	L8	57	GLU	2.7
12	3A	104	VAL	2.7

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Mol	Chain	Res	Type	RSRZ
31	41	37	VAL	2.7
32	59	44	VAL	2.7
1	13	575	G	2.7
1	1G	26	A	2.7
7	6E	147	ALA	2.7
19	AA	74	PHE	2.7
29	21	123	ALA	2.7
37	88	114	ALA	2.7
4	3E	54	TYR	2.7
10	1A	88	LEU	2.7
26	1H	270(Y)	G	2.7
26	1H	1839	G	2.7
26	14	599	G	2.7
26	14	1980	G	2.7
40	75	45	PHE	2.7
37	88	42	ILE	2.7
45	C5	14	LEU	2.7
48	F5	82	LEU	2.7
1	1G	956	U	2.7
3	2E	108	ASN	2.7
50	H5	18	ASP	2.7
8	72	87	SER	2.7
8	72	67	PRO	2.7
3	22	38	ARG	2.7
11	2I	91	ARG	2.7
1	13	897	C	2.7
1	1G	555	C	2.7
1	1G	1063	C	2.7
1	1G	1066	C	2.7
26	1H	270(P)	C	2.7
26	1H	1270	C	2.7
26	14	736	C	2.7
26	14	1925	C	2.7
39	65	8	GLU	2.7
7	62	69	VAL	2.7
32	59	43	VAL	2.7
44	F8	51	VAL	2.7
3	22	87	LEU	2.7
7	62	16	LEU	2.7
18	9I	78	LEU	2.7
33	69	53	ALA	2.7
4	3E	123	HIS	2.7

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Mol	Chain	Res	Type	RSRZ
26	1H	1655	A	2.7
26	14	2809	A	2.7
1	13	1034	G	2.7
1	1G	14	U	2.7
1	1G	164	U	2.7
1	1G	799	G	2.7
1	1G	953	G	2.7
1	1G	1391	U	2.7
26	1H	588	U	2.7
26	1H	696	G	2.7
26	1H	2604	U	2.7
26	14	600	G	2.7
26	14	715	G	2.7
26	14	1346	G	2.7
26	14	2421	G	2.7
41	85	44	ASN	2.7
3	2E	15	THR	2.7
5	42	98	THR	2.7
10	1A	92	THR	2.7
50	H5	40	THR	2.7
10	1I	93	GLY	2.7
19	AA	8	GLY	2.7
29	21	89	ASP	2.7
10	1I	37	PRO	2.7
10	1A	91	PRO	2.7
33	69	137	PRO	2.7
30	39	50	SER	2.7
48	J8	8	SER	2.7
15	6A	71	GLN	2.7
32	51	139	GLN	2.7
54	M5	43	GLN	2.7
28	11	18	VAL	2.7
29	21	116	VAL	2.7
1	13	1399	C	2.7
1	1G	824	C	2.7
2	12	39	ILE	2.7
7	6E	121	ALA	2.7
9	8E	50	LEU	2.7
10	1I	27	ALA	2.7
26	14	641	C	2.7
26	14	1988	C	2.7
29	29	52	LEU	2.7

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Mol	Chain	Res	Type	RSRZ
30	39	58	ALA	2.7
33	61	55	ALA	2.7
46	D5	172	ALA	2.7
48	F5	15	ALA	2.7
15	6A	44	LYS	2.7
26	1H	1759	A	2.7
26	14	492	A	2.7
26	14	637	A	2.7
26	14	646	A	2.7
26	14	689	A	2.7
26	14	1553	A	2.7
26	14	2051	A	2.7
26	14	2059	A	2.7
1	1G	723	U	2.7
2	1E	190	THR	2.7
19	AI	79	THR	2.7
26	1H	273(E)	U	2.7
26	1H	2514	U	2.7
26	14	384	U	2.7
26	14	822	U	2.7
26	14	1679	U	2.7
26	14	2398	U	2.7
29	29	158	GLY	2.7
35	25	96	THR	2.7
45	G8	83	THR	2.7
28	11	99	ASP	2.7
32	51	36	PRO	2.7
42	D8	50	PRO	2.7
1	13	438	G	2.7
22	1L	49	G	2.7
26	1H	2307	G	2.7
26	1H	2574	G	2.7
26	14	2891	G	2.7
4	32	157	LEU	2.7
4	3E	79	PHE	2.7
6	52	25	ILE	2.7
42	D8	71	LEU	2.7
14	5I	37	PHE	2.7
45	G8	65	ALA	2.7
2	12	74	LYS	2.7
3	2E	199	LYS	2.7
4	32	169	LYS	2.7

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Mol	Chain	Res	Type	RSRZ
29	21	155	LYS	2.7
48	J8	92	LYS	2.7
53	L5	2	LYS	2.7
28	19	250	TRP	2.7
1	13	899	C	2.7
1	1G	764	C	2.7
22	1L	27	C	2.7
26	14	1399	C	2.7
26	14	2021	C	2.7
2	12	82	ARG	2.7
28	19	69	ARG	2.7
47	E5	44	ARG	2.7
2	12	14	GLY	2.7
4	3E	29	PRO	2.7
14	5A	51	GLY	2.7
31	41	177	GLY	2.7
1	13	313	A	2.7
1	13	321	A	2.7
1	13	819	A	2.7
1	1G	195	A	2.7
26	1H	2547	U	2.7
26	14	1019	U	2.7
26	14	2656	U	2.7
7	62	139	GLU	2.7
12	3I	43	VAL	2.7
30	39	88	VAL	2.7
31	49	109	VAL	2.7
31	49	149	VAL	2.7
33	69	145	VAL	2.7
34	58	96	GLU	2.7
38	98	73	VAL	2.7
40	75	140	GLU	2.7
47	E5	81	VAL	2.7
2	1E	215	LEU	2.7
3	22	111	LEU	2.7
17	8A	22	LEU	2.7
34	15	34	LEU	2.7
9	8E	33	PHE	2.6
20	BA	74	LYS	2.6
40	B8	45	PHE	2.6
42	95	84	LYS	2.6
40	75	135	ALA	2.6

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Mol	Chain	Res	Type	RSRZ
46	H8	21	ALA	2.6
26	1H	638	G	2.6
26	1H	1792	G	2.6
26	1H	2112	G	2.6
26	14	1325	G	2.6
26	14	2166	G	2.6
9	82	92	TYR	2.6
30	39	97	TYR	2.6
13	4A	108	ARG	2.6
47	E5	39	ARG	2.6
22	1K	69	C	2.6
26	1H	40	C	2.6
26	1H	1075	C	2.6
26	1H	1941	C	2.6
26	1H	2594	C	2.6
26	14	270(Q)	C	2.6
4	3E	167	GLY	2.6
12	3A	5	PRO	2.6
29	29	86	PRO	2.6
50	H5	41	PRO	2.6
1	1G	13	U	2.6
2	1E	213	LEU	2.6
3	2E	111	LEU	2.6
3	22	76	VAL	2.6
5	4E	68	GLU	2.6
7	62	87	VAL	2.6
17	8A	84	LEU	2.6
16	7I	33	ILE	2.6
20	BA	30	LYS	2.6
26	1H	380	U	2.6
26	1H	403	U	2.6
28	19	102	LYS	2.6
32	59	34	GLU	2.6
33	69	38	LEU	2.6
35	68	120	GLU	2.6
37	45	96	VAL	2.6
39	A8	8	GLU	2.6
41	C8	90	VAL	2.6
42	95	72	VAL	2.6
26	14	718	A	2.6
31	49	88	ILE	2.6
34	15	30	ILE	2.6

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Mol	Chain	Res	Type	RSRZ
47	E5	46	LYS	2.6
26	1H	1246	A	2.6
3	2E	133	ALA	2.6
7	62	65	ALA	2.6
29	29	156	MET	2.6
37	88	83	MET	2.6
40	B8	80	SER	2.6
40	75	131	ALA	2.6
43	A5	58	ALA	2.6
44	F8	84	ALA	2.6
1	13	1171	G	2.6
1	1G	184	G	2.6
1	1G	823	G	2.6
1	1G	1193	G	2.6
1	1G	1379	G	2.6
1	1G	1385	G	2.6
1	1G	1523	G	2.6
4	3E	73	ARG	2.6
5	42	27	ARG	2.6
7	6E	149	ARG	2.6
26	1H	101	G	2.6
26	1H	928	G	2.6
26	1H	1649	G	2.6
26	1H	2210	G	2.6
26	14	651	G	2.6
26	14	2124	G	2.6
35	25	48	PRO	2.6
36	78	109	GLY	2.6
45	C5	22	GLY	2.6
10	1I	80	LYS	2.6
10	1A	99	LYS	2.6
14	5I	13	THR	2.6
1	13	339	C	2.6
1	13	345	C	2.6
14	5A	53	LEU	2.6
16	7I	20	VAL	2.6
18	9A	76	LEU	2.6
26	1H	1064	C	2.6
26	14	456	C	2.6
38	98	9	LYS	2.6
41	C8	19	LYS	2.6
30	39	124	LEU	2.6

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Mol	Chain	Res	Type	RSRZ
45	G8	31	LEU	2.6
3	2E	152	ILE	2.6
6	5E	31	GLU	2.6
11	2A	92	GLU	2.6
36	78	70	GLN	2.6
26	14	2068	U	2.6
35	25	80	ASP	2.6
13	4A	75	ALA	2.6
28	19	53	PHE	2.6
29	21	122	PHE	2.6
47	E5	18	ALA	2.6
8	72	115	SER	2.6
26	14	829	A	2.6
26	14	953	A	2.6
27	16	58	A	2.6
29	21	132	HIS	2.6
29	29	144	ARG	2.6
33	69	103	ARG	2.6
36	78	50	ARG	2.6
43	A5	84	ARG	2.6
18	9I	80	PRO	2.6
33	61	106	GLY	2.6
46	H8	147	GLY	2.6
2	1E	179	LYS	2.6
1	13	350	G	2.6
1	13	493	G	2.6
2	1E	15	VAL	2.6
3	22	15	THR	2.6
4	3E	89	THR	2.6
12	3I	36	VAL	2.6
20	BA	104	LEU	2.6
26	1H	954	G	2.6
26	14	545	G	2.6
26	14	1044	G	2.6
31	49	3	LEU	2.6
31	49	135	LEU	2.6
34	58	32	THR	2.6
38	98	20	LEU	2.6
8	72	132	GLU	2.6
30	31	27	GLU	2.6
46	D5	98	MET	2.6
10	1A	20	ALA	2.6

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Mol	Chain	Res	Type	RSRZ
29	21	68	ALA	2.6
33	61	53	ALA	2.6
33	69	46	ALA	2.6
36	78	134	ALA	2.6
26	14	1600	C	2.6
27	1J	90	C	2.6
1	1G	1512	U	2.6
26	1H	2423	U	2.6
10	1A	35	SER	2.6
20	BI	11	SER	2.6
28	19	96	HIS	2.6
30	39	31	HIS	2.6
4	32	76	ARG	2.6
29	29	37	ARG	2.6
38	55	68	ARG	2.6
1	1G	781	A	2.6
26	1H	547	A	2.6
30	39	7	TYR	2.6
32	51	175	LYS	2.6
45	G8	63	LYS	2.6
21	1F	16	GLY	2.6
42	95	48	GLY	2.6
47	E5	83	PRO	2.6
48	F5	84	GLY	2.6
3	22	101	LEU	2.6
42	95	25	LEU	2.6
48	J8	94	LEU	2.6
54	M5	50	LEU	2.6
12	3A	82	VAL	2.6
12	3A	110	VAL	2.6
15	6I	22	THR	2.6
28	11	141	VAL	2.6
33	69	79	ILE	2.6
34	15	122	VAL	2.6
36	35	30	THR	2.6
33	61	99	GLU	2.6
38	55	91	GLN	2.6
54	M5	35	GLN	2.6
2	12	37	ASN	2.6
2	12	55	PHE	2.6
3	2E	63	ASN	2.6
12	3A	68	ALA	2.6

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Mol	Chain	Res	Type	RSRZ
20	BI	52	ALA	2.6
1	1G	21	G	2.5
5	42	147	ASP	2.6
24	3K	63	G	2.5
26	1H	647	G	2.5
26	1H	1056	G	2.5
26	14	648	G	2.5
26	14	1568	G	2.5
26	14	2024	G	2.5
26	14	2052	G	2.5
1	1G	571	U	2.5
15	6I	68	ARG	2.5
16	7I	75	ARG	2.5
24	3K	32	U	2.5
26	1H	639	U	2.5
26	1H	1898	U	2.5
26	14	1433	U	2.5
26	14	1523	U	2.5
26	14	1693	U	2.5
26	14	1779	U	2.5
32	59	54	ARG	2.5
36	35	55	ARG	2.5
1	13	280	C	2.5
1	1G	1129	C	2.5
26	1H	1076	C	2.5
26	14	1908	C	2.5
36	78	36	LYS	2.5
1	1G	196	A	2.5
1	1G	694	A	2.5
1	1G	728	A	2.5
2	1E	167	PRO	2.5
8	72	76	PRO	2.5
22	1K	9	A	2.5
23	2K	38	A	2.5
26	1H	1057	A	2.5
26	1H	1510	A	2.5
26	1H	2005	A	2.5
26	1H	2820	A	2.5
26	14	195	A	2.5
26	14	1536	A	2.5
20	BI	102	GLY	2.5
42	95	30	GLY	2.5

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Mol	Chain	Res	Type	RSRZ
51	M8	41	PRO	2.5
29	21	151	TYR	2.5
33	61	6	LEU	2.5
39	A8	80	LEU	2.5
2	12	185	ILE	2.5
34	58	16	ILE	2.5
34	15	62	VAL	2.5
36	78	114	ILE	2.5
42	95	52	VAL	2.5
3	2E	118	GLN	2.5
5	4E	83	GLU	2.5
5	42	56	GLN	2.5
8	7E	42	GLU	2.5
18	9I	82	THR	2.5
29	29	163	GLU	2.5
31	41	168	GLU	2.5
9	82	33	PHE	2.5
10	1I	11	PHE	2.5
28	11	6	PHE	2.5
38	55	71	GLN	2.5
31	41	46	ALA	2.5
40	B8	127	ALA	2.5
52	J5	53	ALA	2.5
53	P8	45	ALA	2.5
2	12	21	ARG	2.5
14	5I	26	ARG	2.5
17	8A	81	ARG	2.5
28	11	200	ASP	2.5
37	88	56	ARG	2.5
46	H8	81	ARG	2.5
26	14	380	U	2.5
34	58	84	LYS	2.5
36	78	131	SER	2.5
48	J8	91	LYS	2.5
53	L5	48	LYS	2.5
1	1G	776	G	2.5
1	1G	895	G	2.5
26	1H	1661	G	2.5
24	3K	48	C	2.5
26	1H	1663	C	2.5
2	12	98	LEU	2.5
14	5I	44	LEU	2.5

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Mol	Chain	Res	Type	RSRZ
16	7I	6	LEU	2.5
32	59	103	LEU	2.5
32	59	166	GLY	2.5
33	61	128	LEU	2.5
36	35	105	LEU	2.5
39	A8	48	LEU	2.5
43	A5	82	LEU	2.5
2	1E	172	ILE	2.5
16	7I	19	ILE	2.5
31	49	160	VAL	2.5
34	15	4	TYR	2.5
38	98	94	TYR	2.5
44	B5	69	TYR	2.5
26	14	6	A	2.5
26	14	2654	A	2.5
7	6E	11	GLN	2.5
20	BA	45	GLN	2.5
47	E5	45	PHE	2.5
3	2E	126	ARG	2.5
3	22	156	ARG	2.5
6	5E	86	ARG	2.5
9	82	121	ARG	2.5
17	8I	91	ARG	2.5
36	78	79	ARG	2.5
40	75	111	ARG	2.5
41	85	14	HIS	2.5
52	J5	23	HIS	2.5
3	2E	135	LYS	2.5
1	13	1159	U	2.5
1	13	1498	U	2.5
1	1G	1472	U	2.5
1	1G	1506	U	2.5
26	14	1796	U	2.5
3	22	91	LEU	2.5
4	32	155	LEU	2.5
4	32	181	MET	2.5
31	49	43	LEU	2.5
46	D5	167	PRO	2.5
50	H5	26	LEU	2.5
51	M8	7	PRO	2.5
12	3A	87	GLY	2.5
17	8A	80	GLY	2.5

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Mol	Chain	Res	Type	RSRZ
29	21	77	ILE	2.5
37	45	30	GLY	2.5
41	85	80	ILE	2.5
46	H8	115	GLY	2.5
50	H5	43	ILE	2.5
51	M8	22	ILE	2.5
2	12	71	VAL	2.5
2	12	164	VAL	2.5
30	31	132	VAL	2.5
30	39	4	VAL	2.5
1	13	817	C	2.5
1	13	1134	G	2.5
1	13	1471	G	2.5
1	1G	524	G	2.5
3	2E	184	TYR	2.5
26	1H	2081	C	2.5
26	1H	2774	C	2.5
26	14	791	C	2.5
26	14	2420	C	2.5
23	2L	5	G	2.5
26	1H	2246	G	2.5
26	1H	2334	G	2.5
26	1H	2570	G	2.5
26	1H	2677	G	2.5
26	14	188	G	2.5
26	14	805	G	2.5
26	14	2513	G	2.5
26	14	2793	G	2.5
35	25	7	TYR	2.5
2	12	50	GLU	2.5
17	8A	58	GLU	2.5
36	78	74	GLU	2.5
4	3E	111	ALA	2.5
19	AA	75	ALA	2.5
30	31	198	ALA	2.5
39	A8	5	THR	2.5
45	C5	16	ALA	2.5
46	H8	164	ALA	2.5
1	13	900	A	2.5
1	13	969	A	2.5
26	14	782	A	2.5
26	14	1825	A	2.5

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Mol	Chain	Res	Type	RSRZ
26	14	2361	A	2.5
26	14	2432	A	2.5
31	41	170	ARG	2.5
10	1A	90	LEU	2.5
36	78	62	LEU	2.5
30	31	81	PRO	2.5
1	13	1135	U	2.5
6	5E	58	GLY	2.5
26	14	270(L)	U	2.5
32	51	120	GLY	2.5
39	A8	22	GLY	2.5
46	D5	114	GLY	2.5
49	G5	41	ILE	2.5
2	1E	71	VAL	2.5
42	D8	58	VAL	2.5
46	D5	39	VAL	2.5
46	D5	141	VAL	2.5
34	58	42	TRP	2.5
9	82	12	GLU	2.5
30	31	139	PHE	2.5
39	65	112	PHE	2.5
41	85	106	PHE	2.5
7	62	134	ALA	2.5
29	29	68	ALA	2.5
38	98	63	ARG	2.5
47	I8	40	GLN	2.5
48	F5	76	ARG	2.5
1	1G	19	C	2.5
23	2L	40	C	2.5
24	3K	69	C	2.5
26	1H	1295	C	2.5
26	14	772	C	2.5
26	14	2040	C	2.5
26	14	2573	C	2.5
37	45	21	THR	2.5
41	85	85	LYS	2.5
48	F5	23	LYS	2.5
1	13	765	G	2.5
1	13	1435	G	2.5
26	1H	270(R)	G	2.5
26	1H	1271	G	2.5
26	1H	2125	G	2.5

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Mol	Chain	Res	Type	RSRZ
26	1H	2655	G	2.5
26	14	124	G	2.5
26	14	636	G	2.5
26	14	666	G	2.5
26	14	1400	G	2.5
26	14	2717	G	2.5
1	1G	572	A	2.5
26	14	654(T)	A	2.5
33	69	133	HIS	2.5
29	21	60	ASN	2.5
5	42	10	MET	2.4
13	4A	83	ASP	2.4
34	15	99	LEU	2.4
36	78	85	LEU	2.4
48	J8	85	LEU	2.4
6	52	51	PRO	2.4
8	72	131	GLY	2.4
14	5A	55	GLY	2.4
15	6I	23	GLY	2.4
20	BI	96	GLY	2.4
45	C5	17	SER	2.4
49	K8	63	VAL	2.4
49	G5	25	VAL	2.4
5	42	45	PHE	2.4
12	3A	113	ARG	2.4
46	D5	145	GLU	2.4
47	E5	11	ARG	2.4
3	22	135	LYS	2.4
5	42	57	LYS	2.4
9	8E	88	TYR	2.4
30	39	166	ALA	2.4
41	C8	116	ALA	2.4
1	1G	241	C	2.4
26	1H	273(F)	C	2.4
26	14	2142	C	2.4
26	14	2785	C	2.4
7	62	144	MET	2.4
8	72	10	LEU	2.4
8	72	36	LEU	2.4
46	H8	155	LEU	2.4
49	K8	44	LEU	2.4
1	1G	300	A	2.4

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Mol	Chain	Res	Type	RSRZ
26	1H	959	A	2.4
26	14	532	A	2.4
1	13	28	G	2.4
1	13	317	G	2.4
1	13	885	G	2.4
1	1G	191(E)	G	2.4
1	1G	836	G	2.4
1	1G	1338	G	2.4
3	2E	73	PRO	2.4
26	1H	629	G	2.4
26	1H	2276	G	2.4
26	1H	2807	G	2.4
26	14	2529	G	2.4
28	19	270	ILE	2.4
33	69	120	ILE	2.4
45	C5	66	PRO	2.4
4	32	90	GLY	2.4
29	21	188	VAL	2.4
41	C8	87	GLY	2.4
30	39	15	SER	2.4
37	45	6	ARG	2.4
46	H8	142	SER	2.4
50	H5	29	ARG	2.4
1	13	261	U	2.4
1	13	294	U	2.4
1	1G	191(D)	U	2.4
26	1H	1693	U	2.4
26	14	1659	U	2.4
41	85	79	PHE	2.4
45	G8	26	LYS	2.4
3	22	113	ALA	2.4
11	2I	94	ALA	2.4
13	4A	18	ALA	2.4
30	39	26	ALA	2.4
31	41	151	ALA	2.4
31	49	46	ALA	2.4
9	82	62	TYR	2.4
29	29	90	THR	2.4
10	1A	56	HIS	2.4
31	41	173	LEU	2.4
37	45	17	LEU	2.4
42	D8	39	LEU	2.4

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Mol	Chain	Res	Type	RSRZ
28	19	203	ASN	2.4
36	35	84	ASN	2.4
43	A5	40	ASN	2.4
2	12	127	ILE	2.4
2	12	183	PRO	2.4
7	6E	42	ILE	2.4
10	1A	50	ILE	2.4
1	13	75	C	2.4
13	4I	113	PRO	2.4
26	14	1607	C	2.4
29	21	74	PRO	2.4
30	39	102	PRO	2.4
32	59	10	PRO	2.4
46	D5	133	ILE	2.4
22	1L	29	C	2.4
24	3K	51	C	2.4
8	72	54	ASP	2.4
13	4I	112	GLY	2.4
34	15	58	ASP	2.4
47	E5	28	GLY	2.4
1	13	919	A	2.4
1	13	1004	A	2.4
1	13	1492	A	2.4
26	1H	2662	A	2.4
26	14	590	A	2.4
26	14	2013	A	2.4
2	1E	147	LYS	2.4
2	12	96	ARG	2.4
3	22	127	ARG	2.4
4	3E	151	LYS	2.4
9	8E	113	LYS	2.4
9	82	70	LYS	2.4
14	5A	15	LYS	2.4
30	39	137	LYS	2.4
32	51	170	ARG	2.4
41	85	28	ARG	2.4
1	13	916	G	2.4
1	1G	577	G	2.4
4	3E	80	GLU	2.4
11	2I	43	SER	2.4
20	BA	46	GLU	2.4
22	1L	53	G	2.4

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Mol	Chain	Res	Type	RSRZ
26	1H	1248	G	2.4
26	1H	1277	G	2.4
26	14	629	G	2.4
26	14	1106	G	2.4
26	14	2239	G	2.4
27	16	87	G	2.4
29	21	94	GLU	2.4
37	45	104	PHE	2.4
36	35	89	ALA	2.4
1	1G	1281	U	2.4
22	1K	33	U	2.4
26	1H	1097	U	2.4
26	1H	2172	U	2.4
8	7E	94	TYR	2.4
29	21	160	TYR	2.4
9	82	7	THR	2.4
10	1I	92	THR	2.4
13	4A	20	THR	2.4
34	15	73	THR	2.4
8	7E	1	MET	2.4
52	J5	43	HIS	2.4
12	3I	10	LEU	2.4
17	8A	6	LEU	2.4
32	51	171	LEU	2.4
33	69	101	LEU	2.4
2	1E	214	ILE	2.4
46	D5	146	ILE	2.4
8	72	72	PRO	2.4
33	69	119	PRO	2.4
13	4A	74	VAL	2.4
29	21	124	GLY	2.4
29	29	71	GLY	2.4
32	51	141	VAL	2.4
32	51	174	GLY	2.4
42	95	46	VAL	2.4
54	Q8	38	GLY	2.4
54	M5	22	VAL	2.4
12	3A	114	LYS	2.4
20	BI	79	ARG	2.4
29	29	36	ARG	2.4
35	25	31	LYS	2.4
41	85	93	LYS	2.4

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Mol	Chain	Res	Type	RSRZ
45	G8	84	ARG	2.4
47	E5	14	ARG	2.4
48	F5	26	ARG	2.4
49	G5	30	ARG	2.4
1	1G	880	C	2.4
1	1G	899	C	2.4
1	1G	1426	C	2.4
26	1H	967	C	2.4
26	1H	2510	C	2.4
26	14	2791	C	2.4
2	12	57	PHE	2.4
26	1H	2657	A	2.4
26	14	654(A)	A	2.4
26	14	2657	A	2.4
26	14	2835	A	2.4
42	D8	23	GLU	2.4
42	D8	93	GLU	2.4
3	2E	53	ALA	2.4
3	2E	200	ALA	2.4
3	22	168	ALA	2.4
18	9I	60	ALA	2.4
30	39	146	ALA	2.4
37	88	44	ALA	2.4
31	41	100	TRP	2.4
1	13	690	G	2.4
1	1G	29	G	2.4
22	1L	15	G	2.4
26	1H	636	G	2.4
26	1H	969	U	2.4
26	1H	1647	G	2.4
26	1H	2399	G	2.4
26	14	798	G	2.4
26	14	975	G	2.4
26	14	2455	G	2.4
26	14	2802	G	2.4
26	14	2894	G	2.4
33	69	78	THR	2.4
17	8I	43	LEU	2.4
33	69	116	LEU	2.4
31	41	17	PRO	2.4
2	12	197	VAL	2.3
3	2E	130	VAL	2.3

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Mol	Chain	Res	Type	RSRZ
18	9I	86	VAL	2.3
20	BA	34	LYS	2.3
32	51	26	VAL	2.3
33	69	113	ARG	2.3
40	B8	89	VAL	2.3
41	85	15	LYS	2.3
42	D8	24	LYS	2.3
13	4I	6	GLY	2.3
29	21	193	GLY	2.3
47	E5	8	GLY	2.3
39	65	87	PHE	2.3
3	22	60	ALA	2.3
32	59	32	GLU	2.3
37	88	121	ALA	2.3
41	85	35	ALA	2.3
26	14	1767	C	2.3
26	1H	1096	A	2.3
26	1H	2448	A	2.3
26	14	1609	A	2.3
26	14	2057	A	2.3
26	14	2478	A	2.3
15	6I	25	THR	2.3
17	8I	76	LEU	2.3
34	58	3	THR	2.3
1	13	249	U	2.3
1	1G	1062	U	2.3
26	14	270(M)	U	2.3
26	14	1014	U	2.3
26	14	2716	U	2.3
41	C8	17	ILE	2.3
41	85	88	ILE	2.3
48	J8	7	ILE	2.3
8	72	101	PRO	2.3
1	13	887	G	2.3
1	13	941	G	2.3
2	1E	174	VAL	2.3
3	22	103	VAL	2.3
9	8E	51	ARG	2.3
10	1A	45	ARG	2.3
26	1H	1845	G	2.3
26	14	2211	G	2.3
26	14	2373	G	2.3

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Mol	Chain	Res	Type	RSRZ
26	14	2582	G	2.3
29	21	196	VAL	2.3
38	98	32	GLY	2.3
38	98	92	GLY	2.3
46	D5	22	GLY	2.3
28	19	28	GLU	2.3
31	41	156	ASP	2.3
7	6E	2	ALA	2.3
37	45	136	ALA	2.3
17	8A	16	GLN	2.3
32	59	41	MET	2.3
4	3E	176	LEU	2.3
4	32	58	LEU	2.3
17	8I	74	LEU	2.3
31	41	103	LEU	2.3
46	D5	117	LEU	2.3
48	J8	82	LEU	2.3
50	L8	8	LEU	2.3
4	32	125	HIS	2.3
8	72	138	TRP	2.3
1	13	574	A	2.3
1	13	781	A	2.3
4	3E	68	TYR	2.3
26	1H	1882	C	2.3
26	1H	2128	C	2.3
26	14	2263	C	2.3
32	59	61	HIS	2.3
26	14	750	A	2.3
26	14	1365	A	2.3
26	14	2020	A	2.3
29	21	26	ILE	2.3
33	69	129	THR	2.3
26	1H	270(A)	A	2.3
16	7A	31	LYS	2.3
29	29	69	LYS	2.3
42	95	78	LYS	2.3
1	1G	561	U	2.3
2	1E	125	PRO	2.3
2	1E	137	ARG	2.3
3	2E	127	ARG	2.3
5	42	152	ARG	2.3
12	3I	15	ARG	2.3

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Mol	Chain	Res	Type	RSRZ
13	4A	110	ARG	2.3
26	14	504	U	2.3
28	19	36	PRO	2.3
32	59	36	PRO	2.3
52	N8	32	PRO	2.3
19	AA	60	VAL	2.3
42	D8	52	VAL	2.3
19	AA	54	GLY	2.3
20	BA	102	GLY	2.3
6	5E	32	ASN	2.3
41	C8	32	PHE	2.3
1	13	76	G	2.3
1	13	685	G	2.3
1	13	803	G	2.3
1	13	818	G	2.3
1	1G	1441	G	2.3
7	62	128	ALA	2.3
26	1H	180	G	2.3
26	1H	363(B)	G	2.3
26	14	628	G	2.3
26	14	1151	G	2.3
26	14	1674	G	2.3
26	14	2141	G	2.3
27	1J	23	G	2.3
29	21	28	ALA	2.3
30	31	130	ALA	2.3
40	B8	94	ALA	2.3
43	E8	77	ASP	2.3
2	12	196	LEU	2.3
3	22	33	LEU	2.3
3	22	204	LEU	2.3
35	68	122	LEU	2.3
36	78	99	LEU	2.3
42	95	38	LEU	2.3
13	4A	9	ILE	2.3
16	7I	36	ILE	2.3
28	19	151	LYS	2.3
34	15	109	LYS	2.3
37	88	123	HIS	2.3
41	85	54	LYS	2.3
43	A5	95	ILE	2.3
45	G8	94	LYS	2.3

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Mol	Chain	Res	Type	RSRZ
32	59	129	THR	2.3
10	1I	45	ARG	2.3
36	35	15	ARG	2.3
8	72	74	PRO	2.3
1	13	1189	C	2.3
1	1G	564	C	2.3
1	1G	797	C	2.3
13	4A	54	VAL	2.3
26	14	228	A	2.3
26	14	1018	C	2.3
26	14	1105	U	2.3
26	14	1618	A	2.3
29	29	93	VAL	2.3
36	78	83	VAL	2.3
36	35	78	PRO	2.3
26	1H	270(D)	C	2.3
26	1H	749	C	2.3
26	1H	1644	C	2.3
26	1H	1684	C	2.3
1	1G	2	U	2.3
26	1H	2491	U	2.3
26	14	1993	U	2.3
7	62	133	GLY	2.3
4	3E	34	GLU	2.3
5	4E	122	GLU	2.3
30	31	73	ALA	2.3
32	59	75	ALA	2.3
42	D8	34	GLU	2.3
52	J5	35	GLU	2.3
6	52	18	GLN	2.3
30	39	192	LEU	2.3
31	41	3	LEU	2.3
34	15	67	LEU	2.3
34	15	120	LEU	2.3
44	F8	82	GLN	2.3
10	1A	57	LYS	2.3
36	35	39	LYS	2.3
1	13	836	G	2.3
1	1G	902	G	2.3
10	1I	38	ILE	2.3
26	1H	270(N)	G	2.3
26	1H	952	G	2.3

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Mol	Chain	Res	Type	RSRZ
26	1H	1542	G	2.3
26	1H	2569	G	2.3
26	14	187	G	2.3
26	14	573	G	2.3
39	65	18	ILE	2.3
40	B8	42	ILE	2.3
46	D5	120	ILE	2.3
46	D5	124	ILE	2.3
55	3L	45	G	2.3
5	42	107	ARG	2.3
9	82	20	ARG	2.3
20	BI	22	ARG	2.3
31	49	71	THR	2.3
38	55	22	ARG	2.3
49	K8	51	ARG	2.3
3	22	120	VAL	2.3
5	42	70	PRO	2.3
29	29	75	VAL	2.3
30	39	11	VAL	2.3
30	39	92	PRO	2.3
41	C8	24	TYR	2.3
34	58	9	VAL	2.3
24	3K	60	U	2.3
26	1H	2449	U	2.3
26	14	1263	U	2.3
26	14	2047	U	2.3
55	3L	16	U	2.3
1	13	307	C	2.2
1	1G	768	A	2.2
1	1G	1145	C	2.2
1	1G	1466	C	2.2
22	1L	56	C	2.2
26	1H	548	A	2.2
26	1H	1257	C	2.2
26	1H	1685	C	2.2
26	1H	1909	C	2.2
26	14	183	C	2.2
26	14	462	C	2.2
26	14	1013	C	2.2
26	14	1608	A	2.2
26	14	2170	A	2.2
26	14	2240	C	2.2

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Mol	Chain	Res	Type	RSRZ
26	14	2456	C	2.2
26	14	2804	C	2.2
2	1E	63	MET	2.2
3	22	3	ASN	2.2
4	32	80	GLU	2.2
4	32	163	GLU	2.2
29	29	46	ALA	2.2
30	39	113	ALA	2.2
32	51	47	GLU	2.2
54	M5	56	GLU	2.2
4	32	94	LEU	2.2
18	9I	40	LEU	2.2
29	21	52	LEU	2.2
34	15	138	LEU	2.2
31	49	36	LYS	2.2
42	D8	68	LYS	2.2
36	35	87	ASP	2.2
40	B8	122	ASP	2.2
2	12	32	ILE	2.2
33	61	79	ILE	2.2
43	A5	6	ILE	2.2
46	D5	171	ILE	2.2
3	22	31	HIS	2.2
32	59	130	ARG	2.2
54	M5	7	HIS	2.2
2	1E	164	VAL	2.2
2	12	26	PRO	2.2
2	12	150	SER	2.2
4	3E	203	VAL	2.2
6	52	96	PRO	2.2
8	7E	101	PRO	2.2
10	1A	42	THR	2.2
9	8E	17	VAL	2.2
13	4I	98	VAL	2.2
19	AI	76	PRO	2.2
32	59	154	PRO	2.2
38	98	114	VAL	2.2
46	D5	126	VAL	2.2
47	E5	63	VAL	2.2
1	1G	238	G	2.2
1	1G	837	G	2.2
24	3K	53	G	2.2

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Mol	Chain	Res	Type	RSRZ
26	1H	1429	G	2.2
26	1H	1964	G	2.2
26	14	189	G	2.2
50	H5	14	GLY	2.2
4	32	93	PHE	2.2
26	1H	1113	U	2.2
26	1H	2504	U	2.2
26	14	206	U	2.2
26	14	270(F)	U	2.2
8	7E	133	LEU	2.2
9	8E	110	GLU	2.2
9	82	61	ALA	2.2
1	1G	120	A	2.2
1	1G	780	A	2.2
1	1G	974	A	2.2
4	3E	97	LEU	2.2
4	32	199	ASN	2.2
5	42	53	LEU	2.2
13	4A	52	GLU	2.2
15	6A	85	LEU	2.2
18	9I	83	GLU	2.2
37	45	105	GLU	2.2
38	98	101	ALA	2.2
39	65	55	ALA	2.2
19	AA	22	LEU	2.2
30	39	181	LEU	2.2
37	45	118	LEU	2.2
42	95	69	LYS	2.2
45	G8	43	ASN	2.2
46	H8	144	LEU	2.2
48	F5	6	GLU	2.2
26	1H	719	C	2.2
26	1H	900	A	2.2
48	J8	16	ASN	2.2
49	K8	41	ILE	2.2
3	22	59	ARG	2.2
30	31	119	ARG	2.2
40	B8	51	ARG	2.2
46	H8	32	HIS	2.2
48	J8	41	ARG	2.2
16	7I	69	THR	2.2
32	51	29	PRO	2.2

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Mol	Chain	Res	Type	RSRZ
34	58	28	THR	2.2
34	15	28	THR	2.2
36	78	97	PRO	2.2
40	B8	49	VAL	2.2
52	J5	46	CYS	2.2
6	52	59	TYR	2.2
29	21	44	TYR	2.2
41	85	76	TYR	2.2
29	21	125	GLY	2.2
30	39	87	GLY	2.2
37	45	86	GLY	2.2
2	12	51	LEU	2.2
4	3E	64	LEU	2.2
5	4E	153	LYS	2.2
1	13	927	G	2.2
6	52	99	ALA	2.2
9	8E	99	LEU	2.2
18	9I	68	LYS	2.2
28	11	38	LYS	2.2
34	15	37	LYS	2.2
43	E8	82	LEU	2.2
54	Q8	3	LYS	2.2
22	1L	34	G	2.2
22	1L	46	G	2.2
26	1H	929	G	2.2
26	1H	1131	G	2.2
26	1H	1266	G	2.2
26	14	2472	G	2.2
26	14	2578	G	2.2
54	Q8	60	LEU	2.2
1	13	686	U	2.2
1	13	1070	U	2.2
26	1H	1680	U	2.2
26	1H	2492	U	2.2
26	14	2076	U	2.2
26	14	2130	U	2.2
7	62	37	ASN	2.2
36	35	9	ASN	2.2
17	8I	25	ARG	2.2
33	61	120	ILE	2.2
34	15	131	GLN	2.2
39	65	40	ILE	2.2

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Mol	Chain	Res	Type	RSRZ
40	75	7	ILE	2.2
45	G8	23	ARG	2.2
49	K8	46	GLN	2.2
1	13	196	A	2.2
1	13	553	A	2.2
1	13	573	A	2.2
1	13	794	A	2.2
1	13	914	A	2.2
1	13	1502	A	2.2
1	13	1534	A	2.2
9	82	117	HIS	2.2
26	1H	1900	A	2.2
26	1H	2577	A	2.2
26	1H	2629	A	2.2
26	14	460	A	2.2
26	14	529	A	2.2
55	3L	59	A	2.2
1	13	123	C	2.2
1	13	1006	C	2.2
1	1G	904	C	2.2
1	1G	1051	C	2.2
26	1H	654(R)	C	2.2
26	1H	1493	C	2.2
26	14	673	C	2.2
2	12	43	ASP	2.2
4	3E	92	VAL	2.2
10	1A	39	PRO	2.2
33	69	132	PRO	2.2
48	J8	4	VAL	2.2
49	G5	18	PRO	2.2
52	J5	31	VAL	2.2
30	39	34	TRP	2.2
42	95	7	THR	2.2
32	51	38	SER	2.2
34	58	36	GLY	2.2
6	5E	60	PHE	2.2
8	7E	44	PHE	2.2
10	1I	55	LYS	2.2
15	6I	48	LYS	2.2
31	49	125	PHE	2.2
33	69	141	LYS	2.2
36	78	17	LYS	2.2

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Mol	Chain	Res	Type	RSRZ
36	35	113	LYS	2.2
10	1A	85	LEU	2.2
28	11	215	LEU	2.2
36	78	123	LEU	2.2
2	1E	117	GLU	2.2
13	4A	51	ALA	2.2
14	5A	30	ALA	2.2
20	BI	12	ALA	2.2
41	85	99	ALA	2.2
43	E8	5	ALA	2.2
2	12	182	ILE	2.2
4	32	5	ILE	2.2
5	42	89	ILE	2.2
1	1G	323	U	2.2
1	1G	340	U	2.2
1	1G	1425	U	2.2
10	1I	51	ARG	2.2
20	BA	17	ARG	2.2
28	19	204	ILE	2.2
28	19	262	ARG	2.2
29	29	77	ILE	2.2
41	C8	80	ILE	2.2
26	1H	1396	U	2.2
26	14	2016	U	2.2
27	16	22	U	2.2
46	D5	72	ARG	2.2
50	H5	19	GLN	2.2
55	3L	8	U	2.2
1	13	258	G	2.2
1	1G	142	G	2.2
1	1G	760	G	2.2
1	1G	1190	G	2.2
1	1G	1525	G	2.2
26	1H	2508	G	2.2
26	1H	2891	G	2.2
26	14	186	G	2.2
26	14	832	G	2.2
26	14	2035	G	2.2
26	14	2349	G	2.2
29	21	137	HIS	2.2
1	13	243	A	2.2
3	2E	116	VAL	2.2

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Mol	Chain	Res	Type	RSRZ
4	3E	133	VAL	2.2
12	3I	82	VAL	2.2
22	1K	38	A	2.2
26	1H	1085	A	2.2
26	14	1020	A	2.2
26	14	2173	A	2.2
26	14	2542	A	2.2
40	75	15	VAL	2.2
45	G8	3	VAL	2.2
46	D5	87	ASP	2.2
1	13	764	C	2.2
1	13	822	C	2.2
1	13	1407	C	2.2
1	1G	186(D)	C	2.2
26	1H	1403	C	2.2
26	1H	1498	C	2.2
26	1H	1965	C	2.2
26	1H	2137	C	2.2
26	14	47	C	2.2
26	14	246	C	2.2
26	14	1402	C	2.2
5	42	16	THR	2.2
12	3I	61	THR	2.2
29	29	146	THR	2.2
38	98	35	THR	2.2
45	G8	5	MET	2.2
29	29	142	GLY	2.2
33	69	84	GLY	2.2
33	69	112	LYS	2.2
36	35	118	GLY	2.2
37	45	15	GLY	2.2
42	D8	10	LYS	2.2
45	G8	95	LYS	2.2
46	H8	110	GLY	2.2
5	4E	133	TYR	2.2
15	6I	78	TYR	2.2
40	75	22	PHE	2.2
3	22	196	LEU	2.2
30	31	12	LEU	2.2
31	41	176	LEU	2.2
34	58	99	LEU	2.2
46	H8	125	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
18	9I	38	GLU	2.2
28	19	23	GLU	2.2
36	35	31	ALA	2.2
43	E8	3	ALA	2.2
3	22	57	ILE	2.1
13	4I	108	ARG	2.1
13	4A	84	ILE	2.1
32	59	9	ILE	2.1
40	B8	129	ARG	2.1
47	E5	41	ARG	2.1
48	J8	13	ILE	2.1
37	45	12	GLN	2.1
1	13	1257	U	2.1
6	52	11	ASN	2.1
22	1K	66	U	2.1
26	1H	1489	U	2.1
26	1H	2437	U	2.1
26	1H	2808	U	2.1
26	14	963	U	2.1
32	59	65	HIS	2.1
33	61	133	HIS	2.1
49	K8	47	ASN	2.1
4	32	198	VAL	2.1
13	4A	10	PRO	2.1
31	41	159	VAL	2.1
33	61	142	VAL	2.1
33	69	134	PRO	2.1
42	D8	90	PRO	2.1
37	45	7	MET	2.1
41	C8	91	ASP	2.1
46	D5	40	ASP	2.1
1	13	1166	G	2.1
1	1G	1405	G	2.1
13	4I	115	LYS	2.1
1	1G	1519	A	2.1
2	12	18	GLY	2.1
22	1K	67	A	2.1
26	1H	2057	A	2.1
26	1H	2351	G	2.1
26	1H	2630	G	2.1
26	14	959	A	2.1
26	14	1174	A	2.1

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Mol	Chain	Res	Type	RSRZ
26	14	2027	G	2.1
26	14	2157	G	2.1
26	14	2168	G	2.1
26	14	2831	G	2.1
27	1J	87	G	2.1
29	21	57	LYS	2.1
33	69	108	THR	2.1
41	85	22	LYS	2.1
28	11	110	GLY	2.1
29	21	186	GLY	2.1
38	55	108	GLY	2.1
48	J8	9	GLY	2.1
48	J8	36	GLY	2.1
17	8I	27	PHE	2.1
21	1F	14	TRP	2.1
1	13	1426	C	2.1
1	13	1431	C	2.1
1	1G	822	C	2.1
2	12	158	LEU	2.1
26	1H	2085	C	2.1
26	14	867	C	2.1
26	14	1386	C	2.1
37	45	58	PHE	2.1
38	98	100	LEU	2.1
44	B5	66	LEU	2.1
45	C5	31	LEU	2.1
35	68	84	ALA	2.1
4	32	156	GLU	2.1
20	BA	80	ARG	2.1
33	61	122	GLU	2.1
38	98	115	GLU	2.1
10	1I	50	ILE	2.1
28	11	82	ILE	2.1
32	59	72	ILE	2.1
39	65	82	ILE	2.1
3	2E	110	ASN	2.1
35	25	13	ASN	2.1
3	22	66	VAL	2.1
6	5E	9	VAL	2.1
10	1I	39	PRO	2.1
19	AI	58	VAL	2.1
26	1H	164	U	2.1

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Mol	Chain	Res	Type	RSRZ
26	14	185	U	2.1
33	61	137	PRO	2.1
36	35	63	PRO	2.1
36	35	72	PRO	2.1
36	35	83	VAL	2.1
38	55	85	PRO	2.1
39	A8	98	VAL	2.1
46	H8	161	VAL	2.1
2	12	169	LYS	2.1
31	41	74	LYS	2.1
38	98	40	LYS	2.1
54	M5	12	LYS	2.1
10	1A	17	ASP	2.1
10	1I	31	GLY	2.1
29	21	130	GLY	2.1
36	78	30	THR	2.1
36	35	142	GLY	2.1
3	22	47	LEU	2.1
7	62	12	LEU	2.1
36	35	91	PHE	2.1
49	K8	16	LEU	2.1
1	13	767	A	2.1
5	4E	126	ARG	2.1
5	42	30	ALA	2.1
9	82	82	ALA	2.1
24	3K	9	A	2.1
26	1H	320	A	2.1
26	1H	689	A	2.1
26	1H	2453	A	2.1
26	14	480	A	2.1
26	14	1655	A	2.1
26	14	1755	A	2.1
26	14	2621	A	2.1
29	29	20	ALA	2.1
29	29	119	ARG	2.1
36	35	120	ALA	2.1
37	88	53	ALA	2.1
55	3L	21	A	2.1
1	13	348	G	2.1
2	12	134	GLU	2.1
14	5A	32	SER	2.1
24	3K	15	G	2.1

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Mol	Chain	Res	Type	RSRZ
26	1H	171	G	2.1
26	1H	717	G	2.1
26	1H	2061	G	2.1
26	1H	2104	G	2.1
26	1H	2115	G	2.1
26	14	83	G	2.1
26	14	799	G	2.1
29	21	14	ILE	2.1
39	A8	43	GLU	2.1
41	85	108	GLU	2.1
42	95	34	GLU	2.1
42	95	99	ILE	2.1
47	I8	36	ILE	2.1
47	E5	68	GLU	2.1
1	1G	121	C	2.1
1	1G	934	C	2.1
1	1G	1383	C	2.1
26	1H	1499	C	2.1
26	1H	1806	C	2.1
26	1H	2745	C	2.1
26	14	1765	C	2.1
26	14	1924	C	2.1
26	14	2579	C	2.1
41	85	117	GLN	2.1
3	2E	151	VAL	2.1
6	52	88	VAL	2.1
7	6E	61	VAL	2.1
20	BI	14	LYS	2.1
29	21	121	ASN	2.1
42	95	51	VAL	2.1
43	E8	50	VAL	2.1
44	F8	53	LYS	2.1
44	F8	81	VAL	2.1
45	G8	37	VAL	2.1
38	55	110	PRO	2.1
46	D5	83	PRO	2.1
1	1G	686	U	2.1
1	1G	1341	U	2.1
26	1H	2130	U	2.1
26	14	2580	U	2.1
5	4E	31	LEU	2.1
12	3A	52	LEU	2.1

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Mol	Chain	Res	Type	RSRZ
19	AI	30	LEU	2.1
20	BI	53	LEU	2.1
46	H8	22	GLY	2.1
46	D5	33	LEU	2.1
50	H5	23	LEU	2.1
37	45	65	PHE	2.1
48	F5	34	THR	2.1
2	1E	97	TRP	2.1
3	22	88	ARG	2.1
7	62	3	ARG	2.1
9	82	93	ARG	2.1
21	1B	14	TRP	2.1
29	21	37	ARG	2.1
31	49	100	TRP	2.1
38	98	12	ARG	2.1
42	D8	82	ARG	2.1
51	M8	58	ARG	2.1
53	L5	47	ARG	2.1
2	1E	236	TYR	2.1
4	3E	204	ILE	2.1
29	29	162	ALA	2.1
29	29	187	ALA	2.1
37	45	107	ALA	2.1
7	62	142	GLU	2.1
38	55	94	TYR	2.1
40	B8	121	ILE	2.1
42	D8	59	ALA	2.1
43	A5	81	ALA	2.1
30	39	27	GLU	2.1
32	51	32	GLU	2.1
46	D5	99	TYR	2.1
52	J5	52	TYR	2.1
54	M5	16	ILE	2.1
4	3E	152	SER	2.1
22	1K	21	A	2.1
22	1L	67	A	2.1
26	1H	1927	A	2.1
26	14	572	A	2.1
26	14	2031	A	2.1
26	14	2360	A	2.1
26	14	2629	A	2.1
44	F8	87	GLN	2.1

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Mol	Chain	Res	Type	RSRZ
1	13	306	G	2.1
1	13	413	G	2.1
1	13	1131	G	2.1
1	1G	586	C	2.1
1	1G	898	G	2.1
1	1G	1282	C	2.1
2	1E	48	MET	2.1
2	12	19	HIS	2.1
8	7E	129	VAL	2.1
8	72	95	VAL	2.1
9	82	11	LYS	2.1
13	4A	17	VAL	2.1
24	3K	24	G	2.1
26	1H	242	G	2.1
26	1H	391	G	2.1
26	1H	530	G	2.1
26	1H	672	C	2.1
26	1H	902	C	2.1
26	1H	1662	C	2.1
26	1H	1666	G	2.1
26	1H	1728	G	2.1
26	1H	2103	C	2.1
26	1H	2145	C	2.1
3	22	195	VAL	2.1
4	3E	121	VAL	2.1
26	1H	2349	G	2.1
26	1H	2470	G	2.1
26	1H	2567	G	2.1
26	1H	2718	G	2.1
26	1H	2780	G	2.1
26	14	493	G	2.1
26	14	593	G	2.1
26	14	1011	G	2.1
26	14	1806	C	2.1
26	14	2246	G	2.1
27	1J	12	C	2.1
55	3L	72	C	2.1
36	78	125	VAL	2.1
43	A5	59	VAL	2.1
46	D5	139	VAL	2.1
3	2E	114	PRO	2.1
10	1A	69	ASN	2.1

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Mol	Chain	Res	Type	RSRZ
20	BI	10	LEU	2.1
36	35	106	LEU	2.1
1	13	561	U	2.1
1	1G	1065	U	2.1
26	14	905	U	2.1
26	14	2511	U	2.1
26	14	2878	U	2.1
32	51	108	GLY	2.1
3	22	67	THR	2.1
3	22	190	ARG	2.1
7	62	76	ARG	2.1
29	21	111	ARG	2.1
37	45	138	ASP	2.1
2	12	41	ILE	2.1
8	72	13	ILE	2.1
10	1I	74	ILE	2.1
10	1I	75	ILE	2.1
13	4I	5	ALA	2.1
28	19	80	ALA	2.1
33	61	59	ALA	2.1
38	98	62	ALA	2.1
38	98	109	ALA	2.1
40	75	48	ILE	2.1
45	C5	75	ILE	2.1
46	H8	152	ALA	2.1
13	4I	69	GLU	2.1
32	51	119	GLU	2.1
33	69	70	GLU	2.1
52	N8	48	GLU	2.1
5	42	60	TYR	2.1
8	72	58	TYR	2.1
10	1I	57	LYS	2.0
12	3A	62	SER	2.0
42	D8	73	SER	2.0
7	62	106	GLN	2.0
46	H8	156	LYS	2.0
50	H5	10	LYS	2.0
42	95	64	HIS	2.0
1	1G	1130	A	2.0
1	1G	1507	A	2.0
7	62	105	VAL	2.0
25	4K	13	A	2.0

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Mol	Chain	Res	Type	RSRZ
25	4K	25	A	2.0
26	1H	181	A	2.0
26	14	644	A	2.0
29	29	196	VAL	2.0
34	15	46	VAL	2.0
46	H8	141	VAL	2.0
2	12	131	PRO	2.0
36	78	48	PRO	2.0
1	1G	842	C	2.0
1	1G	931	C	2.0
1	1G	1128	C	2.0
2	1E	138	LEU	2.0
4	32	21	LEU	2.0
9	82	19	LEU	2.0
26	1H	1180	C	2.0
26	1H	1430	C	2.0
26	1H	1914	C	2.0
26	1H	2515	C	2.0
26	1H	2558	C	2.0
26	1H	2680	C	2.0
26	1H	2871	C	2.0
26	14	1387	C	2.0
30	39	169	ASN	2.0
31	41	152	LEU	2.0
31	49	53	LEU	2.0
38	55	18	LEU	2.0
50	L8	46	ASN	2.0
1	1G	186(C)	G	2.0
1	1G	769	G	2.0
1	1G	774	G	2.0
1	1G	1462	G	2.0
4	3E	139	ARG	2.0
4	32	110	PHE	2.0
11	2A	49	GLY	2.0
13	4A	91	ARG	2.0
24	3K	4	G	2.0
26	1H	628	G	2.0
26	1H	651	G	2.0
26	1H	654(S)	G	2.0
26	1H	686	G	2.0
26	1H	1987	G	2.0
26	14	273(A)	G	2.0

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Mol	Chain	Res	Type	RSRZ
26	14	776	G	2.0
26	14	2210	G	2.0
28	19	256	GLY	2.0
30	39	85	GLY	2.0
40	75	76	PHE	2.0
50	H5	35	ARG	2.0
7	62	49	ILE	2.0
24	3K	8	U	2.0
26	1H	270(L)	U	2.0
26	14	243	U	2.0
55	3L	6	U	2.0
32	51	57	ASP	2.0
39	65	105	ALA	2.0
48	F5	63	ALA	2.0
29	21	69	LYS	2.0
29	29	154	LYS	2.0
32	59	138	LYS	2.0
34	58	104	LYS	2.0
34	15	66	LYS	2.0
44	B5	18	TYR	2.0
2	1E	233	SER	2.0
4	32	42	GLN	2.0
7	62	61	VAL	2.0
9	82	53	VAL	2.0
33	61	92	VAL	2.0
1	13	195	A	2.0
1	1G	695	A	2.0
1	1G	790	A	2.0
19	AA	16	LEU	2.0
20	BI	72	LEU	2.0
22	1L	28	A	2.0
26	1H	1384	A	2.0
26	1H	2320	A	2.0
26	14	257	A	2.0
26	14	1321	A	2.0
26	14	2614	A	2.0
27	16	89(A)	A	2.0
31	49	152	LEU	2.0
34	58	23	LEU	2.0
36	78	6	LEU	2.0
50	H5	53	LEU	2.0
52	N8	25	LEU	2.0

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Mol	Chain	Res	Type	RSRZ
12	3I	41	ARG	2.0
30	31	160	ASN	2.0
2	12	203	GLY	2.0
42	D8	75	PHE	2.0
44	F8	94	GLY	2.0
1	1G	784	C	2.0
2	12	222	ILE	2.0
26	1H	287	C	2.0
26	1H	1793	C	2.0
26	14	544	C	2.0
26	14	2283	C	2.0
26	14	2394	C	2.0
32	51	136	ILE	2.0
5	4E	17	ALA	2.0
6	52	101	ALA	2.0
10	1I	32	ALA	2.0
33	61	83	ALA	2.0
34	58	47	ALA	2.0
1	13	905	U	2.0
1	1G	1498	U	2.0
16	7I	83	GLU	2.0
26	1H	1944	U	2.0
26	14	1808	U	2.0
26	14	2605	U	2.0
40	B8	11	GLU	2.0
41	85	97	ASP	2.0
1	13	227	G	2.0
1	13	1462	G	2.0
1	1G	1181	G	2.0
26	1H	2080	G	2.0
26	1H	2553	G	2.0
26	14	1110	G	2.0
26	14	1998	G	2.0
26	14	2811	G	2.0
31	41	84	LYS	2.0
40	B8	113	LYS	2.0
52	J5	56	LYS	2.0
31	41	148	MET	2.0
40	B8	1	MET	2.0
6	5E	63	TYR	2.0
2	12	15	VAL	2.0
9	8E	41	VAL	2.0

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Mol	Chain	Res	Type	RSRZ
17	8I	85	VAL	2.0
36	78	126	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
22	H2U	1K	17	20/21	0.33	0.15	153,168,175,178	0
55	PSU	3L	55	20/21	0.46	0.14	140,146,152,152	0
55	5MU	3L	54	21/22	0.52	0.12	136,142,145,152	0
22	5MU	1L	54	21/22	0.55	0.21	122,128,134,140	0
22	H2U	1L	17	20/21	0.64	0.14	153,166,172,174	0
22	PSU	1L	55	20/21	0.69	0.14	122,134,145,147	0
22	5MU	1K	54	21/22	0.74	0.16	100,111,121,127	0
23	7MG	2L	47	24/25	0.75	0.14	113,120,131,141	0
23	5MU	2L	55	21/22	0.75	0.10	116,121,123,124	0
23	5MU	2K	55	21/22	0.79	0.13	99,109,114,119	0
23	PSU	2L	56	20/21	0.79	0.09	108,116,121,124	0
22	PSU	1K	55	20/21	0.83	0.13	104,115,130,130	0
23	7MG	2K	47	24/25	0.83	0.14	94,102,111,114	0
22	AET	1L	37	33/34	0.85	0.25	94,112,119,124	0
23	PSU	2K	56	20/21	0.86	0.10	96,104,114,115	0
23	4SU	2L	8	20/21	0.88	0.10	99,111,114,120	0
23	4SU	2K	8	20/21	0.89	0.13	85,93,98,99	0
22	AET	1K	37	33/34	0.89	0.23	69,82,106,115	0
23	OMC	2K	33	21/22	0.93	0.16	71,78,80,88	0
23	OMC	2L	33	21/22	0.94	0.10	93,95,98,101	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, 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
56	MG	13	1686	1/1	-0.09	0.58	129,129,129,129	0
56	MG	13	1685	1/1	0.20	0.36	114,114,114,114	0
56	MG	13	1608	1/1	0.24	0.29	111,111,111,111	0
56	MG	1G	1646	1/1	0.24	0.42	116,116,116,116	0
56	MG	14	3029	1/1	0.27	0.42	96,96,96,96	0
56	MG	1J	201	1/1	0.28	0.43	95,95,95,95	0
56	MG	1H	3304	1/1	0.29	0.32	106,106,106,106	0
56	MG	13	1659	1/1	0.30	0.37	115,115,115,115	0
56	MG	13	1665	1/1	0.31	0.42	117,117,117,117	0
56	MG	16	211	1/1	0.34	0.39	79,79,79,79	0
56	MG	1H	3303	1/1	0.34	0.52	106,106,106,106	0
56	MG	1H	3198	1/1	0.36	0.47	108,108,108,108	0
56	MG	14	3280	1/1	0.37	0.46	89,89,89,89	0
56	MG	14	3285	1/1	0.39	0.52	95,95,95,95	0
56	MG	13	1741	1/1	0.40	0.43	99,99,99,99	0
56	MG	16	210	1/1	0.40	0.47	101,101,101,101	0
56	MG	1H	3328	1/1	0.41	0.47	86,86,86,86	0
56	MG	13	1618	1/1	0.41	0.40	97,97,97,97	0
56	MG	1H	3026	1/1	0.43	0.47	92,92,92,92	0
56	MG	14	3245	1/1	0.44	0.45	104,104,104,104	0
56	MG	1H	3386	1/1	0.44	0.42	96,96,96,96	0
56	MG	1G	1666	1/1	0.45	0.27	122,122,122,122	0
56	MG	1G	1642	1/1	0.45	0.37	110,110,110,110	0
56	MG	13	1690	1/1	0.45	0.28	118,118,118,118	0
56	MG	14	3298	1/1	0.46	0.41	100,100,100,100	0
56	MG	1G	1651	1/1	0.46	0.27	107,107,107,107	0
56	MG	1J	205	1/1	0.46	0.19	118,118,118,118	0
56	MG	14	3286	1/1	0.47	0.37	93,93,93,93	0
56	MG	14	3218	1/1	0.47	0.17	104,104,104,104	0
56	MG	1H	3153	1/1	0.48	0.42	92,92,92,92	0
56	MG	1H	3165	1/1	0.48	0.56	98,98,98,98	0
56	MG	14	3222	1/1	0.49	0.17	94,94,94,94	0
56	MG	1H	3345	1/1	0.49	0.37	87,87,87,87	0
56	MG	14	3077	1/1	0.49	0.49	87,87,87,87	0
56	MG	13	1711	1/1	0.49	0.30	114,114,114,114	0
56	MG	1H	3101	1/1	0.50	0.45	91,91,91,91	0
56	MG	14	3210	1/1	0.51	0.43	100,100,100,100	0
56	MG	1H	3177	1/1	0.52	0.38	79,79,79,79	0
56	MG	1G	1607	1/1	0.52	0.36	104,104,104,104	0
56	MG	1G	1696	1/1	0.52	0.28	103,103,103,103	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	13	1657	1/1	0.52	0.36	101,101,101,101	0
56	MG	1H	3302	1/1	0.52	0.31	98,98,98,98	0
56	MG	1G	1656	1/1	0.54	0.20	99,99,99,99	0
56	MG	13	1682	1/1	0.54	0.34	116,116,116,116	0
56	MG	14	3211	1/1	0.54	0.32	111,111,111,111	0
56	MG	14	3071	1/1	0.54	0.39	83,83,83,83	0
56	MG	13	1738	1/1	0.55	0.39	96,96,96,96	0
56	MG	1G	1658	1/1	0.55	0.29	108,108,108,108	0
56	MG	13	1689	1/1	0.55	0.23	105,105,105,105	0
56	MG	14	3171	1/1	0.55	0.34	89,89,89,89	0
56	MG	1J	202	1/1	0.55	0.30	92,92,92,92	0
56	MG	1G	1655	1/1	0.55	0.26	121,121,121,121	0
56	MG	88	201	1/1	0.56	0.49	79,79,79,79	0
56	MG	14	3126	1/1	0.56	0.33	102,102,102,102	0
56	MG	1H	3337	1/1	0.56	0.35	99,99,99,99	0
56	MG	14	3065	1/1	0.57	0.33	90,90,90,90	0
56	MG	14	3216	1/1	0.57	0.40	91,91,91,91	0
56	MG	1H	3081	1/1	0.57	0.35	91,91,91,91	0
56	MG	13	1634	1/1	0.57	0.34	118,118,118,118	0
56	MG	1G	1605	1/1	0.58	0.21	105,105,105,105	0
56	MG	13	1669	1/1	0.58	0.32	109,109,109,109	0
56	MG	1H	3258	1/1	0.58	0.36	115,115,115,115	0
56	MG	1G	1691	1/1	0.58	0.28	106,106,106,106	0
56	MG	13	1671	1/1	0.59	0.37	99,99,99,99	0
56	MG	1H	3199	1/1	0.59	0.17	116,116,116,116	0
56	MG	14	3246	1/1	0.59	0.37	86,86,86,86	0
56	MG	14	3179	1/1	0.59	0.20	83,83,83,83	0
56	MG	14	3183	1/1	0.59	0.19	96,96,96,96	0
56	MG	1H	3108	1/1	0.60	0.33	87,87,87,87	0
56	MG	1H	3292	1/1	0.60	0.27	108,108,108,108	0
56	MG	5I	101	1/1	0.60	0.26	85,85,85,85	0
56	MG	13	1619	1/1	0.61	0.35	95,95,95,95	0
56	MG	1H	3175	1/1	0.61	0.24	103,103,103,103	0
56	MG	14	3262	1/1	0.61	0.39	87,87,87,87	0
56	MG	1H	3080	1/1	0.61	0.40	80,80,80,80	0
56	MG	14	3162	1/1	0.61	0.32	89,89,89,89	0
56	MG	35	201	1/1	0.61	0.30	84,84,84,84	0
56	MG	1H	3405	1/1	0.62	0.47	80,80,80,80	0
56	MG	13	1706	1/1	0.62	0.16	111,111,111,111	0
56	MG	1G	1626	1/1	0.62	0.45	102,102,102,102	0
56	MG	13	1684	1/1	0.62	0.42	99,99,99,99	0
56	MG	14	3069	1/1	0.62	0.34	85,85,85,85	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1H	3227	1/1	0.62	0.48	99,99,99,99	0
56	MG	1G	1673	1/1	0.62	0.31	104,104,104,104	0
56	MG	14	3045	1/1	0.63	0.31	91,91,91,91	0
56	MG	14	3217	1/1	0.63	0.31	96,96,96,96	0
56	MG	16	201	1/1	0.63	0.32	79,79,79,79	0
56	MG	13	1735	1/1	0.63	0.35	85,85,85,85	0
56	MG	1H	3294	1/1	0.63	0.18	112,112,112,112	0
56	MG	1H	3036	1/1	0.64	0.26	73,73,73,73	0
56	MG	14	3080	1/1	0.64	0.36	86,86,86,86	0
56	MG	13	1674	1/1	0.64	0.31	101,101,101,101	0
56	MG	13	1650	1/1	0.64	0.30	100,100,100,100	0
56	MG	1G	1653	1/1	0.65	0.33	112,112,112,112	0
56	MG	1H	3305	1/1	0.65	0.35	100,100,100,100	0
56	MG	14	3137	1/1	0.65	0.33	90,90,90,90	0
56	MG	4A	201	1/1	0.65	0.27	116,116,116,116	0
56	MG	4L	401	1/1	0.65	0.22	99,99,99,99	0
56	MG	1H	3333	1/1	0.65	0.34	96,96,96,96	0
56	MG	1H	3054	1/1	0.66	0.46	78,78,78,78	0
56	MG	1H	3279	1/1	0.66	0.28	93,93,93,93	0
56	MG	1H	3406	1/1	0.66	0.37	91,91,91,91	0
56	MG	13	1667	1/1	0.66	0.28	86,86,86,86	0
56	MG	1G	1654	1/1	0.66	0.24	98,98,98,98	0
56	MG	1G	1615	1/1	0.66	0.40	87,87,87,87	0
56	MG	14	3193	1/1	0.66	0.38	88,88,88,88	0
56	MG	1H	3374	1/1	0.66	0.31	101,101,101,101	0
56	MG	14	3225	1/1	0.67	0.18	111,111,111,111	0
56	MG	16	207	1/1	0.67	0.30	110,110,110,110	0
56	MG	16	209	1/1	0.67	0.42	81,81,81,81	0
56	MG	13	1721	1/1	0.67	0.32	74,74,74,74	0
56	MG	13	1615	1/1	0.67	0.23	103,103,103,103	0
56	MG	13	1622	1/1	0.67	0.30	72,72,72,72	0
56	MG	1G	1700	1/1	0.67	0.23	113,113,113,113	0
56	MG	13	1656	1/1	0.67	0.22	91,91,91,91	0
56	MG	1H	3421	1/1	0.67	0.43	92,92,92,92	0
56	MG	1H	3178	1/1	0.67	0.24	91,91,91,91	0
56	MG	14	3164	1/1	0.67	0.29	105,105,105,105	0
56	MG	14	3224	1/1	0.67	0.27	101,101,101,101	0
56	MG	13	1716	1/1	0.68	0.23	94,94,94,94	0
56	MG	13	1623	1/1	0.68	0.29	106,106,106,106	0
56	MG	14	3042	1/1	0.68	0.41	82,82,82,82	0
56	MG	14	3124	1/1	0.68	0.36	82,82,82,82	0
56	MG	1H	3041	1/1	0.68	0.41	65,65,65,65	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1H	3162	1/1	0.68	0.32	70,70,70,70	0
56	MG	14	3154	1/1	0.68	0.40	87,87,87,87	0
56	MG	1H	3272	1/1	0.68	0.30	85,85,85,85	0
56	MG	1G	1622	1/1	0.69	0.35	87,87,87,87	0
56	MG	14	3219	1/1	0.69	0.20	100,100,100,100	0
56	MG	1G	1694	1/1	0.69	0.29	102,102,102,102	0
56	MG	13	1683	1/1	0.69	0.32	99,99,99,99	0
56	MG	13	1718	1/1	0.69	0.23	105,105,105,105	0
56	MG	13	1714	1/1	0.69	0.24	114,114,114,114	0
56	MG	1G	1609	1/1	0.69	0.30	96,96,96,96	0
56	MG	13	1727	1/1	0.69	0.16	103,103,103,103	0
56	MG	14	3261	1/1	0.70	0.34	93,93,93,93	0
56	MG	1G	1687	1/1	0.70	0.27	96,96,96,96	0
56	MG	14	3268	1/1	0.70	0.40	83,83,83,83	0
56	MG	1G	1624	1/1	0.70	0.28	109,109,109,109	0
56	MG	1H	3129	1/1	0.70	0.42	77,77,77,77	0
56	MG	13	1621	1/1	0.70	0.30	74,74,74,74	0
56	MG	14	3209	1/1	0.70	0.23	97,97,97,97	0
56	MG	13	1666	1/1	0.70	0.41	92,92,92,92	0
56	MG	14	3238	1/1	0.70	0.39	85,85,85,85	0
56	MG	1H	3113	1/1	0.70	0.32	67,67,67,67	0
56	MG	1H	3379	1/1	0.70	0.33	85,85,85,85	0
56	MG	14	3259	1/1	0.71	0.33	87,87,87,87	0
56	MG	14	3260	1/1	0.71	0.30	91,91,91,91	0
56	MG	1G	1650	1/1	0.71	0.16	81,81,81,81	0
56	MG	1H	3179	1/1	0.71	0.23	93,93,93,93	0
56	MG	14	3055	1/1	0.71	0.23	89,89,89,89	0
56	MG	14	3276	1/1	0.71	0.39	92,92,92,92	0
56	MG	1G	1659	1/1	0.71	0.31	104,104,104,104	0
56	MG	13	1620	1/1	0.71	0.37	69,69,69,69	0
56	MG	42	201	1/1	0.71	0.33	103,103,103,103	0
56	MG	1H	3297	1/1	0.71	0.10	80,80,80,80	0
56	MG	14	3079	1/1	0.71	0.28	91,91,91,91	0
56	MG	1G	1674	1/1	0.71	0.23	106,106,106,106	0
56	MG	14	3081	1/1	0.71	0.28	114,114,114,114	0
56	MG	1H	3248	1/1	0.71	0.29	86,86,86,86	0
56	MG	35	203	1/1	0.71	0.44	81,81,81,81	0
56	MG	13	1694	1/1	0.72	0.22	96,96,96,96	0
56	MG	14	3004	1/1	0.72	0.31	73,73,73,73	0
56	MG	1H	3361	1/1	0.72	0.21	89,89,89,89	0
56	MG	14	3082	1/1	0.72	0.37	91,91,91,91	0
56	MG	14	3096	1/1	0.72	0.47	87,87,87,87	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	14	3275	1/1	0.72	0.17	77,77,77,77	0
56	MG	14	3041	1/1	0.72	0.42	85,85,85,85	0
56	MG	1H	3252	1/1	0.72	0.25	102,102,102,102	0
56	MG	1G	1692	1/1	0.72	0.36	87,87,87,87	0
56	MG	16	206	1/1	0.72	0.44	80,80,80,80	0
56	MG	13	1680	1/1	0.72	0.32	103,103,103,103	0
56	MG	1G	1665	1/1	0.72	0.29	107,107,107,107	0
56	MG	14	3230	1/1	0.72	0.14	90,90,90,90	0
56	MG	13	1678	1/1	0.72	0.21	97,97,97,97	0
56	MG	14	3074	1/1	0.72	0.22	84,84,84,84	0
56	MG	1H	3163	1/1	0.72	0.33	74,74,74,74	0
56	MG	1H	3090	1/1	0.73	0.30	73,73,73,73	0
56	MG	13	1737	1/1	0.73	0.23	79,79,79,79	0
56	MG	1H	3029	1/1	0.73	0.23	69,69,69,69	0
56	MG	1G	1608	1/1	0.73	0.26	108,108,108,108	0
56	MG	1H	3035	1/1	0.73	0.36	90,90,90,90	0
56	MG	1H	3205	1/1	0.73	0.43	94,94,94,94	0
56	MG	13	1663	1/1	0.73	0.20	105,105,105,105	0
56	MG	1H	3134	1/1	0.73	0.40	85,85,85,85	0
56	MG	14	3151	1/1	0.74	0.34	88,88,88,88	0
56	MG	1H	3193	1/1	0.74	0.17	89,89,89,89	0
56	MG	1H	3334	1/1	0.74	0.41	93,93,93,93	0
56	MG	13	1606	1/1	0.74	0.34	81,81,81,81	0
56	MG	1H	3230	1/1	0.74	0.21	96,96,96,96	0
56	MG	1H	3062	1/1	0.74	0.31	72,72,72,72	0
56	MG	14	3182	1/1	0.74	0.27	91,91,91,91	0
56	MG	14	3023	1/1	0.74	0.31	82,82,82,82	0
56	MG	14	3223	1/1	0.74	0.29	93,93,93,93	0
56	MG	14	3147	1/1	0.74	0.33	94,94,94,94	0
56	MG	14	3272	1/1	0.74	0.42	94,94,94,94	0
56	MG	1H	3253	1/1	0.75	0.31	72,72,72,72	0
56	MG	14	3111	1/1	0.75	0.31	78,78,78,78	0
56	MG	1H	3191	1/1	0.75	0.19	99,99,99,99	0
56	MG	1G	1701	1/1	0.75	0.53	94,94,94,94	0
56	MG	1H	3028	1/1	0.75	0.37	64,64,64,64	0
56	MG	1H	3340	1/1	0.75	0.36	83,83,83,83	0
56	MG	13	1739	1/1	0.75	0.24	74,74,74,74	0
56	MG	1H	3290	1/1	0.75	0.19	94,94,94,94	0
56	MG	13	1736	1/1	0.75	0.31	96,96,96,96	0
56	MG	1H	3202	1/1	0.75	0.39	84,84,84,84	0
56	MG	13	1668	1/1	0.75	0.44	101,101,101,101	0
56	MG	14	3266	1/1	0.75	0.36	85,85,85,85	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1G	1662	1/1	0.75	0.38	96,96,96,96	0
56	MG	1G	1663	1/1	0.75	0.24	100,100,100,100	0
56	MG	1G	1664	1/1	0.75	0.18	106,106,106,106	0
56	MG	1H	3221	1/1	0.75	0.19	89,89,89,89	0
56	MG	14	3197	1/1	0.75	0.29	91,91,91,91	0
56	MG	1G	1616	1/1	0.75	0.15	100,100,100,100	0
56	MG	5I	102	1/1	0.75	0.19	100,100,100,100	0
56	MG	1H	3023	1/1	0.75	0.33	72,72,72,72	0
56	MG	1G	1678	1/1	0.75	0.33	86,86,86,86	0
56	MG	1H	3061	1/1	0.75	0.27	66,66,66,66	0
56	MG	1G	1628	1/1	0.75	0.33	89,89,89,89	0
56	MG	13	1658	1/1	0.75	0.27	96,96,96,96	0
56	MG	1G	1644	1/1	0.75	0.18	100,100,100,100	0
56	MG	16	204	1/1	0.76	0.26	77,77,77,77	0
56	MG	16	205	1/1	0.76	0.33	70,70,70,70	0
56	MG	1H	3312	1/1	0.76	0.11	100,100,100,100	0
56	MG	1H	3368	1/1	0.76	0.33	106,106,106,106	0
56	MG	1G	1633	1/1	0.76	0.37	94,94,94,94	0
56	MG	14	3034	1/1	0.76	0.18	63,63,63,63	0
56	MG	1G	1671	1/1	0.76	0.19	92,92,92,92	0
56	MG	1H	3327	1/1	0.76	0.32	65,65,65,65	0
56	MG	13	1681	1/1	0.76	0.34	98,98,98,98	0
56	MG	14	3047	1/1	0.76	0.13	80,80,80,80	0
56	MG	1G	1675	1/1	0.76	0.23	92,92,92,92	0
56	MG	1H	3010	1/1	0.76	0.29	70,70,70,70	0
56	MG	14	3269	1/1	0.76	0.27	80,80,80,80	0
56	MG	1G	1684	1/1	0.76	0.21	89,89,89,89	0
56	MG	14	3070	1/1	0.76	0.24	72,72,72,72	0
56	MG	14	3201	1/1	0.76	0.19	91,91,91,91	0
56	MG	1H	3396	1/1	0.76	0.13	71,71,71,71	0
56	MG	1G	1690	1/1	0.76	0.43	75,75,75,75	0
56	MG	D8	201	1/1	0.76	0.21	76,76,76,76	0
56	MG	14	3294	1/1	0.76	0.25	94,94,94,94	0
56	MG	1H	3401	1/1	0.76	0.45	77,77,77,77	0
56	MG	1H	3276	1/1	0.76	0.45	68,68,68,68	0
56	MG	13	1728	1/1	0.76	0.21	97,97,97,97	0
56	MG	13	1705	1/1	0.76	0.17	111,111,111,111	0
56	MG	1H	3422	1/1	0.76	0.25	90,90,90,90	0
56	MG	1H	3148	1/1	0.76	0.32	89,89,89,89	0
56	MG	14	3235	1/1	0.77	0.23	88,88,88,88	0
56	MG	1G	1621	1/1	0.77	0.28	89,89,89,89	0
56	MG	14	3170	1/1	0.77	0.26	105,105,105,105	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1H	3207	1/1	0.77	0.40	87,87,87,87	0
56	MG	1H	3291	1/1	0.77	0.22	97,97,97,97	0
56	MG	1G	1625	1/1	0.77	0.22	111,111,111,111	0
56	MG	13	1717	1/1	0.77	0.29	98,98,98,98	0
56	MG	1H	3224	1/1	0.77	0.29	85,85,85,85	0
56	MG	13	1649	1/1	0.77	0.27	76,76,76,76	0
56	MG	14	3198	1/1	0.77	0.29	96,96,96,96	0
56	MG	14	3200	1/1	0.77	0.23	72,72,72,72	0
56	MG	1H	3299	1/1	0.77	0.35	87,87,87,87	0
56	MG	14	3095	1/1	0.77	0.28	92,92,92,92	0
56	MG	1H	3300	1/1	0.77	0.28	86,86,86,86	0
56	MG	1H	3301	1/1	0.77	0.33	95,95,95,95	0
56	MG	14	3281	1/1	0.77	0.20	89,89,89,89	0
56	MG	14	3117	1/1	0.77	0.29	79,79,79,79	0
56	MG	14	3123	1/1	0.77	0.16	86,86,86,86	0
56	MG	13	1628	1/1	0.77	0.31	79,79,79,79	0
56	MG	1G	1606	1/1	0.77	0.17	97,97,97,97	0
56	MG	1H	3418	1/1	0.77	0.21	90,90,90,90	0
56	MG	1H	3093	1/1	0.77	0.15	56,56,56,56	0
56	MG	1H	3346	1/1	0.77	0.30	91,91,91,91	0
56	MG	1H	3356	1/1	0.77	0.41	76,76,76,76	0
56	MG	1H	3358	1/1	0.77	0.34	83,83,83,83	0
56	MG	13	1707	1/1	0.78	0.09	108,108,108,108	0
56	MG	BA	202	1/1	0.78	0.34	113,113,113,113	0
56	MG	1H	3183	1/1	0.78	0.38	80,80,80,80	0
56	MG	13	1703	1/1	0.78	0.30	93,93,93,93	0
56	MG	14	3006	1/1	0.78	0.16	56,56,56,56	0
56	MG	1H	3114	1/1	0.78	0.31	90,90,90,90	0
56	MG	14	3178	1/1	0.78	0.13	85,85,85,85	0
56	MG	13	1720	1/1	0.78	0.15	97,97,97,97	0
56	MG	1H	3238	1/1	0.78	0.47	87,87,87,87	0
56	MG	1H	3382	1/1	0.78	0.39	73,73,73,73	0
56	MG	1H	3247	1/1	0.78	0.32	65,65,65,65	0
56	MG	14	3290	1/1	0.78	0.26	85,85,85,85	0
56	MG	13	1624	1/1	0.78	0.16	102,102,102,102	0
56	MG	1H	3143	1/1	0.78	0.18	78,78,78,78	0
56	MG	1H	3339	1/1	0.78	0.15	74,74,74,74	0
56	MG	14	3248	1/1	0.78	0.40	80,80,80,80	0
56	MG	1J	204	1/1	0.78	0.16	95,95,95,95	0
56	MG	1H	3204	1/1	0.78	0.34	92,92,92,92	0
56	MG	1J	206	1/1	0.78	0.32	68,68,68,68	0
56	MG	13	1664	1/1	0.78	0.34	91,91,91,91	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1H	3269	1/1	0.78	0.42	80,80,80,80	0
56	MG	14	3150	1/1	0.79	0.13	73,73,73,73	0
56	MG	13	1643	1/1	0.79	0.35	78,78,78,78	0
56	MG	1H	3176	1/1	0.79	0.28	93,93,93,93	0
56	MG	13	1729	1/1	0.79	0.22	95,95,95,95	0
56	MG	3E	301	1/1	0.79	0.19	121,121,121,121	0
56	MG	1H	3261	1/1	0.79	0.31	92,92,92,92	0
56	MG	1H	3030	1/1	0.79	0.29	75,75,75,75	0
56	MG	13	1655	1/1	0.79	0.33	94,94,94,94	0
56	MG	1G	1652	1/1	0.79	0.32	87,87,87,87	0
56	MG	13	1696	1/1	0.79	0.36	104,104,104,104	0
56	MG	13	1644	1/1	0.79	0.31	89,89,89,89	0
56	MG	1H	3282	1/1	0.79	0.22	94,94,94,94	0
56	MG	1H	3363	1/1	0.79	0.11	83,83,83,83	0
56	MG	1H	3283	1/1	0.79	0.29	79,79,79,79	0
56	MG	1H	3322	1/1	0.79	0.13	94,94,94,94	0
56	MG	13	1632	1/1	0.79	0.41	86,86,86,86	0
56	MG	14	3131	1/1	0.79	0.37	78,78,78,78	0
56	MG	39	301	1/1	0.79	0.29	94,94,94,94	0
56	MG	1G	1699	1/1	0.79	0.38	90,90,90,90	0
56	MG	1H	3059	1/1	0.79	0.26	60,60,60,60	0
56	MG	1G	1634	1/1	0.80	0.24	89,89,89,89	0
56	MG	1G	1693	1/1	0.80	0.34	84,84,84,84	0
56	MG	1H	3187	1/1	0.80	0.33	75,75,75,75	0
56	MG	1H	3350	1/1	0.80	0.23	85,85,85,85	0
56	MG	1H	3190	1/1	0.80	0.27	80,80,80,80	0
56	MG	14	3233	1/1	0.80	0.15	72,72,72,72	0
56	MG	1G	1648	1/1	0.80	0.30	85,85,85,85	0
56	MG	1H	3233	1/1	0.80	0.14	85,85,85,85	0
56	MG	1G	1672	1/1	0.80	0.24	96,96,96,96	0
56	MG	13	1662	1/1	0.80	0.24	105,105,105,105	0
56	MG	14	3299	1/1	0.80	0.37	78,78,78,78	0
56	MG	14	3204	1/1	0.80	0.39	76,76,76,76	0
56	MG	1H	3271	1/1	0.80	0.32	93,93,93,93	0
56	MG	1H	3412	1/1	0.80	0.30	86,86,86,86	0
56	MG	1H	3417	1/1	0.80	0.29	93,93,93,93	0
56	MG	13	1673	1/1	0.80	0.45	88,88,88,88	0
56	MG	1H	3034	1/1	0.80	0.29	64,64,64,64	0
56	MG	13	1630	1/1	0.80	0.23	74,74,74,74	0
56	MG	1H	3425	1/1	0.80	0.46	101,101,101,101	0
56	MG	13	1710	1/1	0.81	0.21	103,103,103,103	0
56	MG	1H	3281	1/1	0.81	0.30	86,86,86,86	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1H	3214	1/1	0.81	0.39	93,93,93,93	0
56	MG	14	3251	1/1	0.81	0.28	77,77,77,77	0
56	MG	1H	3021	1/1	0.81	0.23	67,67,67,67	0
56	MG	14	3076	1/1	0.81	0.28	78,78,78,78	0
56	MG	1G	1668	1/1	0.81	0.24	106,106,106,106	0
56	MG	1G	1669	1/1	0.81	0.27	85,85,85,85	0
56	MG	1H	3347	1/1	0.81	0.50	89,89,89,89	0
56	MG	1H	3195	1/1	0.81	0.21	84,84,84,84	0
56	MG	1H	3049	1/1	0.81	0.19	95,95,95,95	0
56	MG	1H	3265	1/1	0.81	0.20	72,72,72,72	0
56	MG	14	3009	1/1	0.81	0.26	78,78,78,78	0
56	MG	14	3208	1/1	0.81	0.15	89,89,89,89	0
56	MG	14	3019	1/1	0.81	0.13	70,70,70,70	0
56	MG	1H	3326	1/1	0.81	0.33	67,67,67,67	0
56	MG	14	3119	1/1	0.81	0.09	91,91,91,91	0
56	MG	1H	3424	1/1	0.81	0.20	65,65,65,65	0
56	MG	1H	3293	1/1	0.81	0.15	95,95,95,95	0
56	MG	1H	3174	1/1	0.81	0.39	86,86,86,86	0
56	MG	16	203	1/1	0.81	0.28	85,85,85,85	0
56	MG	1H	3186	1/1	0.81	0.31	97,97,97,97	0
56	MG	13	1651	1/1	0.81	0.30	91,91,91,91	0
56	MG	14	3049	1/1	0.81	0.10	89,89,89,89	0
56	MG	14	3051	1/1	0.81	0.21	75,75,75,75	0
56	MG	14	3228	1/1	0.81	0.13	79,79,79,79	0
56	MG	1H	3335	1/1	0.81	0.37	103,103,103,103	0
56	MG	14	3064	1/1	0.81	0.16	53,53,53,53	0
56	MG	14	3163	1/1	0.81	0.27	90,90,90,90	0
56	MG	1H	3160	1/1	0.81	0.13	66,66,66,66	0
56	MG	45	201	1/1	0.81	0.19	95,95,95,95	0
56	MG	1H	3016	1/1	0.82	0.33	66,66,66,66	0
56	MG	1H	3044	1/1	0.82	0.20	66,66,66,66	0
56	MG	1H	3459	1/1	0.82	0.18	102,102,102,102	0
56	MG	13	1609	1/1	0.82	0.14	83,83,83,83	0
56	MG	1H	3118	1/1	0.82	0.22	74,74,74,74	0
56	MG	1H	3385	1/1	0.82	0.35	75,75,75,75	0
56	MG	14	3273	1/1	0.82	0.20	70,70,70,70	0
56	MG	13	1638	1/1	0.82	0.30	85,85,85,85	0
56	MG	13	1726	1/1	0.82	0.13	99,99,99,99	0
56	MG	1H	3201	1/1	0.82	0.31	77,77,77,77	0
56	MG	BA	201	1/1	0.82	0.14	102,102,102,102	0
56	MG	14	3075	1/1	0.82	0.29	94,94,94,94	0
56	MG	1H	3404	1/1	0.82	0.45	80,80,80,80	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1H	3321	1/1	0.82	0.21	99,99,99,99	0
56	MG	1G	1641	1/1	0.82	0.21	95,95,95,95	0
56	MG	1H	3266	1/1	0.82	0.20	83,83,83,83	0
56	MG	78	202	1/1	0.82	0.22	87,87,87,87	0
56	MG	14	3237	1/1	0.82	0.20	81,81,81,81	0
56	MG	1H	3407	1/1	0.82	0.28	81,81,81,81	0
56	MG	14	3239	1/1	0.82	0.14	53,53,53,53	0
56	MG	1H	3268	1/1	0.82	0.21	86,86,86,86	0
56	MG	1G	1604	1/1	0.82	0.34	87,87,87,87	0
56	MG	1H	3231	1/1	0.82	0.22	83,83,83,83	0
56	MG	1H	3168	1/1	0.82	0.14	84,84,84,84	0
56	MG	13	1604	1/1	0.82	0.21	77,77,77,77	0
56	MG	1H	3365	1/1	0.82	0.17	83,83,83,83	0
56	MG	1G	1722	1/1	0.83	0.22	111,111,111,111	0
56	MG	1H	3083	1/1	0.83	0.27	82,82,82,82	0
56	MG	2K	102	1/1	0.83	0.35	81,81,81,81	0
56	MG	14	3068	1/1	0.83	0.13	78,78,78,78	0
56	MG	14	3143	1/1	0.83	0.40	86,86,86,86	0
56	MG	14	3213	1/1	0.83	0.27	87,87,87,87	0
56	MG	14	3146	1/1	0.83	0.28	83,83,83,83	0
56	MG	13	1763	1/1	0.83	0.10	131,131,131,131	0
56	MG	16	208	1/1	0.83	0.11	95,95,95,95	0
56	MG	1H	3338	1/1	0.83	0.37	83,83,83,83	0
56	MG	14	3220	1/1	0.83	0.17	95,95,95,95	0
56	MG	14	3152	1/1	0.83	0.23	77,77,77,77	0
56	MG	1H	3310	1/1	0.83	0.27	82,82,82,82	0
56	MG	1H	3147	1/1	0.83	0.30	83,83,83,83	0
56	MG	21	302	1/1	0.83	0.16	76,76,76,76	0
56	MG	1G	1689	1/1	0.83	0.33	81,81,81,81	0
56	MG	13	1764	1/1	0.83	0.15	128,128,128,128	0
56	MG	1G	1660	1/1	0.83	0.16	91,91,91,91	0
56	MG	14	3300	1/1	0.83	0.38	84,84,84,84	0
56	MG	14	3421	1/1	0.83	0.25	72,72,72,72	0
56	MG	1H	3423	1/1	0.83	0.16	74,74,74,74	0
56	MG	14	3035	1/1	0.83	0.20	67,67,67,67	0
56	MG	14	3083	1/1	0.83	0.21	73,73,73,73	0
56	MG	13	1642	1/1	0.83	0.34	66,66,66,66	0
56	MG	13	1731	1/1	0.83	0.26	75,75,75,75	0
56	MG	1H	3226	1/1	0.83	0.25	77,77,77,77	0
56	MG	1H	3354	1/1	0.83	0.20	81,81,81,81	0
56	MG	13	1734	1/1	0.83	0.41	87,87,87,87	0
56	MG	BI	202	1/1	0.83	0.13	122,122,122,122	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1G	1635	1/1	0.84	0.19	106,106,106,106	0
56	MG	1G	1639	1/1	0.84	0.18	113,113,113,113	0
56	MG	1H	3280	1/1	0.84	0.29	90,90,90,90	0
56	MG	14	3252	1/1	0.84	0.25	76,76,76,76	0
56	MG	1H	3235	1/1	0.84	0.13	66,66,66,66	0
56	MG	14	3090	1/1	0.84	0.25	59,59,59,59	0
56	MG	1H	3415	1/1	0.84	0.28	77,77,77,77	0
56	MG	13	1654	1/1	0.84	0.34	86,86,86,86	0
56	MG	14	3264	1/1	0.84	0.29	82,82,82,82	0
56	MG	1G	1647	1/1	0.84	0.34	92,92,92,92	0
56	MG	1G	1679	1/1	0.84	0.22	74,74,74,74	0
56	MG	1G	1681	1/1	0.84	0.32	89,89,89,89	0
56	MG	1H	3102	1/1	0.84	0.34	63,63,63,63	0
56	MG	1H	3206	1/1	0.84	0.18	73,73,73,73	0
56	MG	1H	3103	1/1	0.84	0.31	64,64,64,64	0
56	MG	1H	3210	1/1	0.84	0.24	68,68,68,68	0
56	MG	1H	3332	1/1	0.84	0.13	83,83,83,83	0
56	MG	1H	3171	1/1	0.84	0.31	90,90,90,90	0
56	MG	14	3283	1/1	0.84	0.37	84,84,84,84	0
56	MG	14	3284	1/1	0.84	0.18	77,77,77,77	0
56	MG	1H	3172	1/1	0.84	0.35	96,96,96,96	0
56	MG	13	1725	1/1	0.84	0.14	101,101,101,101	0
56	MG	14	3287	1/1	0.84	0.31	86,86,86,86	0
56	MG	16	202	1/1	0.84	0.28	77,77,77,77	0
56	MG	1H	3084	1/1	0.84	0.22	72,72,72,72	0
56	MG	13	1672	1/1	0.84	0.08	80,80,80,80	0
56	MG	14	3153	1/1	0.84	0.09	90,90,90,90	0
56	MG	1H	3228	1/1	0.84	0.29	85,85,85,85	0
56	MG	14	3321	1/1	0.84	0.12	131,131,131,131	0
56	MG	14	3226	1/1	0.84	0.28	60,60,60,60	0
56	MG	1H	3397	1/1	0.84	0.27	60,60,60,60	0
56	MG	1G	1738	1/1	0.84	0.13	105,105,105,105	0
56	MG	1H	3229	1/1	0.84	0.25	83,83,83,83	0
56	MG	14	3165	1/1	0.84	0.27	83,83,83,83	0
56	MG	14	3166	1/1	0.84	0.17	88,88,88,88	0
56	MG	1H	3155	1/1	0.84	0.22	73,73,73,73	0
56	MG	13	1627	1/1	0.84	0.25	93,93,93,93	0
56	MG	14	3244	1/1	0.84	0.23	67,67,67,67	0
56	MG	1H	3119	1/1	0.84	0.29	76,76,76,76	0
56	MG	14	3001	1/1	0.85	0.30	76,76,76,76	0
56	MG	1H	3157	1/1	0.85	0.32	78,78,78,78	0
56	MG	1G	1637	1/1	0.85	0.14	121,121,121,121	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1H	3086	1/1	0.85	0.19	83,83,83,83	0
56	MG	1H	3055	1/1	0.85	0.19	69,69,69,69	0
56	MG	13	1712	1/1	0.85	0.08	106,106,106,106	0
56	MG	14	3101	1/1	0.85	0.34	79,79,79,79	0
56	MG	13	1723	1/1	0.85	0.20	98,98,98,98	0
56	MG	14	3030	1/1	0.85	0.19	78,78,78,78	0
56	MG	1H	3409	1/1	0.85	0.37	75,75,75,75	0
56	MG	1H	3037	1/1	0.85	0.21	57,57,57,57	0
56	MG	1H	3413	1/1	0.85	0.24	81,81,81,81	0
56	MG	1H	3307	1/1	0.85	0.21	89,89,89,89	0
56	MG	14	3277	1/1	0.85	0.35	90,90,90,90	0
56	MG	14	3279	1/1	0.85	0.41	96,96,96,96	0
56	MG	14	3215	1/1	0.85	0.24	94,94,94,94	0
56	MG	14	3129	1/1	0.85	0.40	84,84,84,84	0
56	MG	1H	3188	1/1	0.85	0.07	90,90,90,90	0
56	MG	1H	3237	1/1	0.85	0.11	72,72,72,72	0
56	MG	1H	3208	1/1	0.85	0.28	86,86,86,86	0
56	MG	14	3145	1/1	0.85	0.30	88,88,88,88	0
56	MG	1H	3240	1/1	0.85	0.24	64,64,64,64	0
56	MG	14	3288	1/1	0.85	0.35	94,94,94,94	0
56	MG	1H	3145	1/1	0.85	0.43	91,91,91,91	0
56	MG	1H	3367	1/1	0.85	0.12	97,97,97,97	0
56	MG	14	3295	1/1	0.85	0.28	91,91,91,91	0
56	MG	13	1719	1/1	0.85	0.27	106,106,106,106	0
56	MG	14	3066	1/1	0.85	0.26	67,67,67,67	0
56	MG	1G	1617	1/1	0.85	0.14	92,92,92,92	0
56	MG	1H	3249	1/1	0.85	0.15	70,70,70,70	0
56	MG	14	3330	1/1	0.85	0.12	82,82,82,82	0
56	MG	1G	1661	1/1	0.85	0.31	94,94,94,94	0
56	MG	13	1747	1/1	0.85	0.17	93,93,93,93	0
56	MG	14	3073	1/1	0.85	0.19	72,72,72,72	0
56	MG	1J	203	1/1	0.85	0.12	98,98,98,98	0
56	MG	1H	3222	1/1	0.85	0.28	78,78,78,78	0
56	MG	1H	3255	1/1	0.85	0.29	75,75,75,75	0
56	MG	14	3169	1/1	0.85	0.58	73,73,73,73	0
56	MG	1H	3256	1/1	0.85	0.27	85,85,85,85	0
56	MG	1H	3391	1/1	0.85	0.24	61,61,61,61	0
56	MG	1H	3031	1/1	0.85	0.26	56,56,56,56	0
56	MG	13	1660	1/1	0.85	0.29	83,83,83,83	0
56	MG	1H	3184	1/1	0.86	0.52	79,79,79,79	0
56	MG	14	3102	1/1	0.86	0.18	67,67,67,67	0
56	MG	14	3053	1/1	0.86	0.14	72,72,72,72	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	14	3173	1/1	0.86	0.19	77,77,77,77	0
56	MG	14	3112	1/1	0.86	0.22	83,83,83,83	0
56	MG	1H	3185	1/1	0.86	0.14	87,87,87,87	0
56	MG	1H	3097	1/1	0.86	0.15	70,70,70,70	0
56	MG	1H	3009	1/1	0.86	0.23	66,66,66,66	0
56	MG	14	3191	1/1	0.86	0.16	84,84,84,84	0
56	MG	1H	3213	1/1	0.86	0.11	69,69,69,69	0
56	MG	1G	1631	1/1	0.86	0.20	85,85,85,85	0
56	MG	14	3291	1/1	0.86	0.28	86,86,86,86	0
56	MG	14	3293	1/1	0.86	0.27	81,81,81,81	0
56	MG	1H	3136	1/1	0.86	0.26	68,68,68,68	0
56	MG	1H	3139	1/1	0.86	0.31	79,79,79,79	0
56	MG	1H	3082	1/1	0.86	0.28	76,76,76,76	0
56	MG	1H	3025	1/1	0.86	0.15	49,49,49,49	0
56	MG	14	3022	1/1	0.86	0.26	78,78,78,78	0
56	MG	1H	3104	1/1	0.86	0.29	65,65,65,65	0
56	MG	1H	3550	1/1	0.86	0.12	70,70,70,70	0
56	MG	13	1693	1/1	0.86	0.12	82,82,82,82	0
56	MG	1H	3150	1/1	0.86	0.20	88,88,88,88	0
56	MG	1G	1697	1/1	0.86	0.15	106,106,106,106	0
56	MG	1H	3357	1/1	0.86	0.07	66,66,66,66	0
56	MG	13	1633	1/1	0.86	0.30	82,82,82,82	0
56	MG	14	3043	1/1	0.86	0.10	73,73,73,73	0
56	MG	14	3271	1/1	0.86	0.28	73,73,73,73	0
56	MG	14	3089	1/1	0.86	0.21	72,72,72,72	0
56	MG	1H	3065	1/1	0.86	0.18	69,69,69,69	0
56	MG	13	1605	1/1	0.86	0.09	86,86,86,86	0
56	MG	1H	3096	1/1	0.86	0.14	63,63,63,63	0
56	MG	85	201	1/1	0.86	0.50	75,75,75,75	0
56	MG	1G	1698	1/1	0.87	0.33	88,88,88,88	0
56	MG	1H	3131	1/1	0.87	0.29	65,65,65,65	0
56	MG	1H	3161	1/1	0.87	0.34	76,76,76,76	0
56	MG	1H	3018	1/1	0.87	0.28	49,49,49,49	0
56	MG	1H	3019	1/1	0.87	0.13	53,53,53,53	0
56	MG	1H	3020	1/1	0.87	0.15	56,56,56,56	0
56	MG	1G	1632	1/1	0.87	0.38	83,83,83,83	0
56	MG	14	3278	1/1	0.87	0.10	74,74,74,74	0
56	MG	1H	3003	1/1	0.87	0.29	56,56,56,56	0
56	MG	14	3148	1/1	0.87	0.18	84,84,84,84	0
56	MG	1H	3056	1/1	0.87	0.17	73,73,73,73	0
56	MG	1H	3275	1/1	0.87	0.08	70,70,70,70	0
56	MG	1H	3058	1/1	0.87	0.24	69,69,69,69	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1H	3353	1/1	0.87	0.24	77,77,77,77	0
56	MG	1H	3306	1/1	0.87	0.45	87,87,87,87	0
56	MG	1H	3246	1/1	0.87	0.14	81,81,81,81	0
56	MG	1H	3218	1/1	0.87	0.24	70,70,70,70	0
56	MG	14	3227	1/1	0.87	0.38	75,75,75,75	0
56	MG	14	3011	1/1	0.87	0.09	70,70,70,70	0
56	MG	14	3292	1/1	0.87	0.23	88,88,88,88	0
56	MG	1G	1645	1/1	0.87	0.25	101,101,101,101	0
56	MG	1G	1602	1/1	0.87	0.17	83,83,83,83	0
56	MG	1H	3219	1/1	0.87	0.43	98,98,98,98	0
56	MG	1G	1683	1/1	0.87	0.42	87,87,87,87	0
56	MG	1H	3317	1/1	0.87	0.11	102,102,102,102	0
56	MG	13	1746	1/1	0.87	0.14	96,96,96,96	0
56	MG	14	3240	1/1	0.87	0.25	86,86,86,86	0
56	MG	1H	3364	1/1	0.87	0.19	87,87,87,87	0
56	MG	14	3099	1/1	0.87	0.11	66,66,66,66	0
56	MG	1H	3149	1/1	0.87	0.33	64,64,64,64	0
56	MG	1H	3285	1/1	0.87	0.60	85,85,85,85	0
56	MG	14	3184	1/1	0.87	0.30	85,85,85,85	0
56	MG	14	3190	1/1	0.87	0.29	81,81,81,81	0
56	MG	14	3108	1/1	0.87	0.10	81,81,81,81	0
56	MG	1H	3287	1/1	0.87	0.14	80,80,80,80	0
56	MG	1H	3116	1/1	0.87	0.26	71,71,71,71	0
56	MG	13	1687	1/1	0.87	0.34	82,82,82,82	0
56	MG	1H	3015	1/1	0.87	0.21	47,47,47,47	0
56	MG	13	1677	1/1	0.87	0.24	94,94,94,94	0
56	MG	14	3052	1/1	0.87	0.11	78,78,78,78	0
56	MG	14	3167	1/1	0.88	0.11	81,81,81,81	0
56	MG	1H	3076	1/1	0.88	0.17	88,88,88,88	0
56	MG	1H	3319	1/1	0.88	0.22	85,85,85,85	0
56	MG	1H	3274	1/1	0.88	0.26	79,79,79,79	0
56	MG	1H	3142	1/1	0.88	0.13	79,79,79,79	0
56	MG	98	201	1/1	0.88	0.26	56,56,56,56	0
56	MG	1H	3323	1/1	0.88	0.10	69,69,69,69	0
56	MG	14	3180	1/1	0.88	0.12	82,82,82,82	0
56	MG	13	1692	1/1	0.88	0.12	102,102,102,102	0
56	MG	1H	3232	1/1	0.88	0.20	82,82,82,82	0
56	MG	13	1724	1/1	0.88	0.12	97,97,97,97	0
56	MG	13	1614	1/1	0.88	0.14	69,69,69,69	0
56	MG	1H	3105	1/1	0.88	0.23	54,54,54,54	0
56	MG	14	3274	1/1	0.88	0.11	64,64,64,64	0
56	MG	13	1704	1/1	0.88	0.11	85,85,85,85	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	14	3194	1/1	0.88	0.18	75,75,75,75	0
56	MG	1H	3024	1/1	0.88	0.22	54,54,54,54	0
56	MG	14	3097	1/1	0.88	0.10	76,76,76,76	0
56	MG	1H	3244	1/1	0.88	0.08	70,70,70,70	0
56	MG	14	3017	1/1	0.88	0.17	77,77,77,77	0
56	MG	1H	3289	1/1	0.88	0.20	85,85,85,85	0
56	MG	14	3282	1/1	0.88	0.25	67,67,67,67	0
56	MG	14	3106	1/1	0.88	0.23	80,80,80,80	0
56	MG	1H	3245	1/1	0.88	0.24	57,57,57,57	0
56	MG	1H	3182	1/1	0.88	0.12	85,85,85,85	0
56	MG	1H	3341	1/1	0.88	0.11	80,80,80,80	0
56	MG	14	3114	1/1	0.88	0.29	60,60,60,60	0
56	MG	1H	3048	1/1	0.88	0.27	67,67,67,67	0
56	MG	1H	3211	1/1	0.88	0.25	80,80,80,80	0
56	MG	1H	3087	1/1	0.88	0.16	54,54,54,54	0
56	MG	1H	3156	1/1	0.88	0.37	69,69,69,69	0
56	MG	1G	1630	1/1	0.88	0.28	95,95,95,95	0
56	MG	1H	3217	1/1	0.88	0.22	87,87,87,87	0
56	MG	13	1670	1/1	0.88	0.15	84,84,84,84	0
56	MG	1H	3050	1/1	0.88	0.22	51,51,51,51	0
56	MG	14	3140	1/1	0.88	0.18	88,88,88,88	0
56	MG	1H	3469	1/1	0.88	0.14	93,93,93,93	0
56	MG	1G	1686	1/1	0.88	0.36	69,69,69,69	0
56	MG	1H	3120	1/1	0.88	0.24	75,75,75,75	0
56	MG	1H	3095	1/1	0.88	0.09	64,64,64,64	0
56	MG	1H	3264	1/1	0.88	0.25	74,74,74,74	0
56	MG	14	3057	1/1	0.88	0.20	78,78,78,78	0
56	MG	14	3061	1/1	0.88	0.09	74,74,74,74	0
56	MG	1H	3223	1/1	0.88	0.10	65,65,65,65	0
56	MG	1H	3068	1/1	0.88	0.23	65,65,65,65	0
56	MG	1H	3070	1/1	0.88	0.25	78,78,78,78	0
56	MG	1H	3366	1/1	0.88	0.24	89,89,89,89	0
56	MG	1H	3194	1/1	0.88	0.29	62,62,62,62	0
56	MG	1H	3098	1/1	0.88	0.28	66,66,66,66	0
56	MG	1H	3313	1/1	0.88	0.23	87,87,87,87	0
56	MG	1H	3376	1/1	0.88	0.20	113,113,113,113	0
56	MG	E5	101	1/1	0.88	0.09	67,67,67,67	0
56	MG	1H	3267	1/1	0.89	0.16	84,84,84,84	0
56	MG	13	1709	1/1	0.89	0.24	73,73,73,73	0
56	MG	13	1745	1/1	0.89	0.11	87,87,87,87	0
56	MG	1H	3270	1/1	0.89	0.44	87,87,87,87	0
56	MG	1H	3039	1/1	0.89	0.25	62,62,62,62	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1H	3309	1/1	0.89	0.13	76,76,76,76	0
56	MG	14	3087	1/1	0.89	0.22	60,60,60,60	0
56	MG	13	1691	1/1	0.89	0.21	94,94,94,94	0
56	MG	14	3012	1/1	0.89	0.35	66,66,66,66	0
56	MG	1H	3001	1/1	0.89	0.26	55,55,55,55	0
56	MG	1H	3362	1/1	0.89	0.14	69,69,69,69	0
56	MG	1H	3047	1/1	0.89	0.26	60,60,60,60	0
56	MG	1G	1629	1/1	0.89	0.46	84,84,84,84	0
56	MG	13	1697	1/1	0.89	0.16	98,98,98,98	0
56	MG	1H	3547	1/1	0.89	0.13	85,85,85,85	0
56	MG	14	3033	1/1	0.89	0.30	86,86,86,86	0
56	MG	1H	3005	1/1	0.89	0.20	56,56,56,56	0
56	MG	13	1702	1/1	0.89	0.07	87,87,87,87	0
56	MG	14	3037	1/1	0.89	0.24	61,61,61,61	0
56	MG	14	3040	1/1	0.89	0.21	62,62,62,62	0
56	MG	1H	3152	1/1	0.89	0.12	75,75,75,75	0
56	MG	13	1679	1/1	0.89	0.16	83,83,83,83	0
56	MG	14	3122	1/1	0.89	0.16	55,55,55,55	0
56	MG	1G	1636	1/1	0.89	0.17	99,99,99,99	0
56	MG	1H	3011	1/1	0.89	0.08	46,46,46,46	0
56	MG	1H	3375	1/1	0.89	0.18	70,70,70,70	0
56	MG	1G	1688	1/1	0.89	0.16	89,89,89,89	0
56	MG	14	3130	1/1	0.89	0.14	65,65,65,65	0
56	MG	1H	3014	1/1	0.89	0.16	62,62,62,62	0
56	MG	1H	3057	1/1	0.89	0.24	52,52,52,52	0
56	MG	1H	3329	1/1	0.89	0.20	75,75,75,75	0
56	MG	1H	3220	1/1	0.89	0.34	79,79,79,79	0
56	MG	1H	3091	1/1	0.89	0.20	68,68,68,68	0
56	MG	14	3297	1/1	0.89	0.31	91,91,91,91	0
56	MG	1H	3254	1/1	0.89	0.23	68,68,68,68	0
56	MG	14	3063	1/1	0.89	0.16	80,80,80,80	0
56	MG	1H	3393	1/1	0.89	0.14	65,65,65,65	0
56	MG	1H	3123	1/1	0.89	0.21	70,70,70,70	0
56	MG	1H	3125	1/1	0.89	0.11	52,52,52,52	0
56	MG	14	3231	1/1	0.89	0.24	57,57,57,57	0
56	MG	14	3067	1/1	0.89	0.10	62,62,62,62	0
56	MG	13	1765	1/1	0.89	0.18	129,129,129,129	0
56	MG	1H	3259	1/1	0.89	0.12	69,69,69,69	0
56	MG	14	3156	1/1	0.89	0.31	68,68,68,68	0
56	MG	14	3159	1/1	0.89	0.26	66,66,66,66	0
56	MG	1H	3130	1/1	0.89	0.24	70,70,70,70	0
56	MG	14	3241	1/1	0.89	0.24	59,59,59,59	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1H	3196	1/1	0.89	0.12	68,68,68,68	0
56	MG	1H	3344	1/1	0.89	0.14	89,89,89,89	0
56	MG	13	1708	1/1	0.89	0.20	76,76,76,76	0
56	MG	1H	3410	1/1	0.89	0.40	71,71,71,71	0
56	MG	13	1730	1/1	0.89	0.14	100,100,100,100	0
56	MG	14	3157	1/1	0.90	0.31	86,86,86,86	0
56	MG	1H	3071	1/1	0.90	0.07	71,71,71,71	0
56	MG	1H	3325	1/1	0.90	0.24	90,90,90,90	0
56	MG	14	3247	1/1	0.90	0.21	59,59,59,59	0
56	MG	1G	1729	1/1	0.90	0.11	113,113,113,113	0
56	MG	14	3072	1/1	0.90	0.08	69,69,69,69	0
56	MG	13	1647	1/1	0.90	0.09	97,97,97,97	0
56	MG	1G	1752	1/1	0.90	0.16	139,139,139,139	0
56	MG	13	1613	1/1	0.90	0.18	78,78,78,78	0
56	MG	13	1661	1/1	0.90	0.18	75,75,75,75	0
56	MG	13	1626	1/1	0.90	0.12	78,78,78,78	0
56	MG	14	3263	1/1	0.90	0.36	81,81,81,81	0
56	MG	1H	3419	1/1	0.90	0.13	77,77,77,77	0
56	MG	1B	101	1/1	0.90	0.17	92,92,92,92	0
56	MG	1H	3420	1/1	0.90	0.30	75,75,75,75	0
56	MG	1H	3043	1/1	0.90	0.21	48,48,48,48	0
56	MG	13	1793	1/1	0.90	0.14	114,114,114,114	0
56	MG	1H	3370	1/1	0.90	0.13	84,84,84,84	0
56	MG	1H	3372	1/1	0.90	0.24	71,71,71,71	0
56	MG	1G	1619	1/1	0.90	0.12	94,94,94,94	0
56	MG	14	3094	1/1	0.90	0.28	64,64,64,64	0
56	MG	1H	3241	1/1	0.90	0.18	93,93,93,93	0
56	MG	14	3192	1/1	0.90	0.07	77,77,77,77	0
56	MG	1G	1667	1/1	0.90	0.15	104,104,104,104	0
56	MG	14	3018	1/1	0.90	0.21	66,66,66,66	0
56	MG	1H	3426	1/1	0.90	0.31	80,80,80,80	0
56	MG	1H	3137	1/1	0.90	0.32	74,74,74,74	0
56	MG	1H	3466	1/1	0.90	0.08	115,115,115,115	0
56	MG	1H	3164	1/1	0.90	0.13	78,78,78,78	0
56	MG	1H	3192	1/1	0.90	0.17	75,75,75,75	0
56	MG	1H	3138	1/1	0.90	0.17	75,75,75,75	0
56	MG	1H	3618	1/1	0.90	0.20	104,104,104,104	0
56	MG	1G	1676	1/1	0.90	0.14	81,81,81,81	0
56	MG	1H	3383	1/1	0.90	0.25	58,58,58,58	0
56	MG	14	3038	1/1	0.90	0.20	63,63,63,63	0
56	MG	1H	3060	1/1	0.90	0.19	63,63,63,63	0
56	MG	1G	1680	1/1	0.90	0.25	69,69,69,69	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1H	3278	1/1	0.90	0.32	69,69,69,69	0
56	MG	1H	3112	1/1	0.90	0.13	57,57,57,57	0
56	MG	1H	3046	1/1	0.90	0.11	73,73,73,73	0
56	MG	13	1645	1/1	0.90	0.19	74,74,74,74	0
56	MG	1H	3311	1/1	0.90	0.13	98,98,98,98	0
56	MG	14	3133	1/1	0.90	0.35	78,78,78,78	0
56	MG	1G	1638	1/1	0.90	0.22	93,93,93,93	0
56	MG	14	3138	1/1	0.90	0.15	71,71,71,71	0
56	MG	1H	3399	1/1	0.90	0.24	61,61,61,61	0
56	MG	14	3372	1/1	0.90	0.15	91,91,91,91	0
56	MG	1H	3115	1/1	0.90	0.13	69,69,69,69	0
56	MG	14	3054	1/1	0.90	0.09	48,48,48,48	0
56	MG	14	3229	1/1	0.90	0.23	92,92,92,92	0
56	MG	1H	3063	1/1	0.90	0.22	54,54,54,54	0
56	MG	1G	1643	1/1	0.90	0.25	92,92,92,92	0
56	MG	1H	3284	1/1	0.90	0.38	79,79,79,79	0
56	MG	16	212	1/1	0.90	0.49	65,65,65,65	0
56	MG	14	3236	1/1	0.90	0.16	69,69,69,69	0
56	MG	21	301	1/1	0.90	0.07	64,64,64,64	0
56	MG	13	1698	1/1	0.90	0.14	99,99,99,99	0
56	MG	68	201	1/1	0.90	0.13	84,84,84,84	0
56	MG	1H	3022	1/1	0.90	0.20	51,51,51,51	0
56	MG	13	1653	1/1	0.90	0.13	82,82,82,82	0
56	MG	1H	3180	1/1	0.91	0.32	88,88,88,88	0
56	MG	14	3158	1/1	0.91	0.25	80,80,80,80	0
56	MG	1H	3403	1/1	0.91	0.23	76,76,76,76	0
56	MG	14	3160	1/1	0.91	0.41	86,86,86,86	0
56	MG	1H	3296	1/1	0.91	0.08	68,68,68,68	0
56	MG	13	1795	1/1	0.91	0.09	100,100,100,100	0
56	MG	1H	3033	1/1	0.91	0.18	64,64,64,64	0
56	MG	14	3254	1/1	0.91	0.26	55,55,55,55	0
56	MG	14	3258	1/1	0.91	0.27	50,50,50,50	0
56	MG	13	1648	1/1	0.91	0.40	77,77,77,77	0
56	MG	2I	201	1/1	0.91	0.14	91,91,91,91	0
56	MG	2L	101	1/1	0.91	0.21	86,86,86,86	0
56	MG	1H	3349	1/1	0.91	0.28	74,74,74,74	0
56	MG	1H	3262	1/1	0.91	0.10	73,73,73,73	0
56	MG	1H	3351	1/1	0.91	0.08	68,68,68,68	0
56	MG	14	3265	1/1	0.91	0.21	83,83,83,83	0
56	MG	13	1629	1/1	0.91	0.19	71,71,71,71	0
56	MG	14	3267	1/1	0.91	0.14	77,77,77,77	0
56	MG	14	3084	1/1	0.91	0.17	77,77,77,77	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1H	3088	1/1	0.91	0.21	62,62,62,62	0
56	MG	14	3010	1/1	0.91	0.25	68,68,68,68	0
56	MG	13	1688	1/1	0.91	0.30	86,86,86,86	0
56	MG	14	3092	1/1	0.91	0.20	79,79,79,79	0
56	MG	1H	3189	1/1	0.91	0.36	77,77,77,77	0
56	MG	13	1603	1/1	0.91	0.06	52,52,52,52	0
56	MG	1H	3121	1/1	0.91	0.23	67,67,67,67	0
56	MG	1H	3159	1/1	0.91	0.20	66,66,66,66	0
56	MG	1K	500	1/1	0.91	0.12	101,101,101,101	0
56	MG	1G	1623	1/1	0.91	0.15	86,86,86,86	0
56	MG	14	3195	1/1	0.91	0.13	84,84,84,84	0
56	MG	14	3026	1/1	0.91	0.17	65,65,65,65	0
56	MG	14	3105	1/1	0.91	0.17	64,64,64,64	0
56	MG	2K	101	1/1	0.91	0.23	69,69,69,69	0
56	MG	13	1713	1/1	0.91	0.13	82,82,82,82	0
56	MG	14	3110	1/1	0.91	0.38	85,85,85,85	0
56	MG	1H	3067	1/1	0.91	0.16	68,68,68,68	0
56	MG	1G	1677	1/1	0.91	0.09	94,94,94,94	0
56	MG	1H	3439	1/1	0.91	0.15	59,59,59,59	0
56	MG	13	1631	1/1	0.91	0.15	88,88,88,88	0
56	MG	13	1715	1/1	0.91	0.13	102,102,102,102	0
56	MG	14	3120	1/1	0.91	0.21	70,70,70,70	0
56	MG	1H	3166	1/1	0.91	0.14	87,87,87,87	0
56	MG	1H	3519	1/1	0.91	0.10	73,73,73,73	0
56	MG	1H	3239	1/1	0.91	0.13	78,78,78,78	0
56	MG	1H	3167	1/1	0.91	0.12	83,83,83,83	0
56	MG	14	3128	1/1	0.91	0.26	82,82,82,82	0
56	MG	1H	3135	1/1	0.91	0.22	59,59,59,59	0
56	MG	13	1616	1/1	0.91	0.12	79,79,79,79	0
56	MG	14	3301	1/1	0.91	0.14	85,85,85,85	0
56	MG	1H	3073	1/1	0.91	0.24	58,58,58,58	0
56	MG	1H	3380	1/1	0.91	0.28	66,66,66,66	0
56	MG	13	1774	1/1	0.91	0.12	87,87,87,87	0
56	MG	1H	3331	1/1	0.91	0.11	69,69,69,69	0
56	MG	1H	3286	1/1	0.91	0.23	68,68,68,68	0
56	MG	13	1779	1/1	0.91	0.15	106,106,106,106	0
56	MG	1H	3141	1/1	0.91	0.21	71,71,71,71	0
56	MG	1H	3392	1/1	0.91	0.27	54,54,54,54	0
56	MG	1H	3106	1/1	0.91	0.14	77,77,77,77	0
56	MG	13	1701	1/1	0.91	0.14	95,95,95,95	0
56	MG	29	301	1/1	0.91	0.07	78,78,78,78	0
56	MG	1H	3110	1/1	0.91	0.21	50,50,50,50	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	11	301	1/1	0.91	0.30	47,47,47,47	0
56	MG	1G	1710	1/1	0.91	0.13	102,102,102,102	0
56	MG	1G	1712	1/1	0.91	0.07	132,132,132,132	0
56	MG	1H	3215	1/1	0.91	0.10	61,61,61,61	0
56	MG	1H	3400	1/1	0.91	0.24	48,48,48,48	0
56	MG	13	1757	1/1	0.92	0.07	119,119,119,119	0
56	MG	1H	3053	1/1	0.92	0.07	53,53,53,53	0
56	MG	1H	3151	1/1	0.92	0.31	78,78,78,78	0
56	MG	1H	3170	1/1	0.92	0.18	73,73,73,73	0
56	MG	1H	3427	1/1	0.92	0.21	64,64,64,64	0
56	MG	1H	3434	1/1	0.92	0.07	86,86,86,86	0
56	MG	1G	1613	1/1	0.92	0.12	88,88,88,88	0
56	MG	14	3007	1/1	0.92	0.21	61,61,61,61	0
56	MG	14	3008	1/1	0.92	0.18	72,72,72,72	0
56	MG	14	3172	1/1	0.92	0.06	77,77,77,77	0
56	MG	1H	3387	1/1	0.92	0.35	71,71,71,71	0
56	MG	14	3174	1/1	0.92	0.07	81,81,81,81	0
56	MG	14	3177	1/1	0.92	0.12	92,92,92,92	0
56	MG	1H	3441	1/1	0.92	0.07	115,115,115,115	0
56	MG	1H	3445	1/1	0.92	0.22	90,90,90,90	0
56	MG	1H	3314	1/1	0.92	0.11	72,72,72,72	0
56	MG	1H	3209	1/1	0.92	0.28	80,80,80,80	0
56	MG	1H	3318	1/1	0.92	0.11	68,68,68,68	0
56	MG	1H	3471	1/1	0.92	0.12	91,91,91,91	0
56	MG	1H	3472	1/1	0.92	0.08	108,108,108,108	0
56	MG	1H	3394	1/1	0.92	0.20	67,67,67,67	0
56	MG	1H	3352	1/1	0.92	0.13	68,68,68,68	0
56	MG	14	3027	1/1	0.92	0.26	61,61,61,61	0
56	MG	1H	3288	1/1	0.92	0.13	79,79,79,79	0
56	MG	1H	3568	1/1	0.92	0.12	89,89,89,89	0
56	MG	14	3032	1/1	0.92	0.22	73,73,73,73	0
56	MG	1H	3608	1/1	0.92	0.07	110,110,110,110	0
56	MG	1H	3320	1/1	0.92	0.17	94,94,94,94	0
56	MG	1G	1682	1/1	0.92	0.13	79,79,79,79	0
56	MG	14	3203	1/1	0.92	0.20	83,83,83,83	0
56	MG	1H	3621	1/1	0.92	0.09	52,52,52,52	0
56	MG	14	3205	1/1	0.92	0.11	75,75,75,75	0
56	MG	1H	3069	1/1	0.92	0.22	80,80,80,80	0
56	MG	13	1652	1/1	0.92	0.12	75,75,75,75	0
56	MG	1H	3402	1/1	0.92	0.14	58,58,58,58	0
56	MG	1H	3236	1/1	0.92	0.10	80,80,80,80	0
56	MG	1H	3173	1/1	0.92	0.20	67,67,67,67	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	13	1617	1/1	0.92	0.16	84,84,84,84	0
56	MG	1H	3012	1/1	0.92	0.08	40,40,40,40	0
56	MG	1G	1640	1/1	0.92	0.08	82,82,82,82	0
56	MG	1H	3216	1/1	0.92	0.13	81,81,81,81	0
56	MG	13	1602	1/1	0.92	0.21	59,59,59,59	0
56	MG	14	3132	1/1	0.92	0.21	58,58,58,58	0
56	MG	14	3221	1/1	0.92	0.13	88,88,88,88	0
56	MG	1G	1695	1/1	0.92	0.44	96,96,96,96	0
56	MG	14	3135	1/1	0.92	0.12	90,90,90,90	0
56	MG	1H	3243	1/1	0.92	0.20	60,60,60,60	0
56	MG	14	3311	1/1	0.92	0.08	105,105,105,105	0
56	MG	14	3317	1/1	0.92	0.22	153,153,153,153	0
56	MG	14	3318	1/1	0.92	0.12	84,84,84,84	0
56	MG	1H	3042	1/1	0.92	0.10	79,79,79,79	0
56	MG	14	3056	1/1	0.92	0.13	80,80,80,80	0
56	MG	13	1743	1/1	0.92	0.09	91,91,91,91	0
56	MG	14	3400	1/1	0.92	0.15	87,87,87,87	0
56	MG	1H	3414	1/1	0.92	0.14	68,68,68,68	0
56	MG	1H	3197	1/1	0.92	0.19	65,65,65,65	0
56	MG	1H	3416	1/1	0.92	0.21	75,75,75,75	0
56	MG	1G	1708	1/1	0.92	0.13	105,105,105,105	0
56	MG	31	301	1/1	0.92	0.05	67,67,67,67	0
56	MG	13	1625	1/1	0.92	0.19	75,75,75,75	0
56	MG	13	1785	1/1	0.92	0.13	105,105,105,105	0
56	MG	13	1636	1/1	0.92	0.14	85,85,85,85	0
56	MG	13	1637	1/1	0.92	0.09	67,67,67,67	0
56	MG	1G	1748	1/1	0.92	0.10	107,107,107,107	0
56	MG	1H	3203	1/1	0.92	0.10	70,70,70,70	0
56	MG	P8	101	1/1	0.92	0.21	68,68,68,68	0
56	MG	55	201	1/1	0.92	0.40	85,85,85,85	0
56	MG	1G	1601	1/1	0.92	0.08	71,71,71,71	0
56	MG	13	1748	1/1	0.92	0.10	122,122,122,122	0
56	MG	68	202	1/1	0.93	0.16	90,90,90,90	0
56	MG	13	1635	1/1	0.93	0.18	75,75,75,75	0
56	MG	1H	3355	1/1	0.93	0.12	62,62,62,62	0
56	MG	1H	3478	1/1	0.93	0.11	68,68,68,68	0
56	MG	1H	3109	1/1	0.93	0.21	44,44,44,44	0
56	MG	I8	101	1/1	0.93	0.41	83,83,83,83	0
56	MG	1H	3040	1/1	0.93	0.09	62,62,62,62	0
56	MG	14	3103	1/1	0.93	0.24	78,78,78,78	0
56	MG	14	3161	1/1	0.93	0.12	66,66,66,66	0
56	MG	14	3104	1/1	0.93	0.17	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2L	102	1/1	0.93	0.07	113,113,113,113	0
56	MG	Q8	101	1/1	0.93	0.28	68,68,68,68	0
56	MG	13	1612	1/1	0.93	0.12	71,71,71,71	0
56	MG	1H	3200	1/1	0.93	0.05	79,79,79,79	0
56	MG	1G	1603	1/1	0.93	0.15	78,78,78,78	0
56	MG	1H	3580	1/1	0.93	0.16	77,77,77,77	0
56	MG	1H	3599	1/1	0.93	0.10	85,85,85,85	0
56	MG	14	3289	1/1	0.93	0.32	79,79,79,79	0
56	MG	14	3116	1/1	0.93	0.12	57,57,57,57	0
56	MG	1H	3124	1/1	0.93	0.14	52,52,52,52	0
56	MG	14	3118	1/1	0.93	0.06	66,66,66,66	0
56	MG	1H	3234	1/1	0.93	0.18	67,67,67,67	0
56	MG	BI	201	1/1	0.93	0.07	113,113,113,113	0
56	MG	14	3121	1/1	0.93	0.18	65,65,65,65	0
56	MG	1H	3158	1/1	0.93	0.30	81,81,81,81	0
56	MG	1H	3127	1/1	0.93	0.17	81,81,81,81	0
56	MG	1H	3342	1/1	0.93	0.17	75,75,75,75	0
56	MG	14	3242	1/1	0.93	0.19	66,66,66,66	0
56	MG	14	3243	1/1	0.93	0.13	52,52,52,52	0
56	MG	14	3306	1/1	0.93	0.09	66,66,66,66	0
56	MG	1H	3298	1/1	0.93	0.07	82,82,82,82	0
56	MG	14	3021	1/1	0.93	0.16	47,47,47,47	0
56	MG	1H	3257	1/1	0.93	0.09	82,82,82,82	0
56	MG	1H	3128	1/1	0.93	0.14	60,60,60,60	0
56	MG	1H	3428	1/1	0.93	0.24	57,57,57,57	0
56	MG	14	3352	1/1	0.93	0.14	90,90,90,90	0
56	MG	14	3367	1/1	0.93	0.13	86,86,86,86	0
56	MG	1H	3430	1/1	0.93	0.22	80,80,80,80	0
56	MG	14	3393	1/1	0.93	0.07	67,67,67,67	0
56	MG	1H	3373	1/1	0.93	0.28	84,84,84,84	0
56	MG	14	3405	1/1	0.93	0.08	108,108,108,108	0
56	MG	14	3420	1/1	0.93	0.06	86,86,86,86	0
56	MG	13	1740	1/1	0.93	0.34	76,76,76,76	0
56	MG	14	3424	1/1	0.93	0.07	94,94,94,94	0
56	MG	14	3136	1/1	0.93	0.17	58,58,58,58	0
56	MG	13	1639	1/1	0.93	0.19	76,76,76,76	0
56	MG	14	3199	1/1	0.93	0.09	67,67,67,67	0
56	MG	1H	3078	1/1	0.93	0.06	59,59,59,59	0
56	MG	1H	3451	1/1	0.93	0.21	85,85,85,85	0
56	MG	1H	3242	1/1	0.93	0.14	82,82,82,82	0
56	MG	1H	3132	1/1	0.93	0.20	46,46,46,46	0
56	MG	29	302	1/1	0.93	0.09	57,57,57,57	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	29	303	1/1	0.93	0.16	64,64,64,64	0
56	MG	21	303	1/1	0.93	0.17	51,51,51,51	0
56	MG	1H	3107	1/1	0.93	0.12	63,63,63,63	0
56	MG	41	201	1/1	0.93	0.12	69,69,69,69	0
56	MG	1H	3470	1/1	0.93	0.15	94,94,94,94	0
56	MG	14	3093	1/1	0.93	0.14	56,56,56,56	0
56	MG	14	3270	1/1	0.93	0.21	70,70,70,70	0
56	MG	14	3212	1/1	0.93	0.13	91,91,91,91	0
56	MG	1G	1685	1/1	0.94	0.26	76,76,76,76	0
56	MG	13	1640	1/1	0.94	0.07	65,65,65,65	0
56	MG	1H	3324	1/1	0.94	0.21	78,78,78,78	0
56	MG	88	203	1/1	0.94	0.36	79,79,79,79	0
56	MG	14	3098	1/1	0.94	0.10	67,67,67,67	0
56	MG	14	3175	1/1	0.94	0.12	70,70,70,70	0
56	MG	14	3176	1/1	0.94	0.09	73,73,73,73	0
56	MG	1H	3475	1/1	0.94	0.11	58,58,58,58	0
56	MG	1H	3260	1/1	0.94	0.10	69,69,69,69	0
56	MG	1H	3498	1/1	0.94	0.07	70,70,70,70	0
56	MG	14	3031	1/1	0.94	0.14	63,63,63,63	0
56	MG	14	3181	1/1	0.94	0.17	87,87,87,87	0
56	MG	13	1744	1/1	0.94	0.07	81,81,81,81	0
56	MG	1H	3384	1/1	0.94	0.21	49,49,49,49	0
56	MG	13	1762	1/1	0.94	0.05	128,128,128,128	0
56	MG	14	3185	1/1	0.94	0.30	78,78,78,78	0
56	MG	14	3186	1/1	0.94	0.11	77,77,77,77	0
56	MG	1G	1649	1/1	0.94	0.12	90,90,90,90	0
56	MG	14	3109	1/1	0.94	0.10	69,69,69,69	0
56	MG	14	3036	1/1	0.94	0.07	71,71,71,71	0
56	MG	1H	3085	1/1	0.94	0.20	46,46,46,46	0
56	MG	1H	3575	1/1	0.94	0.10	63,63,63,63	0
56	MG	1H	3579	1/1	0.94	0.10	81,81,81,81	0
56	MG	1H	3126	1/1	0.94	0.17	54,54,54,54	0
56	MG	1H	3581	1/1	0.94	0.08	87,87,87,87	0
56	MG	1H	3583	1/1	0.94	0.08	52,52,52,52	0
56	MG	1H	3032	1/1	0.94	0.10	57,57,57,57	0
56	MG	14	3046	1/1	0.94	0.06	56,56,56,56	0
56	MG	1G	1657	1/1	0.94	0.12	117,117,117,117	0
56	MG	14	3048	1/1	0.94	0.07	66,66,66,66	0
56	MG	1H	3308	1/1	0.94	0.10	78,78,78,78	0
56	MG	14	3206	1/1	0.94	0.21	87,87,87,87	0
56	MG	14	3050	1/1	0.94	0.08	62,62,62,62	0
56	MG	14	3125	1/1	0.94	0.11	84,84,84,84	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1G	1718	1/1	0.94	0.05	140,140,140,140	0
56	MG	1G	1721	1/1	0.94	0.18	143,143,143,143	0
56	MG	1G	1611	1/1	0.94	0.15	86,86,86,86	0
56	MG	1G	1725	1/1	0.94	0.09	111,111,111,111	0
56	MG	13	1789	1/1	0.94	0.08	63,63,63,63	0
56	MG	14	3296	1/1	0.94	0.12	68,68,68,68	0
56	MG	1G	1734	1/1	0.94	0.10	94,94,94,94	0
56	MG	13	1675	1/1	0.94	0.19	80,80,80,80	0
56	MG	14	3060	1/1	0.94	0.12	64,64,64,64	0
56	MG	1G	1741	1/1	0.94	0.13	98,98,98,98	0
56	MG	1G	1742	1/1	0.94	0.14	131,131,131,131	0
56	MG	14	3305	1/1	0.94	0.10	60,60,60,60	0
56	MG	1H	3089	1/1	0.94	0.14	62,62,62,62	0
56	MG	1H	3072	1/1	0.94	0.14	86,86,86,86	0
56	MG	13	1722	1/1	0.94	0.07	99,99,99,99	0
56	MG	14	3144	1/1	0.94	0.18	65,65,65,65	0
56	MG	2A	201	1/1	0.94	0.14	85,85,85,85	0
56	MG	1G	1620	1/1	0.94	0.09	83,83,83,83	0
56	MG	1H	3074	1/1	0.94	0.14	57,57,57,57	0
56	MG	14	3365	1/1	0.94	0.09	89,89,89,89	0
56	MG	1H	3316	1/1	0.94	0.08	106,106,106,106	0
56	MG	14	3149	1/1	0.94	0.12	74,74,74,74	0
56	MG	14	3388	1/1	0.94	0.14	87,87,87,87	0
56	MG	14	3391	1/1	0.94	0.10	106,106,106,106	0
56	MG	13	1732	1/1	0.94	0.13	65,65,65,65	0
56	MG	1H	3077	1/1	0.94	0.06	62,62,62,62	0
56	MG	14	3402	1/1	0.94	0.09	94,94,94,94	0
56	MG	1H	3343	1/1	0.94	0.09	76,76,76,76	0
56	MG	14	3234	1/1	0.94	0.11	60,60,60,60	0
56	MG	5E	201	1/1	0.94	0.17	79,79,79,79	0
56	MG	13	1766	1/1	0.94	0.08	70,70,70,70	0
56	MG	1H	3456	1/1	0.94	0.11	100,100,100,100	0
56	MG	1H	3100	1/1	0.94	0.05	69,69,69,69	0
56	MG	1H	3460	1/1	0.94	0.13	94,94,94,94	0
56	MG	1H	3463	1/1	0.94	0.07	101,101,101,101	0
56	MG	1H	3464	1/1	0.94	0.07	71,71,71,71	0
56	MG	1H	3465	1/1	0.94	0.07	111,111,111,111	0
56	MG	19	301	1/1	0.94	0.06	53,53,53,53	0
56	MG	1H	3051	1/1	0.94	0.05	46,46,46,46	0
56	MG	1H	3468	1/1	0.94	0.06	92,92,92,92	0
56	MG	14	3013	1/1	0.94	0.14	50,50,50,50	0
56	MG	14	3014	1/1	0.94	0.09	50,50,50,50	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1H	3348	1/1	0.94	0.06	87,87,87,87	0
56	MG	1H	3377	1/1	0.94	0.17	49,49,49,49	0
56	MG	14	3250	1/1	0.94	0.16	66,66,66,66	0
56	MG	14	3168	1/1	0.94	0.10	65,65,65,65	0
56	MG	78	201	1/1	0.94	0.10	62,62,62,62	0
56	MG	14	3253	1/1	0.94	0.19	59,59,59,59	0
56	MG	1H	3094	1/1	0.95	0.14	48,48,48,48	0
56	MG	1H	3529	1/1	0.95	0.07	49,49,49,49	0
56	MG	1G	1746	1/1	0.95	0.16	95,95,95,95	0
56	MG	1G	1747	1/1	0.95	0.07	95,95,95,95	0
56	MG	14	3058	1/1	0.95	0.15	78,78,78,78	0
56	MG	13	1801	1/1	0.95	0.11	113,113,113,113	0
56	MG	1H	3075	1/1	0.95	0.16	72,72,72,72	0
56	MG	14	3134	1/1	0.95	0.24	81,81,81,81	0
56	MG	1H	3562	1/1	0.95	0.08	97,97,97,97	0
56	MG	14	3207	1/1	0.95	0.16	67,67,67,67	0
56	MG	1H	3565	1/1	0.95	0.08	110,110,110,110	0
56	MG	13	1805	1/1	0.95	0.06	115,115,115,115	0
56	MG	1H	3169	1/1	0.95	0.12	56,56,56,56	0
56	MG	14	3139	1/1	0.95	0.08	69,69,69,69	0
56	MG	1G	1610	1/1	0.95	0.10	83,83,83,83	0
56	MG	14	3142	1/1	0.95	0.26	70,70,70,70	0
56	MG	1H	3144	1/1	0.95	0.22	57,57,57,57	0
56	MG	1H	3251	1/1	0.95	0.06	66,66,66,66	0
56	MG	1G	1614	1/1	0.95	0.12	71,71,71,71	0
56	MG	13	1601	1/1	0.95	0.15	58,58,58,58	0
56	MG	1H	3381	1/1	0.95	0.15	97,97,97,97	0
56	MG	1H	3597	1/1	0.95	0.07	92,92,92,92	0
56	MG	1H	3122	1/1	0.95	0.08	49,49,49,49	0
56	MG	1H	3603	1/1	0.95	0.08	121,121,121,121	0
56	MG	1H	3225	1/1	0.95	0.16	76,76,76,76	0
56	MG	1H	3616	1/1	0.95	0.25	73,73,73,73	0
56	MG	1H	3315	1/1	0.95	0.07	101,101,101,101	0
56	MG	1H	3004	1/1	0.95	0.08	35,35,35,35	0
56	MG	14	3155	1/1	0.95	0.10	65,65,65,65	0
56	MG	13	1676	1/1	0.95	0.10	68,68,68,68	0
56	MG	1H	3006	1/1	0.95	0.14	52,52,52,52	0
56	MG	1H	3008	1/1	0.95	0.16	47,47,47,47	0
56	MG	14	3304	1/1	0.95	0.05	103,103,103,103	0
56	MG	14	3015	1/1	0.95	0.08	51,51,51,51	0
56	MG	13	1751	1/1	0.95	0.06	106,106,106,106	0
56	MG	14	3307	1/1	0.95	0.13	89,89,89,89	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	14	3308	1/1	0.95	0.09	80,80,80,80	0
56	MG	1H	3437	1/1	0.95	0.06	90,90,90,90	0
56	MG	14	3315	1/1	0.95	0.06	93,93,93,93	0
56	MG	1H	3045	1/1	0.95	0.19	75,75,75,75	0
56	MG	1H	3154	1/1	0.95	0.09	74,74,74,74	0
56	MG	13	1755	1/1	0.95	0.07	94,94,94,94	0
56	MG	14	3322	1/1	0.95	0.06	123,123,123,123	0
56	MG	13	1646	1/1	0.95	0.12	58,58,58,58	0
56	MG	14	3343	1/1	0.95	0.08	54,54,54,54	0
56	MG	14	3345	1/1	0.95	0.14	89,89,89,89	0
56	MG	14	3025	1/1	0.95	0.09	46,46,46,46	0
56	MG	1H	3295	1/1	0.95	0.19	65,65,65,65	0
56	MG	8I	201	1/1	0.95	0.19	98,98,98,98	0
56	MG	1H	3359	1/1	0.95	0.12	58,58,58,58	0
56	MG	14	3385	1/1	0.95	0.15	84,84,84,84	0
56	MG	16	213	1/1	0.95	0.06	98,98,98,98	0
56	MG	1H	3013	1/1	0.95	0.16	42,42,42,42	0
56	MG	1H	3133	1/1	0.95	0.14	67,67,67,67	0
56	MG	14	3395	1/1	0.95	0.06	89,89,89,89	0
56	MG	13	1788	1/1	0.95	0.14	123,123,123,123	0
56	MG	1H	3330	1/1	0.95	0.11	70,70,70,70	0
56	MG	14	3403	1/1	0.95	0.07	101,101,101,101	0
56	MG	1H	3212	1/1	0.95	0.46	91,91,91,91	0
56	MG	14	3408	1/1	0.95	0.06	91,91,91,91	0
56	MG	14	3410	1/1	0.95	0.07	81,81,81,81	0
56	MG	14	3416	1/1	0.95	0.06	98,98,98,98	0
56	MG	14	3417	1/1	0.95	0.08	80,80,80,80	0
56	MG	14	3249	1/1	0.95	0.16	54,54,54,54	0
56	MG	31	302	1/1	0.95	0.26	76,76,76,76	0
56	MG	13	1699	1/1	0.95	0.07	94,94,94,94	0
56	MG	14	3427	1/1	0.95	0.09	104,104,104,104	0
56	MG	14	3429	1/1	0.95	0.06	91,91,91,91	0
56	MG	14	3434	1/1	0.95	0.08	61,61,61,61	0
56	MG	1H	3408	1/1	0.95	0.30	60,60,60,60	0
56	MG	13	1607	1/1	0.95	0.33	78,78,78,78	0
56	MG	1G	1704	1/1	0.95	0.07	85,85,85,85	0
56	MG	14	3256	1/1	0.95	0.12	75,75,75,75	0
56	MG	14	3257	1/1	0.95	0.12	62,62,62,62	0
56	MG	1H	3092	1/1	0.95	0.16	62,62,62,62	0
56	MG	1H	3473	1/1	0.95	0.05	112,112,112,112	0
56	MG	14	3044	1/1	0.95	0.06	71,71,71,71	0
56	MG	1H	3411	1/1	0.95	0.10	71,71,71,71	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1G	1713	1/1	0.95	0.05	119,119,119,119	0
56	MG	1H	3477	1/1	0.95	0.11	90,90,90,90	0
56	MG	1H	3369	1/1	0.95	0.07	95,95,95,95	0
56	MG	1H	3479	1/1	0.95	0.05	107,107,107,107	0
56	MG	1H	3480	1/1	0.95	0.08	113,113,113,113	0
56	MG	1H	3489	1/1	0.95	0.07	53,53,53,53	0
56	MG	13	1695	1/1	0.95	0.11	86,86,86,86	0
56	MG	1H	3506	1/1	0.95	0.09	58,58,58,58	0
56	MG	13	1610	1/1	0.96	0.06	56,56,56,56	0
56	MG	1H	3590	1/1	0.96	0.09	107,107,107,107	0
56	MG	1H	3591	1/1	0.96	0.06	70,70,70,70	0
56	MG	1H	3388	1/1	0.96	0.22	54,54,54,54	0
56	MG	14	3002	1/1	0.96	0.09	49,49,49,49	0
56	MG	13	1780	1/1	0.96	0.10	106,106,106,106	0
56	MG	14	3005	1/1	0.96	0.15	58,58,58,58	0
56	MG	1H	3601	1/1	0.96	0.06	84,84,84,84	0
56	MG	1H	3429	1/1	0.96	0.14	63,63,63,63	0
56	MG	14	3214	1/1	0.96	0.04	90,90,90,90	0
56	MG	1H	3064	1/1	0.96	0.07	59,59,59,59	0
56	MG	1H	3431	1/1	0.96	0.10	54,54,54,54	0
56	MG	13	1800	1/1	0.96	0.06	118,118,118,118	0
56	MG	1H	3436	1/1	0.96	0.10	98,98,98,98	0
56	MG	1H	3066	1/1	0.96	0.09	66,66,66,66	0
56	MG	1H	3002	1/1	0.96	0.13	40,40,40,40	0
56	MG	1G	1612	1/1	0.96	0.10	79,79,79,79	0
56	MG	1H	3481	1/1	0.96	0.08	122,122,122,122	0
56	MG	14	3078	1/1	0.96	0.05	54,54,54,54	0
56	MG	14	3016	1/1	0.96	0.13	51,51,51,51	0
56	MG	1H	3482	1/1	0.96	0.26	142,142,142,142	0
56	MG	1H	3484	1/1	0.96	0.06	45,45,45,45	0
56	MG	1H	3487	1/1	0.96	0.08	50,50,50,50	0
56	MG	14	3020	1/1	0.96	0.10	55,55,55,55	0
56	MG	1G	1702	1/1	0.96	0.06	101,101,101,101	0
56	MG	14	3085	1/1	0.96	0.15	62,62,62,62	0
56	MG	14	3086	1/1	0.96	0.10	59,59,59,59	0
56	MG	14	3313	1/1	0.96	0.06	82,82,82,82	0
56	MG	14	3232	1/1	0.96	0.14	66,66,66,66	0
56	MG	1H	3488	1/1	0.96	0.07	53,53,53,53	0
56	MG	14	3088	1/1	0.96	0.13	61,61,61,61	0
56	MG	14	3319	1/1	0.96	0.05	104,104,104,104	0
56	MG	14	3320	1/1	0.96	0.22	120,120,120,120	0
56	MG	1G	1706	1/1	0.96	0.10	95,95,95,95	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	14	3024	1/1	0.96	0.12	57,57,57,57	0
56	MG	1H	3440	1/1	0.96	0.06	59,59,59,59	0
56	MG	1G	1709	1/1	0.96	0.11	108,108,108,108	0
56	MG	1H	3491	1/1	0.96	0.08	57,57,57,57	0
56	MG	14	3028	1/1	0.96	0.05	53,53,53,53	0
56	MG	14	3364	1/1	0.96	0.10	108,108,108,108	0
56	MG	1G	1711	1/1	0.96	0.08	109,109,109,109	0
56	MG	14	3366	1/1	0.96	0.06	87,87,87,87	0
56	MG	13	1742	1/1	0.96	0.29	92,92,92,92	0
56	MG	14	3371	1/1	0.96	0.06	84,84,84,84	0
56	MG	1H	3505	1/1	0.96	0.08	51,51,51,51	0
56	MG	14	3382	1/1	0.96	0.05	88,88,88,88	0
56	MG	1G	1716	1/1	0.96	0.09	109,109,109,109	0
56	MG	14	3100	1/1	0.96	0.16	65,65,65,65	0
56	MG	1H	3398	1/1	0.96	0.11	47,47,47,47	0
56	MG	1H	3516	1/1	0.96	0.10	59,59,59,59	0
56	MG	1H	3446	1/1	0.96	0.07	87,87,87,87	0
56	MG	1H	3450	1/1	0.96	0.16	84,84,84,84	0
56	MG	13	1802	1/1	0.96	0.12	114,114,114,114	0
56	MG	1G	1670	1/1	0.96	0.08	99,99,99,99	0
56	MG	14	3404	1/1	0.96	0.14	85,85,85,85	0
56	MG	14	3107	1/1	0.96	0.07	68,68,68,68	0
56	MG	14	3039	1/1	0.96	0.08	61,61,61,61	0
56	MG	1G	1735	1/1	0.96	0.06	112,112,112,112	0
56	MG	13	1804	1/1	0.96	0.17	137,137,137,137	0
56	MG	1H	3554	1/1	0.96	0.23	108,108,108,108	0
56	MG	1H	3558	1/1	0.96	0.12	100,100,100,100	0
56	MG	14	3113	1/1	0.96	0.15	69,69,69,69	0
56	MG	1G	1745	1/1	0.96	0.18	124,124,124,124	0
56	MG	14	3115	1/1	0.96	0.09	57,57,57,57	0
56	MG	13	1750	1/1	0.96	0.12	122,122,122,122	0
56	MG	14	3432	1/1	0.96	0.09	91,91,91,91	0
56	MG	14	3433	1/1	0.96	0.07	87,87,87,87	0
56	MG	14	3187	1/1	0.96	0.14	62,62,62,62	0
56	MG	14	3435	1/1	0.96	0.09	121,121,121,121	0
56	MG	14	3188	1/1	0.96	0.08	68,68,68,68	0
56	MG	14	3189	1/1	0.96	0.09	63,63,63,63	0
56	MG	1H	3263	1/1	0.96	0.10	64,64,64,64	0
56	MG	1H	3017	1/1	0.96	0.10	51,51,51,51	0
56	MG	1H	3571	1/1	0.96	0.13	58,58,58,58	0
56	MG	1G	1753	1/1	0.96	0.04	109,109,109,109	0
56	MG	1G	1754	1/1	0.96	0.12	104,104,104,104	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1G	1755	1/1	0.96	0.08	119,119,119,119	0
56	MG	14	3196	1/1	0.96	0.06	78,78,78,78	0
56	MG	1H	3574	1/1	0.96	0.07	53,53,53,53	0
56	MG	1H	3111	1/1	0.96	0.17	54,54,54,54	0
56	MG	25	201	1/1	0.96	0.06	123,123,123,123	0
56	MG	1H	3578	1/1	0.96	0.08	65,65,65,65	0
56	MG	9A	101	1/1	0.96	0.10	115,115,115,115	0
56	MG	1H	3250	1/1	0.96	0.08	67,67,67,67	0
56	MG	45	202	1/1	0.96	0.27	84,84,84,84	0
56	MG	14	3202	1/1	0.96	0.16	71,71,71,71	0
56	MG	13	1611	1/1	0.96	0.18	65,65,65,65	0
56	MG	1H	3181	1/1	0.96	0.09	71,71,71,71	0
56	MG	13	1761	1/1	0.97	0.05	110,110,110,110	0
56	MG	1H	3336	1/1	0.97	0.21	81,81,81,81	0
56	MG	13	1753	1/1	0.97	0.06	121,121,121,121	0
56	MG	1H	3277	1/1	0.97	0.06	66,66,66,66	0
56	MG	1H	3360	1/1	0.97	0.10	50,50,50,50	0
56	MG	1H	3443	1/1	0.97	0.13	74,74,74,74	0
56	MG	14	3303	1/1	0.97	0.06	69,69,69,69	0
56	MG	1H	3496	1/1	0.97	0.08	66,66,66,66	0
56	MG	1H	3444	1/1	0.97	0.06	78,78,78,78	0
56	MG	13	1754	1/1	0.97	0.07	108,108,108,108	0
56	MG	13	1781	1/1	0.97	0.07	97,97,97,97	0
56	MG	1H	3512	1/1	0.97	0.12	65,65,65,65	0
56	MG	14	3309	1/1	0.97	0.10	87,87,87,87	0
56	MG	1H	3513	1/1	0.97	0.24	83,83,83,83	0
56	MG	14	3312	1/1	0.97	0.05	99,99,99,99	0
56	MG	1H	3447	1/1	0.97	0.07	65,65,65,65	0
56	MG	1H	3448	1/1	0.97	0.09	96,96,96,96	0
56	MG	1H	3521	1/1	0.97	0.06	66,66,66,66	0
56	MG	14	3091	1/1	0.97	0.20	57,57,57,57	0
56	MG	1H	3524	1/1	0.97	0.07	56,56,56,56	0
56	MG	1H	3526	1/1	0.97	0.06	57,57,57,57	0
56	MG	1H	3527	1/1	0.97	0.12	50,50,50,50	0
56	MG	13	1784	1/1	0.97	0.10	104,104,104,104	0
56	MG	14	3323	1/1	0.97	0.13	100,100,100,100	0
56	MG	14	3324	1/1	0.97	0.05	50,50,50,50	0
56	MG	1G	1707	1/1	0.97	0.05	92,92,92,92	0
56	MG	14	3333	1/1	0.97	0.06	80,80,80,80	0
56	MG	14	3335	1/1	0.97	0.06	57,57,57,57	0
56	MG	14	3339	1/1	0.97	0.06	61,61,61,61	0
56	MG	14	3340	1/1	0.97	0.05	57,57,57,57	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1H	3535	1/1	0.97	0.05	80,80,80,80	0
56	MG	1H	3543	1/1	0.97	0.07	59,59,59,59	0
56	MG	1H	3146	1/1	0.97	0.05	71,71,71,71	0
56	MG	14	3358	1/1	0.97	0.06	80,80,80,80	0
56	MG	14	3360	1/1	0.97	0.10	69,69,69,69	0
56	MG	14	3362	1/1	0.97	0.07	96,96,96,96	0
56	MG	14	3363	1/1	0.97	0.05	98,98,98,98	0
56	MG	1H	3453	1/1	0.97	0.06	94,94,94,94	0
56	MG	1H	3389	1/1	0.97	0.15	52,52,52,52	0
56	MG	88	202	1/1	0.97	0.38	69,69,69,69	0
56	MG	1G	1715	1/1	0.97	0.11	119,119,119,119	0
56	MG	14	3368	1/1	0.97	0.05	101,101,101,101	0
56	MG	1H	3457	1/1	0.97	0.09	99,99,99,99	0
56	MG	1G	1717	1/1	0.97	0.05	129,129,129,129	0
56	MG	14	3373	1/1	0.97	0.16	117,117,117,117	0
56	MG	14	3374	1/1	0.97	0.05	55,55,55,55	0
56	MG	14	3376	1/1	0.97	0.05	75,75,75,75	0
56	MG	14	3378	1/1	0.97	0.13	69,69,69,69	0
56	MG	1H	3561	1/1	0.97	0.08	78,78,78,78	0
56	MG	14	3383	1/1	0.97	0.08	62,62,62,62	0
56	MG	14	3384	1/1	0.97	0.11	81,81,81,81	0
56	MG	1G	1720	1/1	0.97	0.12	112,112,112,112	0
56	MG	13	1733	1/1	0.97	0.28	64,64,64,64	0
56	MG	13	1641	1/1	0.97	0.07	55,55,55,55	0
56	MG	14	3392	1/1	0.97	0.08	62,62,62,62	0
56	MG	1H	3462	1/1	0.97	0.06	95,95,95,95	0
56	MG	1G	1727	1/1	0.97	0.14	108,108,108,108	0
56	MG	1H	3079	1/1	0.97	0.04	59,59,59,59	0
56	MG	1H	3573	1/1	0.97	0.08	51,51,51,51	0
56	MG	13	1760	1/1	0.97	0.21	127,127,127,127	0
56	MG	1H	3395	1/1	0.97	0.05	54,54,54,54	0
56	MG	1G	1739	1/1	0.97	0.09	107,107,107,107	0
56	MG	14	3407	1/1	0.97	0.07	84,84,84,84	0
56	MG	1G	1740	1/1	0.97	0.14	93,93,93,93	0
56	MG	13	1792	1/1	0.97	0.10	73,73,73,73	0
56	MG	14	3411	1/1	0.97	0.04	109,109,109,109	0
56	MG	14	3412	1/1	0.97	0.06	102,102,102,102	0
56	MG	1H	3467	1/1	0.97	0.07	102,102,102,102	0
56	MG	1G	1744	1/1	0.97	0.12	101,101,101,101	0
56	MG	1H	3007	1/1	0.97	0.04	60,60,60,60	0
56	MG	1H	3371	1/1	0.97	0.11	72,72,72,72	0
56	MG	14	3422	1/1	0.97	0.14	72,72,72,72	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1H	3099	1/1	0.97	0.12	55,55,55,55	0
56	MG	14	3425	1/1	0.97	0.10	95,95,95,95	0
56	MG	1H	3587	1/1	0.97	0.06	51,51,51,51	0
56	MG	1G	1751	1/1	0.97	0.05	95,95,95,95	0
56	MG	1H	3052	1/1	0.97	0.07	41,41,41,41	0
56	MG	14	3127	1/1	0.97	0.13	61,61,61,61	0
56	MG	13	1767	1/1	0.97	0.06	61,61,61,61	0
56	MG	1H	3592	1/1	0.97	0.07	96,96,96,96	0
56	MG	1H	3593	1/1	0.97	0.10	61,61,61,61	0
56	MG	14	3059	1/1	0.97	0.14	41,41,41,41	0
56	MG	1H	3595	1/1	0.97	0.04	99,99,99,99	0
56	MG	13	1794	1/1	0.97	0.08	79,79,79,79	0
56	MG	14	3062	1/1	0.97	0.07	59,59,59,59	0
56	MG	1H	3474	1/1	0.97	0.06	83,83,83,83	0
56	MG	13	1770	1/1	0.97	0.05	89,89,89,89	0
56	MG	1G	1618	1/1	0.97	0.12	74,74,74,74	0
56	MG	1H	3476	1/1	0.97	0.06	92,92,92,92	0
56	MG	13	1796	1/1	0.97	0.07	79,79,79,79	0
56	MG	1H	3611	1/1	0.97	0.08	88,88,88,88	0
56	MG	14	3141	1/1	0.97	0.29	74,74,74,74	0
56	MG	1H	3614	1/1	0.97	0.28	97,97,97,97	0
56	MG	35	202	1/1	0.97	0.09	79,79,79,79	0
56	MG	1H	3378	1/1	0.97	0.16	56,56,56,56	0
56	MG	1H	3432	1/1	0.97	0.18	83,83,83,83	0
56	MG	1H	3433	1/1	0.97	0.06	51,51,51,51	0
56	MG	14	3003	1/1	0.97	0.16	47,47,47,47	0
56	MG	1H	3140	1/1	0.97	0.33	78,78,78,78	0
56	MG	1G	1627	1/1	0.97	0.10	88,88,88,88	0
56	MG	14	3332	1/1	0.98	0.04	57,57,57,57	0
56	MG	1H	3540	1/1	0.98	0.06	85,85,85,85	0
56	MG	14	3255	1/1	0.98	0.09	72,72,72,72	0
56	MG	1H	3542	1/1	0.98	0.12	68,68,68,68	0
56	MG	13	1768	1/1	0.98	0.14	92,92,92,92	0
56	MG	14	3342	1/1	0.98	0.06	51,51,51,51	0
56	MG	1H	3485	1/1	0.98	0.06	55,55,55,55	0
56	MG	1H	3486	1/1	0.98	0.05	45,45,45,45	0
56	MG	14	3347	1/1	0.98	0.04	53,53,53,53	0
56	MG	13	1791	1/1	0.98	0.07	85,85,85,85	0
56	MG	14	3353	1/1	0.98	0.05	64,64,64,64	0
56	MG	14	3354	1/1	0.98	0.04	68,68,68,68	0
56	MG	1H	3555	1/1	0.98	0.20	85,85,85,85	0
56	MG	1H	3556	1/1	0.98	0.04	58,58,58,58	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1H	3557	1/1	0.98	0.04	59,59,59,59	0
56	MG	13	1803	1/1	0.98	0.04	97,97,97,97	0
56	MG	1H	3560	1/1	0.98	0.09	84,84,84,84	0
56	MG	1H	3273	1/1	0.98	0.04	73,73,73,73	0
56	MG	1H	3490	1/1	0.98	0.05	63,63,63,63	0
56	MG	1H	3564	1/1	0.98	0.09	95,95,95,95	0
56	MG	16	214	1/1	0.98	0.06	82,82,82,82	0
56	MG	14	3369	1/1	0.98	0.10	87,87,87,87	0
56	MG	1H	3117	1/1	0.98	0.09	59,59,59,59	0
56	MG	1H	3493	1/1	0.98	0.06	48,48,48,48	0
56	MG	1H	3570	1/1	0.98	0.04	54,54,54,54	0
56	MG	13	1769	1/1	0.98	0.08	82,82,82,82	0
56	MG	14	3375	1/1	0.98	0.05	75,75,75,75	0
56	MG	1H	3572	1/1	0.98	0.04	73,73,73,73	0
56	MG	13	1700	1/1	0.98	0.05	90,90,90,90	0
56	MG	14	3380	1/1	0.98	0.06	92,92,92,92	0
56	MG	1H	3501	1/1	0.98	0.05	57,57,57,57	0
56	MG	1H	3502	1/1	0.98	0.05	49,49,49,49	0
56	MG	1H	3577	1/1	0.98	0.04	49,49,49,49	0
56	MG	13	1783	1/1	0.98	0.07	77,77,77,77	0
56	MG	14	3386	1/1	0.98	0.04	54,54,54,54	0
56	MG	1G	1703	1/1	0.98	0.09	87,87,87,87	0
56	MG	14	3390	1/1	0.98	0.09	66,66,66,66	0
56	MG	13	1773	1/1	0.98	0.10	96,96,96,96	0
56	MG	1H	3511	1/1	0.98	0.07	42,42,42,42	0
56	MG	13	1758	1/1	0.98	0.04	111,111,111,111	0
56	MG	14	3394	1/1	0.98	0.05	98,98,98,98	0
56	MG	1H	3582	1/1	0.98	0.05	56,56,56,56	0
56	MG	14	3396	1/1	0.98	0.04	54,54,54,54	0
56	MG	14	3398	1/1	0.98	0.04	81,81,81,81	0
56	MG	1H	3454	1/1	0.98	0.05	93,93,93,93	0
56	MG	1H	3585	1/1	0.98	0.05	95,95,95,95	0
56	MG	1H	3435	1/1	0.98	0.10	68,68,68,68	0
56	MG	I8	102	1/1	0.98	0.08	66,66,66,66	0
56	MG	1H	3588	1/1	0.98	0.06	52,52,52,52	0
56	MG	14	3406	1/1	0.98	0.07	60,60,60,60	0
56	MG	1G	1714	1/1	0.98	0.11	123,123,123,123	0
56	MG	1H	3589	1/1	0.98	0.07	60,60,60,60	0
56	MG	1H	3038	1/1	0.98	0.20	44,44,44,44	0
56	MG	1H	3520	1/1	0.98	0.05	54,54,54,54	0
56	MG	1H	3458	1/1	0.98	0.10	85,85,85,85	0
56	MG	14	3414	1/1	0.98	0.12	86,86,86,86	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	14	3415	1/1	0.98	0.12	101,101,101,101	0
56	MG	1G	1719	1/1	0.98	0.07	112,112,112,112	0
56	MG	1H	3522	1/1	0.98	0.11	59,59,59,59	0
56	MG	14	3419	1/1	0.98	0.05	84,84,84,84	0
56	MG	1H	3523	1/1	0.98	0.14	82,82,82,82	0
56	MG	13	1798	1/1	0.98	0.13	80,80,80,80	0
56	MG	1H	3525	1/1	0.98	0.05	58,58,58,58	0
56	MG	1G	1726	1/1	0.98	0.14	86,86,86,86	0
56	MG	1H	3600	1/1	0.98	0.06	84,84,84,84	0
56	MG	14	3426	1/1	0.98	0.05	108,108,108,108	0
56	MG	14	3302	1/1	0.98	0.04	56,56,56,56	0
56	MG	14	3428	1/1	0.98	0.05	81,81,81,81	0
56	MG	1G	1728	1/1	0.98	0.16	96,96,96,96	0
56	MG	14	3430	1/1	0.98	0.05	90,90,90,90	0
56	MG	14	3431	1/1	0.98	0.09	104,104,104,104	0
56	MG	1H	3438	1/1	0.98	0.07	94,94,94,94	0
56	MG	1G	1731	1/1	0.98	0.07	99,99,99,99	0
56	MG	1G	1732	1/1	0.98	0.10	102,102,102,102	0
56	MG	1H	3602	1/1	0.98	0.04	88,88,88,88	0
56	MG	1H	3461	1/1	0.98	0.03	102,102,102,102	0
56	MG	1G	1737	1/1	0.98	0.21	127,127,127,127	0
56	MG	13	1799	1/1	0.98	0.04	93,93,93,93	0
56	MG	1H	3610	1/1	0.98	0.17	106,106,106,106	0
56	MG	1H	3533	1/1	0.98	0.04	46,46,46,46	0
56	MG	14	3314	1/1	0.98	0.22	126,126,126,126	0
56	MG	1H	3613	1/1	0.98	0.12	78,78,78,78	0
56	MG	14	3316	1/1	0.98	0.21	79,79,79,79	0
56	MG	1H	3534	1/1	0.98	0.04	51,51,51,51	0
56	MG	1G	1743	1/1	0.98	0.16	122,122,122,122	0
56	MG	1H	3615	1/1	0.98	0.10	108,108,108,108	0
56	MG	13	1776	1/1	0.98	0.11	93,93,93,93	0
56	MG	1H	3617	1/1	0.98	0.28	127,127,127,127	0
56	MG	1H	3538	1/1	0.98	0.05	46,46,46,46	0
56	MG	1H	3620	1/1	0.98	0.06	73,73,73,73	0
56	MG	1G	1749	1/1	0.98	0.12	114,114,114,114	0
56	MG	14	3327	1/1	0.98	0.04	63,63,63,63	0
56	MG	14	3329	1/1	0.98	0.04	57,57,57,57	0
56	MG	1G	1750	1/1	0.98	0.10	109,109,109,109	0
56	MG	14	3331	1/1	0.98	0.15	82,82,82,82	0
58	ZN	5A	101	1/1	0.98	0.04	125,125,125,125	0
56	MG	1H	3536	1/1	0.99	0.04	62,62,62,62	0
56	MG	14	3361	1/1	0.99	0.02	80,80,80,80	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1H	3537	1/1	0.99	0.04	52,52,52,52	0
56	MG	1H	3452	1/1	0.99	0.02	81,81,81,81	0
56	MG	1H	3539	1/1	0.99	0.07	76,76,76,76	0
56	MG	1H	3497	1/1	0.99	0.07	40,40,40,40	0
56	MG	1H	3594	1/1	0.99	0.15	95,95,95,95	0
56	MG	1H	3541	1/1	0.99	0.03	75,75,75,75	0
56	MG	1H	3596	1/1	0.99	0.05	75,75,75,75	0
56	MG	1G	1723	1/1	0.99	0.05	72,72,72,72	0
56	MG	14	3370	1/1	0.99	0.05	70,70,70,70	0
56	MG	13	1786	1/1	0.99	0.03	65,65,65,65	0
56	MG	1H	3598	1/1	0.99	0.08	105,105,105,105	0
56	MG	1H	3499	1/1	0.99	0.07	49,49,49,49	0
56	MG	1H	3546	1/1	0.99	0.10	60,60,60,60	0
56	MG	1H	3027	1/1	0.99	0.07	40,40,40,40	0
56	MG	1G	1730	1/1	0.99	0.03	72,72,72,72	0
56	MG	14	3377	1/1	0.99	0.04	51,51,51,51	0
56	MG	1H	3549	1/1	0.99	0.03	61,61,61,61	0
56	MG	14	3379	1/1	0.99	0.03	66,66,66,66	0
56	MG	1H	3455	1/1	0.99	0.03	92,92,92,92	0
56	MG	14	3381	1/1	0.99	0.09	89,89,89,89	0
56	MG	1G	1733	1/1	0.99	0.17	121,121,121,121	0
56	MG	1H	3604	1/1	0.99	0.10	118,118,118,118	0
56	MG	1H	3605	1/1	0.99	0.05	90,90,90,90	0
56	MG	1G	1736	1/1	0.99	0.12	111,111,111,111	0
56	MG	1H	3606	1/1	0.99	0.04	85,85,85,85	0
56	MG	14	3387	1/1	0.99	0.06	61,61,61,61	0
56	MG	1H	3551	1/1	0.99	0.04	53,53,53,53	0
56	MG	14	3389	1/1	0.99	0.05	54,54,54,54	0
56	MG	1H	3552	1/1	0.99	0.11	78,78,78,78	0
56	MG	1H	3553	1/1	0.99	0.05	62,62,62,62	0
56	MG	1H	3612	1/1	0.99	0.12	62,62,62,62	0
56	MG	1H	3504	1/1	0.99	0.04	56,56,56,56	0
56	MG	13	1787	1/1	0.99	0.15	109,109,109,109	0
56	MG	13	1752	1/1	0.99	0.08	86,86,86,86	0
56	MG	1H	3507	1/1	0.99	0.16	65,65,65,65	0
56	MG	14	3397	1/1	0.99	0.10	70,70,70,70	0
56	MG	1H	3508	1/1	0.99	0.09	74,74,74,74	0
56	MG	14	3399	1/1	0.99	0.07	47,47,47,47	0
56	MG	1H	3559	1/1	0.99	0.06	73,73,73,73	0
56	MG	14	3401	1/1	0.99	0.04	85,85,85,85	0
56	MG	1H	3619	1/1	0.99	0.04	55,55,55,55	0
56	MG	1H	3509	1/1	0.99	0.07	77,77,77,77	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	14	3310	1/1	0.99	0.04	53,53,53,53	0
56	MG	1H	3510	1/1	0.99	0.11	54,54,54,54	0
56	MG	1H	3622	1/1	0.99	0.03	76,76,76,76	0
56	MG	1H	3390	1/1	0.99	0.10	53,53,53,53	0
56	MG	1H	3563	1/1	0.99	0.03	81,81,81,81	0
56	MG	14	3409	1/1	0.99	0.05	80,80,80,80	0
56	MG	13	1777	1/1	0.99	0.07	69,69,69,69	0
56	MG	13	1790	1/1	0.99	0.06	59,59,59,59	0
56	MG	1H	3566	1/1	0.99	0.03	93,93,93,93	0
56	MG	14	3413	1/1	0.99	0.04	93,93,93,93	0
56	MG	1H	3567	1/1	0.99	0.03	51,51,51,51	0
56	MG	1H	3514	1/1	0.99	0.05	84,84,84,84	0
56	MG	1H	3569	1/1	0.99	0.04	73,73,73,73	0
56	MG	13	1778	1/1	0.99	0.03	79,79,79,79	0
56	MG	14	3418	1/1	0.99	0.10	99,99,99,99	0
56	MG	1H	3442	1/1	0.99	0.07	73,73,73,73	0
56	MG	13	1749	1/1	0.99	0.05	92,92,92,92	0
56	MG	13	1771	1/1	0.99	0.14	81,81,81,81	0
56	MG	14	3325	1/1	0.99	0.11	63,63,63,63	0
56	MG	14	3423	1/1	0.99	0.12	95,95,95,95	0
56	MG	14	3326	1/1	0.99	0.04	53,53,53,53	0
56	MG	13	1772	1/1	0.99	0.07	93,93,93,93	0
56	MG	14	3328	1/1	0.99	0.05	58,58,58,58	0
56	MG	13	1782	1/1	0.99	0.05	81,81,81,81	0
56	MG	16	215	1/1	0.99	0.11	71,71,71,71	0
56	MG	1H	3576	1/1	0.99	0.08	68,68,68,68	0
56	MG	13	1759	1/1	0.99	0.04	105,105,105,105	0
56	MG	13	1797	1/1	0.99	0.19	105,105,105,105	0
56	MG	14	3334	1/1	0.99	0.03	51,51,51,51	0
56	MG	1H	3449	1/1	0.99	0.04	88,88,88,88	0
56	MG	14	3336	1/1	0.99	0.03	60,60,60,60	0
56	MG	14	3337	1/1	0.99	0.05	53,53,53,53	0
56	MG	14	3338	1/1	0.99	0.03	51,51,51,51	0
56	MG	1G	1705	1/1	0.99	0.11	84,84,84,84	0
56	MG	13	1756	1/1	0.99	0.03	95,95,95,95	0
56	MG	14	3341	1/1	0.99	0.05	46,46,46,46	0
56	MG	1H	3492	1/1	0.99	0.03	54,54,54,54	0
56	MG	1H	3531	1/1	0.99	0.12	66,66,66,66	0
56	MG	14	3344	1/1	0.99	0.06	66,66,66,66	0
56	MG	1H	3532	1/1	0.99	0.12	85,85,85,85	0
56	MG	14	3346	1/1	0.99	0.10	60,60,60,60	0
56	MG	1H	3584	1/1	0.99	0.06	58,58,58,58	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	14	3348	1/1	0.99	0.04	59,59,59,59	0
56	MG	14	3349	1/1	0.99	0.05	60,60,60,60	0
56	MG	14	3351	1/1	0.99	0.08	76,76,76,76	0
56	MG	13	1775	1/1	0.99	0.06	68,68,68,68	0
56	MG	1H	3586	1/1	0.99	0.04	53,53,53,53	0
56	MG	1H	3494	1/1	0.99	0.04	40,40,40,40	0
56	MG	14	3355	1/1	0.99	0.11	75,75,75,75	0
56	MG	14	3356	1/1	0.99	0.16	81,81,81,81	0
56	MG	14	3357	1/1	0.99	0.06	67,67,67,67	0
56	MG	1H	3495	1/1	0.99	0.03	48,48,48,48	0
57	SF4	3E	302	8/8	0.99	0.04	85,90,93,95	0
57	SF4	32	301	8/8	0.99	0.04	95,103,111,112	0
58	ZN	5I	103	1/1	0.99	0.06	97,97,97,97	0
56	MG	14	3359	1/1	0.99	0.16	105,105,105,105	0
56	MG	1H	3503	1/1	1.00	0.07	55,55,55,55	0
56	MG	1G	1724	1/1	1.00	0.04	75,75,75,75	0
56	MG	14	3350	1/1	1.00	0.07	45,45,45,45	0
56	MG	21	304	1/1	1.00	0.02	54,54,54,54	0
56	MG	1H	3548	1/1	1.00	0.02	50,50,50,50	0
56	MG	1H	3530	1/1	1.00	0.03	54,54,54,54	0
56	MG	1H	3517	1/1	1.00	0.04	54,54,54,54	0
56	MG	1H	3518	1/1	1.00	0.02	51,51,51,51	0
56	MG	1H	3607	1/1	1.00	0.04	61,61,61,61	0
56	MG	1H	3483	1/1	1.00	0.07	63,63,63,63	0
56	MG	1H	3609	1/1	1.00	0.12	90,90,90,90	0
56	MG	1H	3500	1/1	1.00	0.09	43,43,43,43	0
56	MG	1H	3515	1/1	1.00	0.02	41,41,41,41	0
56	MG	1H	3544	1/1	1.00	0.08	57,57,57,57	0
56	MG	1H	3545	1/1	1.00	0.04	63,63,63,63	0
56	MG	1H	3528	1/1	1.00	0.04	49,49,49,49	0

6.5 Other polymers (i)

There are no such residues in this entry.