Full wwPDB X-ray Structure Validation Report (i)

Mar 5, 2026 – 08:40 AM UTC

PDB ID	:	4WQY / pdb_00004wqy
Title	:	Crystal structure of the Thermus thermophilus 70S ribosome in complex with elongation factor G in the post-translocational state (without fusitic acid)
Authors	:	Lin, J.; Gagnon, M.G.; Steitz, T.A.
Deposited on	:	2014-10-22
Resolution	:	2.80 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 (i) 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 (i)) were used in the production of this report:

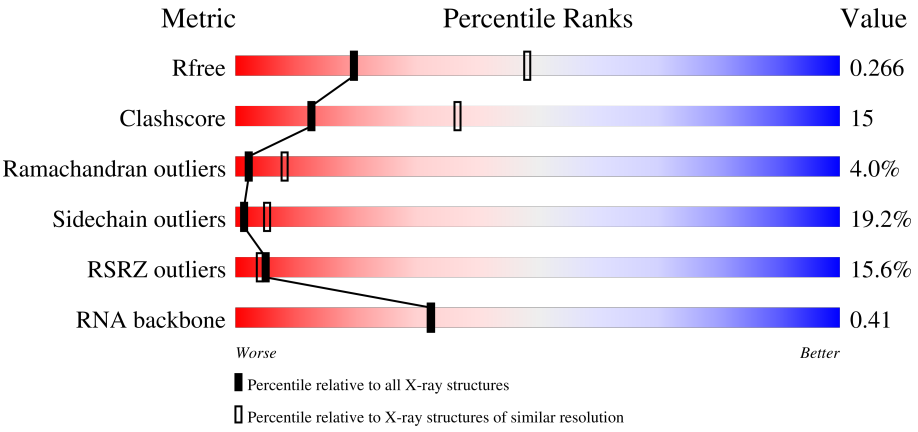
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal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

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.80 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	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)
RNA backbone	3983	1114 (3.00-2.60)

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	AA	2915	4% 47% 41% 9%
1	CA	2915	7% 45% 43% 9%
2	AB	121	% 52% 40% 7%
2	CB	121	4% 45% 48% 7%

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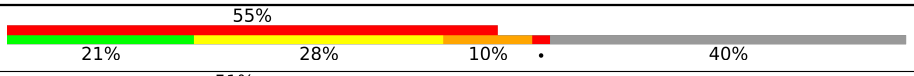
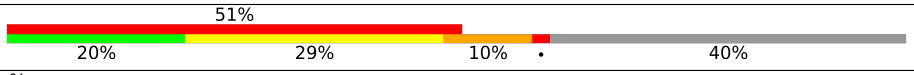
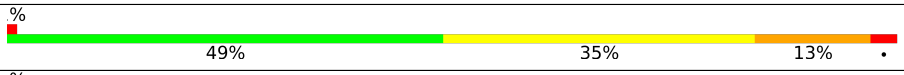
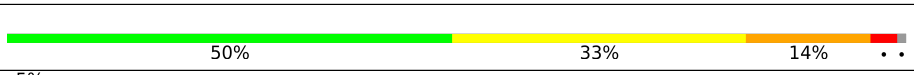
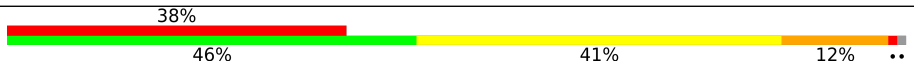
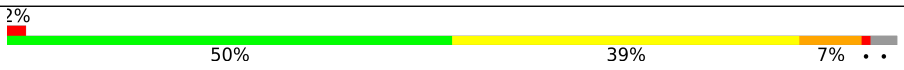
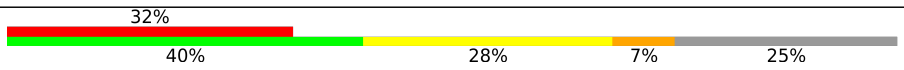
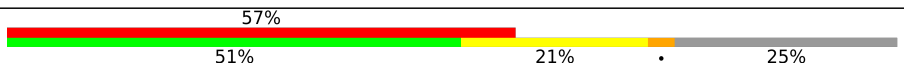
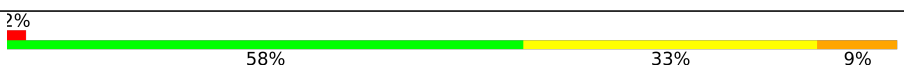
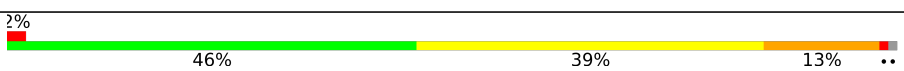
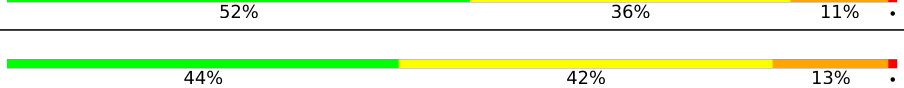
Mol	Chain	Length	Quality of chain
3	AC	228	
3	CC	228	
4	AD	276	
4	CD	276	
5	AE	206	
5	CE	206	
6	AF	210	
6	CF	210	
7	AG	182	
7	CG	182	
8	AH	180	
8	CH	180	
9	AK	173	
9	CK	173	
10	AL	147	
10	CL	147	
11	AN	140	
11	CN	140	
12	AO	122	
12	CO	122	
13	AP	150	
13	CP	150	
14	AQ	141	
14	CQ	141	
15	AR	118	

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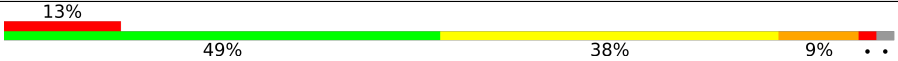
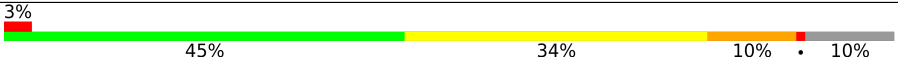
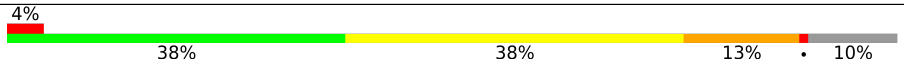
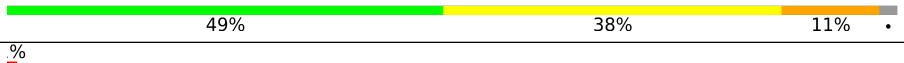
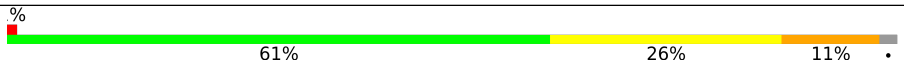
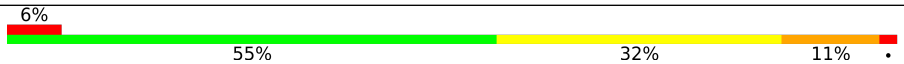
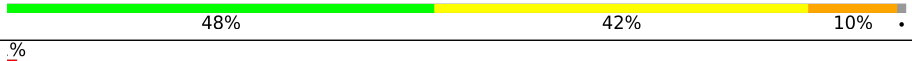
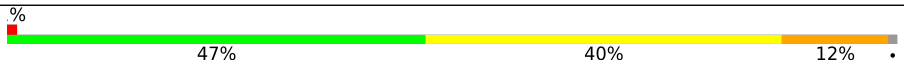
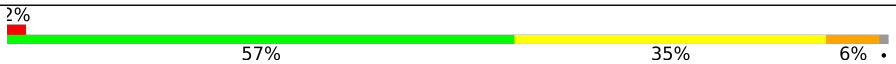
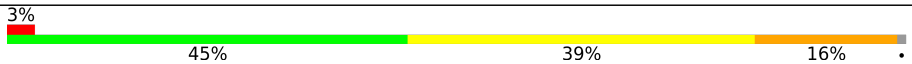
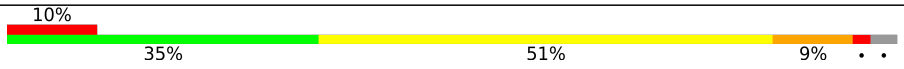
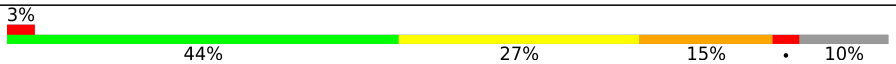
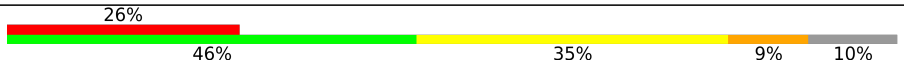
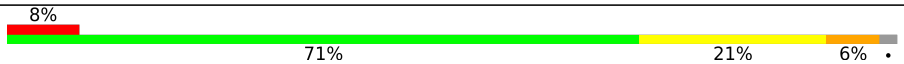
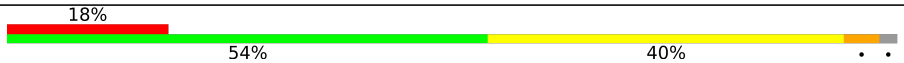
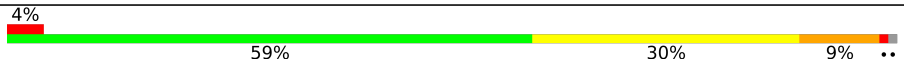
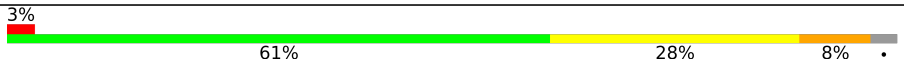
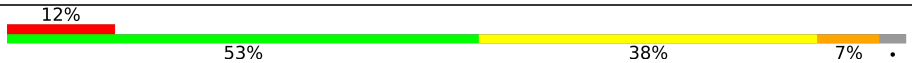
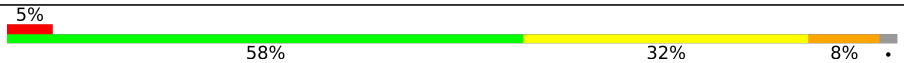
Mol	Chain	Length	Quality of chain
15	CR	118	
16	AS	112	
16	CS	112	
17	AT	146	
17	CT	146	
18	AU	118	
18	CU	118	
19	AV	101	
19	CV	101	
20	AW	113	
20	CW	113	
21	AX	96	
21	CX	96	
22	AY	110	
22	CY	110	
23	AZ	206	
23	CZ	206	
24	A0	85	
24	C0	85	
25	A1	98	
25	C1	98	
26	A2	72	
26	C2	72	
27	A3	60	
27	C3	60	

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Mol	Chain	Length	Quality of chain
28	A4	71	34% 31% 54% 10%
28	C4	71	38% 37% 51% 10%
29	A5	60	40% 50% 8%
29	C5	60	58% 35% 5%
30	A6	54	35% 56% 6%
30	C6	54	52% 35% 11%
31	A7	49	4% 51% 41%
31	C7	49	8% 55% 27% 16%
32	A8	65	35% 52% 9%
32	C8	65	54% 37% 8%
33	A9	37	43% 46% 11%
33	C9	37	22% 35% 57% 8%
34	BA	1521	10% 40% 48% 10%
34	DA	1521	12% 39% 50% 9%
35	BB	256	21% 35% 40% 13% 10%
35	DB	256	27% 43% 38% 9% 10%
36	BC	239	25% 48% 35% 14%
36	DC	239	35% 46% 33% 7% 14%
37	BD	209	20% 48% 37% 12%
37	DD	209	16% 49% 35% 13%
38	BE	162	4% 39% 42% 10% 9%
38	DE	162	6% 40% 40% 9% 9%
39	BF	101	4% 56% 35% 7%
39	DF	101	% 56% 37% 6%
40	BG	156	28% 56% 35% 7%

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Mol	Chain	Length	Quality of chain
40	DG	156	39% 66% 29%
41	BH	138	% 41% 43% 10% 5%
41	DH	138	9% 53% 37% 8%
42	BI	128	55% 52% 36% 11%
42	DI	128	62% 51% 42% 6%
43	BJ	105	47% 54% 30% 9% 8%
43	DJ	105	55% 50% 33% 9% 9%
44	BK	129	11% 50% 33% 5% 12%
44	DK	129	10% 50% 33% 5% 12%
45	BL	132	3% 58% 25% 10% 8%
45	DL	132	8% 52% 33% 7% 8%
46	BM	126	45% 52% 33% 7% 7%
46	DM	126	51% 57% 29% 11%
47	BN	61	56% 52% 38% 7%
47	DN	61	79% 44% 44% 10%
48	BO	89	4% 42% 49% 7%
48	DO	89	10% 45% 40% 13%
49	BP	88	14% 36% 39% 17% 7%
49	DP	88	10% 43% 42% 7% 7%
50	BQ	105	7% 49% 34% 10% 6%
50	DQ	105	12% 51% 34% 9% 6%
51	BR	88	6% 48% 24% 6% 23%
51	DR	88	5% 38% 28% 11% 23%
52	BS	93	55% 44% 42% 10%
52	DS	93	65% 44% 38% 6% 11%

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Mol	Chain	Length	Quality of chain
53	BT	106	26% 42% 37% 10% 9%
53	DT	106	22% 48% 37% 6% 9%
54	BU	27	74% 56% 22% 7% 15%
54	DU	27	52% 48% 37% 15%
55	BV	24	42% 21% 21% 12% 46%
55	DV	24	12% 21% 75%
56	BX	77	4% 52% 36% 10%
56	DX	77	9% 55% 32% 10%
57	BZ	758	32% 53% 30% 12%
57	DZ	758	44% 51% 32% 12%

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
58	MG	CA	3071	-	-	-	X

2 Entry composition

There are 63 unique types of molecules in this entry. The entry contains 305548 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 23S Ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AA	2852	Total	C	N	O	P	0	0	0
			61426	27339	11489	19747	2851			
1	CA	2848	Total	C	N	O	P	0	0	0
			61337	27299	11470	19721	2847			

- Molecule 2 is a RNA chain called 5S Ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	AB	120	Total	C	N	O	P	0	0	0
			2573	1146	476	832	119			
2	CB	120	Total	C	N	O	P	0	0	0
			2573	1146	476	832	119			

- Molecule 3 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	AC	137	Total	C	N	O	S	0	0	0
			1063	669	201	192	1			
3	CC	137	Total	C	N	O	S	0	0	0
			1063	669	201	192	1			

- Molecule 4 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	AD	275	Total	C	N	O	S	0	0	0
			2136	1349	423	361	3			
4	CD	275	Total	C	N	O	S	0	0	0
			2142	1352	426	361	3			

- Molecule 5 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	AE	204	Total	C	N	O	S	0	0	0
			1559	985	298	270	6			
5	CE	204	Total	C	N	O	S	0	0	0
			1559	985	298	270	6			

- Molecule 6 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	AF	203	Total	C	N	O	S	0	0	1
			1584	1009	298	275	2			
6	CF	203	Total	C	N	O	S	0	0	1
			1580	1007	297	274	2			

- Molecule 7 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	AG	181	Total	C	N	O	S	0	0	0
			1425	914	256	251	4			
7	CG	181	Total	C	N	O	S	0	0	0
			1424	911	258	251	4			

- Molecule 8 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	AH	174	Total	C	N	O	S	0	0	0
			1330	845	248	236	1			
8	CH	174	Total	C	N	O	S	0	0	0
			1330	845	248	236	1			

- Molecule 9 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
9	AK	130	Total	C	N	O	0	0	0
			641	381	130	130			
9	CK	130	Total	C	N	O	0	0	0
			641	381	130	130			

- Molecule 10 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	AL	139	Total	C	N	O	S	0	0	0
			1025	653	181	186	5			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	CL	139	Total	C	N	O	S	0	0	0
			1025	653	181	186	5			

- Molecule 11 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	AN	140	Total	C	N	O	S	0	0	0
			1117	719	207	187	4			
11	CN	140	Total	C	N	O	S	0	0	0
			1117	719	207	187	4			

- Molecule 12 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	AO	122	Total	C	N	O	S	0	0	0
			933	588	171	170	4			
12	CO	122	Total	C	N	O	S	0	0	0
			933	588	171	170	4			

- Molecule 13 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	AP	149	Total	C	N	O	S	0	0	0
			1139	709	231	196	3			
13	CP	149	Total	C	N	O	S	0	0	0
			1135	706	230	196	3			

- Molecule 14 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	AQ	141	Total	C	N	O	S	0	0	0
			1122	715	212	188	7			
14	CQ	141	Total	C	N	O	S	0	0	0
			1122	715	212	188	7			

- Molecule 15 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
15	AR	118	Total	C	N	O	S	0	0	0
			968	604	203	160	1			
15	CR	118	Total	C	N	O	S	0	0	0
			968	604	203	160	1			

- Molecule 16 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
16	AS	110	Total	C	N	O	0	0	0
			877	553	175	149			
16	CS	110	Total	C	N	O	0	0	0
			870	549	173	148			

- Molecule 17 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
17	AT	131	Total	C	N	O	S	0	0	0
			1091	680	225	185	1			
17	CT	131	Total	C	N	O	S	0	0	0
			1083	675	224	183	1			

- Molecule 18 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
18	AU	116	Total	C	N	O	S	0	0	0
			959	608	201	149	1			
18	CU	116	Total	C	N	O	S	0	0	0
			959	608	201	149	1			

- Molecule 19 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	AV	101	Total	C	N	O	S	0	0	0
			771	495	140	135	1			
19	CV	101	Total	C	N	O	S	0	0	0
			771	495	140	135	1			

- Molecule 20 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	AW	112	Total	C	N	O	S	0	0	0
			886	557	174	153	2			
20	CW	112	Total	C	N	O	S	0	0	0
			886	557	174	153	2			

- Molecule 21 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
21	AX	95	Total	C	N	O	S	0	0	0
			750	488	135	126	1			
21	CX	95	Total	C	N	O	S	0	0	0
			750	488	135	126	1			

- Molecule 22 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	AY	107	Total	C	N	O	S	0	0	0
			806	517	152	131	6			
22	CY	107	Total	C	N	O	S	0	0	0
			806	517	152	131	6			

- Molecule 23 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
23	AZ	185	Total	C	N	O	S	0	0	0
			1451	927	258	264	2			
23	CZ	185	Total	C	N	O	S	0	0	0
			1451	927	258	264	2			

- Molecule 24 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
24	A0	83	Total	C	N	O	S	0	0	0
			653	404	139	109	1			
24	C0	83	Total	C	N	O	S	0	0	0
			653	404	139	109	1			

- Molecule 25 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
25	A1	97	Total	C	N	O	S	0	0	0
			755	475	148	131	1			
25	C1	97	Total	C	N	O	S	0	0	0
			755	475	148	131	1			

- Molecule 26 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	A2	70	Total	C	N	O	S	0	0	0
			588	365	118	103	2			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	C2	70	Total	C	N	O	S	0	0	0
			588	365	118	103	2			

- Molecule 27 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
27	A3	59	Total	C	N	O	0	0	0
			469	298	90	81			
27	C3	59	Total	C	N	O	0	0	0
			464	296	90	78			

- Molecule 28 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
28	A4	69	Total	C	N	O	S	0	0	0
			558	352	102	99	5			
28	C4	69	Total	C	N	O	S	0	0	0
			532	339	97	91	5			

- Molecule 29 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
29	A5	59	Total	C	N	O	S	0	0	0
			455	285	89	76	5			
29	C5	59	Total	C	N	O	S	0	0	0
			455	285	89	76	5			

- Molecule 30 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
30	A6	53	Total	C	N	O	S	0	0	0
			453	281	91	77	4			
30	C6	53	Total	C	N	O	S	0	0	0
			449	279	91	75	4			

- Molecule 31 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
31	A7	48	Total	C	N	O	S	0	0	0
			418	257	104	55	2			
31	C7	48	Total	C	N	O	S	0	0	0
			418	257	104	55	2			

- Molecule 32 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
32	A8	64	Total	C	N	O	S	0	0	0
			517	331	102	82	2			
32	C8	64	Total	C	N	O	S	0	0	0
			517	331	102	82	2			

- Molecule 33 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
33	A9	37	Total	C	N	O	S	0	0	0
			307	188	68	47	4			
33	C9	37	Total	C	N	O	S	0	0	0
			307	188	68	47	4			

- Molecule 34 is a RNA chain called 16S Ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
34	BA	1495	Total	C	N	O	P	0	0	0
			32141	14304	5958	10384	1495			
34	DA	1501	Total	C	N	O	P	0	0	0
			32268	14361	5980	10426	1501			

- Molecule 35 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
35	BB	231	Total	C	N	O	S	0	0	0
			1846	1179	331	331	5			
35	DB	231	Total	C	N	O	S	0	0	0
			1825	1167	326	327	5			

- Molecule 36 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
36	BC	206	Total	C	N	O	S	0	0	0
			1552	976	302	273	1			
36	DC	206	Total	C	N	O	S	0	0	0
			1544	970	300	273	1			

- Molecule 37 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
37	BD	208	Total	C	N	O	S	0	0	0
			1659	1040	326	286	7			
37	DD	208	Total	C	N	O	S	0	0	0
			1678	1052	333	286	7			

- Molecule 38 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
38	BE	148	Total	C	N	O	S	0	0	0
			1129	714	213	198	4			
38	DE	148	Total	C	N	O	S	0	0	0
			1133	716	214	199	4			

- Molecule 39 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
39	BF	100	Total	C	N	O	S	0	0	0
			812	514	146	149	3			
39	DF	100	Total	C	N	O	S	0	0	0
			820	518	147	152	3			

- Molecule 40 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
40	BG	155	Total	C	N	O	S	0	0	0
			1231	766	243	216	6			
40	DG	155	Total	C	N	O	S	0	0	0
			1235	769	244	216	6			

- Molecule 41 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
41	BH	137	Total	C	N	O	S	0	0	0
			1088	689	206	191	2			
41	DH	137	Total	C	N	O	S	0	0	0
			1088	689	206	191	2			

- Molecule 42 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
42	BI	127	Total	C	N	O	0	0	0
			986	626	193	167			

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
42	DI	127	Total 978	C 619	N 190	O 169	0	0	0

- Molecule 43 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
43	BJ	97	Total 709	C 440	N 138	O 131	0	0	0
43	DJ	96	Total 714	C 445	N 138	O 131	0	0	0

- Molecule 44 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
44	BK	114	Total 833	C 519	N 156	O 155	S 3	0	0	0
44	DK	114	Total 833	C 519	N 156	O 155	S 3	0	0	0

- Molecule 45 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
45	BL	122	Total 930	C 585	N 185	O 159	S 1	0	0	0
45	DL	122	Total 930	C 585	N 185	O 159	S 1	0	0	0

- Molecule 46 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
46	BM	117	Total 923	C 570	N 191	O 160	S 2	0	0	0
46	DM	122	Total 950	C 586	N 197	O 165	S 2	0	0	0

- Molecule 47 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
47	BN	60	Total 492	C 312	N 104	O 72	S 4	0	0	0
47	DN	60	Total 492	C 312	N 104	O 72	S 4	0	0	0

- Molecule 48 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
48	BO	88	Total	C	N	O	S	0	0	0
			728	456	144	126	2			
48	DO	88	Total	C	N	O	S	0	0	0
			728	456	144	126	2			

- Molecule 49 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
49	BP	82	Total	C	N	O	S	0	0	0
			681	433	134	113	1			
49	DP	82	Total	C	N	O	S	0	0	0
			677	430	133	113	1			

- Molecule 50 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
50	BQ	99	Total	C	N	O	S	0	0	0
			823	528	151	142	2			
50	DQ	99	Total	C	N	O	S	0	0	0
			823	528	151	142	2			

- Molecule 51 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
51	BR	68	Total	C	N	O	0	0	0
			555	355	108	92			
51	DR	68	Total	C	N	O	0	0	0
			555	355	108	92			

- Molecule 52 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
52	BS	84	Total	C	N	O	S	0	0	0
			661	423	122	114	2			
52	DS	83	Total	C	N	O	S	0	0	0
			646	412	119	113	2			

- Molecule 53 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
53	BT	96	Total	C	N	O	S	0	0	0
			728	446	156	124	2			
53	DT	96	Total	C	N	O	S	0	0	0
			731	449	156	124	2			

- Molecule 54 is a protein called 30S ribosomal protein Thx.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
54	BU	23	Total	C	N	O	0	0	0
			199	122	48	29			
54	DU	23	Total	C	N	O	0	0	0
			199	122	48	29			

- Molecule 55 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
55	BV	13	Total	C	N	O	P	0	0	0
			277	125	51	88	13			
55	DV	6	Total	C	N	O	P	0	0	0
			128	59	27	37	5			

- Molecule 56 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
56	BX	76	Total	C	N	O	P	S	0	0	0
			1625	725	294	529	76	1			
56	DX	76	Total	C	N	O	P	S	0	0	0
			1621	723	292	529	76	1			

- Molecule 57 is a protein called 50S ribosomal protein L9,Elongation factor G.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
57	BZ	730	Total	C	N	O	S	0	0	0
			4869	3031	886	942	10			
57	DZ	730	Total	C	N	O	S	0	0	0
			4867	3029	886	942	10			

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
58	AA	820	Total	Mg	0	0
			820	820		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
58	AB	23	Total Mg 23 23	0	0
58	AD	12	Total Mg 12 12	0	0
58	AE	5	Total Mg 5 5	0	0
58	AF	8	Total Mg 8 8	0	0
58	AG	2	Total Mg 2 2	0	0
58	AH	2	Total Mg 2 2	0	0
58	AN	3	Total Mg 3 3	0	0
58	AO	1	Total Mg 1 1	0	0
58	AP	3	Total Mg 3 3	0	0
58	AQ	3	Total Mg 3 3	0	0
58	AR	2	Total Mg 2 2	0	0
58	AU	3	Total Mg 3 3	0	0
58	AV	5	Total Mg 5 5	0	0
58	AW	4	Total Mg 4 4	0	0
58	AX	1	Total Mg 1 1	0	0
58	AZ	2	Total Mg 2 2	0	0
58	A0	5	Total Mg 5 5	0	0
58	A1	1	Total Mg 1 1	0	0
58	A2	1	Total Mg 1 1	0	0
58	A4	1	Total Mg 1 1	0	0
58	A5	3	Total Mg 3 3	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
58	A6	1	Total Mg 1 1	0	0
58	A7	5	Total Mg 5 5	0	0
58	A8	2	Total Mg 2 2	0	0
58	A9	1	Total Mg 1 1	0	0
58	BA	212	Total Mg 212 212	0	0
58	BB	1	Total Mg 1 1	0	0
58	BD	1	Total Mg 1 1	0	0
58	BE	1	Total Mg 1 1	0	0
58	BF	1	Total Mg 1 1	0	0
58	BK	1	Total Mg 1 1	0	0
58	BL	4	Total Mg 4 4	0	0
58	BN	2	Total Mg 2 2	0	0
58	BT	1	Total Mg 1 1	0	0
58	BV	1	Total Mg 1 1	0	0
58	BX	10	Total Mg 10 10	0	0
58	BZ	1	Total Mg 1 1	0	0
58	CA	666	Total Mg 666 666	0	0
58	CB	13	Total Mg 13 13	0	0
58	CD	3	Total Mg 3 3	0	0
58	CE	7	Total Mg 7 7	0	0
58	CF	4	Total Mg 4 4	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
58	CG	1	Total Mg 1 1	0	0
58	CN	1	Total Mg 1 1	0	0
58	CO	2	Total Mg 2 2	0	0
58	CQ	4	Total Mg 4 4	0	0
58	CR	1	Total Mg 1 1	0	0
58	CU	2	Total Mg 2 2	0	0
58	CV	2	Total Mg 2 2	0	0
58	CY	1	Total Mg 1 1	0	0
58	C0	1	Total Mg 1 1	0	0
58	C1	1	Total Mg 1 1	0	0
58	C3	1	Total Mg 1 1	0	0
58	C7	1	Total Mg 1 1	0	0
58	C8	1	Total Mg 1 1	0	0
58	DA	166	Total Mg 166 166	0	0
58	DD	1	Total Mg 1 1	0	0
58	DE	2	Total Mg 2 2	0	0
58	DF	1	Total Mg 1 1	0	0
58	DJ	1	Total Mg 1 1	0	0
58	DK	1	Total Mg 1 1	0	0
58	DL	2	Total Mg 2 2	0	0
58	DT	1	Total Mg 1 1	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
58	DZ	3	Total Mg 3 3	0	0

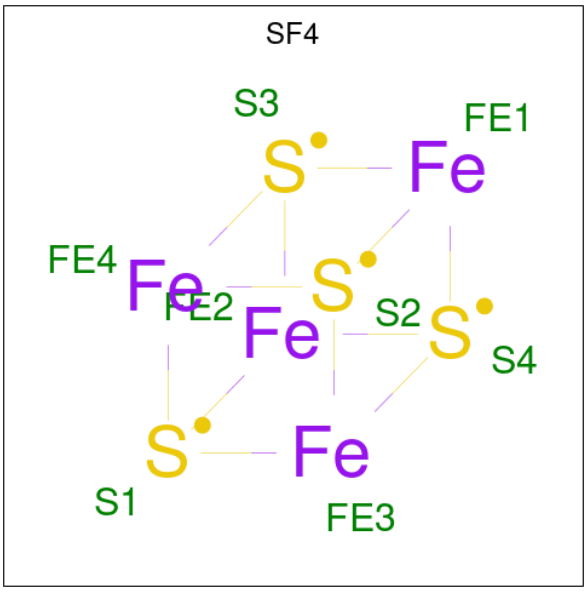
- Molecule 59 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
59	AA	1	Total K 1 1	0	0

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

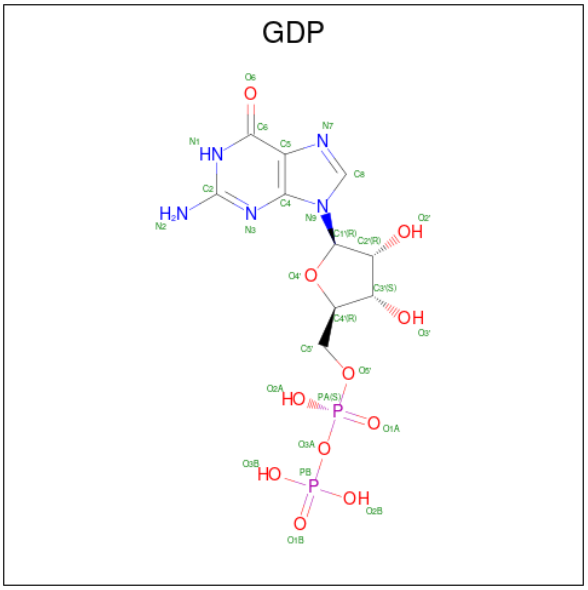
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
60	AY	1	Total Zn 1 1	0	0
60	A4	1	Total Zn 1 1	0	0
60	A5	1	Total Zn 1 1	0	0
60	A6	1	Total Zn 1 1	0	0
60	A9	1	Total Zn 1 1	0	0
60	BN	1	Total Zn 1 1	0	0
60	CY	1	Total Zn 1 1	0	0
60	C4	1	Total Zn 1 1	0	0
60	C5	1	Total Zn 1 1	0	0
60	C6	1	Total Zn 1 1	0	0
60	C9	1	Total Zn 1 1	0	0
60	DN	1	Total Zn 1 1	0	0

- Molecule 61 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe_4S_4).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
61	BD	1	Total Fe S 8 4 4	0	0
61	DD	1	Total Fe S 8 4 4	0	0

- Molecule 62 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
62	BZ	1	Total C N O P 28 10 5 11 2	0	0
62	DZ	1	Total C N O P 28 10 5 11 2	0	0

- Molecule 63 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
63	AA	1406	Total O 1406 1406	0	0
63	AB	37	Total O 37 37	0	0
63	AD	16	Total O 16 16	0	0
63	AE	14	Total O 14 14	0	0
63	AF	6	Total O 6 6	0	0
63	AG	3	Total O 3 3	0	0
63	AH	1	Total O 1 1	0	0
63	AN	3	Total O 3 3	0	0
63	AO	1	Total O 1 1	0	0
63	AP	18	Total O 18 18	0	0
63	AQ	5	Total O 5 5	0	0
63	AR	2	Total O 2 2	0	0
63	AS	1	Total O 1 1	0	0
63	AT	3	Total O 3 3	0	0
63	AU	4	Total O 4 4	0	0
63	AV	1	Total O 1 1	0	0
63	AW	1	Total O 1 1	0	0
63	AX	4	Total O 4 4	0	0
63	AZ	1	Total O 1 1	0	0
63	A0	9	Total O 9 9	0	0
63	A1	2	Total O 2 2	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
63	A2	1	Total O 1 1	0	0
63	A3	2	Total O 2 2	0	0
63	A5	4	Total O 4 4	0	0
63	A7	4	Total O 4 4	0	0
63	A8	9	Total O 9 9	0	0
63	A9	1	Total O 1 1	0	0
63	BA	203	Total O 203 203	0	0
63	BD	3	Total O 3 3	0	0
63	BE	2	Total O 2 2	0	0
63	BG	1	Total O 1 1	0	0
63	BJ	1	Total O 1 1	0	0
63	BL	1	Total O 1 1	0	0
63	BM	1	Total O 1 1	0	0
63	BO	2	Total O 2 2	0	0
63	BP	1	Total O 1 1	0	0
63	BV	3	Total O 3 3	0	0
63	BX	5	Total O 5 5	0	0
63	BZ	2	Total O 2 2	0	0
63	CA	974	Total O 974 974	0	0
63	CB	9	Total O 9 9	0	0
63	CD	17	Total O 17 17	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
63	CE	14	Total O 14 14	0	0
63	CF	6	Total O 6 6	0	0
63	CN	2	Total O 2 2	0	0
63	CP	12	Total O 12 12	0	0
63	CQ	2	Total O 2 2	0	0
63	CT	3	Total O 3 3	0	0
63	CU	2	Total O 2 2	0	0
63	CV	2	Total O 2 2	0	0
63	CW	1	Total O 1 1	0	0
63	CX	2	Total O 2 2	0	0
63	CY	2	Total O 2 2	0	0
63	C0	5	Total O 5 5	0	0
63	C1	1	Total O 1 1	0	0
63	C3	2	Total O 2 2	0	0
63	C6	1	Total O 1 1	0	0
63	C7	1	Total O 1 1	0	0
63	C8	3	Total O 3 3	0	0
63	DA	154	Total O 154 154	0	0
63	DE	3	Total O 3 3	0	0
63	DH	1	Total O 1 1	0	0
63	DJ	1	Total O 1 1	0	0

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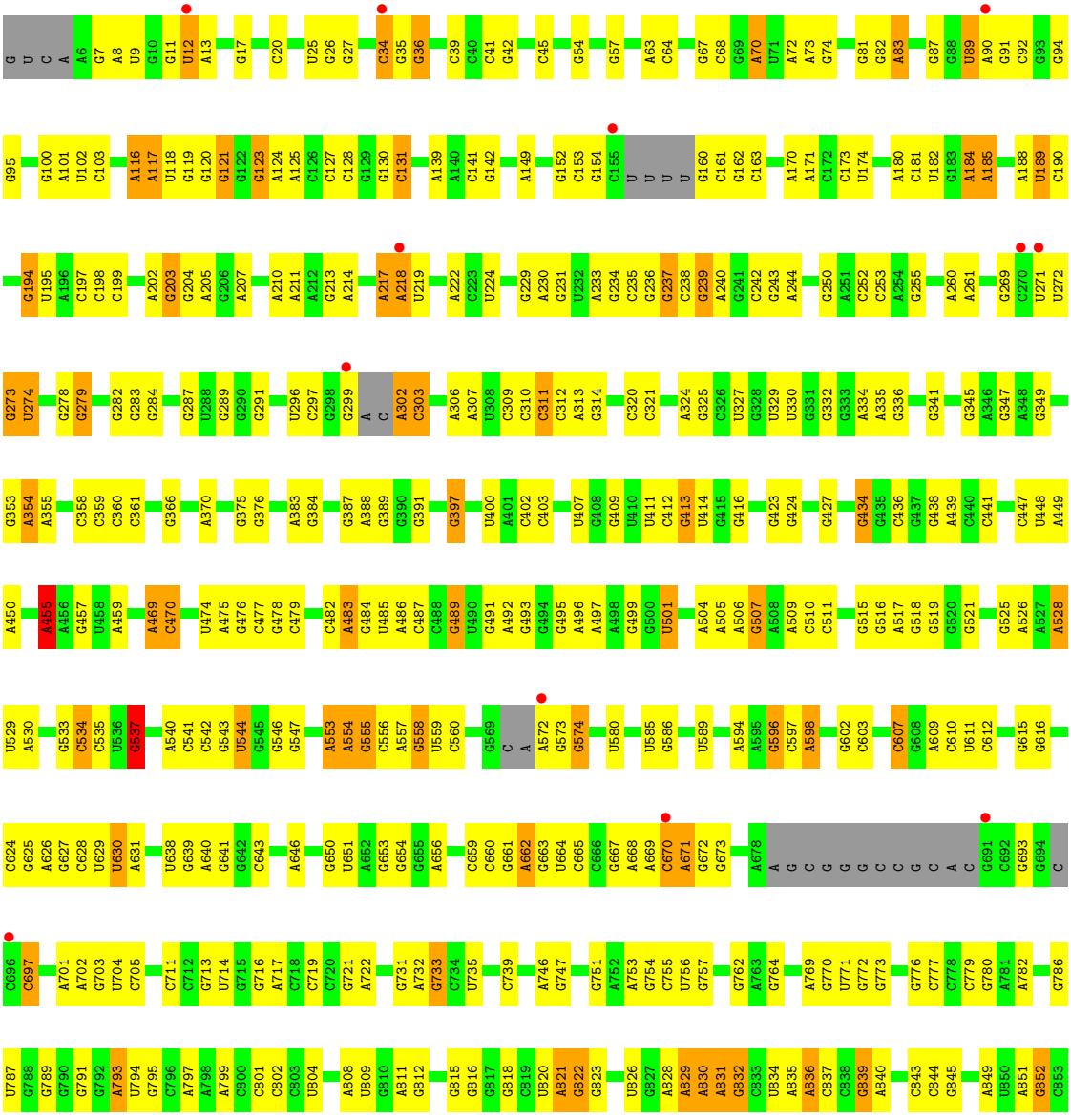
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
63	DK	2	Total O 2 2	0	0
63	DP	1	Total O 1 1	0	0
63	DT	1	Total O 1 1	0	0
63	DV	1	Total O 1 1	0	0
63	DZ	1	Total O 1 1	0	0

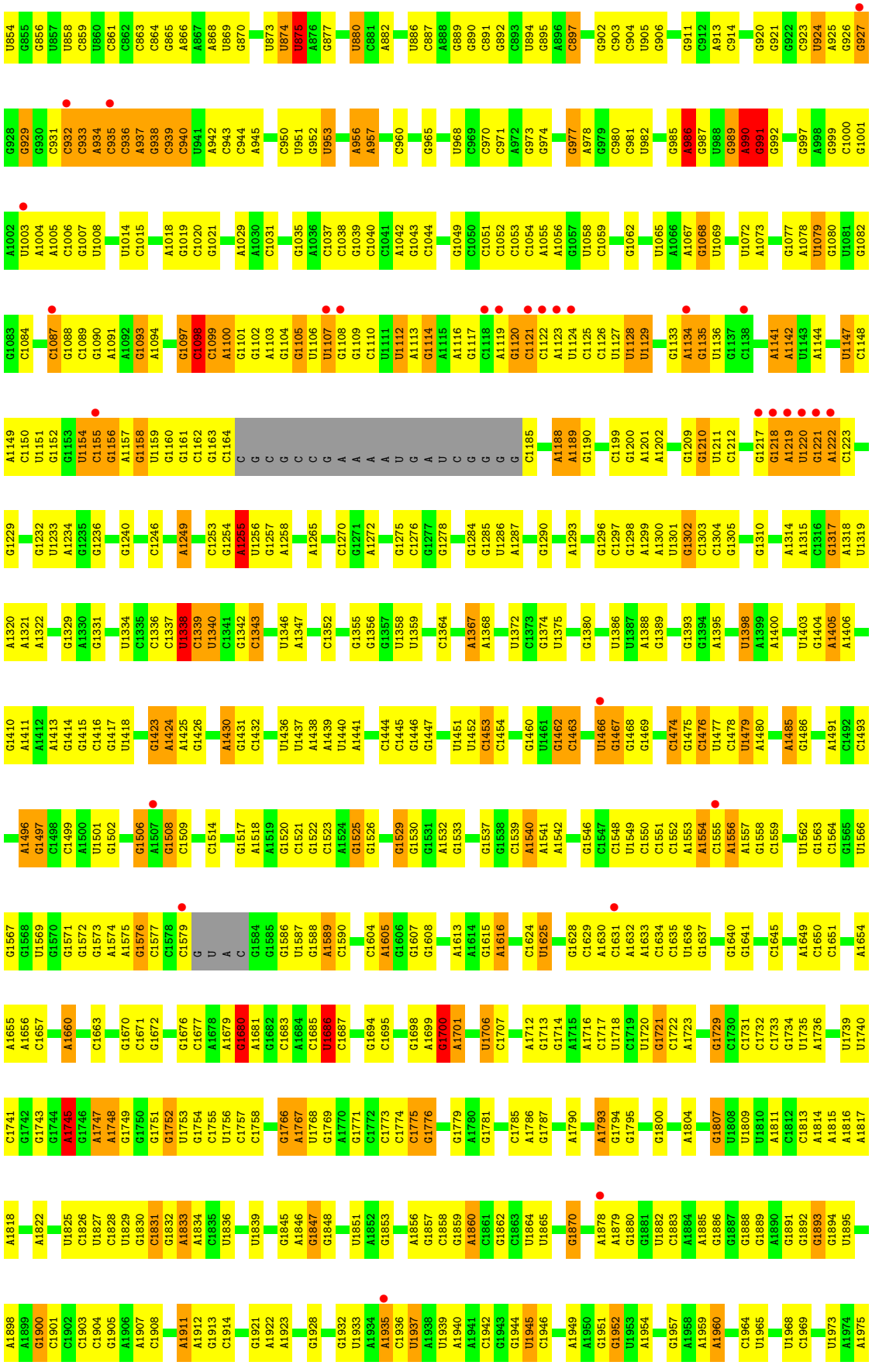
3 Residue-property plots (i)

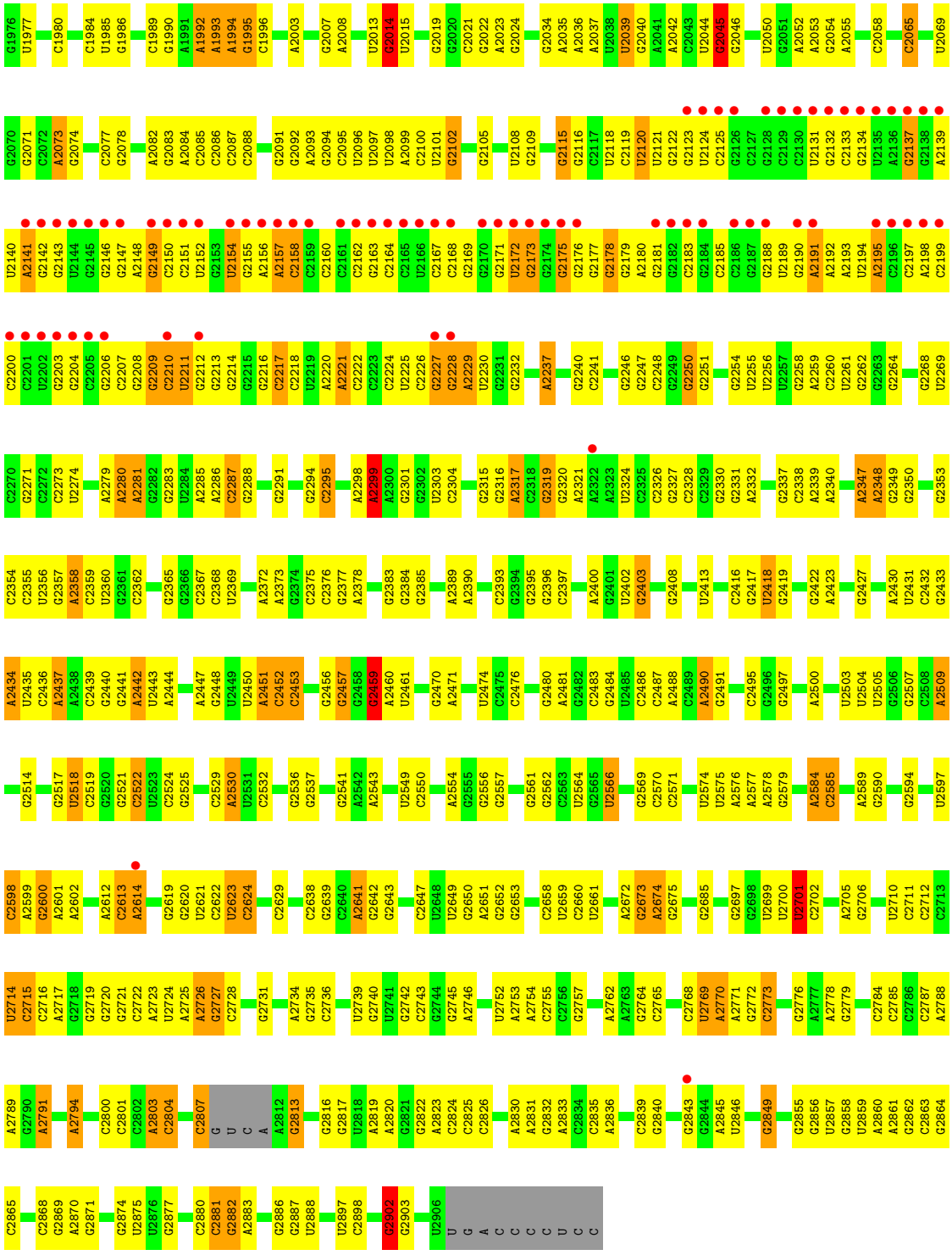
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

- Molecule 1: 23S Ribosomal RNA

Chain AA:

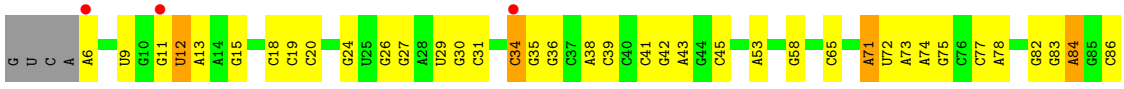


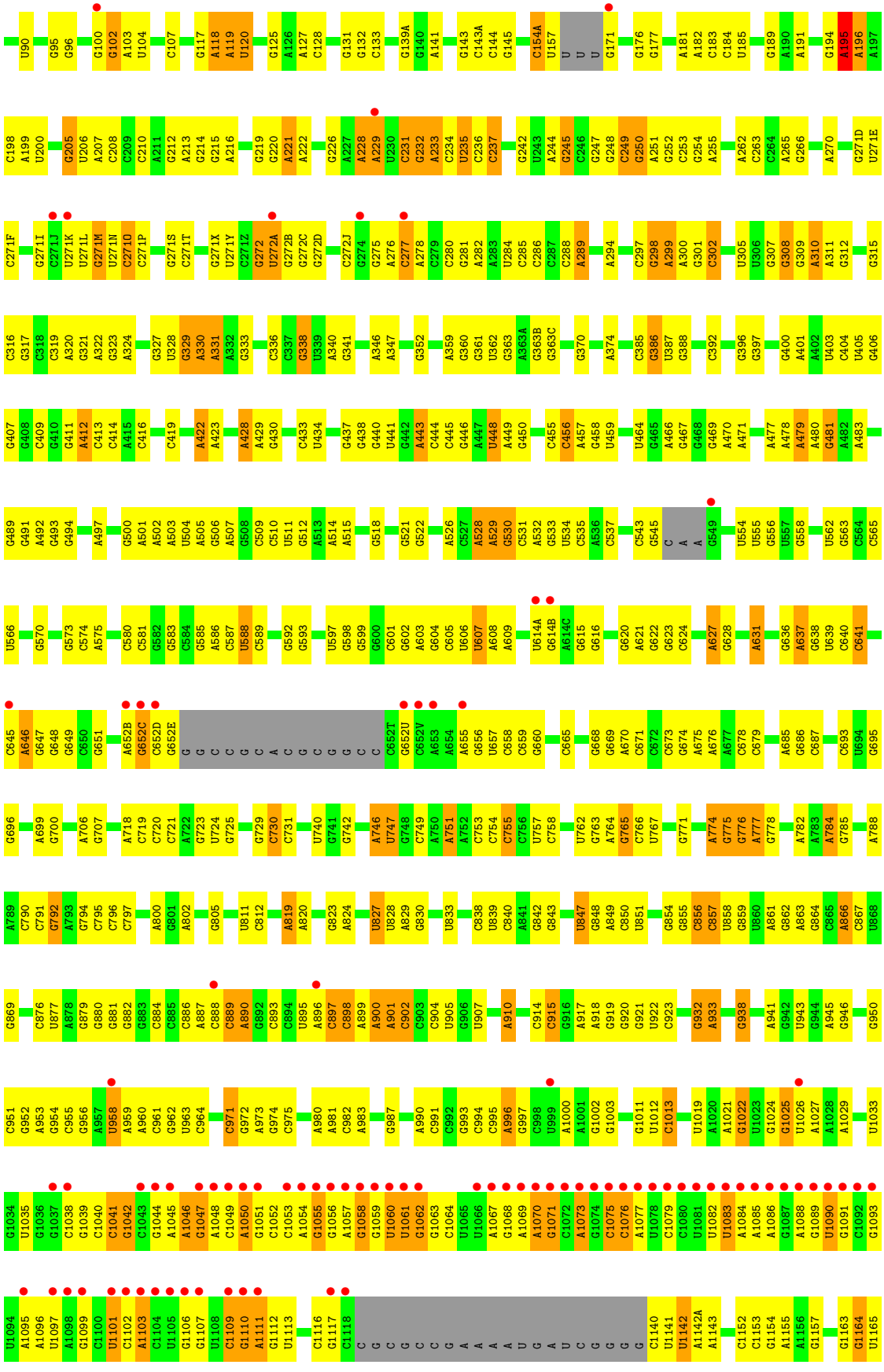


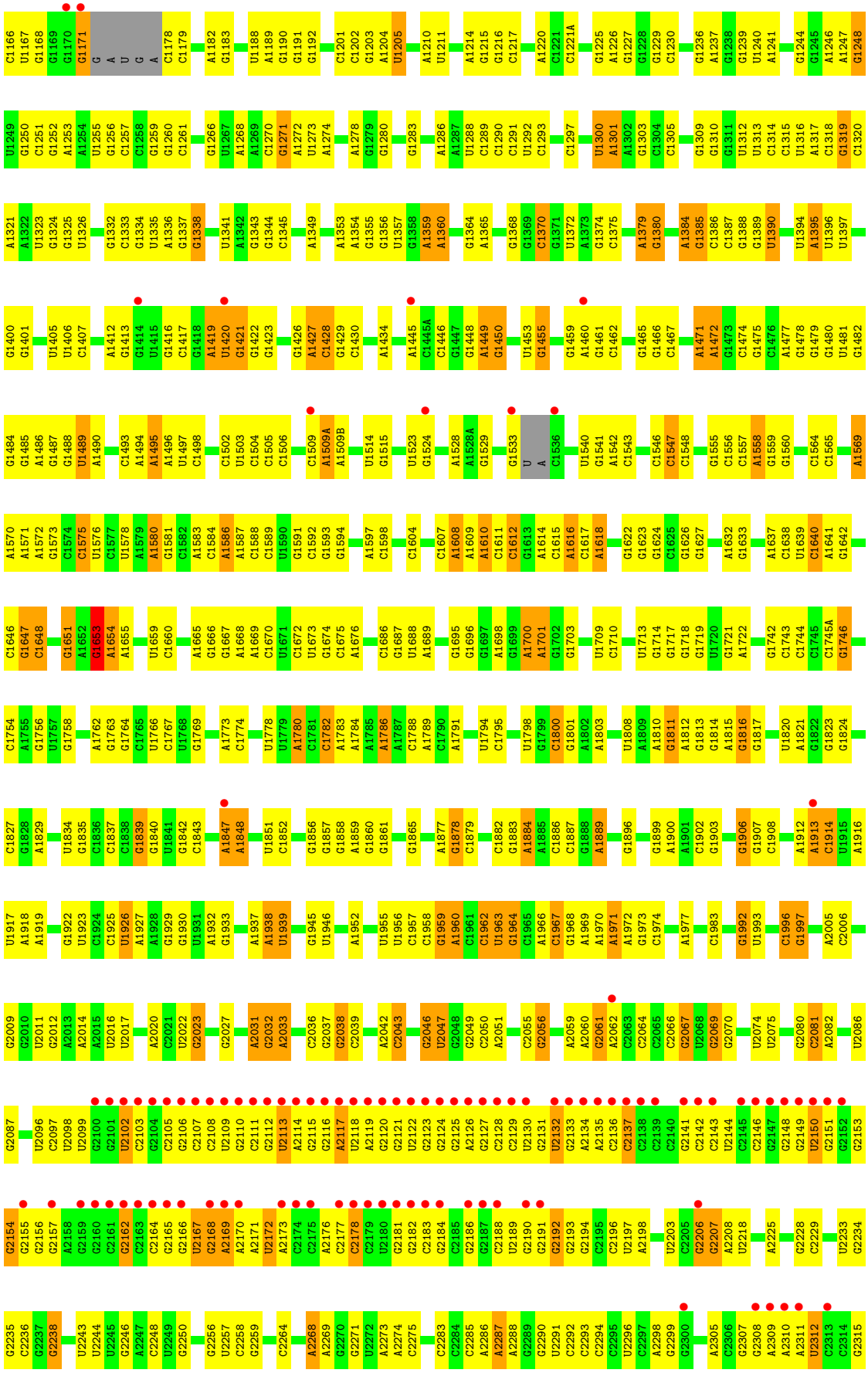


• Molecule 1: 23S Ribosomal RNA

Chain CA:



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A1321 A1322 U1323 G1324 G1325 U1326 G1332 C1333 G1334 U1335 A1336 G1337 G1338 U1341 A1342 G1343 G1344 C1345 A1349 A1353 A1354 G1355 G1356 U1357 G1358 A1359 A1360 G1364 A1365 G1368 G1369 C1370 G1371 U1372 A1373 G1374 C1375 A1379 G1380 A1384 G1385 C1386 C1387 G1388 G1389 U1390 U1394 A1395 U1396 U1397
G1400 G1401 U1405 U1406 C1407 A1412 G1413 G1414 U1415 G1416 C1417 G1418 A1419 U1420 G1421 G1422 G1423 G1426 A1427 C1428 G1429 C1430 A1434 A1445 C1445A C1446 G1447 G1448 A1449 G1450 U1453 G1455 G1459 A1460 G1461 C1462 G1465 G1466 C1467 A1471 A1472 G1473 C1474 G1475 C1476 A1477 G1478 G1479 G1480 U1481 G1482
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C1754 A1755 G1756 U1757 G1758 A1762 G1763 G1764 C1765 U1766 C1767 U1768 G1769 A1773 C1774 U1778 U1779 A1780 C1781 C1782 A1783 A1784 A1785 A1786 A1787 C1788 A1789 C1790 A1791 U1794 C1795 U1798 G1799 C1800 G1801 A1802 A1803 U1808 A1809 A1810 G1811 A1812 G1813 G1814 A1815 G1816 G1817 U1820 A1821 G1822 G1823 G1824
C1827 G1828 A1829 U1834 G1835 C1836 C1837 C1838 G1839 G1840 U1841 G1842 C1843 A1847 A1848 U1851 C1852 G1856 G1857 G1858 A1859 G1860 G1861 G1865 A1877 G1878 C1879 C1882 G1883 A1884 A1885 C1886 C1887 G1888 A1889 G1896 G1899 A1900 A1901 C1902 G1903 G1906 G1907 C1908 A1912 A1913 C1914 U1915 A1916
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G2009 G2010 U2011 G2012 A2013 A2014 A2015 U2016 U2017 A2020 C2021 U2022 G2023 G2027 A2031 G2032 A2033 C2036 G2037 G2038 C2039 A2042 C2043 G2046 U2047 G2048 G2049 C2050 A2051 C2055 G2056 A2059 A2060 G2061 A2062 C2063 C2064 C2065 C2066 G2067 U2068 G2069 G2070 U2074 U2075 G2080 G2081 A2082 U2086
G2087 U2096 C2097 U2098 U2099 G2100 G2101 U2102 C2103 G2104 C2105 G2106 C2107 C2108 U2109 G2110 C2111 G2112 U2113 A2114 G2115 G2116 A2117 U2118 A2119 G2120 G2121 G2122 G2123 G2124 G2125 A2126 G2127 C2128 C2129 U2130 G2131 U2132 G2133 A2134 A2135 C2136 C2137 C2138 C2139 C2140 G2141 C2142 C2143 U2144 C2145 C2146 G2147 G2148 G2149 U2150 G2151 G2152 G2153
G2154 G2155 G2156 G2157 A2158 G2159 G2160 C2161 G2162 C2163 C2164 G2165 G2166 U2167 G2168 A2169 A2170 A2171 U2172 A2173 C2174 G2175 A2176 A2177 C2178 A2179 U2180 G2181 G2182 G2183 G2184 C2185 G2186 G2187 C2188 U2189 G2190 G2191 G2192 G2193 G2194 C2195 C2196 U2197 A2198 U2203 C2205 G2206 G2207 A2208 U2218 A2225 G2228 C2229 U2233 G2234
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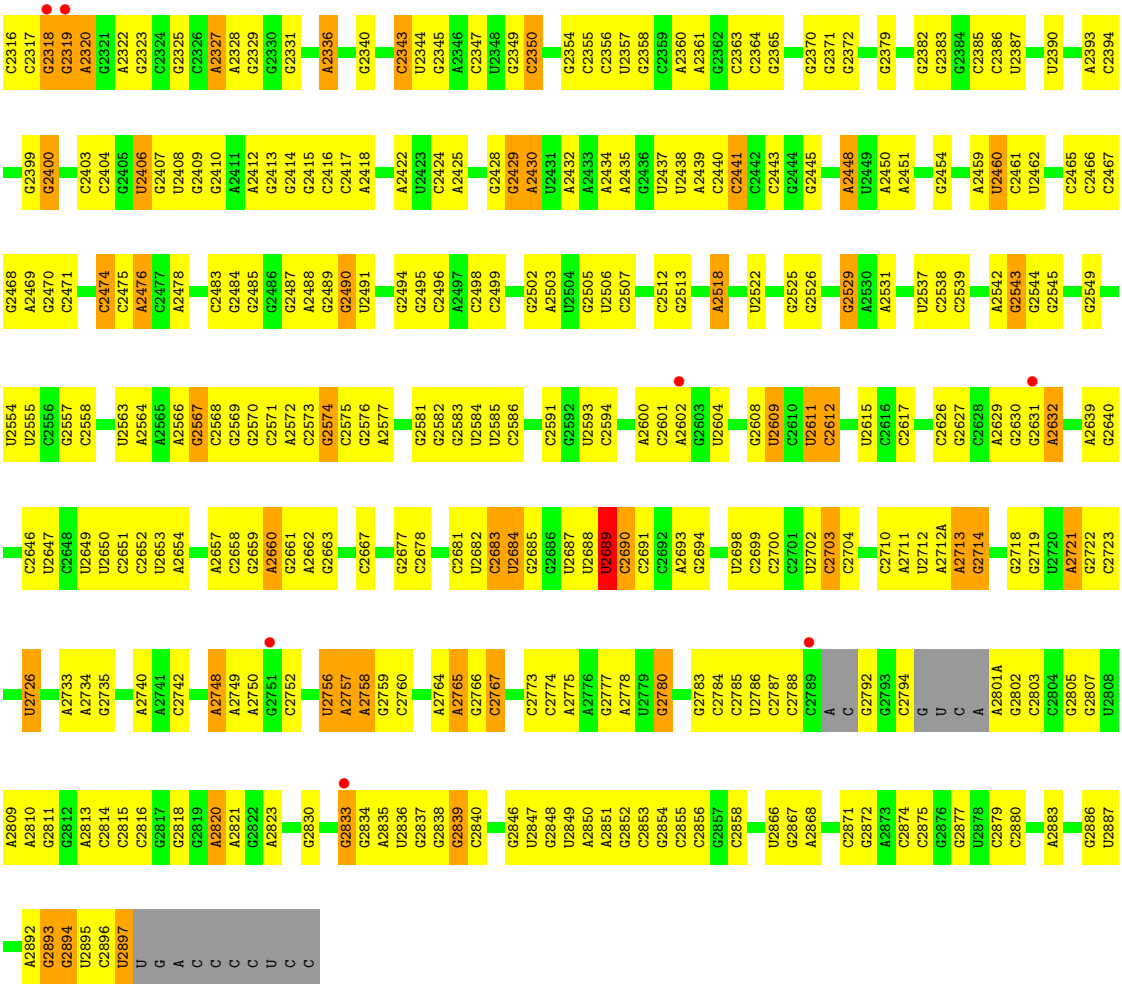
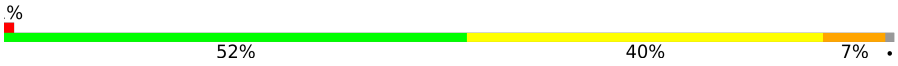
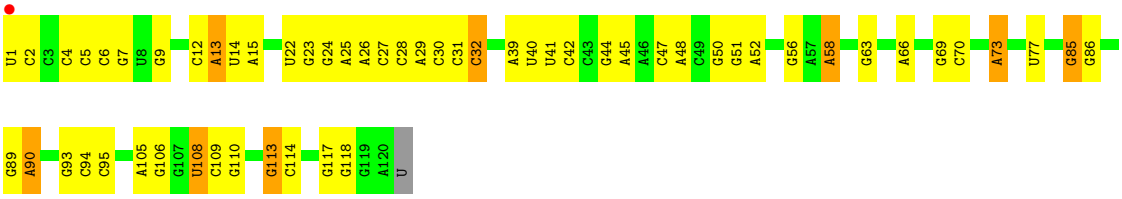


• Molecule 2: 5S Ribosomal RNA

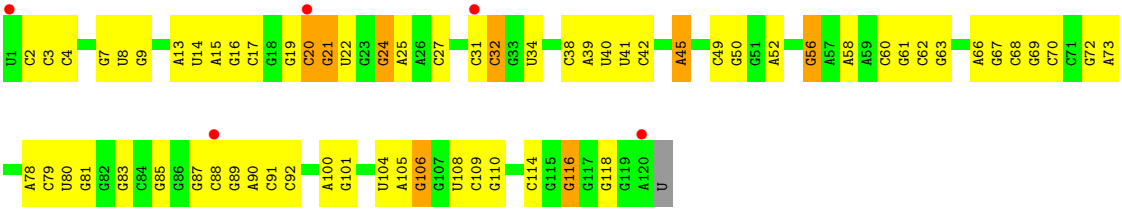
Chain AB:





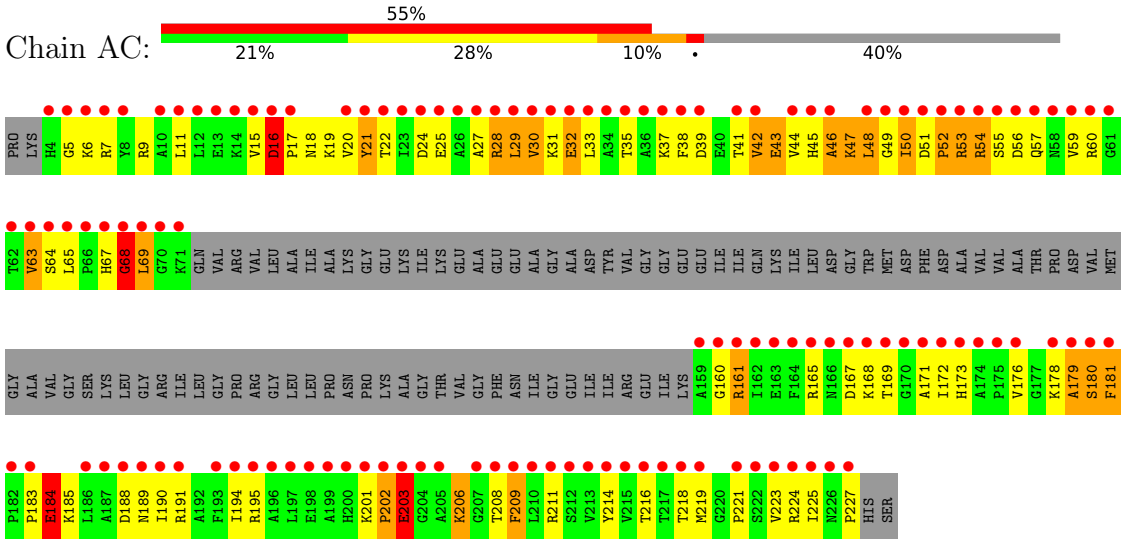
• Molecule 2: 5S Ribosomal RNA

Chain CB:



• Molecule 3: 50S ribosomal protein L1

Chain AC:



• Molecule 3: 50S ribosomal protein L1

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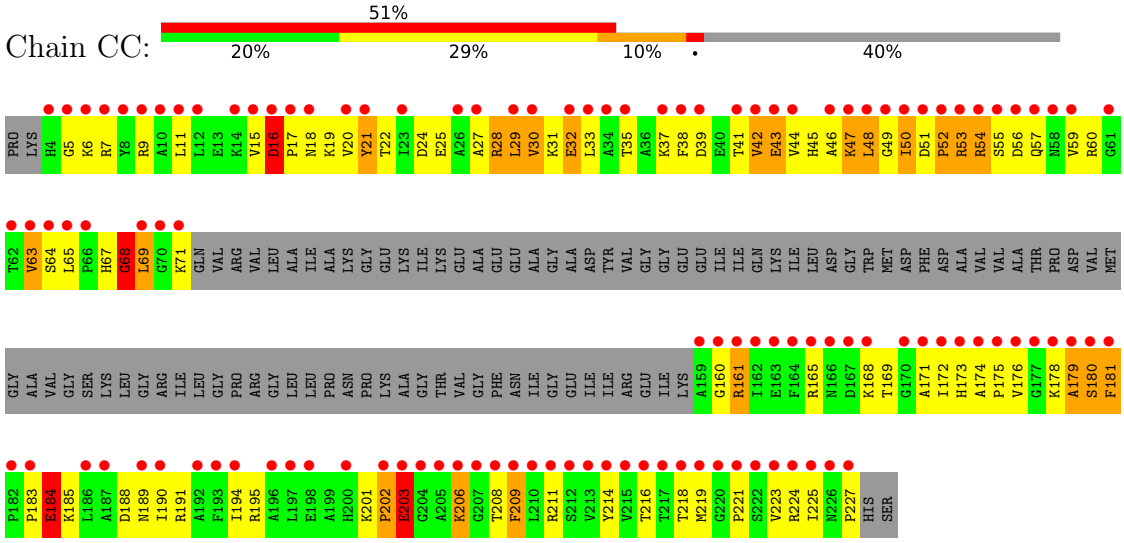

• Molecule 4: 50S ribosomal protein L2

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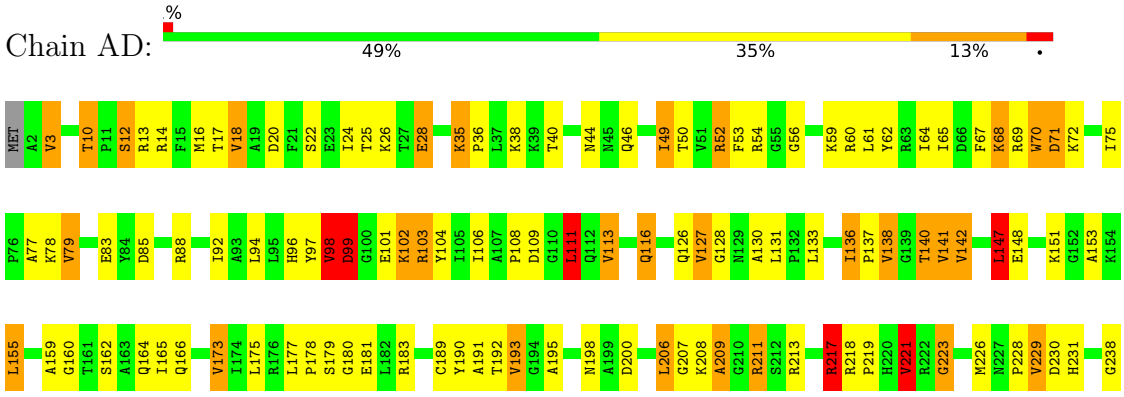
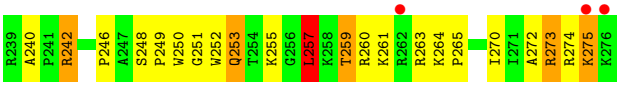
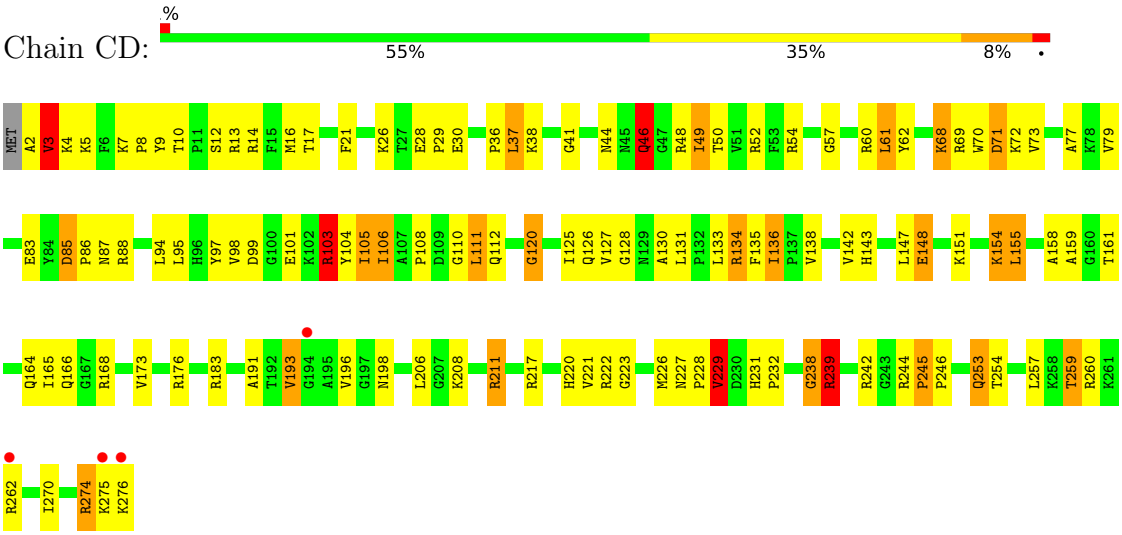




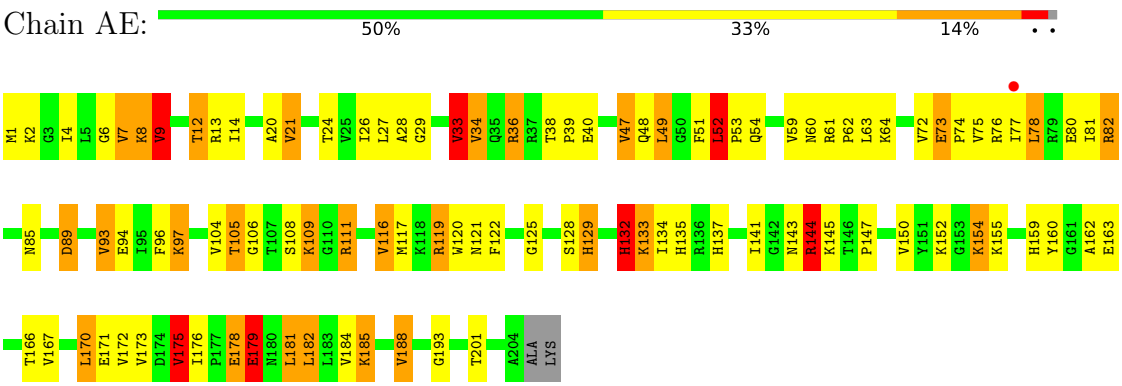
• Molecule 4: 50S ribosomal protein L2

Chain CD:



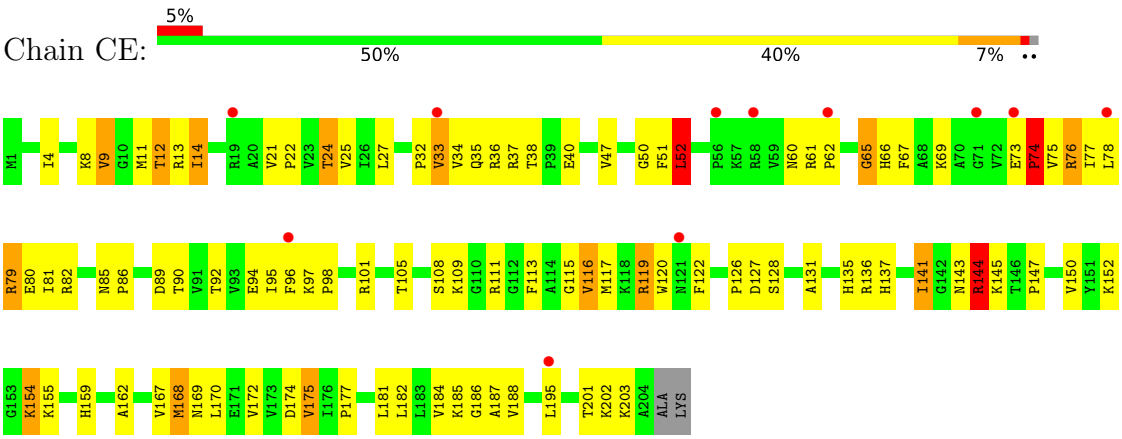
• Molecule 5: 50S ribosomal protein L3

Chain AE:



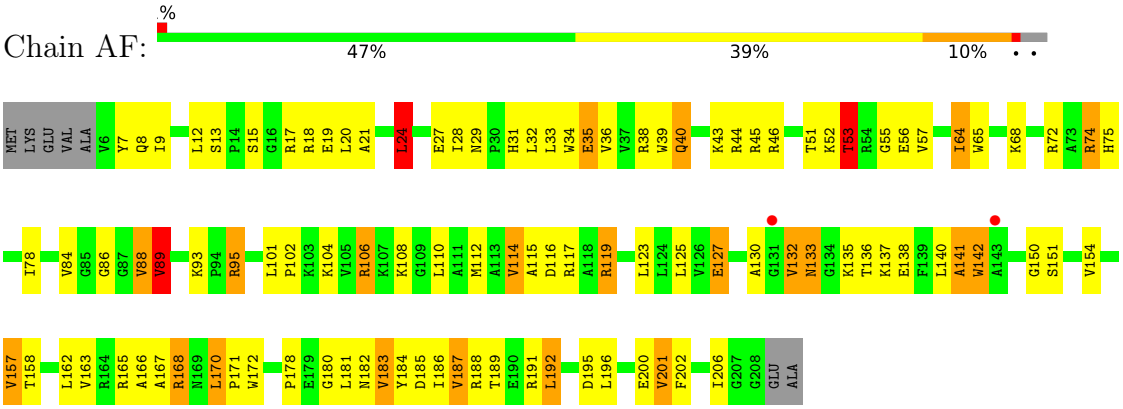
• Molecule 5: 50S ribosomal protein L3

Chain CE:



• Molecule 6: 50S ribosomal protein L4

Chain AF:



• Molecule 6: 50S ribosomal protein L4

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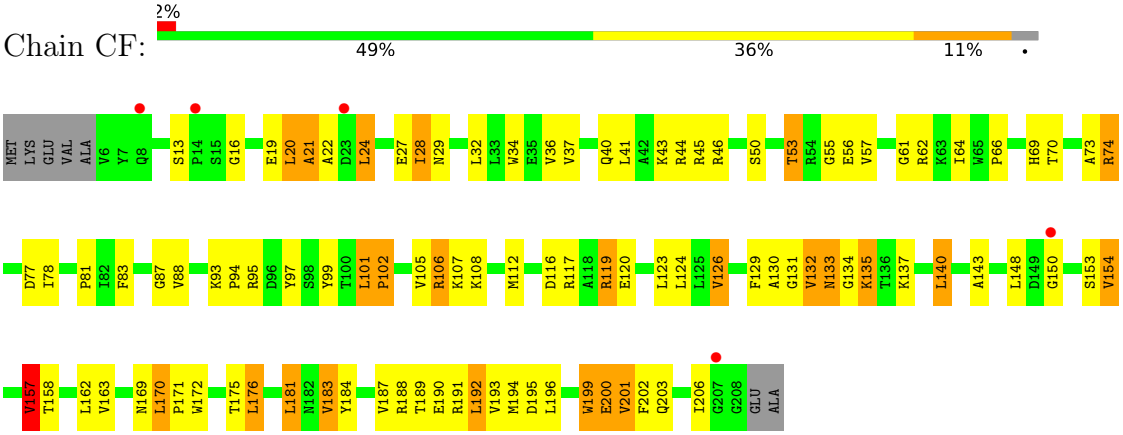
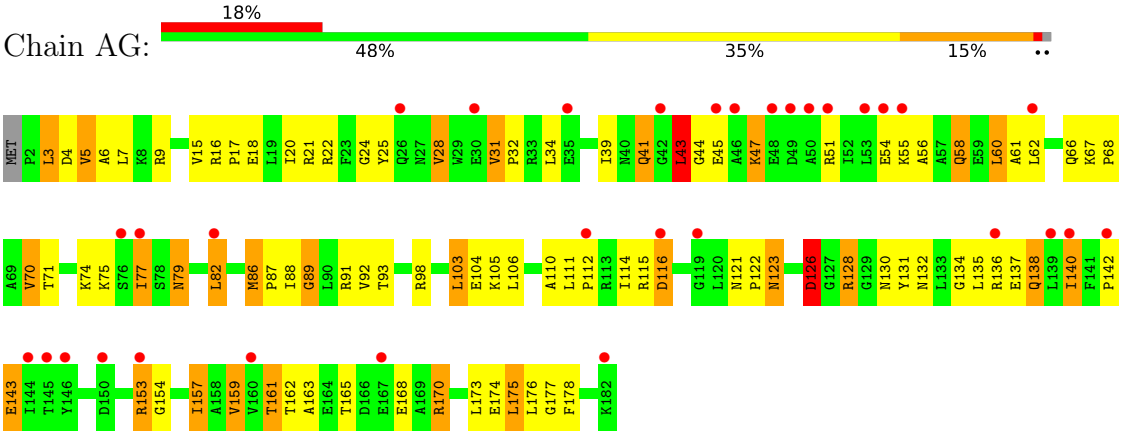


• Molecule 7: 50S ribosomal protein L5

Chain AG:



• Molecule 7: 50S ribosomal protein L5

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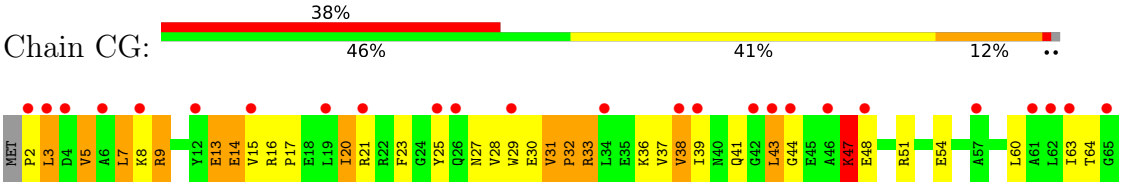
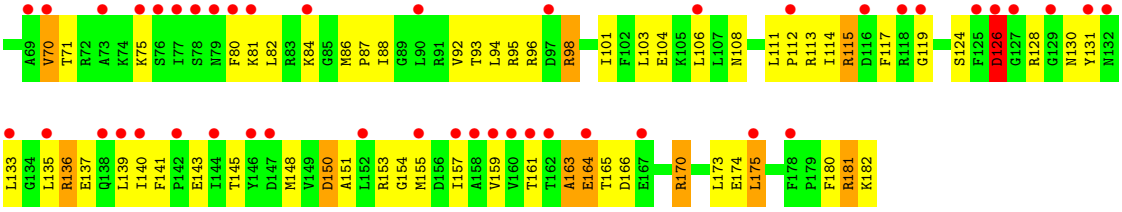
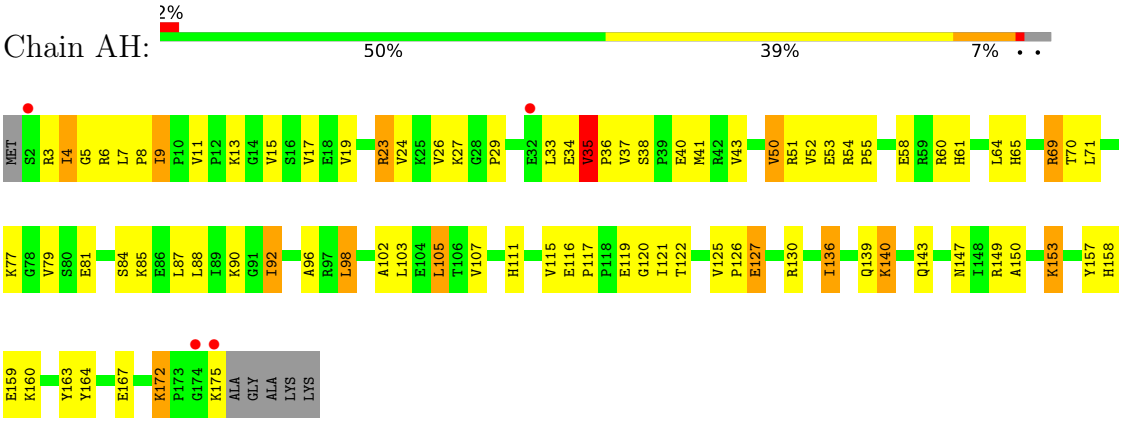




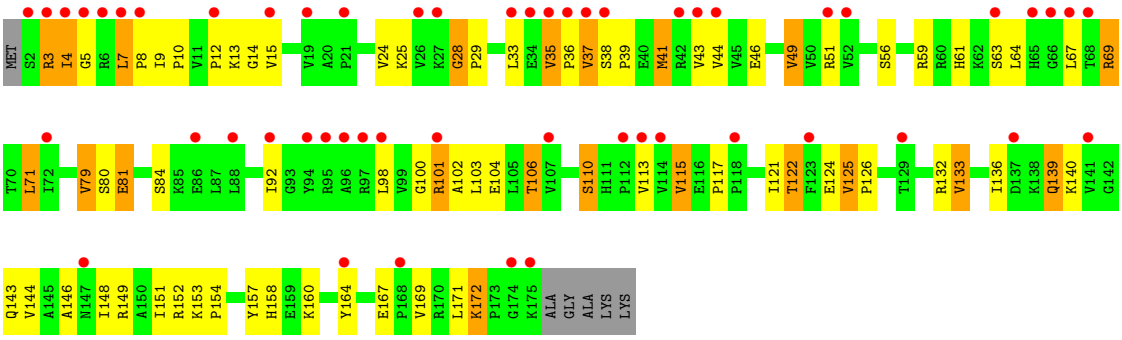


• Molecule 8: 50S ribosomal protein L6

Chain AH:

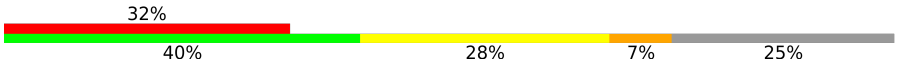
• Molecule 8: 50S ribosomal protein L6

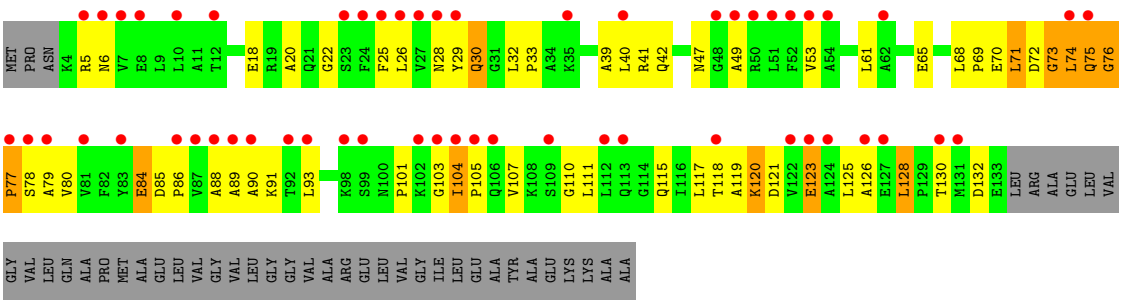
Chain CH:



• Molecule 9: 50S ribosomal protein L10

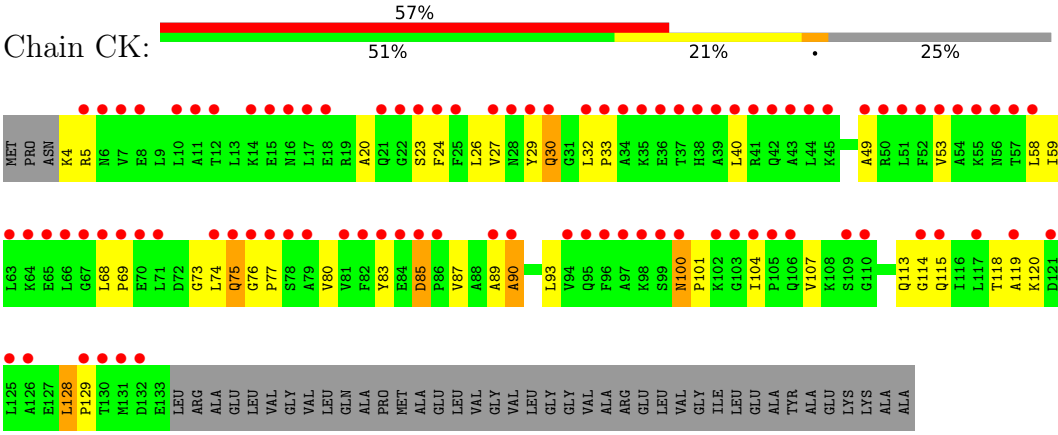
Chain AK:





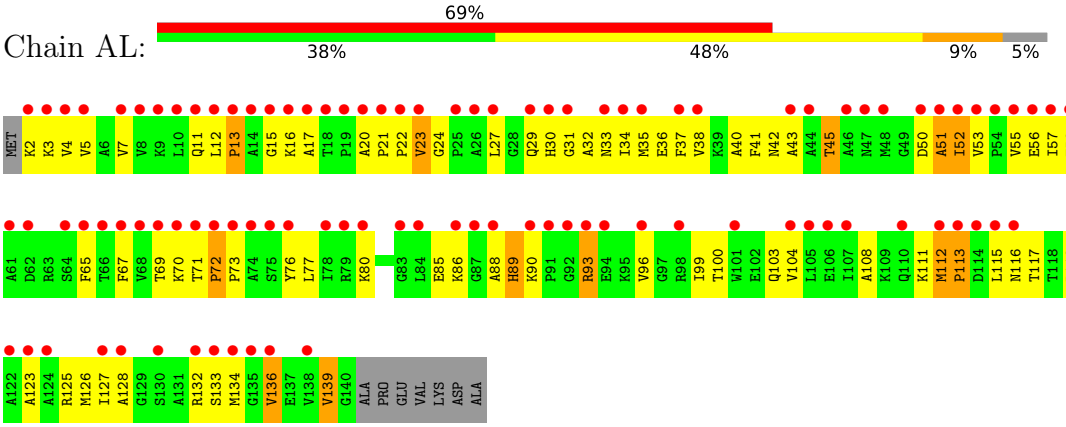
• Molecule 9: 50S ribosomal protein L10

Chain CK:



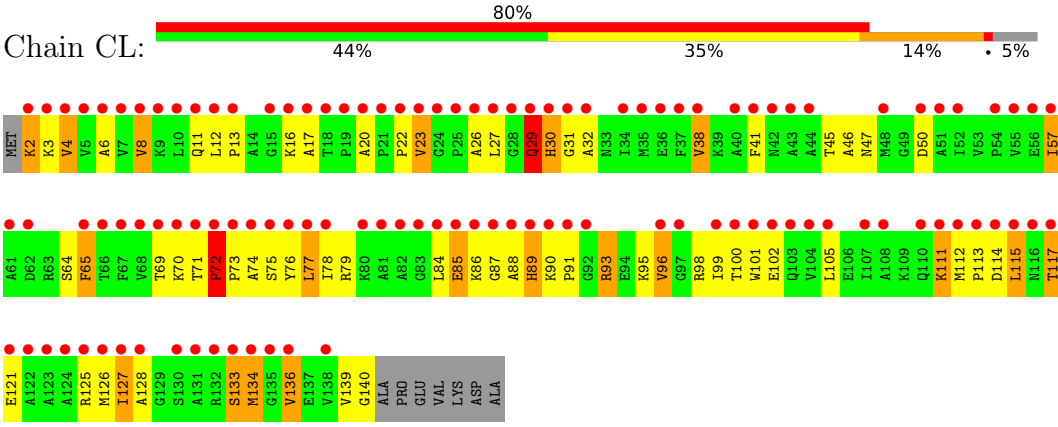
• Molecule 10: 50S ribosomal protein L11

Chain AL:



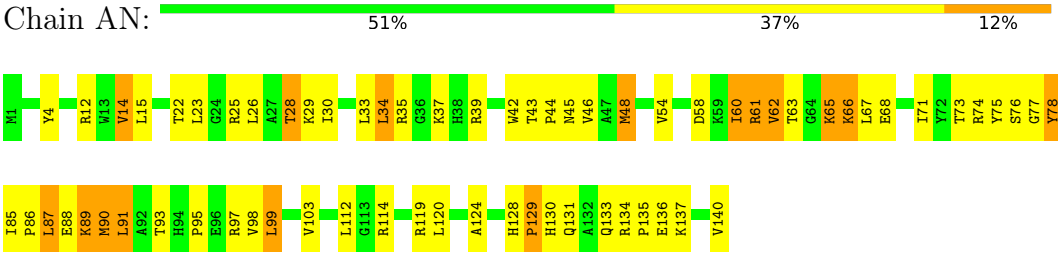
• Molecule 10: 50S ribosomal protein L11

Chain CL:



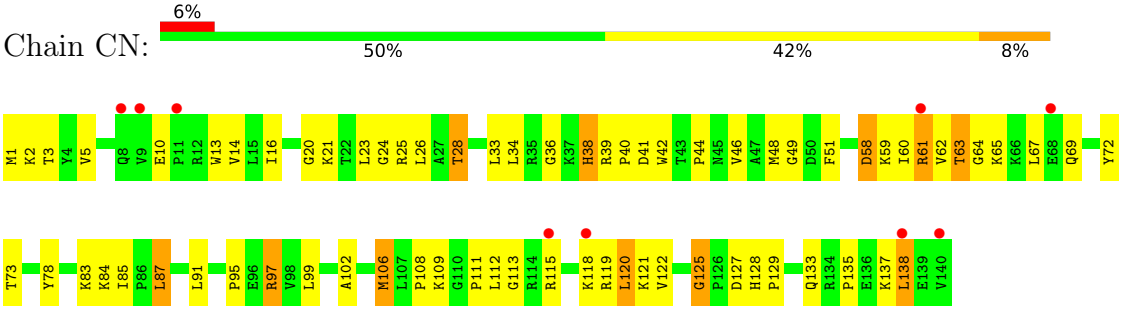
• Molecule 11: 50S ribosomal protein L13

Chain AN:



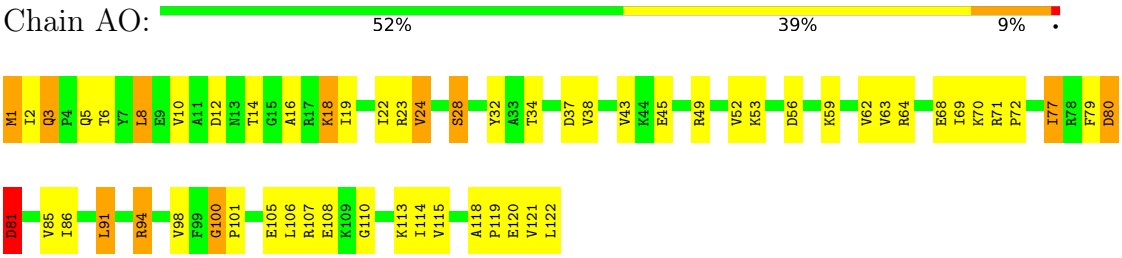
• Molecule 11: 50S ribosomal protein L13

Chain CN:



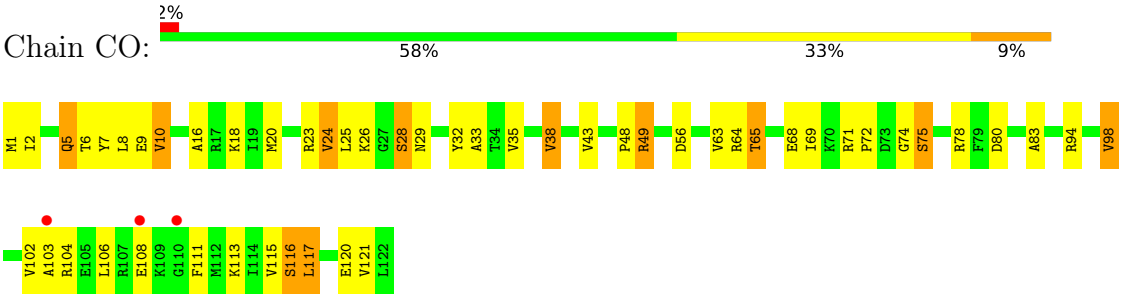
• Molecule 12: 50S ribosomal protein L14

Chain AO:



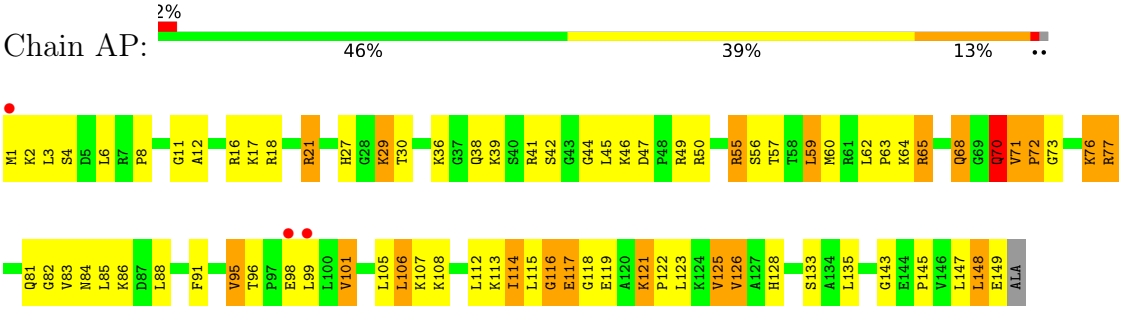
• Molecule 12: 50S ribosomal protein L14

Chain CO:



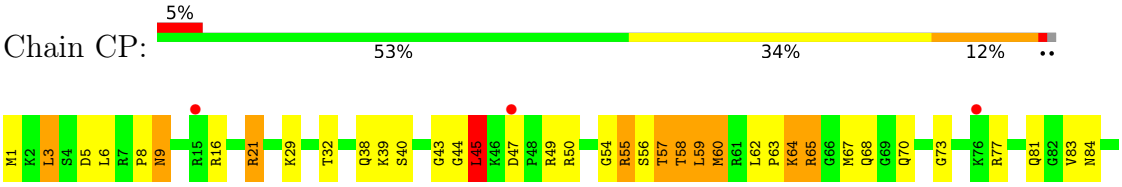
• Molecule 13: 50S ribosomal protein L15

Chain AP:

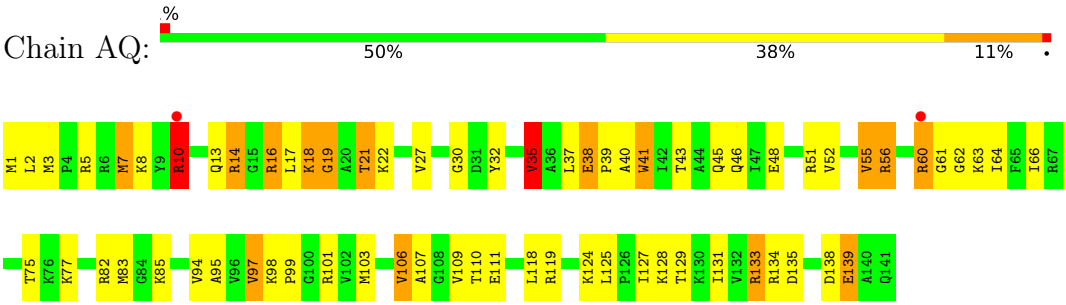


• Molecule 13: 50S ribosomal protein L15

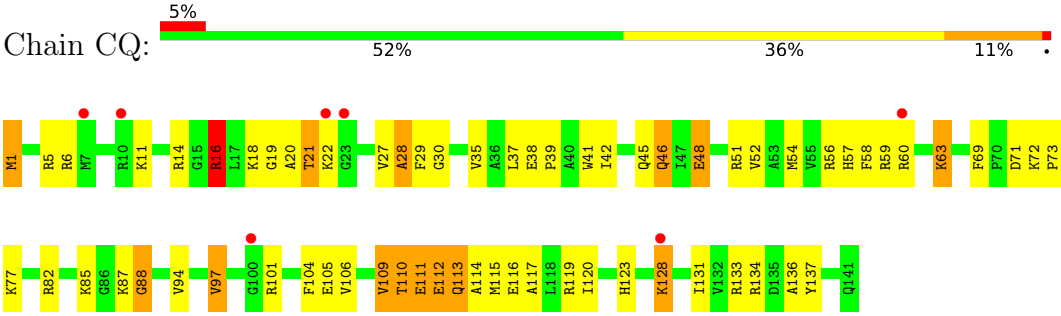
Chain CP:



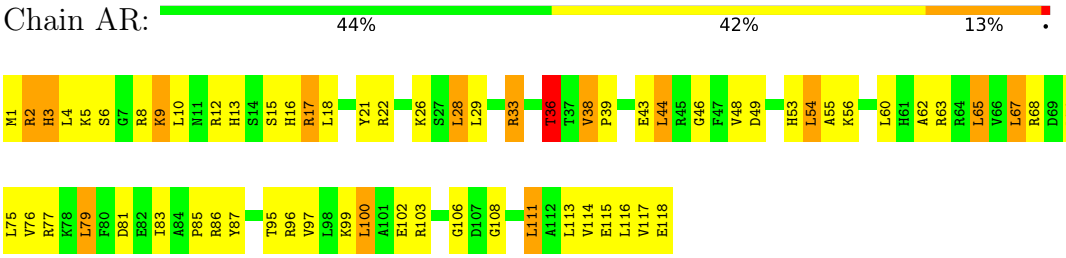
• Molecule 14: 50S ribosomal protein L16



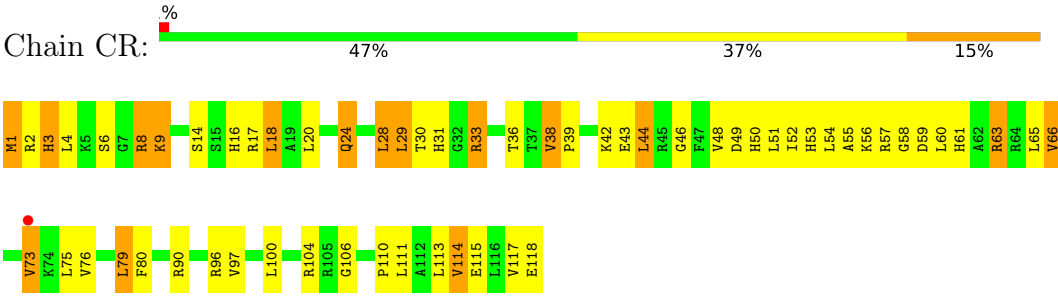
• Molecule 14: 50S ribosomal protein L16



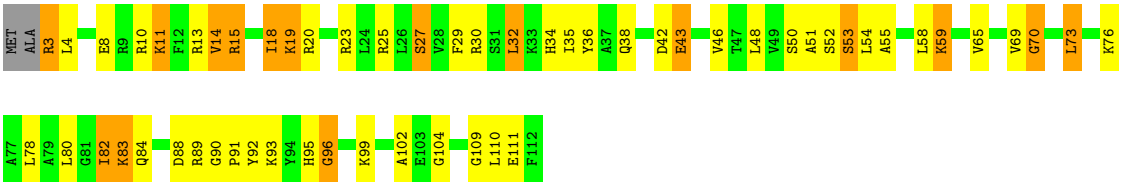
• Molecule 15: 50S ribosomal protein L17



• Molecule 15: 50S ribosomal protein L17

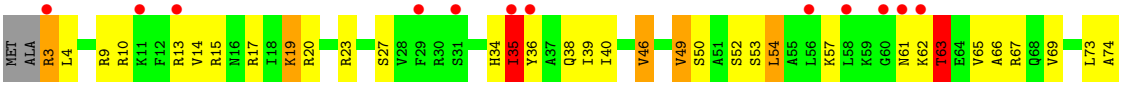


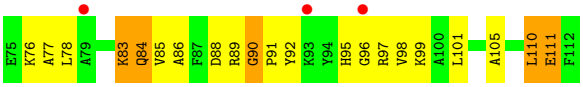
• Molecule 16: 50S ribosomal protein L18



• Molecule 16: 50S ribosomal protein L18

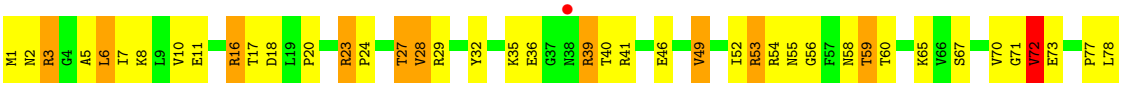
Chain CS:





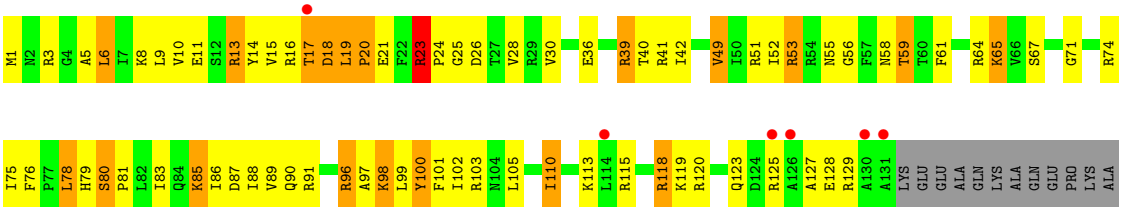
• Molecule 17: 50S ribosomal protein L19

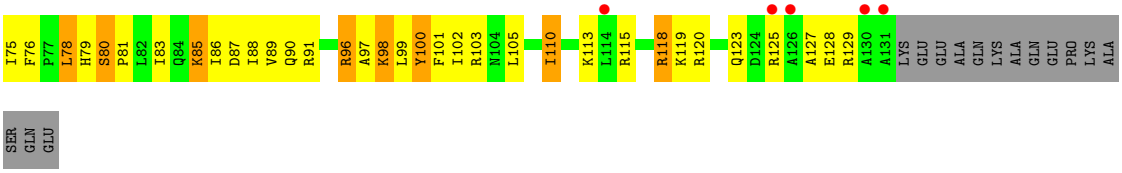
Chain AT:



• Molecule 17: 50S ribosomal protein L19

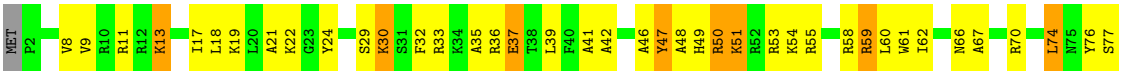
Chain CT:

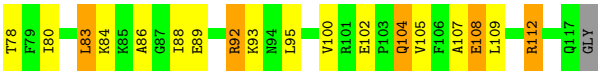




• Molecule 18: 50S ribosomal protein L20

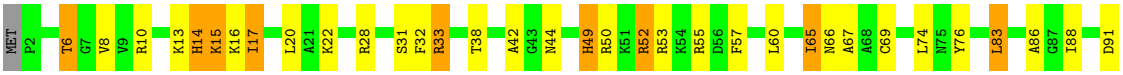
Chain AU:

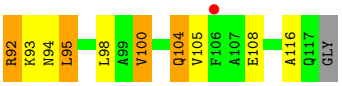




• Molecule 18: 50S ribosomal protein L20

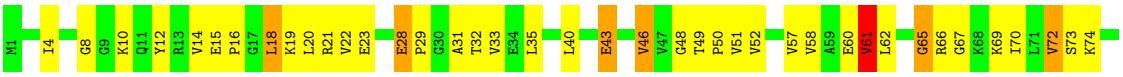
Chain CU:





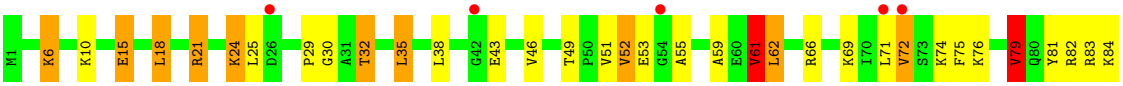
• Molecule 19: 50S ribosomal protein L21

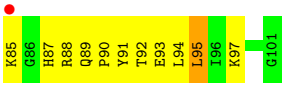
Chain AV:



• Molecule 19: 50S ribosomal protein L21

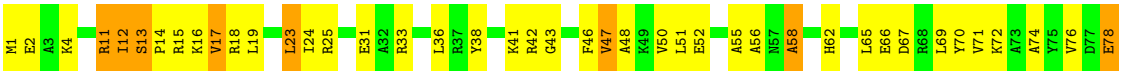
Chain CV:





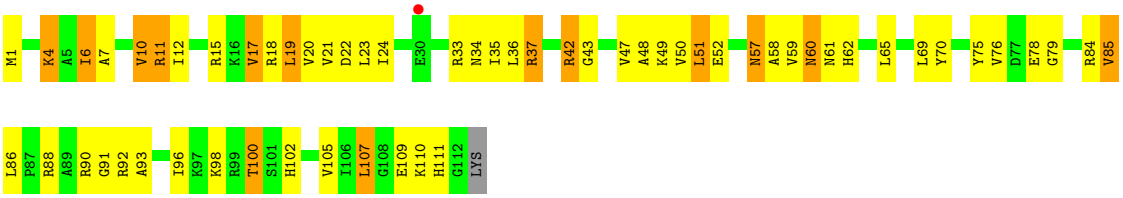
• Molecule 20: 50S ribosomal protein L22

Chain AW:

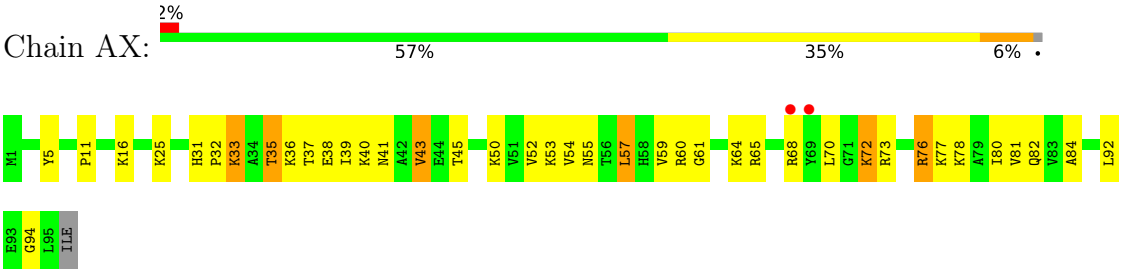


• Molecule 20: 50S ribosomal protein L22

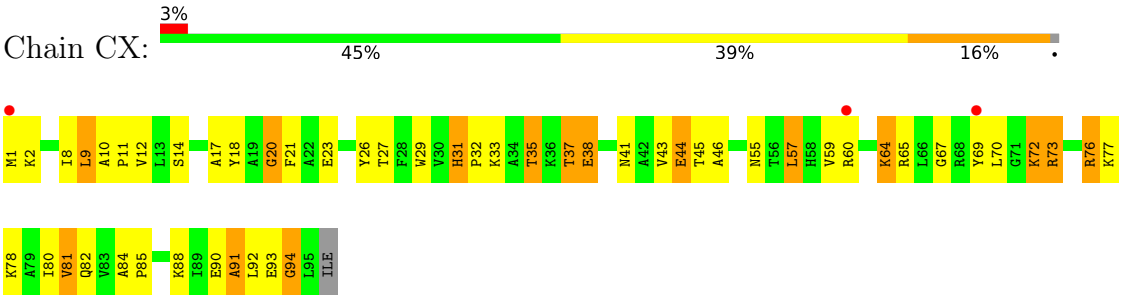
Chain CW:



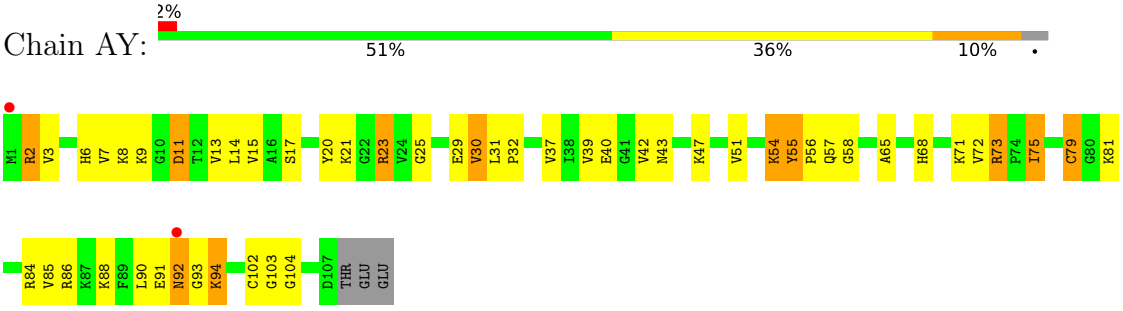
• Molecule 21: 50S ribosomal protein L23



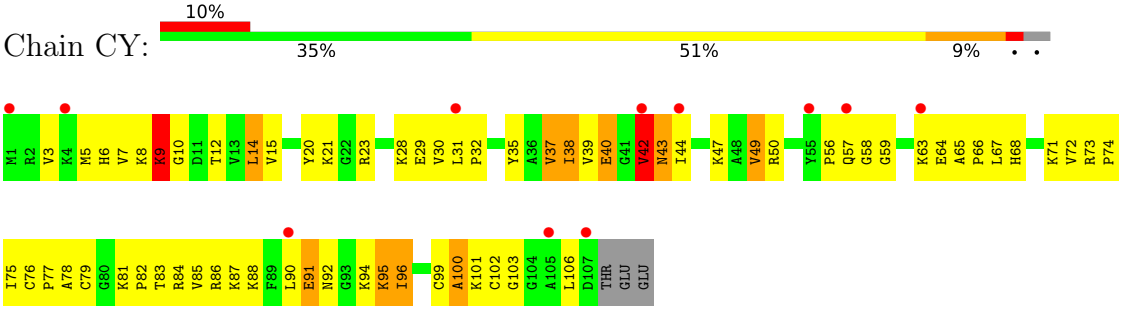
• Molecule 21: 50S ribosomal protein L23



• Molecule 22: 50S ribosomal protein L24

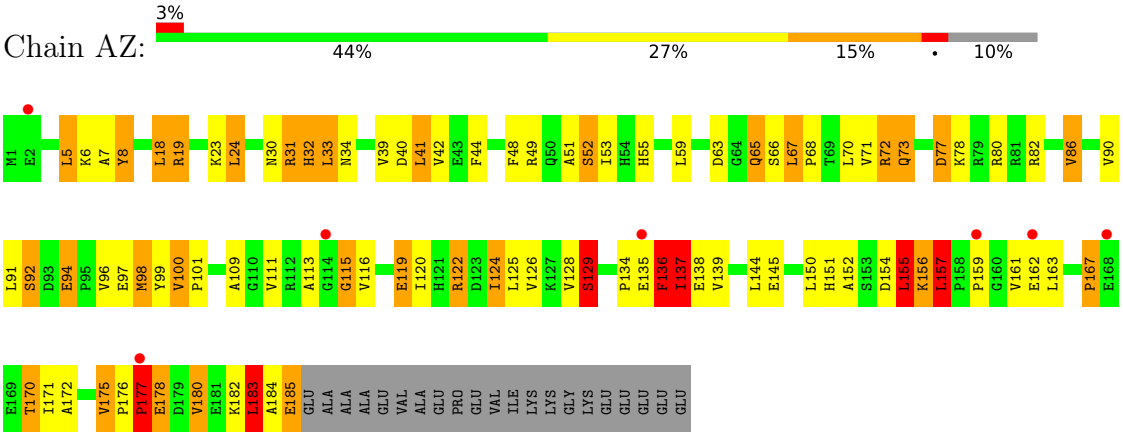


• Molecule 22: 50S ribosomal protein L24



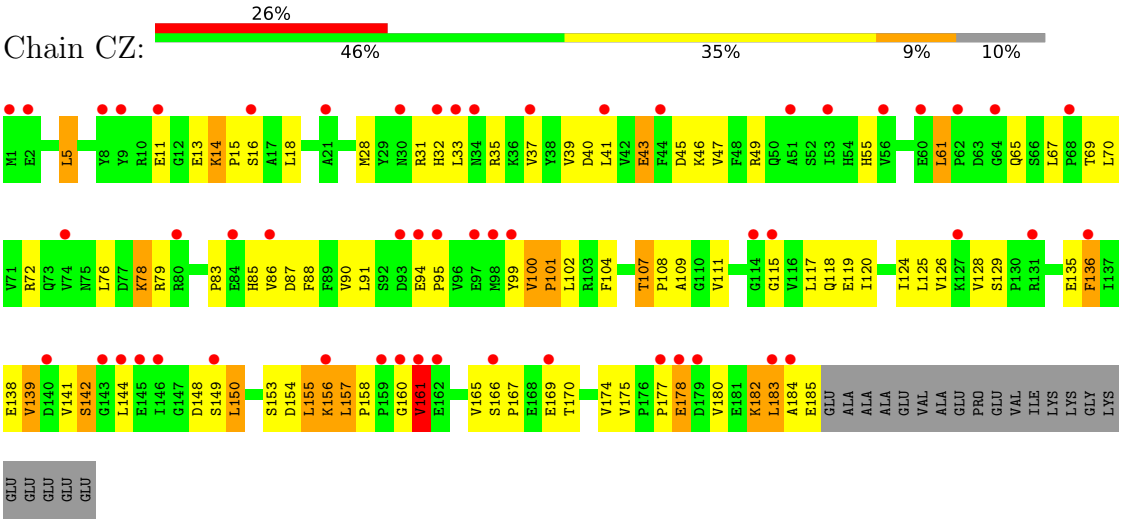
• Molecule 23: 50S ribosomal protein L25

Chain AZ:



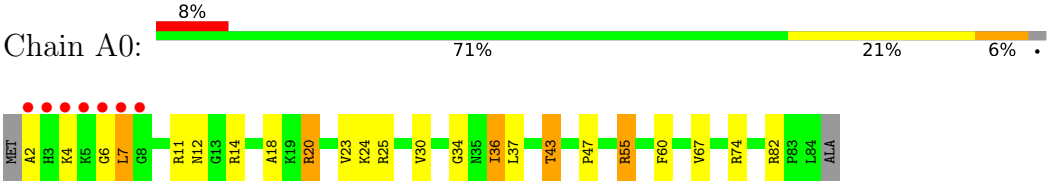
• Molecule 23: 50S ribosomal protein L25

Chain CZ:



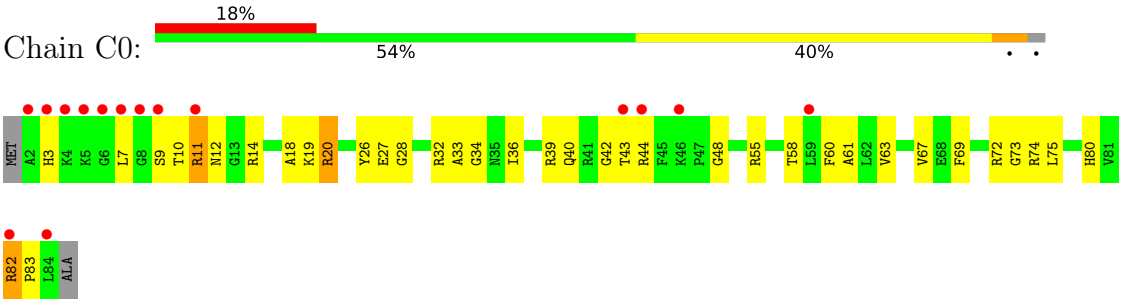
• Molecule 24: 50S ribosomal protein L27

Chain A0:



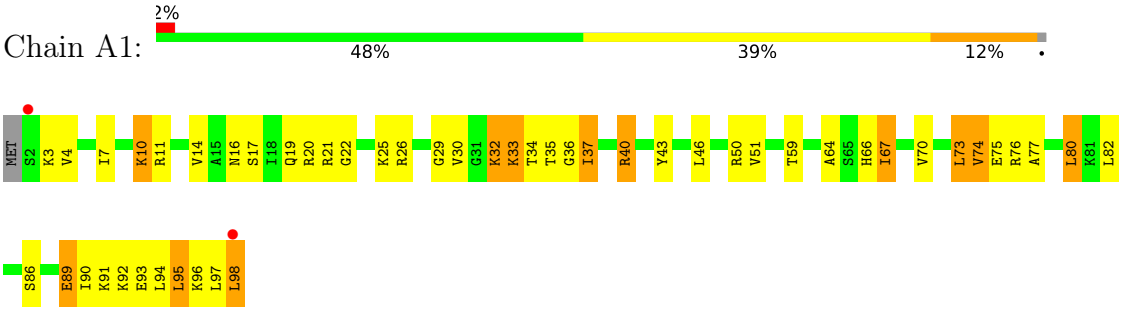
• Molecule 24: 50S ribosomal protein L27

Chain C0:



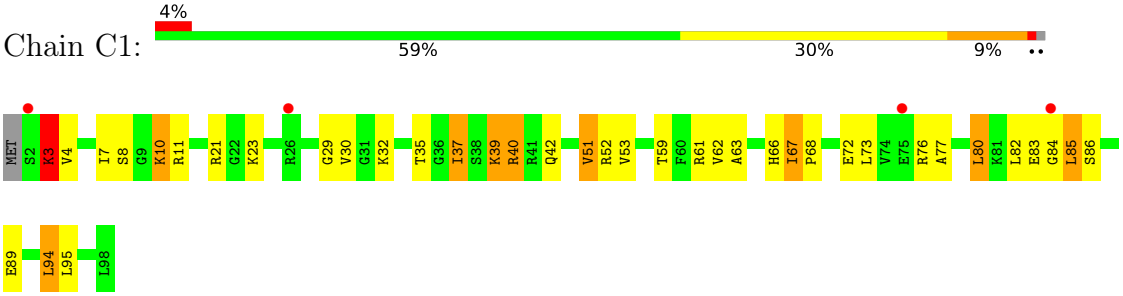
• Molecule 25: 50S ribosomal protein L28

Chain A1:



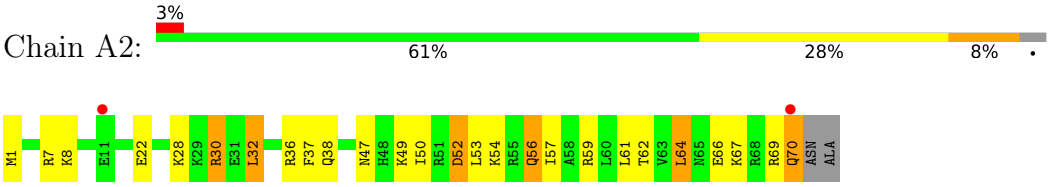
• Molecule 25: 50S ribosomal protein L28

Chain C1:



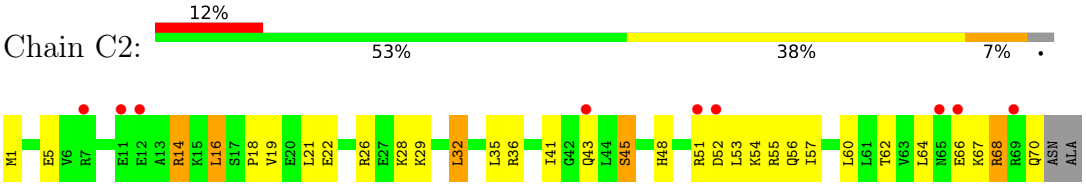
• Molecule 26: 50S ribosomal protein L29

Chain A2:



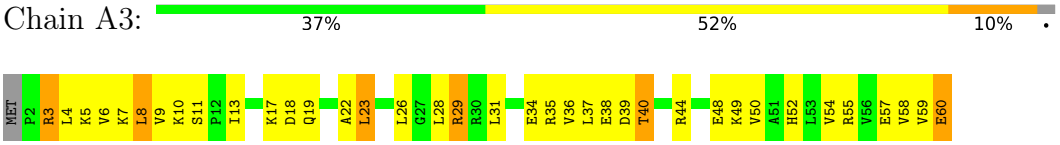
• Molecule 26: 50S ribosomal protein L29

Chain C2:



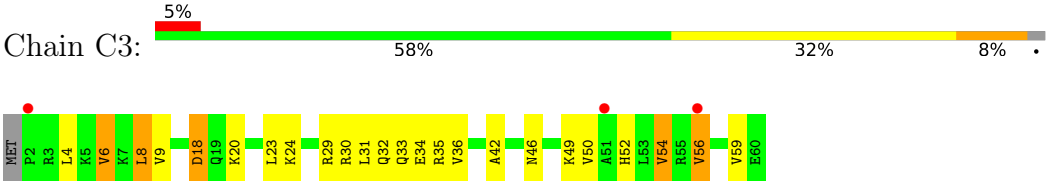
• Molecule 27: 50S ribosomal protein L30

Chain A3:



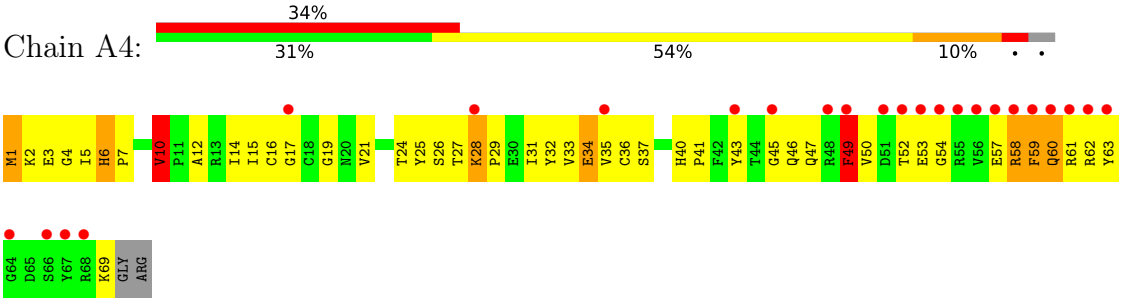
• Molecule 27: 50S ribosomal protein L30

Chain C3:



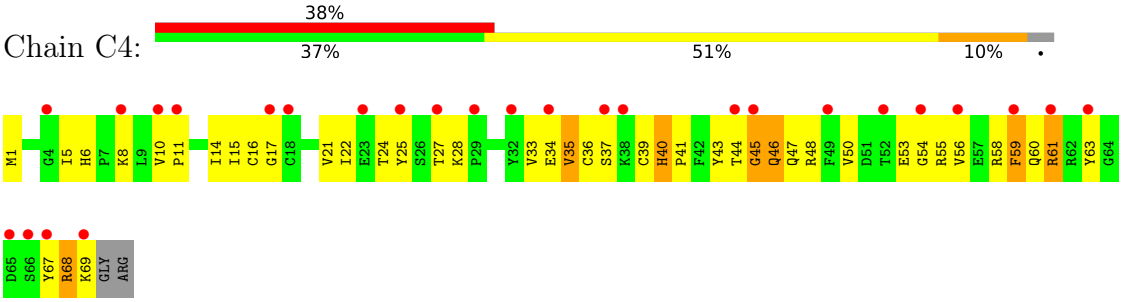
• Molecule 28: 50S ribosomal protein L31

Chain A4:



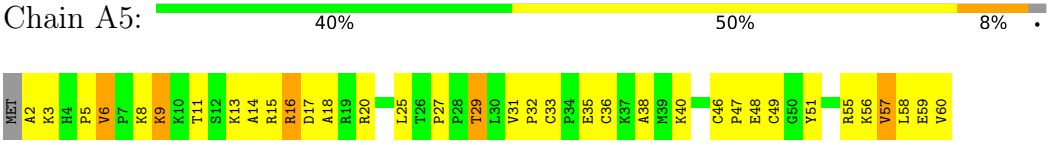
• Molecule 28: 50S ribosomal protein L31

Chain C4:



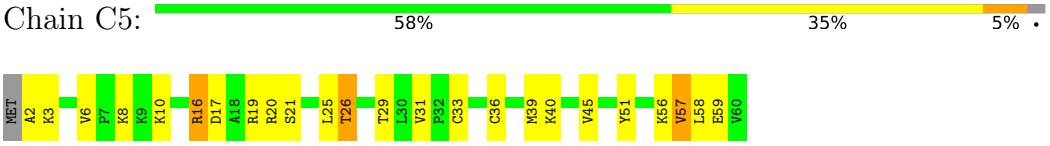
• Molecule 29: 50S ribosomal protein L32

Chain A5:



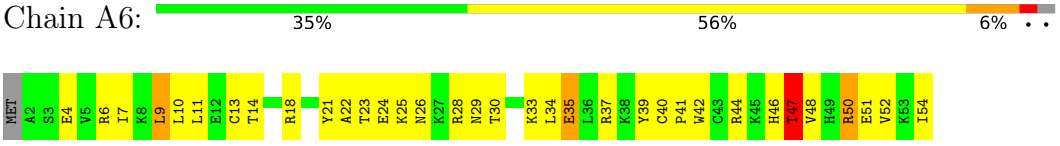
• Molecule 29: 50S ribosomal protein L32

Chain C5:



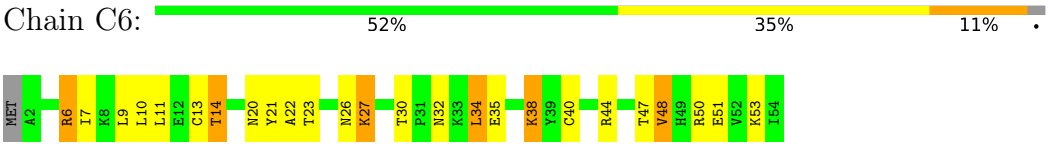
• Molecule 30: 50S ribosomal protein L33

Chain A6:



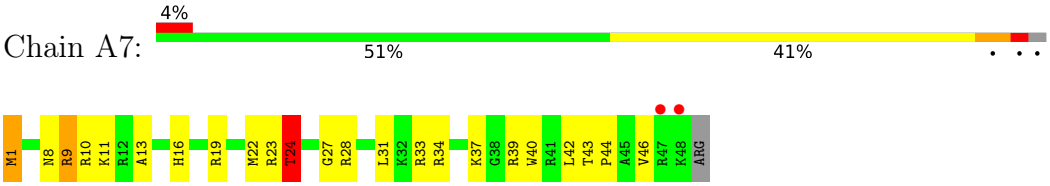
• Molecule 30: 50S ribosomal protein L33

Chain C6:



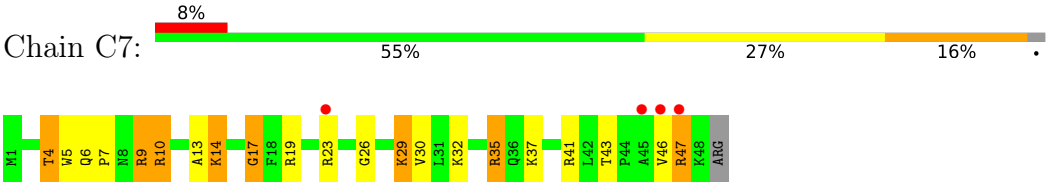
• Molecule 31: 50S ribosomal protein L34

Chain A7:



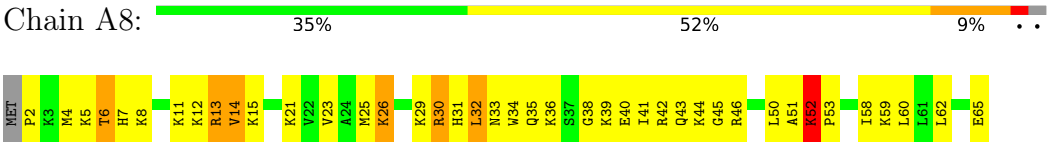
• Molecule 31: 50S ribosomal protein L34

Chain C7:



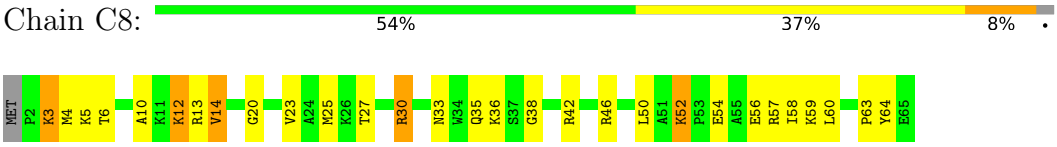
• Molecule 32: 50S ribosomal protein L35

Chain A8:



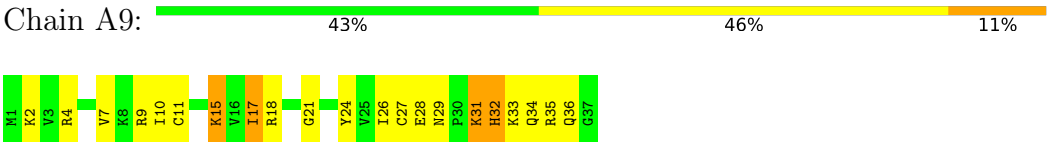
• Molecule 32: 50S ribosomal protein L35

Chain C8:



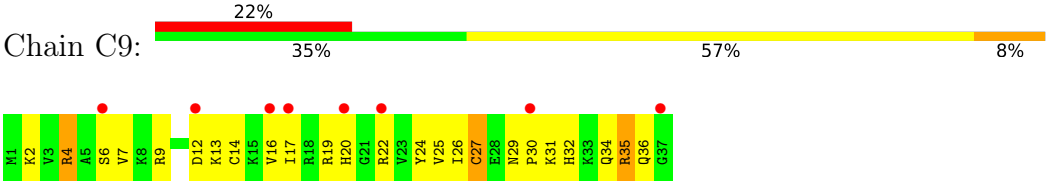
• Molecule 33: 50S ribosomal protein L36

Chain A9:



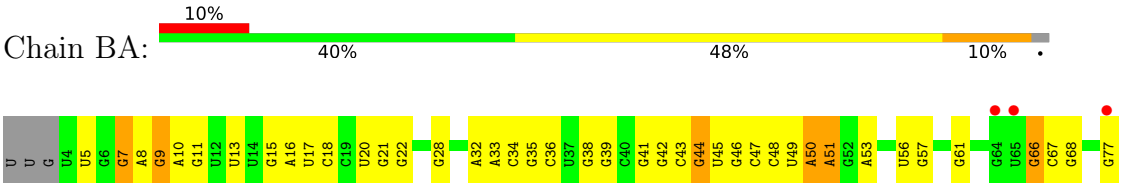
• Molecule 33: 50S ribosomal protein L36

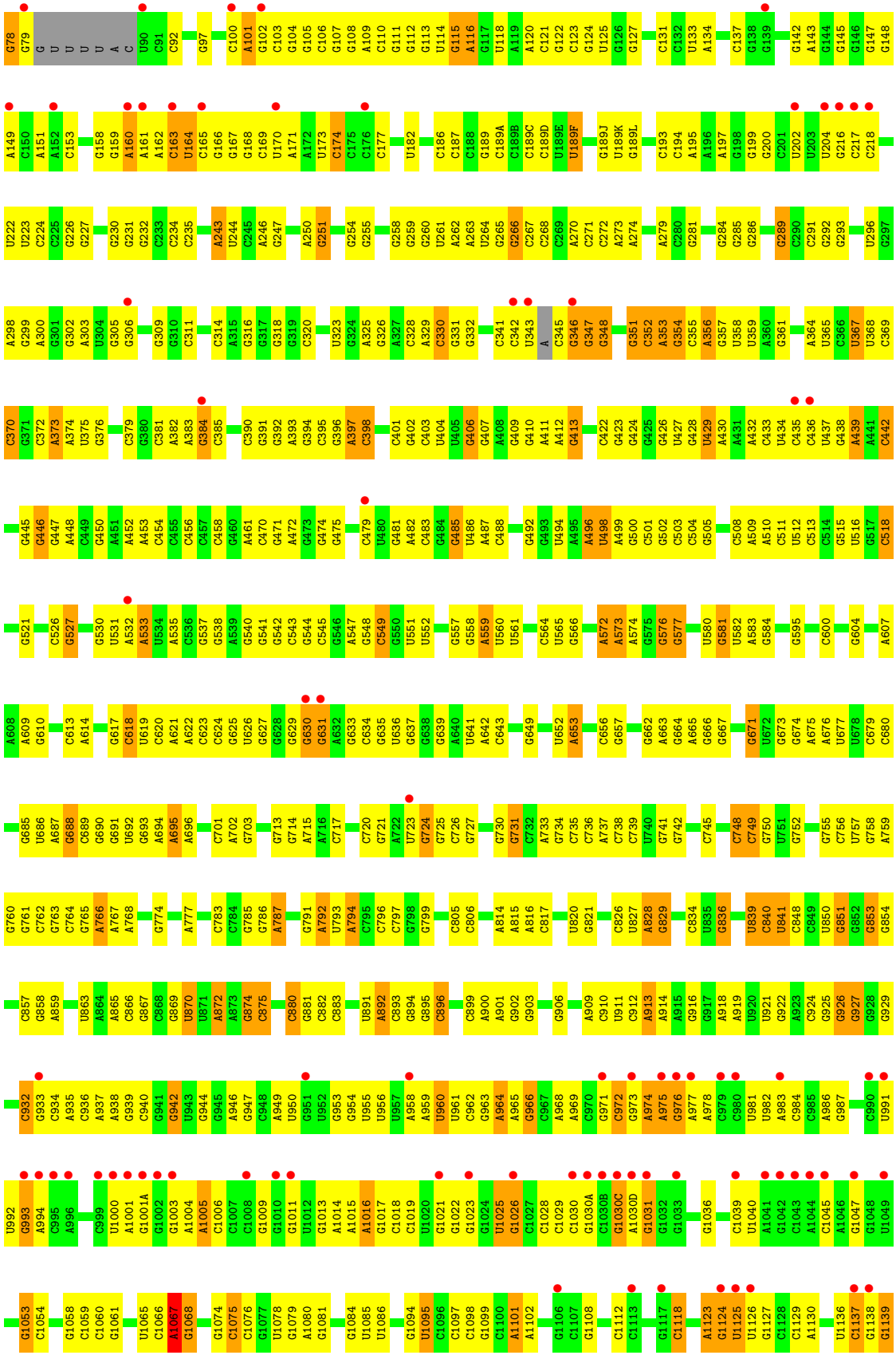
Chain C9:

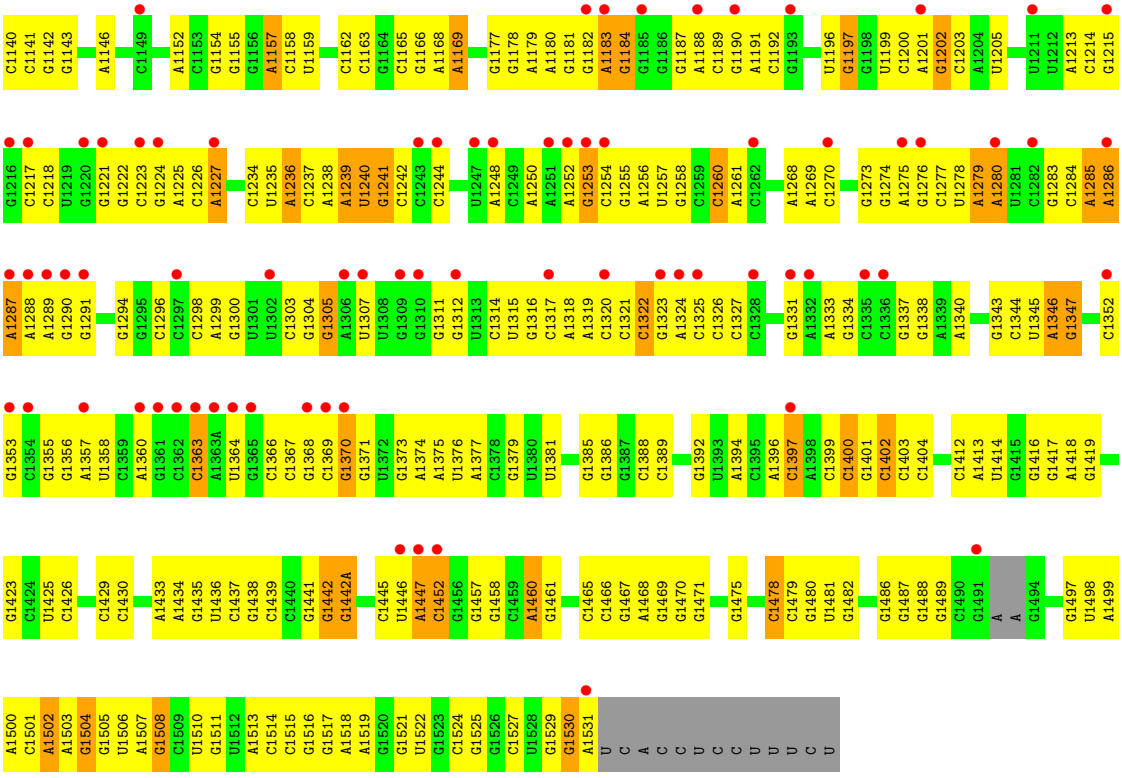


• Molecule 34: 16S Ribosomal RNA

Chain BA:

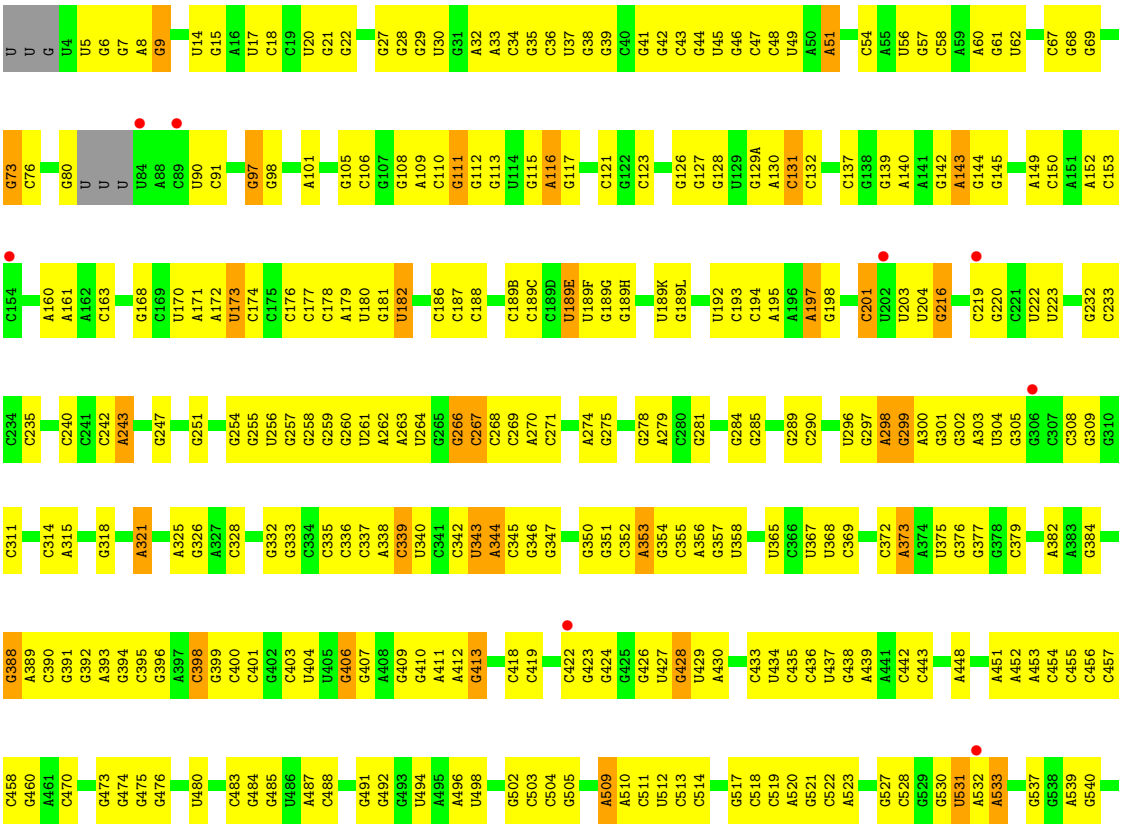


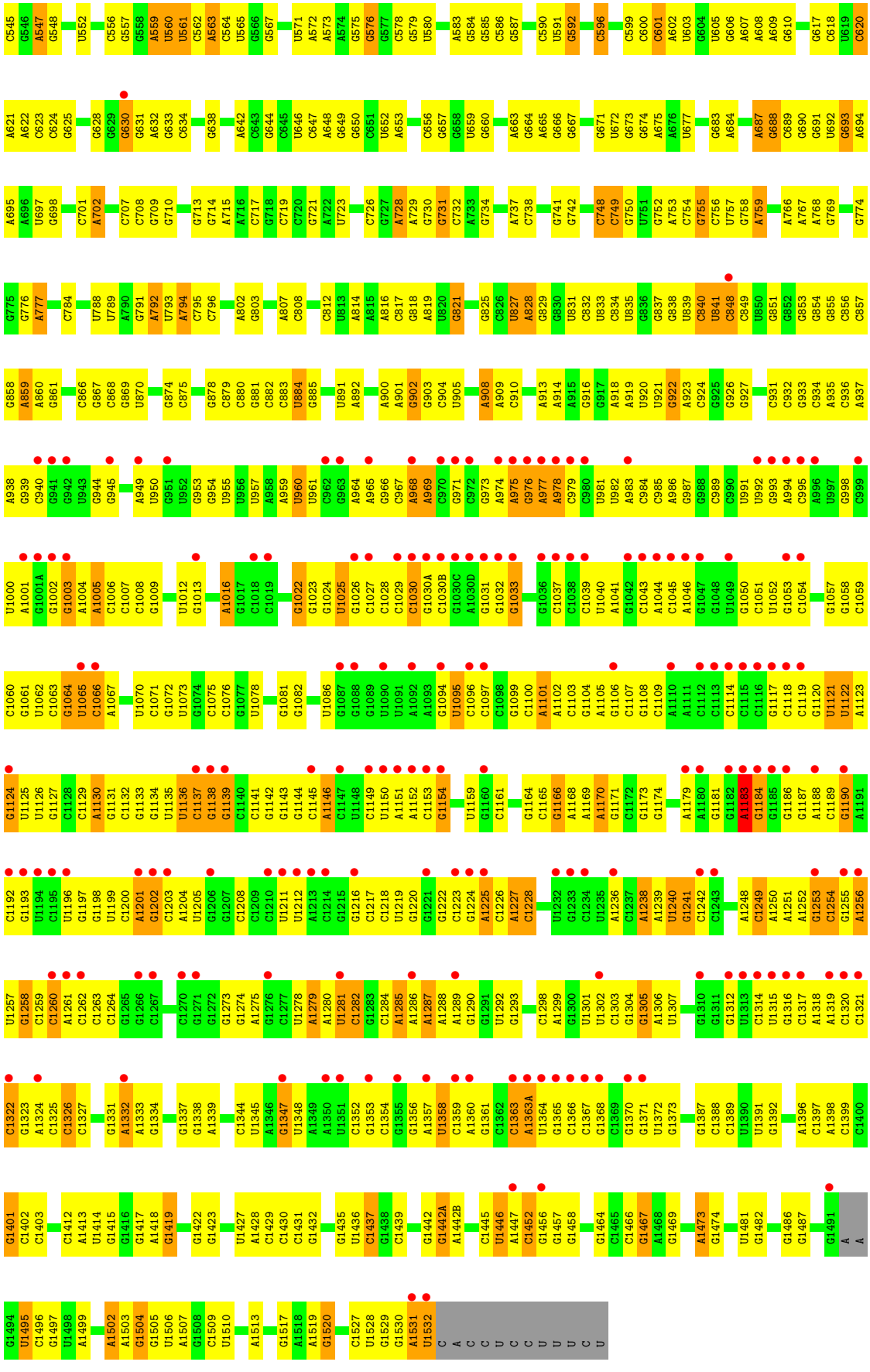




• Molecule 34: 16S Ribosomal RNA

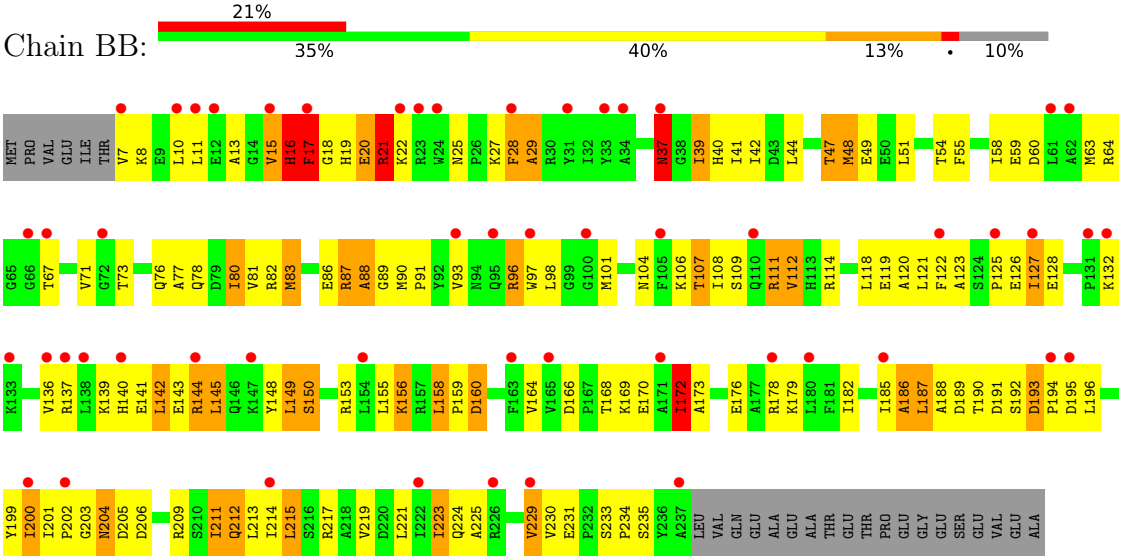
Chain DA:





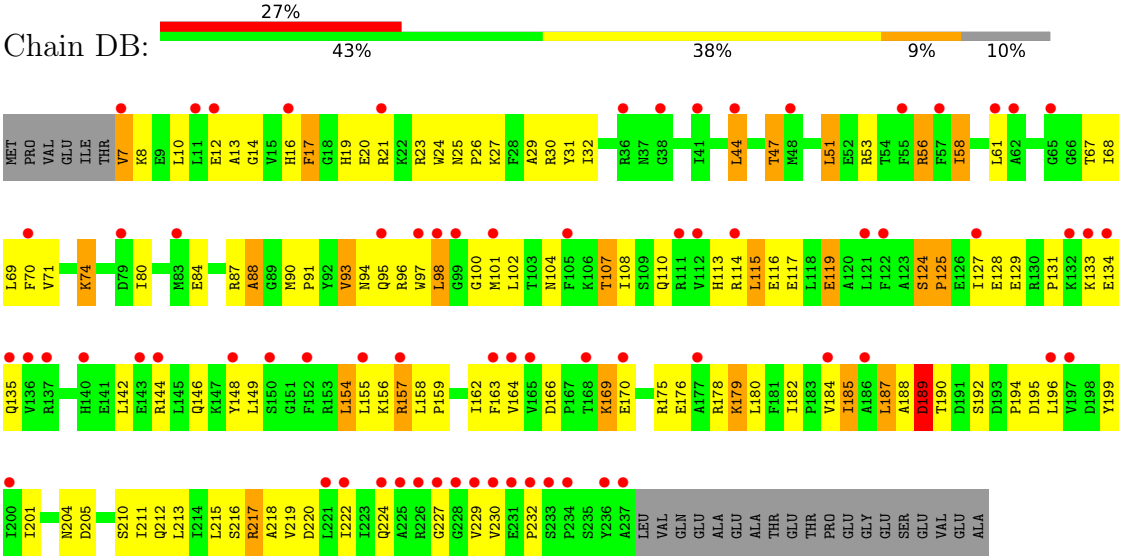
• Molecule 35: 30S ribosomal protein S2

Chain BB:



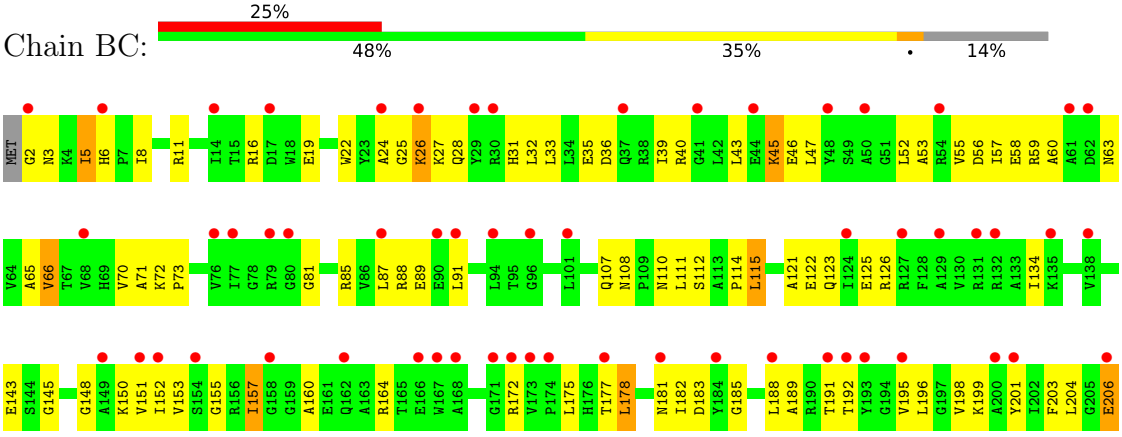
• Molecule 35: 30S ribosomal protein S2

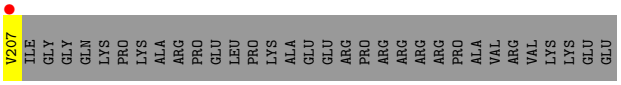
Chain DB:



• Molecule 36: 30S ribosomal protein S3

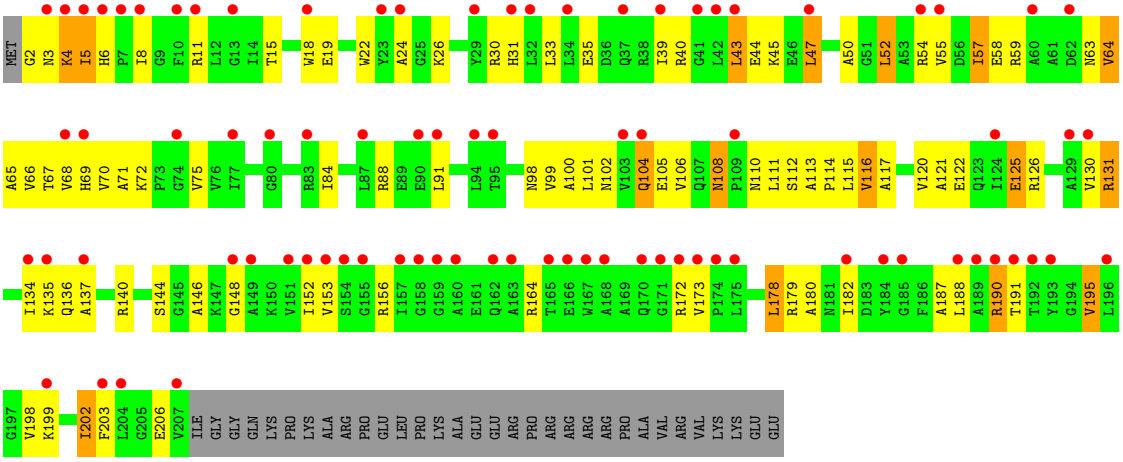
Chain BC:





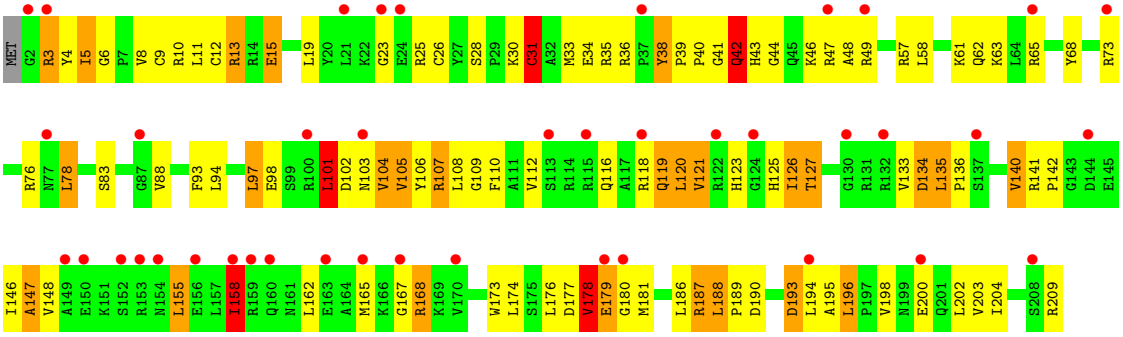
• Molecule 36: 30S ribosomal protein S3

Chain DC:



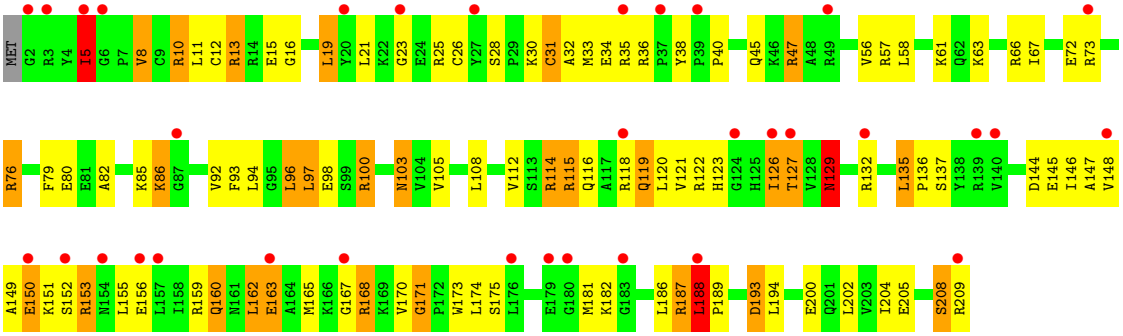
• Molecule 37: 30S ribosomal protein S4

Chain BD:



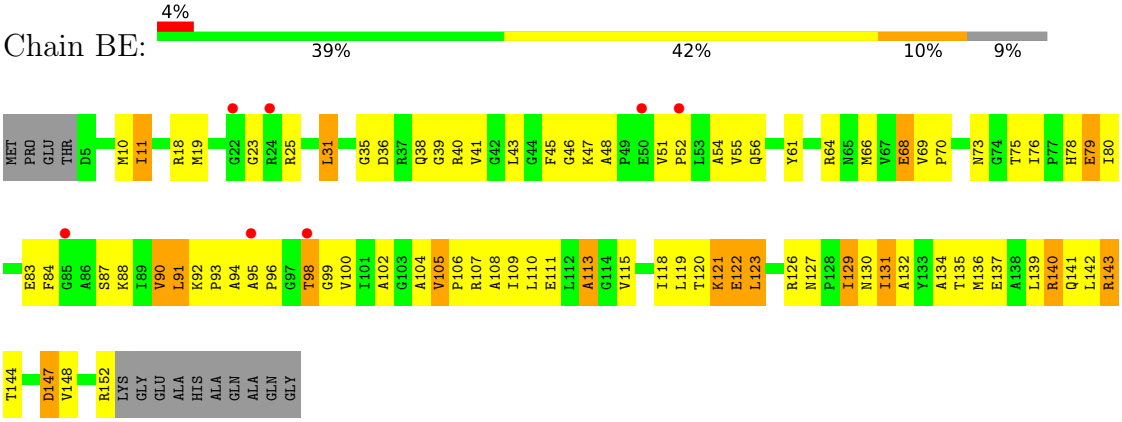
• Molecule 37: 30S ribosomal protein S4

Chain DD:



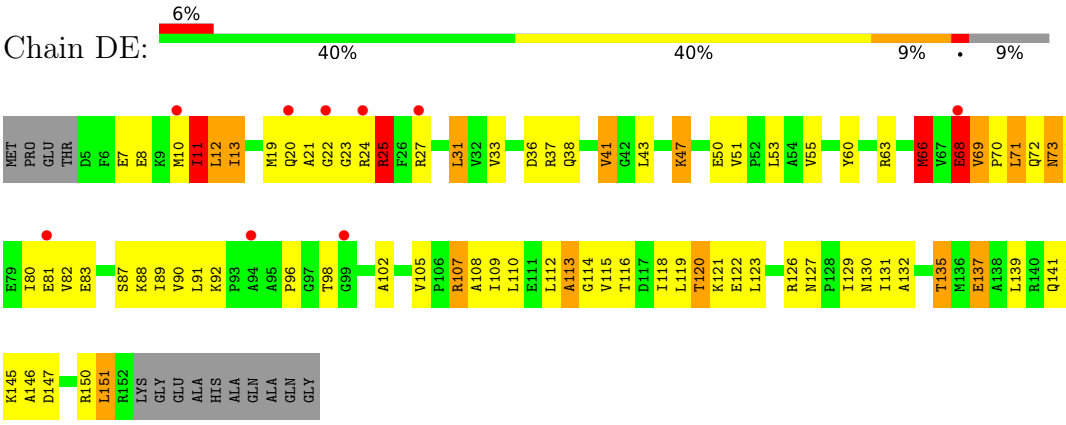
• Molecule 38: 30S ribosomal protein S5

Chain BE:



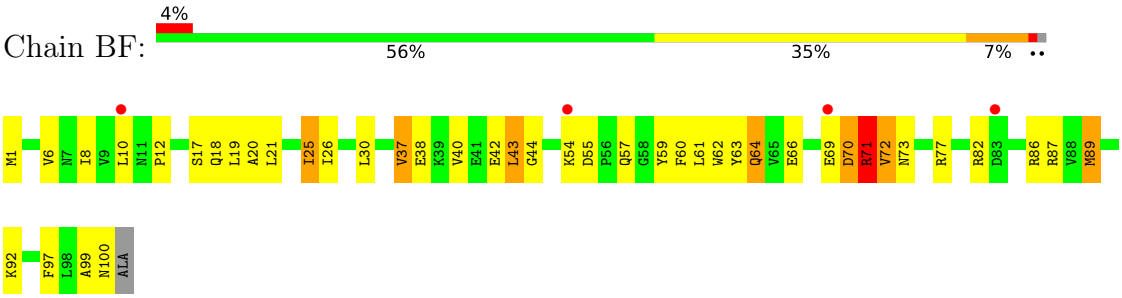
• Molecule 38: 30S ribosomal protein S5

Chain DE:



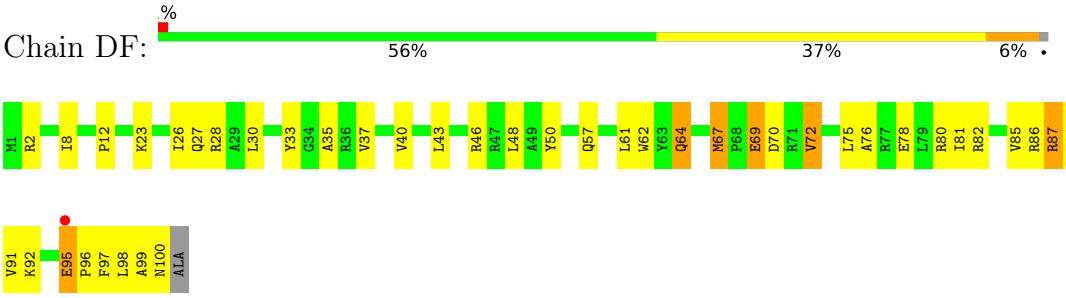
• Molecule 39: 30S ribosomal protein S6

Chain BF:



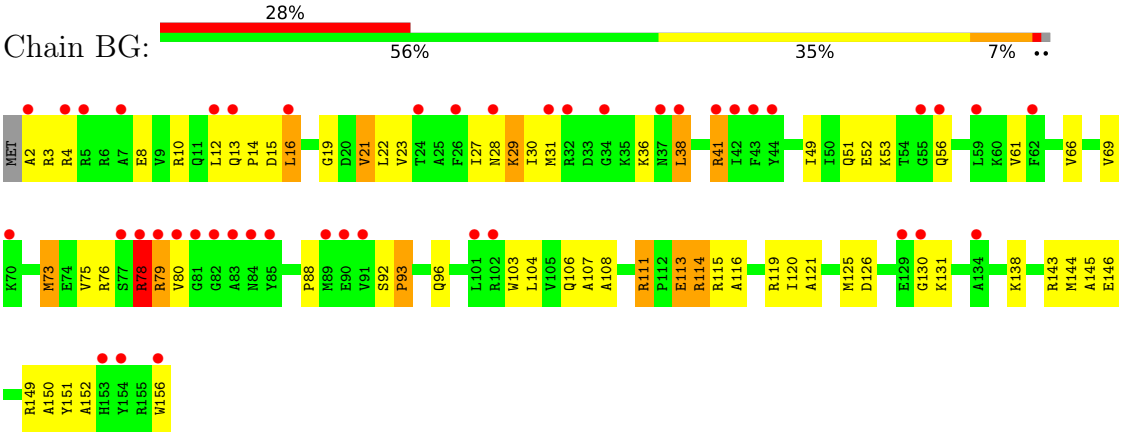
• Molecule 39: 30S ribosomal protein S6

Chain DF:



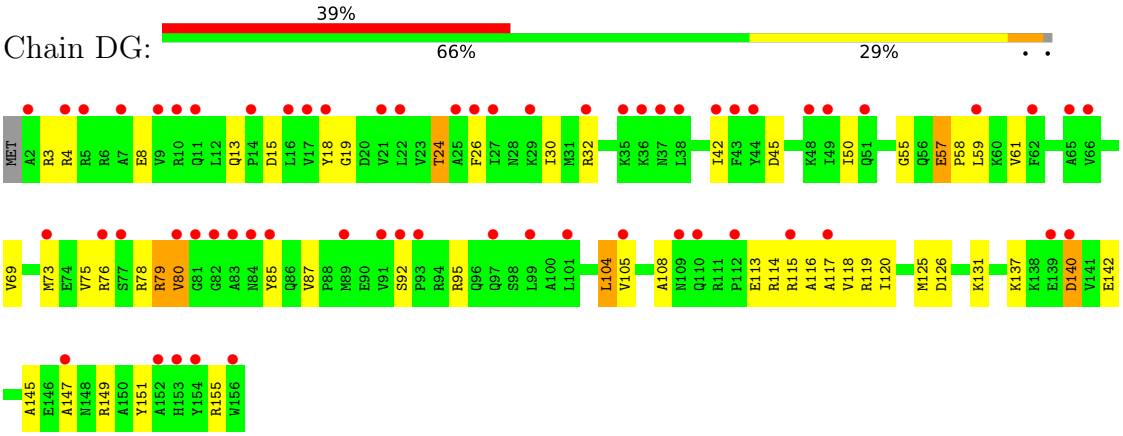
• Molecule 40: 30S ribosomal protein S7

Chain BG:



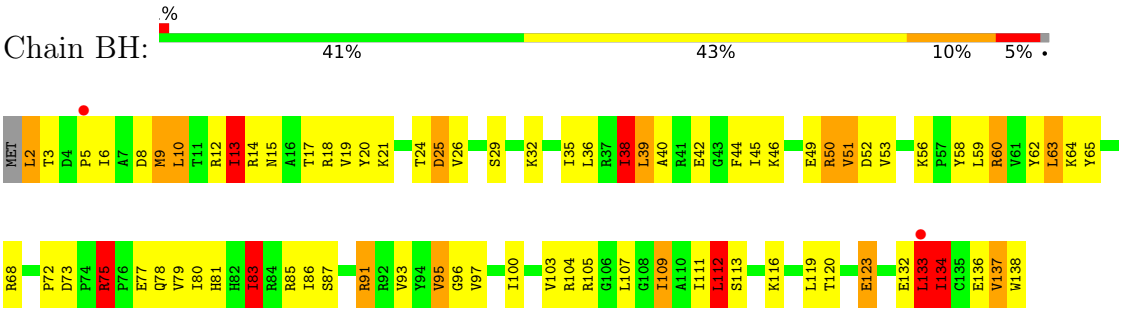
• Molecule 40: 30S ribosomal protein S7

Chain DG:



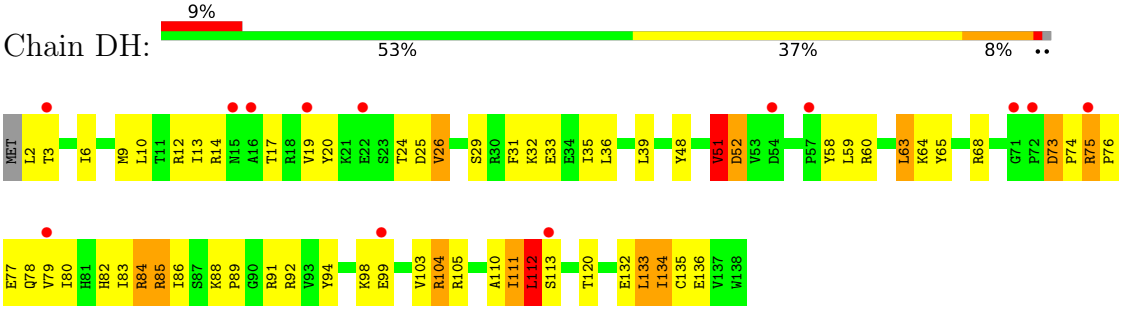
• Molecule 41: 30S ribosomal protein S8

Chain BH:



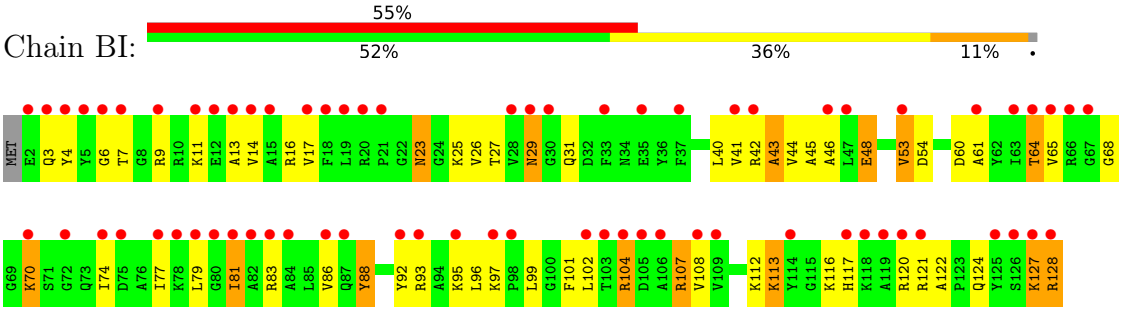
• Molecule 41: 30S ribosomal protein S8

Chain DH:



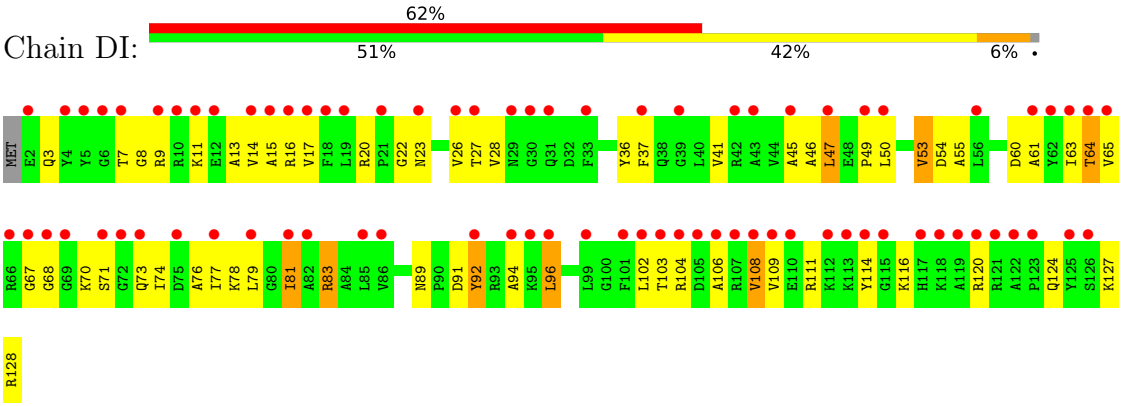
• Molecule 42: 30S ribosomal protein S9

Chain BI:



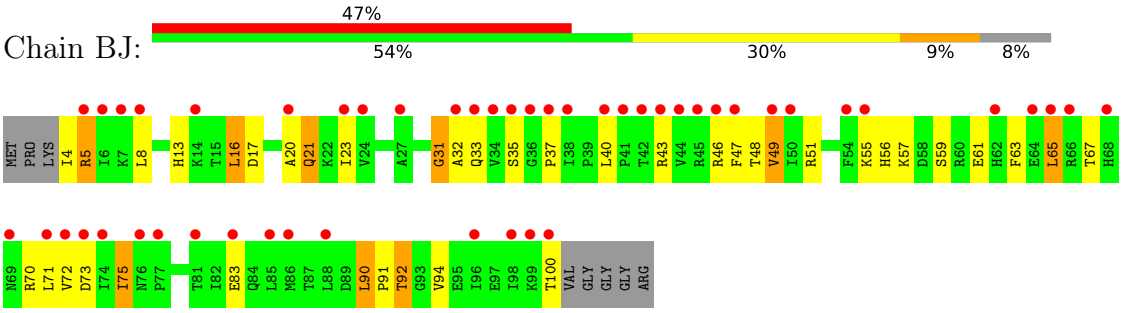
• Molecule 42: 30S ribosomal protein S9

Chain DI:



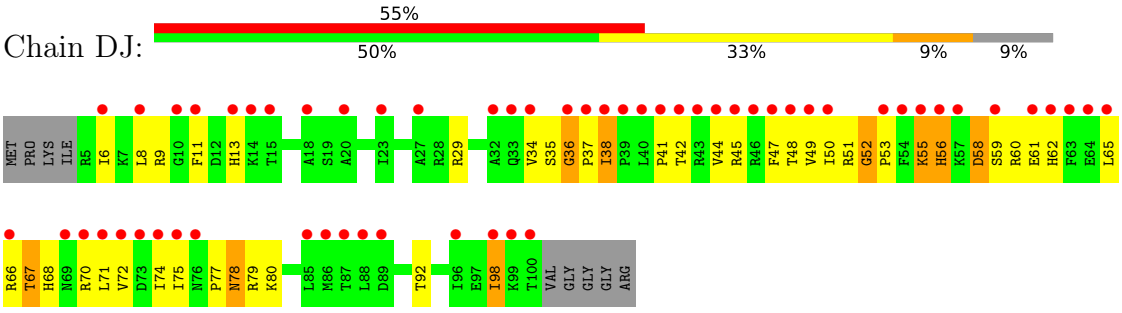
• Molecule 43: 30S ribosomal protein S10

Chain BJ:



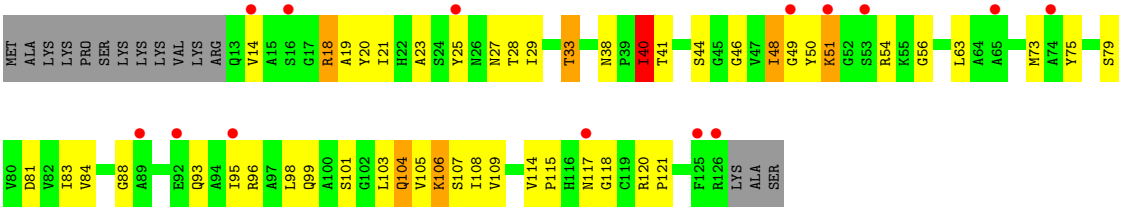
• Molecule 43: 30S ribosomal protein S10

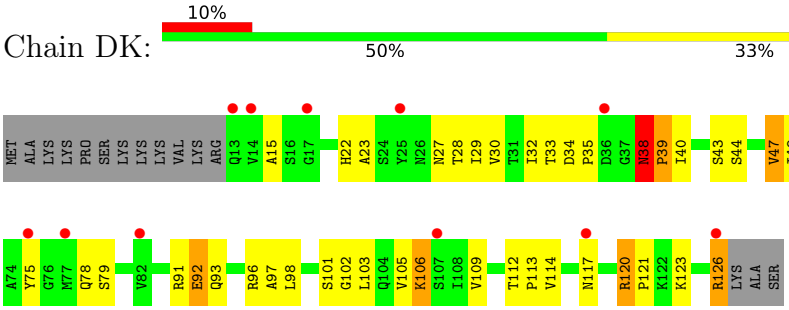
Chain DJ:



• Molecule 44: 30S ribosomal protein S11

Chain BK:



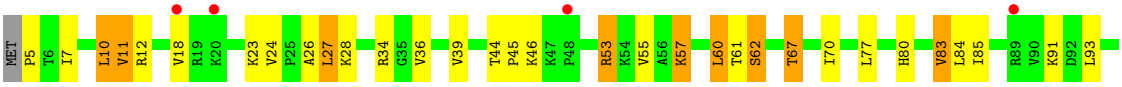


• Molecule 44: 30S ribosomal protein S11

Chain DK:

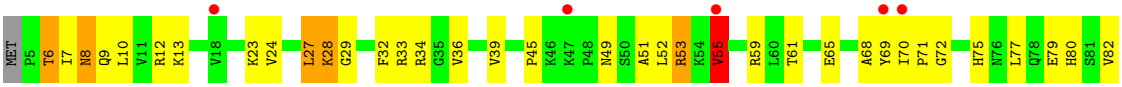
• Molecule 45: 30S ribosomal protein S12

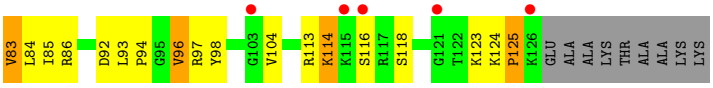
Chain BL:



• Molecule 45: 30S ribosomal protein S12

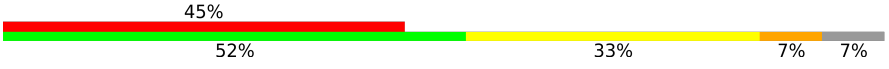
Chain DL:

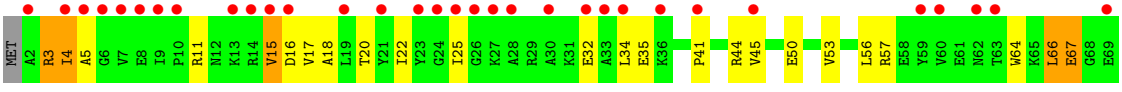


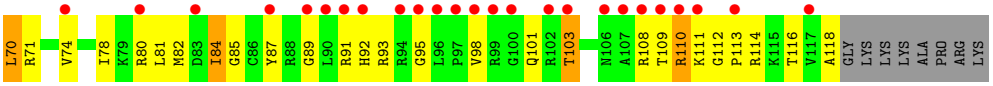


• Molecule 46: 30S ribosomal protein S13

Chain BM:

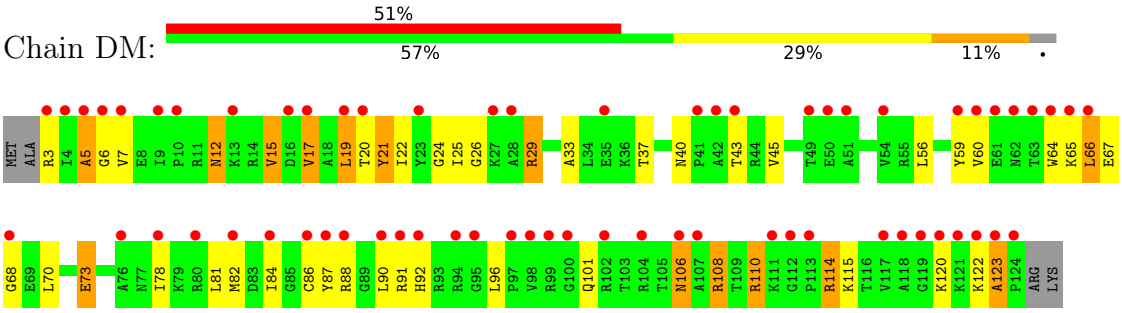






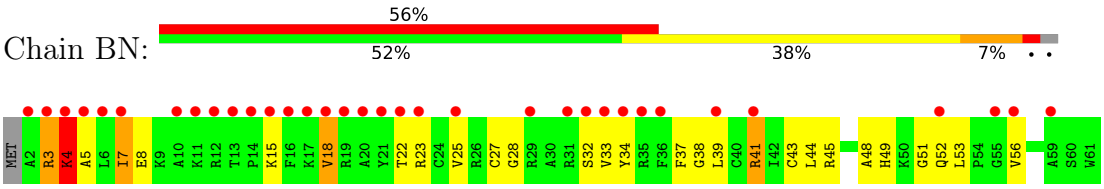
• Molecule 46: 30S ribosomal protein S13

Chain DM:



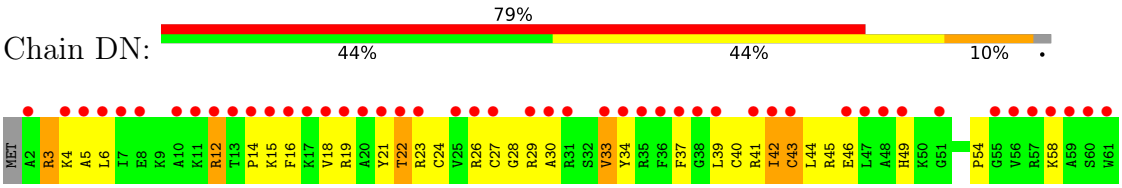
• Molecule 47: 30S ribosomal protein S14 type Z

Chain BN:



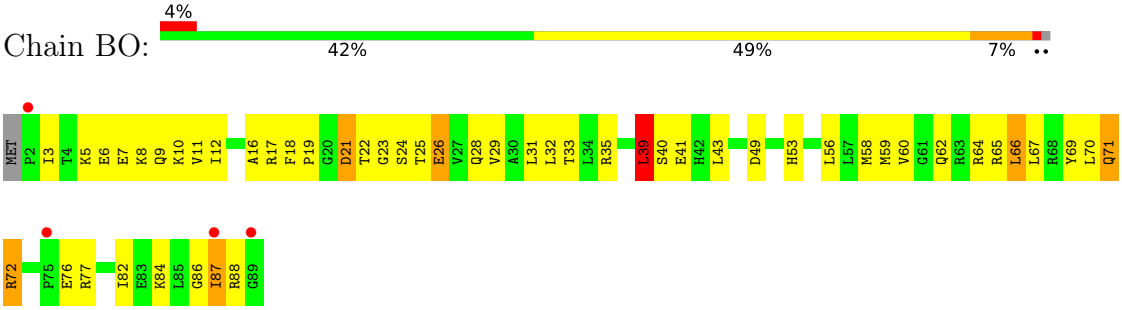
• Molecule 47: 30S ribosomal protein S14 type Z

Chain DN:



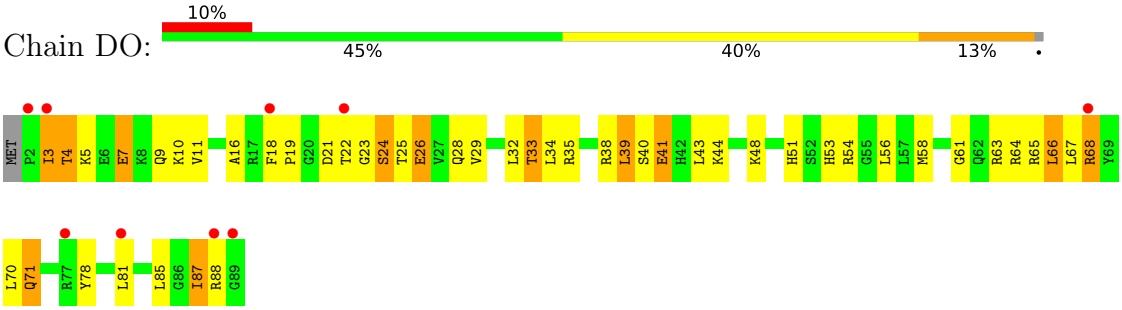
• Molecule 48: 30S ribosomal protein S15

Chain BO:



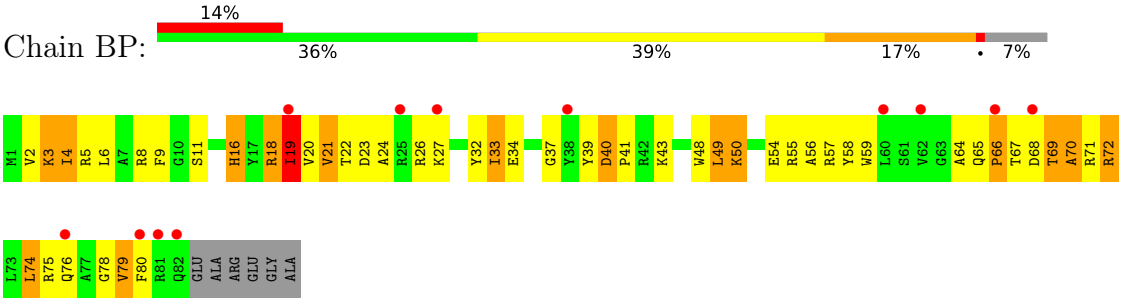
• Molecule 48: 30S ribosomal protein S15

Chain DO:



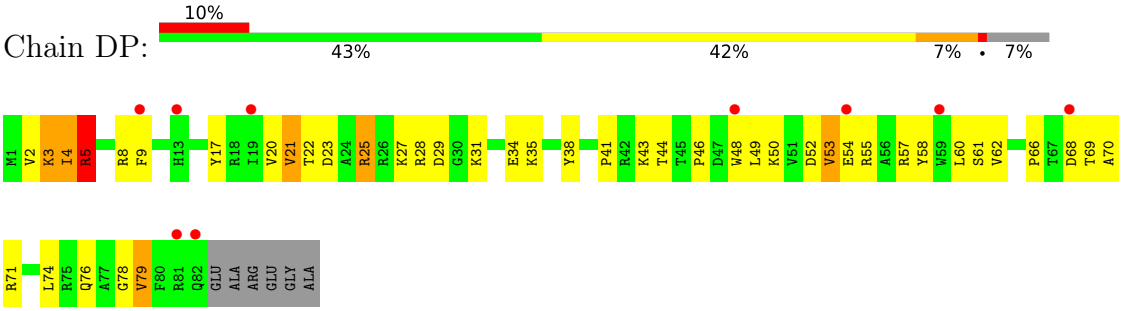
• Molecule 49: 30S ribosomal protein S16

Chain BP:



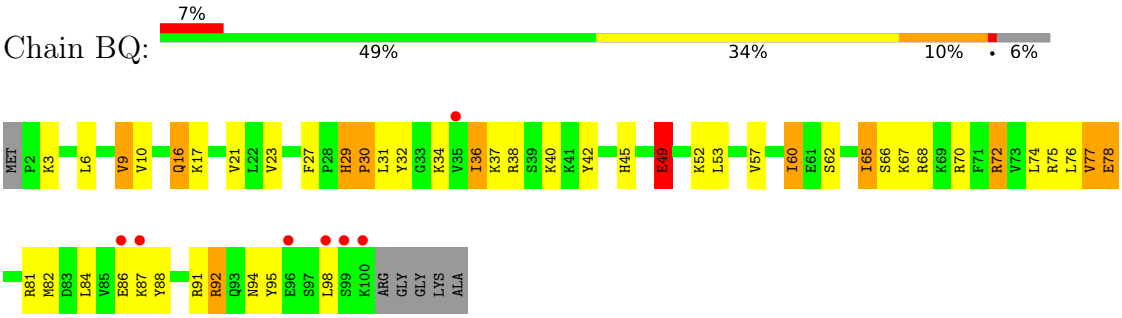
• Molecule 49: 30S ribosomal protein S16

Chain DP:



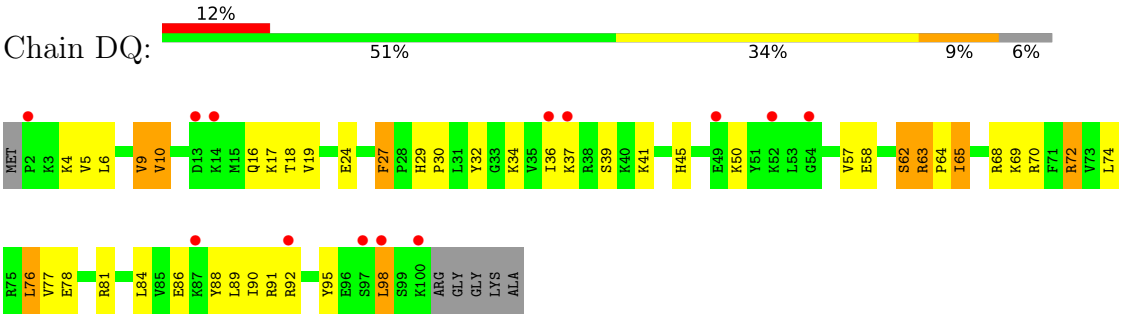
• Molecule 50: 30S ribosomal protein S17

Chain BQ:



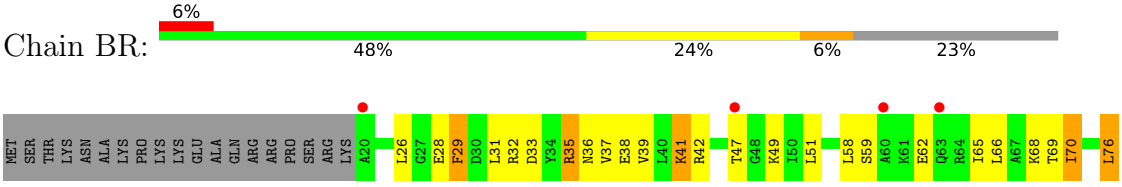
• Molecule 50: 30S ribosomal protein S17

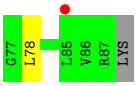
Chain DQ:



• Molecule 51: 30S ribosomal protein S18

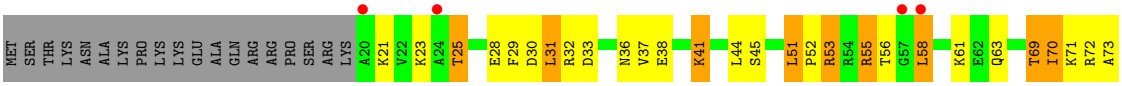
Chain BR:

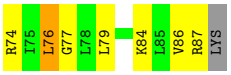




• Molecule 51: 30S ribosomal protein S18

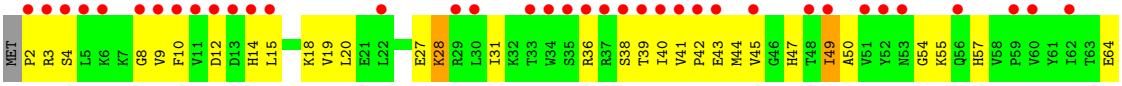
Chain DR:

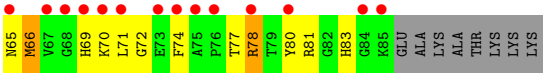




• Molecule 52: 30S ribosomal protein S19

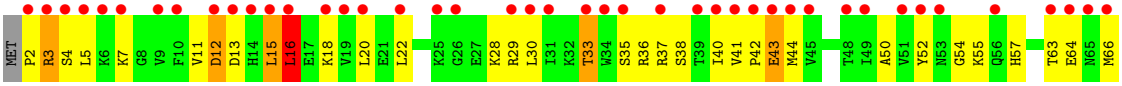
Chain BS:

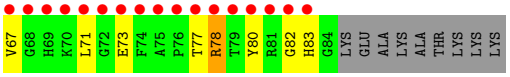




• Molecule 52: 30S ribosomal protein S19

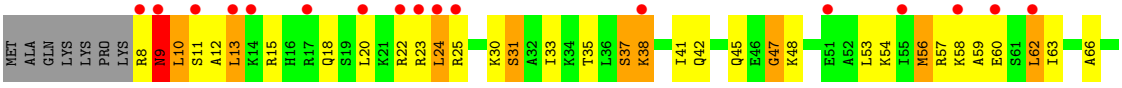
Chain DS:

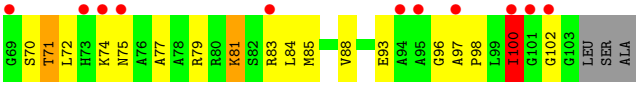




• Molecule 53: 30S ribosomal protein S20

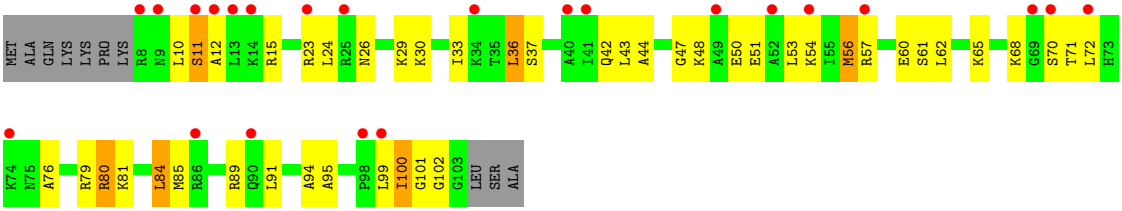
Chain BT:



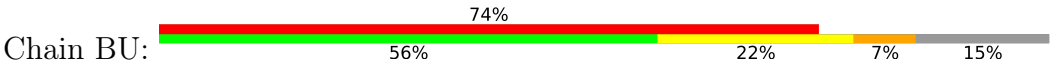


• Molecule 53: 30S ribosomal protein S20

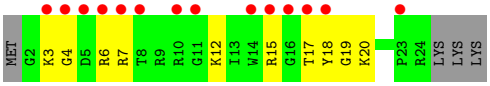
Chain DT:



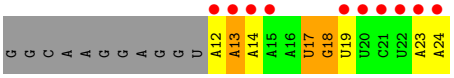
• Molecule 54: 30S ribosomal protein Thx



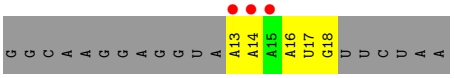
• Molecule 54: 30S ribosomal protein Thx



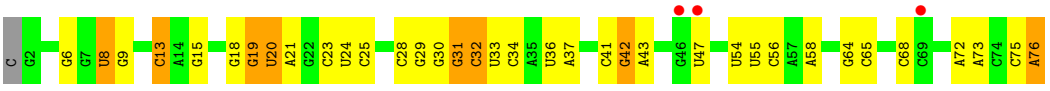
• Molecule 55: mRNA



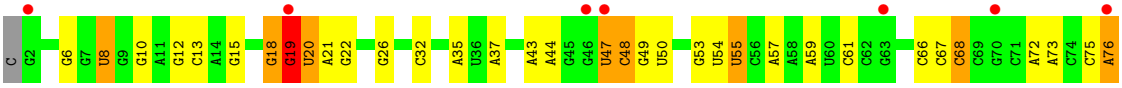
• Molecule 55: mRNA



• Molecule 56: P-site tRNA

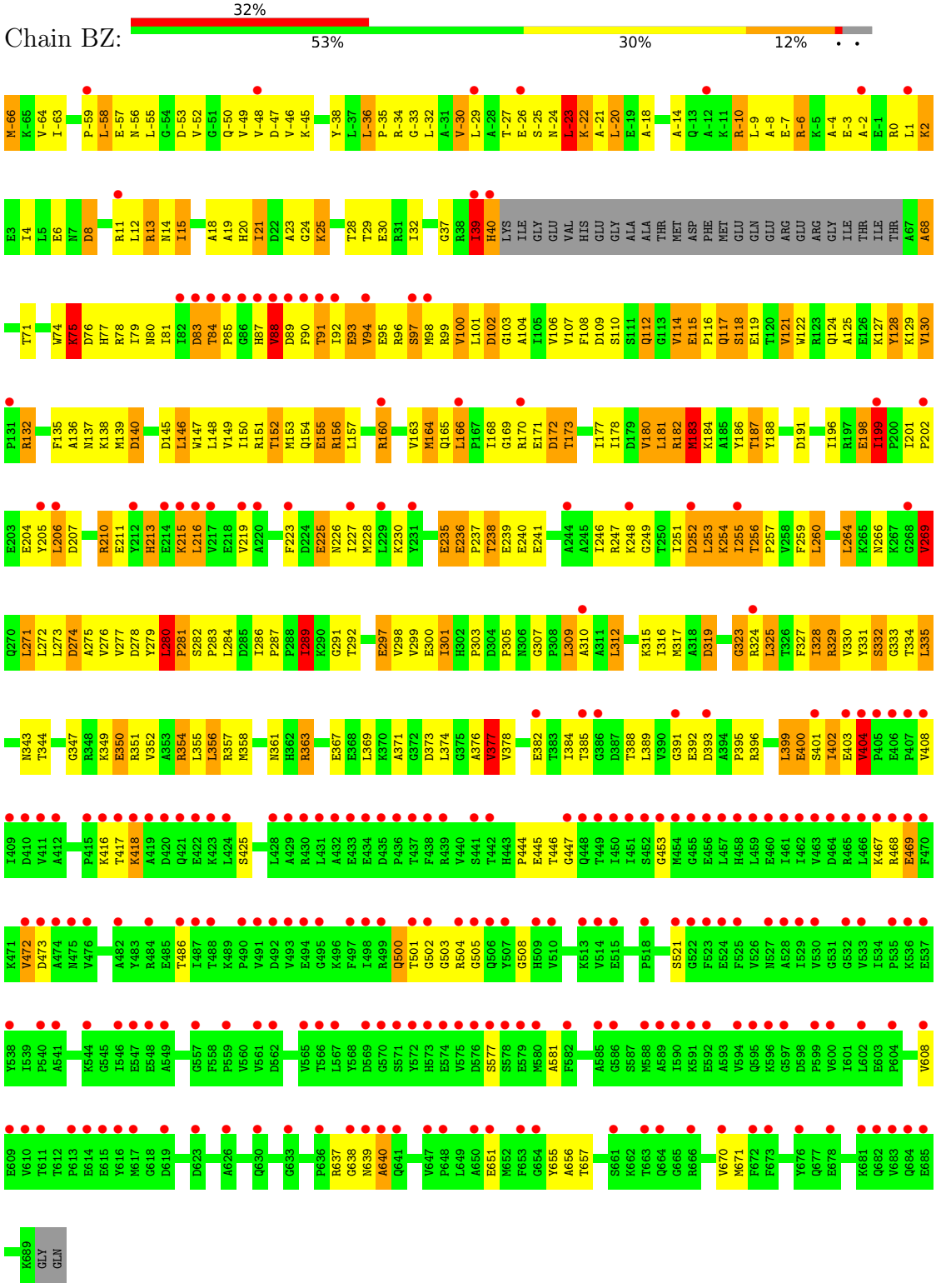


• Molecule 56: P-site tRNA



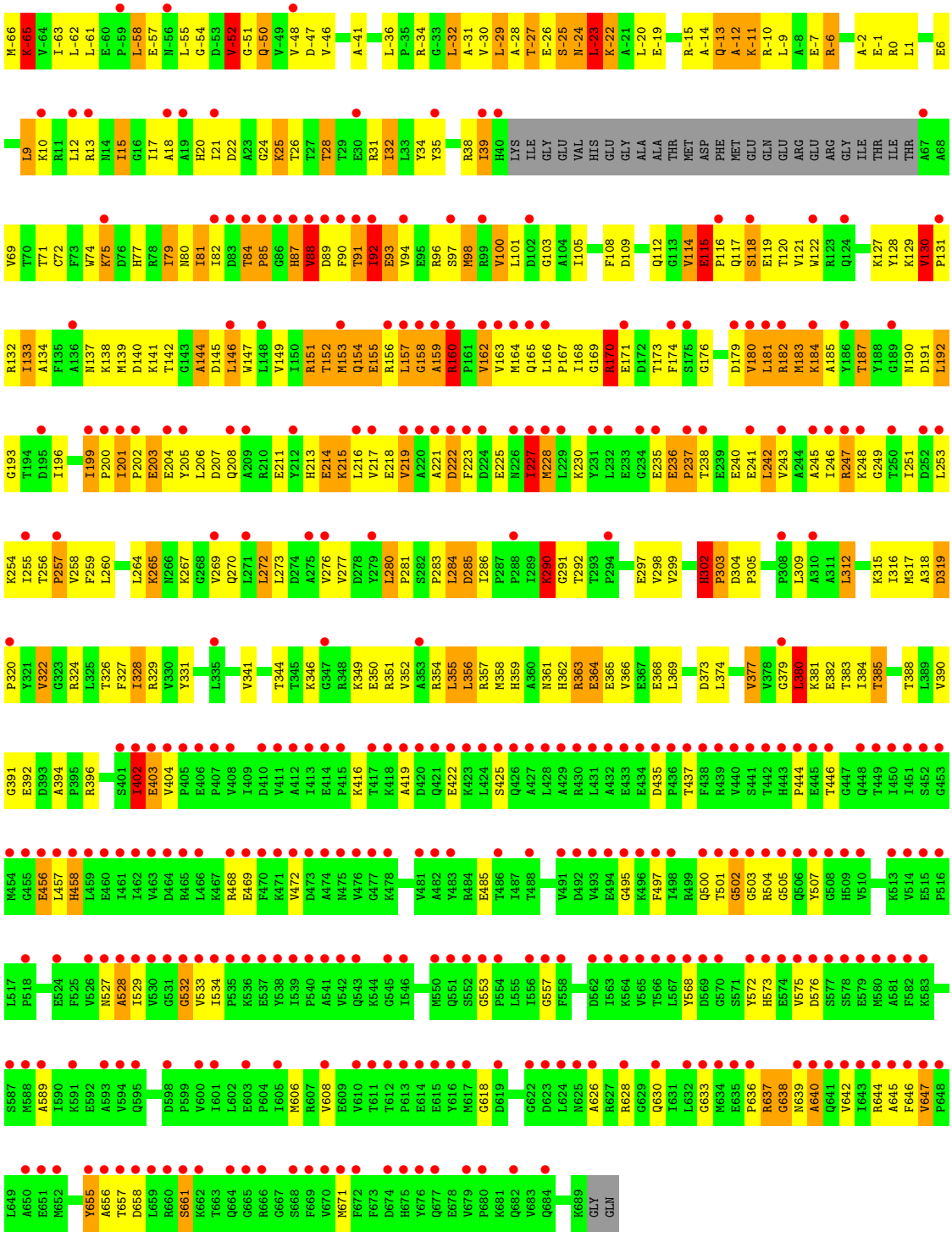
• Molecule 57: 50S ribosomal protein L9,Elongation factor G

Chain BZ:



• Molecule 57: 50S ribosomal protein L9,Elongation factor G

Chain DZ:


M-66 K-65 V-64 I-63 L-62 L-61 E-60 P-59 L-58 E-57 N-56 L-55 G-54 D-53 V-52 G-51 Q-50 V-49 V-48 D-47 V-46 A-41 L-36 P-35 R-34 G-33 L-32 A-31 V-30 L-29 A-28 T-27 E-26 S-25 N-24 L-23 K-22 A-21 L-20 E-19 R-15 A-14 Q-13 A-12 K-11 R-10 L-9 A-8 E-7 R-6 A-2 E-1 R0 L1 E6
L9 K10 R11 L12 R13 N14 I15 G16 I17 A18 A19 H20 I21 D22 A23 G24 K25 T26 T27 T28 T29 E30 R31 I32 L33 Y34 Y35 R38 I39 H40 LYS ILE GLY GLU VAL HIS GLU GLY ALA ALA THR MET ASP PHE MET GLU GLN GLU ARG GLU ARG GLY ILE THR ILE THR A67 A68
V69 T70 T71 C72 F73 W74 K75 D76 H77 R78 I79 N80 I81 I82 D83 T84 P85 G86 H87 V88 D89 P90 T91 I92 E93 V94 E95 R96 S97 M98 R99 V100 L101 D102 G103 A104 I105 F108 D109 Q112 G113 V114 E115 P116 Q117 S118 E119 T120 V121 W122 R123 Q124 K127 Y128 K129 V130 P131
R132 I133 A134 F135 A136 N137 K138 M139 D140 K141 T142 G143 A144 D145 L146 W147 L148 V149 I150 R151 T152 M153 Q154 E155 R156 L157 G158 A159 R160 P161 V162 V163 M164 Q165 L166 P167 I168 G169 R170 E171 D172 T173 F174 S175 G176 D179 V180 L181 R182 M183 K184 A185 Y186 T187 Y188 G189 N190 D191 L192
G193 T194 D195 I196 I199 P200 I201 P202 E203 E204 Y205 L206 D207 Q208 A209 R210 E211 Y212 H213 E214 K215 L216 V217 E218 V219 A220 A221 D222 F223 D224 E225 N226 I227 M228 L229 K230 Y231 L232 E233 G234 E235 E236 P237 T238 E239 E240 E241 L242 V243 A244 A245 I246 R247 K248 G249 T250 I251 D252 L253
K254 I255 T256 P257 V258 F259 L260 L264 K265 N266 K267 G268 V269 Q270 L271 L272 L273 D274 A275 V276 V277 D278 Y279 L280 P281 S282 P283 L284 D285 I286 P287 P288 I289 K290 G291 T292 T293 P294 E297 V298 V299 H302 P303 D304 P305 P308 L309 A310 A311 L312 K315 I316 M317 A318 D319
P320 Y321 V322 G323 R324 L325 T326 F327 I328 R329 V330 Y331 L335 V341 T344 T345 K346 G347 R348 K349 E350 R351 V352 A353 R354 L355 L356 R357 M358 H359 A360 N361 H362 R363 E364 E365 V366 E367 E368 L369 D373 L374 V377 V378 G379 I380 K381 E382 T383 I384 T385 T388 L389 V390
G391 E392 D393 A394 P395 R396 S401 I402 E403 V404 P405 E406 P407 V408 I409 D410 V411 A412 I413 E414 P415 K416 T417 K418 A419 D420 Q421 E422 K423 L424 S425 Q426 A427 L428 A429 R430 L431 A432 E433 E434 D435 P436 T437 F438 R439 V440 S441 T442 H443 P444 E445 T446 G447 Q448 T449 I450 I451 S452 G453
M454 G455 E456 L457 H458 L459 E460 I461 I462 V463 D464 R465 L466 K467 R468 E469 F470 K471 V472 D473 A474 N475 V476 G477 K478 V481 A482 Y483 R484 E485 T486 I487 T488 V491 D492 V493 E494 G495 K496 F497 I498 R499 Q500 T501 G502 G503 R504 G505 Q506 Y507 G508 H509 V510 K513 V514 E515 P516
L517 P518 E524 F525 V526 N527 A528 I529 V530 G531 G532 V533 I534 P535 K536 E537 Y538 I539 P540 A541 V542 Q543 K544 G545 I546 M550 Q551 S552 G553 P554 L555 I556 G557 F558 D562 I563 K564 V565 T566 L567 Y568 D569 G570 S571 Y572 H573 E574 V575 D576 S577 S578 E579 M580 A581 F582 K583
S587 M588 A589 I590 K591 E592 A593 V594 Q595 D598 P599 V600 I601 L602 E603 P604 I605 M606 R607 V608 E609 V610 T611 T612 P613 E614 E615 Y616 M617 G618 D619 G622 D623 L624 N625 A626 R627 R628 G629 Q630 I631 L632 G633 M634 E635 P636 R637 G638 N639 A640 Q641 V642 I643 R644 A645 F646 V647 P648
L649 A650 E651 M652 Y655 A656 T657 D658 L659 R660 S661 K662 T663 Q664 G665 R666 G667 S668 P669 V670 M671 F672 F673 D674 H675 Y676 Q677 E678 V679 P680 K681 Q682 V683 Q684 K689 GLY GLN

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	209.48Å 448.89Å 622.84Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.31 – 2.80 49.31 – 2.80	Depositor EDS
% Data completeness (in resolution range)	96.8 (49.31-2.80) 96.7 (49.31-2.80)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.37 (at 2.81Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE: 1.8.2_1309)	Depositor
R, R_{free}	0.221 , 0.266 0.222 , 0.266	Depositor DCC
R_{free} test set	69082 reflections (4.86%)	wwPDB-VP
Wilson B-factor (Å^2)	47.2	Xtriage
Anisotropy	0.111	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.30 , 77.8	EDS
L-test for twinning[2]	$< \|L\| > = 0.38$, $< L^2 > = 0.20$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.89	EDS
Total number of atoms	305548	wwPDB-VP
Average B, all atoms (Å^2)	78.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.88% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SF4, K, PSU, MG, GDP, ZN, 4SU, 5MU, 5MC

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	AA	0.76	0/68792	0.95	47/107377 (0.0%)
1	CA	0.54	0/68691	0.74	7/107219 (0.0%)
2	AB	0.63	0/2878	0.90	2/4490 (0.0%)
2	CB	0.38	0/2878	0.58	0/4490
3	AC	0.42	0/1083	0.97	6/1460 (0.4%)
3	CC	0.42	0/1083	0.97	5/1460 (0.3%)
4	AD	1.17	5/2186 (0.2%)	1.49	26/2944 (0.9%)
4	CD	0.94	1/2192 (0.0%)	1.37	22/2951 (0.7%)
5	AE	1.30	9/1592 (0.6%)	1.62	31/2149 (1.4%)
5	CE	0.87	0/1592	1.26	12/2149 (0.6%)
6	AF	1.16	2/1619 (0.1%)	1.43	23/2193 (1.0%)
6	CF	0.80	0/1615	1.27	11/2188 (0.5%)
7	AG	0.74	0/1450	1.20	8/1959 (0.4%)
7	CG	0.54	0/1449	1.09	10/1958 (0.5%)
8	AH	1.05	2/1356 (0.1%)	1.40	14/1834 (0.8%)
8	CH	0.55	0/1356	1.04	10/1834 (0.5%)
9	AK	0.69	0/640	1.68	11/889 (1.2%)
9	CK	0.50	0/640	1.71	13/889 (1.5%)
10	AL	0.57	0/1044	1.10	9/1416 (0.6%)
10	CL	0.64	0/1044	1.10	15/1416 (1.1%)
11	AN	1.30	3/1144 (0.3%)	1.49	13/1543 (0.8%)
11	CN	0.72	0/1144	1.16	6/1543 (0.4%)
12	AO	1.13	1/943 (0.1%)	1.47	12/1269 (0.9%)
12	CO	0.91	0/943	1.18	1/1269 (0.1%)
13	AP	1.05	0/1156	1.39	11/1537 (0.7%)
13	CP	0.75	0/1152	1.19	8/1533 (0.5%)
14	AQ	1.21	0/1143	1.42	12/1527 (0.8%)
14	CQ	0.80	0/1143	1.17	9/1527 (0.6%)
15	AR	1.29	4/982 (0.4%)	1.41	5/1312 (0.4%)
15	CR	0.83	1/982 (0.1%)	1.16	3/1312 (0.2%)
16	AS	0.92	0/887	1.26	9/1180 (0.8%)
16	CS	0.64	0/880	1.11	2/1172 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
17	AT	1.11	2/1105 (0.2%)	1.36	7/1477 (0.5%)
17	CT	0.81	0/1097	1.18	9/1468 (0.6%)
18	AU	1.42	4/977 (0.4%)	1.52	11/1301 (0.8%)
18	CU	0.81	0/977	1.12	3/1301 (0.2%)
19	AV	1.32	3/782 (0.4%)	1.57	14/1049 (1.3%)
19	CV	0.71	0/782	1.11	4/1049 (0.4%)
20	AW	1.43	6/897 (0.7%)	1.54	9/1205 (0.7%)
20	CW	1.02	2/897 (0.2%)	1.35	10/1205 (0.8%)
21	AX	1.22	3/764 (0.4%)	1.44	6/1025 (0.6%)
21	CX	0.86	0/764	1.34	10/1025 (1.0%)
22	AY	1.09	1/819 (0.1%)	1.47	11/1095 (1.0%)
22	CY	0.74	0/819	1.19	13/1095 (1.2%)
23	AZ	0.91	1/1483 (0.1%)	1.36	17/2017 (0.8%)
23	CZ	0.60	0/1483	1.18	12/2017 (0.6%)
24	A0	1.14	2/662 (0.3%)	1.31	3/881 (0.3%)
24	C0	0.79	0/662	1.22	5/881 (0.6%)
25	A1	1.15	1/762 (0.1%)	1.39	6/1014 (0.6%)
25	C1	0.88	1/762 (0.1%)	1.27	6/1014 (0.6%)
26	A2	1.05	0/590	1.22	2/781 (0.3%)
26	C2	0.71	0/590	1.12	3/781 (0.4%)
27	A3	1.23	0/474	1.55	7/635 (1.1%)
27	C3	0.77	0/469	1.11	1/630 (0.2%)
28	A4	0.62	1/571 (0.2%)	1.27	9/768 (1.2%)
28	C4	0.50	0/545	1.07	6/737 (0.8%)
29	A5	1.44	5/469 (1.1%)	1.64	9/635 (1.4%)
29	C5	0.87	0/469	1.32	5/635 (0.8%)
30	A6	1.09	1/460 (0.2%)	1.25	4/613 (0.7%)
30	C6	0.84	0/456	1.22	3/608 (0.5%)
31	A7	1.31	2/426 (0.5%)	1.44	1/561 (0.2%)
31	C7	0.96	0/426	1.27	3/561 (0.5%)
32	A8	1.25	0/525	1.43	2/691 (0.3%)
32	C8	0.88	0/525	1.24	3/691 (0.4%)
33	A9	1.22	1/310 (0.3%)	1.61	5/407 (1.2%)
33	C9	0.79	0/310	1.14	1/407 (0.2%)
34	BA	0.43	0/35976	0.64	4/56145 (0.0%)
34	DA	0.38	0/36119	0.59	1/56370 (0.0%)
35	BB	0.57	0/1881	1.10	16/2542 (0.6%)
35	DB	0.52	0/1860	1.02	8/2518 (0.3%)
36	BC	0.52	0/1576	0.93	0/2130
36	DC	0.51	0/1568	0.95	4/2122 (0.2%)
37	BD	0.63	0/1689	1.09	10/2267 (0.4%)
37	DD	0.61	0/1708	1.10	6/2289 (0.3%)
38	BE	0.77	0/1145	1.21	11/1543 (0.7%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
38	DE	0.73	0/1149	1.22	10/1548 (0.6%)
39	BF	0.66	0/825	1.02	1/1118 (0.1%)
39	DF	0.69	0/833	1.06	3/1128 (0.3%)
40	BG	0.54	0/1250	1.00	5/1679 (0.3%)
40	DG	0.45	0/1254	0.93	3/1683 (0.2%)
41	BH	0.77	0/1108	1.18	6/1494 (0.4%)
41	DH	0.63	0/1108	1.10	7/1494 (0.5%)
42	BI	0.51	0/1005	1.04	5/1350 (0.4%)
42	DI	0.50	0/997	0.93	1/1343 (0.1%)
43	BJ	0.49	0/722	1.09	4/982 (0.4%)
43	DJ	0.54	0/727	1.00	3/988 (0.3%)
44	BK	0.66	0/848	1.14	2/1149 (0.2%)
44	DK	0.66	0/848	1.08	4/1149 (0.3%)
45	BL	0.82	0/946	1.21	6/1274 (0.5%)
45	DL	0.71	0/946	1.12	4/1274 (0.3%)
46	BM	0.49	0/933	0.97	4/1253 (0.3%)
46	DM	0.48	0/961	0.93	2/1291 (0.2%)
47	BN	0.55	0/501	0.96	0/664
47	DN	0.47	0/501	0.79	0/664
48	BO	0.78	1/739 (0.1%)	1.15	5/985 (0.5%)
48	DO	0.71	0/739	1.12	4/985 (0.4%)
49	BP	0.71	0/697	1.17	5/939 (0.5%)
49	DP	0.65	0/693	1.13	4/935 (0.4%)
50	BQ	0.74	0/836	1.09	4/1117 (0.4%)
50	DQ	0.70	0/836	1.09	8/1117 (0.7%)
51	BR	0.67	0/560	1.10	2/746 (0.3%)
51	DR	0.69	0/560	0.99	2/746 (0.3%)
52	BS	0.44	0/676	0.90	0/911
52	DS	0.48	0/661	0.92	2/893 (0.2%)
53	BT	0.71	0/730	1.15	1/965 (0.1%)
53	DT	0.64	0/733	1.10	3/969 (0.3%)
54	BU	0.45	0/203	1.02	1/266 (0.4%)
54	DU	0.43	0/203	0.87	0/266
55	BV	0.67	0/310	0.66	0/480
55	DV	0.47	0/144	0.67	0/223
56	BX	0.54	3/1725 (0.2%)	0.72	3/2689 (0.1%)
56	DX	0.46	2/1719 (0.1%)	0.60	0/2677
57	BZ	0.84	1/4927 (0.0%)	1.31	36/6727 (0.5%)
57	DZ	0.74	1/4925 (0.0%)	1.21	37/6724 (0.6%)
All	All	0.68	72/325388 (0.0%)	0.93	840/485060 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected

by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
4	AD	0	3
5	AE	0	1
8	AH	0	1
12	AO	0	2
21	CX	0	1
23	AZ	0	1
37	BD	0	1
53	BT	0	1
57	BZ	0	1
57	DZ	0	4
All	All	0	16

All (72) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
25	A1	67	ILE	CA-CB	-11.79	1.48	1.54
6	AF	84	VAL	CA-CB	-9.77	1.42	1.54
19	AV	61	VAL	CA-CB	9.57	1.64	1.53
56	BX	18	G	O3'-P	7.99	1.73	1.61
56	BX	15	G	O3'-P	-7.88	1.49	1.61
5	AE	21	VAL	CA-C	-7.73	1.47	1.52
56	DX	19	G	O3'-P	-7.58	1.49	1.61
22	AY	39	VAL	CA-CB	-6.99	1.46	1.54
15	AR	38	VAL	CA-CB	-6.76	1.50	1.54
5	AE	132	HIS	CE1-NE2	-6.73	1.25	1.32
11	AN	63	THR	CA-CB	6.72	1.64	1.53
33	A9	15	LYS	CA-C	6.70	1.60	1.52
18	AU	105	VAL	CA-CB	-6.63	1.46	1.54
20	CW	10	VAL	CA-CB	-6.58	1.46	1.54
21	AX	80	ILE	CA-CB	-6.51	1.46	1.53
5	AE	173	VAL	CA-CB	-6.30	1.47	1.54
29	A5	18	ALA	CA-CB	-6.22	1.43	1.53
15	AR	97	VAL	CA-CB	-6.19	1.46	1.54
11	AN	62	VAL	CA-C	6.12	1.59	1.52
5	AE	9	VAL	CA-CB	6.11	1.62	1.54
5	AE	144	ARG	N-CA	5.90	1.50	1.46
29	A5	16	ARG	CG-CD	5.88	1.70	1.52
31	A7	13	ALA	CA-CB	-5.87	1.44	1.53
5	AE	132	HIS	CG-ND1	5.87	1.44	1.38
21	AX	40	LYS	CA-C	-5.77	1.45	1.52
21	AX	76	ARG	CA-C	-5.70	1.45	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
18	AU	46	ALA	CA-C	5.66	1.60	1.52
20	AW	47	VAL	C-O	-5.66	1.17	1.24
20	AW	103	ILE	CA-CB	-5.64	1.47	1.54
15	AR	36	THR	CA-CB	-5.61	1.44	1.53
5	AE	12	THR	CA-C	-5.58	1.46	1.52
4	AD	64	ILE	CA-CB	-5.57	1.47	1.53
4	AD	192	THR	CA-C	-5.56	1.45	1.52
4	AD	240	ALA	CA-CB	-5.55	1.45	1.54
56	DX	8	4SU	O3'-P	5.55	1.61	1.56
57	BZ	404	VAL	CA-CB	5.54	1.61	1.54
20	AW	56	ALA	CA-CB	-5.54	1.44	1.53
20	AW	78	GLU	CA-C	-5.54	1.45	1.52
11	AN	66	LYS	CA-C	5.50	1.60	1.52
17	AT	110	ILE	CA-CB	5.48	1.60	1.54
19	AV	81	TYR	C-O	5.46	1.30	1.23
4	AD	217	ARG	C-O	-5.44	1.17	1.24
5	AE	133	LYS	N-CA	-5.40	1.38	1.46
20	AW	33	ARG	C-O	-5.36	1.18	1.24
29	A5	6	VAL	C-O	-5.34	1.17	1.24
31	A7	8	ASN	CA-C	-5.33	1.47	1.53
15	AR	3	HIS	CG-CD2	5.32	1.41	1.35
23	AZ	90	VAL	CA-CB	-5.31	1.47	1.53
24	A0	30	VAL	CA-CB	-5.30	1.47	1.53
57	DZ	199	ILE	CA-C	5.23	1.58	1.52
4	AD	138	VAL	CA-CB	5.22	1.59	1.54
20	CW	85	VAL	CA-CB	-5.21	1.48	1.54
18	AU	49	HIS	N-CA	-5.18	1.39	1.46
24	A0	25	ARG	CA-C	-5.16	1.46	1.52
29	A5	18	ALA	CA-C	5.14	1.59	1.52
17	AT	72	VAL	CA-CB	-5.14	1.47	1.54
8	AH	111	HIS	CA-C	5.13	1.57	1.52
6	AF	84	VAL	CA-C	-5.13	1.47	1.52
48	BO	40	SER	CA-C	-5.13	1.46	1.52
25	C1	67	ILE	CA-CB	-5.13	1.51	1.54
4	CD	239	ARG	CA-C	-5.12	1.46	1.52
20	AW	96	ILE	CA-CB	-5.12	1.48	1.54
12	AO	62	VAL	CA-CB	-5.10	1.49	1.54
15	CR	38	VAL	CA-CB	-5.10	1.51	1.54
19	AV	33	VAL	CA-CB	-5.10	1.46	1.55
29	A5	16	ARG	CB-CG	5.08	1.67	1.52
18	AU	105	VAL	CA-C	-5.06	1.46	1.52
28	A4	10	VAL	CA-C	5.04	1.56	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
30	A6	23	THR	CA-CB	5.03	1.60	1.53
8	AH	35	VAL	CA-C	-5.02	1.49	1.53
56	BX	8	4SU	O3'-P	5.02	1.61	1.56
5	AE	4	ILE	CA-CB	-5.00	1.50	1.55

All (840) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
9	CK	128	LEU	CA-C-N	17.30	141.47	119.84
9	CK	128	LEU	C-N-CA	17.30	141.47	119.84
9	AK	76	GLY	CA-C-N	16.63	140.62	119.84
9	AK	76	GLY	C-N-CA	16.63	140.62	119.84
4	AD	71	ASP	N-CA-C	-15.53	94.84	114.56
9	CK	76	GLY	CA-C-N	14.59	138.08	119.84
9	CK	76	GLY	C-N-CA	14.59	138.08	119.84
9	AK	128	LEU	CA-C-N	13.82	135.26	120.47
9	AK	128	LEU	C-N-CA	13.82	135.26	120.47
9	CK	32	LEU	CA-C-N	12.51	135.47	119.84
9	CK	32	LEU	C-N-CA	12.51	135.47	119.84
4	AD	10	THR	CA-C-N	-12.06	107.06	120.45
4	AD	10	THR	C-N-CA	-12.06	107.06	120.45
49	BP	79	VAL	N-CA-C	-12.06	100.89	112.83
14	AQ	38	GLU	N-CA-C	11.65	121.77	108.25
33	A9	29	ASN	CA-C-N	-11.64	108.02	120.47
33	A9	29	ASN	C-N-CA	-11.64	108.02	120.47
57	DZ	319	ASP	CA-C-N	11.34	134.01	119.84
57	DZ	319	ASP	C-N-CA	11.34	134.01	119.84
38	BE	104	ALA	N-CA-C	-11.15	99.38	113.43
21	CX	10	ALA	CA-C-N	-10.25	109.27	120.14
21	CX	10	ALA	C-N-CA	-10.25	109.27	120.14
28	A4	60	GLN	N-CA-C	-10.02	100.80	113.23
57	BZ	280	LEU	CA-C-N	9.97	131.54	119.98
57	BZ	280	LEU	C-N-CA	9.97	131.54	119.98
10	CL	71	THR	CA-C-N	9.86	130.54	120.38
10	CL	71	THR	C-N-CA	9.86	130.54	120.38
24	C0	82	ARG	CA-C-N	9.83	132.13	119.84
24	C0	82	ARG	C-N-CA	9.83	132.13	119.84
9	AK	104	ILE	CA-C-N	9.83	132.12	119.84
9	AK	104	ILE	C-N-CA	9.83	132.12	119.84
5	AE	52	LEU	CA-C-N	9.73	131.26	119.98
5	AE	52	LEU	C-N-CA	9.73	131.26	119.98
1	AA	2014	G	C2'-C3'-O3'	9.58	123.87	109.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
20	AW	17	VAL	CB-CA-C	-9.51	99.31	112.14
29	A5	6	VAL	CA-C-N	-9.44	110.32	119.76
29	A5	6	VAL	C-N-CA	-9.44	110.32	119.76
7	CG	31	VAL	CA-C-N	9.14	131.26	119.84
7	CG	31	VAL	C-N-CA	9.14	131.26	119.84
6	AF	64	ILE	N-CA-C	9.08	119.89	110.62
6	AF	40	GLN	N-CA-C	-8.98	100.44	111.40
6	AF	89	VAL	CA-C-N	-8.97	108.00	122.62
6	AF	89	VAL	C-N-CA	-8.97	108.00	122.62
22	AY	25	GLY	N-CA-C	8.95	123.60	110.63
57	DZ	-22	LYS	N-CA-C	-8.81	101.75	111.36
5	AE	20	ALA	CA-C-N	-8.76	115.70	123.33
5	AE	20	ALA	C-N-CA	-8.76	115.70	123.33
37	DD	188	LEU	CA-C-N	8.75	129.28	119.83
37	DD	188	LEU	C-N-CA	8.75	129.28	119.83
22	AY	65	ALA	CA-C-N	-8.74	111.13	120.66
22	AY	65	ALA	C-N-CA	-8.74	111.13	120.66
7	AG	89	GLY	N-CA-C	8.68	121.29	110.96
44	DK	38	ASN	CA-C-N	8.65	130.66	119.84
44	DK	38	ASN	C-N-CA	8.65	130.66	119.84
24	C0	44	ARG	N-CA-C	-8.63	102.89	113.50
13	CP	44	GLY	CA-C-O	-8.62	116.62	122.22
57	DZ	160	ARG	CA-C-N	-8.57	111.05	120.14
57	DZ	160	ARG	C-N-CA	-8.57	111.05	120.14
13	CP	44	GLY	N-CA-C	-8.54	103.83	111.95
10	AL	72	PRO	CA-C-N	8.52	128.58	119.89
10	AL	72	PRO	C-N-CA	8.52	128.58	119.89
45	BL	62	SER	N-CA-C	-8.52	102.89	113.28
57	DZ	280	LEU	CA-C-N	8.50	130.47	119.84
57	DZ	280	LEU	C-N-CA	8.50	130.47	119.84
12	AO	100	GLY	CA-C-N	-8.49	111.41	120.66
12	AO	100	GLY	C-N-CA	-8.49	111.41	120.66
57	BZ	319	ASP	CA-C-N	8.48	127.79	118.97
57	BZ	319	ASP	C-N-CA	8.48	127.79	118.97
23	AZ	129	SER	CA-C-N	8.46	129.28	119.47
23	AZ	129	SER	C-N-CA	8.46	129.28	119.47
23	AZ	86	VAL	CB-CA-C	-8.45	98.03	110.62
27	A3	11	SER	CA-C-N	-8.31	112.35	120.83
27	A3	11	SER	C-N-CA	-8.31	112.35	120.83
28	A4	10	VAL	N-CA-C	8.31	117.06	107.84
7	AG	31	VAL	CA-C-N	8.29	130.21	119.84
7	AG	31	VAL	C-N-CA	8.29	130.21	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
18	AU	105	VAL	N-CA-C	-8.22	102.53	110.42
1	AA	1700	G	C2'-C3'-O3'	8.20	121.80	109.50
57	BZ	128	TYR	N-CA-C	-8.14	100.32	113.19
51	BR	51	LEU	CA-C-N	8.11	129.19	120.11
51	BR	51	LEU	C-N-CA	8.11	129.19	120.11
4	CD	120	GLY	CA-C-N	8.10	129.97	119.84
4	CD	120	GLY	C-N-CA	8.10	129.97	119.84
23	CZ	14	LYS	CA-C-N	8.09	128.03	119.05
23	CZ	14	LYS	C-N-CA	8.09	128.03	119.05
11	CN	125	GLY	CA-C-N	8.06	128.25	119.87
11	CN	125	GLY	C-N-CA	8.06	128.25	119.87
4	CD	148	GLU	CA-C-N	8.05	128.54	119.93
4	CD	148	GLU	C-N-CA	8.05	128.54	119.93
5	AE	73	GLU	CA-C-N	8.02	128.51	119.93
5	AE	73	GLU	C-N-CA	8.02	128.51	119.93
23	CZ	100	VAL	CA-C-N	8.00	129.84	119.84
23	CZ	100	VAL	C-N-CA	8.00	129.84	119.84
26	A2	56	GLN	N-CA-C	-7.99	100.93	111.24
4	CD	223	GLY	N-CA-C	-7.99	102.83	112.49
5	AE	137	HIS	CA-C-N	-7.95	109.90	119.84
5	AE	137	HIS	C-N-CA	-7.95	109.90	119.84
5	CE	81	ILE	CB-CA-C	-7.95	101.27	110.73
19	AV	48	GLY	N-CA-C	-7.89	101.93	112.82
29	A5	14	ALA	N-CA-C	-7.89	102.63	111.07
23	AZ	67	LEU	CA-C-N	7.88	129.70	119.84
23	AZ	67	LEU	C-N-CA	7.88	129.70	119.84
4	CD	238	GLY	N-CA-C	7.88	123.86	114.48
56	BX	15	G	O3'-P-O5'	-7.88	92.18	104.00
18	AU	83	LEU	N-CA-C	-7.87	102.32	112.23
6	CF	24	LEU	CA-C-N	-7.81	111.86	120.14
6	CF	24	LEU	C-N-CA	-7.81	111.86	120.14
20	AW	79	GLY	CA-C-N	7.80	129.83	120.23
20	AW	79	GLY	C-N-CA	7.80	129.83	120.23
5	AE	9	VAL	CB-CA-C	7.80	118.78	111.30
11	CN	106	MET	N-CA-C	-7.77	103.32	114.12
43	BJ	90	LEU	CA-C-N	7.76	128.81	120.11
43	BJ	90	LEU	C-N-CA	7.76	128.81	120.11
4	CD	103	ARG	N-CA-C	7.73	118.19	108.45
57	BZ	670	VAL	N-CA-C	7.72	117.72	111.62
8	AH	172	LYS	CA-C-N	-7.71	112.81	120.21
8	AH	172	LYS	C-N-CA	-7.71	112.81	120.21
53	DT	11	SER	N-CA-C	-7.71	102.07	112.94

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
6	AF	9	ILE	CA-C-N	7.70	129.47	119.84
6	AF	9	ILE	C-N-CA	7.70	129.47	119.84
1	AA	2902	G	C4'-C3'-O3'	7.70	120.95	109.40
14	CQ	69	PHE	CA-C-N	7.63	129.38	119.84
14	CQ	69	PHE	C-N-CA	7.63	129.38	119.84
4	CD	220	HIS	CA-C-N	-7.62	113.27	123.10
4	CD	220	HIS	C-N-CA	-7.62	113.27	123.10
19	AV	99	ILE	CB-CA-C	-7.61	101.64	111.53
1	AA	991	G	O5'-P-OP1	-7.61	85.17	108.00
20	CW	79	GLY	CA-C-N	7.60	127.66	119.90
20	CW	79	GLY	C-N-CA	7.60	127.66	119.90
15	AR	36	THR	CB-CA-C	-7.60	95.30	110.42
25	A1	11	ARG	CA-C-N	-7.55	112.22	119.85
25	A1	11	ARG	C-N-CA	-7.55	112.22	119.85
38	DE	69	VAL	CA-C-N	7.53	129.25	119.84
38	DE	69	VAL	C-N-CA	7.53	129.25	119.84
5	AE	144	ARG	CB-CA-C	-7.50	105.58	116.54
42	BI	46	ALA	N-CA-C	-7.47	104.19	113.38
4	AD	221	VAL	N-CA-C	7.47	119.04	108.36
5	CE	137	HIS	N-CA-C	7.46	118.71	110.13
19	AV	89	GLN	CA-C-N	-7.43	113.08	120.21
19	AV	89	GLN	C-N-CA	-7.43	113.08	120.21
38	BE	23	GLY	N-CA-C	7.41	120.15	111.63
21	CX	38	GLU	N-CA-C	-7.41	103.15	111.07
23	AZ	115	GLY	N-CA-C	7.39	121.66	112.79
57	DZ	302	HIS	CA-C-N	7.36	129.04	119.84
57	DZ	302	HIS	C-N-CA	7.36	129.04	119.84
26	C2	68	ARG	N-CA-C	-7.34	104.47	113.50
12	AO	38	VAL	CB-CA-C	-7.30	101.86	110.91
35	BB	166	ASP	CA-C-N	7.30	126.93	119.56
35	BB	166	ASP	C-N-CA	7.30	126.93	119.56
46	DM	123	ALA	N-CA-C	7.30	118.91	109.64
13	AP	65	ARG	N-CA-C	7.29	121.22	108.75
18	AU	49	HIS	N-CA-C	-7.26	104.57	113.50
7	CG	48	GLU	N-CA-C	-7.25	104.81	112.93
4	AD	71	ASP	N-CA-CB	-7.23	101.39	111.00
21	CX	20	GLY	N-CA-C	-7.22	104.07	112.73
4	CD	229	VAL	CB-CA-C	-7.22	100.97	112.16
8	AH	92	ILE	N-CA-C	7.21	117.73	110.23
49	DP	79	VAL	N-CA-C	-7.20	105.59	113.43
48	BO	40	SER	N-CA-C	-7.18	103.14	110.97
15	CR	43	GLU	N-CA-C	-7.13	103.80	114.64

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
53	BT	11	SER	N-CA-C	-7.12	102.41	113.02
45	BL	124	LYS	CA-C-N	7.12	128.74	119.84
45	BL	124	LYS	C-N-CA	7.12	128.74	119.84
11	AN	43	THR	N-CA-C	-7.09	97.07	109.48
24	A0	12	ASN	N-CA-C	7.08	122.09	113.17
57	DZ	-11	LYS	N-CA-C	-7.08	103.27	112.68
4	AD	28	GLU	CA-C-N	-7.07	113.21	120.85
4	AD	28	GLU	C-N-CA	-7.07	113.21	120.85
21	AX	60	ARG	CA-C-N	7.06	126.70	119.92
21	AX	60	ARG	C-N-CA	7.06	126.70	119.92
1	AA	2902	G	P-O3'-C3'	7.06	130.79	120.20
32	C8	10	ALA	N-CA-C	-7.06	101.88	112.04
21	AX	40	LYS	N-CA-C	-7.05	103.28	110.97
18	AU	78	THR	N-CA-C	-7.04	103.03	111.69
4	CD	85	ASP	CA-C-N	7.04	127.64	120.04
4	CD	85	ASP	C-N-CA	7.04	127.64	120.04
28	C4	40	HIS	CA-C-N	7.04	127.34	119.32
28	C4	40	HIS	C-N-CA	7.04	127.34	119.32
11	AN	134	ARG	CA-C-N	7.03	128.13	119.98
11	AN	134	ARG	C-N-CA	7.03	128.13	119.98
25	C1	37	ILE	CB-CA-C	-7.02	102.82	111.32
20	CW	42	ARG	N-CA-C	-7.02	104.53	113.23
49	BP	40	ASP	CA-C-N	7.01	128.60	119.84
49	BP	40	ASP	C-N-CA	7.01	128.60	119.84
57	BZ	93	GLU	N-CA-C	-7.00	103.34	110.97
17	CT	23	ARG	CA-C-N	-7.00	112.76	119.76
17	CT	23	ARG	C-N-CA	-7.00	112.76	119.76
11	CN	38	HIS	N-CA-C	-7.00	105.28	113.88
5	AE	132	HIS	N-CA-C	6.99	121.13	107.57
4	CD	57	GLY	N-CA-C	6.98	120.01	112.33
16	AS	18	ILE	CB-CA-C	-6.98	102.88	112.02
4	AD	250	TRP	N-CA-C	-6.97	103.96	113.30
23	CZ	43	GLU	N-CA-C	-6.94	103.40	110.97
57	DZ	98	MET	N-CA-C	-6.93	104.46	113.12
43	BJ	83	GLU	N-CA-C	-6.92	104.86	113.38
22	CY	65	ALA	N-CA-C	6.92	118.51	109.93
21	CX	31	HIS	CA-C-N	-6.90	112.67	119.64
21	CX	31	HIS	C-N-CA	-6.90	112.67	119.64
44	DK	75	TYR	N-CA-C	-6.89	104.45	112.92
8	AH	9	ILE	CB-CA-C	-6.89	102.91	111.04
57	BZ	130	VAL	CA-C-N	-6.87	111.86	120.51
57	BZ	130	VAL	C-N-CA	-6.87	111.86	120.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
43	BJ	23	ILE	N-CA-C	-6.82	107.23	113.71
37	DD	148	VAL	N-CA-C	-6.78	97.73	107.77
20	AW	71	VAL	CB-CA-C	-6.76	104.97	112.68
50	DQ	27	PHE	CA-C-N	-6.76	112.97	120.14
50	DQ	27	PHE	C-N-CA	-6.76	112.97	120.14
8	CH	100	GLY	N-CA-C	-6.75	104.19	111.21
4	AD	206	LEU	CA-C-N	-6.74	116.16	123.30
4	AD	206	LEU	C-N-CA	-6.74	116.16	123.30
11	AN	124	ALA	N-CA-C	-6.74	101.84	110.53
3	AC	203	GLU	N-CA-C	-6.72	104.64	114.39
53	DT	101	GLY	N-CA-C	6.72	122.64	110.95
18	AU	47	TYR	CB-CA-C	-6.71	99.65	110.79
9	AK	6	ASN	N-CA-C	-6.71	104.84	113.16
25	A1	37	ILE	CB-CA-C	-6.70	99.69	110.28
3	CC	203	GLU	N-CA-C	-6.70	104.68	114.39
6	CF	87	GLY	CA-C-N	-6.70	114.46	123.10
6	CF	87	GLY	C-N-CA	-6.70	114.46	123.10
4	CD	136	ILE	CA-C-N	6.69	128.20	119.84
4	CD	136	ILE	C-N-CA	6.69	128.20	119.84
15	CR	3	HIS	N-CA-C	6.69	120.33	110.30
23	AZ	100	VAL	CB-CA-C	-6.69	103.16	110.85
31	A7	24	THR	N-CA-CB	-6.69	101.94	110.03
12	AO	19	ILE	N-CA-C	6.67	118.20	108.53
28	A4	52	THR	N-CA-C	-6.67	102.41	111.55
38	BE	113	ALA	N-CA-C	-6.66	104.90	113.16
40	BG	78	ARG	N-CA-C	6.66	118.25	108.86
12	AO	94	ARG	N-CA-C	-6.62	103.89	112.23
14	AQ	10	ARG	N-CA-C	6.62	120.57	112.23
4	AD	12	SER	N-CA-C	-6.62	105.36	113.50
1	CA	1992	G	C2'-C3'-O3'	6.61	119.41	109.50
40	BG	13	GLN	CA-C-N	6.60	128.09	119.84
40	BG	13	GLN	C-N-CA	6.60	128.09	119.84
21	AX	59	VAL	CB-CA-C	-6.59	102.43	110.99
16	AS	53	SER	N-CA-C	-6.58	103.60	111.69
20	CW	61	ASN	N-CA-C	6.55	118.08	111.07
48	DO	43	LEU	N-CA-C	-6.55	104.22	111.82
1	AA	2716	C	OP2-P-O3'	-6.54	88.37	108.00
1	AA	2530	A	OP1-P-OP2	-6.54	99.99	119.60
57	BZ	256	THR	CB-CA-C	-6.53	103.67	110.33
57	DZ	572	TYR	N-CA-C	6.51	116.46	107.73
8	AH	4	ILE	N-CA-C	-6.51	106.21	111.81
6	CF	201	VAL	N-CA-C	6.51	117.20	110.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
15	AR	4	LEU	N-CA-C	-6.51	105.29	113.23
5	AE	12	THR	N-CA-C	-6.49	98.27	108.14
23	AZ	122	ARG	N-CA-C	-6.48	105.30	113.72
8	AH	11	VAL	CB-CA-C	-6.46	103.34	110.52
4	CD	46	GLN	N-CA-C	-6.46	103.91	113.61
48	BO	23	GLY	N-CA-C	6.45	124.84	114.90
41	DH	134	ILE	N-CA-C	6.45	116.59	110.53
22	AY	30	VAL	CB-CA-C	-6.45	102.22	111.19
27	A3	9	VAL	CB-CA-C	-6.45	103.66	110.62
37	BD	141	ARG	CA-C-N	6.44	127.89	119.84
37	BD	141	ARG	C-N-CA	6.44	127.89	119.84
40	BG	92	SER	CA-C-N	6.44	127.89	119.84
40	BG	92	SER	C-N-CA	6.44	127.89	119.84
11	AN	90	MET	N-CA-C	-6.44	103.95	110.97
5	AE	82	ARG	N-CA-C	6.43	119.02	110.53
3	AC	16	ASP	CA-C-N	6.42	125.65	118.97
3	AC	16	ASP	C-N-CA	6.42	125.65	118.97
44	BK	40	ILE	N-CA-C	-6.42	106.73	112.12
14	AQ	19	GLY	N-CA-C	6.42	122.31	112.81
41	BH	38	ILE	N-CA-C	6.40	116.51	110.30
48	DO	18	PHE	CA-C-N	6.40	127.84	119.84
48	DO	18	PHE	C-N-CA	6.40	127.84	119.84
57	DZ	133	ILE	N-CA-C	-6.40	101.29	109.80
13	AP	57	THR	N-CA-C	6.39	119.51	110.50
35	DB	195	ASP	N-CA-C	-6.39	105.64	113.50
57	DZ	130	VAL	N-CA-C	6.38	113.87	107.55
3	CC	16	ASP	CA-C-N	6.38	125.60	118.97
3	CC	16	ASP	C-N-CA	6.38	125.60	118.97
5	CE	128	SER	CB-CA-C	-6.38	105.24	114.87
45	DL	72	GLY	N-CA-C	6.37	119.86	111.70
4	AD	35	LYS	CA-C-N	-6.37	113.41	119.85
4	AD	35	LYS	C-N-CA	-6.37	113.41	119.85
1	AA	1078	A	O5'-P-OP1	-6.37	88.90	108.00
41	DH	88	LYS	CA-C-N	-6.37	113.16	120.04
41	DH	88	LYS	C-N-CA	-6.37	113.16	120.04
1	AA	495	G	O3'-P-O5'	6.35	113.52	104.00
5	AE	8	LYS	CA-C-N	-6.31	116.54	122.66
5	AE	8	LYS	C-N-CA	-6.31	116.54	122.66
4	AD	270	ILE	CB-CA-C	6.29	119.60	110.98
22	CY	31	LEU	CA-C-N	6.29	126.03	119.05
22	CY	31	LEU	C-N-CA	6.29	126.03	119.05
36	DC	125	GLU	N-CA-C	-6.28	105.62	113.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
57	DZ	0	ARG	N-CA-C	-6.28	104.49	111.71
37	DD	189	PRO	CB-CA-C	-6.27	103.74	111.64
35	DB	114	ARG	N-CA-C	-6.26	107.48	114.62
4	CD	245	PRO	CA-C-N	6.25	126.28	119.90
4	CD	245	PRO	C-N-CA	6.25	126.28	119.90
8	AH	115	VAL	CB-CA-C	-6.25	102.50	111.19
23	AZ	167	PRO	N-CA-C	-6.25	105.83	114.27
6	AF	182	ASN	CA-C-N	-6.25	112.56	120.56
6	AF	182	ASN	C-N-CA	-6.25	112.56	120.56
11	AN	86	PRO	CA-C-O	-6.24	114.38	122.12
38	DE	105	VAL	CA-C-N	-6.24	113.52	120.45
38	DE	105	VAL	C-N-CA	-6.24	113.52	120.45
28	C4	6	HIS	CA-C-N	6.22	126.73	120.14
28	C4	6	HIS	C-N-CA	6.22	126.73	120.14
23	CZ	107	THR	CA-C-N	6.21	126.23	119.89
23	CZ	107	THR	C-N-CA	6.21	126.23	119.89
31	C7	6	GLN	CA-C-N	6.21	127.60	119.84
31	C7	6	GLN	C-N-CA	6.21	127.60	119.84
37	BD	188	LEU	CA-C-N	6.20	127.59	119.84
37	BD	188	LEU	C-N-CA	6.20	127.59	119.84
15	CR	66	VAL	N-CA-C	-6.20	103.89	112.50
13	AP	27	HIS	CA-C-N	-6.19	116.14	122.27
13	AP	27	HIS	C-N-CA	-6.19	116.14	122.27
57	BZ	-2	ALA	N-CA-C	-6.19	105.75	113.55
5	AE	36	ARG	N-CA-C	-6.19	99.31	109.40
14	CQ	136	ALA	N-CA-C	-6.19	104.80	112.90
57	BZ	307	GLY	CA-C-N	-6.19	113.41	119.90
57	BZ	307	GLY	C-N-CA	-6.19	113.41	119.90
39	DF	95	GLU	CA-C-N	6.19	127.57	119.84
39	DF	95	GLU	C-N-CA	6.19	127.57	119.84
10	CL	98	ARG	N-CA-C	6.18	117.54	108.14
7	AG	55	LYS	N-CA-C	-6.18	105.56	113.23
57	BZ	287	PRO	CA-C-N	6.18	126.13	119.76
57	BZ	287	PRO	C-N-CA	6.18	126.13	119.76
19	AV	58	VAL	CB-CA-C	-6.18	102.44	110.84
16	AS	109	GLY	N-CA-C	6.17	124.19	115.30
4	AD	68	LYS	N-CA-C	-6.17	103.68	112.13
6	AF	53	THR	N-CA-CB	-6.17	101.05	110.42
5	AE	12	THR	CB-CA-C	-6.16	99.87	110.95
23	AZ	98	MET	N-CA-C	6.15	116.36	108.24
45	BL	10	LEU	N-CA-C	-6.14	105.92	113.41
6	CF	199	TRP	N-CA-C	-6.14	105.75	113.18

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
49	DP	3	LYS	N-CA-C	6.13	118.72	109.41
10	CL	29	GLN	N-CA-C	-6.12	105.45	113.17
4	CD	154	LYS	N-CA-C	-6.12	106.79	114.56
14	AQ	35	VAL	N-CA-C	6.12	117.11	108.36
17	AT	53	ARG	CB-CA-C	-6.11	101.56	110.06
22	CY	100	ALA	N-CA-C	-6.11	105.35	114.64
57	DZ	458	HIS	N-CA-C	-6.10	105.87	113.55
27	A3	40	THR	CA-C-N	-6.09	112.21	118.85
27	A3	40	THR	C-N-CA	-6.09	112.21	118.85
6	CF	176	LEU	N-CA-C	6.08	118.40	108.55
38	DE	68	GLU	N-CA-C	6.08	117.91	111.28
25	A1	14	VAL	CB-CA-C	-6.07	102.58	110.84
57	DZ	236	GLU	CA-C-N	6.07	127.43	119.84
57	DZ	236	GLU	C-N-CA	6.07	127.43	119.84
5	AE	125	GLY	CA-C-N	-6.07	113.72	119.85
5	AE	125	GLY	C-N-CA	-6.07	113.72	119.85
4	AD	56	GLY	N-CA-C	6.06	124.42	115.08
1	CA	2689	U	C2'-C3'-O3'	6.06	118.59	109.50
8	AH	9	ILE	N-CA-C	6.06	113.55	107.55
57	DZ	469	GLU	N-CA-C	-6.06	105.93	113.38
19	AV	65	GLY	N-CA-C	6.05	119.34	110.80
57	BZ	400	GLU	N-CA-C	6.05	123.68	110.80
36	DC	88	ARG	N-CA-C	-6.05	105.94	113.38
28	A4	28	LYS	CA-C-N	6.03	127.38	119.84
28	A4	28	LYS	C-N-CA	6.03	127.38	119.84
5	CE	65	GLY	N-CA-C	-6.03	106.25	115.66
41	BH	75	ARG	CA-C-N	6.03	126.05	119.90
41	BH	75	ARG	C-N-CA	6.03	126.05	119.90
57	DZ	160	ARG	N-CA-C	6.03	123.13	109.81
1	AA	1255	A	C4'-C3'-O3'	6.03	118.44	109.40
22	AY	73	ARG	CA-C-N	-6.03	114.06	120.03
22	AY	73	ARG	C-N-CA	-6.03	114.06	120.03
57	BZ	-22	LYS	N-CA-C	-6.03	105.19	112.54
57	DZ	319	ASP	N-CA-C	6.03	117.25	109.72
30	C6	7	ILE	CB-CA-C	-6.03	102.69	112.03
17	AT	127	ALA	N-CA-C	-6.02	100.60	109.81
48	DO	71	GLN	N-CA-C	-6.02	104.84	111.82
37	BD	38	TYR	CA-C-N	-6.02	114.18	120.38
37	BD	38	TYR	C-N-CA	-6.02	114.18	120.38
24	A0	30	VAL	N-CA-C	6.00	116.45	107.51
1	AA	2299	A	N9-C1'-C2'	-5.99	105.01	114.00
20	CW	85	VAL	N-CA-C	5.99	116.74	107.99

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
23	CZ	157	LEU	CA-C-N	5.99	126.55	120.38
23	CZ	157	LEU	C-N-CA	5.99	126.55	120.38
35	DB	188	ALA	N-CA-C	5.98	118.18	108.26
4	CD	239	ARG	N-CA-C	-5.97	98.09	110.80
51	DR	51	LEU	CA-C-N	5.96	127.29	119.84
51	DR	51	LEU	C-N-CA	5.96	127.29	119.84
6	CF	101	LEU	CA-C-N	5.96	127.29	119.84
6	CF	101	LEU	C-N-CA	5.96	127.29	119.84
34	BA	1067	A	C2'-C3'-O3'	5.96	118.44	109.50
25	C1	11	ARG	CA-C-N	-5.95	113.40	120.13
25	C1	11	ARG	C-N-CA	-5.95	113.40	120.13
8	AH	120	GLY	N-CA-C	-5.94	107.41	114.48
33	C9	16	VAL	CB-CA-C	-5.94	105.09	112.45
18	AU	59	ARG	N-CA-C	-5.93	104.82	111.28
21	AX	41	ASN	N-CA-C	5.92	117.73	111.28
9	CK	40	LEU	N-CA-C	-5.92	105.65	114.64
5	CE	50	GLY	N-CA-C	-5.92	102.15	110.96
23	AZ	177	PRO	N-CA-C	5.91	124.65	112.47
29	A5	31	VAL	CA-C-N	5.91	125.85	119.76
29	A5	31	VAL	C-N-CA	5.91	125.85	119.76
1	AA	985	G	OP1-P-O3'	-5.91	90.27	108.00
8	AH	19	VAL	CB-CA-C	-5.90	102.28	111.26
12	AO	3	GLN	CA-C-N	-5.90	113.61	119.93
12	AO	3	GLN	C-N-CA	-5.90	113.61	119.93
19	AV	70	ILE	CB-CA-C	-5.90	101.84	110.81
38	DE	98	THR	N-CA-C	5.90	118.95	111.69
12	CO	29	ASN	N-CA-C	5.89	119.61	111.71
4	AD	251	GLY	N-CA-C	5.89	121.69	114.69
4	AD	98	VAL	N-CA-C	5.88	117.33	110.62
26	A2	38	GLN	N-CA-C	-5.88	104.95	111.36
1	AA	455	A	C5'-C4'-C3'	-5.87	107.19	116.00
15	AR	9	LYS	N-CA-C	-5.87	106.76	114.04
1	AA	1317	G	O5'-P-OP2	-5.86	90.43	108.00
40	DG	69	VAL	N-CA-C	-5.86	108.15	113.71
57	BZ	323	GLY	N-CA-C	5.85	121.54	111.47
22	AY	17	SER	N-CA-C	5.85	117.42	108.42
23	AZ	94	GLU	CA-C-N	-5.84	112.54	119.84
23	AZ	94	GLU	C-N-CA	-5.84	112.54	119.84
23	AZ	33	LEU	N-CA-C	5.83	118.05	109.24
16	AS	15	ARG	N-CA-C	5.83	117.50	111.03
35	DB	25	ASN	CA-C-N	5.83	127.13	119.84
35	DB	25	ASN	C-N-CA	5.83	127.13	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
57	DZ	84	THR	N-CA-C	-5.82	102.08	110.40
35	BB	158	LEU	CA-C-N	5.82	127.11	119.84
35	BB	158	LEU	C-N-CA	5.82	127.11	119.84
46	BM	112	GLY	CA-C-N	5.82	127.11	119.84
46	BM	112	GLY	C-N-CA	5.82	127.11	119.84
57	BZ	15	ILE	N-CA-C	5.81	118.06	108.99
13	AP	12	ALA	N-CA-C	-5.80	104.92	112.23
57	DZ	642	VAL	N-CA-C	5.79	116.20	107.75
19	AV	28	GLU	CA-C-N	-5.78	113.98	119.76
19	AV	28	GLU	C-N-CA	-5.78	113.98	119.76
5	AE	33	VAL	N-CA-C	-5.78	102.07	109.30
57	BZ	91	THR	N-CA-C	5.78	119.14	111.75
57	BZ	453	GLY	N-CA-C	5.77	119.72	111.12
6	AF	86	GLY	N-CA-C	5.77	122.00	112.66
6	AF	84	VAL	N-CA-C	-5.76	102.10	109.30
27	A3	22	ALA	N-CA-C	-5.76	105.00	111.28
57	BZ	108	PHE	N-CA-C	5.76	118.50	108.76
1	AA	1729	G	OP1-P-O3'	-5.76	90.73	108.00
15	AR	17	ARG	N-CA-C	-5.76	105.09	111.36
10	AL	20	ALA	CA-C-N	5.75	126.31	120.38
10	AL	20	ALA	C-N-CA	5.75	126.31	120.38
41	DH	19	VAL	N-CA-C	-5.75	106.88	112.29
29	A5	27	PRO	CA-C-N	5.75	125.70	119.78
29	A5	27	PRO	C-N-CA	5.75	125.70	119.78
1	CA	448	U	OP1-P-O3'	-5.75	90.75	108.00
1	AA	2858	G	O4'-C1'-N9	5.74	116.81	108.20
22	AY	31	LEU	CA-C-N	5.74	125.10	118.85
22	AY	31	LEU	C-N-CA	5.74	125.10	118.85
19	CV	35	LEU	CA-C-N	-5.74	114.84	120.98
19	CV	35	LEU	C-N-CA	-5.74	114.84	120.98
22	AY	92	ASN	N-CA-C	5.73	117.98	111.11
57	DZ	647	VAL	N-CA-C	5.72	114.42	107.61
23	AZ	32	HIS	N-CA-C	-5.72	106.95	114.04
1	AA	1745	A	N9-C1'-C2'	5.71	122.56	114.00
14	CQ	22	LYS	N-CA-C	-5.71	104.75	110.97
30	A6	28	ARG	N-CA-C	-5.70	106.88	113.88
8	CH	101	ARG	N-CA-C	-5.69	106.19	113.02
10	CL	136	VAL	N-CA-C	5.69	117.05	109.37
1	CA	1653	G	P-O3'-C3'	5.68	128.73	120.20
12	AO	118	ALA	CA-C-N	5.68	125.15	119.24
12	AO	118	ALA	C-N-CA	5.68	125.15	119.24
18	AU	67	ALA	N-CA-C	-5.68	104.70	111.69

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
10	AL	71	THR	CA-C-N	5.68	126.23	120.38
10	AL	71	THR	C-N-CA	5.68	126.23	120.38
2	AB	27	C	OP2-P-O3'	5.67	125.02	108.00
41	BH	112	LEU	N-CA-C	5.67	117.89	108.13
50	DQ	57	VAL	N-CA-C	5.67	118.31	108.95
8	AH	105	LEU	N-CA-C	-5.67	99.65	108.90
35	BB	128	GLU	N-CA-C	-5.67	106.22	113.02
6	AF	114	VAL	CB-CA-C	-5.67	104.63	111.88
42	BI	3	GLN	N-CA-C	5.67	117.73	108.55
33	A9	32	HIS	N-CA-C	5.66	118.39	111.82
22	CY	39	VAL	CB-CA-C	-5.66	103.32	111.19
38	DE	69	VAL	N-CA-C	5.66	121.11	108.88
14	CQ	19	GLY	N-CA-C	5.66	121.18	112.81
16	AS	34	HIS	N-CA-C	5.65	118.89	109.96
9	CK	85	ASP	CA-C-N	5.65	126.90	119.84
9	CK	85	ASP	C-N-CA	5.65	126.90	119.84
29	C5	8	LYS	N-CA-C	-5.65	106.38	113.72
7	AG	54	GLU	N-CA-C	-5.64	106.28	112.72
9	AK	32	LEU	CA-C-N	5.64	126.90	119.84
9	AK	32	LEU	C-N-CA	5.64	126.90	119.84
20	CW	75	TYR	N-CA-C	5.64	117.42	108.79
14	AQ	119	ARG	N-CA-C	-5.64	105.04	111.07
1	AA	1185	C	O5'-P-OP1	-5.64	91.09	108.00
20	AW	105	VAL	CA-C-N	-5.63	114.58	122.75
20	AW	105	VAL	C-N-CA	-5.63	114.58	122.75
48	BO	22	THR	N-CA-C	-5.63	102.56	110.50
56	BX	15	G	P-O3'-C3'	5.63	128.64	120.20
10	CL	46	ALA	N-CA-C	-5.63	106.27	113.02
45	BL	11	VAL	N-CA-C	-5.63	105.02	110.42
22	CY	91	GLU	N-CA-C	-5.62	105.16	111.28
17	AT	98	LYS	N-CA-C	-5.61	100.03	109.07
24	A0	82	ARG	N-CA-C	-5.61	102.70	109.83
6	AF	29	ASN	CA-C-N	5.61	125.07	119.24
6	AF	29	ASN	C-N-CA	5.61	125.07	119.24
14	AQ	97	VAL	N-CA-C	5.61	115.96	108.11
28	A4	40	HIS	CA-C-N	5.60	126.84	119.84
28	A4	40	HIS	C-N-CA	5.60	126.84	119.84
35	BB	193	ASP	CA-C-N	5.60	126.84	119.84
35	BB	193	ASP	C-N-CA	5.60	126.84	119.84
14	CQ	16	ARG	N-CA-C	5.60	117.48	109.14
15	AR	116	LEU	N-CA-C	-5.59	101.43	110.32
10	CL	72	PRO	N-CA-C	5.59	117.52	110.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
29	C5	26	THR	CA-C-N	5.59	126.14	120.38
29	C5	26	THR	C-N-CA	5.59	126.14	120.38
1	AA	2641	A	N9-C1'-C2'	5.59	122.38	114.00
21	CX	73	ARG	CA-C-N	5.59	125.54	119.78
21	CX	73	ARG	C-N-CA	5.59	125.54	119.78
1	AA	991	G	O5'-P-OP2	5.59	124.76	108.00
14	CQ	28	ALA	N-CA-C	5.59	122.70	110.80
57	BZ	408	VAL	CB-CA-C	-5.58	104.79	110.88
5	AE	179	GLU	N-CA-C	5.58	120.07	112.88
10	CL	20	ALA	CA-C-N	5.57	126.12	120.38
10	CL	20	ALA	C-N-CA	5.57	126.12	120.38
36	DC	108	ASN	CA-C-N	5.57	125.66	119.87
36	DC	108	ASN	C-N-CA	5.57	125.66	119.87
7	CG	13	GLU	N-CA-C	-5.57	102.67	110.35
26	C2	45	SER	N-CA-C	-5.55	105.23	112.23
4	AD	223	GLY	N-CA-C	-5.55	106.07	112.73
12	AO	43	VAL	CB-CA-C	-5.55	105.23	111.23
57	BZ	577	SER	N-CA-C	5.55	117.70	110.43
35	DB	156	LYS	N-CA-C	-5.55	106.20	114.64
1	AA	1098	C	C2'-C3'-O3'	5.55	122.02	113.70
1	AA	2459	G	OP1-P-O3'	-5.55	91.36	108.00
57	DZ	-47	ASP	N-CA-C	5.55	117.72	108.02
9	AK	42	GLN	N-CA-C	-5.54	105.39	111.82
57	BZ	264	LEU	N-CA-C	5.54	118.03	111.33
5	AE	129	HIS	CA-C-N	-5.54	114.78	122.86
5	AE	129	HIS	C-N-CA	-5.54	114.78	122.86
57	BZ	-23	LEU	N-CA-C	-5.54	99.01	110.80
37	BD	158	ILE	N-CA-C	-5.53	105.13	110.72
48	BO	21	ASP	N-CA-C	5.53	118.19	109.39
5	AE	201	THR	N-CA-C	5.52	117.42	110.24
11	AN	135	PRO	CA-C-O	-5.52	115.48	121.27
37	DD	114	ARG	N-CA-C	-5.52	105.18	111.14
20	AW	85	VAL	N-CA-C	5.51	116.17	108.89
33	A9	31	LYS	N-CA-C	-5.51	105.43	111.82
29	A5	32	PRO	CA-C-O	-5.51	115.06	121.34
35	BB	123	ALA	N-CA-C	-5.50	106.64	113.19
32	C8	38	GLY	N-CA-C	-5.49	105.74	112.77
6	AF	35	GLU	CA-C-N	5.49	127.59	120.56
6	AF	35	GLU	C-N-CA	5.49	127.59	120.56
17	AT	3	ARG	N-CA-C	-5.49	105.45	111.82
41	BH	134	ILE	N-CA-C	5.48	115.68	110.53
14	AQ	64	ILE	CB-CA-C	-5.48	102.66	110.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
57	BZ	289	ILE	CB-CA-C	-5.48	104.17	111.13
23	AZ	175	VAL	CA-C-N	5.48	126.02	120.38
23	AZ	175	VAL	C-N-CA	5.48	126.02	120.38
12	AO	91	LEU	CB-CA-C	-5.48	104.52	111.86
5	CE	97	LYS	CA-C-N	-5.47	114.14	119.78
5	CE	97	LYS	C-N-CA	-5.47	114.14	119.78
6	AF	9	ILE	N-CA-C	5.47	113.85	107.89
17	AT	116	ALA	N-CA-C	5.46	118.15	110.23
9	CK	89	ALA	N-CA-C	-5.46	105.29	112.72
11	AN	78	TYR	CA-C-N	-5.46	114.09	119.93
11	AN	78	TYR	C-N-CA	-5.46	114.09	119.93
25	A1	66	HIS	N-CA-C	5.46	119.57	113.02
8	CH	35	VAL	CA-C-N	5.46	125.46	119.89
8	CH	35	VAL	C-N-CA	5.46	125.46	119.89
37	BD	42	GLN	N-CA-C	5.46	122.42	110.80
50	BQ	21	VAL	N-CA-C	5.46	116.32	106.61
14	AQ	17	LEU	N-CA-C	5.45	118.73	112.57
7	CG	54	GLU	N-CA-C	-5.45	106.48	113.02
44	DK	23	ALA	N-CA-C	5.45	118.65	107.69
57	DZ	419	ALA	N-CA-C	-5.45	106.60	113.20
14	CQ	120	ILE	CB-CA-C	-5.45	105.00	111.81
19	AV	14	VAL	N-CA-C	5.45	115.73	108.11
20	CW	100	THR	N-CA-C	5.44	118.06	108.75
24	C0	28	GLY	N-CA-C	-5.44	107.84	114.92
5	AE	106	GLY	N-CA-C	-5.44	103.02	111.12
11	AN	135	PRO	CB-CA-C	-5.44	104.64	111.71
10	CL	31	GLY	N-CA-C	-5.44	107.74	115.30
8	CH	28	GLY	CA-C-N	5.44	125.09	119.05
8	CH	28	GLY	C-N-CA	5.44	125.09	119.05
19	AV	94	LEU	N-CA-C	5.43	118.34	109.59
4	AD	102	LYS	N-CA-C	5.43	118.67	109.76
44	BK	56	GLY	N-CA-C	-5.43	106.33	115.62
1	CA	2689	U	P-O3'-C3'	5.43	128.34	120.20
27	C3	59	VAL	N-CA-C	5.43	115.15	108.53
20	AW	12	ILE	N-CA-C	-5.43	100.05	107.75
1	CA	191	A	OP1-P-O3'	-5.42	91.74	108.00
18	AU	37	GLU	N-CA-C	-5.42	104.79	111.40
7	CG	163	ALA	N-CA-C	5.41	117.12	108.41
23	CZ	177	PRO	N-CA-C	5.41	121.36	114.92
57	DZ	382	GLU	N-CA-C	-5.41	105.50	113.61
4	AD	257	LEU	CA-C-N	-5.41	113.69	121.42
4	AD	257	LEU	C-N-CA	-5.41	113.69	121.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
45	DL	23	LYS	N-CA-C	-5.41	106.06	113.30
5	CE	168	MET	N-CA-C	5.41	118.09	110.14
16	CS	63	THR	N-CA-C	5.40	116.86	110.97
1	AA	1807	G	O5'-P-OP2	-5.40	91.81	108.00
17	CT	25	GLY	N-CA-C	-5.39	107.58	114.37
57	DZ	-54	GLY	N-CA-C	5.39	117.28	110.38
22	CY	81	LYS	CA-C-N	5.39	125.56	119.90
22	CY	81	LYS	C-N-CA	5.39	125.56	119.90
35	BB	29	ALA	N-CA-C	5.38	116.83	111.07
53	DT	94	ALA	N-CA-C	-5.38	104.93	112.25
1	AA	2518	U	P-O3'-C3'	5.37	128.26	120.20
50	BQ	9	VAL	CB-CA-C	-5.37	103.85	111.21
57	BZ	118	SER	N-CA-C	-5.37	105.99	112.54
26	C2	16	LEU	N-CA-C	5.37	117.45	110.53
39	BF	6	VAL	N-CA-C	5.36	115.35	107.15
6	AF	187	VAL	N-CA-C	5.36	116.09	110.62
41	DH	112	LEU	N-CA-C	5.36	116.77	107.93
54	BU	9	ARG	N-CA-C	-5.36	105.44	111.28
4	CD	41	GLY	N-CA-C	-5.35	108.46	115.47
45	DL	28	LYS	N-CA-C	5.35	118.51	111.28
57	DZ	272	LEU	N-CA-C	-5.35	106.43	113.12
4	AD	49	ILE	CB-CA-C	-5.35	102.87	111.59
35	BB	211	ILE	N-CA-C	-5.35	105.50	110.53
9	CK	100	ASN	CA-C-N	5.35	126.53	119.84
9	CK	100	ASN	C-N-CA	5.35	126.53	119.84
1	AA	1660	A	O5'-P-OP1	-5.35	91.96	108.00
37	DD	193	ASP	N-CA-C	5.34	118.58	111.75
12	AO	81	ASP	N-CA-C	-5.34	99.62	108.75
17	AT	32	TYR	N-CA-C	5.34	117.78	108.76
30	A6	47	THR	N-CA-C	-5.34	99.99	109.06
45	BL	39	VAL	CB-CA-C	-5.33	102.54	111.29
16	AS	43	GLU	N-CA-C	-5.33	105.55	111.36
1	AA	2045	G	O5'-P-OP1	-5.33	92.01	108.00
20	AW	101	SER	N-CA-C	5.33	118.25	109.72
1	AA	537	G	O4'-C1'-N9	5.33	116.19	108.20
5	AE	172	VAL	N-CA-CB	5.33	116.33	110.53
19	CV	15	GLU	CA-C-N	5.32	126.49	119.84
19	CV	15	GLU	C-N-CA	5.32	126.49	119.84
32	A8	40	GLU	N-CA-C	5.32	116.77	110.97
1	AA	184	A	P-O3'-C3'	5.31	128.17	120.20
38	DE	25	ARG	N-CA-C	5.31	116.70	107.93
13	AP	11	GLY	N-CA-C	5.31	122.42	115.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
50	DQ	9	VAL	N-CA-C	5.31	115.54	108.11
17	AT	58	ASN	N-CA-C	5.31	119.47	113.15
35	BB	160	ASP	N-CA-C	-5.31	106.48	113.17
38	BE	123	LEU	CA-CB-CG	-5.31	97.73	116.30
14	AQ	41	TRP	N-CA-C	-5.30	100.46	108.67
13	CP	96	THR	CA-C-N	5.29	125.36	119.32
13	CP	96	THR	C-N-CA	5.29	125.36	119.32
25	C1	86	SER	CA-C-N	5.29	124.74	119.24
25	C1	86	SER	C-N-CA	5.29	124.74	119.24
1	CA	195	A	P-O3'-C3'	5.29	128.14	120.20
43	DJ	52	GLY	CA-C-N	5.29	127.29	120.89
43	DJ	52	GLY	C-N-CA	5.29	127.29	120.89
57	DZ	-65	LYS	N-CA-C	-5.29	99.54	110.80
8	CH	153	LYS	CA-C-N	5.29	126.45	119.84
8	CH	153	LYS	C-N-CA	5.29	126.45	119.84
4	AD	109	ASP	N-CA-C	-5.28	102.04	109.96
17	CT	90	GLN	N-CA-C	5.28	116.43	108.46
39	DF	64	GLN	N-CA-C	-5.28	100.43	109.24
57	DZ	227	ILE	N-CA-C	-5.28	107.61	112.83
20	CW	61	ASN	CA-C-N	-5.27	114.38	122.60
20	CW	61	ASN	C-N-CA	-5.27	114.38	122.60
19	AV	61	VAL	CB-CA-C	5.27	117.94	111.25
34	BA	115	G	P-O3'-C3'	5.27	128.10	120.20
14	CQ	71	ASP	N-CA-C	-5.27	105.93	114.09
24	C0	32	ARG	N-CA-C	-5.27	101.97	110.14
38	BE	105	VAL	CA-C-N	-5.27	113.20	119.05
38	BE	105	VAL	C-N-CA	-5.27	113.20	119.05
7	AG	70	VAL	CA-C-N	-5.26	115.04	122.94
7	AG	70	VAL	C-N-CA	-5.26	115.04	122.94
1	AA	2536	G	OP1-P-O3'	-5.26	92.23	108.00
1	AA	2536	G	OP2-P-O3'	5.25	123.76	108.00
6	AF	154	VAL	N-CA-C	5.25	115.42	107.75
46	DM	122	LYS	N-CA-C	5.25	117.08	108.52
5	AE	182	LEU	N-CA-C	-5.25	100.34	108.90
5	AE	21	VAL	CB-CA-C	5.25	115.22	110.13
57	DZ	658	ASP	N-CA-C	-5.25	105.62	112.23
30	C6	40	CYS	CA-C-N	-5.24	114.69	121.04
30	C6	40	CYS	C-N-CA	-5.24	114.69	121.04
41	BH	80	ILE	CB-CA-C	-5.24	105.57	111.23
13	CP	60	MET	N-CA-C	-5.24	106.28	113.30
22	CY	42	VAL	N-CA-C	5.24	117.24	109.17
11	CN	78	TYR	CA-C-N	-5.24	114.38	119.78

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
11	CN	78	TYR	C-N-CA	-5.24	114.38	119.78
10	CL	121	GLU	N-CA-C	-5.24	107.06	113.50
42	DI	47	LEU	N-CA-C	-5.24	107.42	112.97
18	AU	30	LYS	CA-C-N	-5.23	116.04	122.84
18	AU	30	LYS	C-N-CA	-5.23	116.04	122.84
19	AV	57	VAL	N-CA-C	-5.23	100.58	108.12
35	BB	172	ILE	CB-CA-C	-5.23	102.71	111.29
22	CY	9	LYS	N-CA-C	-5.23	101.75	110.17
4	CD	168	ARG	N-CA-C	-5.23	100.87	109.40
17	CT	80	SER	CA-C-N	5.23	124.94	119.82
17	CT	80	SER	C-N-CA	5.23	124.94	119.82
57	BZ	281	PRO	N-CA-C	5.23	119.42	110.95
1	AA	1860	A	O5'-P-OP1	-5.22	92.33	108.00
52	DS	82	GLY	N-CA-C	5.22	119.54	111.08
1	AA	470	C	O5'-P-OP1	5.22	123.66	108.00
3	CC	68	GLY	N-CA-C	5.22	125.55	113.18
42	BI	48	GLU	CA-C-N	-5.22	114.37	119.64
42	BI	48	GLU	C-N-CA	-5.22	114.37	119.64
7	CG	141	PHE	CA-C-N	5.22	124.67	119.24
7	CG	141	PHE	C-N-CA	5.22	124.67	119.24
1	AA	985	G	O3'-P-O5'	5.21	111.82	104.00
1	AA	1680	G	OP1-P-O3'	-5.21	92.36	108.00
3	AC	68	GLY	N-CA-C	5.21	125.54	113.18
18	AU	48	ALA	N-CA-C	-5.21	105.77	111.82
3	CC	201	LYS	N-CA-C	-5.21	102.88	110.08
38	BE	122	GLU	CB-CA-C	-5.21	102.44	111.30
10	CL	23	VAL	N-CA-C	-5.21	106.35	111.77
21	AX	43	VAL	N-CA-C	-5.21	104.58	111.09
41	DH	75	ARG	CA-C-N	5.21	126.35	119.84
41	DH	75	ARG	C-N-CA	5.21	126.35	119.84
57	DZ	485	GLU	N-CA-C	5.21	117.11	109.24
23	CZ	129	SER	CA-C-N	5.21	125.01	119.28
23	CZ	129	SER	C-N-CA	5.21	125.01	119.28
13	AP	70	GLN	N-CA-C	5.20	116.89	109.14
20	CW	110	LYS	N-CA-C	-5.20	102.58	110.28
3	AC	201	LYS	N-CA-C	-5.20	102.91	110.08
16	AS	59	LYS	N-CA-C	5.20	121.87	110.80
9	CK	59	ILE	N-CA-C	-5.20	106.48	112.98
13	CP	128	HIS	N-CA-C	-5.20	107.11	113.50
46	BM	109	THR	N-CA-C	-5.20	106.63	113.12
8	AH	19	VAL	N-CA-C	5.19	116.28	109.58
22	AY	79	CYS	N-CA-C	5.19	119.46	113.18

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
50	DQ	10	VAL	CB-CA-C	-5.19	105.69	111.35
5	CE	172	VAL	CB-CA-C	-5.19	106.30	111.80
25	C1	7	ILE	CB-CA-C	-5.19	106.51	111.44
2	AB	27	C	OP1-P-O3'	-5.19	92.44	108.00
5	AE	152	LYS	N-CA-C	-5.19	102.93	110.24
1	AA	1686	U	O5'-P-OP2	-5.18	92.45	108.00
35	BB	186	ALA	N-CA-C	5.18	117.87	109.06
30	A6	6	ARG	CA-C-N	-5.18	116.62	122.48
30	A6	6	ARG	C-N-CA	-5.18	116.62	122.48
1	AA	797	A	O5'-P-OP1	5.18	123.53	108.00
49	BP	70	ALA	N-CA-C	-5.17	106.65	113.12
32	C8	52	LYS	N-CA-C	5.17	119.98	113.25
57	BZ	140	ASP	N-CA-C	-5.17	107.00	113.72
10	CL	85	GLU	N-CA-C	-5.17	108.00	114.56
31	C7	17	GLY	N-CA-C	5.16	118.01	112.33
14	AQ	55	VAL	N-CA-C	-5.16	105.51	110.72
57	BZ	472	VAL	N-CA-C	5.16	120.07	109.34
34	DA	1183	A	P-O3'-C3'	5.16	127.94	120.20
35	BB	188	ALA	N-CA-C	5.16	116.82	108.26
6	AF	157	VAL	N-CA-C	5.15	114.92	106.72
16	CS	83	LYS	N-CA-C	-5.15	101.92	109.81
28	C4	28	LYS	CA-C-N	5.15	124.95	119.28
28	C4	28	LYS	C-N-CA	5.15	124.95	119.28
13	AP	116	GLY	N-CA-C	5.15	123.94	115.34
38	BE	127	ASN	CA-C-N	5.15	124.33	118.97
38	BE	127	ASN	C-N-CA	5.15	124.33	118.97
1	AA	1249	A	O4'-C1'-N9	5.15	115.93	108.20
10	AL	112	MET	CA-C-N	-5.14	113.41	119.84
10	AL	112	MET	C-N-CA	-5.14	113.41	119.84
34	BA	1067	A	P-O3'-C3'	5.14	127.92	120.20
11	AN	26	LEU	N-CA-C	-5.14	105.31	112.45
35	BB	88	ALA	N-CA-C	-5.14	106.94	114.39
49	DP	5	ARG	N-CA-C	5.13	115.02	108.24
38	BE	35	GLY	N-CA-C	5.13	120.63	110.83
38	DE	113	ALA	N-CA-C	-5.13	105.92	113.61
21	CX	41	ASN	N-CA-C	5.13	116.87	111.28
42	BI	88	TYR	N-CA-C	-5.13	105.34	111.03
57	BZ	377	VAL	N-CA-C	5.13	115.29	108.11
29	A5	13	LYS	N-CA-C	-5.12	105.77	112.23
1	AA	1278	G	O5'-P-OP2	5.12	123.37	108.00
7	AG	28	VAL	CB-CA-C	-5.12	102.89	111.29
4	AD	147	LEU	N-CA-C	-5.12	107.69	114.04

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
40	DG	13	GLN	CA-C-N	5.12	126.24	119.84
40	DG	13	GLN	C-N-CA	5.12	126.24	119.84
50	DQ	62	SER	N-CA-C	5.12	116.85	109.07
32	A8	6	THR	CB-CA-C	-5.11	102.17	109.84
4	AD	60	ARG	N-CA-C	5.11	117.58	109.50
3	AC	46	ALA	CA-C-O	5.11	120.90	117.94
57	DZ	394	ALA	CA-C-N	-5.11	114.36	120.13
57	DZ	394	ALA	C-N-CA	-5.11	114.36	120.13
8	CH	117	PRO	CA-C-N	5.10	125.31	120.31
8	CH	117	PRO	C-N-CA	5.10	125.31	120.31
49	DP	70	ALA	N-CA-C	-5.10	105.89	112.68
37	BD	88	VAL	N-CA-C	5.10	115.68	107.98
11	AN	76	SER	N-CA-C	5.10	118.60	112.38
49	BP	3	LYS	N-CA-C	5.10	117.13	109.23
19	AV	12	TYR	N-CA-C	5.09	117.65	108.48
50	BQ	29	HIS	CA-C-N	5.09	126.20	119.84
50	BQ	29	HIS	C-N-CA	5.09	126.20	119.84
52	DS	16	LEU	N-CA-C	-5.09	105.43	111.69
1	AA	989	G	C3'-C2'-O2'	-5.09	103.07	110.70
14	AQ	77	LYS	CA-C-N	-5.09	114.71	119.85
14	AQ	77	LYS	C-N-CA	-5.09	114.71	119.85
18	CU	49	HIS	N-CA-C	-5.09	107.20	113.41
35	DB	129	GLU	N-CA-C	-5.08	107.03	113.18
5	AE	193	GLY	N-CA-C	-5.08	108.60	115.21
10	CL	72	PRO	CA-C-N	5.08	125.08	119.90
10	CL	72	PRO	C-N-CA	5.08	125.08	119.90
9	AK	89	ALA	N-CA-C	-5.08	107.11	113.15
1	AA	2701	U	C2'-C3'-O3'	5.08	117.12	109.50
1	AA	990	A	N9-C1'-C2'	5.07	121.61	114.00
34	BA	880	C	O5'-P-OP2	-5.07	92.78	108.00
6	CF	97	TYR	N-CA-C	-5.07	106.87	113.16
43	DJ	98	ILE	N-CA-C	5.07	115.58	108.17
16	AS	90	GLY	CA-C-N	5.07	126.00	120.83
16	AS	90	GLY	C-N-CA	5.07	126.00	120.83
45	DL	55	VAL	N-CA-C	5.07	114.88	107.88
11	AN	71	ILE	CB-CA-C	-5.07	103.56	110.96
50	DQ	63	ARG	CA-C-N	5.07	125.07	119.90
50	DQ	63	ARG	C-N-CA	5.07	125.07	119.90
5	CE	8	LYS	N-CA-C	-5.07	102.36	109.96
8	AH	140	LYS	N-CA-C	-5.06	105.85	112.23
6	CF	157	VAL	N-CA-C	5.06	115.14	107.75
1	AA	1814	A	O4'-C1'-N9	-5.06	100.91	108.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
22	CY	65	ALA	CA-C-N	5.05	126.16	119.84
22	CY	65	ALA	C-N-CA	5.05	126.16	119.84
28	A4	6	HIS	CA-C-N	5.05	126.15	119.84
28	A4	6	HIS	C-N-CA	5.05	126.15	119.84
35	BB	17	PHE	N-CA-C	5.05	121.56	110.80
57	BZ	608	VAL	N-CA-C	5.05	115.24	108.17
6	AF	196	LEU	N-CA-C	-5.05	106.63	112.89
5	AE	175	VAL	N-CA-C	5.05	115.39	108.12
1	AA	1338	U	O3'-P-O5'	-5.05	96.43	104.00
27	A3	50	VAL	CB-CA-C	-5.05	105.75	112.46
57	DZ	379	GLY	N-CA-C	-5.04	101.23	113.18
13	AP	96	THR	CA-C-N	-5.04	113.73	119.28
13	AP	96	THR	C-N-CA	-5.04	113.73	119.28
1	AA	875	U	OP1-P-O3'	-5.04	92.88	108.00
6	AF	24	LEU	CA-C-N	5.04	126.14	119.84
6	AF	24	LEU	C-N-CA	5.04	126.14	119.84
33	A9	15	LYS	N-CA-C	5.04	117.11	108.90
48	BO	39	LEU	N-CA-C	-5.04	105.87	111.36
1	AA	986	A	O5'-P-OP1	-5.03	92.90	108.00
1	AA	544	U	O3'-P-O5'	-5.03	96.45	104.00
13	AP	71	VAL	CB-CA-C	5.03	116.47	110.68
17	CT	5	ALA	N-CA-C	-5.03	105.88	111.36
38	DE	66	MET	N-CA-C	5.03	117.77	109.72
57	BZ	68	ALA	N-CA-C	5.03	117.42	111.33
21	CX	35	THR	N-CA-C	5.03	118.15	110.20
1	AA	986	A	O5'-P-OP2	5.03	123.08	108.00
7	CG	111	LEU	CA-C-N	-5.03	114.64	119.87
7	CG	111	LEU	C-N-CA	-5.03	114.64	119.87
35	DB	88	ALA	N-CA-C	-5.03	106.31	112.90
8	AH	35	VAL	CB-CA-C	-5.03	105.40	111.18
5	CE	137	HIS	CA-C-N	-5.03	113.56	119.84
5	CE	137	HIS	C-N-CA	-5.03	113.56	119.84
29	C5	10	LYS	CA-C-N	-5.02	114.44	121.72
29	C5	10	LYS	C-N-CA	-5.02	114.44	121.72
25	A1	91	LYS	N-CA-C	-5.02	105.94	111.71
57	BZ	104	ALA	CA-C-N	-5.02	116.47	122.90
57	BZ	104	ALA	C-N-CA	-5.02	116.47	122.90
37	BD	187	ARG	N-CA-C	5.02	116.59	108.26
56	BX	18	G	O3'-P-O5'	-5.02	96.47	104.00
17	CT	127	ALA	N-CA-C	-5.02	104.06	110.53
17	CT	128	GLU	N-CA-C	-5.02	105.82	112.24
57	DZ	655	TYR	N-CA-C	-5.01	106.33	112.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
18	CU	14	HIS	N-CA-C	-5.01	106.34	112.90
13	CP	9	ASN	CA-C-N	-5.00	114.60	119.76
13	CP	9	ASN	C-N-CA	-5.00	114.60	119.76
10	AL	31	GLY	N-CA-C	-5.00	106.17	114.48
18	CU	57	PHE	N-CA-C	5.00	116.42	111.07
38	BE	90	VAL	N-CA-C	5.00	115.17	107.77
46	BM	35	GLU	N-CA-C	-5.00	106.87	113.12
22	CY	96	ILE	CB-CA-C	-5.00	104.35	111.40

There are no chirality outliers.

All (16) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	AD	141	VAL	Peptide
4	AD	70	TRP	Peptide
4	AD	98	VAL	Peptide
5	AE	132	HIS	Sidechain
8	AH	23	ARG	Peptide
12	AO	80	ASP	Peptide
12	AO	81	ASP	Peptide
23	AZ	176	PRO	Peptide
37	BD	147	ALA	Peptide
53	BT	9	ASN	Peptide
57	BZ	404	VAL	Peptide
21	CX	93	GLU	Peptide
57	DZ	159	ALA	Peptide
57	DZ	87	HIS	Peptide
57	DZ	88	VAL	Peptide
57	DZ	91	THR	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	AA	61426	0	30938	1079	0
1	CA	61337	0	30928	1189	0
2	AB	2573	0	1306	32	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	CB	2573	0	1306	45	0
3	AC	1063	0	1089	156	0
3	CC	1063	0	1091	216	0
4	AD	2136	0	2218	113	0
4	CD	2142	0	2229	86	0
5	AE	1559	0	1618	68	0
5	CE	1559	0	1618	60	0
6	AF	1584	0	1625	70	0
6	CF	1580	0	1619	81	0
7	AG	1425	0	1443	65	0
7	CG	1424	0	1434	62	0
8	AH	1330	0	1407	47	0
8	CH	1330	0	1407	50	0
9	AK	641	0	309	22	0
9	CK	641	0	309	11	0
10	AL	1025	0	1066	54	0
10	CL	1025	0	1066	51	0
11	AN	1117	0	1184	34	0
11	CN	1117	0	1184	42	0
12	AO	933	0	996	37	0
12	CO	933	0	996	29	0
13	AP	1139	0	1223	54	0
13	CP	1135	0	1212	55	0
14	AQ	1122	0	1179	55	0
14	CQ	1122	0	1179	53	0
15	AR	968	0	1033	50	0
15	CR	968	0	1033	49	0
16	AS	877	0	938	46	0
16	CS	870	0	923	37	0
17	AT	1091	0	1151	55	0
17	CT	1083	0	1136	47	0
18	AU	959	0	1019	41	0
18	CU	959	0	1018	35	0
19	AV	771	0	829	22	0
19	CV	771	0	830	30	0
20	AW	886	0	940	27	0
20	CW	886	0	940	37	0
21	AX	750	0	814	30	0
21	CX	750	0	814	40	0
22	AY	806	0	881	26	0
22	CY	806	0	881	35	0
23	AZ	1451	0	1457	64	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
23	CZ	1451	0	1457	51	0
24	A0	653	0	674	21	0
24	C0	653	0	674	26	0
25	A1	755	0	826	34	0
25	C1	755	0	826	25	0
26	A2	588	0	643	15	0
26	C2	588	0	643	20	0
27	A3	469	0	518	26	0
27	C3	464	0	514	12	0
28	A4	558	0	545	29	0
28	C4	532	0	504	21	0
29	A5	455	0	466	20	0
29	C5	455	0	465	12	0
30	A6	453	0	473	20	0
30	C6	449	0	469	16	0
31	A7	418	0	467	24	0
31	C7	418	0	467	20	0
32	A8	517	0	582	30	0
32	C8	517	0	582	26	0
33	A9	307	0	335	15	0
33	C9	307	0	335	16	0
34	BA	32141	0	16222	669	0
34	DA	32268	0	16287	689	0
35	BB	1846	0	1867	101	0
35	DB	1825	0	1828	92	0
36	BC	1552	0	1546	55	0
36	DC	1544	0	1524	53	0
37	BD	1659	0	1677	97	0
37	DD	1678	0	1719	70	0
38	BE	1129	0	1185	56	0
38	DE	1133	0	1191	66	0
39	BF	812	0	804	29	0
39	DF	820	0	814	31	0
40	BG	1231	0	1238	38	0
40	DG	1235	0	1249	24	0
41	BH	1088	0	1126	56	0
41	DH	1088	0	1126	47	0
42	BI	986	0	995	38	0
42	DI	978	0	966	43	0
43	BJ	709	0	650	31	0
43	DJ	714	0	672	38	0
44	BK	833	0	836	34	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	DK	833	0	836	27	0
45	BL	930	0	980	25	0
45	DL	930	0	980	42	0
46	BM	923	0	970	33	0
46	DM	950	0	988	40	0
47	BN	492	0	529	19	0
47	DN	492	0	531	34	0
48	BO	728	0	760	37	0
48	DO	728	0	760	32	0
49	BP	681	0	697	36	0
49	DP	677	0	686	28	0
50	BQ	823	0	891	29	0
50	DQ	823	0	891	37	0
51	BR	555	0	618	20	0
51	DR	555	0	618	26	0
52	BS	661	0	675	34	0
52	DS	646	0	644	30	0
53	BT	728	0	798	36	0
53	DT	731	0	807	30	0
54	BU	199	0	208	5	0
54	DU	199	0	208	8	0
55	BV	277	0	140	4	0
55	DV	128	0	67	5	0
56	BX	1625	0	829	23	0
56	DX	1621	0	826	21	0
57	BZ	4869	0	4164	261	0
57	DZ	4867	0	4166	247	0
58	A0	5	0	0	0	0
58	A1	1	0	0	0	0
58	A2	1	0	0	0	0
58	A4	1	0	0	0	0
58	A5	3	0	0	0	0
58	A6	1	0	0	0	0
58	A7	5	0	0	0	0
58	A8	2	0	0	0	0
58	A9	1	0	0	0	0
58	AA	820	0	0	0	0
58	AB	23	0	0	0	0
58	AD	12	0	0	0	0
58	AE	5	0	0	0	0
58	AF	8	0	0	0	0
58	AG	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
58	AH	2	0	0	0	0
58	AN	3	0	0	0	0
58	AO	1	0	0	0	0
58	AP	3	0	0	0	0
58	AQ	3	0	0	0	0
58	AR	2	0	0	0	0
58	AU	3	0	0	0	0
58	AV	5	0	0	0	0
58	AW	4	0	0	0	0
58	AX	1	0	0	0	0
58	AZ	2	0	0	0	0
58	BA	212	0	0	0	0
58	BB	1	0	0	0	0
58	BD	1	0	0	0	0
58	BE	1	0	0	0	0
58	BF	1	0	0	0	0
58	BK	1	0	0	0	0
58	BL	4	0	0	0	0
58	BN	2	0	0	0	0
58	BT	1	0	0	0	0
58	BV	1	0	0	0	0
58	BX	10	0	0	0	0
58	BZ	1	0	0	0	0
58	C0	1	0	0	0	0
58	C1	1	0	0	0	0
58	C3	1	0	0	0	0
58	C7	1	0	0	0	0
58	C8	1	0	0	0	0
58	CA	666	0	0	0	0
58	CB	13	0	0	0	0
58	CD	3	0	0	0	0
58	CE	7	0	0	0	0
58	CF	4	0	0	0	0
58	CG	1	0	0	0	0
58	CN	1	0	0	0	0
58	CO	2	0	0	0	0
58	CQ	4	0	0	0	0
58	CR	1	0	0	0	0
58	CU	2	0	0	0	0
58	CV	2	0	0	0	0
58	CY	1	0	0	0	0
58	DA	166	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
58	DD	1	0	0	0	0
58	DE	2	0	0	0	0
58	DF	1	0	0	0	0
58	DJ	1	0	0	0	0
58	DK	1	0	0	0	0
58	DL	2	0	0	0	0
58	DT	1	0	0	0	0
58	DZ	3	0	0	0	0
59	AA	1	0	0	0	0
60	A4	1	0	0	0	0
60	A5	1	0	0	0	0
60	A6	1	0	0	0	0
60	A9	1	0	0	0	0
60	AY	1	0	0	0	0
60	BN	1	0	0	0	0
60	C4	1	0	0	0	0
60	C5	1	0	0	0	0
60	C6	1	0	0	0	0
60	C9	1	0	0	0	0
60	CY	1	0	0	0	0
60	DN	1	0	0	0	0
61	BD	8	0	0	0	0
61	DD	8	0	0	0	0
62	BZ	28	0	12	4	0
62	DZ	28	0	12	7	0
63	A0	9	0	0	2	0
63	A1	2	0	0	1	0
63	A2	1	0	0	0	0
63	A3	2	0	0	0	0
63	A5	4	0	0	1	0
63	A7	4	0	0	2	0
63	A8	9	0	0	3	0
63	A9	1	0	0	0	0
63	AA	1406	0	0	76	0
63	AB	37	0	0	3	0
63	AD	16	0	0	0	0
63	AE	14	0	0	3	0
63	AF	6	0	0	2	0
63	AG	3	0	0	0	0
63	AH	1	0	0	0	0
63	AN	3	0	0	0	0
63	AO	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
63	AP	18	0	0	1	0
63	AQ	5	0	0	1	0
63	AR	2	0	0	0	0
63	AS	1	0	0	0	0
63	AT	3	0	0	0	0
63	AU	4	0	0	0	0
63	AV	1	0	0	0	0
63	AW	1	0	0	0	0
63	AX	4	0	0	0	0
63	AZ	1	0	0	0	0
63	BA	203	0	0	15	0
63	BD	3	0	0	0	0
63	BE	2	0	0	0	0
63	BG	1	0	0	0	0
63	BJ	1	0	0	0	0
63	BL	1	0	0	0	0
63	BM	1	0	0	0	0
63	BO	2	0	0	0	0
63	BP	1	0	0	0	0
63	BV	3	0	0	0	0
63	BX	5	0	0	0	0
63	BZ	2	0	0	0	0
63	C0	5	0	0	0	0
63	C1	1	0	0	0	0
63	C3	2	0	0	0	0
63	C6	1	0	0	1	0
63	C7	1	0	0	0	0
63	C8	3	0	0	0	0
63	CA	974	0	0	87	0
63	CB	9	0	0	0	0
63	CD	17	0	0	0	0
63	CE	14	0	0	3	0
63	CF	6	0	0	0	0
63	CN	2	0	0	0	0
63	CP	12	0	0	2	0
63	CQ	2	0	0	1	0
63	CT	3	0	0	0	0
63	CU	2	0	0	1	0
63	CV	2	0	0	0	0
63	CW	1	0	0	0	0
63	CX	2	0	0	0	0
63	CY	2	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
63	DA	154	0	0	11	0
63	DE	3	0	0	0	0
63	DH	1	0	0	0	0
63	DJ	1	0	0	0	0
63	DK	2	0	0	0	0
63	DP	1	0	0	0	0
63	DT	1	0	0	0	0
63	DV	1	0	0	0	0
63	DZ	1	0	0	0	0
All	All	305548	0	205094	7474	0

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 (7474) 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)
1:CA:2128:C:H5"	3:CC:219:MET:CE	1.49	1.42
1:CA:2132:U:O2	3:CC:6:LYS:CB	1.64	1.41
1:CA:2128:C:OP1	3:CC:219:MET:CE	1.71	1.39
1:CA:2176:A:H4'	3:CC:45:HIS:CD2	1.60	1.37
1:AA:2143:G:N2	3:AC:169:THR:OG1	1.58	1.36
1:AA:2143:G:O4'	3:AC:168:LYS:NZ	1.59	1.35
1:CA:2121:G:N2	3:CC:169:THR:OG1	1.64	1.28
1:CA:2177:C:H1'	3:CC:171:ALA:CB	1.62	1.27
1:CA:2128:C:C5'	3:CC:219:MET:HE1	1.65	1.26
1:CA:2132:U:C2	3:CC:6:LYS:HB2	1.69	1.24
1:AA:2154:U:C5	3:AC:6:LYS:HB2	1.74	1.23
1:AA:2143:G:C1'	3:AC:168:LYS:HD3	1.67	1.23
1:CA:2121:G:O2'	3:CC:168:LYS:HB3	1.31	1.22
1:AA:2143:G:O4'	3:AC:168:LYS:CE	1.88	1.20
1:AA:2143:G:H1'	3:AC:168:LYS:CD	1.71	1.20
1:AA:2143:G:C1'	3:AC:168:LYS:CD	2.20	1.19
1:CA:2132:U:O2	3:CC:6:LYS:HB2	1.23	1.19
1:CA:2132:U:O2	3:CC:6:LYS:CA	1.92	1.15
1:CA:2177:C:H1'	3:CC:171:ALA:HB1	1.28	1.14
1:CA:2177:C:H4'	3:CC:46:ALA:O	1.48	1.13
1:CA:2124:G:H4'	3:CC:175:PRO:HG3	1.30	1.13
1:AA:2143:G:C1'	3:AC:168:LYS:CE	2.28	1.11
1:CA:2176:A:O2'	3:CC:45:HIS:ND1	1.85	1.09
57:BZ:210:ARG:HB2	57:BZ:210:ARG:HH11	1.16	1.08

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:DA:396:G:OP1	57:DZ:349:LYS:NZ	1.84	1.08
1:CA:2121:G:H1'	3:CC:168:LYS:CD	1.85	1.06
1:AA:2143:G:O2'	3:AC:168:LYS:HB3	1.55	1.06
1:CA:2132:U:H1'	3:CC:6:LYS:HB3	1.38	1.06
57:BZ:160:ARG:NH1	57:BZ:256:THR:OG1	1.90	1.04
1:AA:535:C:OP1	63:AA:3901:HOH:O	1.75	1.03
1:CA:2121:G:C1'	3:CC:168:LYS:HD3	1.87	1.03
1:CA:2177:C:H1'	3:CC:171:ALA:HB2	1.37	1.03
1:CA:2124:G:H4'	3:CC:175:PRO:CG	1.91	1.01
1:CA:1860:G:O4'	3:CC:206:LYS:HD3	1.56	1.00
1:CA:1860:G:O4'	3:CC:206:LYS:CD	2.01	1.00
1:AA:525:G:H22	1:AA:528:A:H5'	1.28	0.99
1:CA:1798:U:H5'	4:CD:259:THR:HG22	1.45	0.99
1:AA:2143:G:C1'	3:AC:168:LYS:HE2	1.92	0.99
34:BA:1502:A:H2	34:BA:1505:G:H1	1.02	0.99
39:DF:87:ARG:HH11	39:DF:87:ARG:HG3	1.27	0.98
1:AA:656:A:OP1	13:AP:65:ARG:NH1	1.96	0.98
1:AA:2154:U:C5	3:AC:6:LYS:CB	2.47	0.98
35:DB:185:ILE:HG22	35:DB:199:TYR:HB2	1.46	0.97
4:CD:60:ARG:HD3	4:CD:86:PRO:HB2	1.45	0.97
1:CA:2128:C:P	3:CC:219:MET:HE2	2.04	0.96
34:DA:1502:A:H2	34:DA:1505:G:H1	1.07	0.96
1:AA:2143:G:C2'	3:AC:168:LYS:HD3	1.96	0.96
1:CA:2176:A:O2'	3:CC:45:HIS:CG	2.17	0.96
1:CA:2176:A:C4'	3:CC:45:HIS:CD2	2.49	0.95
45:DL:36:VAL:HG11	57:DZ:425:SER:HB3	1.46	0.95
57:DZ:92:ILE:HG23	57:DZ:93:GLU:HG2	1.49	0.94
1:AA:1829:U:H5'	4:AD:259:THR:HG22	1.49	0.94
1:CA:2177:C:O2	3:CC:171:ALA:HB3	1.68	0.94
1:CA:2206:G:H3'	1:CA:2207:G:C8	2.02	0.94
1:AA:542:C:OP1	29:A5:16:ARG:NH2	2.00	0.93
1:CA:1056:G:HO2'	1:CA:1086:A:H8	1.00	0.93
1:CA:1332:G:OP1	63:CA:3702:HOH:O	1.86	0.93
1:AA:1740:U:O2'	4:AD:14:ARG:NH2	2.01	0.93
1:CA:731:C:OP2	63:CA:3701:HOH:O	1.85	0.93
34:DA:922:G:H4'	38:DE:20:GLN:HA	1.49	0.93
1:AA:1219:A:H1'	1:AA:1220:U:H5"	1.50	0.93
34:BA:78:G:H22	34:BA:92:C:H42	1.17	0.93
12:AO:49:ARG:NH2	34:BA:1423:G:OP1	2.02	0.93
1:CA:2120:G:H21	3:CC:168:LYS:HE2	1.34	0.92
1:CA:2121:G:O2'	3:CC:168:LYS:CB	2.17	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:2128:C:OP1	3:CC:219:MET:HE2	0.75	0.92
34:BA:559:A:OP1	38:BE:126:ARG:NH2	2.01	0.92
34:BA:1158:C:H5	34:BA:1181:G:H1	1.17	0.92
1:CA:400:G:N7	63:CA:3712:HOH:O	2.01	0.92
50:BQ:66:SER:O	50:BQ:70:ARG:NH1	2.01	0.92
7:AG:41:GLN:HG3	7:AG:60:LEU:HD21	1.49	0.91
1:CA:2124:G:C4'	3:CC:175:PRO:HG3	2.01	0.91
1:CA:1859:A:O2'	3:CC:206:LYS:HE3	1.68	0.91
1:CA:2176:A:O2'	3:CC:45:HIS:CE1	2.23	0.91
57:DZ:169:GLY:H	57:DZ:170:ARG:HH12	1.07	0.91
1:CA:1859:A:H2'	3:CC:206:LYS:CD	2.00	0.91
1:AA:2143:G:H1'	3:AC:168:LYS:CE	1.96	0.91
1:AA:2199:C:O2	3:AC:173:HIS:CE1	2.24	0.91
1:CA:1859:A:C2'	3:CC:206:LYS:CD	2.48	0.91
15:CR:97:VAL:HG22	15:CR:114:VAL:HG13	1.53	0.91
1:CA:1359:A:N1	1:CA:1372:U:N3	2.17	0.91
1:CA:1798:U:OP2	4:CD:274:ARG:NH2	2.03	0.90
1:CA:2177:C:O2	3:CC:171:ALA:CB	2.18	0.90
1:CA:2137:C:H42	1:CA:2154:G:H1	1.19	0.90
1:CA:631:A:OP1	13:CP:65:ARG:NH1	2.05	0.90
1:AA:894:U:OP2	63:AA:3903:HOH:O	1.90	0.90
1:CA:2132:U:O2	3:CC:6:LYS:HA	1.68	0.89
41:DH:51:VAL:HG11	41:DH:60:ARG:HH11	1.36	0.89
34:BA:167:G:H2'	34:BA:168:G:H8	1.36	0.89
57:DZ:357:ARG:NH1	57:DZ:373:ASP:OD1	2.06	0.89
34:BA:1182:G:H4'	34:BA:1183:A:H5'	1.54	0.89
1:CA:2177:C:C1'	3:CC:171:ALA:HB2	2.02	0.89
1:AA:1716:A:OP2	63:AA:3904:HOH:O	1.91	0.88
1:CA:1782:C:OP1	63:CA:3703:HOH:O	1.89	0.88
1:AA:1249:A:H2	1:AA:1287:A:H62	1.22	0.88
1:AA:839:G:O6	63:AA:3902:HOH:O	1.90	0.88
3:CC:31:LYS:NZ	3:CC:181:PHE:O	2.06	0.88
53:DT:57:ARG:HH22	53:DT:100:ILE:HD12	1.36	0.88
34:BA:1125:U:H4'	43:BJ:5:ARG:HH22	1.39	0.88
1:CA:2849:U:O4	17:CT:23:ARG:NH2	2.06	0.87
57:DZ:92:ILE:HD13	57:DZ:93:GLU:H	1.37	0.87
7:AG:41:GLN:NE2	7:AG:154:GLY:O	2.07	0.87
57:BZ:87:HIS:O	57:BZ:90:PHE:N	2.06	0.87
1:CA:1153:C:OP1	18:CU:92:ARG:NH1	2.07	0.87
1:AA:2143:G:O4'	3:AC:168:LYS:CD	2.21	0.87
20:CW:34:ASN:OD1	20:CW:37:ARG:NH2	2.08	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:2143:G:H1'	3:AC:168:LYS:CG	2.03	0.87
15:AR:33:ARG:NH1	15:AR:115:GLU:OE2	2.06	0.87
1:CA:1021:A:H62	1:CA:1141:U:H3	1.22	0.87
1:AA:1100:A:H62	1:AA:1151:U:H3	1.22	0.87
14:AQ:14:ARG:HG2	14:AQ:41:TRP:HH2	1.38	0.87
3:AC:31:LYS:NZ	3:AC:181:PHE:O	2.06	0.87
1:AA:2154:U:C6	3:AC:6:LYS:HB3	2.10	0.86
15:AR:86:ARG:NH1	15:AR:87:TYR:OH	2.08	0.86
1:CA:2714:G:OP2	63:CA:3704:HOH:O	1.93	0.86
34:DA:1307:U:OP1	46:DM:101:GLN:NE2	2.08	0.86
1:AA:2198:A:O2'	3:AC:45:HIS:CD2	2.29	0.86
1:CA:2121:G:C1'	3:CC:168:LYS:CD	2.51	0.86
34:BA:1375:A:H4'	40:BG:29:LYS:HE2	1.55	0.86
4:AD:85:ASP:OD2	4:AD:88:ARG:NH1	2.08	0.86
4:AD:206:LEU:HD22	4:AD:211:ARG:HG2	1.58	0.86
57:BZ:275:ALA:HA	57:BZ:278:ASP:HB2	1.57	0.86
38:DE:122:GLU:O	38:DE:126:ARG:NH1	2.09	0.86
34:BA:937:A:OP2	63:BA:3301:HOH:O	1.94	0.85
37:BD:98:GLU:OE1	37:BD:103:ASN:ND2	2.10	0.85
12:CO:7:TYR:HE1	12:CO:20:MET:HE3	1.39	0.85
34:DA:881:G:OP2	45:DL:12:ARG:NH2	2.09	0.85
3:AC:52:PRO:HG2	3:AC:53:ARG:HD3	1.57	0.85
13:CP:38:GLN:HG2	13:CP:45:LEU:H	1.39	0.85
15:CR:38:VAL:HG12	15:CR:42:LYS:HD2	1.58	0.85
1:AA:2143:G:O2'	3:AC:168:LYS:HD3	1.76	0.85
24:A0:11:ARG:O	24:A0:14:ARG:NH2	2.08	0.85
1:AA:1099:C:H2'	1:AA:1100:A:H5"	1.58	0.85
36:BC:58:GLU:HB3	43:BJ:92:THR:HG21	1.58	0.85
37:BD:13:ARG:NH1	37:BD:38:TYR:O	2.09	0.85
3:CC:52:PRO:HG2	3:CC:53:ARG:HD3	1.57	0.85
1:AA:2444:A:OP1	63:AA:3905:HOH:O	1.94	0.85
10:CL:101:TRP:HE1	10:CL:140:GLY:HA3	1.42	0.85
1:CA:195:A:N7	63:CA:3716:HOH:O	2.10	0.84
37:BD:107:ARG:HH22	37:BD:194:LEU:HD11	1.42	0.84
1:CA:1022:G:H22	1:CA:1142(A):A:H2	1.21	0.84
7:CG:38:VAL:HG22	7:CG:93:THR:HG23	1.59	0.84
1:AA:2459:G:OP2	63:AA:3907:HOH:O	1.94	0.84
7:AG:126:ASP:HB3	7:AG:128:ARG:H	1.41	0.84
41:BH:86:ILE:HG21	41:BH:133:LEU:HD13	1.57	0.84
57:BZ:191:ASP:O	57:BZ:266:ASN:ND2	2.09	0.84
1:CA:1859:A:N6	1:CA:1883:G:O2'	2.11	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:2121:G:H1'	3:CC:168:LYS:CE	2.07	0.84
34:DA:812:C:N3	63:DA:1806:HOH:O	2.09	0.84
1:CA:1648:C:OP1	63:CA:3705:HOH:O	1.95	0.84
1:CA:1913:A:H4'	1:CA:1914:C:H5'	1.60	0.84
45:DL:75:HIS:HD2	45:DL:77:LEU:H	1.20	0.84
1:CA:9:U:H3	1:CA:2629:A:H2	1.22	0.83
34:BA:1326:C:OP1	54:BU:12:LYS:NZ	2.10	0.83
1:CA:1859:A:C2'	3:CC:206:LYS:HE3	2.09	0.83
1:CA:2176:A:H4'	3:CC:45:HIS:NE2	1.93	0.83
1:CA:1310:G:OP2	31:C7:9:ARG:NH1	2.11	0.83
52:DS:15:LEU:HD22	52:DS:33:THR:HB	1.59	0.83
57:DZ:373:ASP:OD2	57:DZ:374:LEU:N	2.11	0.83
1:AA:327:U:O4	63:AA:3908:HOH:O	1.95	0.83
1:AA:615:G:O6	63:AA:3906:HOH:O	1.94	0.83
1:CA:2046:G:H5'	29:C5:19:ARG:HA	1.61	0.83
21:CX:35:THR:HG22	21:CX:37:THR:H	1.42	0.83
34:BA:200:G:H1	34:BA:217:C:H42	1.24	0.83
34:BA:429:U:OP2	37:BD:36:ARG:NH2	2.12	0.83
37:DD:13:ARG:NH1	37:DD:38:TYR:O	2.12	0.83
34:BA:456:C:H42	34:BA:475:G:H1	1.22	0.82
57:DZ:-66:MET:N	57:DZ:-46:VAL:O	2.12	0.82
35:BB:77:ALA:HB2	35:BB:211:ILE:HD13	1.60	0.82
57:BZ:210:ARG:HH11	57:BZ:210:ARG:CB	1.91	0.82
34:BA:1047:G:O2'	34:BA:1215:G:O2'	1.96	0.82
37:BD:187:ARG:NH2	37:BD:193:ASP:OD1	2.11	0.82
57:DZ:553:GLY:H	57:DZ:557:GLY:HA2	1.42	0.82
34:BA:881:G:OP2	45:BL:12:ARG:NH2	2.12	0.82
44:BK:99:GLN:HG2	44:BK:105:VAL:HG21	1.60	0.82
21:AX:31:HIS:HD2	21:AX:33:LYS:H	1.25	0.82
1:CA:2287:A:H62	1:CA:2344:U:H3	1.23	0.82
5:CE:127:ASP:OD2	63:CE:401:HOH:O	1.97	0.82
1:AA:2495:C:N3	14:AQ:124:LYS:NZ	2.27	0.82
1:CA:2660:A:N6	57:DZ:661:SER:OG	2.13	0.82
34:BA:167:G:H2'	34:BA:168:G:C8	2.14	0.82
14:AQ:38:GLU:HA	14:AQ:99:PRO:HG3	1.59	0.82
22:AY:92:ASN:HB2	22:AY:94:LYS:H	1.45	0.82
1:CA:1268:A:OP1	63:CA:3706:HOH:O	1.97	0.82
1:CA:2177:C:C1'	3:CC:171:ALA:CB	2.53	0.82
30:C6:10:LEU:HD23	30:C6:22:ALA:HB2	1.62	0.81
3:AC:54:ARG:NH2	3:AC:56:ASP:HB3	1.95	0.81
13:CP:95:VAL:HG23	13:CP:99:LEU:HD11	1.62	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:BA:437:U:H5'	37:BD:155:LEU:HD21	1.63	0.81
1:CA:526:A:OP1	63:CA:3707:HOH:O	1.98	0.81
2:CB:66:A:H61	2:CB:109:C:H5"	1.42	0.81
46:DM:15:VAL:HG13	46:DM:45:VAL:HG22	1.62	0.81
30:A6:13:CYS:SG	30:A6:47:THR:HG21	2.21	0.81
1:AA:39:C:O2	6:AF:46:ARG:NH2	2.14	0.81
2:AB:14:U:OP2	2:AB:70:C:O2'	1.98	0.81
3:CC:54:ARG:NH2	3:CC:56:ASP:HB3	1.95	0.81
1:AA:2154:U:C6	3:AC:6:LYS:CB	2.64	0.81
1:CA:861:A:N3	2:CB:79:C:O2'	2.14	0.81
1:CA:2128:C:C5'	3:CC:219:MET:CE	2.41	0.81
16:AS:52:SER:HB2	16:AS:55:ALA:H	1.44	0.81
20:AW:14:PRO:HG2	20:AW:78:GLU:HG2	1.61	0.81
1:CA:2847:U:O4	63:CA:3708:HOH:O	1.98	0.81
1:AA:818:G:OP1	31:A7:10:ARG:NH1	2.14	0.81
57:DZ:182:ARG:O	57:DZ:184:LYS:N	2.14	0.81
17:AT:118:ARG:HG3	17:AT:118:ARG:HH11	1.46	0.80
1:CA:2124:G:O3'	3:CC:175:PRO:CG	2.28	0.80
1:AA:9:U:H3	1:AA:2641:A:H2	1.28	0.80
1:AA:2349:G:OP1	63:AA:3911:HOH:O	1.99	0.80
13:AP:38:GLN:HG2	13:AP:45:LEU:HD23	1.62	0.80
1:CA:95:G:HO2'	26:C2:48:HIS:HD1	0.83	0.80
34:DA:1238:A:OP2	63:DA:1801:HOH:O	1.98	0.80
57:DZ:169:GLY:N	57:DZ:170:ARG:HH12	1.78	0.80
1:CA:2518:A:OP2	63:CA:3709:HOH:O	1.99	0.80
49:BP:71:ARG:O	49:BP:75:ARG:N	2.13	0.80
1:CA:1817:G:OP1	4:CD:88:ARG:NH2	2.14	0.80
10:CL:87:GLY:HA2	10:CL:134:MET:HE3	1.63	0.80
1:AA:553:A:H2'	1:AA:554:A:H5'	1.63	0.80
34:BA:946:A:O2'	34:BA:1333:A:N3	2.14	0.80
1:CA:1627:G:OP1	63:CA:3710:HOH:O	2.00	0.80
37:BD:187:ARG:NH1	37:BD:190:ASP:OD1	2.14	0.80
57:DZ:165:GLN:HA	57:DZ:180:VAL:HG13	1.64	0.80
1:AA:64:C:O2	1:AA:482:C:N4	2.16	0.79
1:AA:2143:G:C4'	3:AC:168:LYS:NZ	2.45	0.79
1:AA:2442:A:OP2	63:AA:3910:HOH:O	1.99	0.79
6:AF:31:HIS:NE2	6:AF:35:GLU:OE2	2.16	0.79
34:BA:664:G:H22	34:BA:741:G:H1	1.30	0.79
44:BK:79:SER:HA	44:BK:104:GLN:HB2	1.63	0.79
34:DA:839:U:H5"	34:DA:840:C:H5	1.47	0.79
34:DA:1320:C:N3	52:DS:36:ARG:NH2	2.30	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:DD:187:ARG:NH2	37:DD:193:ASP:OD2	2.14	0.79
36:BC:19:GLU:HB3	36:BC:40:ARG:HH22	1.47	0.79
1:CA:1093:G:H1'	1:CA:1099:G:H22	1.47	0.79
1:CA:2357:U:OP1	24:C0:20:ARG:NH1	2.16	0.79
14:CQ:21:THR:HG21	14:CQ:101:ARG:HD3	1.64	0.79
37:DD:121:VAL:HG22	37:DD:126:ILE:HG13	1.65	0.79
57:BZ:246:ILE:HG23	57:BZ:255:ILE:HD11	1.63	0.79
34:DA:656:C:O2'	48:DO:28:GLN:NE2	2.16	0.79
1:AA:2143:G:O4'	3:AC:168:LYS:HD3	1.81	0.79
22:AY:54:LYS:HA	22:AY:56:PRO:HD3	1.63	0.79
36:BC:153:VAL:HG22	36:BC:198:VAL:HG22	1.65	0.79
49:BP:67:THR:HG22	49:BP:69:THR:H	1.47	0.79
1:CA:555:U:O2'	1:CA:556:G:N7	2.14	0.79
34:DA:1129:C:H42	34:DA:1143:G:H1	1.31	0.79
14:AQ:10:ARG:NH1	63:AQ:301:HOH:O	2.05	0.79
23:AZ:53:ILE:HG22	23:AZ:71:VAL:HG12	1.65	0.79
57:BZ:-53:ASP:H	57:BZ:-50:GLN:HE21	1.30	0.79
1:AA:1117:G:O2'	1:AA:1135:G:OP2	2.01	0.79
1:AA:2418:U:OP1	63:AA:3909:HOH:O	1.99	0.79
1:AA:1657:C:OP1	63:AA:3912:HOH:O	2.01	0.79
57:BZ:91:THR:OG1	57:BZ:124:GLN:NE2	2.16	0.79
1:AA:1135:G:N2	1:AA:1147:U:O4	2.15	0.79
34:BA:166:G:H2'	34:BA:167:G:H8	1.47	0.79
34:BA:564:C:O2'	41:BH:91:ARG:NH2	2.16	0.79
34:BA:1304:G:OP2	63:BA:3302:HOH:O	1.99	0.79
1:AA:1848:G:OP1	4:AD:62:TYR:OH	1.99	0.78
1:AA:2199:C:O2	3:AC:173:HIS:HE1	1.66	0.78
17:CT:55:ASN:H	17:CT:59:THR:HG22	1.47	0.78
34:DA:1224:G:OP1	63:DA:1802:HOH:O	2.01	0.78
34:BA:1458:G:H5"	53:BT:31:SER:HB3	1.65	0.78
37:BD:167:GLY:H	37:BD:168:ARG:HH12	1.31	0.78
50:BQ:6:LEU:HD23	50:BQ:23:VAL:HG11	1.63	0.78
1:AA:1151:U:H2'	1:AA:1152:G:H8	1.48	0.78
14:AQ:111:GLU:OE1	14:AQ:133:ARG:NH2	2.16	0.78
34:DA:512:U:H2'	34:DA:513:C:H6	1.48	0.78
57:BZ:264:LEU:HB2	62:BZ:801:GDP:C6	2.19	0.78
34:DA:891:U:OP2	63:DA:1803:HOH:O	2.02	0.78
15:AR:100:LEU:HB2	15:AR:111:LEU:O	1.84	0.78
34:DA:590:C:H2'	34:DA:591:U:H6	1.48	0.78
1:AA:553:A:C8	1:AA:553:A:H3'	2.18	0.78
1:AA:1831:C:OP1	4:AD:260:ARG:NH2	2.17	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:BZ:247:ARG:HG3	57:BZ:279:TYR:HA	1.65	0.78
1:CA:184:C:H2'	1:CA:185:U:C6	2.18	0.78
57:DZ:170:ARG:N	57:DZ:170:ARG:HH11	1.82	0.78
63:AA:3928:HOH:O	15:AR:3:HIS:NE2	2.17	0.78
57:BZ:14:ASN:HB2	57:BZ:102:ASP:OD2	1.84	0.78
1:CA:1019:U:H3	1:CA:1142(A):A:H62	1.29	0.78
1:CA:847:U:OP2	63:CA:3711:HOH:O	2.00	0.78
3:CC:20:VAL:O	3:CC:21:TYR:HB2	1.83	0.78
34:DA:1004:A:H62	34:DA:1037:C:H2'	1.48	0.78
1:AA:153:C:OP2	25:A1:92:LYS:NZ	2.16	0.77
20:CW:33:ARG:NH2	20:CW:52:GLU:OE1	2.17	0.77
48:DO:4:THR:OG1	48:DO:7:GLU:OE1	2.01	0.77
1:AA:11:G:H2'	1:AA:12:U:H5"	1.66	0.77
1:AA:1094:A:OP2	1:AA:1155:C:N4	2.16	0.77
7:AG:161:THR:HG23	7:AG:163:ALA:H	1.49	0.77
43:BJ:35:SER:HB3	43:BJ:73:ASP:HB2	1.64	0.77
1:CA:302:C:N4	1:CA:315:G:O6	2.17	0.77
1:CA:2128:C:H5"	3:CC:219:MET:HE1	0.78	0.77
34:DA:278:G:OP2	50:DQ:41:LYS:NZ	2.18	0.77
1:AA:1087:C:H42	1:AA:1160:G:H1	1.33	0.77
18:CU:50:ARG:NH1	19:CV:71:LEU:O	2.18	0.77
34:DA:266:G:H5"	34:DA:268:C:H41	1.49	0.77
1:AA:482:C:O2'	21:AX:68:ARG:NH1	2.16	0.77
1:AA:868:A:H2'	1:AA:991:G:H5"	1.66	0.77
23:AZ:119:GLU:OE1	23:AZ:122:ARG:NH1	2.17	0.77
11:CN:21:LYS:HD3	11:CN:26:LEU:HD13	1.67	0.77
57:BZ:114:VAL:HG23	57:BZ:152:THR:HB	1.66	0.77
22:AY:102:CYS:SG	22:AY:103:GLY:N	2.56	0.77
33:A9:2:LYS:HE2	33:A9:31:LYS:O	1.85	0.77
20:CW:12:ILE:HD13	20:CW:17:VAL:HG13	1.67	0.77
3:AC:20:VAL:O	3:AC:21:TYR:HB2	1.83	0.77
3:AC:24:ASP:O	3:AC:28:ARG:HG3	1.85	0.77
1:CA:1423:G:N7	63:CA:3746:HOH:O	2.17	0.77
37:DD:129:ASN:HD21	37:DD:144:ASP:HA	1.47	0.77
37:BD:127:THR:HG23	37:BD:147:ALA:HB3	1.66	0.77
37:BD:167:GLY:H	37:BD:168:ARG:NH1	1.82	0.77
1:AA:434:G:N2	1:AA:447:C:O2	2.17	0.77
1:AA:1718:U:O4	63:AA:3904:HOH:O	2.02	0.77
34:BA:504:C:OP1	63:BA:3303:HOH:O	2.02	0.77
1:AA:1001:G:OP2	14:AQ:14:ARG:NH2	2.18	0.76
16:AS:11:LYS:HG3	16:AS:91:PRO:HD3	1.66	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:BA:164:U:H2'	34:BA:165:C:C6	2.20	0.76
1:CA:309:G:N3	1:CA:329:G:O2'	2.18	0.76
1:CA:397:G:N7	63:CA:3745:HOH:O	2.17	0.76
1:CA:2499:C:OP2	63:CA:3713:HOH:O	2.03	0.76
18:CU:76:TYR:OH	18:CU:92:ARG:NH1	2.18	0.76
1:AA:2143:G:H1'	3:AC:168:LYS:HE2	1.60	0.76
15:AR:67:LEU:HD13	15:AR:76:VAL:HG21	1.67	0.76
34:BA:881:G:P	45:BL:12:ARG:HH22	2.08	0.76
1:AA:1462:G:N2	1:AA:1629:C:O2	2.16	0.76
9:AK:73:GLY:O	9:AK:75:GLN:N	2.18	0.76
1:CA:601:C:OP1	6:CF:108:LYS:NZ	2.18	0.76
3:CC:24:ASP:O	3:CC:28:ARG:HG3	1.85	0.76
36:DC:122:GLU:O	36:DC:126:ARG:NH1	2.18	0.76
3:AC:27:ALA:O	3:AC:30:VAL:HG22	1.85	0.76
1:CA:11:G:H2'	1:CA:12:U:H5"	1.67	0.76
3:CC:27:ALA:O	3:CC:30:VAL:HG22	1.85	0.76
1:CA:336:C:HO2'	22:CY:35:TYR:HH	1.32	0.76
1:AA:2390:A:H4'	16:AS:23:ARG:NH1	2.00	0.76
1:AA:2643:G:N2	1:AA:2800:C:O2	2.15	0.76
37:BD:41:GLY:O	37:BD:43:HIS:N	2.15	0.76
1:CA:1689:A:H62	1:CA:1698:A:H2	1.34	0.76
1:CA:2317:C:N4	1:CA:2318:G:O6	2.19	0.76
1:AA:9:U:N3	1:AA:2641:A:H2	1.84	0.76
1:AA:1090:G:O2'	1:AA:1157:A:N6	2.19	0.76
57:BZ:210:ARG:HB2	57:BZ:210:ARG:NH1	2.00	0.76
34:DA:117:G:OP2	63:DA:1804:HOH:O	2.04	0.76
21:CX:60:ARG:HH22	31:C7:47:ARG:HH22	1.33	0.76
24:C0:11:ARG:O	24:C0:14:ARG:NH2	2.19	0.76
1:AA:2287:C:H6	1:AA:2287:C:H5'	1.50	0.75
14:AQ:14:ARG:HG2	14:AQ:41:TRP:CH2	2.22	0.75
25:A1:34:THR:HG22	25:A1:36:GLY:H	1.49	0.75
1:CA:1336:A:OP2	21:CX:64:LYS:NZ	2.19	0.75
10:CL:100:THR:HA	10:CL:139:VAL:HB	1.67	0.75
44:DK:22:HIS:HB3	44:DK:29:ILE:HB	1.68	0.75
40:BG:111:ARG:NH2	40:BG:126:ASP:OD2	2.19	0.75
57:BZ:182:ARG:O	57:BZ:184:LYS:N	2.19	0.75
1:CA:1754:C:OP1	17:CT:96:ARG:NH1	2.20	0.75
27:A3:39:ASP:OD2	27:A3:44:ARG:NH2	2.18	0.75
1:CA:1056:G:H4'	1:CA:1086:A:N7	2.02	0.75
4:CD:206:LEU:HD22	4:CD:211:ARG:HG2	1.69	0.75
7:CG:113:ARG:NH1	7:CG:139:LEU:O	2.19	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:DK:48:ILE:O	44:DK:50:TYR:N	2.19	0.75
8:AH:7:LEU:HD12	8:AH:8:PRO:HD2	1.68	0.75
37:DD:57:ARG:NH2	37:DD:205:GLU:OE2	2.15	0.75
1:AA:185:A:H62	13:AP:38:GLN:HE22	1.33	0.75
1:AA:2007:G:OP2	63:AA:3913:HOH:O	2.02	0.75
12:AO:64:ARG:NH1	12:AO:81:ASP:OD1	2.19	0.75
1:CA:370:G:N7	63:CA:3749:HOH:O	2.19	0.75
1:CA:2022:U:OP1	63:CA:3714:HOH:O	2.04	0.75
13:CP:39:LYS:HA	13:CP:45:LEU:HG	1.68	0.75
17:AT:54:ARG:HA	17:AT:59:THR:HB	1.66	0.75
57:BZ:13:ARG:NH1	57:BZ:280:LEU:O	2.19	0.75
1:CA:2850:A:N7	1:CA:2868:A:O2'	2.20	0.75
1:AA:403:C:OP1	63:AA:3914:HOH:O	2.04	0.75
1:CA:528:A:N1	1:CA:2042:A:H2'	2.02	0.75
6:CF:157:VAL:HG13	6:CF:176:LEU:HB3	1.69	0.75
7:AG:138:GLN:HE22	7:AG:153:ARG:HH21	1.35	0.75
53:DT:56:MET:HE1	53:DT:85:MET:HG2	1.69	0.75
17:CT:18:ASP:N	17:CT:18:ASP:OD1	2.20	0.74
34:DA:979:C:O2	47:DN:19:ARG:NE	2.15	0.74
6:AF:18:ARG:NH2	6:AF:127:GLU:OE1	2.20	0.74
34:BA:738:C:H2'	34:BA:739:C:H6	1.52	0.74
1:CA:2178:C:OP1	3:CC:47:LYS:HG2	1.87	0.74
43:BJ:61:GLU:OE2	47:BN:45:ARG:NE	2.19	0.74
56:BX:36:U:H1'	57:BZ:503:GLY:H	1.52	0.74
1:CA:1315:C:OP2	63:CA:3702:HOH:O	2.04	0.74
1:CA:1446:C:H42	1:CA:1465:G:H1	1.33	0.74
34:DA:1417:G:O6	63:DA:1805:HOH:O	2.05	0.74
34:BA:148:G:H1	34:BA:174:C:H42	1.35	0.74
34:DA:959:A:O2'	34:DA:984:C:O2'	2.06	0.74
40:DG:151:TYR:OH	44:DK:54:ARG:NH1	2.20	0.74
1:CA:2120:G:N2	3:CC:168:LYS:HE2	2.02	0.74
7:CG:136:ARG:HH11	7:CG:137:GLU:H	1.34	0.74
28:C4:40:HIS:HB3	28:C4:43:TYR:HB2	1.69	0.74
1:AA:121:G:OP2	63:AA:3916:HOH:O	2.06	0.74
35:BB:16:HIS:HB2	35:BB:204:ASN:HB3	1.70	0.74
47:BN:48:ALA:HB2	47:BN:53:LEU:HD12	1.70	0.74
35:DB:69:LEU:HB3	35:DB:162:ILE:HG22	1.68	0.74
1:AA:717:A:O2'	63:AA:3915:HOH:O	2.05	0.74
34:BA:1417:G:H22	34:BA:1482:G:H2'	1.53	0.74
34:BA:1502:A:H2	34:BA:1505:G:N1	1.83	0.74
12:CO:63:VAL:HG12	12:CO:106:LEU:HD11	1.69	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:BA:1303:C:OP1	63:BA:3302:HOH:O	2.05	0.74
37:DD:165:MET:SD	37:DD:168:ARG:NH1	2.57	0.74
3:CC:48:LEU:HB3	3:CC:50:ILE:HD12	1.70	0.73
14:CQ:58:PHE:O	14:CQ:60:ARG:N	2.21	0.73
6:AF:75:HIS:ND1	63:AF:402:HOH:O	2.20	0.73
57:BZ:225:GLU:HA	57:BZ:228:MET:HB3	1.69	0.73
35:DB:16:HIS:CG	35:DB:17:PHE:H	2.06	0.73
36:DC:180:ALA:HB1	36:DC:182:ILE:HG13	1.70	0.73
1:AA:1065:U:HO2'	1:AA:1067:A:H2	1.35	0.73
57:BZ:169:GLY:O	57:BZ:173:THR:OG1	2.05	0.73
1:CA:2121:G:H1'	3:CC:168:LYS:HE2	1.68	0.73
10:CL:76:TYR:HD1	10:CL:79:ARG:HH21	1.36	0.73
41:DH:10:LEU:HD22	41:DH:83:ILE:HD11	1.70	0.73
20:AW:18:ARG:NH1	20:AW:76:VAL:O	2.20	0.73
1:CA:1434:A:H61	1:CA:1558:A:H62	1.36	0.73
34:DA:44:G:N2	34:DA:398:C:O2	2.18	0.73
46:DM:82:MET:HE2	46:DM:92:HIS:HB3	1.69	0.73
6:AF:89:VAL:O	63:AF:401:HOH:O	2.07	0.73
57:BZ:329:ARG:HB2	57:BZ:374:LEU:HG	1.69	0.73
1:CA:2107:C:H42	1:CA:2182:G:H1	1.35	0.73
1:AA:607:C:O2	1:AA:1302:G:N2	2.19	0.73
1:CA:198:C:OP2	63:CA:3716:HOH:O	2.07	0.73
46:DM:33:ALA:HA	46:DM:59:TYR:HE2	1.53	0.73
57:BZ:388:THR:OG1	57:BZ:399:LEU:N	2.13	0.73
1:CA:2120:G:H21	3:CC:168:LYS:CE	2.00	0.73
1:CA:2132:U:H1'	3:CC:6:LYS:CB	2.18	0.73
3:CC:55:SER:O	3:CC:57:GLN:N	2.22	0.73
1:AA:2143:G:H1'	3:AC:168:LYS:HG2	1.69	0.73
34:BA:1503:A:O2'	55:BV:13:A:N1	2.21	0.73
1:CA:2132:U:O2	3:CC:6:LYS:HB3	1.86	0.73
5:CE:9:VAL:HG23	17:CT:3:ARG:HG2	1.71	0.73
9:CK:73:GLY:O	9:CK:75:GLN:N	2.18	0.73
35:BB:16:HIS:O	35:BB:18:GLY:N	2.20	0.73
34:DA:1189:C:OP1	43:DJ:51:ARG:NH2	2.22	0.73
1:AA:345:G:OP1	6:AF:135:LYS:NZ	2.19	0.73
1:AA:611:U:H2'	1:AA:612:C:C6	2.24	0.73
24:A0:18:ALA:HB3	24:A0:20:ARG:HH21	1.53	0.73
1:CA:530:G:N1	63:CA:3714:HOH:O	2.22	0.73
1:CA:1054:A:O2'	9:CK:30:GLN:O	2.05	0.73
1:CA:1062:G:N3	10:CL:133:SER:OG	2.17	0.73
1:CA:2206:G:H3'	1:CA:2207:G:H8	1.53	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:CL:88:ALA:O	10:CL:90:LYS:N	2.22	0.73
24:C0:10:THR:HG22	24:C0:12:ASN:H	1.54	0.73
39:DF:50:TYR:CE2	51:DR:77:GLY:HA2	2.24	0.73
3:AC:48:LEU:HB3	3:AC:50:ILE:HD12	1.70	0.72
17:CT:97:ALA:O	17:CT:98:LYS:NZ	2.21	0.72
22:CY:87:LYS:HD2	22:CY:95:LYS:HD2	1.70	0.72
1:AA:2143:G:C4'	3:AC:168:LYS:HD3	2.19	0.72
1:CA:1237:A:OP1	63:CA:3719:HOH:O	2.08	0.72
17:AT:55:ASN:H	17:AT:59:THR:HG22	1.54	0.72
34:DA:976:G:OP2	34:DA:1358:U:O2'	2.05	0.72
38:DE:131:ILE:O	38:DE:135:THR:OG1	2.05	0.72
57:DZ:187:THR:HB	57:DZ:199:ILE:HD11	1.71	0.72
1:AA:1480:A:H61	1:AA:1605:A:H62	1.34	0.72
1:AA:1533:G:N2	1:AA:1548:C:O2	2.19	0.72
1:AA:2476:C:H1'	63:AA:4446:HOH:O	1.89	0.72
2:AB:13:A:N1	2:AB:69:G:O2'	2.23	0.72
1:CA:2615:U:OP2	63:CA:3715:HOH:O	2.06	0.72
34:DA:1137:C:O2'	34:DA:1138:G:N2	2.22	0.72
35:DB:16:HIS:CD2	35:DB:17:PHE:H	2.07	0.72
57:BZ:-34:ARG:HG3	57:BZ:-32:LEU:HG	1.70	0.72
1:CA:2124:G:O3'	3:CC:175:PRO:HG3	1.89	0.72
1:AA:1055:A:OP2	11:AN:37:LYS:NZ	2.23	0.72
34:BA:1296:C:OP1	46:BM:44:ARG:NH2	2.21	0.72
34:BA:1320:C:OP1	52:BS:70:LYS:NZ	2.22	0.72
57:BZ:122:TRP:HH2	57:BZ:256:THR:HG1	1.36	0.72
1:CA:2307:G:N1	7:CG:43:LEU:O	2.23	0.72
22:CY:29:GLU:HB3	22:CY:38:ILE:HG13	1.69	0.72
34:DA:473:G:H2'	34:DA:474:G:H8	1.55	0.72
1:AA:2448:G:O6	63:AA:3918:HOH:O	2.07	0.72
36:BC:45:LYS:HD3	36:BC:46:GLU:HG2	1.71	0.72
1:CA:1064:C:H4'	10:CL:89:HIS:HA	1.72	0.72
1:CA:1095:A:O4'	57:DZ:618:GLY:HA2	1.90	0.72
57:DZ:88:VAL:O	57:DZ:91:THR:N	2.23	0.72
1:AA:2859:U:O4	17:AT:23:ARG:NH2	2.22	0.72
1:CA:1056:G:H4'	1:CA:1086:A:C8	2.24	0.72
57:DZ:167:PRO:O	57:DZ:170:ARG:NH2	2.23	0.72
1:AA:629:U:OP1	63:AA:3919:HOH:O	2.08	0.72
1:AA:2154:U:C4	3:AC:6:LYS:HB2	2.25	0.72
1:CA:1183:G:O2'	27:C3:29:ARG:NH1	2.23	0.72
1:CA:2286:A:H4'	1:CA:2287:A:O4'	1.90	0.72
6:CF:53:THR:HB	6:CF:56:GLU:OE2	1.89	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:931:C:N4	1:AA:938:G:O6	2.19	0.72
57:BZ:-53:ASP:H	57:BZ:-50:GLN:NE2	1.88	0.72
23:CZ:45:ASP:OD1	23:CZ:49:ARG:NH1	2.23	0.72
57:DZ:92:ILE:O	57:DZ:94:VAL:N	2.23	0.72
32:A8:29:LYS:HB2	32:A8:33:ASN:HD21	1.55	0.71
34:BA:735:C:H2'	34:BA:736:C:H6	1.55	0.71
34:DA:838:G:H1	34:DA:848:C:H42	1.37	0.71
35:BB:201:ILE:HG21	35:BB:214:ILE:HG21	1.71	0.71
34:DA:687:A:O2'	34:DA:701:C:N4	2.23	0.71
1:AA:1549:U:H2'	1:AA:1550:C:H6	1.54	0.71
21:AX:31:HIS:CD2	21:AX:33:LYS:H	2.07	0.71
35:DB:189:ASP:OD1	35:DB:189:ASP:N	2.23	0.71
57:DZ:97:SER:HA	57:DZ:100:VAL:HG12	1.73	0.71
1:CA:2124:G:C3'	3:CC:175:PRO:HG3	2.21	0.71
1:CA:2132:U:C1'	3:CC:6:LYS:HB3	2.16	0.71
16:CS:27:SER:HA	16:CS:88:ASP:HB3	1.72	0.71
34:DA:596:C:O2	34:DA:644:G:N2	2.18	0.71
1:AA:560:C:O3'	18:AU:53:ARG:NH1	2.22	0.71
10:AL:17:ALA:HB3	10:AL:38:VAL:HG13	1.71	0.71
1:CA:1859:A:C2'	3:CC:206:LYS:CE	2.68	0.71
3:CC:51:ASP:HB3	3:CC:57:GLN:OE1	1.91	0.71
57:DZ:285:ASP:OD2	57:DZ:285:ASP:N	2.17	0.71
1:AA:920:G:O6	1:AA:950:C:N4	2.19	0.71
25:A1:3:LYS:HG2	25:A1:4:VAL:HG23	1.72	0.71
1:CA:1300:U:H4'	1:CA:1301:A:H5'	1.72	0.71
12:CO:2:ILE:HD12	12:CO:6:THR:HG21	1.72	0.71
34:DA:1502:A:H2	34:DA:1505:G:N1	1.87	0.71
46:DM:25:ILE:HG13	46:DM:29:ARG:HG2	1.70	0.71
34:BA:826:C:O2	41:BH:15:ASN:ND2	2.23	0.71
48:BO:26:GLU:OE2	48:BO:77:ARG:NE	2.18	0.71
56:BX:37:A:H5'	57:BZ:500:GLN:O	1.91	0.71
1:CA:855:G:O2'	24:C0:27:GLU:OE2	2.09	0.71
45:DL:75:HIS:CD2	45:DL:77:LEU:H	2.07	0.71
7:AG:15:VAL:HG22	7:AG:175:LEU:HB3	1.73	0.71
34:BA:1305:G:H22	34:BA:1331:G:H1'	1.54	0.71
40:BG:111:ARG:NH1	40:BG:113:GLU:OE2	2.22	0.71
8:CH:113:VAL:HG11	8:CH:151:ILE:HG21	1.72	0.71
21:CX:35:THR:HB	21:CX:38:GLU:HB2	1.70	0.71
1:AA:1426:G:OP2	63:AA:3917:HOH:O	2.07	0.71
2:AB:22:U:O4	63:AB:3101:HOH:O	2.09	0.71
4:AD:69:ARG:NH2	4:AD:128:GLY:O	2.24	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1333:C:OP2	63:CA:3720:HOH:O	2.08	0.71
8:CH:38:SER:HB3	8:CH:41:MET:HG2	1.73	0.71
34:DA:932:C:H2'	34:DA:933:G:H8	1.55	0.71
7:AG:41:GLN:HE22	7:AG:153:ARG:HB3	1.57	0.70
1:CA:2038:G:O6	63:CA:3721:HOH:O	2.09	0.70
52:DS:15:LEU:HG	52:DS:18:LYS:HD3	1.72	0.70
53:DT:56:MET:HE3	53:DT:84:LEU:HD13	1.72	0.70
1:AA:1749:G:N7	63:AA:3954:HOH:O	2.25	0.70
32:A8:6:THR:HB	32:A8:8:LYS:HE2	1.73	0.70
10:CL:78:ILE:HD12	10:CL:127:ILE:HG22	1.74	0.70
34:DA:590:C:H2'	34:DA:591:U:C6	2.26	0.70
34:DA:986:A:N3	52:DS:52:TYR:OH	2.22	0.70
40:DG:113:GLU:HB2	40:DG:119:ARG:HG2	1.74	0.70
1:AA:427:G:N7	63:AA:3952:HOH:O	2.24	0.70
5:AE:179:GLU:HB3	5:AE:181:LEU:HD22	1.72	0.70
7:AG:143:GLU:O	28:A4:28:LYS:NZ	2.23	0.70
1:CA:2839:G:O2'	15:CR:49:ASP:OD2	2.08	0.70
2:CB:62:C:H2'	2:CB:63:G:H8	1.55	0.70
34:DA:369:C:OP2	34:DA:388:G:N2	2.23	0.70
34:BA:406:G:N3	37:BD:119:GLN:NE2	2.40	0.70
34:BA:1289:A:N1	34:BA:1371:G:O2'	2.21	0.70
35:BB:212:GLN:NE2	35:BB:234:PRO:O	2.24	0.70
34:DA:691:G:H2'	34:DA:692:U:C6	2.26	0.70
1:AA:2143:G:O2'	3:AC:168:LYS:CB	2.38	0.70
1:AA:2735:G:OP2	63:AA:3920:HOH:O	2.09	0.70
34:BA:933:G:O6	40:BG:3:ARG:NH2	2.25	0.70
1:CA:1637:A:OP2	63:CA:3717:HOH:O	2.07	0.70
1:CA:2448:A:N1	63:CA:3768:HOH:O	2.24	0.70
57:DZ:222:ASP:OD2	57:DZ:222:ASP:N	2.21	0.70
12:AO:16:ALA:HB2	12:AO:52:VAL:HG21	1.74	0.70
1:CA:1670:C:OP1	63:CA:3718:HOH:O	2.08	0.70
1:CA:2121:G:C1'	3:CC:168:LYS:CE	2.70	0.70
7:CG:9:ARG:NH1	7:CG:13:GLU:OE1	2.24	0.70
34:DA:62:U:N3	34:DA:105:G:O6	2.14	0.70
34:BA:406:G:OP2	63:BA:3304:HOH:O	2.10	0.70
3:AC:51:ASP:HB3	3:AC:57:GLN:OE1	1.90	0.70
10:AL:134:MET:HG3	10:AL:136:VAL:HG12	1.72	0.70
53:BT:10:LEU:HB3	53:BT:12:ALA:H	1.57	0.70
1:CA:441:U:O2	6:CF:46:ARG:NH2	2.25	0.70
1:CA:1665:A:OP2	63:CA:3722:HOH:O	2.09	0.70
30:C6:6:ARG:NH1	30:C6:26:ASN:HB2	2.07	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:DZ:183:MET:SD	57:DZ:213:HIS:HD2	2.14	0.70
1:CA:6:A:N6	1:CA:2897:U:O4	2.19	0.70
1:CA:323:G:O2'	1:CA:1205:U:N3	2.24	0.70
1:CA:1842:G:O3'	4:CD:253:GLN:NE2	2.25	0.70
8:CH:15:VAL:HG23	8:CH:28:GLY:HA3	1.73	0.70
35:DB:67:THR:HA	35:DB:90:MET:HE2	1.72	0.70
1:AA:2013:U:H2'	1:AA:2014:G:H5"	1.73	0.70
34:BA:671:G:H5'	39:BF:77:ARG:HH22	1.57	0.70
1:CA:2466:C:H5"	33:C9:6:SER:HB2	1.72	0.70
34:DA:1075:C:OP1	35:DB:179:LYS:NZ	2.24	0.70
17:AT:16:ARG:NH2	17:AT:83:ILE:O	2.25	0.69
38:DE:12:LEU:HB3	38:DE:31:LEU:HB2	1.72	0.69
41:DH:36:LEU:HA	41:DH:39:LEU:HD23	1.73	0.69
1:AA:2285:A:H2'	1:AA:2286:A:C8	2.26	0.69
1:AA:2564:U:OP2	63:AA:3921:HOH:O	2.10	0.69
29:A5:11:THR:HG22	29:A5:15:ARG:HB3	1.73	0.69
34:BA:1053:G:O2'	34:BA:1199:U:OP2	2.08	0.69
1:CA:300:A:OP1	22:CY:86:ARG:NH2	2.25	0.69
1:CA:2125:G:OP1	3:CC:71:LYS:NZ	2.25	0.69
13:CP:54:GLY:O	63:CP:201:HOH:O	2.10	0.69
2:AB:4:C:H42	2:AB:117:G:H1	1.37	0.69
23:AZ:48:PHE:CE2	23:AZ:71:VAL:HG11	2.27	0.69
34:BA:44:G:H2'	34:BA:45:U:O4'	1.93	0.69
42:BI:40:LEU:O	42:BI:42:ARG:N	2.25	0.69
57:BZ:148:LEU:O	57:BZ:152:THR:OG1	2.09	0.69
36:DC:134:ILE:HD11	36:DC:153:VAL:HG23	1.73	0.69
1:AA:868:A:C2'	1:AA:991:G:H5"	2.21	0.69
3:AC:183:PRO:HG2	3:AC:184:GLU:OE2	1.92	0.69
34:BA:972:C:O2'	43:BJ:55:LYS:O	2.09	0.69
57:BZ:13:ARG:HH12	57:BZ:247:ARG:HH12	1.41	0.69
57:BZ:324:ARG:HG3	57:BZ:324:ARG:HH11	1.57	0.69
14:CQ:85:LYS:HG2	24:C0:7:LEU:HB3	1.73	0.69
34:DA:27:G:N2	34:DA:557:G:H1'	2.07	0.69
3:AC:57:GLN:HG3	3:AC:57:GLN:O	1.93	0.69
42:BI:17:VAL:HG21	42:BI:81:ILE:HG22	1.74	0.69
7:CG:28:VAL:O	7:CG:31:VAL:HG12	1.91	0.69
25:C1:3:LYS:HB2	25:C1:61:ARG:NH1	2.07	0.69
1:AA:801:C:H2'	1:AA:802:C:C6	2.28	0.69
3:CC:46:ALA:HB3	3:CC:172:ILE:HG22	1.75	0.69
18:CU:65:ILE:HD11	18:CU:95:LEU:HB3	1.72	0.69
34:DA:984:C:H2'	34:DA:985:C:C6	2.27	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:2291:G:N7	24:A0:14:ARG:NH1	2.41	0.69
34:BA:1445:C:O2'	34:BA:1447:A:N6	2.25	0.69
1:CA:437:G:N7	63:CA:3780:HOH:O	2.26	0.69
34:DA:978:A:O2'	34:DA:1322:C:N3	2.26	0.69
35:DB:27:LYS:HG3	35:DB:194:PRO:HD2	1.75	0.69
43:DJ:6:ILE:HG12	43:DJ:98:ILE:HG12	1.74	0.69
1:AA:1444:C:OP1	21:AX:53:LYS:NZ	2.23	0.69
1:AA:1499:C:H42	1:AA:1506:G:H1	1.38	0.69
3:AC:55:SER:O	3:AC:57:GLN:N	2.22	0.69
34:BA:903:G:OP1	63:BA:3305:HOH:O	2.10	0.69
37:BD:13:ARG:HB3	37:BD:13:ARG:HH11	1.57	0.69
1:CA:403:U:H4'	1:CA:404:C:H5'	1.74	0.69
1:CA:1815:A:OP2	4:CD:54:ARG:NH2	2.26	0.69
1:CA:1840:G:OP2	63:CA:3723:HOH:O	2.09	0.69
1:CA:2470:G:O6	1:CA:2476:A:O2'	2.11	0.69
8:CH:98:LEU:HD22	8:CH:125:VAL:HG23	1.75	0.69
12:CO:35:VAL:HG13	12:CO:65:THR:HG23	1.75	0.69
20:CW:1:MET:HE2	20:CW:62:HIS:HB3	1.75	0.69
36:DC:47:LEU:HB3	36:DC:52:LEU:HB3	1.74	0.69
57:DZ:117:GLN:NE2	57:DZ:120:THR:OG1	2.25	0.69
57:DZ:160:ARG:NH1	57:DZ:256:THR:OG1	2.26	0.69
1:AA:2497:G:OP1	14:AQ:46:GLN:NE2	2.23	0.69
30:C6:11:LEU:HB2	30:C6:21:TYR:HB2	1.74	0.69
1:AA:1410:G:N7	25:A1:3:LYS:HE2	2.07	0.69
5:AE:29:GLY:HA3	63:AE:406:HOH:O	1.92	0.69
57:BZ:18:ALA:HB1	57:BZ:121:VAL:HG21	1.75	0.69
1:CA:1843:C:H5'	4:CD:253:GLN:NE2	2.07	0.69
1:CA:1859:A:H2'	3:CC:206:LYS:HD3	1.74	0.69
1:CA:2631:G:O2'	1:CA:2810:A:N1	2.23	0.69
29:A5:5:PRO:O	63:A5:201:HOH:O	2.10	0.68
41:BH:113:SER:HB2	41:BH:134:ILE:HD11	1.74	0.68
1:CA:848:G:H2'	1:CA:849:A:C8	2.27	0.68
1:CA:1062:G:H21	10:CL:133:SER:HA	1.57	0.68
28:C4:14:ILE:HG22	28:C4:22:ILE:HB	1.74	0.68
51:DR:56:THR:HB	51:DR:58:LEU:HD23	1.75	0.68
3:CC:57:GLN:O	3:CC:57:GLN:HG3	1.93	0.68
1:AA:1604:C:OP2	1:AA:1605:A:O2'	2.12	0.68
34:BA:677:U:H3	34:BA:713:G:H22	1.39	0.68
42:BI:45:ALA:HA	42:BI:48:GLU:HB2	1.75	0.68
57:BZ:357:ARG:NH1	57:BZ:373:ASP:OD1	2.27	0.68
3:CC:15:VAL:O	3:CC:16:ASP:HB3	1.92	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:CC:30:VAL:HG23	3:CC:31:LYS:H	1.58	0.68
27:C3:6:VAL:HG13	27:C3:56:VAL:HG13	1.73	0.68
34:DA:677:U:H3	34:DA:713:G:H22	1.39	0.68
34:DA:932:C:H2'	34:DA:933:G:C8	2.28	0.68
43:DJ:52:GLY:O	47:DN:41:ARG:NH2	2.27	0.68
49:DP:52:ASP:O	49:DP:54:GLU:N	2.27	0.68
53:DT:65:LYS:HA	53:DT:68:LYS:HD3	1.75	0.68
8:AH:51:ARG:NH2	8:AH:53:GLU:OE1	2.26	0.68
34:BA:1498:U:O2'	55:BV:17:U:OP1	2.08	0.68
14:CQ:27:VAL:O	14:CQ:29:PHE:N	2.23	0.68
30:C6:6:ARG:NH2	63:C6:4001:HOH:O	2.26	0.68
38:DE:43:LEU:HD21	38:DE:132:ALA:HB1	1.75	0.68
3:AC:25:GLU:HA	3:AC:28:ARG:HD2	1.74	0.68
34:BA:656:C:O2'	48:BO:28:GLN:NE2	2.26	0.68
34:BA:765:G:H5"	34:BA:766:A:OP1	1.93	0.68
1:CA:1412:A:H2'	1:CA:1413:G:H8	1.59	0.68
1:CA:2121:G:O2'	3:CC:168:LYS:HD3	1.93	0.68
3:CC:183:PRO:HG2	3:CC:184:GLU:OE2	1.92	0.68
15:CR:33:ARG:HG3	15:CR:115:GLU:HB3	1.76	0.68
24:C0:27:GLU:HB2	24:C0:69:PHE:HD1	1.58	0.68
7:AG:131:TYR:HB3	7:AG:159:VAL:HG12	1.74	0.68
39:BF:97:PHE:HB2	51:BR:32:ARG:HH11	1.58	0.68
1:CA:997:G:OP1	18:CU:92:ARG:HG2	1.94	0.68
1:CA:1647:G:OP1	63:CA:3705:HOH:O	2.10	0.68
8:CH:3:ARG:NH2	8:CH:5:GLY:H	1.91	0.68
15:CR:33:ARG:HE	15:CR:113:LEU:HD22	1.58	0.68
34:DA:878:G:H5'	41:DH:89:PRO:HG2	1.75	0.68
34:DA:1137:C:HO2'	34:DA:1138:G:N2	1.91	0.68
39:DF:8:ILE:HD13	39:DF:26:ILE:HD13	1.76	0.68
41:DH:6:ILE:O	41:DH:10:LEU:HG	1.93	0.68
1:AA:553:A:H3'	1:AA:553:A:H8	1.57	0.68
23:AZ:52:SER:OG	23:AZ:53:ILE:N	2.19	0.68
31:A7:24:THR:HG22	31:A7:27:GLY:H	1.58	0.68
57:BZ:21:ILE:HD13	57:BZ:21:ILE:H	1.58	0.68
57:BZ:202:PRO:O	57:BZ:206:LEU:HB2	1.94	0.68
3:CC:30:VAL:HG23	3:CC:31:LYS:N	2.09	0.68
6:CF:101:LEU:HD12	6:CF:102:PRO:HD2	1.75	0.68
34:DA:512:U:H2'	34:DA:513:C:C6	2.29	0.68
1:AA:2291:G:O6	24:A0:14:ARG:HD2	1.93	0.68
3:AC:15:VAL:O	3:AC:16:ASP:HB3	1.92	0.68
6:AF:53:THR:CG2	6:AF:55:GLY:H	2.07	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:987:G:O2'	1:CA:1000:A:N3	2.24	0.68
1:CA:1412:A:H2'	1:CA:1413:G:C8	2.28	0.68
1:CA:2499:C:OP2	63:CA:3725:HOH:O	2.11	0.68
3:CC:25:GLU:HA	3:CC:28:ARG:HD2	1.74	0.68
39:DF:2:ARG:NE	39:DF:69:GLU:HG2	2.09	0.68
1:AA:1940:A:O2'	1:AA:1942:C:N4	2.25	0.68
9:AK:39:ALA:O	9:AK:41:ARG:N	2.26	0.68
8:CH:41:MET:HE2	8:CH:64:LEU:HB3	1.76	0.68
34:DA:578:C:OP1	63:DA:1807:HOH:O	2.12	0.68
1:AA:553:A:OP2	11:AN:114:ARG:NH1	2.26	0.68
1:AA:1800:G:O2'	1:AA:1980:C:OP1	2.11	0.68
1:AA:2326:C:H2'	1:AA:2327:G:H8	1.59	0.68
3:AC:46:ALA:HB3	3:AC:172:ILE:CG2	2.23	0.68
11:AN:129:PRO:HD2	11:AN:130:HIS:CD2	2.28	0.68
53:BT:33:ILE:O	53:BT:37:SER:OG	2.10	0.68
1:CA:1309:G:H4'	31:C7:7:PRO:HB2	1.75	0.68
1:CA:2177:C:C2'	3:CC:171:ALA:HB2	2.24	0.68
36:DC:113:ALA:HB2	36:DC:202:ILE:HG13	1.76	0.68
1:AA:1338:U:H2'	1:AA:1339:C:C6	2.29	0.67
1:AA:2152:U:H4'	1:AA:2155:G:H4'	1.74	0.67
3:AC:46:ALA:HB3	3:AC:172:ILE:HG22	1.75	0.67
47:BN:51:GLY:O	47:BN:53:LEU:N	2.26	0.67
1:CA:2327:A:H2'	1:CA:2328:A:C8	2.29	0.67
3:CC:46:ALA:HB3	3:CC:172:ILE:CG2	2.23	0.67
19:CV:21:ARG:NH2	19:CV:91:TYR:OH	2.26	0.67
35:DB:212:GLN:O	35:DB:216:SER:OG	2.12	0.67
41:DH:73:ASP:OD2	41:DH:75:ARG:NH1	2.28	0.67
46:DM:17:VAL:O	46:DM:20:THR:OG1	2.12	0.67
1:AA:237:G:OP1	63:AA:3923:HOH:O	2.12	0.67
1:AA:1834:A:O2'	4:AD:259:THR:HG21	1.94	0.67
30:A6:18:ARG:HD3	30:A6:42:TRP:NE1	2.09	0.67
34:BA:453:A:O2'	49:BP:68:ASP:O	2.11	0.67
34:BA:542:G:OP1	37:BD:10:ARG:NH2	2.16	0.67
38:BE:40:ARG:NH2	38:BE:68:GLU:HA	2.10	0.67
1:CA:2886:G:H2'	1:CA:2887:U:H6	1.57	0.67
7:CG:180:PHE:O	7:CG:182:LYS:N	2.28	0.67
19:CV:74:LYS:HB2	19:CV:83:ARG:HB2	1.77	0.67
33:C9:22:ARG:HB2	33:C9:24:TYR:CE1	2.29	0.67
42:DI:13:ALA:HB2	42:DI:68:GLY:HA3	1.75	0.67
1:AA:2162:C:O2	1:AA:2173:G:N2	2.28	0.67
9:AK:28:ASN:O	9:AK:30:GLN:N	2.27	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:DA:1078:U:H1'	38:DE:130:ASN:HD21	1.58	0.67
34:DA:1279:A:O2'	34:DA:1282:C:N4	2.26	0.67
34:BA:942:G:H21	42:BI:124:GLN:NE2	1.93	0.67
3:CC:41:THR:O	3:CC:42:VAL:HB	1.94	0.67
34:BA:714:G:H2'	34:BA:715:A:C8	2.29	0.67
37:BD:178:VAL:O	37:BD:180:GLY:N	2.27	0.67
1:CA:2345:G:OP2	30:C6:38:LYS:NZ	2.22	0.67
34:DA:376:G:H5"	49:DP:5:ARG:HD3	1.77	0.67
34:DA:1132:C:H2'	34:DA:1133:G:C8	2.29	0.67
34:DA:1251:A:H2'	34:DA:1252:A:C8	2.29	0.67
1:AA:801:C:H2'	1:AA:802:C:H6	1.60	0.67
1:AA:1935:A:H4'	1:AA:1936:C:H5"	1.76	0.67
1:AA:1993:A:OP2	4:AD:242:ARG:NH2	2.27	0.67
3:AC:30:VAL:HG23	3:AC:31:LYS:H	1.58	0.67
3:AC:30:VAL:HG23	3:AC:31:LYS:N	2.09	0.67
34:BA:279:A:OP2	50:BQ:95:TYR:OH	2.09	0.67
1:CA:2124:G:O3'	3:CC:175:PRO:HG2	1.94	0.67
35:DB:178:ARG:HH22	41:DH:68:ARG:HH22	1.42	0.67
1:AA:2262:G:OP1	14:AQ:85:LYS:NZ	2.22	0.67
17:AT:24:PRO:HA	17:AT:49:VAL:HG22	1.76	0.67
26:A2:1:MET:N	26:A2:52:ASP:OD1	2.26	0.67
34:BA:486:U:H2'	34:BA:487:A:H8	1.59	0.67
34:BA:538:G:H5"	45:BL:114:LYS:HB2	1.77	0.67
1:CA:922:U:H2'	1:CA:923:C:C6	2.30	0.67
1:CA:1783:A:OP1	63:CA:3728:HOH:O	2.13	0.67
23:CZ:108:PRO:HG2	23:CZ:117:LEU:HD13	1.76	0.67
34:DA:920:U:H2'	34:DA:921:U:C6	2.30	0.67
37:DD:23:GLY:N	37:DD:26:CYS:SG	2.60	0.67
57:DZ:363:ARG:HG2	57:DZ:363:ARG:HH11	1.58	0.67
1:AA:1151:U:H2'	1:AA:1152:G:C8	2.30	0.67
16:AS:15:ARG:O	16:AS:19:LYS:HG2	1.95	0.67
35:BB:204:ASN:OD1	35:BB:205:ASP:N	2.27	0.67
1:CA:1270:C:O2'	1:CA:1648:C:OP2	2.09	0.67
1:CA:2123:G:H21	3:CC:45:HIS:HE1	1.42	0.67
1:AA:868:A:N1	63:AA:3962:HOH:O	2.27	0.67
14:AQ:37:LEU:HB2	14:AQ:128:LYS:HB2	1.75	0.67
44:BK:27:ASN:OD1	44:BK:28:THR:N	2.26	0.67
1:CA:299:A:N3	1:CA:319:C:O2'	2.28	0.67
1:CA:1899:G:H2'	1:CA:1899:G:N3	2.10	0.67
10:CL:6:ALA:HB3	10:CL:30:HIS:HE1	1.60	0.67
1:AA:630:U:OP1	6:AF:102:PRO:HA	1.93	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:2787:C:OP2	63:AA:3922:HOH:O	2.11	0.67
34:BA:406:G:H21	37:BD:119:GLN:HE22	1.43	0.67
37:BD:108:LEU:HD11	37:BD:174:LEU:HD22	1.76	0.67
1:CA:991:C:OP2	63:CA:3730:HOH:O	2.13	0.67
23:AZ:152:ALA:HB1	23:AZ:163:LEU:HD21	1.78	0.66
36:BC:152:ILE:HB	36:BC:199:LYS:HB2	1.78	0.66
1:CA:1971:A:OP1	63:CA:3726:HOH:O	2.11	0.66
2:CB:106:G:H5'	23:CZ:31:ARG:HG2	1.76	0.66
17:CT:85:LYS:NZ	17:CT:87:ASP:OD2	2.28	0.66
34:DA:1499:A:H1'	34:DA:1520:G:H5'	1.77	0.66
57:DZ:115:GLU:O	57:DZ:118:SER:HB2	1.95	0.66
57:DZ:214:GLU:OE2	57:DZ:218:GLU:OE2	2.12	0.66
1:AA:482:C:H4'	63:AA:4405:HOH:O	1.95	0.66
1:AA:1525:G:H2'	1:AA:1526:G:H8	1.60	0.66
3:AC:176:VAL:HG11	3:AC:190:ILE:HD13	1.76	0.66
6:AF:132:VAL:HG22	6:AF:163:VAL:HG22	1.77	0.66
3:CC:31:LYS:NZ	3:CC:180:SER:O	2.28	0.66
3:CC:42:VAL:HG13	3:CC:43:GLU:N	2.10	0.66
17:CT:39:ARG:NH2	34:DA:345:C:OP2	2.28	0.66
35:DB:101:MET:HA	35:DB:108:ILE:HG13	1.77	0.66
21:AX:5:TYR:CZ	26:A2:30:ARG:HD2	2.30	0.66
33:A9:11:CYS:HB3	33:A9:32:HIS:HE1	1.61	0.66
1:CA:2582:G:OP2	63:CA:3727:HOH:O	2.13	0.66
5:CE:11:MET:HG2	5:CE:24:THR:HG22	1.78	0.66
3:AC:65:LEU:HB3	3:AC:189:ASN:ND2	2.11	0.66
4:AD:16:MET:HG3	4:AD:211:ARG:HH21	1.59	0.66
3:AC:41:THR:O	3:AC:42:VAL:HB	1.94	0.66
3:AC:42:VAL:HG13	3:AC:43:GLU:N	2.10	0.66
10:AL:72:PRO:O	10:AL:111:LYS:NZ	2.28	0.66
34:BA:1305:G:N2	34:BA:1331:G:H1'	2.10	0.66
34:BA:1347:G:N2	34:BA:1373:G:H2'	2.10	0.66
1:CA:2682:U:O2'	17:CT:58:ASN:ND2	2.28	0.66
7:CG:126:ASP:HB3	7:CG:128:ARG:H	1.60	0.66
13:CP:126:VAL:HG12	13:CP:148:LEU:HD22	1.77	0.66
25:C1:67:ILE:N	25:C1:68:PRO:HD2	2.10	0.66
5:AE:93:VAL:HG22	63:AE:406:HOH:O	1.94	0.66
17:AT:105:LEU:HD13	17:AT:109:GLU:HB3	1.77	0.66
34:BA:1355:G:H2'	34:BA:1356:G:C8	2.30	0.66
37:BD:78:LEU:HB3	37:BD:93:PHE:HE1	1.61	0.66
57:BZ:184:LYS:NZ	57:BZ:198:GLU:OE1	2.27	0.66
1:CA:1429:G:H2'	1:CA:1430:C:C6	2.30	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1688:U:O2	1:CA:1700:A:H5'	1.96	0.66
38:DE:53:LEU:H	38:DE:53:LEU:HD12	1.59	0.66
1:AA:1157:A:H8	1:AA:1158:G:H1'	1.60	0.66
1:AA:1995:G:H2'	1:AA:1996:C:C6	2.30	0.66
8:AH:61:HIS:HA	8:AH:64:LEU:HD12	1.76	0.66
25:A1:86:SER:O	25:A1:90:ILE:HG13	1.96	0.66
1:CA:120:U:OP2	63:CA:3735:HOH:O	2.14	0.66
16:CS:34:HIS:O	16:CS:97:ARG:NH2	2.27	0.66
37:DD:13:ARG:HB2	37:DD:40:PRO:HD3	1.77	0.66
1:AA:2299:A:H62	1:AA:2356:U:H3	1.44	0.66
4:AD:77:ALA:O	4:AD:116:GLN:HG3	1.96	0.66
35:BB:179:LYS:HA	41:BH:72:PRO:HG3	1.78	0.66
53:BT:56:MET:HE2	53:BT:85:MET:HA	1.76	0.66
4:CD:17:THR:O	4:CD:211:ARG:NH2	2.28	0.66
34:DA:67:C:H2'	34:DA:68:G:C8	2.31	0.66
57:DZ:75:LYS:O	57:DZ:77:HIS:HD2	1.79	0.66
32:A8:38:GLY:O	32:A8:42:ARG:HB2	1.96	0.66
34:BA:653:A:OP1	41:BH:56:LYS:NZ	2.27	0.66
34:BA:738:C:H2'	34:BA:739:C:C6	2.31	0.66
57:BZ:-38:TYR:O	57:BZ:-35:PRO:HD2	1.96	0.66
1:CA:775:G:O3'	63:CA:3729:HOH:O	2.13	0.66
1:CA:2292:C:OP1	16:CS:17:ARG:NH2	2.23	0.66
1:CA:2611:U:C4	29:C5:3:LYS:HG3	2.31	0.66
1:CA:2823:A:OP1	5:CE:159:HIS:NE2	2.20	0.66
21:CX:31:HIS:HD2	21:CX:33:LYS:H	1.43	0.66
34:DA:728:A:H2'	34:DA:729:A:C8	2.31	0.66
14:AQ:21:THR:HG21	14:AQ:101:ARG:HD3	1.78	0.66
19:AV:29:PRO:HA	19:AV:61:VAL:HG22	1.78	0.66
1:CA:301:G:N7	63:CA:3793:HOH:O	2.28	0.66
1:CA:2880:C:O3'	15:CR:90:ARG:NH1	2.29	0.66
3:CC:65:LEU:HB3	3:CC:189:ASN:ND2	2.11	0.66
4:CD:110:GLY:O	4:CD:112:GLN:NE2	2.29	0.66
6:CF:53:THR:HG23	6:CF:55:GLY:H	1.61	0.66
34:DA:339:C:H2'	34:DA:340:U:C6	2.31	0.66
34:DA:807:A:H2'	34:DA:808:C:C6	2.31	0.66
57:DZ:169:GLY:H	57:DZ:170:ARG:NH1	1.87	0.66
19:AV:72:VAL:HG13	19:AV:85:LYS:HB3	1.78	0.65
34:BA:193:C:H2'	34:BA:194:C:C6	2.31	0.65
57:BZ:166:LEU:HB3	57:BZ:178:ILE:HD12	1.78	0.65
1:CA:1045:A:H4'	1:CA:1046:A:H5"	1.77	0.65
1:CA:2006:C:OP2	63:CA:3734:HOH:O	2.14	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:2121:G:H1'	3:CC:168:LYS:CG	2.26	0.65
1:CA:2124:G:H4'	3:CC:175:PRO:CD	2.25	0.65
11:CN:49:GLY:O	11:CN:119:ARG:NH1	2.29	0.65
34:DA:503:C:H2'	34:DA:504:C:H6	1.61	0.65
1:AA:1529:G:O6	1:AA:1553:A:N6	2.29	0.65
3:AC:31:LYS:NZ	3:AC:180:SER:O	2.28	0.65
23:AZ:115:GLY:HA2	23:AZ:177:PRO:HB3	1.78	0.65
37:BD:162:LEU:O	37:BD:165:MET:N	2.29	0.65
41:BH:83:ILE:HB	41:BH:137:VAL:HG13	1.78	0.65
1:CA:1780:A:OP1	63:CA:3703:HOH:O	2.13	0.65
8:CH:80:SER:OG	8:CH:81:GLU:N	2.26	0.65
17:CT:23:ARG:HG3	17:CT:120:ARG:NH1	2.11	0.65
20:CW:18:ARG:NH1	20:CW:76:VAL:O	2.29	0.65
28:C4:24:THR:OG1	28:C4:25:TYR:N	2.29	0.65
1:AA:455:A:OP2	1:AA:455:A:H8	1.80	0.65
1:AA:1355:G:OP1	31:A7:9:ARG:HB2	1.97	0.65
34:BA:356:A:N3	34:BA:368:U:O2'	2.27	0.65
35:BB:88:ALA:HB2	35:BB:219:VAL:HG13	1.79	0.65
1:CA:1364:G:N7	25:C1:3:LYS:HE2	2.11	0.65
3:CC:176:VAL:HG11	3:CC:190:ILE:HD13	1.76	0.65
4:CD:238:GLY:O	4:CD:239:ARG:HB2	1.95	0.65
22:CY:23:ARG:HG2	22:CY:42:VAL:HG22	1.78	0.65
34:DA:1016:A:O2'	34:DA:1217:C:O2'	2.13	0.65
39:DF:30:LEU:HB3	39:DF:35:ALA:HB3	1.78	0.65
57:DZ:169:GLY:O	57:DZ:173:THR:OG1	2.09	0.65
1:AA:2430:A:H2'	1:AA:2431:U:C6	2.31	0.65
3:AC:63:VAL:O	3:AC:161:ARG:HA	1.96	0.65
7:AG:131:TYR:HB3	7:AG:159:VAL:CG1	2.26	0.65
50:BQ:45:HIS:HB2	50:BQ:65:ILE:HD13	1.78	0.65
1:CA:53:A:OP2	63:CA:3736:HOH:O	2.14	0.65
1:CA:658:C:H2'	1:CA:659:C:C6	2.31	0.65
3:CC:63:VAL:O	3:CC:161:ARG:HA	1.96	0.65
20:CW:51:LEU:HD23	20:CW:105:VAL:HG11	1.78	0.65
34:DA:189(F):U:O2	50:DQ:63:ARG:NH2	2.29	0.65
46:DM:5:ALA:HB3	46:DM:22:ILE:HD12	1.77	0.65
1:AA:1342:G:OP1	1:AA:2721:G:O2'	2.12	0.65
1:CA:1466:G:HO2'	1:CA:1546:C:HO2'	1.43	0.65
45:DL:59:ARG:NH1	45:DL:65:GLU:OE1	2.30	0.65
49:DP:43:LYS:HG2	49:DP:48:TRP:CD2	2.32	0.65
1:AA:661:G:N7	13:AP:113:LYS:NZ	2.44	0.65
1:AA:1154:U:O2'	1:AA:1155:C:O4'	2.15	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:AF:184:TYR:O	6:AF:188:ARG:HG3	1.96	0.65
34:DA:921:U:O2'	38:DE:19:MET:O	2.13	0.65
1:AA:2365:G:N7	63:AA:3974:HOH:O	2.29	0.65
34:BA:411:A:OP1	37:BD:30:LYS:NZ	2.26	0.65
1:CA:2124:G:C4'	3:CC:175:PRO:CG	2.69	0.65
1:CA:2150:U:H2'	1:CA:2151:G:H8	1.62	0.65
8:CH:164:TYR:N	8:CH:167:GLU:OE1	2.24	0.65
34:DA:116:A:OP1	63:DA:1804:HOH:O	2.15	0.65
57:DZ:168:ILE:HG23	57:DZ:205:TYR:HE2	1.61	0.65
1:AA:1736:A:H62	1:AA:1745:A:H2	1.45	0.65
3:AC:206:LYS:HB3	3:AC:206:LYS:NZ	2.12	0.65
6:AF:101:LEU:HD12	6:AF:102:PRO:HD2	1.78	0.65
40:BG:78:ARG:HH21	40:BG:156:TRP:HB3	1.60	0.65
57:BZ:264:LEU:HB2	62:BZ:801:GDP:C5	2.32	0.65
57:BZ:355:LEU:HD23	57:BZ:369:LEU:HD13	1.79	0.65
1:CA:778:G:OP2	63:CA:3732:HOH:O	2.14	0.65
6:CF:131:GLY:O	6:CF:133:ASN:N	2.21	0.65
7:CG:166:ASP:O	7:CG:170:ARG:N	2.29	0.65
19:CV:21:ARG:HG2	19:CV:91:TYR:CE2	2.32	0.65
34:DA:404:U:H5'	37:DD:122:ARG:HE	1.61	0.65
35:DB:84:GLU:HB3	35:DB:219:VAL:HG21	1.79	0.65
35:DB:178:ARG:HH21	41:DH:74:PRO:HB3	1.62	0.65
50:DQ:86:GLU:HG3	50:DQ:90:ILE:HD11	1.79	0.65
57:DZ:169:GLY:N	57:DZ:170:ARG:NH1	2.45	0.65
57:DZ:637:ARG:C	57:DZ:639:ASN:H	2.05	0.65
1:AA:1154:U:O2'	1:AA:1155:C:H5"	1.97	0.65
1:AA:2207:C:H2'	1:AA:2208:G:H8	1.62	0.65
1:AA:2864:G:H2'	1:AA:2865:C:C6	2.32	0.65
10:AL:99:ILE:O	10:AL:139:VAL:N	2.30	0.65
34:BA:690:G:C6	34:BA:691:G:C6	2.84	0.65
38:BE:78:HIS:HD1	41:BH:104:ARG:HD2	1.61	0.65
1:CA:2032:G:O2'	5:CE:145:LYS:HE2	1.97	0.65
1:CA:2758:A:C2	1:CA:2759:G:H1'	2.32	0.65
1:CA:2850:A:OP2	1:CA:2866:U:H5	1.80	0.65
3:CC:206:LYS:NZ	3:CC:206:LYS:HB3	2.12	0.65
17:CT:16:ARG:HD2	17:CT:19:LEU:HD11	1.78	0.65
47:DN:24:CYS:HB3	47:DN:28:GLY:H	1.61	0.65
1:AA:1154:U:O2'	1:AA:1155:C:H6	1.80	0.65
28:A4:53:GLU:HB3	28:A4:54:GLY:HA2	1.79	0.65
32:A8:39:LYS:O	32:A8:43:GLN:HG3	1.96	0.65
1:CA:1188:U:H4'	19:CV:79:VAL:HG22	1.79	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:CT:11:GLU:O	17:CT:15:VAL:HG23	1.97	0.65
35:DB:155:LEU:HD11	35:DB:159:PRO:HD3	1.79	0.65
57:DZ:24:GLY:HA2	62:DZ:704:GDP:O2A	1.97	0.65
57:DZ:151:ARG:O	57:DZ:155:GLU:HB2	1.97	0.65
1:CA:1090:U:H2'	1:CA:1091:G:C8	2.31	0.64
1:CA:2176:A:H4'	3:CC:45:HIS:HD2	1.48	0.64
10:CL:27:LEU:HD11	10:CL:57:ILE:HD13	1.78	0.64
10:CL:101:TRP:NE1	10:CL:140:GLY:HA3	2.10	0.64
34:DA:222:U:H2'	34:DA:223:U:C6	2.32	0.64
34:DA:982:U:H5"	47:DN:6:LEU:HD21	1.78	0.64
45:DL:79:GLU:HB3	45:DL:80:HIS:CD2	2.32	0.64
1:AA:1068:G:OP2	11:AN:65:LYS:NZ	2.30	0.64
3:AC:69:LEU:O	3:AC:178:LYS:HG3	1.98	0.64
8:AH:54:ARG:HD3	8:AH:65:HIS:ND1	2.12	0.64
40:BG:93:PRO:HA	40:BG:96:GLN:HB2	1.79	0.64
3:CC:69:LEU:O	3:CC:178:LYS:HG3	1.97	0.64
10:CL:8:VAL:HG21	10:CL:26:ALA:HB1	1.77	0.64
34:DA:1101:A:H4'	34:DA:1102:A:O5'	1.97	0.64
34:DA:1387:G:H2'	34:DA:1388:C:C6	2.32	0.64
35:DB:88:ALA:HB2	35:DB:219:VAL:HG13	1.79	0.64
57:DZ:363:ARG:HG2	57:DZ:363:ARG:NH1	2.10	0.64
6:AF:123:LEU:HD13	6:AF:192:LEU:HD13	1.78	0.64
10:AL:41:PHE:HE1	10:AL:53:VAL:HB	1.60	0.64
20:AW:43:GLY:O	20:AW:47:VAL:HG23	1.97	0.64
21:AX:43:VAL:HG21	21:AX:81:VAL:HG11	1.78	0.64
34:BA:503:C:H2'	34:BA:504:C:H6	1.62	0.64
37:BD:57:ARG:HG2	37:BD:202:LEU:HD22	1.79	0.64
25:C1:8:SER:HB3	25:C1:66:HIS:CD2	2.33	0.64
34:DA:1071:C:H2'	34:DA:1072:G:H8	1.62	0.64
41:DH:13:ILE:O	41:DH:17:THR:HG23	1.97	0.64
50:DQ:18:THR:OG1	50:DQ:69:LYS:NZ	2.20	0.64
1:AA:354:A:H2	1:AA:1255:A:HO2'	1.41	0.64
1:AA:1249:A:H61	1:AA:1286:U:H2'	1.63	0.64
1:AA:2023:A:H2'	1:AA:2024:G:C8	2.31	0.64
1:AA:2457:G:OP1	6:AF:74:ARG:NH2	2.29	0.64
4:AD:273:ARG:HB3	4:AD:273:ARG:HH11	1.63	0.64
5:AE:49:LEU:HD22	5:AE:81:ILE:HD13	1.80	0.64
34:BA:166:G:H2'	34:BA:167:G:C8	2.30	0.64
35:BB:109:SER:HA	35:BB:112:VAL:HG13	1.78	0.64
35:BB:111:ARG:HG2	35:BB:111:ARG:HH11	1.62	0.64
44:BK:23:ALA:HB1	44:BK:88:GLY:HA3	1.78	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:2022:U:O2'	1:CA:2617:C:H5'	1.97	0.64
1:CA:2430:A:OP2	63:CA:3737:HOH:O	2.14	0.64
1:CA:2723:C:H5"	15:CR:1:MET:HE2	1.79	0.64
6:CF:170:LEU:HG	6:CF:172:TRP:NE1	2.12	0.64
7:CG:64:THR:HB	7:CG:94:LEU:HD21	1.78	0.64
34:DA:407:G:H5"	37:DD:115:ARG:HD2	1.78	0.64
34:DA:663:A:H5"	51:DR:61:LYS:HE3	1.78	0.64
36:DC:58:GLU:HB3	43:DJ:92:THR:HG21	1.80	0.64
1:AA:786:G:OP1	63:AA:3924:HOH:O	2.14	0.64
1:AA:2137:G:H21	1:AA:2193:A:H61	1.45	0.64
16:AS:48:LEU:HD23	16:AS:82:ILE:HD11	1.78	0.64
29:A5:16:ARG:HD2	29:A5:17:ASP:OD1	1.97	0.64
57:BZ:223:PHE:HB3	57:BZ:248:LYS:HD3	1.80	0.64
1:CA:2177:C:H5'	3:CC:45:HIS:HB3	1.80	0.64
1:CA:2287:A:N6	1:CA:2344:U:H3	1.94	0.64
7:CG:126:ASP:HB2	7:CG:130:ASN:H	1.63	0.64
57:DZ:532:GLY:O	57:DZ:534:ILE:N	2.31	0.64
1:AA:1452:U:H2'	1:AA:1453:C:C6	2.32	0.64
6:AF:53:THR:HG23	6:AF:55:GLY:H	1.61	0.64
22:AY:20:TYR:CE1	22:AY:43:ASN:HA	2.32	0.64
39:BF:89:MET:HE3	51:BR:76:LEU:HD22	1.80	0.64
1:CA:271(E):U:H2'	1:CA:271(F):C:C6	2.33	0.64
1:CA:2837:G:N7	63:CA:3800:HOH:O	2.30	0.64
5:CE:115:GLY:O	5:CE:119:ARG:HB2	1.98	0.64
15:CR:52:ILE:O	15:CR:55:ALA:N	2.31	0.64
34:BA:148:G:H2'	34:BA:149:A:H8	1.63	0.64
34:BA:1510:U:H2'	34:BA:1511:G:C8	2.33	0.64
1:CA:253:C:OP2	32:C8:5:LYS:NZ	2.24	0.64
1:CA:2033:A:OP1	63:CA:3741:HOH:O	2.15	0.64
1:AA:957:A:OP1	63:AA:3926:HOH:O	2.15	0.64
2:AB:29:A:O2'	2:AB:58:A:N1	2.29	0.64
5:AE:141:ILE:HD12	5:AE:150:VAL:HG21	1.80	0.64
34:DA:427:U:OP1	37:DD:13:ARG:NH2	2.30	0.64
57:DZ:159:ALA:HB1	57:DZ:160:ARG:HG3	1.80	0.64
1:AA:325:G:OP2	22:AY:84:ARG:NH2	2.31	0.64
1:AA:2157:A:N6	1:AA:2178:G:O2'	2.25	0.64
1:AA:2623:U:H6	1:AA:2623:U:H5'	1.63	0.64
8:AH:69:ARG:HG3	8:AH:70:THR:N	2.12	0.64
23:AZ:151:HIS:HA	23:AZ:170:THR:HA	1.79	0.64
37:BD:23:GLY:N	37:BD:26:CYS:SG	2.69	0.64
57:BZ:402:ILE:HG23	57:BZ:403:GLU:H	1.62	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:2032:G:N7	63:CA:3802:HOH:O	2.30	0.64
1:CA:2296:U:OP2	16:CS:9:ARG:NH2	2.31	0.64
1:CA:2788:C:OP1	5:CE:61:ARG:NH2	2.26	0.64
34:DA:7:G:O2'	38:DE:120:THR:O	2.16	0.64
36:DC:173:VAL:HG13	36:DC:182:ILE:HD13	1.78	0.64
49:DP:53:VAL:HG22	49:DP:79:VAL:HG22	1.79	0.64
3:AC:68:GLY:N	3:AC:189:ASN:HD21	1.96	0.64
1:CA:1058:G:O2'	10:CL:114:ASP:O	2.16	0.64
1:CA:1996:C:H4'	1:CA:1997:G:OP1	1.98	0.64
3:CC:44:VAL:CG2	3:CC:176:VAL:HG21	2.28	0.64
4:CD:276:LYS:H	4:CD:276:LYS:HD3	1.63	0.64
12:CO:7:TYR:CE1	12:CO:20:MET:HE3	2.29	0.64
12:CO:120:GLU:OE1	17:CT:67:SER:OG	2.15	0.64
39:DF:100:ASN:HD21	51:DR:23:LYS:HE3	1.63	0.64
41:DH:85:ARG:HH21	41:DH:134:ILE:HG23	1.62	0.64
47:DN:27:CYS:SG	47:DN:28:GLY:N	2.71	0.64
57:DZ:169:GLY:HA3	57:DZ:174:PHE:HA	1.80	0.64
1:AA:516:G:H2'	1:AA:517:A:C8	2.33	0.63
1:AA:732:A:H1'	1:AA:735:U:O4	1.98	0.63
1:AA:1410:G:OP2	25:A1:3:LYS:HD2	1.97	0.63
44:BK:48:ILE:O	44:BK:50:TYR:N	2.30	0.63
57:BZ:637:ARG:C	57:BZ:639:ASN:H	2.06	0.63
1:CA:528:A:O2'	1:CA:529:A:H5"	1.97	0.63
1:CA:1029:A:N1	1:CA:2465:C:O2'	2.31	0.63
3:CC:29:LEU:O	3:CC:32:GLU:N	2.31	0.63
10:CL:30:HIS:HA	10:CL:59:ILE:HD12	1.78	0.63
33:C9:9:ARG:HG2	33:C9:14:CYS:HB2	1.80	0.63
34:DA:474:G:H2'	34:DA:475:G:H8	1.63	0.63
1:AA:553:A:C2'	1:AA:554:A:H5'	2.26	0.63
1:AA:1633:A:H2'	1:AA:1634:C:C6	2.34	0.63
3:AC:44:VAL:CG2	3:AC:176:VAL:HG21	2.28	0.63
57:BZ:-38:TYR:O	57:BZ:-34:ARG:HG2	1.97	0.63
57:BZ:19:ALA:HB3	57:BZ:25:LYS:HE3	1.79	0.63
1:CA:2162:G:OP1	1:CA:2172:U:O2'	2.16	0.63
34:DA:1086:U:H3	34:DA:1099:G:H22	1.46	0.63
42:DI:16:ARG:HB2	42:DI:64:THR:HG23	1.80	0.63
1:AA:2717:A:O2'	1:AA:2862:G:OP1	2.08	0.63
3:AC:7:ARG:O	3:AC:11:LEU:HD23	1.99	0.63
3:AC:29:LEU:O	3:AC:32:GLU:N	2.32	0.63
38:BE:51:VAL:O	38:BE:55:VAL:HG23	1.98	0.63
7:CG:161:THR:HG22	7:CG:163:ALA:H	1.63	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:DD:76:ARG:NH2	37:DD:80:GLU:OE1	2.26	0.63
46:DM:65:LYS:NZ	46:DM:73:GLU:OE2	2.29	0.63
27:A3:8:LEU:HD13	27:A3:31:LEU:HD23	1.79	0.63
34:BA:1239:A:H4'	34:BA:1240:U:H5"	1.81	0.63
36:BC:157:ILE:HD13	36:BC:164:ARG:HB3	1.80	0.63
57:BZ:20:HIS:ND1	57:BZ:116:PRO:O	2.32	0.63
57:BZ:273:LEU:O	57:BZ:276:VAL:N	2.30	0.63
1:CA:2722:G:OP2	63:CA:3740:HOH:O	2.15	0.63
48:DO:16:ALA:HB1	48:DO:21:ASP:HB3	1.80	0.63
57:DZ:402:ILE:HG23	57:DZ:403:GLU:H	1.62	0.63
5:AE:111:ARG:HG3	5:AE:160:TYR:CD2	2.33	0.63
18:AU:104:GLN:CD	18:AU:104:GLN:H	2.05	0.63
5:AE:120:TRP:CE3	5:AE:155:LYS:HE2	2.34	0.63
21:AX:57:LEU:HD13	21:AX:78:LYS:HB2	1.80	0.63
38:BE:93:PRO:HG2	41:BH:105:ARG:HG3	1.81	0.63
57:BZ:273:LEU:HA	57:BZ:276:VAL:HG23	1.81	0.63
1:CA:2871:C:N4	63:CA:3804:HOH:O	2.30	0.63
3:CC:7:ARG:O	3:CC:11:LEU:HD23	1.99	0.63
3:CC:68:GLY:N	3:CC:189:ASN:HD21	1.96	0.63
1:AA:2096:U:H2'	1:AA:2097:U:C6	2.33	0.63
11:AN:46:VAL:HG23	11:AN:48:MET:HG2	1.79	0.63
34:BA:1125:U:H4'	43:BJ:5:ARG:NH2	2.14	0.63
44:BK:18:ARG:NH1	44:BK:20:TYR:OH	2.31	0.63
7:CG:41:GLN:NE2	7:CG:154:GLY:O	2.27	0.63
35:DB:74:LYS:NZ	35:DB:205:ASP:O	2.32	0.63
40:BG:113:GLU:HB2	40:BG:119:ARG:HG2	1.80	0.63
57:BZ:329:ARG:HD3	57:BZ:331:TYR:CZ	2.34	0.63
1:CA:2121:G:C2'	3:CC:168:LYS:HD3	2.28	0.63
16:CS:39:ILE:HB	16:CS:49:VAL:HG12	1.81	0.63
34:DA:646:U:H2'	34:DA:647:C:C6	2.34	0.63
34:DA:1003:G:N2	34:DA:1025:U:O4	2.31	0.63
36:DC:187:ALA:HB3	36:DC:198:VAL:HB	1.81	0.63
24:A0:18:ALA:HB3	24:A0:20:ARG:NH2	2.13	0.63
1:CA:2150:U:H2'	1:CA:2151:G:C8	2.34	0.63
3:CC:6:LYS:HG3	3:CC:7:ARG:N	2.14	0.63
19:CV:21:ARG:HG2	19:CV:91:TYR:CD2	2.34	0.63
55:DV:18:G:H4'	57:DZ:504:ARG:HA	1.80	0.63
1:AA:2034:G:OP1	20:AW:11:ARG:NH2	2.32	0.62
3:AC:6:LYS:HG3	3:AC:7:ARG:N	2.14	0.62
46:BM:92:HIS:CE1	46:BM:98:VAL:HG21	2.34	0.62
1:CA:1044:G:H21	1:CA:1111:A:H2	1.45	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1786:A:H1'	1:CA:1938:A:N6	2.13	0.62
1:CA:2640:G:OP1	11:CN:97:ARG:NH2	2.32	0.62
10:CL:125:ARG:HA	10:CL:128:ALA:HB3	1.81	0.62
34:DA:60:A:H4'	34:DA:61:G:O5'	1.99	0.62
34:DA:1353:G:H2'	34:DA:1354:C:H6	1.64	0.62
57:DZ:211:GLU:O	57:DZ:215:LYS:HE2	1.99	0.62
1:AA:2886:G:H4'	17:AT:2:ASN:ND2	2.14	0.62
38:BE:78:HIS:CD2	38:BE:142:LEU:HD23	2.34	0.62
1:CA:1040:C:H2'	1:CA:1041:C:O4'	1.99	0.62
34:DA:1251:A:N1	34:DA:1354:C:O2'	2.32	0.62
57:DZ:82:ILE:HD12	57:DZ:101:LEU:HD23	1.81	0.62
57:DZ:264:LEU:HB2	62:DZ:704:GDP:C5	2.34	0.62
1:AA:2324:U:H5'	7:AG:88:ILE:HD11	1.81	0.62
16:AS:27:SER:HA	16:AS:88:ASP:HB3	1.81	0.62
34:BA:735:C:H2'	34:BA:736:C:C6	2.34	0.62
48:BO:25:THR:HG21	48:BO:70:LEU:HB2	1.81	0.62
57:BZ:508:GLY:HA3	57:BZ:581:ALA:O	1.98	0.62
1:CA:854:G:O6	63:CA:3733:HOH:O	2.14	0.62
10:CL:84:LEU:HD21	10:CL:96:VAL:HB	1.81	0.62
34:DA:176:C:OP1	53:DT:29:LYS:NZ	2.23	0.62
34:DA:1095:U:H5'	34:DA:1109:C:O2	2.00	0.62
35:DB:178:ARG:NH2	41:DH:68:ARG:HH22	1.98	0.62
1:AA:650:G:N7	13:AP:107:LYS:NZ	2.47	0.62
1:AA:2319:G:N1	7:AG:43:LEU:O	2.28	0.62
1:CA:898:C:H2'	1:CA:899:A:O4'	2.00	0.62
1:CA:1820:U:H4'	1:CA:1821:A:OP2	1.98	0.62
34:DA:875:C:O2'	41:DH:14:ARG:NH1	2.32	0.62
57:DZ:-61:LEU:HG	57:DZ:-31:ALA:HA	1.81	0.62
57:DZ:363:ARG:HH11	57:DZ:363:ARG:CG	2.12	0.62
57:DZ:497:PHE:O	57:DZ:507:TYR:HA	1.98	0.62
3:AC:68:GLY:H	3:AC:189:ASN:HD21	1.47	0.62
10:AL:100:THR:HA	10:AL:139:VAL:HB	1.82	0.62
29:A5:8:LYS:O	29:A5:9:LYS:HG2	1.98	0.62
32:A8:33:ASN:HA	32:A8:36:LYS:HD2	1.82	0.62
34:BA:1355:G:H2'	34:BA:1356:G:H8	1.63	0.62
43:BJ:16:LEU:HD21	43:BJ:70:ARG:HG2	1.81	0.62
13:CP:84:ASN:HA	13:CP:115:LEU:O	2.00	0.62
34:DA:438:G:O2'	34:DA:494:U:O4	2.16	0.62
1:AA:667:G:N2	1:AA:670:C:OP2	2.27	0.62
1:AA:965:G:N2	1:AA:2281:A:OP2	2.32	0.62
1:AA:1775:C:H5'	1:AA:1776:G:OP2	2.00	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:AK:118:THR:O	9:AK:120:LYS:N	2.33	0.62
34:BA:255:G:H1'	50:BQ:16:GLN:HE21	1.64	0.62
49:BP:34:GLU:OE2	49:BP:59:TRP:NE1	2.30	0.62
57:BZ:330:VAL:HG12	57:BZ:371:ALA:HA	1.81	0.62
34:DA:1260:C:O5'	34:DA:1284:C:H4'	2.00	0.62
34:DA:1387:G:H2'	34:DA:1388:C:H6	1.65	0.62
39:DF:43:LEU:HD22	39:DF:46:ARG:HH12	1.63	0.62
43:DJ:34:VAL:HG12	43:DJ:74:ILE:HG12	1.82	0.62
49:DP:5:ARG:HH12	49:DP:28:ARG:HA	1.64	0.62
1:AA:261:A:N7	1:AA:283:G:N2	2.48	0.62
37:BD:173:TRP:CD1	37:BD:173:TRP:H	2.15	0.62
45:BL:34:ARG:O	45:BL:61:THR:HG23	1.99	0.62
46:BM:84:ILE:HB	52:BS:74:PHE:HE1	1.64	0.62
48:BO:17:ARG:HG3	48:BO:17:ARG:HH11	1.63	0.62
48:BO:62:GLN:HA	48:BO:65:ARG:NH1	2.15	0.62
49:BP:43:LYS:HG2	49:BP:48:TRP:CD2	2.35	0.62
1:CA:2298:A:H2'	1:CA:2299:G:O4'	2.00	0.62
3:CC:53:ARG:HD3	3:CC:53:ARG:H	1.65	0.62
41:DH:25:ASP:HB3	41:DH:58:TYR:HD2	1.65	0.62
1:AA:2456:G:OP2	6:AF:68:LYS:NZ	2.26	0.62
3:AC:53:ARG:HD3	3:AC:53:ARG:H	1.65	0.62
9:AK:39:ALA:C	9:AK:41:ARG:H	2.07	0.62
34:BA:624:C:H2'	34:BA:625:G:H8	1.65	0.62
34:BA:742:G:OP2	48:BO:35:ARG:NH2	2.33	0.62
36:BC:53:ALA:HB2	36:BC:115:LEU:HD13	1.81	0.62
1:CA:1341:U:OP2	1:CA:1394:U:O2'	2.16	0.62
10:CL:99:ILE:O	10:CL:139:VAL:N	2.25	0.62
34:DA:1226:C:OP2	46:DM:91:ARG:NH1	2.32	0.62
34:DA:1352:C:OP1	54:DU:3:LYS:NZ	2.30	0.62
38:DE:110:LEU:HD13	38:DE:118:ILE:HG21	1.81	0.62
1:AA:1199:C:OP1	18:AU:92:ARG:NH1	2.33	0.62
1:AA:1549:U:H2'	1:AA:1550:C:C6	2.34	0.62
17:AT:88:ILE:HD12	17:AT:91:ARG:HH12	1.64	0.62
34:BA:406:G:N2	37:BD:119:GLN:HE22	1.97	0.62
37:BD:194:LEU:HD12	37:BD:195:ALA:H	1.64	0.62
39:BF:70:ASP:O	39:BF:72:VAL:N	2.33	0.62
1:CA:1082:U:H5'	10:CL:117:THR:HA	1.81	0.62
1:CA:2177:C:H5'	3:CC:45:HIS:CB	2.30	0.62
1:CA:2218:U:O4'	25:C1:52:ARG:NH2	2.33	0.62
1:CA:2689:U:P	1:CA:2719:G:H22	2.22	0.62
12:CO:24:VAL:HB	12:CO:33:ALA:HB2	1.82	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A3:29:ARG:HG2	27:A3:29:ARG:HH11	1.65	0.62
34:BA:1425:U:H2'	34:BA:1426:C:H6	1.64	0.62
38:BE:102:ALA:HB1	38:BE:106:PRO:HB2	1.81	0.62
1:CA:1557:C:OP2	1:CA:1558:A:O2'	2.13	0.62
1:CA:2285:C:OP2	30:C6:6:ARG:NH1	2.33	0.62
2:CB:104:U:O3'	23:CZ:72:ARG:NH1	2.32	0.62
15:CR:9:LYS:HA	15:CR:17:ARG:HE	1.63	0.62
51:DR:25:THR:O	51:DR:25:THR:OG1	2.16	0.62
1:AA:1117:G:H1'	1:AA:1135:G:C8	2.34	0.61
1:AA:2490:A:OP2	33:A9:2:LYS:NZ	2.30	0.61
10:AL:13:PRO:HA	10:AL:52:ILE:HG12	1.81	0.61
34:BA:1307:U:OP1	46:BM:101:GLN:NE2	2.32	0.61
35:BB:213:LEU:HD22	35:BB:214:ILE:HD13	1.82	0.61
3:CC:11:LEU:HD12	3:CC:33:LEU:HA	1.82	0.61
3:CC:68:GLY:H	3:CC:189:ASN:HD21	1.47	0.61
11:CN:72:TYR:N	11:CN:85:ILE:O	2.32	0.61
36:DC:65:ALA:HA	36:DC:100:ALA:HB3	1.81	0.61
53:DT:10:LEU:HG	53:DT:11:SER:H	1.65	0.61
1:AA:202:A:H2'	1:AA:203:G:O4'	2.00	0.61
16:AS:52:SER:HB2	16:AS:55:ALA:N	2.13	0.61
39:BF:99:ALA:HB3	51:BR:29:PHE:HE2	1.65	0.61
21:CX:9:LEU:HB2	21:CX:29:TRP:O	2.00	0.61
23:CZ:104:PHE:HA	23:CZ:139:VAL:HG22	1.83	0.61
36:DC:55:VAL:HG13	36:DC:68:VAL:HG22	1.81	0.61
36:DC:111:LEU:HD22	36:DC:146:ALA:HB2	1.82	0.61
36:DC:136:GLN:O	36:DC:140:ARG:N	2.30	0.61
1:AA:1099:C:C2'	1:AA:1100:A:H5"	2.30	0.61
1:AA:2316:G:O6	63:AA:3927:HOH:O	2.15	0.61
1:AA:2331:G:H22	16:AS:3:ARG:HG2	1.64	0.61
34:BA:688:G:H2'	34:BA:689:C:H6	1.64	0.61
38:BE:48:ALA:H	38:BE:54:ALA:HB2	1.66	0.61
38:BE:92:LYS:HB3	38:BE:119:LEU:HB2	1.83	0.61
1:CA:271(O):C:H2'	1:CA:271(P):C:C6	2.35	0.61
1:CA:2612:C:OP2	29:C5:2:ALA:N	2.33	0.61
30:C6:6:ARG:HH12	30:C6:26:ASN:HB2	1.64	0.61
34:DA:368:U:P	57:DZ:351:ARG:HH11	2.23	0.61
34:DA:473:G:H2'	34:DA:474:G:C8	2.35	0.61
7:AG:18:GLU:O	7:AG:21:ARG:HB2	2.00	0.61
16:AS:95:HIS:CG	16:AS:96:GLY:H	2.19	0.61
37:BD:30:LYS:HA	37:BD:35:ARG:HH11	1.65	0.61
57:BZ:187:THR:HB	57:BZ:199:ILE:HD11	1.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1021:A:C8	1:CA:1021:A:H3'	2.36	0.61
7:CG:108:ASN:HB3	28:C4:22:ILE:HD13	1.82	0.61
13:CP:97:PRO:HD3	13:CP:126:VAL:O	2.01	0.61
34:DA:664:G:H22	34:DA:741:G:H1	1.47	0.61
34:DA:828:A:N6	34:DA:858:G:O2'	2.34	0.61
34:DA:1353:G:H2'	34:DA:1354:C:C6	2.34	0.61
1:AA:1201:A:OP1	18:AU:55:ARG:HD3	2.00	0.61
17:AT:105:LEU:HB2	17:AT:110:ILE:HG13	1.81	0.61
34:BA:783:C:OP1	34:BA:1515:C:O2'	2.18	0.61
34:BA:975:A:N1	43:BJ:48:THR:HB	2.16	0.61
35:BB:48:MET:HA	35:BB:51:LEU:HD12	1.83	0.61
1:CA:360:G:H2'	1:CA:361:G:O4'	2.01	0.61
49:DP:23:ASP:OD1	49:DP:25:ARG:HD3	2.01	0.61
6:AF:183:VAL:O	6:AF:187:VAL:HG23	2.01	0.61
17:AT:7:ILE:O	17:AT:11:GLU:HG3	2.00	0.61
57:BZ:319:ASP:HB3	57:BZ:323:GLY:O	2.00	0.61
1:CA:2132:U:C2	3:CC:6:LYS:CB	2.47	0.61
34:DA:1279:A:OP2	43:DJ:9:ARG:NH1	2.33	0.61
35:BB:83:MET:O	35:BB:87:ARG:HB2	2.00	0.61
47:BN:34:TYR:N	47:BN:39:LEU:O	2.31	0.61
1:CA:1800:C:OP2	4:CD:183:ARG:NH2	2.34	0.61
4:CD:68:LYS:HD2	4:CD:70:TRP:CZ2	2.36	0.61
34:DA:976:G:H5'	34:DA:1358:U:O2'	2.00	0.61
34:DA:1063:C:OP2	34:DA:1064:G:O2'	2.17	0.61
52:DS:33:THR:HG21	52:DS:71:LEU:HD21	1.82	0.61
24:A0:20:ARG:NH2	63:A0:201:HOH:O	2.33	0.61
32:A8:30:ARG:O	63:A8:5101:HOH:O	2.15	0.61
34:BA:1425:U:H2'	34:BA:1426:C:C6	2.36	0.61
49:BP:55:ARG:O	49:BP:58:TYR:N	2.34	0.61
1:CA:340:A:H2'	1:CA:341:G:O4'	2.01	0.61
14:CQ:57:HIS:CD2	14:CQ:117:ALA:HB2	2.35	0.61
15:CR:24:GLN:HE22	15:CR:36:THR:HG21	1.65	0.61
38:DE:78:HIS:HA	41:DH:105:ARG:HG3	1.82	0.61
1:AA:843:C:H2'	1:AA:844:C:C6	2.36	0.61
1:AA:1210:G:H2'	1:AA:1211:U:C6	2.34	0.61
1:AA:1221:G:H1'	1:AA:1222:A:H5'	1.83	0.61
1:AA:2576:A:C2	1:AA:2659:U:H4'	2.35	0.61
1:CA:323:G:HO2'	1:CA:1205:U:H3	1.47	0.61
1:CA:2037:G:O6	63:CA:3738:HOH:O	2.15	0.61
23:CZ:144:LEU:HD22	23:CZ:148:ASP:HB3	1.83	0.61
57:DZ:184:LYS:HB2	57:DZ:184:LYS:NZ	2.16	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:DZ:346:LYS:NZ	57:DZ:384:ILE:HG12	2.15	0.61
1:AA:1106:U:H4'	1:AA:1107:U:H5'	1.81	0.61
17:AT:56:GLY:O	17:AT:59:THR:HG23	2.01	0.61
52:BS:3:ARG:NH1	52:BS:8:GLY:O	2.34	0.61
57:BZ:181:LEU:O	57:BZ:183:MET:N	2.34	0.61
2:CB:62:C:H2'	2:CB:63:G:C8	2.36	0.61
17:CT:56:GLY:O	17:CT:59:THR:HG23	2.00	0.61
57:DZ:-14:ALA:O	57:DZ:-12:ALA:N	2.31	0.61
1:AA:1062:G:N7	63:AA:3981:HOH:O	2.31	0.60
34:BA:1118:C:OP1	42:BI:104:ARG:NH1	2.34	0.60
1:CA:1203:G:H2'	1:CA:1204:A:H2	1.65	0.60
1:CA:2393:A:H5"	13:CP:63:PRO:HB3	1.83	0.60
6:CF:34:TRP:CZ2	13:CP:8:PRO:HG3	2.35	0.60
20:CW:18:ARG:HG3	20:CW:76:VAL:HB	1.82	0.60
41:DH:64:LYS:HG2	41:DH:79:VAL:HG21	1.83	0.60
57:DZ:322:VAL:HG22	57:DZ:363:ARG:HH21	1.66	0.60
1:AA:776:G:C6	4:AD:208:LYS:HB2	2.36	0.60
1:AA:794:U:O2	1:AA:2036:A:H1'	2.01	0.60
1:AA:1553:A:O2'	1:AA:1554:A:O5'	2.19	0.60
1:CA:2121:G:O4'	3:CC:168:LYS:HD3	2.00	0.60
11:CN:62:VAL:HG21	11:CN:87:LEU:HD11	1.83	0.60
32:C8:6:THR:HG22	32:C8:63:PRO:HD2	1.81	0.60
34:DA:1123:A:H4'	43:DJ:36:GLY:HA3	1.83	0.60
1:AA:1466:U:O2'	1:AA:1467:G:OP1	2.18	0.60
6:AF:135:LYS:HB2	6:AF:138:GLU:HG3	1.83	0.60
17:AT:6:LEU:O	17:AT:10:VAL:HG23	2.01	0.60
34:BA:1224:G:N2	63:BA:3323:HOH:O	2.33	0.60
37:BD:13:ARG:NH1	37:BD:13:ARG:HB3	2.17	0.60
37:BD:101:LEU:HG	37:BD:121:VAL:HG11	1.83	0.60
41:BH:116:LYS:O	41:BH:119:LEU:HD21	1.99	0.60
1:CA:910:A:N3	1:CA:2264:C:O2'	2.29	0.60
1:CA:2658:C:O3'	8:CH:158:HIS:HE1	1.83	0.60
28:C4:59:PHE:HA	28:C4:61:ARG:N	2.16	0.60
35:DB:12:GLU:C	35:DB:14:GLY:HA3	2.26	0.60
57:DZ:199:ILE:HB	57:DZ:200:PRO:HD2	1.82	0.60
1:AA:1296:G:N7	13:AP:18:ARG:NH2	2.49	0.60
9:AK:70:GLU:O	9:AK:72:ASP:N	2.34	0.60
20:AW:18:ARG:HG3	20:AW:76:VAL:HB	1.82	0.60
34:BA:576:G:O6	34:BA:880:C:O2'	2.19	0.60
34:BA:875:C:O2'	41:BH:14:ARG:NH1	2.34	0.60
34:BA:953:G:H5'	34:BA:965:A:H61	1.66	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:2583:G:OP2	63:CA:3727:HOH:O	2.16	0.60
3:CC:194:ILE:HD11	3:CC:227:PRO:CB	2.32	0.60
16:CS:23:ARG:HH21	16:CS:84:GLN:HB3	1.67	0.60
35:DB:13:ALA:N	35:DB:14:GLY:HA3	2.16	0.60
35:DB:93:VAL:HG21	35:DB:97:TRP:CD1	2.36	0.60
37:DD:153:ARG:HD3	37:DD:181:MET:HE1	1.83	0.60
57:DZ:223:PHE:HB3	57:DZ:248:LYS:HD3	1.82	0.60
4:AD:180:GLY:HA3	4:AD:275:LYS:HD3	1.83	0.60
8:AH:149:ARG:NH1	8:AH:167:GLU:OE2	2.34	0.60
34:BA:662:G:H2'	34:BA:663:A:C8	2.35	0.60
57:BZ:257:PRO:HB2	57:BZ:259:PHE:HE1	1.66	0.60
1:CA:315:G:H2'	1:CA:316:C:C6	2.37	0.60
1:CA:889:C:O2'	1:CA:890:A:O4'	2.18	0.60
4:CD:127:VAL:HA	4:CD:193:VAL:HG22	1.83	0.60
1:AA:956:A:C5	14:AQ:13:GLN:HG3	2.35	0.60
1:AA:2832:G:OP2	63:AA:3928:HOH:O	2.16	0.60
11:AN:30:ILE:HG22	11:AN:34:LEU:HD22	1.83	0.60
35:BB:73:THR:OG1	35:BB:170:GLU:OE2	2.15	0.60
39:BF:18:GLN:HA	39:BF:21:LEU:HD12	1.84	0.60
57:BZ:184:LYS:HE3	57:BZ:186:TYR:OH	2.01	0.60
1:CA:570:G:H5"	63:CA:4298:HOH:O	2.01	0.60
1:CA:614(B):G:H2'	6:CF:44:ARG:HH11	1.65	0.60
1:CA:2576:G:H8	1:CA:2581:G:O6	1.84	0.60
22:CY:56:PRO:O	22:CY:58:GLY:N	2.31	0.60
34:DA:587:G:N2	34:DA:754:C:OP2	2.27	0.60
34:DA:688:G:H2'	34:DA:689:C:H6	1.67	0.60
1:AA:469:A:C5	6:AF:45:ARG:HD2	2.37	0.60
1:AA:483:A:H5"	63:AA:4405:HOH:O	2.00	0.60
4:AD:10:THR:OG1	4:AD:13:ARG:HB2	2.01	0.60
10:AL:53:VAL:HG12	10:AL:69:THR:HB	1.84	0.60
34:BA:148:G:H2'	34:BA:149:A:C8	2.37	0.60
38:BE:135:THR:O	38:BE:139:LEU:HG	2.01	0.60
57:BZ:96:ARG:O	57:BZ:100:VAL:HG23	2.00	0.60
1:CA:592:G:H4'	32:C8:3:LYS:HB3	1.83	0.60
1:CA:1116:C:H2'	1:CA:1117:G:H8	1.66	0.60
1:CA:2168:G:H2'	1:CA:2169:A:C8	2.37	0.60
12:CO:49:ARG:NH1	34:DA:1423:G:OP1	2.35	0.60
1:AA:1388:A:OP2	63:AA:3930:HOH:O	2.16	0.60
1:AA:2044:U:O2'	1:AA:2629:C:H5'	2.02	0.60
7:AG:105:LYS:HG2	28:A4:24:THR:HG21	1.83	0.60
20:AW:14:PRO:HG2	20:AW:78:GLU:CG	2.30	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:AZ:152:ALA:HB3	23:AZ:167:PRO:HA	1.84	0.60
34:BA:673:G:H2'	34:BA:674:G:C8	2.36	0.60
34:BA:1404:C:O2	34:BA:1519:A:O2'	2.20	0.60
57:BZ:14:ASN:HD22	57:BZ:329:ARG:NH2	2.00	0.60
1:CA:443:A:C6	6:CF:45:ARG:HD2	2.37	0.60
1:CA:2478:A:OP2	33:C9:2:LYS:NZ	2.27	0.60
6:CF:53:THR:HG22	6:CF:56:GLU:HG3	1.84	0.60
37:DD:162:LEU:HD13	37:DD:181:MET:HG2	1.83	0.60
1:AA:863:C:H4'	63:AA:4360:HOH:O	2.01	0.60
1:AA:1189:A:OP1	11:AN:25:ARG:NH2	2.35	0.60
1:AA:1937:U:OP2	63:AA:3932:HOH:O	2.17	0.60
23:AZ:98:MET:O	23:AZ:125:LEU:HD12	2.02	0.60
34:BA:1486:G:O6	63:BA:3306:HOH:O	2.15	0.60
35:BB:195:ASP:O	41:BH:68:ARG:NH2	2.34	0.60
52:BS:41:VAL:HG23	52:BS:44:MET:HE3	1.83	0.60
1:CA:422:A:H2'	1:CA:423:A:C8	2.36	0.60
1:CA:1271:G:N2	1:CA:1617:C:O4'	2.35	0.60
1:CA:1523:U:H2'	1:CA:1524:G:H8	1.67	0.60
1:CA:1611:C:OP1	63:CA:3743:HOH:O	2.16	0.60
6:CF:108:LYS:O	6:CF:112:MET:HG3	2.02	0.60
34:DA:235:C:H5'	50:DQ:70:ARG:HG2	1.83	0.60
34:DA:674:G:H2'	34:DA:675:A:H8	1.67	0.60
1:AA:1945:U:H5"	56:BX:24:U:O2	2.02	0.60
3:AC:214:TYR:CE2	3:AC:224:ARG:HG2	2.36	0.60
13:AP:62:LEU:O	32:A8:13:ARG:HD3	2.02	0.60
34:BA:112:G:HO2'	34:BA:354:G:HO2'	1.50	0.60
34:BA:222:U:H2'	34:BA:223:U:C6	2.36	0.60
34:DA:1281:U:P	34:DA:1282:C:H41	2.25	0.60
3:AC:194:ILE:HD11	3:AC:227:PRO:CB	2.32	0.59
50:BQ:57:VAL:HG12	50:BQ:76:LEU:HA	1.84	0.59
57:BZ:-7:GLU:O	57:BZ:-6:ARG:NH1	2.34	0.59
57:BZ:98:MET:HE2	57:BZ:98:MET:HA	1.84	0.59
1:CA:657:U:H2'	1:CA:658:C:C6	2.37	0.59
1:CA:740:U:OP2	63:CA:3728:HOH:O	2.17	0.59
1:CA:2291:U:H2'	1:CA:2292:C:C6	2.37	0.59
20:CW:4:LYS:HE2	20:CW:6:ILE:HD11	1.84	0.59
34:DA:392:G:H2'	34:DA:393:A:C8	2.36	0.59
34:DA:701:C:OP1	34:DA:702:A:O2'	2.14	0.59
35:DB:210:SER:OG	35:DB:211:ILE:N	2.35	0.59
36:DC:22:TRP:HZ3	36:DC:24:ALA:HB2	1.67	0.59
37:DD:127:THR:HG23	37:DD:147:ALA:HB3	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:DP:53:VAL:HG13	49:DP:79:VAL:HG13	1.84	0.59
1:AA:310:C:H2'	1:AA:311:C:C6	2.37	0.59
1:AA:1105:G:H1'	10:AL:126:MET:HE3	1.83	0.59
1:AA:1825:U:H2'	1:AA:1826:C:C6	2.37	0.59
1:AA:2101:U:O3'	25:A1:35:THR:OG1	2.19	0.59
1:AA:2207:C:H2'	1:AA:2208:G:C8	2.37	0.59
1:AA:2255:U:H2'	1:AA:2256:U:H6	1.65	0.59
1:AA:2287:C:H5'	1:AA:2287:C:C6	2.34	0.59
34:BA:189(C):C:H2'	34:BA:189(D):C:O4'	2.03	0.59
34:BA:230:G:OP1	49:BP:33:ILE:HD11	2.02	0.59
34:BA:1118:C:H1'	34:BA:1179:A:C4	2.37	0.59
44:BK:46:GLY:HA2	44:BK:50:TYR:O	2.02	0.59
56:BX:36:U:O2	57:BZ:502:GLY:HA2	2.02	0.59
1:CA:386:G:H5'	63:CA:4468:HOH:O	2.00	0.59
1:CA:881:G:H1	1:CA:895:U:H3	1.48	0.59
1:CA:1157:G:O6	63:CA:3742:HOH:O	2.16	0.59
1:CA:1860:G:C5'	3:CC:206:LYS:C	2.48	0.59
1:CA:2176:A:C4'	3:CC:45:HIS:NE2	2.61	0.59
57:DZ:630:GLN:O	57:DZ:646:PHE:N	2.34	0.59
1:AA:116:A:O5'	1:AA:117:A:H5"	2.02	0.59
1:AA:597:C:H4'	1:AA:598:A:O5'	2.02	0.59
1:AA:821:A:HO2'	1:AA:822:G:H8	1.49	0.59
1:AA:2317:A:H5"	7:AG:134:GLY:HA3	1.83	0.59
6:AF:17:ARG:HG2	6:AF:18:ARG:H	1.67	0.59
29:A5:49:CYS:SG	29:A5:51:TYR:HB2	2.42	0.59
34:BA:165:C:H2'	34:BA:166:G:C8	2.37	0.59
34:BA:401:C:OP2	37:BD:73:ARG:NH1	2.36	0.59
34:BA:966:G:H21	42:BI:127:LYS:NZ	1.99	0.59
37:BD:107:ARG:HH22	37:BD:194:LEU:CD1	2.15	0.59
1:CA:1325:G:OP1	1:CA:1647:G:O2'	2.19	0.59
1:CA:2132:U:C1'	3:CC:6:LYS:CB	2.77	0.59
1:CA:2723:C:OP2	5:CE:109:LYS:NZ	2.35	0.59
31:C7:26:GLY:O	31:C7:30:VAL:HG23	2.02	0.59
34:DA:392:G:H2'	34:DA:393:A:H8	1.66	0.59
48:DO:61:GLY:O	48:DO:64:ARG:N	2.35	0.59
1:AA:310:C:H2'	1:AA:311:C:H6	1.67	0.59
1:AA:1480:A:H61	1:AA:1605:A:N6	2.00	0.59
3:AC:11:LEU:HD12	3:AC:33:LEU:HA	1.82	0.59
4:AD:101:GLU:OE1	4:AD:103:ARG:NH1	2.27	0.59
16:AS:84:GLN:HA	16:AS:111:GLU:HB2	1.83	0.59
34:BA:67:C:H2'	34:BA:68:G:C8	2.37	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:BZ:88:VAL:HG13	57:BZ:117:GLN:NE2	2.16	0.59
57:BZ:639:ASN:HA	57:BZ:640:ALA:O	2.02	0.59
1:CA:2096:U:H2'	1:CA:2097:C:C6	2.37	0.59
1:CA:2113:U:H2'	1:CA:2114:A:H8	1.66	0.59
34:DA:742:G:OP2	48:DO:35:ARG:NH2	2.36	0.59
34:DA:776:G:N2	34:DA:802:A:OP2	2.33	0.59
37:DD:15:GLU:OE2	37:DD:66:ARG:NH1	2.35	0.59
56:DX:47:U:N3	56:DX:50:U:OP1	2.35	0.59
1:AA:1476:C:H2'	1:AA:1477:U:C6	2.37	0.59
3:AC:214:TYR:CZ	3:AC:224:ARG:HG2	2.37	0.59
17:AT:117:ASP:O	17:AT:120:ARG:N	2.36	0.59
34:BA:572:A:H5'	34:BA:573:A:OP2	2.02	0.59
34:BA:630:G:O2'	34:BA:631:G:H5'	2.03	0.59
1:CA:718:A:H3'	1:CA:719:C:H6	1.67	0.59
2:CB:105:A:P	23:CZ:72:ARG:HH12	2.25	0.59
17:CT:99:LEU:O	17:CT:101:PHE:N	2.35	0.59
34:DA:857:C:H2'	34:DA:858:G:O4'	2.03	0.59
39:DF:62:TRP:CH2	39:DF:64:GLN:HB2	2.37	0.59
1:AA:2365:G:H1'	24:A0:34:GLY:HA3	1.83	0.59
5:AE:27:LEU:HD22	17:AT:1:MET:SD	2.43	0.59
18:AU:32:PHE:O	18:AU:35:ALA:HB3	2.02	0.59
23:AZ:171:ILE:HD12	23:AZ:172:ALA:N	2.16	0.59
35:BB:158:LEU:HG	35:BB:182:ILE:HD11	1.85	0.59
57:BZ:21:ILE:H	57:BZ:21:ILE:CD1	2.15	0.59
1:CA:2168:G:H2'	1:CA:2169:A:H8	1.67	0.59
10:CL:73:PRO:O	10:CL:77:LEU:HG	2.02	0.59
1:AA:123:G:H5"	31:A7:19:ARG:HD3	1.83	0.59
1:AA:174:U:H4'	1:AA:207:A:H4'	1.85	0.59
34:BA:49:U:O4	34:BA:365:U:H5	1.85	0.59
50:BQ:78:GLU:OE1	50:BQ:81:ARG:NH1	2.36	0.59
57:BZ:19:ALA:HB1	57:BZ:23:ALA:HB3	1.84	0.59
1:CA:994:C:OP1	18:CU:53:ARG:NH2	2.36	0.59
3:CC:41:THR:HG22	3:CC:42:VAL:N	2.17	0.59
3:CC:214:TYR:CE2	3:CC:224:ARG:HG2	2.37	0.59
14:CQ:109:VAL:HG13	14:CQ:113:GLN:HB3	1.84	0.59
23:CZ:183:LEU:O	23:CZ:185:GLU:N	2.36	0.59
25:C1:62:VAL:HG22	25:C1:63:ALA:O	2.03	0.59
34:DA:113:G:N3	34:DA:353:A:O2'	2.33	0.59
34:DA:336:C:H2'	34:DA:337:C:H6	1.68	0.59
34:DA:338:A:H2'	34:DA:339:C:O4'	2.03	0.59
1:AA:1229:G:OP1	27:A3:29:ARG:HD2	2.01	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:2259:A:H2'	1:AA:2260:C:H6	1.67	0.59
1:AA:2525:G:O6	63:AA:3925:HOH:O	2.14	0.59
34:BA:679:C:H2'	34:BA:680:C:H6	1.67	0.59
34:BA:975:A:N6	34:BA:1367:C:O4'	2.36	0.59
38:BE:43:LEU:HD21	38:BE:132:ALA:HB1	1.84	0.59
57:BZ:357:ARG:NH1	57:BZ:373:ASP:CG	2.61	0.59
1:CA:558:G:OP1	11:CN:111:PRO:HD2	2.03	0.59
1:CA:1102:C:H2'	1:CA:1103:A:C8	2.37	0.59
1:CA:2807:G:N1	1:CA:2893:G:O6	2.32	0.59
3:CC:214:TYR:CZ	3:CC:224:ARG:HG2	2.37	0.59
6:CF:28:ILE:HA	6:CF:112:MET:HE2	1.84	0.59
8:CH:144:VAL:O	8:CH:148:ILE:HG12	2.03	0.59
34:DA:409:G:H1	34:DA:433:C:H42	1.51	0.59
37:DD:10:ARG:HA	37:DD:13:ARG:HG3	1.83	0.59
1:AA:1219:A:H4'	1:AA:1220:U:OP1	2.00	0.59
1:AA:1817:A:H8	63:AA:4147:HOH:O	1.86	0.59
1:AA:2158:C:H42	1:AA:2177:G:H1	1.50	0.59
36:BC:43:LEU:HD22	36:BC:47:LEU:HD11	1.83	0.59
1:CA:2572:A:N7	5:CE:144:ARG:HD2	2.18	0.59
17:CT:88:ILE:HG13	17:CT:91:ARG:NH2	2.17	0.59
34:DA:503:C:H2'	34:DA:504:C:C6	2.37	0.59
34:DA:1187:G:H4'	42:DI:111:ARG:HH11	1.67	0.59
52:DS:33:THR:OG1	52:DS:35:SER:O	2.21	0.59
1:AA:1039:G:OP1	18:AU:50:ARG:NH2	2.35	0.59
1:AA:2504:U:H2'	1:AA:2505:U:C6	2.38	0.59
4:AD:137:PRO:O	4:AD:140:THR:HG23	2.03	0.59
38:BE:110:LEU:HD13	38:BE:118:ILE:HG21	1.84	0.59
57:BZ:309:LEU:HA	57:BZ:333:GLY:HA3	1.85	0.59
1:CA:1063:G:H1'	10:CL:134:MET:HA	1.84	0.59
1:CA:1827:C:OP2	4:CD:222:ARG:NH1	2.36	0.59
1:CA:2356:C:O3'	24:C0:20:ARG:HD3	2.02	0.59
1:CA:2567:G:H2'	1:CA:2568:C:C6	2.38	0.59
2:CB:56:G:H5'	7:CG:27:ASN:ND2	2.18	0.59
16:CS:84:GLN:HA	16:CS:111:GLU:HB2	1.83	0.59
34:DA:1107:C:C4	34:DA:1108:G:C8	2.91	0.59
34:DA:1227:A:N3	52:DS:83:HIS:HB3	2.18	0.59
1:AA:1134:A:N6	10:AL:133:SER:OG	2.36	0.58
1:AA:1586:G:H2'	1:AA:1587:U:O4'	2.03	0.58
1:AA:1828:C:H4'	4:AD:257:LEU:O	2.03	0.58
1:AA:1830:G:N7	4:AD:179:SER:OG	2.35	0.58
4:AD:133:LEU:HB3	4:AD:173:VAL:HG11	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:AP:88:LEU:HD11	13:AP:114:ILE:HD12	1.85	0.58
23:AZ:70:LEU:HD11	23:AZ:98:MET:HE2	1.85	0.58
32:A8:26:LYS:HD3	63:A8:5105:HOH:O	2.02	0.58
34:BA:551:U:H2'	34:BA:552:U:C6	2.37	0.58
34:BA:975:A:H5'	34:BA:975:A:H8	1.68	0.58
34:BA:1274:G:N2	34:BA:1275:A:N7	2.51	0.58
34:BA:1347:G:H22	34:BA:1373:G:H2'	1.68	0.58
48:BO:32:LEU:O	48:BO:35:ARG:N	2.36	0.58
57:BZ:146:LEU:HG	57:BZ:260:LEU:HD22	1.85	0.58
1:CA:528:A:C2	1:CA:2043:C:H4'	2.38	0.58
1:CA:1049:C:H3'	1:CA:1050:A:H8	1.67	0.58
6:CF:36:VAL:HG11	6:CF:183:VAL:CG1	2.33	0.58
34:DA:858:G:O6	34:DA:869:G:H3'	2.03	0.58
57:DZ:164:MET:O	57:DZ:180:VAL:HG22	2.03	0.58
57:DZ:221:ALA:HB1	57:DZ:228:MET:HB2	1.84	0.58
1:AA:1683:C:OP2	63:AA:3931:HOH:O	2.17	0.58
1:AA:1825:U:H2'	1:AA:1826:C:H6	1.68	0.58
1:AA:1993:A:P	4:AD:242:ARG:HH22	2.26	0.58
1:AA:2357:G:H4'	1:AA:2358:A:O5'	2.03	0.58
52:BS:36:ARG:NH2	52:BS:72:GLY:O	2.37	0.58
57:BZ:99:ARG:CZ	57:BZ:312:LEU:HD11	2.33	0.58
1:CA:1803:A:H4'	4:CD:259:THR:CG2	2.32	0.58
1:CA:2886:G:H2'	1:CA:2887:U:C6	2.37	0.58
5:CE:78:LEU:O	5:CE:79:ARG:HG2	2.02	0.58
34:DA:201:C:H42	34:DA:216:G:H1	1.50	0.58
53:DT:10:LEU:HB3	53:DT:12:ALA:H	1.68	0.58
1:AA:1517:G:N7	63:AA:3987:HOH:O	2.32	0.58
1:AA:1520:G:C6	1:AA:1521:C:C4	2.90	0.58
8:AH:164:TYR:HB2	8:AH:167:GLU:HB2	1.84	0.58
34:BA:234:C:H2'	34:BA:235:C:H6	1.68	0.58
34:BA:396:G:OP1	57:BZ:349:LYS:NZ	2.32	0.58
57:BZ:-23:LEU:HA	57:BZ:-20:LEU:HB2	1.85	0.58
1:CA:194:G:H3'	63:CA:3965:HOH:O	2.02	0.58
1:CA:1109:C:H5'	1:CA:1110:G:OP2	2.03	0.58
1:CA:2713:A:OP2	1:CA:2713:A:H4'	2.04	0.58
1:AA:354:A:H2	1:AA:1255:A:O2'	1.87	0.58
1:AA:455:A:OP2	1:AA:455:A:C8	2.55	0.58
1:AA:1636:U:H2'	1:AA:1637:G:C8	2.39	0.58
1:AA:2762:A:OP1	8:AH:3:ARG:NH2	2.31	0.58
3:AC:41:THR:HG22	3:AC:42:VAL:N	2.17	0.58
18:AU:8:VAL:HG23	18:AU:11:ARG:HH21	1.69	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:BA:1467:G:O6	63:BA:3307:HOH:O	2.16	0.58
35:BB:19:HIS:HE1	35:BB:189:ASP:HB3	1.67	0.58
6:CF:32:LEU:HD11	6:CF:105:VAL:HG13	1.84	0.58
34:DA:528:C:H41	45:DL:49:ASN:ND2	2.01	0.58
34:DA:1203:C:OP1	47:DN:3:ARG:HG3	2.02	0.58
34:DA:1241:G:H2'	34:DA:1242:C:C6	2.38	0.58
34:DA:1251:A:N6	34:DA:1285:A:N1	2.51	0.58
1:AA:1563:G:H2'	1:AA:1564:C:H6	1.69	0.58
1:AA:2658:C:H2'	1:AA:2659:U:O4'	2.03	0.58
57:BZ:182:ARG:HH11	57:BZ:182:ARG:HG3	1.67	0.58
1:CA:1063:G:N3	10:CL:91:PRO:HG2	2.18	0.58
1:CA:1379:A:H4'	1:CA:1380:G:OP2	2.02	0.58
21:CX:59:VAL:N	21:CX:76:ARG:O	2.28	0.58
1:AA:831:A:C6	4:AD:229:VAL:HG11	2.38	0.58
1:AA:864:C:H4'	1:AA:977:G:C5	2.39	0.58
1:AA:1834:A:H4'	4:AD:259:THR:HG23	1.85	0.58
4:AD:102:LYS:C	4:AD:103:ARG:HG2	2.29	0.58
10:AL:23:VAL:HA	10:AL:27:LEU:HD22	1.85	0.58
34:BA:749:C:H2'	34:BA:750:G:H8	1.69	0.58
34:BA:1277:C:O2'	34:BA:1279:A:H1'	2.03	0.58
35:BB:192:SER:O	35:BB:194:PRO:HD3	2.03	0.58
36:BC:33:LEU:O	36:BC:36:ASP:HB2	2.04	0.58
1:CA:1859:A:H2'	3:CC:206:LYS:HD2	1.71	0.58
1:CA:2148:G:H2'	1:CA:2149:G:C8	2.38	0.58
2:CB:22:U:H3	2:CB:61:G:H1	1.50	0.58
14:CQ:57:HIS:HD2	14:CQ:117:ALA:HB2	1.68	0.58
15:CR:29:LEU:HD23	15:CR:70:LEU:HD11	1.86	0.58
20:CW:59:VAL:HG12	20:CW:60:ASN:HD22	1.68	0.58
34:DA:509:A:C8	34:DA:509:A:H3'	2.38	0.58
34:DA:922:G:H2'	34:DA:923:A:C8	2.38	0.58
4:AD:108:PRO:HD2	4:AD:111:LEU:HG	1.85	0.58
24:A0:43:THR:O	24:A0:43:THR:HG23	2.03	0.58
27:A3:3:ARG:NH1	27:A3:60:GLU:OE2	2.36	0.58
42:BI:23:ASN:N	42:BI:60:ASP:OD1	2.35	0.58
1:CA:1021:A:H3'	1:CA:1021:A:H8	1.68	0.58
1:CA:1967:C:H2'	1:CA:1968:G:H5'	1.86	0.58
34:DA:56:U:H2'	34:DA:57:G:H8	1.68	0.58
36:DC:57:ILE:HG13	36:DC:66:VAL:HG22	1.84	0.58
1:AA:153:C:H2'	1:AA:154:G:O4'	2.04	0.58
1:AA:2279:A:H5"	1:AA:2280:A:H5'	1.86	0.58
27:A3:7:LYS:HG3	27:A3:34:GLU:HG3	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A3:19:GLN:OE1	27:A3:52:HIS:NE2	2.32	0.58
34:BA:1435:G:H2'	34:BA:1436:U:C6	2.39	0.58
57:BZ:343:ASN:HA	57:BZ:389:LEU:HD12	1.85	0.58
1:CA:938:G:OP1	32:C8:52:LYS:NZ	2.30	0.58
7:CG:37:VAL:O	7:CG:94:LEU:N	2.22	0.58
15:CR:1:MET:HE3	15:CR:3:HIS:CE1	2.39	0.58
21:CX:35:THR:HG22	21:CX:37:THR:N	2.16	0.58
21:CX:57:LEU:HD13	21:CX:78:LYS:HB3	1.86	0.58
34:DA:1119:C:H2'	34:DA:1120:G:C8	2.38	0.58
38:DE:80:ILE:HD13	41:DH:104:ARG:HH21	1.69	0.58
7:AG:170:ARG:NH1	7:AG:174:GLU:OE1	2.37	0.58
17:AT:2:ASN:O	17:AT:6:LEU:HD22	2.03	0.58
34:BA:394:G:H2'	34:BA:395:C:H6	1.68	0.58
40:BG:108:ALA:HA	40:BG:111:ARG:HD2	1.85	0.58
57:BZ:32:ILE:HG23	57:BZ:273:LEU:HD21	1.85	0.58
1:CA:1047:G:O2'	1:CA:1110:G:O6	2.22	0.58
1:CA:1453:U:O2'	1:CA:1455:G:N7	2.35	0.58
1:CA:1612:C:O2'	31:C7:5:TRP:O	2.21	0.58
1:CA:2121:G:C1'	3:CC:168:LYS:HE2	2.32	0.58
8:CH:3:ARG:HH22	8:CH:5:GLY:H	1.51	0.58
12:CO:115:VAL:HG13	12:CO:121:VAL:HG21	1.86	0.58
17:CT:13:ARG:HB3	17:CT:13:ARG:HH11	1.68	0.58
34:DA:1292:U:H2'	34:DA:1293:G:H8	1.69	0.58
1:AA:733:G:O5'	31:A7:11:LYS:NZ	2.37	0.58
1:AA:1079:U:OP1	33:A9:9:ARG:NH2	2.37	0.58
1:AA:2430:A:H2'	1:AA:2431:U:H6	1.69	0.58
2:AB:4:C:N4	2:AB:117:G:H1	2.01	0.58
13:AP:70:GLN:O	13:AP:73:GLY:N	2.26	0.58
17:AT:60:THR:HG22	17:AT:77:PRO:HA	1.86	0.58
30:A6:34:LEU:HB2	30:A6:51:GLU:HB2	1.86	0.58
57:BZ:399:LEU:O	57:BZ:401:SER:N	2.35	0.58
7:CG:136:ARG:HD2	7:CG:137:GLU:N	2.18	0.58
34:DA:1029:C:H2'	34:DA:1030:C:H5"	1.86	0.58
35:DB:162:ILE:HD11	35:DB:184:VAL:HG22	1.85	0.58
57:DZ:20:HIS:HB2	57:DZ:118:SER:OG	2.04	0.58
57:DZ:170:ARG:N	57:DZ:170:ARG:NH1	2.51	0.58
1:AA:1904:C:H2'	1:AA:1905:G:O4'	2.04	0.57
5:AE:128:SER:OG	5:AE:129:HIS:N	2.35	0.57
17:AT:53:ARG:HB3	17:AT:53:ARG:CZ	2.33	0.57
19:AV:49:THR:HG22	19:AV:49:THR:O	2.02	0.57
21:AX:11:PRO:HD3	26:A2:37:PHE:CE1	2.39	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:BA:258:G:H2'	34:BA:259:G:H8	1.69	0.57
34:BA:1137:C:H4'	34:BA:1138:G:C2	2.38	0.57
37:BD:178:VAL:HG12	37:BD:179:GLU:H	1.67	0.57
41:BH:65:TYR:HA	41:BH:79:VAL:HG23	1.85	0.57
56:BX:36:U:H1'	57:BZ:503:GLY:N	2.18	0.57
1:CA:699:A:H2'	1:CA:700:G:O4'	2.03	0.57
1:CA:1167:U:H2'	1:CA:1168:G:C8	2.39	0.57
1:CA:1653:G:C6	15:CR:9:LYS:HG3	2.39	0.57
10:CL:2:LYS:HD3	57:DZ:154:GLN:HE22	1.69	0.57
26:C2:1:MET:HE3	26:C2:5:GLU:HB3	1.85	0.57
27:C3:29:ARG:HB3	27:C3:33:GLN:HE22	1.69	0.57
34:DA:457:C:H2'	34:DA:458:C:H6	1.68	0.57
37:DD:31:CYS:SG	37:DD:33:MET:N	2.77	0.57
1:AA:1314:A:H2'	1:AA:1315:A:O4'	2.04	0.57
1:AA:1735:U:O2	1:AA:1747:A:H5'	2.03	0.57
7:AG:165:THR:OG1	7:AG:168:GLU:HG3	2.04	0.57
34:BA:642:A:H2'	34:BA:643:C:C6	2.40	0.57
34:BA:1086:U:H3	34:BA:1099:G:H22	1.50	0.57
57:BZ:119:GLU:OE1	57:BZ:156:ARG:NH1	2.36	0.57
1:CA:298:G:H5"	1:CA:299:A:OP1	2.04	0.57
4:CD:7:LYS:O	4:CD:9:TYR:N	2.37	0.57
32:C8:33:ASN:HA	32:C8:36:LYS:HG3	1.86	0.57
33:C9:29:ASN:HD22	33:C9:32:HIS:CE1	2.22	0.57
34:DA:858:G:N1	34:DA:870:U:OP2	2.30	0.57
34:DA:1050:G:N2	34:DA:1208:C:O2	2.18	0.57
34:DA:1143:G:H2'	34:DA:1144:G:H8	1.69	0.57
34:DA:1304:G:O2'	34:DA:1333:A:N6	2.37	0.57
57:DZ:24:GLY:O	57:DZ:28:THR:OG1	2.19	0.57
1:AA:173:C:H2'	1:AA:174:U:C6	2.39	0.57
1:AA:1700:G:H3'	15:AR:2:ARG:HD3	1.86	0.57
1:AA:2360:U:OP2	32:A8:42:ARG:NH2	2.36	0.57
1:AA:2776:G:N7	63:AA:3984:HOH:O	2.32	0.57
10:AL:73:PRO:O	10:AL:77:LEU:HG	2.02	0.57
28:A4:58:ARG:O	28:A4:60:GLN:N	2.37	0.57
34:BA:56:U:H2'	34:BA:57:G:C8	2.38	0.57
34:BA:1345:U:OP1	42:BI:120:ARG:NH1	2.33	0.57
34:DA:35:G:O2'	45:DL:118:SER:O	2.19	0.57
50:DQ:95:TYR:HA	50:DQ:98:LEU:HD12	1.84	0.57
57:DZ:344:THR:OG1	57:DZ:388:THR:HB	2.05	0.57
1:AA:821:A:H2'	1:AA:821:A:N3	2.18	0.57
1:AA:2589:A:O2'	29:A5:2:ALA:HB1	2.03	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:2769:U:H1'	1:AA:2770:A:H5"	1.85	0.57
13:AP:63:PRO:HG2	32:A8:25:MET:HB2	1.87	0.57
19:AV:40:LEU:HB2	19:AV:46:VAL:HG13	1.87	0.57
34:BA:381:C:H2'	34:BA:382:A:O4'	2.04	0.57
34:BA:1221:G:H4'	52:BS:77:THR:HG21	1.86	0.57
34:BA:1326:C:H2'	34:BA:1327:C:C6	2.39	0.57
35:BB:170:GLU:HB3	35:BB:173:ALA:HB3	1.85	0.57
1:CA:336:C:H5"	22:CY:6:HIS:ND1	2.20	0.57
34:DA:1314:C:OP2	52:DS:4:SER:OG	2.16	0.57
38:DE:33:VAL:HG13	38:DE:112:LEU:HD12	1.87	0.57
46:DM:3:ARG:N	46:DM:7:VAL:O	2.37	0.57
56:DX:72:A:H2'	56:DX:73:A:C8	2.39	0.57
1:AA:553:A:C8	1:AA:553:A:C3'	2.86	0.57
1:AA:935:C:N3	1:AA:936:C:N4	2.52	0.57
1:AA:1136:U:O2	1:AA:1148:C:H1'	2.05	0.57
1:AA:1255:A:H5"	1:AA:1257:G:O4'	2.04	0.57
1:AA:2585:C:OP1	63:AA:3934:HOH:O	2.18	0.57
8:AH:150:ALA:HA	8:AH:153:LYS:HD3	1.87	0.57
21:AX:53:LYS:NZ	21:AX:55:ASN:OD1	2.36	0.57
36:BC:110:ASN:O	36:BC:111:LEU:HD23	2.05	0.57
37:BD:104:VAL:HG11	37:BD:146:ILE:HD13	1.87	0.57
38:BE:11:ILE:HD11	38:BE:108:ALA:HB3	1.85	0.57
57:BZ:13:ARG:NH1	57:BZ:247:ARG:HH12	2.02	0.57
1:CA:322:A:C5	1:CA:340:A:C2	2.92	0.57
6:CF:20:LEU:HD13	6:CF:21:ALA:H	1.69	0.57
56:DX:19:G:H4'	56:DX:20:U:OP2	2.03	0.57
1:AA:197:C:H2'	1:AA:198:C:H6	1.70	0.57
1:AA:1100:A:N6	1:AA:1151:U:H3	1.99	0.57
1:AA:1104:G:N2	1:AA:1127:U:H1'	2.19	0.57
1:AA:1968:U:H2'	1:AA:1969:C:C6	2.40	0.57
7:AG:68:PRO:HB3	7:AG:92:VAL:HB	1.87	0.57
16:AS:3:ARG:HD3	16:AS:4:LEU:N	2.19	0.57
33:A9:15:LYS:HG2	33:A9:17:ILE:HD13	1.86	0.57
49:BP:19:ILE:HG23	49:BP:37:GLY:O	2.04	0.57
53:BT:56:MET:HE3	53:BT:88:VAL:HB	1.87	0.57
57:BZ:165:GLN:NE2	57:BZ:260:LEU:H	2.03	0.57
57:BZ:324:ARG:HG3	57:BZ:324:ARG:NH1	2.18	0.57
1:CA:1204:A:H2	1:CA:1241:A:H62	1.52	0.57
1:CA:2577:A:H5'	29:C5:3:LYS:HD3	1.85	0.57
4:CD:10:THR:OG1	4:CD:13:ARG:HG2	2.04	0.57
14:CQ:38:GLU:OE2	14:CQ:128:LYS:N	2.30	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:DI:47:LEU:HB3	42:DI:50:LEU:HD12	1.85	0.57
53:DT:42:GLN:O	53:DT:42:GLN:NE2	2.38	0.57
57:DZ:114:VAL:HG21	57:DZ:156:ARG:HB2	1.86	0.57
1:AA:54:G:O2'	1:AA:125:A:N1	2.29	0.57
1:AA:1356:G:OP2	31:A7:9:ARG:NH1	2.38	0.57
1:AA:1496:A:H5'	1:AA:1497:G:OP2	2.05	0.57
1:AA:2264:G:N7	24:A0:4:LYS:NZ	2.52	0.57
2:AB:24:G:H3'	63:AB:3102:HOH:O	2.05	0.57
6:AF:53:THR:HB	6:AF:56:GLU:OE2	2.05	0.57
10:AL:12:LEU:HD11	10:AL:23:VAL:HG22	1.85	0.57
10:AL:112:MET:HG3	10:AL:113:PRO:HD3	1.86	0.57
10:AL:115:LEU:HD22	10:AL:126:MET:HE1	1.85	0.57
15:AR:44:LEU:HD22	15:AR:48:VAL:HG23	1.84	0.57
23:AZ:138:GLU:H	23:AZ:156:LYS:HE3	1.70	0.57
33:A9:11:CYS:HB3	33:A9:32:HIS:CE1	2.39	0.57
34:BA:501:C:H2'	34:BA:502:G:C8	2.40	0.57
36:BC:19:GLU:HB3	36:BC:40:ARG:NH2	2.18	0.57
42:BI:4:TYR:CE1	42:BI:88:TYR:HA	2.40	0.57
1:CA:195:A:H61	1:CA:198:C:H3'	1.69	0.57
1:CA:747:U:O2'	20:CW:92:ARG:NH2	2.38	0.57
1:CA:1071:G:O2'	1:CA:1089:G:OP2	2.19	0.57
1:CA:1462:C:H4'	1:CA:2703:C:H5'	1.86	0.57
10:CL:74:ALA:HB1	10:CL:127:ILE:HD12	1.84	0.57
10:CL:112:MET:HG3	10:CL:113:PRO:HD3	1.86	0.57
34:DA:403:C:H2'	34:DA:404:U:H6	1.69	0.57
34:DA:513:C:H2'	34:DA:514:C:H6	1.70	0.57
34:DA:652:U:O4	34:DA:752:G:O2'	2.22	0.57
35:DB:24:TRP:CZ3	35:DB:26:PRO:HA	2.39	0.57
39:DF:87:ARG:HG3	39:DF:87:ARG:NH1	2.05	0.57
57:DZ:-65:LYS:HB3	57:DZ:-28:ALA:HB3	1.86	0.57
1:AA:836:A:N1	63:AA:3988:HOH:O	2.32	0.57
13:AP:1:MET:HE2	13:AP:6:LEU:HD23	1.87	0.57
34:BA:828:A:H2'	34:BA:829:G:O4'	2.04	0.57
34:BA:1187:G:H5"	42:BI:113:LYS:HD3	1.85	0.57
34:BA:1376:U:H2'	34:BA:1377:A:C8	2.39	0.57
37:BD:4:TYR:O	37:BD:6:GLY:N	2.35	0.57
1:CA:1247:A:OP1	6:CF:95:ARG:NH2	2.37	0.57
1:CA:1860:G:C8	3:CC:206:LYS:HG3	2.39	0.57
34:DA:254:G:OP1	50:DQ:68:ARG:N	2.30	0.57
34:DA:837:G:H1	34:DA:849:C:H42	1.52	0.57
42:DI:28:VAL:HG22	42:DI:63:ILE:HB	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:997:G:OP1	14:AQ:16:ARG:NH2	2.38	0.57
1:AA:1499:C:N4	1:AA:1506:G:H1	2.03	0.57
1:AA:2326:C:H2'	1:AA:2327:G:C8	2.38	0.57
1:AA:2658:C:OP2	1:AA:2745:G:O2'	2.23	0.57
17:AT:24:PRO:HD3	17:AT:52:ILE:HD12	1.86	0.57
23:AZ:48:PHE:HE2	23:AZ:71:VAL:HG11	1.70	0.57
34:BA:895:G:H2'	34:BA:896:C:C6	2.39	0.57
38:BE:90:VAL:O	38:BE:120:THR:HA	2.05	0.57
1:CA:776:G:H4'	1:CA:777:A:O5'	2.05	0.57
1:CA:1803:A:H4'	4:CD:259:THR:HG23	1.85	0.57
2:CB:60:C:H2'	2:CB:61:G:H8	1.68	0.57
6:CF:192:LEU:HD13	6:CF:194:MET:HE2	1.87	0.57
11:CN:67:LEU:HD13	11:CN:87:LEU:HD13	1.87	0.57
34:DA:737:A:H2'	34:DA:738:C:C6	2.40	0.57
46:DM:25:ILE:HG23	46:DM:29:ARG:HB3	1.87	0.57
46:DM:78:ILE:HG22	46:DM:82:MET:HE3	1.86	0.57
57:DZ:32:ILE:HG23	57:DZ:273:LEU:HD21	1.87	0.57
1:AA:139:A:H8	1:AA:1454:C:HO2'	1.50	0.57
1:AA:409:G:OP2	63:AA:3933:HOH:O	2.18	0.57
1:AA:479:C:O2	1:AA:483:A:O2'	2.23	0.57
1:AA:574:G:O2'	1:AA:1265:A:N3	2.28	0.57
1:AA:2268:G:H2'	1:AA:2269:U:O4'	2.05	0.57
13:AP:121:LYS:O	13:AP:123:LEU:N	2.38	0.57
17:AT:27:THR:HB	17:AT:89:VAL:HG23	1.87	0.57
23:AZ:111:VAL:C	23:AZ:113:ALA:H	2.11	0.57
34:BA:376:G:OP2	49:BP:67:THR:HG21	2.04	0.57
34:BA:679:C:H2'	34:BA:680:C:C6	2.39	0.57
34:BA:1373:G:H4'	40:BG:31:MET:SD	2.44	0.57
53:BT:22:ARG:O	53:BT:25:ARG:N	2.38	0.57
1:CA:58:G:O2'	1:CA:73:A:N1	2.37	0.57
1:CA:795:C:H2'	1:CA:796:C:C6	2.39	0.57
1:CA:1334:G:O6	63:CA:3744:HOH:O	2.16	0.57
1:CA:1766:U:H2'	1:CA:1767:C:H6	1.70	0.57
3:CC:29:LEU:O	3:CC:30:VAL:C	2.48	0.57
15:CR:56:LYS:NZ	15:CR:90:ARG:O	2.38	0.57
34:DA:1118:C:OP1	42:DI:104:ARG:NH1	2.37	0.57
1:AA:934:A:OP1	1:AA:935:C:N4	2.36	0.56
1:AA:1093:G:N2	1:AA:1156:G:O2'	2.37	0.56
6:AF:34:TRP:NE1	13:AP:8:PRO:HD3	2.20	0.56
18:AU:74:LEU:HD12	18:AU:74:LEU:H	1.70	0.56
21:AX:57:LEU:CD1	21:AX:78:LYS:HB2	2.34	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:AZ:138:GLU:N	23:AZ:156:LYS:HE3	2.20	0.56
57:BZ:74:TRP:CD1	57:BZ:273:LEU:HB3	2.39	0.56
1:CA:307:G:N1	1:CA:310:A:OP2	2.37	0.56
1:CA:746:A:H2'	1:CA:2612:C:H5"	1.87	0.56
5:CE:101:ARG:HD2	5:CE:169:ASN:OD1	2.04	0.56
13:CP:138:LEU:HD23	13:CP:145:PRO:HG3	1.86	0.56
34:DA:677:U:O2	34:DA:777:A:O2'	2.23	0.56
34:DA:839:U:H5"	34:DA:840:C:C5	2.35	0.56
34:DA:1248:A:H2'	34:DA:1249:C:C6	2.40	0.56
57:DZ:242:LEU:HD23	57:DZ:245:ALA:HB3	1.86	0.56
1:AA:839:G:H5"	1:AA:840:A:H5'	1.86	0.56
1:AA:1120:G:H2'	1:AA:1121:C:C6	2.39	0.56
1:AA:2556:G:H1'	1:AA:2658:C:H4'	1.88	0.56
3:AC:29:LEU:O	3:AC:30:VAL:C	2.48	0.56
11:AN:23:LEU:HD13	11:AN:98:VAL:HG12	1.87	0.56
23:AZ:7:ALA:HB2	23:AZ:59:LEU:HD22	1.87	0.56
34:BA:193:C:H2'	34:BA:194:C:H6	1.69	0.56
34:BA:1202:G:H2'	34:BA:1203:C:O4'	2.05	0.56
35:BB:55:PHE:CD1	35:BB:58:ILE:HD12	2.40	0.56
40:BG:28:ASN:HD21	40:BG:36:LYS:HE3	1.70	0.56
44:BK:21:ILE:HB	44:BK:84:VAL:HG22	1.87	0.56
1:CA:995:C:O2	11:CN:3:THR:OG1	2.14	0.56
4:CD:95:LEU:HD11	4:CD:105:ILE:HG23	1.86	0.56
7:CG:44:GLY:O	7:CG:47:LYS:HB2	2.06	0.56
14:CQ:54:MET:HG2	14:CQ:117:ALA:O	2.05	0.56
21:CX:91:ALA:O	21:CX:92:LEU:HD23	2.05	0.56
34:DA:585:G:H4'	45:DL:8:ASN:OD1	2.04	0.56
42:DI:53:VAL:O	42:DI:55:ALA:N	2.38	0.56
1:AA:347:G:C8	6:AF:171:PRO:HG3	2.40	0.56
1:AA:1836:U:OP1	4:AD:252:TRP:NE1	2.37	0.56
1:AA:1907:A:H2'	1:AA:1908:C:O4'	2.05	0.56
1:AA:2143:G:O2'	3:AC:168:LYS:CD	2.52	0.56
1:AA:2897:U:H2'	1:AA:2898:C:C6	2.40	0.56
3:AC:6:LYS:HG3	3:AC:7:ARG:H	1.69	0.56
5:AE:105:THR:OG1	5:AE:166:THR:OG1	2.23	0.56
12:AO:2:ILE:HD12	12:AO:6:THR:HG21	1.86	0.56
15:AR:49:ASP:OD1	15:AR:95:THR:OG1	2.18	0.56
17:AT:39:ARG:NH1	17:AT:41:ARG:HD3	2.20	0.56
17:AT:65:LYS:HE2	17:AT:67:SER:HB2	1.87	0.56
19:AV:18:LEU:HD13	19:AV:20:LEU:HB2	1.88	0.56
29:A5:16:ARG:HD3	29:A5:20:ARG:NH1	2.20	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:BA:503:C:H2'	34:BA:504:C:C6	2.40	0.56
34:BA:1158:C:H5	34:BA:1181:G:N1	1.96	0.56
34:BA:1183:A:O2'	34:BA:1184:G:OP1	2.19	0.56
34:BA:1441:G:H5"	34:BA:1442:G:H5'	1.86	0.56
57:BZ:93:GLU:HA	57:BZ:93:GLU:OE2	2.04	0.56
57:BZ:278:ASP:HB3	57:BZ:279:TYR:CD2	2.40	0.56
1:CA:1203:G:H2'	1:CA:1204:A:C2	2.39	0.56
1:CA:1240:U:O4	63:CA:3739:HOH:O	2.15	0.56
1:CA:1420:U:O2'	1:CA:1421:G:OP1	2.22	0.56
1:CA:2312:U:H5'	7:CG:88:ILE:HD11	1.86	0.56
13:CP:81:GLN:NE2	13:CP:105:LEU:O	2.38	0.56
25:C1:73:LEU:HB3	25:C1:94:LEU:HD23	1.87	0.56
34:DA:475:G:H2'	34:DA:476:G:H8	1.70	0.56
34:DA:978:A:OP2	34:DA:1363:C:N4	2.38	0.56
34:DA:1150:U:O4	34:DA:1151:A:N6	2.39	0.56
34:DA:1255:G:OP1	43:DJ:45:ARG:NH2	2.38	0.56
34:DA:1256:A:H61	34:DA:1278:U:H1'	1.70	0.56
34:DA:1292:U:H2'	34:DA:1293:G:C8	2.40	0.56
35:DB:29:ALA:HA	35:DB:32:ILE:HD12	1.87	0.56
38:DE:36:ASP:C	38:DE:38:GLN:H	2.14	0.56
45:DL:93:LEU:HB3	45:DL:96:VAL:HG21	1.87	0.56
49:DP:68:ASP:O	49:DP:71:ARG:HG2	2.06	0.56
57:DZ:215:LYS:HD3	57:DZ:215:LYS:N	2.20	0.56
1:AA:397:G:OP2	1:AA:397:G:H8	1.88	0.56
1:AA:791:G:O6	63:AA:3929:HOH:O	2.16	0.56
1:AA:2481:A:O2'	14:AQ:56:ARG:HD2	2.04	0.56
1:AA:2784:C:H2'	1:AA:2785:C:C6	2.39	0.56
10:AL:51:ALA:HB1	10:AL:72:PRO:HB3	1.88	0.56
37:BD:78:LEU:HB3	37:BD:93:PHE:CE1	2.41	0.56
3:CC:6:LYS:HG3	3:CC:7:ARG:H	1.69	0.56
19:CV:69:LYS:HA	19:CV:87:HIS:O	2.05	0.56
30:C6:13:CYS:SG	30:C6:47:THR:HG21	2.46	0.56
34:DA:1401:G:C2	34:DA:1402:C:H1'	2.41	0.56
38:DE:92:LYS:HB3	38:DE:119:LEU:HB2	1.88	0.56
57:DZ:237:PRO:HB3	57:DZ:241:GLU:OE1	2.05	0.56
57:DZ:265:LYS:O	57:DZ:267:LYS:HG3	2.06	0.56
1:AA:244:A:O2'	1:AA:411:U:OP1	2.23	0.56
1:AA:296:U:H2'	1:AA:297:C:C6	2.40	0.56
1:AA:313:A:N6	1:AA:375:G:H1'	2.21	0.56
4:AD:13:ARG:HD2	4:AD:16:MET:HE3	1.86	0.56
9:AK:117:LEU:HA	9:AK:123:GLU:H	1.70	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:AP:29:LYS:HG2	13:AP:30:THR:HG23	1.86	0.56
23:AZ:134:PRO:O	23:AZ:136:PHE:N	2.38	0.56
34:BA:946:A:H2'	34:BA:947:G:C8	2.40	0.56
34:BA:975:A:H4'	34:BA:976:G:H5"	1.87	0.56
57:BZ:184:LYS:HD2	57:BZ:198:GLU:OE2	2.06	0.56
1:CA:1069:A:N7	1:CA:1073:A:N6	2.54	0.56
1:CA:1324:G:O2'	1:CA:1326:U:OP2	2.24	0.56
1:CA:2758:A:H2'	1:CA:2759:G:O4'	2.04	0.56
13:CP:99:LEU:HD12	13:CP:100:LEU:HD23	1.88	0.56
23:CZ:102:LEU:HD11	23:CZ:124:ILE:HB	1.85	0.56
26:C2:16:LEU:O	26:C2:67:LYS:NZ	2.22	0.56
26:C2:32:LEU:HD13	26:C2:36:ARG:NH1	2.21	0.56
30:C6:9:LEU:HD13	30:C6:51:GLU:HG3	1.86	0.56
34:DA:35:G:N3	45:DL:118:SER:HB2	2.20	0.56
49:DP:53:VAL:O	49:DP:57:ARG:N	2.38	0.56
1:AA:152:G:H2'	1:AA:153:C:C6	2.40	0.56
1:AA:886:U:H1'	1:AA:1236:G:H1'	1.87	0.56
1:AA:1298:G:O6	18:AU:36:ARG:HG2	2.05	0.56
1:AA:1817:A:H1'	1:AA:1960:A:N6	2.21	0.56
1:AA:2624:C:OP2	29:A5:2:ALA:N	2.38	0.56
15:AR:63:ARG:O	15:AR:67:LEU:HB2	2.05	0.56
15:AR:118:GLU:H	15:AR:118:GLU:CD	2.14	0.56
28:A4:10:VAL:HG21	28:A4:29:PRO:HG3	1.86	0.56
34:BA:347:G:H2'	34:BA:348:G:O4'	2.05	0.56
34:BA:674:G:H2'	34:BA:675:A:H8	1.70	0.56
34:BA:1129:C:O2'	34:BA:1139:G:N7	2.37	0.56
1:CA:660:G:H5'	6:CF:99:TYR:CE2	2.41	0.56
1:CA:996:A:H4'	18:CU:91:ASP:OD2	2.06	0.56
3:CC:49:GLY:N	3:CC:209:PHE:O	2.39	0.56
6:CF:56:GLU:CD	6:CF:93:LYS:HZ3	2.13	0.56
34:DA:418:C:H2'	34:DA:419:C:C6	2.40	0.56
34:DA:937:A:N6	34:DA:1345:U:O4	2.38	0.56
34:DA:1218:C:OP1	47:DN:12:ARG:NH2	2.39	0.56
1:AA:1882:U:C4	1:AA:1883:C:C4	2.94	0.56
1:AA:2255:U:H2'	1:AA:2256:U:C6	2.40	0.56
4:AD:98:VAL:HG23	4:AD:99:ASP:H	1.70	0.56
23:AZ:51:ALA:HA	23:AZ:55:HIS:HD2	1.70	0.56
27:A3:18:ASP:OD1	27:A3:18:ASP:N	2.39	0.56
27:A3:44:ARG:O	27:A3:48:GLU:HG3	2.06	0.56
30:A6:25:LYS:HE3	30:A6:30:THR:O	2.06	0.56
36:BC:11:ARG:NH2	36:BC:177:THR:O	2.39	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:BP:74:LEU:HG	49:BP:79:VAL:HG21	1.88	0.56
57:BZ:149:VAL:O	57:BZ:153:MET:HG3	2.04	0.56
57:BZ:215:LYS:O	57:BZ:219:VAL:HG13	2.06	0.56
1:CA:2512:C:H2'	1:CA:2513:G:O4'	2.06	0.56
4:CD:83:GLU:OE1	4:CD:104:TYR:OH	2.19	0.56
5:CE:14:ILE:HG13	5:CE:21:VAL:HG13	1.86	0.56
21:CX:8:ILE:HD11	21:CX:43:VAL:HG23	1.87	0.56
34:DA:325:A:OP2	53:DT:70:SER:OG	2.18	0.56
34:DA:1114:C:H42	34:DA:1186:G:H1	1.53	0.56
37:DD:129:ASN:ND2	37:DD:145:GLU:H	2.02	0.56
40:DG:18:TYR:CD2	40:DG:59:LEU:HB2	2.40	0.56
44:DK:48:ILE:C	44:DK:50:TYR:H	2.12	0.56
57:DZ:13:ARG:HH12	57:DZ:77:HIS:CE1	2.24	0.56
57:DZ:15:ILE:HA	57:DZ:103:GLY:O	2.06	0.56
1:AA:329:U:H2'	1:AA:330:U:C6	2.41	0.56
1:AA:1660:A:N1	20:AW:87:PRO:HB3	2.20	0.56
4:AD:72:LYS:HD3	4:AD:97:TYR:CE2	2.41	0.56
20:AW:70:TYR:OH	20:AW:72:LYS:HG3	2.06	0.56
29:A5:57:VAL:HG12	29:A5:58:LEU:HB2	1.87	0.56
34:BA:787:A:H8	34:BA:787:A:H5"	1.71	0.56
37:BD:31:CYS:SG	37:BD:33:MET:N	2.79	0.56
57:BZ:99:ARG:NH1	57:BZ:401:SER:O	2.38	0.56
57:BZ:160:ARG:HE	57:BZ:254:LYS:C	2.14	0.56
1:CA:1977:A:N3	63:CA:3813:HOH:O	2.32	0.56
5:CE:37:ARG:NE	5:CE:80:GLU:OE1	2.35	0.56
34:DA:1040:U:N3	34:DA:1041:A:N7	2.54	0.56
34:DA:1228:C:OP1	46:DM:115:LYS:N	2.31	0.56
49:DP:5:ARG:CZ	49:DP:22:THR:HG21	2.36	0.56
1:AA:546:G:H2'	1:AA:547:G:C8	2.41	0.56
1:AA:1126:C:O2'	10:AL:126:MET:HG3	2.05	0.56
11:AN:75:TYR:CE2	11:AN:77:GLY:HA2	2.41	0.56
13:AP:50:ARG:HD3	32:A8:7:HIS:CD2	2.41	0.56
15:AR:28:LEU:HD12	15:AR:48:VAL:HG21	1.87	0.56
20:AW:23:LEU:CD2	29:A5:25:LEU:HD12	2.36	0.56
23:AZ:135:GLU:O	23:AZ:136:PHE:HB2	2.05	0.56
43:BJ:47:PHE:HB2	43:BJ:63:PHE:HB2	1.87	0.56
49:BP:20:VAL:HG21	49:BP:32:TYR:CG	2.41	0.56
1:CA:2166:G:H3'	1:CA:2167:U:H5"	1.88	0.56
5:CE:36:ARG:HD3	5:CE:47:VAL:HG12	1.88	0.56
7:CG:15:VAL:HA	7:CG:175:LEU:HD23	1.87	0.56
34:DA:502:G:C6	34:DA:503:C:N3	2.74	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:DO:33:THR:HG21	48:DO:85:LEU:HD22	1.88	0.56
48:DO:40:SER:O	48:DO:44:LYS:HG3	2.05	0.56
1:AA:927:G:N2	1:AA:944:C:N3	2.53	0.56
1:AA:2221:A:OP2	1:AA:2222:C:H5	1.89	0.56
1:AA:2474:U:H1'	1:AA:2503:U:O4	2.06	0.56
5:AE:108:SER:O	5:AE:162:ALA:HA	2.06	0.56
5:AE:117:MET:HG3	63:AE:402:HOH:O	2.06	0.56
6:AF:53:THR:HG22	6:AF:56:GLU:HG3	1.88	0.56
7:AG:115:ARG:HG3	7:AG:116:ASP:CG	2.31	0.56
23:AZ:77:ASP:OD2	23:AZ:80:ARG:HB2	2.05	0.56
25:A1:89:GLU:HA	25:A1:92:LYS:HB2	1.86	0.56
34:BA:44:G:C2	34:BA:45:U:H1'	2.41	0.56
34:BA:921:U:O2	38:BE:19:MET:HB2	2.06	0.56
34:BA:959:A:HO2'	34:BA:984:C:HO2'	1.32	0.56
34:BA:1191:A:H2'	34:BA:1192:C:C6	2.41	0.56
35:BB:60:ASP:OD2	35:BB:64:ARG:NH2	2.37	0.56
57:BZ:147:TRP:O	57:BZ:151:ARG:HB2	2.06	0.56
1:CA:1292:U:H2'	1:CA:1293:C:C6	2.41	0.56
1:CA:2424:C:O2	1:CA:2429:G:O2'	2.19	0.56
1:CA:2677:G:H2'	1:CA:2678:C:C6	2.41	0.56
3:CC:42:VAL:O	3:CC:216:THR:O	2.24	0.56
17:CT:19:LEU:HD22	17:CT:86:ILE:HD12	1.86	0.56
20:CW:43:GLY:O	20:CW:47:VAL:HG23	2.06	0.56
34:DA:957:U:H2'	34:DA:959:A:OP2	2.06	0.56
34:DA:1012:U:H2'	34:DA:1013:G:C8	2.40	0.56
1:AA:436:C:OP1	63:AA:3936:HOH:O	2.18	0.55
30:A6:18:ARG:HD3	30:A6:42:TRP:CE2	2.42	0.55
34:BA:1525:G:P	44:BK:120:ARG:HH22	2.29	0.55
36:BC:35:GLU:OE2	36:BC:59:ARG:NH2	2.23	0.55
42:BI:116:LYS:HD2	42:BI:122:ALA:HA	1.89	0.55
1:CA:2572:A:C8	5:CE:144:ARG:HD2	2.41	0.55
13:CP:100:LEU:HB3	13:CP:106:LEU:HB2	1.88	0.55
26:C2:64:LEU:HD11	26:C2:68:ARG:HH21	1.72	0.55
34:DA:297:G:N2	34:DA:300:A:OP2	2.39	0.55
34:DA:1435:G:H2'	34:DA:1436:U:C6	2.41	0.55
35:DB:142:LEU:HG	35:DB:146:GLN:NE2	2.20	0.55
36:DC:110:ASN:ND2	36:DC:144:SER:OG	2.40	0.55
36:DC:179:ARG:HD2	36:DC:206:GLU:HB2	1.87	0.55
44:DK:79:SER:HB2	44:DK:106:LYS:HE3	1.89	0.55
50:DQ:81:ARG:HH21	50:DQ:84:LEU:HD21	1.69	0.55
1:AA:886:U:H2'	1:AA:887:C:C6	2.41	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1154:U:HO2'	1:AA:1155:C:H6	1.53	0.55
6:AF:132:VAL:CG2	6:AF:163:VAL:HG22	2.35	0.55
13:AP:86:LYS:HB3	13:AP:118:GLY:HA3	1.87	0.55
17:AT:118:ARG:HG3	17:AT:118:ARG:NH1	2.15	0.55
34:BA:17:U:H2'	34:BA:18:C:C6	2.41	0.55
34:BA:911:U:H2'	34:BA:912:C:C6	2.41	0.55
36:BC:70:VAL:HG22	36:BC:72:LYS:H	1.71	0.55
36:BC:125:GLU:HA	36:BC:191:THR:HG22	1.87	0.55
42:BI:16:ARG:HH11	42:BI:64:THR:HG21	1.71	0.55
1:CA:96:G:H4'	26:C2:48:HIS:CD2	2.40	0.55
1:CA:800:A:H8	1:CA:800:A:OP1	1.89	0.55
1:CA:1856:G:H1	1:CA:1886:C:N4	2.03	0.55
1:CA:2336:A:H61	24:C0:43:THR:CG2	2.19	0.55
8:CH:56:SER:HB3	8:CH:61:HIS:ND1	2.21	0.55
15:CR:51:LEU:HD13	15:CR:70:LEU:HD21	1.88	0.55
34:DA:671:G:H2'	34:DA:672:U:O4'	2.06	0.55
42:DI:8:GLY:O	42:DI:15:ALA:N	2.32	0.55
45:DL:75:HIS:HD2	45:DL:77:LEU:N	1.99	0.55
1:AA:236:G:H4'	1:AA:413:G:C5	2.41	0.55
1:AA:672:G:H2'	1:AA:673:G:O4'	2.06	0.55
10:AL:55:VAL:HG13	10:AL:57:ILE:HD11	1.89	0.55
13:AP:39:LYS:NZ	63:AP:301:HOH:O	2.34	0.55
34:BA:685:G:O2'	34:BA:686:U:H5'	2.06	0.55
1:CA:771:G:OP1	31:C7:10:ARG:NH1	2.39	0.55
4:CD:71:ASP:CG	4:CD:103:ARG:HH22	2.13	0.55
16:CS:105:ALA:O	16:CS:110:LEU:HB2	2.06	0.55
34:DA:433:C:H2'	34:DA:434:U:H6	1.70	0.55
34:DA:517:G:N1	34:DA:533:A:OP2	2.39	0.55
50:DQ:64:PRO:HB3	50:DQ:70:ARG:HH11	1.70	0.55
10:AL:119:ASP:CG	10:AL:120:LEU:H	2.14	0.55
21:AX:50:LYS:HG2	21:AX:84:ALA:HB2	1.88	0.55
1:CA:537:C:OP1	1:CA:995:C:N4	2.39	0.55
1:CA:774:A:H2'	1:CA:774:A:N3	2.19	0.55
1:CA:1814:G:O6	63:CA:3724:HOH:O	2.09	0.55
1:CA:1842:G:O2'	4:CD:253:GLN:NE2	2.40	0.55
34:DA:409:G:H1	34:DA:433:C:N4	2.03	0.55
34:DA:411:A:H62	34:DA:413:G:H21	1.54	0.55
37:DD:103:ASN:OD1	37:DD:114:ARG:NH2	2.37	0.55
45:DL:69:TYR:CE2	45:DL:71:PRO:HA	2.41	0.55
1:AA:441:C:O2	1:AA:1895:U:O2'	2.24	0.55
1:AA:834:U:H5"	1:AA:835:A:H5'	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:BA:1015:A:H2'	34:BA:1016:A:C8	2.42	0.55
34:BA:1394:A:C5	34:BA:1501:C:H4'	2.42	0.55
35:BB:91:PRO:HG2	35:BB:155:LEU:HD13	1.89	0.55
36:BC:172:ARG:NH2	36:BC:206:GLU:OE2	2.37	0.55
43:BJ:17:ASP:OD1	43:BJ:70:ARG:NH1	2.40	0.55
50:BQ:53:LEU:HD23	50:BQ:82:MET:HE1	1.89	0.55
53:BT:33:ILE:HG13	53:BT:62:LEU:HD22	1.88	0.55
1:CA:1932:A:H2'	1:CA:1933:G:O4'	2.06	0.55
6:CF:116:ASP:OD2	6:CF:117:ARG:NH1	2.40	0.55
6:CF:126:VAL:HG21	6:CF:129:PHE:CZ	2.42	0.55
16:CS:49:VAL:HG11	16:CS:77:ALA:HB2	1.87	0.55
34:DA:1142:G:H3'	34:DA:1143:G:C8	2.41	0.55
35:DB:93:VAL:HG21	35:DB:97:TRP:HD1	1.70	0.55
1:AA:81:G:N2	1:AA:101:A:OP2	2.28	0.55
1:AA:354:A:HO2'	1:AA:355:A:H8	1.53	0.55
1:AA:923:C:H2'	1:AA:924:U:O4'	2.06	0.55
1:AA:1405:A:N1	1:AA:1418:U:C4	2.74	0.55
1:AA:2720:G:H1'	15:AR:71:GLN:HE22	1.72	0.55
25:A1:64:ALA:HA	25:A1:67:ILE:HG13	1.88	0.55
34:BA:921:U:O2'	38:BE:19:MET:O	2.23	0.55
34:BA:937:A:N6	34:BA:1345:U:O4	2.38	0.55
57:BZ:-10:ARG:HB2	57:BZ:-10:ARG:HH11	1.72	0.55
1:CA:38:A:H2'	1:CA:39:C:C6	2.41	0.55
1:CA:1095:A:N7	1:CA:1096:A:N6	2.55	0.55
1:CA:2483:C:H2'	1:CA:2484:G:O4'	2.07	0.55
2:CB:41:U:C4	7:CG:70:VAL:HG23	2.41	0.55
34:DA:987:G:N2	34:DA:1219:U:O2	2.39	0.55
45:DL:53:ARG:HH12	45:DL:92:ASP:HB2	1.72	0.55
1:AA:469:A:C6	6:AF:45:ARG:HD2	2.42	0.55
1:AA:504:A:N1	1:AA:525:G:H4'	2.22	0.55
1:AA:510:C:H2'	1:AA:511:C:C6	2.42	0.55
1:AA:1220:U:O3'	1:AA:1221:G:H4'	2.06	0.55
2:AB:66:A:N6	2:AB:108:U:H2'	2.22	0.55
34:BA:458:C:N4	34:BA:474:G:O6	2.40	0.55
34:BA:1074:G:O2'	34:BA:1101:A:N1	2.37	0.55
1:CA:674:G:O2'	6:CF:74:ARG:HD3	2.06	0.55
1:CA:856:C:H2'	1:CA:857:C:C6	2.42	0.55
1:CA:1107:G:OP1	9:CK:58:LEU:HA	2.06	0.55
1:CA:2474:C:H5"	1:CA:2475:C:OP2	2.06	0.55
1:CA:2721:A:H5"	63:CA:3740:HOH:O	2.06	0.55
4:CD:108:PRO:HD2	4:CD:111:LEU:HG	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:DA:1429:C:H2'	34:DA:1430:C:C6	2.41	0.55
38:DE:71:LEU:HD21	38:DE:113:ALA:O	2.07	0.55
1:AA:239:G:OP2	32:A8:13:ARG:NH2	2.40	0.55
1:AA:546:G:H2'	1:AA:547:G:H8	1.72	0.55
1:AA:1923:A:OP2	4:AD:255:LYS:HE3	2.06	0.55
1:AA:2575:U:H4'	12:AO:28:SER:HA	1.89	0.55
23:AZ:156:LYS:HG2	23:AZ:157:LEU:N	2.22	0.55
35:BB:16:HIS:CG	35:BB:17:PHE:N	2.75	0.55
36:BC:25:GLY:O	36:BC:27:LYS:N	2.40	0.55
38:BE:83:GLU:HG2	38:BE:88:LYS:HD2	1.89	0.55
57:BZ:-58:LEU:HD11	57:BZ:-32:LEU:HD13	1.87	0.55
57:BZ:-23:LEU:H	57:BZ:-21:ALA:H	1.55	0.55
57:BZ:116:PRO:HA	57:BZ:119:GLU:HG3	1.87	0.55
57:BZ:289:ILE:HD11	57:BZ:331:TYR:CG	2.42	0.55
1:CA:184:C:H2'	1:CA:185:U:H6	1.71	0.55
1:CA:338:G:N7	63:CA:3819:HOH:O	2.33	0.55
1:CA:956:G:OP2	14:CQ:14:ARG:NH2	2.35	0.55
1:CA:1058:G:O2'	10:CL:115:LEU:O	2.25	0.55
1:CA:2364:C:OP1	24:C0:55:ARG:NH1	2.38	0.55
26:C2:32:LEU:HD13	26:C2:36:ARG:HH11	1.72	0.55
35:DB:142:LEU:HG	35:DB:146:GLN:HE21	1.72	0.55
57:DZ:13:ARG:NH1	57:DZ:77:HIS:ND1	2.55	0.55
1:AA:559:U:H2'	1:AA:560:C:C6	2.42	0.55
1:AA:865:G:H5'	1:AA:886:U:OP1	2.07	0.55
3:AC:194:ILE:HD11	3:AC:227:PRO:HB3	1.89	0.55
4:AD:71:ASP:OD2	4:AD:103:ARG:NH2	2.40	0.55
6:AF:32:LEU:HB3	6:AF:112:MET:HE1	1.87	0.55
22:AY:56:PRO:C	22:AY:58:GLY:H	2.15	0.55
32:A8:11:LYS:HG3	32:A8:11:LYS:O	2.07	0.55
34:BA:200:G:H1	34:BA:217:C:N4	1.98	0.55
34:BA:486:U:H2'	34:BA:487:A:C8	2.41	0.55
34:BA:826:C:H4'	41:BH:12:ARG:HD3	1.89	0.55
35:BB:20:GLU:HA	35:BB:21:ARG:HH21	1.72	0.55
36:BC:16:ARG:NH1	36:BC:183:ASP:OD1	2.27	0.55
1:CA:154(A):C:H42	1:CA:171:G:H1	1.55	0.55
1:CA:614(B):G:N2	6:CF:44:ARG:O	2.36	0.55
1:CA:1466:G:O2'	1:CA:1546:C:O2'	2.16	0.55
1:CA:2507:C:C2	1:CA:2583:G:C2	2.95	0.55
5:CE:120:TRP:CE3	5:CE:155:LYS:HD3	2.41	0.55
10:CL:6:ALA:HB3	10:CL:30:HIS:CE1	2.40	0.55
19:CV:6:LYS:HB2	19:CV:38:LEU:HD21	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:CY:20:TYR:CE1	22:CY:43:ASN:HA	2.42	0.55
34:DA:254:G:O3'	50:DQ:69:LYS:NZ	2.40	0.55
34:DA:673:G:H2'	34:DA:674:G:C8	2.42	0.55
35:DB:215:LEU:O	35:DB:219:VAL:HG23	2.07	0.55
1:AA:388:A:H2'	1:AA:389:G:H8	1.72	0.55
3:AC:52:PRO:HB2	3:AC:168:LYS:O	2.07	0.55
21:AX:35:THR:HG22	21:AX:38:GLU:H	1.71	0.55
34:BA:619:U:N3	37:BD:134:ASP:OD2	2.23	0.55
37:BD:168:ARG:HH11	37:BD:168:ARG:H	1.55	0.55
41:BH:120:THR:OG1	41:BH:123:GLU:HB2	2.07	0.55
1:CA:2526:G:H5'	1:CA:2742:C:O2'	2.06	0.55
2:CB:45:A:OP2	7:CG:96:ARG:NH2	2.40	0.55
14:CQ:85:LYS:HB2	24:C0:7:LEU:HD12	1.87	0.55
34:DA:869:G:H8	34:DA:869:G:O5'	1.90	0.55
34:DA:986:A:O2'	52:DS:55:LYS:O	2.25	0.55
51:DR:73:ALA:HB3	51:DR:79:LEU:HD12	1.88	0.55
1:AA:1558:G:H2'	1:AA:1559:C:C6	2.42	0.54
1:AA:2787:C:H2'	1:AA:2788:A:O4'	2.06	0.54
2:AB:41:U:C5	7:AG:70:VAL:HB	2.43	0.54
3:AC:42:VAL:O	3:AC:216:THR:O	2.24	0.54
3:AC:54:ARG:CZ	3:AC:56:ASP:HB3	2.38	0.54
1:CA:236:C:H2'	1:CA:237:C:H6	1.71	0.54
1:CA:1046:A:H3'	1:CA:1047:G:H5'	1.88	0.54
1:CA:1374:G:H2'	1:CA:1375:C:C6	2.43	0.54
3:CC:6:LYS:HA	3:CC:9:ARG:HH11	1.73	0.54
20:CW:12:ILE:HG13	20:CW:42:ARG:NH1	2.21	0.54
23:CZ:100:VAL:O	23:CZ:124:ILE:N	2.40	0.54
29:C5:16:ARG:HG2	29:C5:17:ASP:OD1	2.06	0.54
34:DA:8:A:N6	37:DD:209:ARG:HB2	2.21	0.54
34:DA:373:A:H61	34:DA:391:G:H1'	1.72	0.54
34:DA:687:A:H4'	34:DA:688:G:O5'	2.07	0.54
34:DA:1143:G:H2'	34:DA:1144:G:C8	2.42	0.54
45:DL:55:VAL:HG22	45:DL:68:ALA:O	2.07	0.54
57:DZ:108:PHE:O	57:DZ:137:ASN:N	2.36	0.54
57:DZ:316:ILE:HG12	57:DZ:385:THR:HG22	1.88	0.54
1:AA:1587:U:H2'	1:AA:1588:G:O4'	2.07	0.54
1:AA:2705:A:H2'	1:AA:2706:G:C8	2.41	0.54
9:AK:26:LEU:HA	9:AK:84:GLU:HA	1.89	0.54
9:AK:103:GLY:HA3	9:AK:111:LEU:H	1.73	0.54
10:AL:11:GLN:O	10:AL:52:ILE:HD13	2.08	0.54
14:AQ:60:ARG:HA	23:AZ:178:GLU:O	2.06	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:A4:26:SER:OG	28:A4:27:THR:N	2.40	0.54
34:BA:189(K):U:H2'	34:BA:189(L):G:C8	2.42	0.54
34:BA:1000:U:H2'	34:BA:1001:A:H8	1.72	0.54
34:BA:1369:C:H2'	34:BA:1370:G:C8	2.42	0.54
43:BJ:65:LEU:HB2	47:BN:56:VAL:HG22	1.88	0.54
53:BT:9:ASN:O	53:BT:10:LEU:HB2	2.07	0.54
1:CA:621:A:H5'	13:CP:108:LYS:HZ1	1.72	0.54
1:CA:996:A:C2	1:CA:997:G:C8	2.95	0.54
1:CA:2846:G:H2'	1:CA:2847:U:O4'	2.07	0.54
3:CC:52:PRO:HB2	3:CC:168:LYS:O	2.07	0.54
10:CL:12:LEU:HD11	10:CL:23:VAL:HG21	1.90	0.54
13:CP:68:GLN:OE1	13:CP:68:GLN:HA	2.07	0.54
14:CQ:38:GLU:HB2	14:CQ:39:PRO:HD2	1.89	0.54
34:DA:460:G:O6	34:DA:470:C:H5"	2.08	0.54
34:DA:1097:C:O2'	34:DA:1169:A:N3	2.39	0.54
34:DA:1129:C:H2'	34:DA:1139:G:N7	2.22	0.54
1:AA:197:C:H2'	1:AA:198:C:C6	2.43	0.54
1:AA:1141:A:H2'	1:AA:1142:A:C8	2.42	0.54
1:AA:1525:G:O2'	1:AA:1605:A:H2	1.90	0.54
4:AD:155:LEU:HD23	4:AD:177:LEU:HD22	1.90	0.54
10:AL:15:GLY:O	10:AL:17:ALA:N	2.40	0.54
20:AW:14:PRO:CG	20:AW:78:GLU:HG2	2.35	0.54
34:BA:382:A:H2'	34:BA:383:A:H8	1.72	0.54
38:BE:122:GLU:O	38:BE:126:ARG:NH1	2.40	0.54
52:BS:3:ARG:HG2	52:BS:4:SER:H	1.73	0.54
1:CA:1141:U:H2'	11:CN:63:THR:HG21	1.89	0.54
1:CA:2121:G:O4'	3:CC:168:LYS:NZ	2.36	0.54
6:CF:28:ILE:HD11	6:CF:116:ASP:HB2	1.89	0.54
7:CG:170:ARG:NH1	7:CG:174:GLU:OE2	2.40	0.54
34:DA:1000:U:H2'	34:DA:1001:A:C8	2.41	0.54
1:AA:2396:G:OP2	24:A0:55:ARG:NH1	2.40	0.54
3:AC:183:PRO:C	3:AC:185:LYS:H	2.16	0.54
14:AQ:43:THR:HA	14:AQ:94:VAL:HG12	1.90	0.54
34:BA:551:U:H2'	34:BA:552:U:H6	1.71	0.54
37:BD:134:ASP:O	37:BD:136:PRO:HD3	2.07	0.54
37:BD:155:LEU:HD13	37:BD:158:ILE:HD11	1.88	0.54
44:BK:81:ASP:OD2	44:BK:107:SER:OG	2.25	0.54
57:BZ:39:ILE:HD12	57:BZ:40:HIS:H	1.72	0.54
1:CA:491:G:H2'	1:CA:492:A:C8	2.42	0.54
1:CA:932:G:H4'	1:CA:933:A:O5'	2.05	0.54
1:CA:1653:G:H3'	15:CR:2:ARG:HD3	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:CL:74:ALA:HA	10:CL:77:LEU:CD1	2.37	0.54
21:CX:55:ASN:HB2	21:CX:80:ILE:HB	1.88	0.54
34:DA:583:A:H2'	34:DA:584:G:O4'	2.07	0.54
35:DB:44:LEU:HD22	35:DB:44:LEU:H	1.72	0.54
35:DB:71:VAL:HG23	35:DB:164:VAL:HA	1.89	0.54
50:DQ:27:PHE:CE2	50:DQ:36:ILE:HD11	2.42	0.54
56:DX:76:A:H3'	56:DX:76:A:OP2	2.08	0.54
1:AA:1102:G:H5"	1:AA:1103:A:O4'	2.07	0.54
1:AA:2638:C:H2'	1:AA:2639:G:C8	2.42	0.54
3:AC:49:GLY:N	3:AC:209:PHE:O	2.39	0.54
10:AL:33:ASN:HB3	10:AL:36:GLU:HB2	1.90	0.54
12:AO:53:LYS:HG2	12:AO:56:ASP:OD2	2.08	0.54
13:AP:85:LEU:HD12	13:AP:116:GLY:HA2	1.89	0.54
14:AQ:32:TYR:HB2	14:AQ:106:VAL:HG23	1.90	0.54
27:A3:5:LYS:HD3	27:A3:59:VAL:HG11	1.90	0.54
34:BA:1030(D):A:H62	34:BA:1031:G:H21	1.56	0.54
57:BZ:21:ILE:HD13	57:BZ:21:ILE:N	2.23	0.54
1:CA:2683:C:H5"	17:CT:53:ARG:HH12	1.72	0.54
3:CC:44:VAL:HG23	3:CC:176:VAL:HG21	1.89	0.54
3:CC:183:PRO:C	3:CC:185:LYS:H	2.16	0.54
7:CG:5:VAL:HG13	7:CG:8:LYS:HB2	1.90	0.54
13:CP:63:PRO:HG2	32:C8:25:MET:HB2	1.90	0.54
22:CY:28:LYS:N	22:CY:38:ILE:O	2.40	0.54
34:DA:435:C:H2'	34:DA:436:C:C6	2.42	0.54
34:DA:539:A:H2'	34:DA:540:G:H8	1.72	0.54
35:DB:71:VAL:HA	35:DB:93:VAL:HG22	1.89	0.54
38:DE:83:GLU:HA	38:DE:88:LYS:HA	1.88	0.54
46:DM:33:ALA:O	46:DM:37:THR:OG1	2.21	0.54
57:DZ:168:ILE:N	57:DZ:176:GLY:O	2.41	0.54
57:DZ:264:LEU:HD12	62:DZ:704:GDP:C4	2.43	0.54
1:AA:624:C:OP1	6:AF:108:LYS:HE3	2.08	0.54
16:AS:25:ARG:HD3	16:AS:42:ASP:OD2	2.08	0.54
34:BA:1521:G:H2'	34:BA:1522:U:O4'	2.08	0.54
3:CC:194:ILE:HD11	3:CC:227:PRO:HB3	1.89	0.54
4:CD:68:LYS:HD2	4:CD:70:TRP:CH2	2.42	0.54
13:CP:59:LEU:O	32:C8:13:ARG:HD2	2.08	0.54
21:CX:43:VAL:HG11	21:CX:81:VAL:HG21	1.90	0.54
34:DA:757:U:O2'	34:DA:879:C:O2	2.24	0.54
34:DA:982:U:O2	34:DA:1222:G:N1	2.37	0.54
37:DD:135:LEU:C	37:DD:137:SER:H	2.16	0.54
53:DT:50:GLU:H	53:DT:99:LEU:HD12	1.73	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:2150:C:H4'	3:AC:219:MET:HE3	1.89	0.54
1:AA:2714:U:H4'	1:AA:2715:C:OP1	2.06	0.54
1:AA:2789:A:C6	1:AA:2791:A:C6	2.95	0.54
22:AY:55:TYR:N	22:AY:55:TYR:CD1	2.75	0.54
34:BA:33:A:H2'	34:BA:34:C:C6	2.42	0.54
34:BA:345:C:O5'	34:BA:345:C:H6	1.91	0.54
34:BA:1013:G:N2	34:BA:1015:A:H3'	2.22	0.54
37:BD:23:GLY:HA3	37:BD:112:VAL:HG12	1.89	0.54
57:BZ:252:ASP:O	57:BZ:253:LEU:HB2	2.06	0.54
1:CA:938:G:P	32:C8:52:LYS:HZ2	2.30	0.54
1:CA:1063:G:H4'	10:CL:134:MET:HB3	1.88	0.54
34:DA:193:C:H2'	34:DA:194:C:C6	2.43	0.54
34:DA:1306:A:H1'	34:DA:1332:A:N1	2.23	0.54
34:DA:1372:U:H5"	42:DI:71:SER:HB3	1.88	0.54
42:DI:79:LEU:HG	42:DI:83:ARG:HD2	1.88	0.54
43:DJ:8:LEU:HB2	43:DJ:70:ARG:HB2	1.89	0.54
49:DP:5:ARG:NH1	49:DP:28:ARG:HA	2.22	0.54
57:DZ:94:VAL:O	57:DZ:98:MET:HG2	2.08	0.54
1:AA:1067:A:C8	1:AA:1067:A:H3'	2.43	0.54
1:AA:2250:G:N3	1:AA:2250:G:H2'	2.22	0.54
1:AA:2298:A:H4'	1:AA:2299:A:O4'	2.08	0.54
1:AA:2874:G:OP1	17:AT:119:LYS:HD2	2.08	0.54
20:AW:25:ARG:NH2	20:AW:74:ALA:O	2.34	0.54
28:A4:15:ILE:HD13	28:A4:21:VAL:HG22	1.89	0.54
34:BA:664:G:N2	34:BA:741:G:H1	2.04	0.54
35:BB:111:ARG:HH21	35:BB:114:ARG:HG2	1.73	0.54
35:BB:204:ASN:OD1	35:BB:206:ASP:N	2.40	0.54
51:BR:66:LEU:HD11	51:BR:70:ILE:HD11	1.89	0.54
1:CA:2102:U:H2'	1:CA:2103:C:C6	2.43	0.54
22:CY:74:PRO:O	22:CY:82:PRO:HA	2.08	0.54
30:C6:14:THR:OG1	30:C6:48:VAL:O	2.24	0.54
34:DA:1132:C:H2'	34:DA:1133:G:H8	1.73	0.54
35:DB:128:GLU:HG3	35:DB:135:GLN:HE22	1.72	0.54
50:DQ:18:THR:HG23	50:DQ:69:LYS:HD3	1.89	0.54
1:AA:1405:A:C2	1:AA:1418:U:O4	2.61	0.54
1:AA:1563:G:H2'	1:AA:1564:C:C6	2.43	0.54
1:AA:1566:U:H2'	1:AA:1567:G:O4'	2.08	0.54
5:AE:176:ILE:HG22	5:AE:178:GLU:HG2	1.90	0.54
34:BA:36:C:O2'	45:BL:117:ARG:NH2	2.39	0.54
34:BA:757:U:H2'	34:BA:758:G:O4'	2.08	0.54
41:BH:81:HIS:N	41:BH:138:TRP:O	2.36	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:BI:26:VAL:HG13	42:BI:61:ALA:HB3	1.90	0.54
57:BZ:87:HIS:O	57:BZ:89:ASP:N	2.40	0.54
57:BZ:127:LYS:NZ	57:BZ:128:TYR:HE2	2.06	0.54
1:CA:971:C:H2'	1:CA:972:G:O4'	2.08	0.54
1:CA:1514:U:H2'	1:CA:1515:G:H8	1.72	0.54
1:CA:1784:A:O2'	63:CA:3747:HOH:O	2.19	0.54
1:CA:2469:A:O3'	14:CQ:56:ARG:NH2	2.41	0.54
22:CY:49:VAL:N	22:CY:59:GLY:O	2.30	0.54
28:C4:44:THR:O	28:C4:46:GLN:N	2.40	0.54
34:DA:1004:A:H8	34:DA:1005:A:H4'	1.72	0.54
50:DQ:45:HIS:HB2	50:DQ:65:ILE:HD12	1.90	0.54
1:AA:1525:G:N2	1:AA:1562:U:C2	2.76	0.54
1:AA:1895:U:OP1	1:AA:2422:G:O2'	2.21	0.54
1:AA:2228:G:O2'	1:AA:2229:A:OP1	2.24	0.54
34:BA:1442:G:H1	34:BA:1461:G:H21	1.56	0.54
34:BA:1507:A:H2'	34:BA:1508:G:C8	2.42	0.54
35:BB:47:THR:HA	35:BB:202:PRO:HG2	1.89	0.54
56:BX:30:G:N2	56:BX:41:C:C2	2.76	0.54
57:BZ:183:MET:SD	57:BZ:213:HIS:HD2	2.31	0.54
57:BZ:230:LYS:HD2	57:BZ:235:GLU:HB3	1.88	0.54
57:BZ:344:THR:OG1	57:BZ:388:THR:HB	2.08	0.54
57:BZ:503:GLY:O	57:BZ:505:GLY:N	2.41	0.54
1:CA:952:G:OP1	14:CQ:16:ARG:NH2	2.40	0.54
1:CA:1824:G:OP1	4:CD:52:ARG:NH1	2.40	0.54
1:CA:1971:A:OP2	4:CD:242:ARG:NH2	2.40	0.54
1:CA:2118:U:N3	1:CA:2149:G:H1'	2.23	0.54
5:CE:27:LEU:HD13	17:CT:1:MET:SD	2.48	0.54
5:CE:175:VAL:O	5:CE:177:PRO:HD3	2.07	0.54
6:CF:116:ASP:OD1	6:CF:119:ARG:NH2	2.41	0.54
11:CN:40:PRO:HA	18:CU:67:ALA:HB3	1.90	0.54
20:CW:60:ASN:HD22	20:CW:60:ASN:N	2.05	0.54
25:C1:23:LYS:HB3	25:C1:29:GLY:HA3	1.89	0.54
34:DA:1145:C:H4'	34:DA:1146:A:H5'	1.90	0.54
46:DM:108:ARG:HD2	46:DM:114:ARG:HD2	1.90	0.54
1:AA:309:C:H2'	1:AA:310:C:C6	2.43	0.53
1:AA:1043:G:OP2	18:AU:58:ARG:NH1	2.35	0.53
1:AA:1501:U:O2'	1:AA:1502:G:N7	2.41	0.53
1:AA:1551:C:H2'	1:AA:1552:C:H6	1.74	0.53
1:AA:1552:C:N4	1:AA:1553:A:H62	2.05	0.53
3:AC:52:PRO:HG2	3:AC:53:ARG:H	1.73	0.53
34:BA:45:U:H2'	34:BA:46:G:C8	2.43	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:BA:820:U:H4'	34:BA:821:G:OP2	2.07	0.53
38:BE:68:GLU:HG2	38:BE:70:PRO:HD3	1.90	0.53
44:BK:40:ILE:HG23	44:BK:75:TYR:HD2	1.73	0.53
1:CA:2117:A:N6	1:CA:2171:A:N1	2.55	0.53
3:CC:30:VAL:HG23	3:CC:31:LYS:HG2	1.89	0.53
4:CD:26:LYS:NZ	4:CD:30:GLU:HG2	2.22	0.53
7:CG:29:TRP:O	7:CG:33:ARG:NH1	2.41	0.53
8:CH:80:SER:HG	8:CH:81:GLU:H	1.56	0.53
34:DA:537:G:OP1	45:DL:113:ARG:NH1	2.34	0.53
34:DA:859:A:H2'	34:DA:860:A:O4'	2.08	0.53
34:DA:967:C:H2'	34:DA:968:A:N7	2.23	0.53
49:DP:74:LEU:O	49:DP:79:VAL:HG23	2.08	0.53
1:AA:721:G:H1'	6:AF:74:ARG:HD3	1.90	0.53
1:AA:2154:U:C4	3:AC:6:LYS:CB	2.89	0.53
1:AA:2450:U:O2'	1:AA:2452:C:OP1	2.26	0.53
1:AA:2856:G:H2'	1:AA:2857:U:O4'	2.07	0.53
3:AC:44:VAL:HG23	3:AC:176:VAL:HG21	1.89	0.53
8:AH:87:LEU:HA	8:AH:163:TYR:O	2.08	0.53
49:BP:55:ARG:O	49:BP:57:ARG:N	2.41	0.53
57:BZ:-9:LEU:O	57:BZ:-6:ARG:N	2.33	0.53
1:CA:1154:G:H8	1:CA:1154:G:O5'	1.90	0.53
1:CA:2080:G:H2'	1:CA:2081:C:H6	1.72	0.53
1:CA:2432:A:N1	25:C1:35:THR:HG22	2.23	0.53
1:CA:2469:A:H2'	1:CA:2470:G:O4'	2.07	0.53
3:CC:52:PRO:HG2	3:CC:53:ARG:H	1.73	0.53
3:CC:54:ARG:CZ	3:CC:56:ASP:HB3	2.37	0.53
7:CG:7:LEU:HD13	7:CG:104:GLU:HA	1.89	0.53
14:CQ:30:GLY:O	14:CQ:134:ARG:HD3	2.08	0.53
22:CY:102:CYS:SG	22:CY:103:GLY:N	2.81	0.53
23:CZ:138:GLU:H	23:CZ:156:LYS:HZ1	1.56	0.53
29:C5:45:VAL:HG11	29:C5:58:LEU:HD13	1.91	0.53
34:DA:106:C:O2'	34:DA:379:C:OP1	2.25	0.53
34:DA:1317:C:OP1	47:DN:16:PHE:HB3	2.09	0.53
50:DQ:10:VAL:HG13	50:DQ:19:VAL:HB	1.89	0.53
57:DZ:350:GLU:OE2	57:DZ:383:THR:OG1	2.26	0.53
1:AA:2045:G:H5'	1:AA:2629:C:H4'	1.90	0.53
34:BA:1352:C:OP1	54:BU:3:LYS:NZ	2.34	0.53
1:CA:1070:A:H2'	1:CA:1097:U:OP1	2.09	0.53
1:CA:2413:G:N2	1:CA:2414:G:H1'	2.22	0.53
1:CA:2659:G:N2	1:CA:2662:A:OP2	2.42	0.53
11:CN:42:TRP:CH2	11:CN:44:PRO:HB3	2.44	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:CS:35:ILE:HD12	16:CS:101:LEU:HD12	1.91	0.53
34:DA:355:C:C4	34:DA:356:A:N7	2.77	0.53
34:DA:921:U:O2	38:DE:19:MET:HB2	2.08	0.53
34:DA:1119:C:H2'	34:DA:1120:G:H8	1.73	0.53
34:DA:1392:G:H21	34:DA:1502:A:H8	1.55	0.53
43:DJ:78:ASN:C	43:DJ:80:LYS:H	2.16	0.53
53:DT:33:ILE:O	53:DT:37:SER:OG	2.16	0.53
57:DZ:264:LEU:HB2	62:DZ:704:GDP:C6	2.43	0.53
1:AA:1160:G:H2'	1:AA:1161:G:C8	2.43	0.53
1:AA:2118:U:H2'	1:AA:2119:C:C6	2.44	0.53
3:AC:171:ALA:HB1	3:AC:173:HIS:CE1	2.44	0.53
16:AS:70:GLY:HA3	16:AS:104:GLY:HA3	1.91	0.53
18:AU:61:TRP:CH2	18:AU:93:LYS:HB2	2.43	0.53
34:BA:435:C:H2'	34:BA:436:C:H6	1.73	0.53
34:BA:1507:A:H2'	34:BA:1508:G:H8	1.73	0.53
37:BD:31:CYS:SG	37:BD:34:GLU:HG2	2.48	0.53
57:BZ:216:LEU:O	57:BZ:219:VAL:HG22	2.08	0.53
1:CA:125:G:C6	31:C7:10:ARG:HG3	2.44	0.53
1:CA:250:G:H2'	1:CA:251:A:C8	2.44	0.53
2:CB:40:U:O4	28:C4:1:MET:N	2.39	0.53
5:CE:24:THR:HG23	5:CE:186:GLY:O	2.09	0.53
7:CG:37:VAL:HB	7:CG:94:LEU:HB2	1.89	0.53
22:CY:94:LYS:NZ	63:CY:601:HOH:O	2.40	0.53
25:C1:77:ALA:O	25:C1:80:LEU:HB2	2.08	0.53
35:DB:84:GLU:OE1	35:DB:87:ARG:NH1	2.41	0.53
43:DJ:11:PHE:HE1	43:DJ:67:THR:HB	1.73	0.53
57:DZ:201:ILE:HG21	57:DZ:206:LEU:HD13	1.90	0.53
57:DZ:456:GLU:C	57:DZ:458:HIS:H	2.17	0.53
1:AA:980:C:H2'	1:AA:981:C:H6	1.74	0.53
1:AA:1417:G:H2'	1:AA:1418:U:H5	1.73	0.53
1:AA:2660:C:H2'	1:AA:2661:U:C6	2.43	0.53
8:AH:17:VAL:HG22	8:AH:26:VAL:HG22	1.91	0.53
8:AH:102:ALA:HB2	8:AH:116:GLU:OE1	2.08	0.53
33:A9:27:CYS:SG	33:A9:28:GLU:N	2.82	0.53
34:BA:186:C:H2'	34:BA:187:C:H6	1.73	0.53
34:BA:1399:C:H4'	34:BA:1400:C:H5"	1.90	0.53
34:BA:1412:C:H2'	34:BA:1413:A:C8	2.43	0.53
41:BH:87:SER:HA	41:BH:93:VAL:HG23	1.89	0.53
1:CA:247:G:H4'	1:CA:386:G:C5	2.43	0.53
1:CA:300:A:P	22:CY:86:ARG:HH21	2.31	0.53
1:CA:792:G:O6	63:CA:3731:HOH:O	2.13	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:2012:G:OP1	20:CW:11:ARG:NH2	2.42	0.53
6:CF:124:LEU:HB3	6:CF:193:VAL:HG22	1.88	0.53
7:CG:20:ILE:HA	7:CG:25:TYR:HD1	1.73	0.53
12:CO:98:VAL:HG13	12:CO:117:LEU:HB3	1.91	0.53
22:CY:99:CYS:SG	22:CY:100:ALA:N	2.82	0.53
34:DA:73:G:C6	34:DA:76:C:C4	2.97	0.53
34:DA:1070:U:H2'	34:DA:1071:C:H6	1.73	0.53
34:DA:1312:G:N7	52:DS:2:PRO:HD2	2.23	0.53
44:DK:67:ASP:O	44:DK:71:LYS:HG3	2.08	0.53
56:DX:53:G:H1	56:DX:61:C:H42	1.55	0.53
57:DZ:132:ARG:H	57:DZ:132:ARG:HD2	1.73	0.53
57:DZ:225:GLU:HA	57:DZ:228:MET:HB3	1.90	0.53
57:DZ:503:GLY:C	57:DZ:505:GLY:H	2.17	0.53
1:AA:1701:A:OP1	15:AR:1:MET:N	2.42	0.53
1:AA:1846:A:P	4:AD:54:ARG:HH22	2.31	0.53
1:AA:1885:A:H2'	1:AA:1886:G:O4'	2.08	0.53
1:AA:1913:G:C6	1:AA:1914:C:C4	2.97	0.53
3:AC:30:VAL:HG23	3:AC:31:LYS:HG2	1.90	0.53
3:AC:42:VAL:HG13	3:AC:43:GLU:H	1.73	0.53
14:AQ:19:GLY:O	14:AQ:98:LYS:HE3	2.08	0.53
18:AU:9:VAL:O	18:AU:13:LYS:HG2	2.07	0.53
23:AZ:72:ARG:NH2	23:AZ:97:GLU:O	2.42	0.53
40:BG:23:VAL:O	40:BG:27:ILE:HG12	2.08	0.53
44:BK:98:LEU:O	44:BK:101:SER:OG	2.16	0.53
1:CA:1059:G:H5"	1:CA:1060:U:H2'	1.89	0.53
1:CA:1095:A:H3'	1:CA:1096:A:C8	2.43	0.53
1:CA:2542:A:H4'	1:CA:2543:G:H8	1.72	0.53
1:CA:2667:C:N3	8:CH:110:SER:OG	2.42	0.53
3:CC:171:ALA:HB1	3:CC:173:HIS:CE1	2.43	0.53
7:CG:43:LEU:HB3	7:CG:88:ILE:O	2.09	0.53
7:CG:114:ILE:HG23	7:CG:136:ARG:NH2	2.24	0.53
17:CT:102:ILE:HB	17:CT:110:ILE:HD13	1.90	0.53
20:CW:7:ALA:O	20:CW:102:HIS:HA	2.09	0.53
34:DA:406:G:H5'	37:DD:5:ILE:HG12	1.90	0.53
34:DA:422:C:H5'	34:DA:423:G:C5	2.44	0.53
34:DA:1044:A:C6	34:DA:1045:C:H1'	2.44	0.53
34:DA:1255:G:P	43:DJ:45:ARG:HH22	2.30	0.53
35:DB:162:ILE:O	35:DB:185:ILE:HG12	2.09	0.53
40:DG:15:ASP:HB3	40:DG:24:THR:HG23	1.91	0.53
46:DM:66:LEU:O	46:DM:68:GLY:N	2.41	0.53
1:AA:1049:G:O2'	1:AA:1056:A:N1	2.38	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1893:G:H2'	1:AA:1894:G:H8	1.73	0.53
2:AB:39:A:H2'	2:AB:40:U:C6	2.44	0.53
3:AC:6:LYS:HA	3:AC:9:ARG:HH11	1.72	0.53
3:AC:48:LEU:CB	3:AC:50:ILE:HD12	2.38	0.53
8:AH:98:LEU:HD22	8:AH:125:VAL:HG23	1.91	0.53
34:BA:266:G:H5"	34:BA:268:C:H41	1.74	0.53
34:BA:721:G:C6	34:BA:733:A:C2	2.96	0.53
35:BB:59:GLU:O	35:BB:63:MET:HB2	2.09	0.53
48:BO:35:ARG:CZ	48:BO:59:MET:HE2	2.39	0.53
57:BZ:206:LEU:O	57:BZ:210:ARG:NH1	2.42	0.53
1:CA:144:C:H5'	21:CX:2:LYS:HE2	1.90	0.53
1:CA:440:G:H2'	1:CA:441:U:C6	2.43	0.53
1:CA:483:A:H5"	22:CY:50:ARG:NH1	2.23	0.53
1:CA:899:A:O2'	1:CA:900:A:H5'	2.08	0.53
24:C0:48:GLY:HA3	24:C0:80:HIS:ND1	2.23	0.53
34:DA:596:C:N3	34:DA:644:G:N1	2.48	0.53
49:DP:28:ARG:HG3	49:DP:29:ASP:OD1	2.09	0.53
1:AA:123:G:H4'	1:AA:124:A:OP2	2.09	0.53
1:AA:1285:G:H2'	1:AA:1286:U:O4'	2.09	0.53
11:AN:68:GLU:HG3	11:AN:88:GLU:OE2	2.08	0.53
34:BA:35:G:N3	45:BL:118:SER:OG	2.42	0.53
35:BB:25:ASN:H	35:BB:191:ASP:HA	1.73	0.53
40:BG:151:TYR:OH	44:BK:54:ARG:HG2	2.09	0.53
41:BH:119:LEU:HB3	41:BH:123:GLU:HB3	1.90	0.53
56:BX:19:G:H4'	56:BX:20:U:OP2	2.08	0.53
1:CA:1523:U:H2'	1:CA:1524:G:C8	2.43	0.53
1:CA:2086:U:H2'	1:CA:2087:G:C8	2.43	0.53
1:CA:2233:U:H2'	1:CA:2234:G:C8	2.44	0.53
6:CF:132:VAL:HG21	6:CF:163:VAL:HG22	1.91	0.53
34:DA:108:G:OP1	34:DA:326:G:N2	2.30	0.53
34:DA:1106:G:H5"	36:DC:172:ARG:HG2	1.90	0.53
34:DA:1239:A:H4'	34:DA:1240:U:H5"	1.89	0.53
35:DB:16:HIS:HB2	35:DB:204:ASN:CB	2.38	0.53
53:DT:57:ARG:NH2	53:DT:100:ILE:HD12	2.16	0.53
1:AA:2752:U:O2'	1:AA:2753:A:H5'	2.09	0.53
4:AD:52:ARG:HB2	4:AD:53:PHE:CE2	2.44	0.53
16:AS:54:LEU:O	16:AS:54:LEU:HG	2.08	0.53
16:AS:93:LYS:HG2	16:AS:95:HIS:HB2	1.91	0.53
19:AV:8:GLY:O	19:AV:10:LYS:HE2	2.09	0.53
23:AZ:39:VAL:HG21	23:AZ:44:PHE:HB2	1.90	0.53
34:BA:865:A:H5'	34:BA:1078:U:O4	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:BE:137:GLU:O	38:BE:141:GLN:HG3	2.09	0.53
38:BE:147:ASP:OD1	38:BE:147:ASP:N	2.20	0.53
1:CA:1107:G:P	9:CK:58:LEU:HA	2.48	0.53
10:CL:17:ALA:HB3	10:CL:38:VAL:HG13	1.91	0.53
34:DA:451:A:N6	34:DA:480:U:H2'	2.24	0.53
34:DA:924:C:O2'	34:DA:1502:A:N6	2.41	0.53
34:DA:954:G:H21	34:DA:1227:A:H62	1.57	0.53
34:DA:1065:U:OP2	34:DA:1190:G:N2	2.42	0.53
57:DZ:96:ARG:HH11	57:DZ:96:ARG:HB2	1.74	0.53
1:AA:553:A:H2	1:AA:2065:C:H5'	1.73	0.53
1:AA:782:A:N7	1:AA:808:A:H2	2.07	0.53
1:AA:2402:U:P	32:A8:35:GLN:HE22	2.32	0.53
20:AW:13:SER:HB3	20:AW:16:LYS:HG3	1.91	0.53
21:AX:36:LYS:HG2	21:AX:54:VAL:HG12	1.91	0.53
24:A0:37:LEU:HG	24:A0:60:PHE:HA	1.91	0.53
34:BA:368:U:P	57:BZ:351:ARG:HH11	2.32	0.53
34:BA:1189:C:P	43:BJ:51:ARG:HH22	2.32	0.53
35:BB:55:PHE:HD1	35:BB:58:ILE:HD12	1.74	0.53
36:BC:40:ARG:HG2	36:BC:55:VAL:HG11	1.90	0.53
46:BM:80:ARG:NH2	52:BS:69:HIS:HE1	2.07	0.53
57:BZ:350:GLU:OE1	57:BZ:382:GLU:N	2.42	0.53
1:CA:271(D):G:C6	1:CA:271(E):U:C4	2.97	0.53
1:CA:2128:C:H5'	1:CA:2173:A:N3	2.24	0.53
3:CC:51:ASP:OD2	3:CC:54:ARG:HB2	2.09	0.53
8:CH:106:THR:O	8:CH:106:THR:OG1	2.24	0.53
10:CL:79:ARG:NH1	10:CL:85:GLU:O	2.42	0.53
14:CQ:20:ALA:HB2	23:CZ:79:ARG:HB2	1.90	0.53
21:CX:18:TYR:HA	21:CX:21:PHE:CE2	2.44	0.53
38:DE:107:ARG:HG2	38:DE:108:ALA:N	2.23	0.53
42:DI:8:GLY:HA3	42:DI:76:ALA:O	2.08	0.53
1:AA:704:U:H2'	1:AA:705:C:C6	2.44	0.52
1:AA:869:U:O4	1:AA:989:G:H1'	2.08	0.52
1:AA:1141:A:H2'	1:AA:1142:A:H8	1.74	0.52
1:AA:1847:G:O6	4:AD:35:LYS:NZ	2.41	0.52
1:AA:2013:U:C2'	1:AA:2014:G:H5"	2.37	0.52
1:AA:2390:A:H4'	16:AS:23:ARG:HH11	1.71	0.52
3:AC:51:ASP:OD2	3:AC:54:ARG:HB2	2.09	0.52
3:AC:64:SER:HA	3:AC:161:ARG:H	1.74	0.52
7:AG:47:LYS:O	7:AG:51:ARG:HG2	2.09	0.52
7:AG:135:LEU:HD13	7:AG:157:ILE:HG13	1.89	0.52
23:AZ:63:ASP:OD1	23:AZ:65:GLN:HB2	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:BI:77:ILE:O	42:BI:81:ILE:HG23	2.10	0.52
46:BM:87:TYR:O	46:BM:91:ARG:HG2	2.09	0.52
1:CA:1059:G:OP2	1:CA:1060:U:H3'	2.08	0.52
1:CA:1067:A:H2'	1:CA:1068:G:C8	2.44	0.52
1:CA:1615:C:O2'	1:CA:1616:A:H5"	2.10	0.52
1:CA:1939:U:OP1	1:CA:2604:U:O2'	2.22	0.52
22:CY:5:MET:HE3	22:CY:32:PRO:HA	1.90	0.52
39:DF:2:ARG:CZ	39:DF:69:GLU:HG2	2.39	0.52
52:DS:41:VAL:HG12	52:DS:43:GLU:H	1.73	0.52
57:DZ:165:GLN:O	57:DZ:166:LEU:HD12	2.09	0.52
1:AA:180:A:H2'	1:AA:181:C:C6	2.44	0.52
1:AA:1964:C:OP2	1:AA:1965:U:O2'	2.18	0.52
1:AA:1995:G:H2'	1:AA:1996:C:H6	1.72	0.52
1:AA:2200:C:O2'	3:AC:169:THR:HB	2.10	0.52
6:AF:7:TYR:O	6:AF:21:ALA:HA	2.09	0.52
22:AY:92:ASN:N	22:AY:93:GLY:HA2	2.24	0.52
34:BA:1205:U:O2'	36:BC:195:VAL:HG23	2.09	0.52
57:BZ:328:ILE:HD12	57:BZ:377:VAL:HG12	1.90	0.52
1:CA:795:C:H2'	1:CA:796:C:H6	1.74	0.52
1:CA:2064:C:OP2	63:CA:3748:HOH:O	2.19	0.52
1:CA:2316:C:O2'	7:CG:128:ARG:NH2	2.42	0.52
11:CN:1:MET:HE1	18:CU:94:ASN:HD22	1.75	0.52
34:DA:796:C:O5'	34:DA:796:C:H6	1.92	0.52
34:DA:994:A:N7	34:DA:1216:G:H4'	2.24	0.52
35:DB:98:LEU:HB2	35:DB:101:MET:SD	2.50	0.52
37:DD:187:ARG:HG2	37:DD:188:LEU:O	2.10	0.52
42:DI:9:ARG:HG2	42:DI:14:VAL:HG12	1.90	0.52
44:DK:27:ASN:OD1	44:DK:28:THR:N	2.41	0.52
57:DZ:329:ARG:HD3	57:DZ:331:TYR:CZ	2.45	0.52
1:AA:185:A:C4	1:AA:852:G:C6	2.97	0.52
1:AA:1218:G:O2'	1:AA:1219:A:O4'	2.25	0.52
1:AA:1946:C:H4'	56:BX:13:C:H4'	1.92	0.52
2:AB:105:A:H2'	2:AB:106:G:O4'	2.08	0.52
6:AF:185:ASP:HA	6:AF:188:ARG:HD3	1.90	0.52
10:AL:119:ASP:OD1	10:AL:120:LEU:N	2.39	0.52
33:A9:7:VAL:HG12	33:A9:34:GLN:HB3	1.91	0.52
1:CA:636:G:O2'	1:CA:638:G:O2'	2.25	0.52
20:CW:57:ASN:O	20:CW:58:ALA:C	2.53	0.52
21:CX:8:ILE:O	26:C2:36:ARG:NH2	2.42	0.52
23:CZ:101:PRO:O	23:CZ:102:LEU:HD12	2.10	0.52
50:DQ:64:PRO:HB3	50:DQ:70:ARG:NH1	2.25	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:DT:10:LEU:HD23	53:DT:12:ALA:HB2	1.91	0.52
57:DZ:-29:LEU:HB3	57:DZ:-27:THR:HG22	1.91	0.52
1:AA:41:C:H2'	1:AA:42:G:O4'	2.09	0.52
1:AA:1038:C:OP1	18:AU:47:TYR:OH	2.14	0.52
1:AA:1073:A:C2	1:AA:2500:A:H5'	2.45	0.52
1:AA:1478:C:H2'	1:AA:1479:U:O4'	2.09	0.52
1:AA:1766:G:H3'	1:AA:1767:A:H5"	1.91	0.52
1:AA:2102:G:OP1	25:A1:35:THR:HG21	2.09	0.52
4:AD:20:ASP:C	4:AD:22:SER:H	2.16	0.52
15:AR:2:ARG:O	15:AR:5:LYS:HB2	2.09	0.52
16:AS:14:VAL:O	16:AS:18:ILE:HG12	2.09	0.52
34:BA:145:G:H1	34:BA:177:C:H42	1.56	0.52
34:BA:761:G:C6	34:BA:762:C:C4	2.97	0.52
34:BA:872:A:C4	34:BA:874:G:N7	2.78	0.52
34:BA:1068:G:H8	34:BA:1068:G:OP2	1.93	0.52
34:BA:1458:G:OP1	53:BT:35:THR:OG1	2.18	0.52
47:BN:4:LYS:HA	47:BN:7:ILE:HG23	1.91	0.52
57:BZ:357:ARG:NH1	57:BZ:373:ASP:OD2	2.43	0.52
1:CA:219:G:C6	1:CA:220:G:C6	2.98	0.52
1:CA:1095:A:C5	1:CA:1096:A:C6	2.98	0.52
1:CA:1803:A:O2'	4:CD:259:THR:HG21	2.09	0.52
1:CA:2292:C:H42	1:CA:2340:G:H1	1.57	0.52
15:CR:9:LYS:HA	15:CR:17:ARG:NE	2.24	0.52
32:C8:54:GLU:O	32:C8:58:ILE:HG13	2.09	0.52
34:DA:390:C:O3'	49:DP:28:ARG:NH2	2.42	0.52
34:DA:659:U:OP1	48:DO:9:GLN:NE2	2.41	0.52
34:DA:1052:U:O4	34:DA:1200:C:O2'	2.18	0.52
34:DA:1258:G:H2'	34:DA:1259:C:C6	2.45	0.52
50:DQ:6:LEU:O	50:DQ:58:GLU:HA	2.08	0.52
57:DZ:166:LEU:HD13	57:DZ:180:VAL:HG11	1.91	0.52
57:DZ:357:ARG:HG3	57:DZ:364:GLU:HB3	1.90	0.52
1:AA:493:G:OP1	31:A7:33:ARG:NH1	2.43	0.52
1:AA:911:G:OP2	14:AQ:22:LYS:HE2	2.09	0.52
1:AA:1636:U:H2'	1:AA:1637:G:H8	1.74	0.52
2:AB:89:G:H2'	2:AB:90:A:C8	2.45	0.52
3:AC:67:HIS:CG	3:AC:185:LYS:HD2	2.45	0.52
5:AE:7:VAL:HG21	17:AT:1:MET:HE1	1.92	0.52
6:AF:51:THR:HB	6:AF:88:VAL:HG11	1.91	0.52
6:AF:64:ILE:HD12	6:AF:65:TRP:CZ3	2.44	0.52
10:AL:22:PRO:O	10:AL:27:LEU:HD13	2.09	0.52
34:BA:1250:A:H4'	42:BI:68:GLY:N	2.24	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:BD:196:LEU:O	37:BD:198:VAL:N	2.37	0.52
41:BH:35:ILE:O	41:BH:38:ILE:HB	2.10	0.52
1:CA:729:G:H4'	1:CA:763:G:H5'	1.92	0.52
1:CA:1301:A:C8	1:CA:1303:G:C8	2.98	0.52
1:CA:1474:C:H2'	1:CA:1475:G:C8	2.45	0.52
1:CA:1638:C:H5"	1:CA:2710:C:O2'	2.09	0.52
3:CC:64:SER:HA	3:CC:161:ARG:H	1.74	0.52
16:CS:83:LYS:HB2	16:CS:111:GLU:HG3	1.91	0.52
17:CT:17:THR:O	17:CT:17:THR:OG1	2.25	0.52
34:DA:1437:C:H42	34:DA:1464:G:H1	1.58	0.52
37:DD:175:SER:HB3	37:DD:186:LEU:HD11	1.92	0.52
38:DE:126:ARG:HA	38:DE:131:ILE:HD11	1.92	0.52
41:DH:86:ILE:HG21	41:DH:133:LEU:HD13	1.91	0.52
57:DZ:149:VAL:O	57:DZ:152:THR:OG1	2.28	0.52
57:DZ:272:LEU:O	57:DZ:276:VAL:HG23	2.09	0.52
1:AA:1068:G:N2	1:AA:1188:A:C2	2.76	0.52
1:AA:2331:G:H22	16:AS:3:ARG:CG	2.22	0.52
3:AC:65:LEU:HD22	3:AC:189:ASN:HB3	1.91	0.52
4:AD:26:LYS:HE2	4:AD:28:GLU:O	2.09	0.52
11:AN:67:LEU:HD13	11:AN:87:LEU:HD13	1.91	0.52
12:AO:100:GLY:H	12:AO:119:PRO:HG2	1.74	0.52
34:BA:21:G:H2'	34:BA:22:G:C8	2.44	0.52
35:BB:54:THR:O	35:BB:58:ILE:HG13	2.09	0.52
1:CA:914:C:C4	1:CA:915:C:C6	2.97	0.52
34:DA:1059:C:OP2	36:DC:199:LYS:NZ	2.42	0.52
34:DA:1239:A:H62	34:DA:1299:A:N6	2.07	0.52
37:DD:112:VAL:HG22	37:DD:116:GLN:OE1	2.10	0.52
57:DZ:71:THR:HG22	57:DZ:80:ASN:OD1	2.10	0.52
1:AA:1720:U:C2'	1:AA:1721:G:H5'	2.40	0.52
1:AA:2504:U:H2'	1:AA:2505:U:H6	1.73	0.52
18:AU:76:TYR:OH	18:AU:92:ARG:HD3	2.10	0.52
34:BA:537:G:H2'	34:BA:538:G:H8	1.74	0.52
37:BD:104:VAL:O	37:BD:106:TYR:N	2.43	0.52
40:BG:38:LEU:HA	40:BG:41:ARG:HB2	1.91	0.52
57:BZ:14:ASN:HB2	57:BZ:102:ASP:CG	2.34	0.52
1:CA:322:A:H5'	1:CA:340:A:H1'	1.92	0.52
1:CA:1110:G:H2'	1:CA:1110:G:N3	2.25	0.52
1:CA:1798:U:C5'	4:CD:259:THR:HG22	2.31	0.52
1:CA:2203:U:O4'	4:CD:151:LYS:HE2	2.10	0.52
3:CC:48:LEU:CB	3:CC:50:ILE:HD12	2.38	0.52
3:CC:65:LEU:HD22	3:CC:189:ASN:HB3	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:CC:67:HIS:CG	3:CC:185:LYS:HD2	2.45	0.52
7:CG:38:VAL:HA	7:CG:93:THR:HA	1.91	0.52
34:DA:49:U:O4	34:DA:365:U:H5	1.93	0.52
34:DA:1347:G:N2	34:DA:1373:G:H2'	2.25	0.52
36:DC:113:ALA:HA	36:DC:116:VAL:HG23	1.91	0.52
38:DE:33:VAL:HG21	38:DE:109:ILE:HA	1.91	0.52
57:DZ:-13:GLN:HA	57:DZ:-10:ARG:HG2	1.91	0.52
1:AA:1154:U:H1'	1:AA:1155:C:OP1	2.10	0.52
1:AA:2200:C:H4'	3:AC:47:LYS:NZ	2.25	0.52
1:AA:2259:A:H2'	1:AA:2260:C:C6	2.45	0.52
1:AA:2887:G:O2'	1:AA:2888:U:H5'	2.10	0.52
10:AL:123:ALA:O	10:AL:126:MET:HB2	2.10	0.52
17:AT:29:ARG:HB2	17:AT:46:GLU:HG3	1.91	0.52
27:A3:55:ARG:NH2	27:A3:57:GLU:OE1	2.42	0.52
34:BA:1392:G:N2	34:BA:1502:A:C8	2.76	0.52
44:BK:84:VAL:HG21	44:BK:95:ILE:HD11	1.90	0.52
48:BO:67:LEU:O	48:BO:71:GLN:HB2	2.10	0.52
57:BZ:257:PRO:HB2	57:BZ:259:PHE:CE1	2.44	0.52
1:CA:585:G:H2'	1:CA:1251:C:H42	1.75	0.52
1:CA:641:C:O2'	1:CA:2350:C:OP1	2.19	0.52
1:CA:2124:G:H4'	3:CC:175:PRO:HD3	1.91	0.52
5:CE:52:LEU:O	5:CE:76:ARG:N	2.40	0.52
23:CZ:28:MET:HE1	23:CZ:61:LEU:HD21	1.91	0.52
34:DA:1149:C:OP2	42:DI:9:ARG:NH2	2.42	0.52
38:DE:129:ILE:O	38:DE:132:ALA:HB3	2.09	0.52
51:DR:53:ARG:HA	51:DR:56:THR:OG1	2.10	0.52
57:DZ:-27:THR:HG23	57:DZ:-24:ASN:OD1	2.09	0.52
12:AO:101:PRO:HB3	12:AO:120:GLU:HB3	1.92	0.52
25:A1:19:GLN:O	25:A1:35:THR:HG22	2.09	0.52
34:BA:518:C:O2'	34:BA:530:G:N2	2.43	0.52
39:BF:97:PHE:HD1	51:BR:31:LEU:HD21	1.75	0.52
45:BL:57:LYS:HA	45:BL:67:THR:HA	1.91	0.52
47:BN:37:PHE:CE1	47:BN:53:LEU:HD13	2.44	0.52
57:BZ:160:ARG:HD3	57:BZ:160:ARG:H	1.75	0.52
1:CA:1859:A:C2	1:CA:1884:A:H1'	2.45	0.52
9:CK:26:LEU:N	9:CK:115:GLN:O	2.43	0.52
34:DA:368:U:C2	57:DZ:354:ARG:NH1	2.77	0.52
35:DB:69:LEU:HD12	35:DB:70:PHE:N	2.25	0.52
38:DE:10:MET:HB3	38:DE:13:ILE:HD11	1.91	0.52
57:DZ:134:ALA:HB3	57:DZ:153:MET:HE1	1.90	0.52
57:DZ:528:ALA:O	57:DZ:568:TYR:HA	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:AG:110:ALA:HB1	7:AG:140:ILE:HG22	1.92	0.52
10:AL:45:THR:O	10:AL:45:THR:OG1	2.19	0.52
10:AL:56:GLU:O	10:AL:67:PHE:HA	2.09	0.52
16:AS:83:LYS:O	16:AS:111:GLU:N	2.40	0.52
30:A6:18:ARG:HD3	30:A6:42:TRP:CD1	2.44	0.52
34:BA:1154:G:H2'	34:BA:1155:G:H8	1.75	0.52
37:BD:121:VAL:O	37:BD:134:ASP:HA	2.10	0.52
40:BG:103:TRP:HA	40:BG:106:GLN:HB2	1.92	0.52
41:BH:113:SER:CB	41:BH:134:ILE:HD11	2.40	0.52
57:BZ:80:ASN:ND2	57:BZ:374:LEU:HB2	2.25	0.52
57:BZ:177:ILE:HD12	57:BZ:188:TYR:OH	2.10	0.52
57:BZ:273:LEU:O	57:BZ:275:ALA:N	2.43	0.52
1:CA:587:C:C6	1:CA:671:C:H1'	2.45	0.52
1:CA:1865:G:N2	1:CA:1878:G:C5	2.78	0.52
1:CA:2441:C:OP2	1:CA:2586:C:O2'	2.28	0.52
34:DA:649:G:H2'	34:DA:650:G:H8	1.75	0.52
35:DB:163:PHE:HD1	35:DB:185:ILE:HG13	1.75	0.52
57:DZ:72:CYS:SG	57:DZ:79:ILE:HB	2.50	0.52
1:AA:516:G:H2'	1:AA:517:A:H8	1.74	0.51
1:AA:929:G:H1	1:AA:940:C:H42	1.58	0.51
3:AC:218:THR:HG22	3:AC:219:MET:SD	2.50	0.51
5:AE:116:VAL:HG13	5:AE:122:PHE:CD2	2.44	0.51
13:AP:68:GLN:HA	13:AP:68:GLN:OE1	2.09	0.51
16:AS:93:LYS:HE2	16:AS:95:HIS:HB2	1.92	0.51
26:A2:50:ILE:O	26:A2:54:LYS:HG3	2.11	0.51
34:BA:1469:G:H2'	34:BA:1470:G:C8	2.44	0.51
35:BB:21:ARG:HB3	35:BB:39:ILE:HG12	1.91	0.51
42:BI:127:LYS:O	42:BI:128:ARG:HG2	2.09	0.51
48:BO:29:VAL:HG11	48:BO:67:LEU:HD21	1.91	0.51
1:CA:687:C:H5'	31:C7:4:THR:O	2.10	0.51
1:CA:2394:C:OP1	13:CP:64:LYS:HB2	2.10	0.51
1:CA:2484:G:C2	1:CA:2485:G:C8	2.99	0.51
1:CA:2786:U:O2'	5:CE:62:PRO:O	2.20	0.51
3:CC:42:VAL:CG1	3:CC:43:GLU:N	2.73	0.51
4:CD:148:GLU:HB2	4:CD:151:LYS:HD2	1.91	0.51
23:CZ:125:LEU:HB3	23:CZ:165:VAL:HG13	1.92	0.51
34:DA:630:G:H2'	34:DA:631:G:H8	1.75	0.51
34:DA:1359:C:OP1	47:DN:22:THR:OG1	2.29	0.51
36:DC:55:VAL:HG22	36:DC:68:VAL:HG13	1.91	0.51
57:DZ:131:PRO:HG2	57:DZ:281:PRO:HG3	1.92	0.51
1:AA:1065:U:O2'	1:AA:1067:A:H2	1.90	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:2198:A:H2'	1:AA:2199:C:C6	2.45	0.51
1:AA:2764:G:H4'	8:AH:4:ILE:HD11	1.92	0.51
3:AC:54:ARG:HH22	3:AC:56:ASP:HB3	1.76	0.51
12:AO:1:MET:HE3	12:AO:32:TYR:CE2	2.45	0.51
14:AQ:38:GLU:HG2	14:AQ:127:ILE:HB	1.91	0.51
34:BA:515:G:H2'	34:BA:516:U:O4'	2.10	0.51
36:BC:88:ARG:HA	36:BC:91:LEU:HB3	1.92	0.51
36:BC:108:ASN:HB3	36:BC:111:LEU:HG	1.92	0.51
37:BD:101:LEU:O	37:BD:104:VAL:N	2.43	0.51
37:BD:110:PHE:HE2	37:BD:148:VAL:HG23	1.75	0.51
57:BZ:14:ASN:OD1	57:BZ:80:ASN:HB2	2.10	0.51
57:BZ:388:THR:HG23	57:BZ:399:LEU:HD22	1.92	0.51
1:CA:11:G:C2'	1:CA:12:U:H5"	2.39	0.51
1:CA:2177:C:O3'	3:CC:47:LYS:HB2	2.10	0.51
2:CB:50:G:OP1	16:CS:63:THR:HG22	2.10	0.51
17:CT:26:ASP:O	17:CT:49:VAL:HG12	2.10	0.51
24:C0:36:ILE:HD12	24:C0:58:THR:HG21	1.92	0.51
32:C8:52:LYS:O	32:C8:56:GLU:HG3	2.11	0.51
34:DA:502:G:OP2	45:DL:116:SER:HA	2.11	0.51
34:DA:939:G:H1	34:DA:1344:C:H42	1.57	0.51
34:DA:1039:C:H2'	34:DA:1040:U:O4'	2.10	0.51
34:DA:1071:C:H2'	34:DA:1072:G:C8	2.44	0.51
34:DA:1222:G:H5"	52:DS:78:ARG:NH2	2.25	0.51
37:DD:92:VAL:O	37:DD:96:LEU:HD13	2.10	0.51
37:DD:100:ARG:NH2	37:DD:118:ARG:HH12	2.08	0.51
1:AA:1405:A:N6	1:AA:1418:U:H3	2.08	0.51
1:AA:1423:G:H5"	1:AA:1424:A:OP2	2.11	0.51
1:AA:1556:A:H3'	1:AA:1557:A:H8	1.74	0.51
4:AD:16:MET:HG3	4:AD:211:ARG:NH2	2.25	0.51
4:AD:77:ALA:O	4:AD:116:GLN:HA	2.10	0.51
16:AS:11:LYS:O	16:AS:15:ARG:HB2	2.11	0.51
19:AV:16:PRO:HD3	19:AV:99:ILE:HD11	1.92	0.51
27:A3:3:ARG:HD3	27:A3:60:GLU:OE2	2.11	0.51
45:BL:96:VAL:C	45:BL:97:ARG:HG2	2.34	0.51
48:BO:8:LYS:O	48:BO:12:ILE:HG13	2.11	0.51
57:BZ:129:LYS:HD2	57:BZ:253:LEU:CD2	2.40	0.51
57:BZ:140:ASP:OD2	57:BZ:140:ASP:N	2.42	0.51
1:CA:307:G:H2'	1:CA:309:G:OP2	2.11	0.51
1:CA:996:A:O3'	18:CU:91:ASP:HB2	2.09	0.51
1:CA:2218:U:O2	25:C1:52:ARG:NH2	2.42	0.51
1:CA:2235:G:H2'	1:CA:2236:C:C6	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:CC:68:GLY:H	3:CC:189:ASN:ND2	2.08	0.51
14:CQ:106:VAL:HG21	14:CQ:114:ALA:HB1	1.92	0.51
34:DA:475:G:H2'	34:DA:476:G:C8	2.46	0.51
36:DC:121:ALA:HB2	36:DC:187:ALA:HB1	1.93	0.51
1:AA:388:A:H2'	1:AA:389:G:C8	2.46	0.51
63:AA:4286:HOH:O	15:AR:15:SER:HB3	2.09	0.51
7:AG:79:ASN:OD1	7:AG:79:ASN:N	2.42	0.51
8:AH:5:GLY:HA3	8:AH:65:HIS:CD2	2.46	0.51
16:AS:91:PRO:HG2	16:AS:92:TYR:CE1	2.45	0.51
25:A1:50:ARG:HG2	25:A1:59:THR:HB	1.91	0.51
35:BB:97:TRP:HZ3	35:BB:176:GLU:OE2	1.93	0.51
38:BE:78:HIS:NE2	38:BE:142:LEU:HA	2.25	0.51
42:BI:43:ALA:HA	42:BI:74:ILE:HD13	1.91	0.51
1:CA:301:G:OP2	22:CY:84:ARG:NH2	2.43	0.51
1:CA:2121:G:HO2'	3:CC:168:LYS:HB3	1.65	0.51
3:CC:6:LYS:N	3:CC:9:ARG:NH1	2.58	0.51
10:CL:75:SER:HA	10:CL:78:ILE:HG22	1.93	0.51
13:CP:88:LEU:HD11	13:CP:114:ILE:HD12	1.91	0.51
15:CR:38:VAL:CG1	15:CR:42:LYS:HD2	2.36	0.51
34:DA:556:C:C4	34:DA:557:G:N7	2.79	0.51
34:DA:975:A:H61	43:DJ:48:THR:HB	1.75	0.51
39:DF:82:ARG:HB2	39:DF:85:VAL:HG23	1.91	0.51
51:DR:44:LEU:HD21	51:DR:70:ILE:HD13	1.91	0.51
52:DS:13:ASP:HA	52:DS:16:LEU:HB3	1.93	0.51
1:AA:714:U:O2	32:A8:2:PRO:HD2	2.10	0.51
1:AA:1398:U:OP1	63:AA:3937:HOH:O	2.19	0.51
1:AA:1624:C:H2'	1:AA:1625:U:O4'	2.11	0.51
1:AA:1634:C:H2'	1:AA:1635:C:C6	2.46	0.51
1:AA:1809:U:H2'	1:AA:1815:A:N6	2.24	0.51
17:AT:118:ARG:HG2	34:BA:1442(A):G:C8	2.44	0.51
34:BA:1030(C):G:H2'	34:BA:1030(D):A:H8	1.76	0.51
44:BK:48:ILE:HG21	44:BK:63:LEU:HB3	1.93	0.51
1:CA:252:G:P	13:CP:50:ARG:HH12	2.33	0.51
1:CA:477:A:H2'	1:CA:478:A:C8	2.45	0.51
1:CA:1973:G:H2'	1:CA:1974:C:C6	2.45	0.51
1:CA:2128:C:P	3:CC:219:MET:CE	2.81	0.51
1:CA:2336:A:H61	24:C0:43:THR:HG22	1.75	0.51
3:CC:50:ILE:H	3:CC:50:ILE:HD13	1.76	0.51
6:CF:29:ASN:ND2	6:CF:32:LEU:HB2	2.25	0.51
14:CQ:63:LYS:HA	23:CZ:178:GLU:HG3	1.91	0.51
34:DA:909:A:H2'	34:DA:910:C:O4'	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:DA:995:C:H1'	47:DN:4:LYS:HE2	1.93	0.51
43:DJ:61:GLU:OE2	47:DN:49:HIS:NE2	2.36	0.51
45:DL:80:HIS:HA	57:DZ:425:SER:OG	2.11	0.51
57:DZ:302:HIS:O	57:DZ:304:ASP:N	2.40	0.51
1:AA:711:C:OP1	13:AP:17:LYS:HE2	2.11	0.51
1:AA:1340:U:O2'	15:AR:26:LYS:NZ	2.42	0.51
1:AA:1343:C:OP1	1:AA:2722:C:H4'	2.11	0.51
1:AA:2209:G:O2'	1:AA:2210:C:OP1	2.27	0.51
1:AA:2524:C:O2'	5:AE:154:LYS:HE2	2.10	0.51
3:AC:6:LYS:N	3:AC:9:ARG:NH1	2.58	0.51
3:AC:44:VAL:HG21	3:AC:176:VAL:HG21	1.92	0.51
5:AE:24:THR:HG21	5:AE:188:VAL:HB	1.92	0.51
8:AH:43:VAL:HG22	8:AH:52:VAL:HG22	1.92	0.51
34:BA:839:U:H4'	34:BA:840:C:OP2	2.11	0.51
38:BE:143:ARG:NH1	41:BH:77:GLU:OE2	2.42	0.51
53:BT:12:ALA:O	53:BT:15:ARG:HB2	2.11	0.51
1:CA:220:G:O2'	1:CA:233:A:N3	2.36	0.51
1:CA:2177:C:O2'	3:CC:171:ALA:HB2	2.10	0.51
3:CC:57:GLN:HB2	3:CC:202:PRO:HG2	1.93	0.51
3:CC:218:THR:HG22	3:CC:219:MET:SD	2.50	0.51
7:CG:98:ARG:HA	7:CG:101:ILE:HB	1.92	0.51
16:CS:34:HIS:CE1	16:CS:54:LEU:HA	2.46	0.51
17:CT:6:LEU:O	17:CT:9:LEU:HB3	2.10	0.51
26:C2:18:PRO:O	26:C2:22:GLU:HG2	2.10	0.51
39:DF:23:LYS:HG2	39:DF:61:LEU:HD21	1.93	0.51
47:DN:14:PRO:HB2	47:DN:16:PHE:O	2.10	0.51
53:DT:47:GLY:HA2	53:DT:48:LYS:C	2.35	0.51
56:DX:8:4SU:O5'	56:DX:8:4SU:H6	2.09	0.51
57:DZ:122:TRP:CE2	57:DZ:132:ARG:NH1	2.79	0.51
57:DZ:193:GLY:O	57:DZ:196:ILE:HG22	2.11	0.51
1:AA:439:A:O5'	1:AA:439:A:H8	1.94	0.51
1:AA:1249:A:N6	1:AA:1286:U:H2'	2.24	0.51
1:AA:2331:G:N1	16:AS:3:ARG:HA	2.25	0.51
3:AC:54:ARG:HD2	3:AC:55:SER:H	1.76	0.51
3:AC:68:GLY:H	3:AC:189:ASN:ND2	2.09	0.51
6:AF:39:TRP:O	6:AF:43:LYS:HG2	2.10	0.51
6:AF:114:VAL:HG21	6:AF:202:PHE:CZ	2.45	0.51
6:AF:202:PHE:CZ	6:AF:206:ILE:HD13	2.46	0.51
23:AZ:59:LEU:N	23:AZ:67:LEU:O	2.30	0.51
34:BA:1017:G:H2'	34:BA:1018:C:C6	2.46	0.51
37:BD:120:LEU:HB3	37:BD:126:ILE:HD11	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:BJ:33:GLN:O	43:BJ:75:ILE:N	2.43	0.51
45:BL:77:LEU:HD21	45:BL:107:ALA:HA	1.92	0.51
1:CA:1045:A:N6	1:CA:1111:A:H2'	2.26	0.51
1:CA:1960:A:H8	1:CA:1960:A:H5"	1.76	0.51
1:CA:2476:A:H2'	1:CA:2476:A:N3	2.24	0.51
14:CQ:116:GLU:O	14:CQ:119:ARG:N	2.43	0.51
22:CY:14:LEU:HG	22:CY:15:VAL:N	2.25	0.51
34:DA:176:C:H2'	34:DA:177:C:H6	1.76	0.51
34:DA:189(B):C:H2'	34:DA:189(C):C:C6	2.46	0.51
34:DA:1256:A:N6	34:DA:1278:U:O2	2.43	0.51
39:DF:99:ALA:HB3	51:DR:29:PHE:CE1	2.46	0.51
39:DF:100:ASN:ND2	51:DR:23:LYS:HE3	2.25	0.51
1:AA:662:A:H4'	1:AA:663:G:O5'	2.11	0.51
1:AA:771:U:O4	1:AA:772:G:C6	2.64	0.51
1:AA:1532:A:H2'	1:AA:1533:G:H8	1.76	0.51
1:AA:2035:A:O2'	20:AW:94:ASP:OD2	2.26	0.51
1:AA:2120:U:H2'	1:AA:2121:U:O4'	2.11	0.51
7:AG:112:PRO:HG3	28:A4:43:TYR:CE1	2.46	0.51
8:AH:4:ILE:O	8:AH:69:ARG:HG2	2.10	0.51
27:A3:5:LYS:HB3	27:A3:57:GLU:HG2	1.92	0.51
34:BA:111:G:H5"	49:BP:27:LYS:HG2	1.91	0.51
34:BA:153:C:H42	34:BA:169:C:H42	1.56	0.51
34:BA:358:U:O2'	34:BA:359:U:H5'	2.10	0.51
47:BN:3:ARG:O	47:BN:5:ALA:N	2.44	0.51
57:BZ:107:VAL:HG22	57:BZ:135:PHE:HD2	1.74	0.51
57:BZ:639:ASN:N	57:BZ:640:ALA:HB3	2.26	0.51
1:CA:607:U:OP1	6:CF:102:PRO:HA	2.10	0.51
1:CA:1385:G:O2'	1:CA:1396:U:O2	2.24	0.51
3:CC:42:VAL:HG13	3:CC:43:GLU:H	1.73	0.51
7:CG:151:ALA:HB3	7:CG:153:ARG:HH11	1.76	0.51
12:CO:103:ALA:O	12:CO:106:LEU:HB2	2.11	0.51
30:C6:30:THR:O	30:C6:30:THR:HG22	2.11	0.51
34:DA:410:G:OP1	37:DD:30:LYS:NZ	2.34	0.51
34:DA:618:C:N4	34:DA:621:A:N7	2.59	0.51
34:DA:693:G:O4'	55:DV:13:A:H5"	2.11	0.51
34:DA:1312:G:H5'	52:DS:5:LEU:HD11	1.92	0.51
41:DH:51:VAL:HG22	41:DH:60:ARG:HB2	1.92	0.51
42:DI:45:ALA:O	42:DI:78:LYS:HG3	2.09	0.51
44:DK:15:ALA:HB1	44:DK:78:GLN:HG3	1.91	0.51
1:AA:2198:A:O2'	3:AC:45:HIS:CG	2.64	0.51
7:AG:16:ARG:HB2	7:AG:17:PRO:HD3	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:AR:103:ARG:HD3	15:AR:108:GLY:O	2.10	0.51
16:AS:10:ARG:O	16:AS:14:VAL:HG13	2.10	0.51
17:AT:73:GLU:OE1	17:AT:103:ARG:NE	2.41	0.51
34:BA:1234:C:H2'	34:BA:1235:U:C6	2.46	0.51
34:BA:1315:U:H2'	34:BA:1316:G:O4'	2.11	0.51
34:BA:1323:G:H4'	34:BA:1363:C:N3	2.26	0.51
38:BE:36:ASP:OD1	38:BE:39:GLY:N	2.39	0.51
40:BG:28:ASN:ND2	40:BG:36:LYS:HE3	2.26	0.51
41:BH:6:ILE:HG22	41:BH:10:LEU:HD21	1.93	0.51
1:CA:272:G:H4'	1:CA:272(A):U:H5"	1.91	0.51
1:CA:1810:A:H2'	1:CA:1811:G:O4'	2.11	0.51
1:CA:2365:G:H4'	24:C0:60:PHE:CZ	2.46	0.51
1:CA:2850:A:OP2	1:CA:2866:U:C5	2.63	0.51
3:CC:44:VAL:HG21	3:CC:176:VAL:HG21	1.93	0.51
13:CP:59:LEU:HD23	32:C8:58:ILE:HD13	1.92	0.51
23:CZ:69:THR:HG22	23:CZ:90:VAL:HG22	1.91	0.51
26:C2:29:LYS:HG2	26:C2:57:ILE:HD13	1.92	0.51
34:DA:803:G:OP1	63:DA:1808:HOH:O	2.19	0.51
37:DD:93:PHE:O	37:DD:97:LEU:HB2	2.11	0.51
42:DI:8:GLY:HA2	42:DI:79:LEU:HD23	1.93	0.51
43:DJ:13:HIS:HB3	43:DJ:68:HIS:CE1	2.45	0.51
44:DK:38:ASN:OD1	44:DK:38:ASN:N	2.43	0.51
57:DZ:35:TYR:HE2	57:DZ:269:VAL:HB	1.76	0.51
57:DZ:359:HIS:HB2	57:DZ:362:HIS:O	2.11	0.51
1:AA:229:G:OP2	1:AA:230:A:O2'	2.27	0.51
3:AC:42:VAL:CG1	3:AC:43:GLU:N	2.73	0.51
11:AN:42:TRP:CH2	11:AN:44:PRO:HB3	2.45	0.51
14:AQ:62:GLY:O	23:AZ:178:GLU:HG2	2.11	0.51
34:BA:102:G:O2'	34:BA:151:A:N3	2.43	0.51
34:BA:186:C:H2'	34:BA:187:C:C6	2.46	0.51
34:BA:966:G:H21	42:BI:127:LYS:HZ1	1.58	0.51
35:BB:141:GLU:O	35:BB:145:LEU:HB2	2.11	0.51
36:BC:172:ARG:HB2	36:BC:203:PHE:CD2	2.46	0.51
42:BI:23:ASN:ND2	42:BI:60:ASP:OD2	2.44	0.51
1:CA:1859:A:C2'	3:CC:206:LYS:HD2	1.99	0.51
1:CA:2121:G:H1'	3:CC:168:LYS:HG2	1.92	0.51
1:CA:2328:A:H2'	1:CA:2329:G:C8	2.46	0.51
1:CA:2773:C:H2'	1:CA:2774:C:H6	1.76	0.51
1:CA:2823:A:P	5:CE:159:HIS:HE2	2.31	0.51
6:CF:29:ASN:HD22	6:CF:32:LEU:HB2	1.75	0.51
8:CH:98:LEU:HD12	8:CH:102:ALA:O	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:C8:20:GLY:O	32:C8:59:LYS:HE2	2.11	0.51
34:DA:1399:C:C2	34:DA:1502:A:N6	2.79	0.51
46:DM:96:LEU:C	46:DM:110:ARG:HG2	2.36	0.51
57:DZ:117:GLN:NE2	57:DZ:120:THR:HG1	2.08	0.51
1:AA:1301:U:O5'	1:AA:1302:G:H5"	2.10	0.50
3:AC:50:ILE:H	3:AC:50:ILE:HD13	1.76	0.50
3:AC:57:GLN:HB2	3:AC:202:PRO:HG2	1.93	0.50
6:AF:133:ASN:N	6:AF:138:GLU:OE1	2.31	0.50
7:AG:41:GLN:O	7:AG:43:LEU:HB2	2.12	0.50
7:AG:58:GLN:O	7:AG:62:LEU:HG	2.10	0.50
10:AL:93:ARG:CZ	10:AL:93:ARG:HB3	2.39	0.50
16:AS:20:ARG:NH2	24:A0:47:PRO:HB2	2.26	0.50
20:AW:69:LEU:HD13	20:AW:107:LEU:HD23	1.92	0.50
21:AX:32:PRO:HA	21:AX:77:LYS:HB2	1.91	0.50
34:BA:309:G:O2'	34:BA:607:A:N1	2.44	0.50
34:BA:892:A:H2'	34:BA:893:C:C6	2.46	0.50
34:BA:976:G:OP1	47:BN:32:SER:N	2.44	0.50
35:BB:150:SER:O	35:BB:153:ARG:NH1	2.44	0.50
43:BJ:4:ILE:HA	43:BJ:100:THR:HA	1.93	0.50
49:BP:57:ARG:HE	49:BP:79:VAL:HG12	1.76	0.50
57:BZ:93:GLU:O	57:BZ:96:ARG:N	2.45	0.50
57:BZ:164:MET:O	57:BZ:180:VAL:HG13	2.11	0.50
1:CA:2316:C:H2'	1:CA:2317:C:C6	2.45	0.50
1:CA:2400:G:N2	1:CA:2417:C:C2	2.79	0.50
1:CA:2684:U:H2'	1:CA:2685:G:O4'	2.11	0.50
6:CF:157:VAL:HG11	6:CF:181:LEU:HD12	1.92	0.50
14:CQ:11:LYS:NZ	14:CQ:88:GLY:O	2.26	0.50
15:CR:57:ARG:O	15:CR:59:ASP:N	2.43	0.50
16:CS:15:ARG:HG2	16:CS:88:ASP:OD1	2.11	0.50
16:CS:66:ALA:HA	16:CS:69:VAL:HG12	1.91	0.50
34:DA:67:C:H2'	34:DA:68:G:H8	1.75	0.50
34:DA:667:G:H4'	48:DO:51:HIS:ND1	2.26	0.50
37:DD:25:ARG:HG2	37:DD:25:ARG:O	2.11	0.50
46:DM:81:LEU:HD11	46:DM:88:ARG:HH21	1.76	0.50
1:AA:491:G:H2'	1:AA:492:A:C8	2.46	0.50
1:AA:897:C:O3'	27:A3:49:LYS:HE2	2.12	0.50
1:AA:2143:G:C4'	3:AC:168:LYS:CD	2.88	0.50
2:AB:15:A:OP2	2:AB:69:G:N2	2.36	0.50
7:AG:4:ASP:CG	7:AG:9:ARG:HH21	2.20	0.50
11:AN:28:THR:HG22	11:AN:29:LYS:N	2.25	0.50
34:BA:67:C:H2'	34:BA:68:G:H8	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:BA:791:G:C2'	34:BA:792:A:H5'	2.41	0.50
34:BA:1060:C:C5	36:BC:2:GLY:HA3	2.46	0.50
37:BD:68:TYR:OH	37:BD:98:GLU:OE2	2.26	0.50
43:BJ:49:VAL:HG23	47:BN:41:ARG:HB2	1.93	0.50
57:BZ:15:ILE:HA	57:BZ:103:GLY:O	2.12	0.50
1:CA:479:A:N3	1:CA:481:G:H5"	2.26	0.50
1:CA:646:A:H2'	1:CA:647:G:O4'	2.10	0.50
1:CA:1861:G:OP2	3:CC:206:LYS:HA	2.10	0.50
1:CA:2318:G:H4'	1:CA:2319:G:OP2	2.11	0.50
4:CD:69:ARG:NH2	4:CD:128:GLY:O	2.45	0.50
16:CS:83:LYS:HD3	16:CS:111:GLU:OE1	2.11	0.50
34:DA:1051:C:H2'	34:DA:1052:U:H6	1.77	0.50
41:DH:25:ASP:HB3	41:DH:58:TYR:CD2	2.44	0.50
47:DN:37:PHE:HB3	47:DN:39:LEU:HD12	1.92	0.50
57:DZ:154:GLN:C	57:DZ:158:GLY:HA2	2.37	0.50
1:AA:302:A:O2'	1:AA:303:C:OP1	2.28	0.50
1:AA:1336:C:O2'	1:AA:1337:C:H5'	2.11	0.50
1:AA:2294:G:OP1	1:AA:2295:C:H1'	2.11	0.50
1:AA:2408:G:H4'	25:A1:29:GLY:O	2.11	0.50
1:AA:2600:G:OP1	63:AA:3938:HOH:O	2.19	0.50
1:AA:2673:G:C6	1:AA:2674:A:C2	3.00	0.50
8:AH:33:LEU:HD11	8:AH:136:ILE:HG13	1.93	0.50
16:AS:89:ARG:HD2	16:AS:92:TYR:O	2.12	0.50
21:AX:11:PRO:HD3	26:A2:37:PHE:CZ	2.47	0.50
23:AZ:109:ALA:HB3	23:AZ:145:GLU:HG3	1.94	0.50
34:BA:767:A:H2'	34:BA:768:A:O4'	2.12	0.50
34:BA:899:C:O5'	34:BA:899:C:H6	1.95	0.50
38:BE:105:VAL:HB	38:BE:106:PRO:HD3	1.94	0.50
46:BM:84:ILE:HG22	52:BS:66:MET:HE2	1.91	0.50
53:BT:63:ILE:HD12	53:BT:81:LYS:HG2	1.92	0.50
57:BZ:182:ARG:HG3	57:BZ:182:ARG:NH1	2.26	0.50
1:CA:1050:A:O2'	1:CA:2752:C:H1'	2.10	0.50
1:CA:1143:A:OP1	11:CN:25:ARG:NH2	2.44	0.50
1:CA:1557:C:H5"	1:CA:1558:A:OP2	2.11	0.50
1:CA:2322:A:H2'	1:CA:2323:G:O4'	2.11	0.50
1:CA:2820:A:OP2	15:CR:2:ARG:NH2	2.44	0.50
34:DA:519:C:H2'	34:DA:520:A:O4'	2.12	0.50
34:DA:1133:G:H2'	34:DA:1134:G:H8	1.75	0.50
38:DE:72:GLN:C	38:DE:73:ASN:HD22	2.19	0.50
1:AA:1645:C:OP2	21:AX:36:LYS:HD2	2.12	0.50
3:AC:65:LEU:HB3	3:AC:189:ASN:HD22	1.75	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:AZ:24:LEU:HD22	23:AZ:41:LEU:HD23	1.93	0.50
34:BA:364:A:H2'	34:BA:365:U:C6	2.47	0.50
34:BA:545:C:OP2	37:BD:65:ARG:NH2	2.44	0.50
34:BA:853:G:C6	34:BA:854:G:C5	3.00	0.50
34:BA:1417:G:N2	34:BA:1482:G:H2'	2.23	0.50
36:BC:40:ARG:NH2	36:BC:55:VAL:O	2.44	0.50
39:BF:37:VAL:HG12	39:BF:38:GLU:H	1.77	0.50
41:BH:58:TYR:O	41:BH:59:LEU:HD23	2.12	0.50
42:BI:9:ARG:H	42:BI:79:LEU:HD23	1.75	0.50
57:BZ:-36:LEU:HD11	57:BZ:-29:LEU:HD22	1.92	0.50
57:BZ:291:GLY:HA3	57:BZ:301:ILE:HD11	1.93	0.50
1:CA:71:A:N7	21:CX:31:HIS:HE1	2.09	0.50
1:CA:876:C:H2'	1:CA:877:U:O4'	2.10	0.50
1:CA:2394:C:OP1	32:C8:30:ARG:NH1	2.44	0.50
1:CA:2748:A:H5'	8:CH:4:ILE:HD12	1.94	0.50
1:CA:2787:C:H2'	1:CA:2788:C:H6	1.77	0.50
1:CA:2850:A:C2	1:CA:2851:A:C4	2.99	0.50
4:CD:44:ASN:ND2	4:CD:46:GLN:HG3	2.26	0.50
8:CH:103:LEU:HB3	8:CH:115:VAL:HG22	1.93	0.50
12:CO:10:VAL:HG11	12:CO:16:ALA:HB1	1.93	0.50
26:C2:22:GLU:OE2	26:C2:68:ARG:NH2	2.44	0.50
34:DA:143:A:OP2	34:DA:143:A:H8	1.94	0.50
34:DA:1325:C:H4'	54:DU:17:THR:HG21	1.92	0.50
38:DE:69:VAL:HG22	38:DE:71:LEU:HD13	1.94	0.50
43:DJ:11:PHE:CE1	43:DJ:67:THR:HB	2.47	0.50
46:DM:20:THR:HA	46:DM:25:ILE:O	2.11	0.50
57:DZ:103:GLY:H	57:DZ:130:VAL:HG23	1.75	0.50
57:DZ:346:LYS:HZ3	57:DZ:384:ILE:HG12	1.76	0.50
1:AA:89:U:H1'	1:AA:90:A:N7	2.27	0.50
1:AA:313:A:H61	1:AA:375:G:H1'	1.77	0.50
1:AA:596:G:O2'	1:AA:597:C:H3'	2.12	0.50
1:AA:1211:U:H2'	1:AA:1212:C:C6	2.46	0.50
1:AA:1818:A:O4'	1:AA:2601:A:H4'	2.12	0.50
1:AA:2735:G:H2'	1:AA:2736:C:C6	2.46	0.50
8:AH:41:MET:CE	8:AH:65:HIS:HA	2.41	0.50
34:BA:413:G:H1'	34:BA:428:G:H21	1.76	0.50
35:BB:111:ARG:HG2	35:BB:111:ARG:NH1	2.26	0.50
57:BZ:122:TRP:O	57:BZ:122:TRP:CD1	2.65	0.50
1:CA:489:G:N7	20:CW:49:LYS:NZ	2.56	0.50
1:CA:491:G:H2'	1:CA:492:A:H8	1.76	0.50
1:CA:1370:C:HO2'	1:CA:1811:G:HO2'	1.40	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1856:G:C2	1:CA:1887:C:N3	2.80	0.50
1:CA:2570:G:H2'	1:CA:2571:C:O4'	2.12	0.50
3:CC:54:ARG:HD2	3:CC:55:SER:H	1.76	0.50
34:DA:43:C:H2'	34:DA:44:G:O4'	2.12	0.50
34:DA:791:G:C6	34:DA:792:A:N7	2.80	0.50
34:DA:994:A:C2	47:DN:5:ALA:HA	2.47	0.50
34:DA:1060:C:H4'	43:DJ:51:ARG:HB3	1.92	0.50
35:DB:87:ARG:NH2	35:DB:220:ASP:OD1	2.41	0.50
46:DM:86:CYS:SG	46:DM:88:ARG:HB2	2.51	0.50
57:DZ:139:MET:HA	57:DZ:144:ALA:HB1	1.93	0.50
1:AA:181:C:H2'	1:AA:182:U:H5'	1.94	0.50
1:AA:2357:G:N3	1:AA:2393:C:H2'	2.27	0.50
1:AA:2705:A:H2'	1:AA:2706:G:H8	1.77	0.50
9:AK:69:PRO:C	9:AK:71:LEU:H	2.20	0.50
10:AL:51:ALA:HB2	10:AL:76:TYR:CZ	2.46	0.50
34:BA:158:G:H2'	34:BA:159:G:H8	1.77	0.50
34:BA:316:G:OP2	34:BA:351:G:O2'	2.30	0.50
34:BA:1298:C:H2'	40:BG:114:ARG:NH1	2.27	0.50
53:BT:30:LYS:HA	53:BT:33:ILE:HD12	1.93	0.50
1:CA:1141:U:OP1	11:CN:25:ARG:HD2	2.11	0.50
1:CA:1843:C:H5'	4:CD:253:GLN:HE21	1.74	0.50
1:CA:2238:G:H2'	1:CA:2238:G:N3	2.27	0.50
9:CK:118:THR:O	9:CK:120:LYS:N	2.45	0.50
15:CR:33:ARG:NH2	29:C5:57:VAL:O	2.45	0.50
19:CV:72:VAL:HG13	19:CV:85:LYS:HB3	1.93	0.50
33:C9:14:CYS:HA	33:C9:27:CYS:HB2	1.93	0.50
34:DA:181:G:H4'	34:DA:182:U:H5'	1.93	0.50
34:DA:579:G:H2'	34:DA:580:U:H6	1.76	0.50
34:DA:1142:G:H2'	34:DA:1143:G:O4'	2.11	0.50
34:DA:1224:G:O2'	34:DA:1322:C:OP1	2.29	0.50
34:DA:1248:A:H2'	34:DA:1249:C:H6	1.77	0.50
34:DA:1388:C:H2'	34:DA:1389:C:C6	2.47	0.50
36:DC:70:VAL:HG22	36:DC:72:LYS:H	1.77	0.50
37:DD:171:GLY:HA3	37:DD:174:LEU:HB2	1.93	0.50
1:AA:423:G:O2'	25:A1:43:TYR:O	2.30	0.50
1:AA:1100:A:H2'	1:AA:1101:G:O4'	2.11	0.50
1:AA:1714:G:O2'	1:AA:2013:U:O4	2.19	0.50
3:AC:191:ARG:O	3:AC:194:ILE:HG22	2.12	0.50
3:AC:191:ARG:O	3:AC:195:ARG:HG2	2.11	0.50
4:AD:261:LYS:HZ1	4:AD:263:ARG:NH2	2.10	0.50
14:AQ:16:ARG:HG2	14:AQ:18:LYS:HE2	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:AQ:21:THR:CG2	14:AQ:101:ARG:HD3	2.42	0.50
15:AR:81:ASP:O	15:AR:85:PRO:HG2	2.12	0.50
34:BA:1036:G:H2'	34:BA:1036:G:N3	2.27	0.50
57:BZ:-34:ARG:O	57:BZ:-32:LEU:N	2.44	0.50
57:BZ:276:VAL:HG13	57:BZ:280:LEU:HD12	1.92	0.50
1:CA:189:G:H2'	1:CA:205:G:N2	2.26	0.50
1:CA:1386:C:H2'	1:CA:1387:C:H6	1.77	0.50
1:CA:1564:C:H2'	1:CA:1565:C:C6	2.47	0.50
1:CA:2567:G:H2'	1:CA:2568:C:H6	1.76	0.50
1:CA:2712:U:H2'	1:CA:2714:G:H5"	1.94	0.50
3:CC:65:LEU:HB3	3:CC:189:ASN:HD22	1.75	0.50
8:CH:3:ARG:CZ	8:CH:5:GLY:H	2.24	0.50
12:CO:104:ARG:HE	17:CT:36:GLU:HG3	1.77	0.50
13:CP:1:MET:HG3	13:CP:5:ASP:HB2	1.93	0.50
34:DA:186:C:H2'	34:DA:187:C:H6	1.77	0.50
34:DA:403:C:O2'	37:DD:122:ARG:NH2	2.36	0.50
35:DB:71:VAL:HG12	35:DB:93:VAL:HG22	1.93	0.50
37:DD:205:GLU:HA	37:DD:208:SER:HB2	1.94	0.50
40:DG:115:ARG:HB3	40:DG:115:ARG:NH1	2.27	0.50
41:DH:94:TYR:HE1	41:DH:132:GLU:HB2	1.76	0.50
43:DJ:78:ASN:O	43:DJ:80:LYS:N	2.43	0.50
44:DK:98:LEU:O	44:DK:101:SER:OG	2.13	0.50
57:DZ:257:PRO:O	57:DZ:259:PHE:HD1	1.95	0.50
57:DZ:355:LEU:HB3	57:DZ:366:VAL:HG23	1.94	0.50
1:AA:1093:G:H21	1:AA:1157:A:H2	1.60	0.50
1:AA:1681:A:H5"	63:AA:4094:HOH:O	2.12	0.50
1:AA:1686:U:O2'	1:AA:1687:C:H5'	2.11	0.50
1:AA:1716:A:H5"	1:AA:2562:G:OP1	2.12	0.50
1:AA:1993:A:H5'	1:AA:1994:A:H5"	1.92	0.50
1:AA:2132:G:P	1:AA:2140:U:H3	2.35	0.50
4:AD:13:ARG:HD2	4:AD:16:MET:CE	2.42	0.50
4:AD:25:THR:HG21	4:AD:113:VAL:HG11	1.94	0.50
4:AD:162:SER:HB3	4:AD:195:ALA:HB2	1.94	0.50
6:AF:7:TYR:OH	6:AF:119:ARG:HG3	2.12	0.50
6:AF:184:TYR:CE2	6:AF:188:ARG:HD2	2.47	0.50
8:AH:77:LYS:HE2	8:AH:81:GLU:OE2	2.12	0.50
35:BB:86:GLU:C	35:BB:89:GLY:H	2.19	0.50
50:BQ:37:LYS:O	50:BQ:38:ARG:NH2	2.45	0.50
1:CA:658:C:H2'	1:CA:659:C:H6	1.74	0.50
1:CA:700:G:O2'	1:CA:1632:A:N3	2.29	0.50
1:CA:1422:G:C6	1:CA:1423:G:C5	3.00	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1488:G:C6	1:CA:1489:U:N3	2.80	0.50
1:CA:1608:A:H1'	1:CA:1610:A:OP2	2.11	0.50
1:CA:2193:G:H2'	1:CA:2194:G:O4'	2.11	0.50
1:CA:2537:U:H2'	1:CA:2538:C:C6	2.47	0.50
6:CF:36:VAL:HG11	6:CF:183:VAL:HG11	1.94	0.50
6:CF:117:ARG:NH2	6:CF:189:THR:O	2.31	0.50
8:CH:12:PRO:O	8:CH:15:VAL:HG12	2.11	0.50
13:CP:70:GLN:O	13:CP:73:GLY:N	2.34	0.50
34:DA:179:A:H2'	34:DA:180:U:C6	2.47	0.50
34:DA:968:A:C8	34:DA:1062:U:H4'	2.47	0.50
34:DA:1429:C:H2'	34:DA:1430:C:H6	1.76	0.50
48:DO:64:ARG:HH11	48:DO:68:ARG:HH12	1.60	0.50
52:DS:11:VAL:O	52:DS:13:ASP:N	2.45	0.50
57:DZ:-52:VAL:O	57:DZ:-50:GLN:N	2.45	0.50
1:AA:239:G:H5'	13:AP:60:MET:SD	2.52	0.50
1:AA:509:A:C8	1:AA:510:C:C5	3.00	0.50
1:AA:1007:G:H2'	1:AA:1008:U:C6	2.47	0.50
1:AA:2509:A:H5"	63:AA:4234:HOH:O	2.12	0.50
2:AB:7:G:H5'	16:AS:29:PHE:CE2	2.47	0.50
2:AB:42:C:OP2	28:A4:2:LYS:NZ	2.36	0.50
6:AF:13:SER:HA	6:AF:127:GLU:HG3	1.93	0.50
7:AG:61:ALA:HB1	28:A4:7:PRO:HG2	1.94	0.50
12:AO:23:ARG:HG3	12:AO:24:VAL:N	2.26	0.50
34:BA:113:G:H2'	34:BA:114:U:H6	1.77	0.50
34:BA:730:G:C5	34:BA:731:G:H1'	2.47	0.50
34:BA:1465:C:H2'	34:BA:1466:C:O4'	2.11	0.50
37:BD:8:VAL:HA	37:BD:11:LEU:HD13	1.94	0.50
41:BH:9:MET:O	41:BH:12:ARG:N	2.44	0.50
41:BH:112:LEU:HA	41:BH:134:ILE:HG12	1.94	0.50
44:BK:99:GLN:NE2	44:BK:108:ILE:HD11	2.27	0.50
53:BT:37:SER:O	53:BT:41:ILE:HG13	2.12	0.50
56:BX:23:C:H2'	56:BX:24:U:C6	2.47	0.50
57:BZ:226:ASN:O	57:BZ:230:LYS:HG3	2.12	0.50
57:BZ:467:LYS:O	57:BZ:469:GLU:N	2.38	0.50
1:CA:84:A:H5"	22:CY:8:LYS:HE3	1.93	0.50
1:CA:228:A:H8	1:CA:229:A:H5'	1.76	0.50
1:CA:493:G:H2'	1:CA:494:G:O4'	2.11	0.50
1:CA:608:A:H2'	1:CA:609:A:C8	2.47	0.50
1:CA:729:G:H5'	1:CA:730:C:H5"	1.94	0.50
1:CA:2690:C:OP2	15:CR:14:SER:HB2	2.12	0.50
1:CA:2726:U:H4'	12:CO:1:MET:HE1	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:CD:2:ALA:O	4:CD:3:VAL:HB	2.11	0.50
20:CW:70:TYR:O	20:CW:107:LEU:HD12	2.12	0.50
22:CY:99:CYS:SG	22:CY:102:CYS:N	2.85	0.50
34:DA:528:C:H41	45:DL:49:ASN:HD21	1.60	0.50
34:DA:975:A:H4'	34:DA:976:G:H5"	1.93	0.50
34:DA:1003:G:H2'	34:DA:1004:A:O4'	2.12	0.50
35:DB:192:SER:O	35:DB:194:PRO:HD3	2.12	0.50
53:DT:47:GLY:HA2	53:DT:48:LYS:O	2.12	0.50
54:DU:12:LYS:HE3	54:DU:19:GLY:HA3	1.94	0.50
1:AA:771:U:C4	1:AA:772:G:C5	3.00	0.49
1:AA:799:A:H3'	31:A7:1:MET:HE1	1.94	0.49
1:AA:921:G:H5"	23:AZ:175:VAL:HG11	1.94	0.49
1:AA:2660:C:H2'	1:AA:2661:U:H6	1.77	0.49
14:AQ:39:PRO:HA	14:AQ:97:VAL:O	2.12	0.49
34:BA:102:G:H2'	34:BA:103:C:H6	1.76	0.49
34:BA:715:A:H5"	34:BA:805:C:H1'	1.94	0.49
34:BA:1058:G:H2'	34:BA:1059:C:O4'	2.12	0.49
38:BE:51:VAL:HB	38:BE:52:PRO:HD3	1.94	0.49
38:BE:110:LEU:HD13	38:BE:118:ILE:HD13	1.94	0.49
45:BL:7:ILE:O	45:BL:11:VAL:HG23	2.12	0.49
45:BL:85:ILE:HG22	45:BL:100:ILE:HG13	1.93	0.49
46:BM:84:ILE:HG21	52:BS:66:MET:HB3	1.94	0.49
53:BT:79:ARG:HD2	53:BT:83:ARG:NH1	2.26	0.49
1:CA:587:C:C5	1:CA:671:C:H1'	2.47	0.49
1:CA:958:U:H5"	14:CQ:14:ARG:HD3	1.94	0.49
1:CA:1374:G:C5	1:CA:1375:C:C4	3.00	0.49
1:CA:1406:U:H2'	1:CA:1407:C:C6	2.47	0.49
4:CD:143:HIS:CD2	4:CD:196:VAL:HG22	2.47	0.49
8:CH:64:LEU:HD23	8:CH:67:LEU:HD23	1.94	0.49
10:CL:30:HIS:HB3	10:CL:32:ALA:H	1.76	0.49
11:CN:36:GLY:HA2	11:CN:38:HIS:CE1	2.47	0.49
27:C3:18:ASP:OD1	27:C3:18:ASP:N	2.34	0.49
28:C4:59:PHE:HA	28:C4:61:ARG:HB2	1.94	0.49
31:C7:19:ARG:HG2	31:C7:19:ARG:HH11	1.76	0.49
33:C9:22:ARG:HD3	33:C9:35:ARG:HD2	1.92	0.49
34:DA:14:U:O2	34:DA:17:U:H5	1.94	0.49
34:DA:560:U:O2'	34:DA:561:U:OP2	2.27	0.49
48:DO:11:VAL:HG21	48:DO:34:LEU:HD22	1.93	0.49
57:DZ:74:TRP:CD1	57:DZ:273:LEU:HB3	2.46	0.49
1:AA:602:G:H2'	1:AA:603:C:C6	2.46	0.49
1:AA:2328:C:H1'	7:AG:128:ARG:NH2	2.27	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:AR:54:LEU:O	15:AR:62:ALA:HB1	2.12	0.49
34:BA:685:G:C2	34:BA:686:U:C4	3.00	0.49
34:BA:963:G:C2'	34:BA:964:A:H5'	2.42	0.49
53:BT:38:LYS:HA	53:BT:41:ILE:HD12	1.94	0.49
1:CA:236:C:H2'	1:CA:237:C:C6	2.47	0.49
1:CA:253:C:O3'	63:CA:3750:HOH:O	2.19	0.49
1:CA:751:A:H5'	20:CW:90:ARG:HA	1.93	0.49
1:CA:796:C:H2'	1:CA:797:C:C6	2.47	0.49
1:CA:2563:U:H4'	12:CO:28:SER:HA	1.94	0.49
5:CE:36:ARG:HD3	5:CE:47:VAL:CG1	2.42	0.49
7:CG:36:LYS:HD3	7:CG:95:ARG:CZ	2.41	0.49
14:CQ:51:ARG:O	14:CQ:54:MET:N	2.45	0.49
16:CS:49:VAL:HG13	16:CS:73:LEU:HD11	1.94	0.49
17:CT:61:PHE:CE1	17:CT:76:PHE:HB2	2.48	0.49
34:DA:750:G:O2'	48:DO:21:ASP:OD1	2.30	0.49
34:DA:853:G:C6	34:DA:854:G:N7	2.80	0.49
34:DA:1281:U:H5"	34:DA:1282:C:H5	1.77	0.49
34:DA:1402:C:H2'	34:DA:1403:C:O4'	2.12	0.49
1:AA:510:C:OP1	22:AY:51:VAL:HG12	2.12	0.49
1:AA:703:G:H2'	1:AA:704:U:O4'	2.13	0.49
1:AA:2175:G:H2'	1:AA:2176:G:H8	1.77	0.49
1:AA:2742:G:H2'	1:AA:2743:C:O4'	2.12	0.49
12:AO:120:GLU:OE1	17:AT:67:SER:OG	2.28	0.49
22:AY:14:LEU:HD12	22:AY:15:VAL:N	2.28	0.49
34:BA:1399:C:C2	34:BA:1502:A:N6	2.80	0.49
44:BK:40:ILE:HG22	44:BK:41:THR:HG22	1.93	0.49
44:BK:115:PRO:HB2	44:BK:118:GLY:H	1.77	0.49
57:BZ:278:ASP:HB3	57:BZ:279:TYR:CE2	2.47	0.49
1:CA:83:G:O2'	1:CA:102:G:N2	2.45	0.49
1:CA:990:A:OP2	63:CA:3730:HOH:O	2.20	0.49
1:CA:1713:U:H2'	1:CA:1714:G:H8	1.77	0.49
1:CA:2293:C:H2'	1:CA:2294:C:C6	2.47	0.49
1:CA:2740:A:C6	1:CA:2764:A:C8	3.00	0.49
1:CA:2823:A:OP1	5:CE:113:PHE:HB2	2.12	0.49
11:CN:14:VAL:HG11	11:CN:138:LEU:HD12	1.94	0.49
13:CP:43:GLY:HA3	63:CP:203:HOH:O	2.12	0.49
18:CU:66:ASN:HB3	63:CU:3101:HOH:O	2.13	0.49
34:DA:559:A:OP1	38:DE:126:ARG:NH2	2.46	0.49
34:DA:1142:G:H3'	34:DA:1143:G:H8	1.76	0.49
47:DN:40:CYS:SG	47:DN:43:CYS:HB2	2.52	0.49
1:AA:260:A:N6	1:AA:284:G:H1'	2.28	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1699:A:C2'	1:AA:1700:G:H5'	2.42	0.49
3:AC:203:GLU:CD	3:AC:203:GLU:N	2.70	0.49
7:AG:110:ALA:HB1	7:AG:140:ILE:CG2	2.41	0.49
11:AN:65:LYS:NZ	11:AN:65:LYS:HB2	2.27	0.49
18:AU:86:ALA:CB	18:AU:88:ILE:HD12	2.42	0.49
22:AY:13:VAL:HB	22:AY:72:VAL:HG13	1.94	0.49
26:A2:22:GLU:HG2	26:A2:64:LEU:HD11	1.95	0.49
34:BA:624:C:H2'	34:BA:625:G:C8	2.46	0.49
35:BB:81:VAL:HG12	35:BB:215:LEU:HD11	1.95	0.49
44:BK:18:ARG:HA	44:BK:81:ASP:H	1.76	0.49
49:BP:71:ARG:O	49:BP:74:LEU:N	2.46	0.49
57:BZ:13:ARG:HH21	57:BZ:77:HIS:CE1	2.30	0.49
1:CA:724:U:H2'	1:CA:725:G:O4'	2.12	0.49
1:CA:1278:A:OP1	15:CR:36:THR:HG22	2.13	0.49
3:CC:203:GLU:CD	3:CC:203:GLU:N	2.70	0.49
5:CE:12:THR:HG22	5:CE:13:ARG:H	1.78	0.49
10:CL:74:ALA:HB2	10:CL:111:LYS:HE2	1.94	0.49
11:CN:112:LEU:O	11:CN:115:ARG:N	2.44	0.49
14:CQ:16:ARG:HG2	14:CQ:16:ARG:HH11	1.77	0.49
34:DA:1044:A:C5	34:DA:1045:C:H1'	2.46	0.49
34:DA:1060:C:C5	36:DC:2:GLY:HA3	2.48	0.49
34:DA:1124:G:H5"	43:DJ:35:SER:OG	2.12	0.49
35:DB:7:VAL:HG12	35:DB:8:LYS:H	1.77	0.49
35:DB:133:LYS:C	35:DB:135:GLN:H	2.19	0.49
1:AA:70:A:N7	21:AX:31:HIS:HE1	2.10	0.49
1:AA:491:G:C6	1:AA:492:A:N6	2.80	0.49
1:AA:2262:G:C6	14:AQ:83:MET:HB3	2.48	0.49
1:AA:2822:G:C2	1:AA:2823:A:C4	3.00	0.49
7:AG:18:GLU:OE2	7:AG:21:ARG:NH1	2.45	0.49
25:A1:17:SER:HB2	25:A1:40:ARG:HG2	1.95	0.49
27:A3:26:LEU:O	27:A3:35:ARG:NE	2.37	0.49
28:A4:41:PRO:HG3	28:A4:49:PHE:CE2	2.48	0.49
36:BC:114:PRO:HA	36:BC:185:GLY:HA3	1.95	0.49
41:BH:5:PRO:O	41:BH:8:ASP:HB3	2.13	0.49
1:CA:1421:G:C2	1:CA:1422:G:C8	3.01	0.49
1:CA:1925:C:C2'	1:CA:1926:U:H5'	2.42	0.49
1:CA:2801(A):A:H1'	1:CA:2895:U:H1'	1.93	0.49
9:CK:27:VAL:HA	9:CK:113:GLN:HA	1.95	0.49
25:C1:21:ARG:HD3	25:C1:35:THR:HG21	1.93	0.49
34:DA:391:G:C6	34:DA:392:G:C5	3.00	0.49
34:DA:935:A:H61	40:DG:3:ARG:HG3	1.78	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:DA:1227:A:OP1	52:DS:80:TYR:OH	2.27	0.49
34:DA:1356:G:N2	34:DA:1367:C:O2	2.46	0.49
1:AA:139:A:H8	1:AA:1454:C:O2'	1.96	0.49
1:AA:1003:U:OP2	14:AQ:14:ARG:HD3	2.11	0.49
1:AA:1038:C:OP1	19:AV:74:LYS:NZ	2.43	0.49
1:AA:1827:U:H2'	1:AA:1828:C:C6	2.48	0.49
4:AD:68:LYS:HD2	4:AD:70:TRP:CZ2	2.48	0.49
8:AH:38:SER:HB2	8:AH:64:LEU:HD22	1.95	0.49
9:AK:61:LEU:O	9:AK:65:GLU:N	2.46	0.49
13:AP:84:ASN:OD1	13:AP:117:GLU:HB2	2.12	0.49
25:A1:89:GLU:O	25:A1:93:GLU:HG2	2.12	0.49
28:A4:69:LYS:HE2	52:BS:20:LEU:HD13	1.94	0.49
34:BA:102:G:H2'	34:BA:103:C:C6	2.47	0.49
34:BA:284:G:H2'	34:BA:285:G:H8	1.78	0.49
34:BA:826:C:H5'	41:BH:12:ARG:NH1	2.27	0.49
35:BB:108:ILE:O	35:BB:111:ARG:HB2	2.13	0.49
36:BC:87:LEU:O	36:BC:91:LEU:N	2.45	0.49
39:BF:70:ASP:HB2	39:BF:71:ARG:HG2	1.94	0.49
46:BM:4:ILE:HB	46:BM:57:ARG:HG3	1.94	0.49
1:CA:34:C:OP1	1:CA:34:C:H6	1.96	0.49
1:CA:321:G:OP1	6:CF:135:LYS:NZ	2.40	0.49
1:CA:848:G:C4	1:CA:933:A:H8	2.31	0.49
3:CC:191:ARG:O	3:CC:195:ARG:HG2	2.11	0.49
6:CF:61:GLY:HA2	6:CF:77:ASP:HB3	1.94	0.49
7:CG:124:SER:HB2	7:CG:131:TYR:CE1	2.48	0.49
34:DA:767:A:H2'	34:DA:768:A:O4'	2.13	0.49
34:DA:900:A:H2'	34:DA:901:A:C8	2.47	0.49
34:DA:1391:U:H2'	34:DA:1392:G:C8	2.48	0.49
35:DB:163:PHE:HA	35:DB:185:ILE:O	2.12	0.49
37:DD:129:ASN:H	37:DD:129:ASN:HD22	1.61	0.49
43:DJ:38:ILE:HG13	43:DJ:71:LEU:HB3	1.95	0.49
46:DM:12:ASN:OD1	46:DM:12:ASN:N	2.46	0.49
56:DX:15:G:H2'	56:DX:59:A:N1	2.28	0.49
1:AA:100:G:OP1	26:A2:7:ARG:NH2	2.46	0.49
1:AA:185:A:H2'	1:AA:185:A:N3	2.27	0.49
1:AA:1007:G:H2'	1:AA:1008:U:H6	1.76	0.49
4:AD:52:ARG:HB2	4:AD:53:PHE:CD2	2.47	0.49
7:AG:25:TYR:OH	7:AG:168:GLU:OE1	2.24	0.49
8:AH:98:LEU:HD12	8:AH:102:ALA:O	2.12	0.49
11:AN:60:ILE:C	11:AN:61:ARG:HD2	2.38	0.49
34:BA:51:A:H61	34:BA:314:C:H1'	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:BA:78:G:H22	34:BA:92:C:N4	1.99	0.49
57:BZ:-38:TYR:C	57:BZ:-35:PRO:HD2	2.38	0.49
1:CA:443:A:H1'	1:CA:1201:C:O4'	2.13	0.49
1:CA:1337:G:H2'	1:CA:1338:G:O4'	2.12	0.49
1:CA:1400:G:H2'	1:CA:1401:G:C8	2.47	0.49
1:CA:1857:G:C6	1:CA:1858:G:N1	2.81	0.49
3:CC:24:ASP:C	3:CC:24:ASP:OD1	2.55	0.49
3:CC:55:SER:C	3:CC:57:GLN:N	2.71	0.49
3:CC:191:ARG:O	3:CC:194:ILE:HG22	2.12	0.49
5:CE:47:VAL:HG11	5:CE:86:PRO:HD2	1.94	0.49
34:DA:1004:A:H5'	34:DA:1024:G:H22	1.78	0.49
37:DD:149:ALA:O	37:DD:152:SER:N	2.40	0.49
38:DE:143:ARG:HD2	41:DH:77:GLU:OE2	2.12	0.49
49:DP:4:ILE:O	49:DP:66:PRO:HA	2.12	0.49
57:DZ:246:ILE:O	57:DZ:249:GLY:N	2.44	0.49
1:AA:2451:A:C5'	1:AA:2451:A:C8	2.95	0.49
6:AF:34:TRP:CE2	13:AP:8:PRO:HD3	2.48	0.49
29:A5:33:CYS:N	29:A5:38:ALA:O	2.46	0.49
29:A5:46:CYS:SG	29:A5:48:GLU:HB2	2.52	0.49
34:BA:66:G:O4'	34:BA:173:U:C4	2.66	0.49
34:BA:107:G:OP1	34:BA:325:A:N6	2.43	0.49
34:BA:250:A:H4'	34:BA:251:G:O5'	2.11	0.49
34:BA:1347:G:C8	42:BI:107:ARG:HB2	2.48	0.49
36:BC:181:ASN:HB3	36:BC:204:LEU:HB2	1.94	0.49
45:BL:53:ARG:HG3	45:BL:93:LEU:HD21	1.95	0.49
48:BO:18:PHE:HB2	48:BO:19:PRO:HD2	1.94	0.49
57:BZ:310:ALA:O	57:BZ:331:TYR:N	2.43	0.49
1:CA:1461:G:H2'	1:CA:1462:C:C6	2.47	0.49
4:CD:71:ASP:OD2	4:CD:103:ARG:NH2	2.46	0.49
11:CN:128:HIS:CE1	11:CN:135:PRO:HG2	2.48	0.49
17:CT:13:ARG:HB2	17:CT:14:TYR:CD2	2.47	0.49
17:CT:118:ARG:HG2	34:DA:1442(A):G:C8	2.47	0.49
34:DA:314:C:O2'	34:DA:315:A:H5'	2.13	0.49
34:DA:938:A:H2'	34:DA:939:G:O4'	2.13	0.49
34:DA:1153:C:H2'	34:DA:1154:G:H5"	1.93	0.49
37:DD:31:CYS:SG	37:DD:32:ALA:N	2.82	0.49
46:DM:33:ALA:HA	46:DM:59:TYR:CE2	2.42	0.49
57:DZ:168:ILE:HG12	57:DZ:205:TYR:CD2	2.48	0.49
1:AA:424:G:OP2	25:A1:10:LYS:NZ	2.44	0.49
1:AA:469:A:H1'	1:AA:1246:C:O4'	2.13	0.49
1:AA:2451:A:C8	1:AA:2451:A:H5"	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:AQ:62:GLY:HA2	23:AZ:116:VAL:HG21	1.94	0.49
18:AU:108:GLU:OE2	18:AU:112:ARG:NH1	2.38	0.49
26:A2:32:LEU:HD13	26:A2:36:ARG:NH1	2.28	0.49
34:BA:41:G:C2	34:BA:42:G:C5	3.01	0.49
34:BA:109:A:C6	34:BA:326:G:C6	3.00	0.49
34:BA:160:A:N6	34:BA:345:C:OP2	2.42	0.49
35:BB:21:ARG:HA	35:BB:39:ILE:HA	1.95	0.49
35:BB:54:THR:HG22	35:BB:58:ILE:HD11	1.95	0.49
36:BC:148:GLY:HA3	36:BC:172:ARG:O	2.13	0.49
37:BD:13:ARG:HB2	37:BD:40:PRO:HD3	1.94	0.49
42:BI:112:LYS:HE2	42:BI:117:HIS:O	2.13	0.49
44:BK:29:ILE:HG13	44:BK:44:SER:HB3	1.93	0.49
53:BT:57:ARG:HH22	53:BT:100:ILE:HD11	1.78	0.49
1:CA:26:G:H1'	1:CA:514:A:N6	2.28	0.49
1:CA:649:G:C4'	32:C8:46:ARG:HH12	2.25	0.49
1:CA:1225:G:O3'	19:CV:84:LYS:HE2	2.13	0.49
1:CA:2293:C:H2'	1:CA:2294:C:H6	1.78	0.49
1:CA:2538:C:H2'	1:CA:2539:C:H6	1.77	0.49
1:CA:2722:G:H5'	15:CR:4:LEU:HD12	1.93	0.49
6:CF:184:TYR:CE1	13:CP:3:LEU:HD21	2.46	0.49
15:CR:55:ALA:HB2	15:CR:79:LEU:HD13	1.95	0.49
34:DA:137:C:O2'	49:DP:61:SER:O	2.30	0.49
34:DA:714:G:H2'	34:DA:715:A:C8	2.48	0.49
35:DB:67:THR:HG22	35:DB:90:MET:HG2	1.94	0.49
45:DL:45:PRO:HG3	45:DL:51:ALA:HB3	1.95	0.49
57:DZ:181:LEU:HD23	57:DZ:182:ARG:HG3	1.95	0.49
57:DZ:639:ASN:N	57:DZ:640:ALA:HB3	2.27	0.49
1:AA:611:U:O4	1:AA:717:A:H1'	2.13	0.49
1:AA:1700:G:H3'	15:AR:2:ARG:CD	2.43	0.49
1:AA:2247:G:H2'	1:AA:2248:C:C6	2.48	0.49
1:AA:2874:G:H2'	1:AA:2875:U:O4'	2.13	0.49
3:AC:55:SER:C	3:AC:57:GLN:N	2.71	0.49
12:AO:14:THR:HG21	12:AO:86:ILE:HB	1.95	0.49
33:A9:15:LYS:HE2	33:A9:17:ILE:HD11	1.94	0.49
34:BA:691:G:H2'	34:BA:692:U:C6	2.48	0.49
56:BX:75:C:H2'	56:BX:76:A:C2	2.48	0.49
57:BZ:20:HIS:CD2	57:BZ:115:GLU:OE1	2.66	0.49
57:BZ:356:LEU:N	57:BZ:376:ALA:O	2.40	0.49
1:CA:143:G:H2'	1:CA:143(A):C:C6	2.48	0.49
1:CA:621:A:H5'	13:CP:108:LYS:NZ	2.28	0.49
1:CA:1514:U:H2'	1:CA:1515:G:C8	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:2121:G:O2'	3:CC:168:LYS:CD	2.61	0.49
1:CA:2123:G:N2	3:CC:45:HIS:HE1	2.10	0.49
15:CR:1:MET:HE3	15:CR:3:HIS:HE1	1.78	0.49
34:DA:586:C:H42	34:DA:755:G:H1	1.60	0.49
34:DA:692:U:O2'	34:DA:694:A:N7	2.34	0.49
36:DC:44:GLU:HG3	36:DC:52:LEU:HD11	1.94	0.49
43:DJ:42:THR:HG21	43:DJ:66:ARG:HB3	1.94	0.49
46:DM:60:VAL:HG23	46:DM:64:TRP:CE3	2.48	0.49
56:DX:67:C:C2'	56:DX:68:C:H5'	2.42	0.49
57:DZ:-52:VAL:C	57:DZ:-50:GLN:H	2.20	0.49
57:DZ:184:LYS:HG2	57:DZ:185:ALA:H	1.78	0.49
1:AA:116:A:C8	1:AA:117:A:C8	3.01	0.48
1:AA:185:A:O5'	13:AP:46:LYS:NZ	2.45	0.48
1:AA:828:A:H2	1:AA:1807:G:N3	2.11	0.48
1:AA:830:A:O2'	1:AA:832:G:OP1	2.26	0.48
1:AA:1900:G:H2'	1:AA:1901:C:C6	2.48	0.48
1:AA:2653:G:H5"	1:AA:2653:G:H8	1.78	0.48
12:AO:64:ARG:HG2	12:AO:79:PHE:CG	2.48	0.48
15:AR:10:LEU:O	15:AR:12:ARG:HG3	2.13	0.48
15:AR:16:HIS:HD2	15:AR:16:HIS:O	1.96	0.48
34:BA:110:C:H2'	34:BA:111:G:O4'	2.13	0.48
34:BA:565:U:H3'	34:BA:566:G:H2'	1.95	0.48
35:BB:17:PHE:HB2	35:BB:44:LEU:HD21	1.94	0.48
56:BX:37:A:H4'	57:BZ:501:THR:HA	1.95	0.48
1:CA:1152:C:H2'	1:CA:1153:C:H6	1.78	0.48
1:CA:2783:G:H2'	1:CA:2784:C:C6	2.48	0.48
3:CC:42:VAL:HA	3:CC:216:THR:O	2.13	0.48
6:CF:132:VAL:O	6:CF:134:GLY:N	2.45	0.48
14:CQ:104:PHE:O	14:CQ:105:GLU:HG3	2.12	0.48
22:CY:77:PRO:HD3	22:CY:106:LEU:HD23	1.95	0.48
25:C1:85:LEU:HD23	25:C1:89:GLU:HB3	1.95	0.48
34:DA:90:U:H2'	34:DA:91:C:C6	2.48	0.48
34:DA:97:G:O2'	34:DA:98:G:OP2	2.26	0.48
34:DA:259:G:H2'	34:DA:260:G:C8	2.48	0.48
34:DA:683:G:C6	34:DA:684:A:C6	3.01	0.48
1:AA:1112:U:N3	1:AA:1114:G:OP2	2.45	0.48
1:AA:2417:G:O2'	1:AA:2418:U:OP1	2.28	0.48
1:AA:2564:U:H2'	1:AA:2566:U:OP2	2.13	0.48
1:AA:2800:C:H1'	5:AE:62:PRO:HB3	1.93	0.48
4:AD:67:PHE:CD1	4:AD:153:ALA:HB3	2.48	0.48
4:AD:133:LEU:N	4:AD:189:CYS:O	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:AF:181:LEU:HG	6:AF:186:ILE:HD11	1.95	0.48
17:AT:16:ARG:NH1	17:AT:18:ASP:OD1	2.47	0.48
17:AT:35:LYS:HB2	17:AT:40:THR:HG22	1.95	0.48
34:BA:142:G:H2'	34:BA:143:A:H8	1.78	0.48
34:BA:222:U:H2'	34:BA:223:U:H6	1.77	0.48
34:BA:390:C:H2'	34:BA:391:G:C8	2.48	0.48
34:BA:938:A:C6	34:BA:939:G:N7	2.81	0.48
34:BA:974:A:OP2	47:BN:41:ARG:NH1	2.46	0.48
34:BA:1005:A:H1'	34:BA:1036:G:H22	1.78	0.48
57:BZ:637:ARG:C	57:BZ:639:ASN:N	2.70	0.48
1:CA:86:C:H4'	1:CA:104:U:H1'	1.95	0.48
1:CA:308:G:C8	1:CA:501:A:O4'	2.67	0.48
1:CA:310:A:O2'	1:CA:312:G:N7	2.39	0.48
1:CA:819:A:C4	1:CA:1189:A:C2	3.01	0.48
1:CA:1059:G:C4	10:CL:126:MET:HE2	2.49	0.48
1:CA:1097:U:O2	10:CL:22:PRO:HG3	2.13	0.48
1:CA:1865:G:C2	1:CA:1878:G:C6	3.01	0.48
1:CA:2788:C:O2'	1:CA:2809:A:N3	2.44	0.48
1:CA:2855:C:H2'	1:CA:2856:C:C6	2.48	0.48
3:CC:184:GLU:O	3:CC:188:ASP:OD2	2.31	0.48
5:CE:126:PRO:HB2	5:CE:131:ALA:HB2	1.94	0.48
5:CE:168:MET:O	5:CE:170:LEU:HD12	2.12	0.48
11:CN:102:ALA:O	11:CN:106:MET:HG3	2.13	0.48
28:C4:36:CYS:SG	28:C4:37:SER:N	2.86	0.48
34:DA:1072:G:H21	35:DB:107:THR:HG21	1.77	0.48
34:DA:1304:G:OP2	63:DA:1810:HOH:O	2.20	0.48
37:DD:98:GLU:OE1	37:DD:103:ASN:ND2	2.46	0.48
57:DZ:-34:ARG:C	57:DZ:-32:LEU:H	2.21	0.48
1:AA:238:C:O2'	13:AP:64:LYS:HE3	2.13	0.48
1:AA:485:U:OP2	31:A7:39:ARG:NH1	2.47	0.48
1:AA:543:G:H2'	1:AA:544:U:C6	2.48	0.48
1:AA:938:G:C6	1:AA:939:C:C4	3.02	0.48
1:AA:1739:U:H2'	1:AA:1741:C:C5	2.48	0.48
1:AA:1952:G:O2'	1:AA:1990:G:O6	2.29	0.48
1:AA:2183:C:O2'	1:AA:2195:A:H4'	2.12	0.48
1:AA:2651:A:H2'	1:AA:2652:G:O4'	2.13	0.48
3:AC:24:ASP:C	3:AC:24:ASP:OD1	2.55	0.48
4:AD:147:LEU:HD22	4:AD:155:LEU:HD11	1.96	0.48
20:AW:1:MET:HE3	20:AW:2:GLU:H	1.77	0.48
34:BA:263:A:OP1	53:BT:79:ARG:NH1	2.46	0.48
34:BA:292:G:N7	34:BA:293:G:H1'	2.29	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:BA:794:A:OP2	63:BA:3308:HOH:O	2.19	0.48
34:BA:938:A:C6	34:BA:939:G:C5	3.01	0.48
34:BA:1061:G:OP1	43:BJ:59:SER:OG	2.31	0.48
34:BA:1392:G:H21	34:BA:1502:A:H8	1.61	0.48
34:BA:1394:A:C6	34:BA:1501:C:H4'	2.48	0.48
39:BF:97:PHE:CD1	51:BR:31:LEU:HD21	2.48	0.48
57:BZ:160:ARG:HE	57:BZ:254:LYS:CA	2.25	0.48
1:CA:328:U:H4'	22:CY:68:HIS:CE1	2.48	0.48
1:CA:848:G:N9	1:CA:933:A:H8	2.11	0.48
1:CA:914:C:H2'	1:CA:915:C:O5'	2.14	0.48
1:CA:1400:G:H2'	1:CA:1401:G:H8	1.78	0.48
1:CA:1837:C:OP1	34:DA:784:C:H4'	2.13	0.48
1:CA:2646:C:H2'	1:CA:2647:U:O4'	2.13	0.48
2:CB:66:A:N6	2:CB:109:C:H5"	2.18	0.48
4:CD:134:ARG:HD2	4:CD:135:PHE:CZ	2.48	0.48
21:CX:26:TYR:HB3	21:CX:92:LEU:HD12	1.94	0.48
21:CX:60:ARG:HH22	31:C7:47:ARG:NH2	2.04	0.48
28:C4:15:ILE:HD13	28:C4:21:VAL:HG13	1.94	0.48
33:C9:19:ARG:HB3	33:C9:24:TYR:CE1	2.48	0.48
34:DA:17:U:H2'	34:DA:18:C:C6	2.48	0.48
39:DF:70:ASP:OD1	39:DF:70:ASP:N	2.46	0.48
41:DH:51:VAL:HB	41:DH:52:ASP:H	1.41	0.48
43:DJ:13:HIS:HB3	43:DJ:68:HIS:HE1	1.78	0.48
1:AA:311:C:H2'	1:AA:312:C:H6	1.77	0.48
1:AA:558:G:H5'	18:AU:24:TYR:CE1	2.48	0.48
1:AA:1249:A:H2	1:AA:1287:A:N6	2.02	0.48
22:AY:102:CYS:SG	22:AY:104:GLY:N	2.81	0.48
23:AZ:23:LYS:HD2	23:AZ:40:ASP:HA	1.95	0.48
34:BA:676:A:H1'	44:BK:115:PRO:HB3	1.94	0.48
34:BA:932:C:C2	34:BA:1386:G:N2	2.82	0.48
39:BF:17:SER:O	39:BF:20:ALA:HB3	2.13	0.48
41:BH:73:ASP:OD1	41:BH:75:ARG:HD3	2.13	0.48
50:BQ:31:LEU:HD23	50:BQ:32:TYR:CZ	2.49	0.48
1:CA:118:A:H3'	1:CA:119:A:H5"	1.96	0.48
1:CA:981:A:H3'	1:CA:982:C:C6	2.48	0.48
1:CA:1101:U:H2'	1:CA:1102:C:C6	2.48	0.48
1:CA:2394:C:P	32:C8:30:ARG:HH11	2.36	0.48
1:CA:2531:A:N3	1:CA:2658:C:O2'	2.42	0.48
1:CA:2689:U:OP2	1:CA:2719:G:N2	2.46	0.48
1:CA:2839:G:H5'	15:CR:46:GLY:HA2	1.94	0.48
4:CD:5:LYS:HG2	4:CD:17:THR:HG22	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:CD:73:VAL:HG13	4:CD:120:GLY:HA3	1.94	0.48
26:C2:1:MET:N	26:C2:52:ASP:OD1	2.42	0.48
28:C4:53:GLU:O	28:C4:55:ARG:N	2.46	0.48
34:DA:109:A:C6	34:DA:326:G:C6	3.01	0.48
34:DA:255:G:H2'	34:DA:256:U:H6	1.78	0.48
34:DA:426:G:OP1	37:DD:36:ARG:NH1	2.39	0.48
34:DA:502:G:P	45:DL:116:SER:HA	2.54	0.48
34:DA:719:C:N4	51:DR:71:LYS:HE2	2.29	0.48
34:DA:1053:G:O5'	34:DA:1054:C:H5'	2.14	0.48
40:DG:42:ILE:HG22	40:DG:120:ILE:HD12	1.94	0.48
46:DM:29:ARG:HD3	46:DM:64:TRP:CD2	2.49	0.48
57:DZ:184:LYS:HB2	57:DZ:184:LYS:HZ2	1.77	0.48
57:DZ:495:GLY:HA3	57:DZ:589:ALA:HB2	1.95	0.48
57:DZ:638:GLY:C	57:DZ:640:ALA:HB3	2.38	0.48
1:AA:189:U:O2	1:AA:413:G:N2	2.46	0.48
1:AA:1065:U:O2'	1:AA:1067:A:C2	2.65	0.48
1:AA:1110:C:H4'	10:AL:89:HIS:HA	1.94	0.48
1:AA:2131:U:H5'	1:AA:2171:G:H21	1.77	0.48
4:AD:230:ASP:O	4:AD:231:HIS:HB2	2.12	0.48
4:AD:242:ARG:N	4:AD:242:ARG:HD3	2.28	0.48
7:AG:103:LEU:HD23	7:AG:106:LEU:HD23	1.96	0.48
9:AK:25:PHE:C	9:AK:85:ASP:H	2.20	0.48
10:AL:125:ARG:HA	10:AL:128:ALA:HB3	1.96	0.48
11:AN:22:THR:O	11:AN:23:LEU:C	2.55	0.48
13:AP:143:GLY:O	13:AP:145:PRO:HD3	2.12	0.48
34:BA:302:G:C6	34:BA:303:A:C5	3.01	0.48
34:BA:392:G:H2'	34:BA:393:A:H8	1.77	0.48
34:BA:1226:C:H4'	52:BS:80:TYR:OH	2.13	0.48
41:BH:17:THR:HG22	41:BH:63:LEU:HG	1.95	0.48
45:BL:5:PRO:HB2	45:BL:10:LEU:HD21	1.94	0.48
57:BZ:12:LEU:HG	57:BZ:13:ARG:N	2.28	0.48
1:CA:1607:C:N4	1:CA:1622:G:OP2	2.40	0.48
7:CG:112:PRO:HG3	28:C4:43:TYR:CE2	2.49	0.48
18:CU:49:HIS:HA	18:CU:52:ARG:HB3	1.95	0.48
21:CX:72:LYS:HG3	21:CX:73:ARG:O	2.12	0.48
34:DA:868:C:H2'	34:DA:869:G:O4'	2.12	0.48
34:DA:1118:C:H1'	34:DA:1179:A:C4	2.48	0.48
35:DB:69:LEU:HD12	35:DB:70:PHE:H	1.79	0.48
38:DE:11:ILE:HD11	38:DE:108:ALA:HB3	1.94	0.48
1:AA:1067:A:H8	1:AA:1068:G:H5"	1.78	0.48
1:AA:1501:U:OP1	15:AR:77:ARG:NH1	2.44	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1857:G:H4'	4:AD:242:ARG:CZ	2.43	0.48
1:AA:2299:A:C4	1:AA:2301:G:C8	3.01	0.48
1:AA:2368:C:OP1	24:A0:24:LYS:HE3	2.13	0.48
4:AD:218:ARG:HB3	4:AD:219:PRO:HD2	1.94	0.48
5:AE:60:ASN:O	5:AE:64:LYS:HG3	2.14	0.48
7:AG:3:LEU:HD12	7:AG:5:VAL:HG12	1.95	0.48
9:AK:76:GLY:HA3	9:AK:115:GLN:CB	2.44	0.48
11:AN:12:ARG:HE	11:AN:14:VAL:CG2	2.26	0.48
15:AR:13:HIS:CE1	15:AR:16:HIS:HB2	2.49	0.48
25:A1:95:LEU:HD12	25:A1:98:LEU:HD11	1.95	0.48
28:A4:10:VAL:CG2	28:A4:29:PRO:HG3	2.43	0.48
34:BA:46:G:H1'	34:BA:396:G:N2	2.29	0.48
34:BA:78:G:N2	34:BA:92:C:H42	1.98	0.48
34:BA:667:G:O2'	48:BO:49:ASP:OD1	2.29	0.48
34:BA:1388:C:H2'	34:BA:1389:C:C6	2.49	0.48
34:BA:1437:C:H2'	34:BA:1438:G:C8	2.48	0.48
36:BC:112:SER:HB3	36:BC:115:LEU:HD22	1.96	0.48
37:BD:30:LYS:HA	37:BD:35:ARG:NH1	2.28	0.48
40:BG:143:ARG:O	40:BG:146:GLU:N	2.46	0.48
57:BZ:183:MET:SD	57:BZ:213:HIS:CD2	3.06	0.48
1:CA:1061:U:H4'	1:CA:1070:A:H1'	1.96	0.48
1:CA:1192:G:OP2	63:CA:3753:HOH:O	2.20	0.48
1:CA:1386:C:H2'	1:CA:1387:C:C6	2.49	0.48
1:CA:1448:G:H5"	1:CA:1542:A:OP2	2.13	0.48
1:CA:2176:A:HO2'	3:CC:45:HIS:CG	2.25	0.48
1:CA:2218:U:O2	25:C1:52:ARG:NE	2.45	0.48
1:CA:2649:U:H2'	1:CA:2650:U:C6	2.49	0.48
3:CC:17:PRO:HG2	3:CC:18:ASN:H	1.79	0.48
5:CE:67:PHE:CE2	5:CE:74:PRO:HA	2.49	0.48
12:CO:72:PRO:C	12:CO:74:GLY:H	2.22	0.48
24:C0:48:GLY:HA3	24:C0:80:HIS:CE1	2.48	0.48
27:C3:46:ASN:O	27:C3:50:VAL:HG22	2.13	0.48
34:DA:1279:A:O2'	34:DA:1281:U:OP2	2.17	0.48
41:DH:112:LEU:HB3	41:DH:133:LEU:HA	1.96	0.48
46:DM:40:ASN:O	46:DM:43:THR:OG1	2.26	0.48
48:DO:65:ARG:O	48:DO:68:ARG:HB3	2.14	0.48
56:DX:75:C:H2'	56:DX:76:A:C2	2.48	0.48
57:DZ:-9:LEU:O	57:DZ:-6:ARG:N	2.46	0.48
1:AA:139:A:C8	1:AA:1454:C:O2'	2.65	0.48
7:AG:56:ALA:O	7:AG:60:LEU:HD22	2.14	0.48
7:AG:105:LYS:HD3	28:A4:25:TYR:O	2.12	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:AU:102:GLU:HA	18:AU:104:GLN:HE22	1.79	0.48
27:A3:3:ARG:HD3	27:A3:60:GLU:CD	2.38	0.48
34:BA:189(F):U:C4	50:BQ:72:ARG:NH1	2.82	0.48
34:BA:410:G:C2	34:BA:429:U:C2	3.01	0.48
34:BA:763:G:H2'	34:BA:764:C:H6	1.79	0.48
34:BA:1324:A:H2'	34:BA:1325:C:C6	2.48	0.48
46:BM:74:VAL:O	46:BM:78:ILE:HG13	2.14	0.48
1:CA:154(A):C:N4	1:CA:171:G:H1	2.11	0.48
1:CA:652(E):G:H8	1:CA:652(E):G:O5'	1.97	0.48
1:CA:1266:G:O4'	20:CW:15:ARG:NH2	2.46	0.48
1:CA:1686:C:H2'	1:CA:1687:G:O4'	2.13	0.48
1:CA:1839:G:C8	1:CA:1927:A:H1'	2.48	0.48
1:CA:2125:G:O5'	3:CC:71:LYS:NZ	2.44	0.48
1:CA:2315:G:H2'	1:CA:2316:C:C6	2.49	0.48
4:CD:242:ARG:HD3	4:CD:242:ARG:N	2.28	0.48
11:CN:24:GLY:O	11:CN:28:THR:HG23	2.13	0.48
34:DA:586:C:N3	34:DA:755:G:N2	2.57	0.48
34:DA:620:C:C2	37:DD:135:LEU:HG	2.49	0.48
34:DA:814:A:H2'	34:DA:816:A:C5'	2.42	0.48
34:DA:881:G:P	45:DL:12:ARG:HH22	2.36	0.48
34:DA:883:C:C2'	34:DA:884:U:H5'	2.44	0.48
39:DF:80:ARG:NH1	39:DF:88:VAL:O	2.46	0.48
57:DZ:138:LYS:HG2	62:DZ:704:GDP:C6	2.49	0.48
1:AA:306:A:C4	1:AA:383:A:C2	3.02	0.48
1:AA:1162:C:H2'	1:AA:1163:G:C8	2.49	0.48
1:AA:1314:A:C2	1:AA:2035:A:C4	3.02	0.48
1:AA:1320:A:N3	1:AA:1343:C:H1'	2.28	0.48
1:AA:1540:A:H2'	1:AA:1541:A:C8	2.49	0.48
1:AA:2050:U:O4	63:AA:3935:HOH:O	2.18	0.48
1:AA:2612:A:H2'	1:AA:2613:C:C6	2.49	0.48
1:AA:2647:C:H4'	5:AE:48:GLN:HE21	1.79	0.48
3:AC:42:VAL:HA	3:AC:216:THR:O	2.13	0.48
15:AR:83:ILE:O	15:AR:86:ARG:HB2	2.13	0.48
20:AW:2:GLU:OE2	20:AW:72:LYS:NZ	2.33	0.48
30:A6:35:GLU:OE2	30:A6:50:ARG:NH1	2.47	0.48
34:BA:9:G:H2'	34:BA:10:A:H8	1.78	0.48
34:BA:487:A:H2'	34:BA:488:C:O4'	2.13	0.48
34:BA:955:U:H2'	34:BA:956:U:H6	1.79	0.48
34:BA:1516:G:H2'	34:BA:1518:A:OP2	2.13	0.48
39:BF:89:MET:CE	51:BR:76:LEU:HD22	2.42	0.48
42:BI:6:GLY:O	42:BI:17:VAL:HG12	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:BZ:445:GLU:O	57:BZ:447:GLY:N	2.42	0.48
1:CA:300:A:H1'	1:CA:319:C:O4'	2.14	0.48
1:CA:597:U:H2'	1:CA:598:G:C8	2.49	0.48
8:CH:7:LEU:HB3	8:CH:69:ARG:HH11	1.79	0.48
16:CS:74:ALA:O	16:CS:78:LEU:HG	2.14	0.48
20:CW:70:TYR:O	20:CW:107:LEU:HA	2.13	0.48
33:C9:17:ILE:HG21	33:C9:19:ARG:HH21	1.79	0.48
34:DA:171:A:H2'	34:DA:172:A:C8	2.48	0.48
34:DA:255:G:H1'	50:DQ:16:GLN:NE2	2.28	0.48
34:DA:920:U:N3	34:DA:921:U:C4	2.81	0.48
34:DA:1222:G:C2	34:DA:1223:C:C2	3.02	0.48
35:DB:218:ALA:O	35:DB:222:ILE:HG23	2.13	0.48
42:DI:26:VAL:HG22	42:DI:61:ALA:HB3	1.96	0.48
42:DI:127:LYS:O	42:DI:128:ARG:HB3	2.13	0.48
43:DJ:44:VAL:HG13	43:DJ:66:ARG:HG2	1.95	0.48
50:DQ:63:ARG:HG2	50:DQ:64:PRO:HD2	1.96	0.48
50:DQ:76:LEU:HD12	50:DQ:78:GLU:H	1.77	0.48
51:DR:53:ARG:HD2	51:DR:63:GLN:HB2	1.95	0.48
57:DZ:655:TYR:C	57:DZ:657:THR:H	2.22	0.48
1:AA:412:C:O2	13:AP:71:VAL:HG21	2.14	0.48
1:AA:511:C:C2	1:AA:521:G:N2	2.82	0.48
1:AA:2150:C:H4'	3:AC:219:MET:CE	2.43	0.48
1:AA:2569:G:H2'	1:AA:2570:C:C6	2.48	0.48
1:AA:2833:A:OP1	5:AE:159:HIS:NE2	2.40	0.48
2:AB:77:U:OP1	23:AZ:19:ARG:NH2	2.47	0.48
15:AR:77:ARG:O	15:AR:81:ASP:N	2.40	0.48
20:AW:46:PHE:O	20:AW:50:VAL:HG23	2.14	0.48
20:AW:52:GLU:O	20:AW:55:ALA:HB3	2.13	0.48
28:A4:36:CYS:SG	28:A4:37:SER:N	2.87	0.48
34:BA:234:C:H2'	34:BA:235:C:C6	2.47	0.48
34:BA:394:G:H2'	34:BA:395:C:C6	2.49	0.48
34:BA:976:G:H5'	34:BA:1358:U:O2'	2.14	0.48
34:BA:994:A:N1	34:BA:1047:G:H4'	2.29	0.48
34:BA:1402:C:O2	34:BA:1500:A:N1	2.47	0.48
39:BF:60:PHE:CE2	51:BR:78:LEU:HD21	2.49	0.48
50:BQ:75:ARG:NH1	50:BQ:77:VAL:HG23	2.28	0.48
53:BT:54:LYS:HA	53:BT:57:ARG:CZ	2.43	0.48
57:BZ:99:ARG:NH1	57:BZ:312:LEU:HD11	2.29	0.48
1:CA:1859:A:C3'	3:CC:206:LYS:HE3	2.27	0.48
1:CA:2382:G:H21	32:C8:42:ARG:NH1	2.12	0.48
1:CA:2639:A:OP2	63:CA:3752:HOH:O	2.20	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:CB:14:U:H1'	2:CB:108:U:O2'	2.13	0.48
6:CF:21:ALA:HB3	6:CF:22:ALA:HA	1.95	0.48
13:CP:64:LYS:HE2	32:C8:12:LYS:HG2	1.96	0.48
14:CQ:63:LYS:HD3	23:CZ:175:VAL:HG21	1.96	0.48
15:CR:44:LEU:HD22	15:CR:48:VAL:HG23	1.96	0.48
23:CZ:28:MET:HA	23:CZ:88:PHE:O	2.14	0.48
23:CZ:78:LYS:HB3	23:CZ:78:LYS:NZ	2.29	0.48
34:DA:834:C:C4	34:DA:835:U:C5	3.02	0.48
34:DA:882:C:OP2	45:DL:13:LYS:NZ	2.46	0.48
34:DA:919:A:O5'	34:DA:919:A:H8	1.96	0.48
34:DA:1002:G:N3	34:DA:1003:G:H8	2.12	0.48
35:DB:16:HIS:HD2	35:DB:204:ASN:H	1.62	0.48
37:DD:129:ASN:HD22	37:DD:129:ASN:N	2.12	0.48
38:DE:122:GLU:O	38:DE:123:LEU:HD23	2.14	0.48
43:DJ:50:ILE:HB	47:DN:41:ARG:NH2	2.29	0.48
56:DX:37:A:H4'	57:DZ:501:THR:HA	1.96	0.48
1:AA:664:U:H2'	1:AA:665:C:C6	2.48	0.48
1:AA:721:G:OP2	63:AA:3939:HOH:O	2.20	0.48
1:AA:1815:A:H4'	1:AA:1816:A:O5'	2.14	0.48
1:AA:2816:G:C2	1:AA:2817:G:C5	3.02	0.48
5:AE:33:VAL:HG13	5:AE:89:ASP:C	2.39	0.48
6:AF:158:THR:OG1	6:AF:195:ASP:OD2	2.31	0.48
12:AO:18:LYS:HB2	12:AO:45:GLU:HB3	1.96	0.48
15:AR:96:ARG:HD2	15:AR:115:GLU:OE1	2.14	0.48
18:AU:74:LEU:HD12	18:AU:74:LEU:N	2.28	0.48
34:BA:13:U:OP1	63:BA:3309:HOH:O	2.20	0.48
34:BA:44:G:C6	34:BA:45:U:C2	3.02	0.48
34:BA:109:A:H2'	34:BA:326:G:N2	2.29	0.48
34:BA:430:A:OP2	37:BD:8:VAL:HG12	2.13	0.48
34:BA:622:A:C8	34:BA:623:C:C6	3.02	0.48
36:BC:22:TRP:HZ3	36:BC:24:ALA:HB2	1.78	0.48
44:BK:93:GLN:HA	44:BK:93:GLN:HE21	1.78	0.48
45:BL:24:VAL:HB	45:BL:27:LEU:HD22	1.95	0.48
57:BZ:24:GLY:HA2	62:BZ:801:GDP:O2A	2.12	0.48
57:BZ:210:ARG:HH11	57:BZ:210:ARG:CG	2.26	0.48
57:BZ:249:GLY:HA2	57:BZ:252:ASP:HB2	1.96	0.48
1:CA:1259:G:O2'	1:CA:1260:G:H5'	2.14	0.48
1:CA:1356:G:H2'	1:CA:1357:U:O4'	2.13	0.48
1:CA:1607:C:H4'	1:CA:1608:A:O5'	2.14	0.48
1:CA:2113:U:H3	1:CA:2169:A:H62	1.59	0.48
1:CA:2176:A:O2'	3:CC:45:HIS:CD2	2.64	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:2183:C:H2'	1:CA:2184:G:H8	1.79	0.48
1:CA:2495:G:O2'	1:CA:2496:C:H5'	2.13	0.48
6:CF:37:VAL:HG21	13:CP:6:LEU:HD13	1.96	0.48
21:CX:57:LEU:CD1	21:CX:78:LYS:HB3	2.44	0.48
23:CZ:160:GLY:HA2	23:CZ:161:VAL:HG12	1.95	0.48
34:DA:176:C:H2'	34:DA:177:C:C6	2.49	0.48
34:DA:179:A:H2'	34:DA:180:U:H6	1.79	0.48
34:DA:530:G:O2'	34:DA:531:U:OP1	2.27	0.48
34:DA:1151:A:H5'	43:DJ:41:PRO:HA	1.96	0.48
35:DB:166:ASP:OD2	35:DB:169:LYS:N	2.43	0.48
38:DE:71:LEU:O	38:DE:72:GLN:HG2	2.14	0.48
47:DN:23:ARG:HD2	47:DN:28:GLY:O	2.14	0.48
53:DT:50:GLU:HG3	53:DT:100:ILE:HD13	1.96	0.48
57:DZ:190:ASN:ND2	57:DZ:192:LEU:HB2	2.29	0.48
1:AA:1112:U:H2'	1:AA:1113:A:C8	2.49	0.47
1:AA:1451:U:H2'	1:AA:1452:U:C6	2.49	0.47
1:AA:1851:U:C4	4:AD:160:GLY:HA3	2.49	0.47
1:AA:2801:C:O2'	1:AA:2819:A:N3	2.39	0.47
1:AA:2840:G:OP1	5:AE:76:ARG:NH2	2.47	0.47
2:AB:73:A:N1	23:AZ:34:ASN:ND2	2.61	0.47
3:AC:55:SER:C	3:AC:57:GLN:H	2.19	0.47
5:AE:34:VAL:HG23	5:AE:34:VAL:O	2.14	0.47
6:AF:64:ILE:HD12	6:AF:65:TRP:CE3	2.49	0.47
7:AG:173:LEU:HA	7:AG:176:LEU:HD12	1.96	0.47
7:AG:174:GLU:O	7:AG:177:GLY:N	2.42	0.47
23:AZ:128:VAL:HG22	23:AZ:129:SER:O	2.13	0.47
28:A4:16:CYS:SG	28:A4:17:GLY:N	2.86	0.47
34:BA:540:G:H2'	34:BA:541:G:O4'	2.14	0.47
34:BA:652:U:O4	34:BA:752:G:O2'	2.21	0.47
34:BA:1095:U:P	34:BA:1108:G:H1	2.36	0.47
34:BA:1413:A:C6	34:BA:1414:U:C4	3.02	0.47
34:BA:1469:G:H2'	34:BA:1470:G:H8	1.79	0.47
49:BP:3:LYS:O	49:BP:21:VAL:HA	2.14	0.47
52:BS:39:THR:HA	52:BS:70:LYS:HD3	1.96	0.47
57:BZ:655:TYR:O	57:BZ:657:THR:N	2.47	0.47
1:CA:528:A:C2	1:CA:2042:A:H2'	2.48	0.47
1:CA:820:A:H1'	1:CA:943:U:H1'	1.95	0.47
1:CA:1024:G:C6	1:CA:1025:G:C6	3.02	0.47
1:CA:2177:C:O2'	3:CC:47:LYS:HD3	2.14	0.47
1:CA:2750:A:H8	1:CA:2750:A:OP1	1.96	0.47
3:CC:68:GLY:N	3:CC:189:ASN:ND2	2.62	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:CV:32:THR:HA	19:CV:59:ALA:O	2.14	0.47
34:DA:266:G:O2'	34:DA:267:C:OP2	2.21	0.47
36:DC:47:LEU:HG	36:DC:68:VAL:HG11	1.96	0.47
36:DC:131:ARG:HH12	36:DC:135:LYS:HZ3	1.61	0.47
37:DD:135:LEU:O	37:DD:137:SER:N	2.41	0.47
57:DZ:154:GLN:O	57:DZ:158:GLY:HA2	2.14	0.47
1:AA:152:G:H1	1:AA:163:C:H42	1.61	0.47
1:AA:1229:G:N7	63:AA:3995:HOH:O	2.35	0.47
1:AA:1454:C:C2	1:AA:1641:G:N2	2.82	0.47
1:AA:2141:A:O2'	1:AA:2142:G:H5'	2.14	0.47
1:AA:2172:U:H2'	1:AA:2173:G:C8	2.49	0.47
1:AA:2389:A:H2'	1:AA:2390:A:C8	2.49	0.47
1:AA:2413:U:OP1	30:A6:18:ARG:NH2	2.48	0.47
1:AA:2416:C:O3'	13:AP:77:ARG:NH2	2.46	0.47
1:AA:2886:G:H4'	17:AT:2:ASN:HD22	1.79	0.47
2:AB:48:A:H4'	16:AS:95:HIS:HD2	1.80	0.47
3:AC:184:GLU:O	3:AC:188:ASP:OD2	2.31	0.47
21:AX:53:LYS:HB3	21:AX:82:GLN:HB3	1.96	0.47
28:A4:14:ILE:HG12	28:A4:31:ILE:HB	1.96	0.47
34:BA:369:C:O2'	34:BA:370:C:H5'	2.14	0.47
34:BA:863:U:O2'	34:BA:865:A:N7	2.47	0.47
36:BC:134:ILE:HD11	36:BC:153:VAL:HB	1.95	0.47
41:BH:113:SER:H	41:BH:134:ILE:HD11	1.79	0.47
43:BJ:37:PRO:HA	43:BJ:72:VAL:HG12	1.96	0.47
45:BL:84:LEU:HB2	45:BL:105:TYR:CD2	2.49	0.47
53:BT:59:ALA:O	53:BT:63:ILE:HG13	2.14	0.47
53:BT:63:ILE:O	53:BT:66:ALA:HB3	2.14	0.47
1:CA:26:G:C6	1:CA:27:G:N1	2.82	0.47
1:CA:839:U:H2'	1:CA:840:C:C6	2.48	0.47
1:CA:1041:C:H5'	1:CA:1042:G:OP2	2.14	0.47
1:CA:1766:U:H2'	1:CA:1767:C:C6	2.48	0.47
1:CA:2243:U:H2'	1:CA:2244:U:C6	2.49	0.47
28:C4:59:PHE:HA	28:C4:60:GLN:C	2.40	0.47
34:DA:186:C:C2	34:DA:187:C:C5	3.02	0.47
34:DA:474:G:H2'	34:DA:475:G:C8	2.47	0.47
34:DA:841:U:H6	34:DA:841:U:P	2.37	0.47
34:DA:902:G:O2'	34:DA:903:G:H5'	2.14	0.47
34:DA:1263:C:H2'	34:DA:1264:C:C6	2.49	0.47
35:DB:219:VAL:O	35:DB:222:ILE:HG12	2.14	0.47
56:DX:49:G:N2	56:DX:66:C:C2	2.82	0.47
57:DZ:116:PRO:O	57:DZ:117:GLN:HB3	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:990:A:H2	63:AA:4053:HOH:O	1.97	0.47
1:AA:1389:G:N3	1:AA:1430:A:H2	2.12	0.47
1:AA:2674:A:H5"	1:AA:2675:G:OP2	2.14	0.47
5:AE:33:VAL:HG13	5:AE:89:ASP:O	2.15	0.47
6:AF:117:ARG:NH2	6:AF:189:THR:O	2.46	0.47
7:AG:22:ARG:HH12	7:AG:175:LEU:HD11	1.79	0.47
12:AO:79:PHE:CE2	17:AT:72:VAL:HG13	2.50	0.47
22:AY:30:VAL:O	22:AY:32:PRO:HD3	2.13	0.47
34:BA:1241:G:H2'	34:BA:1242:C:C6	2.49	0.47
49:BP:75:ARG:HH11	49:BP:75:ARG:HG3	1.79	0.47
1:CA:271(E):U:H2'	1:CA:271(F):C:H6	1.78	0.47
1:CA:565:C:H2'	1:CA:566:U:O4'	2.13	0.47
1:CA:784:A:C6	4:CD:229:VAL:HG11	2.48	0.47
1:CA:849:A:H3'	1:CA:850:C:C6	2.49	0.47
1:CA:955:C:OP1	14:CQ:87:LYS:HE2	2.14	0.47
1:CA:981:A:OP1	63:CA:3756:HOH:O	2.20	0.47
23:CZ:14:LYS:HA	23:CZ:15:PRO:HD3	1.75	0.47
34:DA:792:A:O2'	34:DA:794:A:N7	2.40	0.47
36:DC:116:VAL:HG21	36:DC:202:ILE:HD11	1.97	0.47
50:DQ:88:TYR:O	50:DQ:91:ARG:HB3	2.13	0.47
57:DZ:-58:LEU:HD21	57:DZ:-32:LEU:HB3	1.96	0.47
1:AA:1123:A:C6	1:AA:1124:U:C2	3.03	0.47
1:AA:1699:A:OP1	15:AR:8:ARG:NH1	2.47	0.47
1:AA:1911:A:N1	1:AA:2246:G:H1'	2.28	0.47
1:AA:2211:U:H2'	1:AA:2212:G:C8	2.49	0.47
12:AO:80:ASP:OD2	17:AT:71:GLY:HA3	2.14	0.47
34:BA:666:G:H5'	34:BA:726:C:H1'	1.96	0.47
34:BA:814:A:N7	34:BA:816:A:C4	2.82	0.47
34:BA:1162:C:H2'	34:BA:1163:C:C6	2.49	0.47
34:BA:1221:G:OP1	34:BA:1320:C:N4	2.42	0.47
43:BJ:8:LEU:HB2	43:BJ:70:ARG:HB2	1.96	0.47
57:BZ:11:ARG:HD3	57:BZ:76:ASP:O	2.14	0.47
57:BZ:153:MET:C	57:BZ:155:GLU:H	2.21	0.47
1:CA:695:G:OP1	1:CA:1380:G:O2'	2.20	0.47
1:CA:2112:G:C5	1:CA:2113:U:H1'	2.49	0.47
1:CA:2849:U:H4'	1:CA:2868:A:C2	2.49	0.47
3:CC:15:VAL:O	3:CC:21:TYR:OH	2.29	0.47
3:CC:206:LYS:HB3	3:CC:206:LYS:HZ2	1.78	0.47
13:CP:62:LEU:HD11	32:C8:50:LEU:HD11	1.97	0.47
25:C1:3:LYS:HB2	25:C1:61:ARG:HH12	1.78	0.47
34:DA:509:A:H3'	34:DA:509:A:H8	1.77	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:DZ:247:ARG:NH2	57:DZ:285:ASP:OD1	2.47	0.47
57:DZ:283:PRO:HA	57:DZ:286:ILE:HD11	1.97	0.47
57:DZ:326:THR:HB	57:DZ:377:VAL:HG13	1.97	0.47
1:AA:722:A:C8	1:AA:851:A:C6	3.03	0.47
1:AA:889:G:N2	1:AA:982:U:C2	2.83	0.47
1:AA:2199:C:H1'	3:AC:173:HIS:HE1	1.80	0.47
2:AB:25:A:OP1	63:AB:3102:HOH:O	2.20	0.47
9:AK:118:THR:O	9:AK:121:ASP:N	2.46	0.47
22:AY:2:ARG:HG3	22:AY:3:VAL:O	2.15	0.47
23:AZ:100:VAL:HG11	23:AZ:137:ILE:HG13	1.96	0.47
34:BA:106:C:O2	34:BA:379:C:H4'	2.14	0.47
34:BA:1030(C):G:N7	34:BA:1031:G:N2	2.60	0.47
41:BH:2:LEU:HD13	41:BH:3:THR:H	1.80	0.47
41:BH:20:TYR:HA	41:BH:65:TYR:OH	2.15	0.47
52:BS:31:ILE:HB	52:BS:49:ILE:HG23	1.95	0.47
57:BZ:25:LYS:HB3	57:BZ:83:ASP:OD2	2.14	0.47
57:BZ:84:THR:HG22	57:BZ:97:SER:HB2	1.96	0.47
57:BZ:181:LEU:HD12	57:BZ:216:LEU:HD21	1.95	0.47
57:BZ:417:THR:HA	57:BZ:418:LYS:CB	2.45	0.47
1:CA:588:U:H2'	1:CA:589:C:C6	2.49	0.47
1:CA:2594:C:C2	1:CA:2600:A:C2	3.03	0.47
1:CA:2780:G:OP1	11:CN:118:LYS:HE2	2.15	0.47
2:CB:100:A:H3'	2:CB:101:G:H8	1.80	0.47
3:CC:6:LYS:HA	3:CC:9:ARG:NH1	2.30	0.47
6:CF:202:PHE:CZ	6:CF:206:ILE:HD13	2.49	0.47
15:CR:51:LEU:HD23	15:CR:66:VAL:HG22	1.97	0.47
15:CR:117:VAL:HG12	15:CR:118:GLU:H	1.79	0.47
23:CZ:128:VAL:HB	23:CZ:161:VAL:HG23	1.96	0.47
24:C0:34:GLY:N	24:C0:61:ALA:O	2.38	0.47
34:DA:955:U:OP1	46:DM:120:LYS:HE3	2.15	0.47
34:DA:1118:C:H1'	34:DA:1179:A:C5	2.50	0.47
34:DA:1431:C:H2'	34:DA:1432:G:O4'	2.14	0.47
49:DP:17:TYR:HE2	49:DP:41:PRO:HG3	1.79	0.47
51:DR:69:THR:HA	51:DR:72:ARG:HB2	1.95	0.47
57:DZ:153:MET:HA	57:DZ:157:LEU:HD11	1.95	0.47
57:DZ:505:GLY:HA2	57:DZ:576:ASP:CB	2.45	0.47
1:AA:693:G:H1	1:AA:697:C:H42	1.62	0.47
1:AA:719:C:C2	1:AA:856:G:N2	2.82	0.47
1:AA:1222:A:H2'	1:AA:1222:A:N3	2.28	0.47
1:AA:2652:G:C6	1:AA:2788:A:C2	3.02	0.47
3:AC:180:SER:O	3:AC:181:PHE:O	2.32	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:AD:26:LYS:HD3	4:AD:83:GLU:OE2	2.15	0.47
5:AE:60:ASN:CG	5:AE:62:PRO:HD2	2.40	0.47
5:AE:134:ILE:C	5:AE:134:ILE:HD12	2.40	0.47
10:AL:30:HIS:CG	10:AL:59:ILE:HB	2.50	0.47
11:AN:128:HIS:O	11:AN:131:GLN:NE2	2.47	0.47
31:A7:31:LEU:HD22	31:A7:42:LEU:HB3	1.95	0.47
35:BB:20:GLU:HA	35:BB:21:ARG:NH2	2.28	0.47
35:BB:132:LYS:O	35:BB:136:VAL:HG23	2.15	0.47
38:BE:84:PHE:HB3	38:BE:134:ALA:HB2	1.95	0.47
42:BI:83:ARG:HA	42:BI:86:VAL:HG22	1.95	0.47
50:BQ:67:LYS:O	50:BQ:68:ARG:HG2	2.15	0.47
1:CA:271(X):G:C2	1:CA:271(Y):U:O4	2.67	0.47
1:CA:500:G:N1	1:CA:503:A:OP2	2.43	0.47
1:CA:639:U:H2'	1:CA:640:C:C6	2.50	0.47
1:CA:1202:C:N4	1:CA:1203:G:C6	2.83	0.47
1:CA:1494:A:C6	1:CA:1495:A:C6	3.02	0.47
1:CA:1745(A):C:H5'	1:CA:1746:G:OP2	2.14	0.47
1:CA:2023:G:H5'	1:CA:2617:C:H4'	1.97	0.47
1:CA:2404:C:O3'	13:CP:77:ARG:NH2	2.48	0.47
1:CA:2758:A:N3	1:CA:2759:G:H1'	2.29	0.47
5:CE:150:VAL:HG13	5:CE:154:LYS:HG3	1.95	0.47
15:CR:38:VAL:HB	15:CR:39:PRO:HD3	1.97	0.47
16:CS:95:HIS:CG	16:CS:96:GLY:N	2.83	0.47
19:CV:66:ARG:HB3	19:CV:88:ARG:HE	1.79	0.47
21:CX:32:PRO:HA	21:CX:77:LYS:HD2	1.96	0.47
31:C7:5:TRP:CD1	31:C7:7:PRO:HD3	2.49	0.47
34:DA:160:A:H2'	34:DA:161:A:O4'	2.15	0.47
34:DA:998:G:H1	34:DA:1043:C:H42	1.62	0.47
34:DA:1107:C:C4	34:DA:1108:G:N7	2.82	0.47
40:DG:18:TYR:OH	40:DG:58:PRO:HB2	2.15	0.47
41:DH:63:LEU:HD23	41:DH:65:TYR:OH	2.14	0.47
42:DI:127:LYS:O	42:DI:127:LYS:HG3	2.14	0.47
43:DJ:38:ILE:HG12	43:DJ:71:LEU:O	2.15	0.47
56:DX:47:U:H3'	56:DX:48:C:C5'	2.44	0.47
56:DX:55:PSU:O2'	56:DX:57:A:N7	2.26	0.47
57:DZ:-11:LYS:O	57:DZ:-7:GLU:HG3	2.15	0.47
57:DZ:20:HIS:CE1	57:DZ:117:GLN:HB3	2.49	0.47
57:DZ:312:LEU:O	57:DZ:328:ILE:HA	2.14	0.47
1:AA:130:G:H2'	1:AA:131:C:H6	1.79	0.47
1:AA:999:G:H5"	14:AQ:13:GLN:HB3	1.97	0.47
1:AA:1067:A:H3'	1:AA:1067:A:H8	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1474:C:C5	1:AA:1616:A:H5"	2.50	0.47
1:AA:1634:C:H2'	1:AA:1635:C:H6	1.79	0.47
1:AA:1944:G:H2'	1:AA:1945:U:O4'	2.15	0.47
1:AA:2602:A:OP2	4:AD:238:GLY:HA2	2.15	0.47
1:AA:2772:G:O2'	1:AA:2773:C:H5'	2.15	0.47
2:AB:66:A:H61	2:AB:108:U:H2'	1.79	0.47
3:AC:6:LYS:HA	3:AC:9:ARG:NH1	2.30	0.47
3:AC:17:PRO:HG2	3:AC:18:ASN:H	1.79	0.47
3:AC:30:VAL:CG2	3:AC:31:LYS:H	2.27	0.47
3:AC:68:GLY:N	3:AC:189:ASN:ND2	2.62	0.47
5:AE:54:GLN:HE21	5:AE:76:ARG:HG2	1.78	0.47
6:AF:7:TYR:CD1	6:AF:24:LEU:HB2	2.50	0.47
7:AG:67:LYS:H	28:A4:6:HIS:CE1	2.33	0.47
12:AO:107:ARG:NE	17:AT:36:GLU:HG2	2.29	0.47
13:AP:98:GLU:O	13:AP:101:VAL:HG12	2.15	0.47
21:AX:5:TYR:CE1	26:A2:30:ARG:HD2	2.49	0.47
22:AY:37:VAL:HG21	22:AY:72:VAL:HG21	1.97	0.47
27:A3:4:LEU:O	27:A3:36:VAL:HA	2.15	0.47
32:A8:14:VAL:HG11	32:A8:58:ILE:HG21	1.95	0.47
34:BA:447:G:H2'	34:BA:485:G:N2	2.29	0.47
34:BA:724:G:C2	34:BA:725:G:C8	3.03	0.47
34:BA:973:G:H3'	34:BA:974:A:H5"	1.97	0.47
39:BF:44:GLY:HA2	39:BF:59:TYR:CZ	2.49	0.47
43:BJ:8:LEU:HD12	43:BJ:20:ALA:HB2	1.96	0.47
48:BO:7:GLU:O	48:BO:11:VAL:HG23	2.14	0.47
57:BZ:68:ALA:HB3	57:BZ:327:PHE:CG	2.50	0.47
57:BZ:145:ASP:O	57:BZ:148:LEU:HB3	2.15	0.47
57:BZ:168:ILE:HG12	57:BZ:205:TYR:CD2	2.50	0.47
57:BZ:169:GLY:HA3	57:BZ:173:THR:O	2.14	0.47
57:BZ:373:ASP:OD2	57:BZ:374:LEU:N	2.48	0.47
1:CA:144:C:H2'	1:CA:145:G:H8	1.79	0.47
1:CA:207:A:H2'	1:CA:208:C:O4'	2.15	0.47
1:CA:253:C:O2'	63:CA:3755:HOH:O	2.20	0.47
1:CA:271(S):G:C6	1:CA:271(T):C:C4	3.03	0.47
1:CA:827:U:H1'	1:CA:2246:G:O2'	2.14	0.47
1:CA:1075:C:H5'	1:CA:1076:C:OP2	2.15	0.47
1:CA:1178:C:H2'	1:CA:1179:C:C6	2.49	0.47
1:CA:1270:C:H5"	1:CA:1271:G:O5'	2.15	0.47
1:CA:1310:G:H1'	1:CA:1611:C:H5'	1.96	0.47
1:CA:1466:G:H2'	1:CA:1547:C:H41	1.80	0.47
1:CA:1479:G:H5'	1:CA:1558:A:C2	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1588:C:H2'	1:CA:1589:C:C6	2.50	0.47
1:CA:1639:U:C2'	1:CA:1640:C:H5"	2.45	0.47
1:CA:1709:U:H2'	1:CA:1710:C:C6	2.50	0.47
1:CA:1778:U:H2'	1:CA:1784:A:N6	2.30	0.47
1:CA:2049:G:OP2	63:CA:3757:HOH:O	2.20	0.47
1:CA:2749:A:O4'	8:CH:63:SER:HA	2.14	0.47
2:CB:116:G:H8	2:CB:116:G:OP2	1.98	0.47
4:CD:275:LYS:HA	4:CD:276:LYS:C	2.40	0.47
7:CG:119:GLY:HA3	7:CG:181:ARG:HB2	1.96	0.47
11:CN:1:MET:HE1	18:CU:94:ASN:ND2	2.29	0.47
12:CO:1:MET:HE2	12:CO:32:TYR:CG	2.50	0.47
12:CO:80:ASP:OD2	17:CT:64:ARG:NH2	2.47	0.47
14:CQ:37:LEU:HA	14:CQ:37:LEU:HD23	1.53	0.47
14:CQ:111:GLU:O	14:CQ:115:MET:HG2	2.15	0.47
16:CS:3:ARG:NE	16:CS:4:LEU:O	2.43	0.47
20:CW:85:VAL:HG13	20:CW:93:ALA:HB1	1.96	0.47
34:DA:7:G:H5'	34:DA:298:A:O4'	2.14	0.47
34:DA:97:G:C4	34:DA:98:G:C8	3.02	0.47
34:DA:539:A:OP1	45:DL:114:LYS:HG2	2.14	0.47
34:DA:922:G:C2	34:DA:923:A:C4	3.02	0.47
34:DA:938:A:C6	34:DA:939:G:C5	3.03	0.47
34:DA:1165:C:H2'	34:DA:1166:G:O4'	2.14	0.47
34:DA:1363(A):A:H1'	34:DA:1365:G:N7	2.29	0.47
35:DB:95:GLN:HB2	35:DB:96:ARG:H	1.46	0.47
38:DE:78:HIS:CD2	38:DE:142:LEU:HD23	2.50	0.47
39:DF:89:MET:HE2	51:DR:76:LEU:HD13	1.97	0.47
45:DL:6:THR:OG1	45:DL:9:GLN:HG3	2.15	0.47
50:DQ:62:SER:CB	50:DQ:72:ARG:HD3	2.44	0.47
57:DZ:-55:LEU:HD22	57:DZ:-48:VAL:HG21	1.96	0.47
57:DZ:230:LYS:HB3	57:DZ:235:GLU:HB3	1.97	0.47
57:DZ:527:ASN:O	57:DZ:529:ILE:N	2.48	0.47
1:AA:217:A:H2'	1:AA:219:U:O4'	2.15	0.47
1:AA:616:G:O4'	32:A8:4:MET:HE2	2.14	0.47
1:AA:986:A:H2'	1:AA:987:G:C8	2.50	0.47
1:AA:1845:G:OP1	4:AD:40:THR:OG1	2.23	0.47
1:AA:2431:U:H2'	1:AA:2432:C:C6	2.50	0.47
1:AA:2574:U:O2'	12:AO:23:ARG:HD3	2.15	0.47
7:AG:103:LEU:HD23	7:AG:103:LEU:HA	1.82	0.47
34:BA:9:G:H2'	34:BA:10:A:C8	2.49	0.47
34:BA:53:A:H8	34:BA:53:A:O5'	1.98	0.47
34:BA:299:G:H2'	34:BA:300:A:C8	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:BA:512:U:H2'	34:BA:513:C:C6	2.50	0.47
34:BA:841:U:H6	34:BA:841:U:OP2	1.97	0.47
35:BB:67:THR:HA	35:BB:90:MET:SD	2.55	0.47
41:BH:85:ARG:O	41:BH:86:ILE:HD13	2.15	0.47
57:BZ:271:LEU:HD12	57:BZ:271:LEU:H	1.79	0.47
1:CA:329:G:N7	22:CY:71:LYS:NZ	2.62	0.47
1:CA:1095:A:OP1	57:DZ:618:GLY:HA3	2.15	0.47
1:CA:1292:U:H2'	1:CA:1293:C:H6	1.79	0.47
1:CA:1575:C:H2'	1:CA:1576:U:H6	1.80	0.47
1:CA:1963:U:H2'	1:CA:1963:U:O2	2.15	0.47
3:CC:180:SER:O	3:CC:181:PHE:O	2.33	0.47
5:CE:33:VAL:HG13	5:CE:89:ASP:HA	1.96	0.47
6:CF:36:VAL:HG11	6:CF:183:VAL:HG13	1.97	0.47
16:CS:14:VAL:HG23	16:CS:15:ARG:N	2.30	0.47
31:C7:13:ALA:O	31:C7:17:GLY:HA3	2.15	0.47
34:DA:110:C:H2'	34:DA:111:G:O4'	2.15	0.47
34:DA:433:C:H2'	34:DA:434:U:C6	2.48	0.47
34:DA:457:C:H2'	34:DA:458:C:C6	2.48	0.47
34:DA:664:G:N2	34:DA:741:G:H1	2.12	0.47
34:DA:953:G:H5'	34:DA:965:A:H61	1.79	0.47
34:DA:1327:C:OP1	54:DU:20:LYS:N	2.47	0.47
34:DA:1366:C:O2'	43:DJ:60:ARG:NH2	2.47	0.47
36:DC:18:TRP:CD1	47:DN:54:PRO:HA	2.50	0.47
39:DF:40:VAL:HG23	39:DF:62:TRP:O	2.15	0.47
41:DH:33:GLU:OE2	41:DH:48:TYR:OH	2.28	0.47
49:DP:21:VAL:HG13	49:DP:34:GLU:O	2.15	0.47
53:DT:54:LYS:HA	53:DT:57:ARG:NH2	2.30	0.47
56:DX:47:U:C2	56:DX:50:U:OP1	2.68	0.47
57:DZ:238:THR:HG22	57:DZ:241:GLU:OE2	2.15	0.47
1:AA:1529:G:C6	1:AA:1553:A:C6	3.03	0.47
1:AA:1698:G:C5'	15:AR:39:PRO:HG2	2.45	0.47
1:AA:2331:G:C2	16:AS:3:ARG:HA	2.50	0.47
3:AC:223:VAL:HG23	3:AC:223:VAL:O	2.15	0.47
8:AH:58:GLU:OE2	8:AH:60:ARG:NH2	2.48	0.47
13:AP:82:GLY:HA2	13:AP:113:LYS:O	2.15	0.47
22:AY:54:LYS:CA	22:AY:56:PRO:HD3	2.41	0.47
25:A1:20:ARG:HD3	63:A1:201:HOH:O	2.15	0.47
34:BA:445:G:C6	34:BA:446:G:C5	3.03	0.47
34:BA:1223:C:OP1	52:BS:78:ARG:NH2	2.48	0.47
34:BA:1525:G:P	44:BK:120:ARG:NH2	2.88	0.47
35:BB:164:VAL:HB	35:BB:186:ALA:HB2	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:BH:97:VAL:HA	41:BH:100:ILE:HG13	1.96	0.47
48:BO:16:ALA:HB1	48:BO:21:ASP:HB3	1.97	0.47
49:BP:6:LEU:HA	49:BP:19:ILE:HA	1.96	0.47
53:BT:77:ALA:O	53:BT:81:LYS:HG3	2.15	0.47
1:CA:20:C:OP1	18:CU:22:LYS:NZ	2.44	0.47
1:CA:656:G:O6	63:CA:3754:HOH:O	2.20	0.47
1:CA:851:U:O2'	27:C3:42:ALA:O	2.33	0.47
1:CA:1055:G:H3'	1:CA:1056:G:H8	1.80	0.47
1:CA:1604:C:P	63:CA:3761:HOH:O	2.73	0.47
1:CA:1637:A:H4'	1:CA:2711:A:O2'	2.15	0.47
1:CA:1847:A:H3'	1:CA:1848:A:H5'	1.96	0.47
1:CA:2489:G:O2'	1:CA:2490:G:H5'	2.15	0.47
18:CU:86:ALA:HB2	18:CU:116:ALA:HB2	1.97	0.47
23:CZ:40:ASP:OD1	23:CZ:43:GLU:HG3	2.15	0.47
34:DA:15:G:C5	34:DA:1396:A:C2	3.03	0.47
34:DA:427:U:H3'	34:DA:428:G:H2'	1.97	0.47
34:DA:487:A:H2'	34:DA:488:C:O4'	2.15	0.47
34:DA:1022:G:H2'	34:DA:1023:G:H8	1.79	0.47
34:DA:1201:A:H1'	34:DA:1202:G:OP2	2.15	0.47
35:DB:98:LEU:HA	35:DB:98:LEU:HD13	1.67	0.47
37:DD:38:TYR:CE1	37:DD:45:GLN:HG3	2.50	0.47
38:DE:69:VAL:HG11	38:DE:113:ALA:HB1	1.97	0.47
38:DE:82:VAL:HG11	38:DE:137:GLU:HB3	1.96	0.47
43:DJ:49:VAL:HG23	47:DN:41:ARG:HB2	1.96	0.47
56:DX:10:G:N2	56:DX:26:G:H1'	2.29	0.47
57:DZ:191:ASP:HA	57:DZ:267:LYS:NZ	2.29	0.47
1:AA:360:C:O2'	1:AA:361:C:H5'	2.15	0.47
1:AA:895:G:O6	1:AA:974:G:H2'	2.15	0.47
1:AA:1293:A:OP1	6:AF:95:ARG:NH2	2.43	0.47
1:AA:1403:U:H2'	1:AA:1404:G:O4'	2.15	0.47
1:AA:1831:C:OP1	4:AD:264:LYS:NZ	2.46	0.47
1:AA:2643:G:O2'	1:AA:2820:A:N1	2.37	0.47
8:AH:40:GLU:OE1	8:AH:60:ARG:NH1	2.48	0.47
20:AW:38:TYR:OH	29:A5:47:PRO:HG3	2.14	0.47
34:BA:273:A:N7	63:BA:3325:HOH:O	2.36	0.47
34:BA:953:G:H2'	34:BA:954:G:O4'	2.15	0.47
34:BA:1305:G:H5"	54:BU:4:GLY:HA3	1.97	0.47
34:BA:1311:G:N2	34:BA:1327:C:C2	2.83	0.47
36:BC:5:ILE:HG12	36:BC:6:HIS:H	1.79	0.47
41:BH:39:LEU:HB3	41:BH:45:ILE:HG12	1.96	0.47
57:BZ:300:GLU:C	57:BZ:301:ILE:HG12	2.40	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:189:G:OP2	25:C1:39:LYS:NZ	2.47	0.47
1:CA:622:G:H2'	1:CA:623:G:H8	1.79	0.47
1:CA:901:A:H5"	1:CA:902:C:OP2	2.14	0.47
1:CA:1474:C:H2'	1:CA:1475:G:H8	1.79	0.47
1:CA:1788:C:H2'	1:CA:1789:A:O4'	2.15	0.47
1:CA:2061:G:H5"	1:CA:2503:A:C2	2.50	0.47
2:CB:24:G:N2	2:CB:27:C:N3	2.61	0.47
3:CC:223:VAL:HG23	3:CC:223:VAL:O	2.15	0.47
10:CL:64:SER:OG	10:CL:65:PHE:N	2.47	0.47
12:CO:68:GLU:HG2	12:CO:68:GLU:O	2.15	0.47
14:CQ:63:LYS:HB3	14:CQ:63:LYS:HE2	1.71	0.47
22:CY:79:CYS:SG	22:CY:102:CYS:HB3	2.55	0.47
31:C7:19:ARG:HG2	31:C7:19:ARG:NH1	2.31	0.47
34:DA:192:U:O2'	53:DT:60:GLU:OE2	2.17	0.47
34:DA:396:G:O2'	34:DA:398:C:OP1	2.27	0.47
34:DA:892:A:O2'	34:DA:1415:G:H4'	2.14	0.47
34:DA:981:U:H5'	47:DN:21:TYR:CE2	2.50	0.47
34:DA:1130:A:O2'	42:DI:3:GLN:OE1	2.23	0.47
34:DA:1139:G:N2	34:DA:1142:G:O6	2.39	0.47
39:DF:43:LEU:HD22	39:DF:46:ARG:NH1	2.30	0.47
1:AA:181:C:O2'	1:AA:849:A:N3	2.43	0.46
1:AA:1209:G:C2'	1:AA:1210:G:H5'	2.45	0.46
1:AA:1879:A:H2'	1:AA:1880:G:H8	1.80	0.46
1:AA:2024:G:P	15:AR:9:LYS:HE3	2.55	0.46
1:AA:2349:G:C2	1:AA:2350:G:C8	3.03	0.46
1:AA:2649:U:C2'	1:AA:2650:G:H5'	2.45	0.46
5:AE:9:VAL:HB	17:AT:3:ARG:HG2	1.98	0.46
5:AE:60:ASN:OD1	5:AE:62:PRO:HD2	2.16	0.46
5:AE:73:GLU:HA	5:AE:74:PRO:HD3	1.74	0.46
5:AE:116:VAL:HG13	5:AE:122:PHE:HB2	1.97	0.46
6:AF:101:LEU:O	6:AF:106:ARG:HD3	2.14	0.46
10:AL:30:HIS:HD2	10:AL:65:PHE:HB2	1.80	0.46
17:AT:105:LEU:CB	17:AT:110:ILE:HG13	2.45	0.46
34:BA:38:G:N7	63:BA:3324:HOH:O	2.35	0.46
34:BA:397:A:C6	34:BA:548:G:N7	2.83	0.46
34:BA:565:U:OP2	34:BA:566:G:O2'	2.30	0.46
37:BD:140:VAL:HG11	37:BD:146:ILE:HD11	1.96	0.46
37:BD:162:LEU:HD13	37:BD:181:MET:HG2	1.97	0.46
40:BG:14:PRO:HB3	40:BG:19:GLY:C	2.39	0.46
51:BR:29:PHE:CD2	51:BR:29:PHE:N	2.78	0.46
1:CA:534:U:H5'	18:CU:42:ALA:HB1	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:602:G:O2'	1:CA:655:A:N6	2.47	0.46
1:CA:718:A:H2'	1:CA:719:C:O4'	2.15	0.46
1:CA:889:C:O2'	1:CA:890:A:O5'	2.31	0.46
1:CA:921:G:H4'	1:CA:2269:A:C5	2.50	0.46
1:CA:993:G:H1'	19:CV:89:GLN:OE1	2.15	0.46
1:CA:1227:G:OP1	18:CU:13:LYS:NZ	2.37	0.46
1:CA:2652:C:H2'	1:CA:2653:U:O4'	2.16	0.46
1:CA:2734:A:H2'	1:CA:2735:G:O4'	2.15	0.46
6:CF:64:ILE:HG21	6:CF:78:ILE:HG23	1.98	0.46
8:CH:140:LYS:O	8:CH:144:VAL:HG23	2.15	0.46
16:CS:23:ARG:HD3	16:CS:86:ALA:HB2	1.96	0.46
34:DA:177:C:H2'	34:DA:178:C:C6	2.50	0.46
34:DA:605:U:H2'	34:DA:606:G:O4'	2.15	0.46
34:DA:748:C:H4'	34:DA:749:C:O5'	2.15	0.46
35:DB:58:ILE:HG23	35:DB:68:ILE:HD11	1.96	0.46
37:DD:36:ARG:HG3	37:DD:38:TYR:CE2	2.49	0.46
45:DL:69:TYR:HE2	45:DL:71:PRO:HA	1.80	0.46
1:AA:662:A:H8	13:AP:117:GLU:HG3	1.80	0.46
1:AA:704:U:H2'	1:AA:705:C:H6	1.80	0.46
1:AA:795:G:C8	20:AW:89:ALA:HB1	2.49	0.46
1:AA:2224:C:O2	4:AD:151:LYS:NZ	2.41	0.46
4:AD:261:LYS:NZ	4:AD:263:ARG:NH2	2.62	0.46
10:AL:41:PHE:C	10:AL:43:ALA:H	2.22	0.46
17:AT:20:PRO:HB2	17:AT:88:ILE:HD11	1.96	0.46
23:AZ:99:TYR:CE2	23:AZ:125:LEU:HD13	2.50	0.46
34:BA:1227:A:OP2	46:BM:111:LYS:HD2	2.14	0.46
35:BB:51:LEU:HD21	35:BB:201:ILE:HG23	1.96	0.46
43:BJ:63:PHE:HZ	47:BN:45:ARG:HG3	1.80	0.46
45:BL:28:LYS:HE2	45:BL:62:SER:HB2	1.96	0.46
1:CA:244:A:C2	1:CA:255:A:C4	3.04	0.46
1:CA:297:C:H2'	1:CA:298:G:O4'	2.15	0.46
1:CA:307:G:H22	1:CA:310:A:P	2.38	0.46
1:CA:324:A:N6	1:CA:338:G:O2'	2.45	0.46
1:CA:964:C:O2'	1:CA:2273:A:N3	2.38	0.46
1:CA:1188:U:C4'	19:CV:79:VAL:HG22	2.43	0.46
1:CA:1860:G:H8	3:CC:206:LYS:HG3	1.81	0.46
1:CA:2155:G:C6	1:CA:2156:G:H1'	2.50	0.46
2:CB:31:C:H2'	2:CB:32:C:H5'	1.97	0.46
3:CC:42:VAL:O	3:CC:216:THR:C	2.59	0.46
3:CC:46:ALA:O	3:CC:47:LYS:HB2	2.15	0.46
6:CF:13:SER:OG	6:CF:16:GLY:O	2.21	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:CF:34:TRP:CE2	13:CP:8:PRO:HG3	2.50	0.46
8:CH:84:SER:HA	8:CH:133:VAL:O	2.16	0.46
34:DA:56:U:H2'	34:DA:57:G:C8	2.49	0.46
34:DA:513:C:H2'	34:DA:514:C:C6	2.48	0.46
34:DA:617:G:H4'	49:DP:44:THR:O	2.15	0.46
34:DA:642:A:N3	41:DH:113:SER:OG	2.46	0.46
34:DA:731:G:C6	34:DA:732:C:C4	3.03	0.46
34:DA:1306:A:H1'	34:DA:1332:A:C2	2.50	0.46
34:DA:1348:U:H4'	42:DI:120:ARG:HD3	1.96	0.46
36:DC:5:ILE:HG12	36:DC:6:HIS:H	1.81	0.46
38:DE:78:HIS:HA	41:DH:105:ARG:CG	2.44	0.46
40:DG:18:TYR:CE2	40:DG:59:LEU:HB2	2.49	0.46
42:DI:70:LYS:O	42:DI:74:ILE:HG13	2.15	0.46
44:DK:123:LYS:O	44:DK:126:ARG:HG3	2.16	0.46
57:DZ:109:ASP:OD2	57:DZ:138:LYS:HD2	2.15	0.46
57:DZ:214:GLU:O	57:DZ:218:GLU:HB2	2.15	0.46
57:DZ:630:GLN:O	57:DZ:645:ALA:HB1	2.15	0.46
1:AA:198:C:C2'	1:AA:199:C:H5'	2.46	0.46
1:AA:560:C:O2'	18:AU:53:ARG:HD3	2.16	0.46
1:AA:713:G:O2'	1:AA:714:U:H5'	2.14	0.46
1:AA:1551:C:H2'	1:AA:1552:C:C6	2.50	0.46
1:AA:1771:G:H8	1:AA:1771:G:O5'	1.99	0.46
1:AA:2124:U:H2'	1:AA:2125:C:C6	2.49	0.46
2:AB:28:C:OP1	16:AS:36:TYR:OH	2.29	0.46
3:AC:42:VAL:O	3:AC:216:THR:C	2.59	0.46
3:AC:42:VAL:CG1	3:AC:43:GLU:H	2.27	0.46
3:AC:46:ALA:O	3:AC:47:LYS:HB2	2.15	0.46
6:AF:141:ALA:O	6:AF:142:TRP:C	2.58	0.46
8:AH:105:LEU:HD12	8:AH:105:LEU:HA	1.80	0.46
34:BA:292:G:C5	34:BA:293:G:H1'	2.50	0.46
34:BA:357:G:N1	34:BA:358:U:C4	2.84	0.46
34:BA:406:G:C2	34:BA:407:G:C8	3.03	0.46
34:BA:1217:C:H2'	34:BA:1218:C:O4'	2.15	0.46
36:BC:22:TRP:CH2	36:BC:32:LEU:HB2	2.51	0.46
36:BC:134:ILE:HG23	36:BC:151:VAL:HB	1.96	0.46
1:CA:1210:A:C2	1:CA:1237:A:C6	3.04	0.46
1:CA:1257:C:H4'	6:CF:83:PHE:CD1	2.50	0.46
1:CA:1300:U:H4'	1:CA:1301:A:C5'	2.44	0.46
1:CA:1668:A:H4'	1:CA:1669:A:O5'	2.15	0.46
1:CA:2196:C:O2'	1:CA:2197:U:H5'	2.16	0.46
1:CA:2459:A:C6	1:CA:2460:U:C2	3.03	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:2830:G:N3	1:CA:2883:A:H2	2.14	0.46
4:CD:44:ASN:HD21	4:CD:46:GLN:HG3	1.79	0.46
7:CG:23:PHE:HB2	7:CG:25:TYR:CE1	2.50	0.46
34:DA:112:G:H5'	34:DA:389:A:O2'	2.15	0.46
34:DA:153:C:H42	34:DA:168:G:H1	1.62	0.46
34:DA:1173:G:H2'	34:DA:1174:G:C8	2.51	0.46
38:DE:51:VAL:O	38:DE:55:VAL:HG23	2.16	0.46
57:DZ:15:ILE:O	57:DZ:81:ILE:HA	2.15	0.46
57:DZ:639:ASN:HA	57:DZ:640:ALA:O	2.15	0.46
1:AA:142:G:H1'	21:AX:37:THR:HG21	1.97	0.46
1:AA:555:G:N3	1:AA:555:G:O4'	2.47	0.46
1:AA:1160:G:H2'	1:AA:1161:G:H8	1.80	0.46
1:AA:1574:A:O2'	1:AA:1575:A:H5'	2.14	0.46
1:AA:1898:A:H8	1:AA:1898:A:OP2	1.98	0.46
1:AA:1903:C:H2'	1:AA:1904:C:H6	1.81	0.46
1:AA:2724:U:O2'	1:AA:2726:A:H5'	2.16	0.46
1:AA:2823:A:O2'	1:AA:2824:C:H5'	2.15	0.46
3:AC:176:VAL:O	3:AC:176:VAL:HG12	2.15	0.46
9:AK:25:PHE:O	9:AK:84:GLU:HA	2.16	0.46
18:AU:89:GLU:HB2	19:AV:50:PRO:HB3	1.96	0.46
34:BA:159:G:N2	34:BA:161:A:O5'	2.48	0.46
34:BA:620:C:C2	37:BD:135:LEU:HG	2.51	0.46
34:BA:1222:G:OP1	34:BA:1321:C:O2'	2.22	0.46
38:BE:61:TYR:HA	38:BE:64:ARG:HB2	1.98	0.46
57:BZ:140:ASP:HA	57:BZ:172:ASP:H	1.80	0.46
1:CA:71:A:C8	21:CX:31:HIS:HE1	2.34	0.46
1:CA:1503:U:H2'	1:CA:1504:C:C6	2.50	0.46
1:CA:1695:G:H1'	4:CD:8:PRO:O	2.16	0.46
1:CA:2360:A:O5'	1:CA:2360:A:H8	1.98	0.46
1:CA:2591:C:OP1	4:CD:239:ARG:HD2	2.16	0.46
3:CC:42:VAL:CG1	3:CC:43:GLU:H	2.28	0.46
5:CE:116:VAL:HG13	5:CE:122:PHE:HB2	1.98	0.46
6:CF:21:ALA:CB	6:CF:22:ALA:HA	2.46	0.46
7:CG:33:ARG:HB2	7:CG:33:ARG:CZ	2.45	0.46
13:CP:96:THR:OG1	13:CP:98:GLU:HG2	2.16	0.46
23:CZ:182:LYS:HB3	23:CZ:183:LEU:H	1.47	0.46
30:C6:14:THR:OG1	30:C6:48:VAL:HG13	2.15	0.46
34:DA:1024:G:H2'	34:DA:1025:U:H5"	1.97	0.46
34:DA:1323:G:H2'	34:DA:1324:A:C8	2.50	0.46
38:DE:7:GLU:OE1	38:DE:37:ARG:NH2	2.44	0.46
38:DE:37:ARG:O	38:DE:114:GLY:HA3	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:DZ:302:HIS:HA	57:DZ:303:PRO:HD2	1.63	0.46
1:AA:141:C:H2'	1:AA:142:G:O4'	2.16	0.46
1:AA:1014:U:H2'	1:AA:1015:C:C6	2.50	0.46
1:AA:1485:A:H2'	1:AA:1486:G:O4'	2.16	0.46
1:AA:2274:U:H4'	1:AA:2340:A:C2	2.51	0.46
1:AA:2731:G:O2'	1:AA:2857:U:OP1	2.33	0.46
11:AN:12:ARG:HE	11:AN:14:VAL:HG21	1.81	0.46
21:AX:5:TYR:CE2	26:A2:30:ARG:HB2	2.51	0.46
30:A6:26:ASN:C	30:A6:26:ASN:OD1	2.57	0.46
34:BA:112:G:C2	34:BA:330:C:N4	2.84	0.46
34:BA:271:C:H2'	34:BA:272:C:C6	2.51	0.46
34:BA:382:A:H2'	34:BA:383:A:C8	2.49	0.46
34:BA:936:C:H2'	34:BA:937:A:O4'	2.15	0.46
34:BA:1225:A:OP1	46:BM:103:THR:N	2.44	0.46
34:BA:1366:C:H2'	34:BA:1367:C:C6	2.51	0.46
34:BA:1434:A:H2'	34:BA:1435:G:O4'	2.14	0.46
38:BE:80:ILE:HG23	38:BE:91:LEU:HD23	1.98	0.46
46:BM:20:THR:HA	46:BM:25:ILE:O	2.15	0.46
49:BP:5:ARG:O	49:BP:20:VAL:N	2.47	0.46
57:BZ:100:VAL:O	57:BZ:100:VAL:HG12	2.15	0.46
57:BZ:273:LEU:C	57:BZ:275:ALA:N	2.73	0.46
10:CL:93:ARG:HE	10:CL:93:ARG:HB3	1.54	0.46
23:CZ:118:GLN:O	23:CZ:120:ILE:N	2.48	0.46
34:DA:263:A:OP1	53:DT:79:ARG:NH1	2.48	0.46
34:DA:284:G:H2'	34:DA:285:G:H8	1.81	0.46
34:DA:375:U:C2	34:DA:376:G:C8	3.04	0.46
34:DA:918:A:H2'	34:DA:919:A:C8	2.51	0.46
34:DA:1189:C:O5'	34:DA:1189:C:H6	1.98	0.46
34:DA:1289:A:C8	34:DA:1290:G:C8	3.03	0.46
35:DB:91:PRO:HD3	35:DB:154:LEU:HD12	1.96	0.46
38:DE:21:ALA:O	38:DE:23:GLY:N	2.44	0.46
41:DH:20:TYR:HA	41:DH:65:TYR:CZ	2.50	0.46
57:DZ:227:ILE:HG23	57:DZ:241:GLU:OE1	2.15	0.46
57:DZ:319:ASP:HA	57:DZ:320:PRO:HD2	1.65	0.46
57:DZ:355:LEU:HD13	57:DZ:355:LEU:HA	1.77	0.46
1:AA:11:G:H2'	1:AA:12:U:C5'	2.42	0.46
1:AA:1616:A:O4'	4:AD:59:LYS:NZ	2.49	0.46
1:AA:1757:C:H2'	1:AA:1758:C:C6	2.50	0.46
1:AA:2191:A:H2'	1:AA:2191:A:N3	2.31	0.46
1:AA:2529:C:C2	1:AA:2554:A:N6	2.83	0.46
4:AD:223:GLY:HA3	4:AD:231:HIS:CE1	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:AF:116:ASP:OD1	6:AF:119:ARG:NH2	2.48	0.46
6:AF:188:ARG:HA	13:AP:3:LEU:HD13	1.97	0.46
12:AO:122:LEU:HD23	12:AO:122:LEU:HA	1.64	0.46
22:AY:68:HIS:H	22:AY:71:LYS:HD3	1.80	0.46
31:A7:34:ARG:NH1	31:A7:39:ARG:HG3	2.31	0.46
34:BA:112:G:O2'	34:BA:354:G:O2'	2.22	0.46
34:BA:720:C:OP2	34:BA:721:G:O2'	2.32	0.46
34:BA:972:C:OP1	63:BA:3310:HOH:O	2.21	0.46
37:BD:39:PRO:HD2	37:BD:44:GLY:HA2	1.98	0.46
37:BD:108:LEU:HB3	37:BD:110:PHE:CE1	2.50	0.46
37:BD:110:PHE:CE2	37:BD:148:VAL:HG23	2.50	0.46
1:CA:182:A:H2'	1:CA:183:C:C6	2.50	0.46
1:CA:387:U:H3'	25:C1:32:LYS:HB2	1.98	0.46
1:CA:676:A:H2	1:CA:2069:G:N3	2.13	0.46
1:CA:1071:G:C8	1:CA:1089:G:C6	3.04	0.46
1:CA:1168:G:C2	1:CA:1182:A:C2	3.03	0.46
1:CA:1239:G:H2'	1:CA:1240:U:O4'	2.15	0.46
1:CA:1962:C:O2'	1:CA:1964:G:OP2	2.30	0.46
1:CA:2191:G:H2'	1:CA:2192:G:O4'	2.15	0.46
1:CA:2399:G:C6	1:CA:2400:G:C5	3.03	0.46
1:CA:2564:A:C2	1:CA:2647:U:H4'	2.50	0.46
2:CB:78:A:H2'	2:CB:79:C:O4'	2.16	0.46
3:CC:54:ARG:HH22	3:CC:56:ASP:HB3	1.75	0.46
8:CH:101:ARG:HH22	8:CH:122:THR:HG23	1.80	0.46
11:CN:65:LYS:HD2	11:CN:69:GLN:NE2	2.31	0.46
14:CQ:75:THR:HG21	14:CQ:87:LYS:HZ2	1.81	0.46
14:CQ:75:THR:HG21	14:CQ:87:LYS:NZ	2.31	0.46
15:CR:16:HIS:O	15:CR:17:ARG:C	2.57	0.46
16:CS:35:ILE:HG12	16:CS:97:ARG:HH21	1.80	0.46
16:CS:90:GLY:C	16:CS:92:TYR:H	2.23	0.46
17:CT:99:LEU:C	17:CT:101:PHE:N	2.73	0.46
23:CZ:5:LEU:HD23	23:CZ:47:VAL:HG21	1.98	0.46
34:DA:576:G:N1	34:DA:759:A:OP1	2.46	0.46
34:DA:938:A:N6	34:DA:939:G:C6	2.83	0.46
34:DA:1131:G:P	42:DI:20:ARG:HH22	2.37	0.46
35:DB:16:HIS:HB2	35:DB:204:ASN:HB3	1.96	0.46
37:DD:150:GLU:OE2	37:DD:151:LYS:N	2.48	0.46
46:DM:25:ILE:HD11	46:DM:66:LEU:HD23	1.97	0.46
57:DZ:280:LEU:CD2	57:DZ:281:PRO:HD2	2.45	0.46
1:AA:7:G:H2'	1:AA:8:A:C8	2.51	0.46
1:AA:589:U:P	19:AV:80:GLN:HE21	2.39	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:671:A:H2'	1:AA:672:G:O4'	2.15	0.46
1:AA:1221:G:H1'	1:AA:1222:A:C5'	2.46	0.46
1:AA:1405:A:N3	1:AA:1405:A:O4'	2.48	0.46
1:AA:1414:G:C2	1:AA:1415:G:C8	3.03	0.46
1:AA:1452:U:H2'	1:AA:1453:C:H6	1.79	0.46
1:AA:1957:G:H1'	1:AA:1986:G:N2	2.31	0.46
9:AK:103:GLY:HA2	9:AK:110:GLY:HA3	1.98	0.46
27:A3:7:LYS:HG3	27:A3:34:GLU:CG	2.44	0.46
27:A3:29:ARG:HG2	27:A3:29:ARG:NH1	2.29	0.46
34:BA:482:A:H3'	34:BA:483:C:H6	1.81	0.46
34:BA:498:U:N3	34:BA:499:A:N7	2.64	0.46
34:BA:688:G:H2'	34:BA:689:C:C6	2.47	0.46
34:BA:1368:G:OP2	42:BI:112:LYS:HG3	2.16	0.46
35:BB:17:PHE:HA	35:BB:44:LEU:HD11	1.98	0.46
35:BB:71:VAL:HG22	35:BB:93:VAL:CG2	2.45	0.46
36:BC:56:ASP:O	36:BC:66:VAL:HA	2.15	0.46
37:BD:93:PHE:O	37:BD:97:LEU:HB2	2.16	0.46
40:BG:121:ALA:O	40:BG:125:MET:HB2	2.16	0.46
41:BH:83:ILE:HA	41:BH:136:GLU:O	2.16	0.46
46:BM:20:THR:C	46:BM:22:ILE:H	2.24	0.46
47:BN:27:CYS:SG	47:BN:28:GLY:N	2.88	0.46
48:BO:66:LEU:HD12	48:BO:66:LEU:HA	1.83	0.46
48:BO:69:TYR:HA	48:BO:72:ARG:HH11	1.81	0.46
57:BZ:227:ILE:HA	57:BZ:230:LYS:HG3	1.97	0.46
57:BZ:238:THR:HG23	57:BZ:241:GLU:OE1	2.15	0.46
1:CA:374:A:C2	1:CA:401:A:C4	3.04	0.46
1:CA:749:C:O2	1:CA:1618:A:H2'	2.14	0.46
1:CA:1247:A:O2'	1:CA:1248:G:H5"	2.16	0.46
1:CA:1353:A:H2'	1:CA:1354:A:C8	2.50	0.46
1:CA:1480:G:C6	1:CA:1481:U:C4	3.04	0.46
1:CA:1494:A:H2'	1:CA:1495:A:C8	2.51	0.46
1:CA:2050:C:C4	1:CA:2051:A:C6	3.03	0.46
1:CA:2108:C:H2'	1:CA:2109:U:C6	2.51	0.46
3:CC:20:VAL:O	3:CC:224:ARG:O	2.33	0.46
4:CD:227:ASN:O	4:CD:228:PRO:C	2.58	0.46
5:CE:35:GLN:OE1	5:CE:66:HIS:HE1	1.99	0.46
10:CL:59:ILE:HG12	10:CL:60:TYR:N	2.31	0.46
14:CQ:72:LYS:HA	14:CQ:73:PRO:HD3	1.81	0.46
20:CW:48:ALA:O	20:CW:52:GLU:N	2.43	0.46
25:C1:40:ARG:NH2	25:C1:42:GLN:HG2	2.30	0.46
34:DA:139:G:H2'	34:DA:140:A:H8	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:DA:177:C:H2'	34:DA:178:C:H6	1.80	0.46
34:DA:488:C:O5'	34:DA:488:C:H6	1.99	0.46
34:DA:908:A:O2'	34:DA:909:A:H5'	2.16	0.46
34:DA:1288:A:N1	34:DA:1371:G:H1'	2.30	0.46
35:DB:47:THR:O	35:DB:51:LEU:HD22	2.16	0.46
35:DB:58:ILE:HA	35:DB:61:LEU:HB3	1.98	0.46
57:DZ:145:ASP:OD2	57:DZ:145:ASP:C	2.59	0.46
57:DZ:637:ARG:O	57:DZ:639:ASN:N	2.47	0.46
1:AA:34:C:H5"	1:AA:35:G:OP2	2.16	0.46
1:AA:68:C:O2	1:AA:72:A:O2'	2.34	0.46
1:AA:1133:G:O6	1:AA:1135:G:C2	2.69	0.46
1:AA:1367:A:H2'	1:AA:1368:A:O4'	2.15	0.46
1:AA:2451:A:H5"	1:AA:2451:A:H8	1.81	0.46
1:AA:2849:G:H5'	15:AR:46:GLY:HA2	1.97	0.46
2:AB:29:A:OP2	16:AS:32:LEU:HD12	2.16	0.46
3:AC:206:LYS:HB3	3:AC:206:LYS:HZ3	1.79	0.46
4:AD:70:TRP:HB3	4:AD:190:TYR:CZ	2.51	0.46
4:AD:70:TRP:HB3	4:AD:190:TYR:CE2	2.50	0.46
4:AD:101:GLU:OE1	4:AD:103:ARG:HD3	2.16	0.46
4:AD:253:GLN:HE21	4:AD:253:GLN:HB3	1.47	0.46
5:AE:12:THR:HG22	5:AE:13:ARG:H	1.80	0.46
13:AP:95:VAL:HG22	13:AP:125:VAL:HB	1.98	0.46
16:AS:51:ALA:CB	16:AS:73:LEU:HB2	2.45	0.46
18:AU:86:ALA:HB3	18:AU:88:ILE:HD12	1.96	0.46
26:A2:54:LYS:O	26:A2:57:ILE:HB	2.15	0.46
34:BA:674:G:H2'	34:BA:675:A:C8	2.49	0.46
34:BA:1014:A:H4'	52:BS:14:HIS:CE1	2.51	0.46
34:BA:1429:C:H2'	34:BA:1430:C:C6	2.51	0.46
35:BB:22:LYS:HA	35:BB:40:HIS:CE1	2.51	0.46
35:BB:42:ILE:HG21	35:BB:202:PRO:O	2.16	0.46
35:BB:200:ILE:HB	35:BB:202:PRO:HD3	1.98	0.46
45:BL:83:VAL:HG21	45:BL:100:ILE:HG12	1.98	0.46
57:BZ:127:LYS:NZ	57:BZ:128:TYR:CE2	2.80	0.46
1:CA:235:U:H2'	1:CA:236:C:C6	2.51	0.46
1:CA:392:C:H5"	1:CA:409:C:H5"	1.96	0.46
1:CA:1084:A:C8	1:CA:1085:A:C8	3.04	0.46
1:CA:1593:G:H2'	1:CA:1594:G:C8	2.51	0.46
8:CH:13:LYS:HA	8:CH:14:GLY:HA2	1.67	0.46
15:CR:24:GLN:NE2	15:CR:36:THR:HG21	2.30	0.46
21:CX:64:LYS:HE3	21:CX:73:ARG:NH2	2.31	0.46
34:DA:129(A):G:C6	34:DA:189(E):U:H4'	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:DA:731:G:H5'	34:DA:766:A:H4'	1.97	0.46
34:DA:1202:G:O4'	47:DN:29:ARG:NH1	2.48	0.46
34:DA:1415:G:C6	34:DA:1486:G:C6	3.04	0.46
57:DZ:606:MET:N	57:DZ:647:VAL:O	2.46	0.46
1:AA:719:C:H4'	6:AF:89:VAL:HG21	1.98	0.46
1:AA:2403:G:O6	1:AA:2437:A:H8	1.98	0.46
1:AA:2697:G:H5'	12:AO:68:GLU:OE1	2.14	0.46
9:AK:88:ALA:C	9:AK:90:ALA:H	2.23	0.46
13:AP:55:ARG:HG2	13:AP:56:SER:N	2.29	0.46
25:A1:76:ARG:NH1	25:A1:97:LEU:HB3	2.31	0.46
30:A6:11:LEU:HB2	30:A6:21:TYR:HB2	1.97	0.46
34:BA:448:A:P	34:BA:485:G:H22	2.39	0.46
34:BA:537:G:H5"	45:BL:113:ARG:HH12	1.80	0.46
34:BA:629:G:H2'	34:BA:630:G:O4'	2.15	0.46
34:BA:836:G:C6	34:BA:851:G:C6	3.04	0.46
37:BD:25:ARG:NH1	37:BD:30:LYS:O	2.45	0.46
57:BZ:-9:LEU:O	57:BZ:-6:ARG:HB2	2.16	0.46
57:BZ:201:ILE:HG21	57:BZ:206:LEU:HA	1.98	0.46
1:CA:521:G:H2'	1:CA:522:G:C8	2.51	0.46
1:CA:1323:U:H2'	1:CA:1324:G:H5'	1.97	0.46
1:CA:2121:G:O2'	3:CC:168:LYS:CG	2.62	0.46
1:CA:2437:U:O2'	1:CA:2438:U:H5'	2.16	0.46
1:CA:2749:A:H1'	8:CH:63:SER:HB3	1.97	0.46
2:CB:31:C:H4'	7:CG:29:TRP:CZ2	2.51	0.46
4:CD:138:VAL:HB	4:CD:166:GLN:O	2.14	0.46
13:CP:139:LYS:C	13:CP:141:ALA:H	2.24	0.46
19:CV:76:LYS:HD2	19:CV:81:TYR:CD2	2.51	0.46
28:C4:35:VAL:HA	28:C4:39:CYS:SG	2.55	0.46
34:DA:674:G:H2'	34:DA:675:A:C8	2.49	0.46
34:DA:730:G:C6	34:DA:731:G:H1'	2.51	0.46
34:DA:807:A:C5	34:DA:808:C:C4	3.04	0.46
35:DB:113:HIS:HA	35:DB:116:GLU:HG2	1.97	0.46
36:DC:71:ALA:HB2	36:DC:106:VAL:HB	1.97	0.46
42:DI:9:ARG:HA	42:DI:13:ALA:O	2.15	0.46
42:DI:77:ILE:O	42:DI:81:ILE:HG22	2.15	0.46
1:AA:217:A:H3'	1:AA:218:A:C5'	2.41	0.46
1:AA:324:A:OP1	22:AY:86:ARG:NH2	2.47	0.46
1:AA:897:C:O5'	1:AA:897:C:H6	1.99	0.46
1:AA:1913:G:C5	1:AA:1914:C:C4	3.04	0.46
1:AA:2649:U:O2'	1:AA:2650:G:H5'	2.16	0.46
11:AN:78:TYR:O	11:AN:79:PRO:C	2.55	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:AR:21:TYR:OH	15:AR:43:GLU:HG2	2.15	0.46
19:AV:91:TYR:CD1	19:AV:91:TYR:C	2.94	0.46
34:BA:232:G:H1'	34:BA:262:A:N1	2.31	0.46
34:BA:577:G:H1'	34:BA:816:A:C4	2.51	0.46
34:BA:690:G:O6	44:BK:51:LYS:HE2	2.17	0.46
34:BA:1075:C:OP1	35:BB:179:LYS:HE3	2.14	0.46
34:BA:1098:C:C2	34:BA:1099:G:C8	3.04	0.46
36:BC:45:LYS:HE3	36:BC:45:LYS:HB2	1.80	0.46
40:BG:16:LEU:HD22	40:BG:16:LEU:H	1.80	0.46
41:BH:25:ASP:OD1	41:BH:60:ARG:HG3	2.15	0.46
42:BI:9:ARG:HB3	42:BI:104:ARG:NH1	2.30	0.46
56:BX:37:A:C4'	57:BZ:501:THR:HA	2.46	0.46
1:CA:1547:C:H2'	1:CA:1548:C:C6	2.51	0.46
1:CA:1743:C:H2'	1:CA:1744:C:C6	2.51	0.46
1:CA:2107:C:N3	1:CA:2182:G:N2	2.46	0.46
2:CB:60:C:H2'	2:CB:61:G:C8	2.47	0.46
13:CP:47:ASP:OD1	13:CP:49:ARG:HB2	2.16	0.46
19:CV:52:VAL:HG22	19:CV:55:ALA:HB3	1.97	0.46
22:CY:73:ARG:HH21	22:CY:83:THR:C	2.24	0.46
34:DA:257:G:C2	34:DA:270:A:C2	3.03	0.46
34:DA:448:A:C4	34:DA:487:A:C2	3.04	0.46
34:DA:1240:U:H5'	34:DA:1241:G:C8	2.51	0.46
34:DA:1412:C:C2	34:DA:1413:A:C8	3.04	0.46
34:DA:1439:C:H6	34:DA:1439:C:O5'	1.99	0.46
38:DE:89:ILE:HD12	38:DE:121:LYS:O	2.16	0.46
44:DK:92:GLU:OE2	51:DR:87:ARG:NH1	2.48	0.46
53:DT:36:LEU:HA	53:DT:36:LEU:HD13	1.57	0.46
1:AA:831:A:C8	1:AA:839:G:C5	3.04	0.45
1:AA:1149:A:C8	1:AA:1150:C:C5	3.04	0.45
1:AA:1240:G:O2'	1:AA:1272:A:N1	2.48	0.45
1:AA:1356:G:OP2	31:A7:9:ARG:HD2	2.16	0.45
3:AC:211:ARG:HG2	3:AC:211:ARG:HH11	1.81	0.45
5:AE:34:VAL:HG13	5:AE:48:GLN:O	2.16	0.45
8:AH:69:ARG:HG3	8:AH:70:THR:H	1.81	0.45
32:A8:26:LYS:HB2	32:A8:44:LYS:O	2.15	0.45
34:BA:499:A:H4'	34:BA:500:G:H5'	1.98	0.45
34:BA:1314:C:OP2	52:BS:4:SER:OG	2.13	0.45
44:BK:120:ARG:HA	44:BK:121:PRO:HD3	1.63	0.45
52:BS:3:ARG:NH1	52:BS:10:PHE:HB2	2.31	0.45
57:BZ:127:LYS:HD3	57:BZ:128:TYR:HE2	1.81	0.45
1:CA:833:U:O2	13:CP:55:ARG:NH2	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1019:U:HO2'	1:CA:1021:A:H2	1.63	0.45
1:CA:1252:G:N3	18:CU:33:ARG:HG2	2.31	0.45
1:CA:1860:G:H8	1:CA:1860:G:OP2	1.99	0.45
1:CA:2256:G:C2'	1:CA:2257:U:H5'	2.46	0.45
3:CC:37:LYS:O	3:CC:38:PHE:HB3	2.17	0.45
6:CF:41:LEU:HD23	6:CF:41:LEU:HA	1.56	0.45
8:CH:15:VAL:HG23	8:CH:28:GLY:CA	2.43	0.45
10:CL:90:LYS:HE3	10:CL:90:LYS:HB3	1.84	0.45
34:DA:198:G:H1	34:DA:219:C:H42	1.64	0.45
34:DA:335:C:H2'	34:DA:336:C:C6	2.51	0.45
34:DA:833:U:H2'	34:DA:834:C:C6	2.51	0.45
34:DA:1205:U:H4'	36:DC:195:VAL:HG23	1.98	0.45
35:DB:104:ASN:O	35:DB:108:ILE:HG12	2.15	0.45
36:DC:63:ASN:HB2	36:DC:98:ASN:HB2	1.97	0.45
38:DE:19:MET:SD	38:DE:24:ARG:HB3	2.56	0.45
42:DI:116:LYS:NZ	42:DI:120:ARG:O	2.47	0.45
43:DJ:58:ASP:N	43:DJ:58:ASP:OD1	2.49	0.45
50:DQ:89:LEU:HA	50:DQ:89:LEU:HD23	1.64	0.45
57:DZ:-26:GLU:HA	57:DZ:-23:LEU:HD22	1.97	0.45
1:AA:242:C:O2'	63:AA:3940:HOH:O	2.20	0.45
1:AA:354:A:H2	1:AA:1255:A:C2'	2.29	0.45
1:AA:2734:A:C2	1:AA:2883:A:C5	3.04	0.45
2:AB:4:C:H2'	2:AB:5:C:O4'	2.16	0.45
4:AD:79:VAL:HG12	4:AD:113:VAL:HA	1.98	0.45
4:AD:159:ALA:HB1	4:AD:198:ASN:O	2.15	0.45
5:AE:80:GLU:C	5:AE:81:ILE:HD12	2.41	0.45
12:AO:34:THR:N	12:AO:37:ASP:OD2	2.45	0.45
25:A1:74:VAL:O	25:A1:77:ALA:N	2.47	0.45
34:BA:107:G:H2'	34:BA:108:G:O4'	2.16	0.45
34:BA:406:G:N3	34:BA:407:G:C8	2.84	0.45
34:BA:1234:C:H1'	34:BA:1364:U:O2	2.16	0.45
34:BA:1279:A:H5"	34:BA:1280:A:OP1	2.17	0.45
34:BA:1530:G:H4'	34:BA:1530:G:OP1	2.15	0.45
35:BB:145:LEU:O	35:BB:149:LEU:HB2	2.16	0.45
36:BC:11:ARG:NH2	36:BC:182:ILE:HD12	2.31	0.45
37:BD:127:THR:O	37:BD:147:ALA:N	2.48	0.45
37:BD:204:ILE:HG21	38:BE:98:THR:O	2.16	0.45
38:BE:144:THR:O	38:BE:148:VAL:HG23	2.16	0.45
40:BG:78:ARG:HD3	40:BG:79:ARG:H	1.81	0.45
46:BM:84:ILE:HG13	46:BM:85:GLY:HA2	1.97	0.45
50:BQ:10:VAL:HG12	50:BQ:53:LEU:HD12	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:BR:33:ASP:OD2	51:BR:36:ASN:HB2	2.16	0.45
57:BZ:153:MET:C	57:BZ:155:GLU:N	2.74	0.45
57:BZ:213:HIS:ND1	57:BZ:213:HIS:C	2.74	0.45
1:CA:205:G:HO2'	1:CA:206:U:P	2.39	0.45
1:CA:272(C):G:H2'	1:CA:272(D):G:O4'	2.16	0.45
1:CA:445:C:H2'	1:CA:446:G:O4'	2.16	0.45
1:CA:580:C:H2'	1:CA:581:C:C6	2.51	0.45
1:CA:657:U:H2'	1:CA:658:C:H6	1.79	0.45
1:CA:718:A:H3'	1:CA:719:C:C6	2.49	0.45
1:CA:2128:C:O4'	1:CA:2173:A:O2'	2.29	0.45
1:CA:2593:U:H2'	1:CA:2594:C:C6	2.51	0.45
2:CB:49:C:H2'	2:CB:50:G:C8	2.51	0.45
5:CE:60:ASN:OD1	5:CE:62:PRO:HD2	2.16	0.45
8:CH:46:GLU:HB2	8:CH:49:VAL:HG12	1.97	0.45
8:CH:121:ILE:HG12	8:CH:140:LYS:HD2	1.97	0.45
14:CQ:16:ARG:HG2	14:CQ:16:ARG:NH1	2.32	0.45
17:CT:96:ARG:CZ	17:CT:96:ARG:HB3	2.47	0.45
30:C6:10:LEU:HA	30:C6:22:ALA:HA	1.98	0.45
34:DA:142:G:C2	34:DA:143:A:C4	3.04	0.45
34:DA:403:C:H2'	34:DA:404:U:C6	2.49	0.45
34:DA:1107:C:N4	34:DA:1108:G:N7	2.64	0.45
35:DB:24:TRP:HZ3	35:DB:29:ALA:HB2	1.81	0.45
38:DE:68:GLU:HG2	38:DE:70:PRO:HD3	1.97	0.45
42:DI:11:LYS:HA	42:DI:108:VAL:HG13	1.97	0.45
57:DZ:31:ARG:HA	57:DZ:31:ARG:NE	2.31	0.45
57:DZ:326:THR:O	57:DZ:377:VAL:N	2.42	0.45
1:AA:651:U:O4	13:AP:81:GLN:NE2	2.47	0.45
1:AA:1249:A:N6	63:AA:4112:HOH:O	2.50	0.45
1:AA:1334:U:O4	15:AR:106:GLY:HA3	2.15	0.45
1:AA:1615:G:H4'	4:AD:59:LYS:HB3	1.99	0.45
1:AA:1660:A:P	1:AA:1660:A:H8	2.40	0.45
1:AA:2221:A:H5"	1:AA:2222:C:OP2	2.17	0.45
1:AA:2303:U:H2'	1:AA:2304:C:C6	2.52	0.45
1:AA:2383:G:O2'	30:A6:46:HIS:ND1	2.40	0.45
3:AC:20:VAL:O	3:AC:224:ARG:O	2.34	0.45
7:AG:44:GLY:HA2	7:AG:88:ILE:HG22	1.98	0.45
11:AN:87:LEU:O	11:AN:88:GLU:C	2.58	0.45
15:AR:55:ALA:HB2	15:AR:79:LEU:HD13	1.98	0.45
34:BA:395:C:O3'	57:BZ:349:LYS:NZ	2.49	0.45
34:BA:410:G:N2	34:BA:429:U:O2	2.50	0.45
34:BA:745:C:H1'	34:BA:836:G:O2'	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:BA:1112:C:C2	36:BC:178:LEU:HB2	2.52	0.45
34:BA:1236:A:H2'	34:BA:1237:C:C6	2.51	0.45
34:BA:1468:A:O5'	34:BA:1468:A:H8	1.99	0.45
39:BF:12:PRO:HG3	39:BF:57:GLN:O	2.16	0.45
1:CA:24:G:O2'	20:CW:78:GLU:O	2.23	0.45
1:CA:305:U:H6	1:CA:305:U:O5'	1.99	0.45
1:CA:500:G:N2	1:CA:502:A:H3'	2.31	0.45
1:CA:628:G:HO2'	1:CA:651:G:HO2'	1.65	0.45
1:CA:1214:A:H2'	1:CA:1215:G:O4'	2.17	0.45
1:CA:1488:G:H5'	1:CA:1489:U:OP2	2.15	0.45
1:CA:2125:G:P	3:CC:71:LYS:NZ	2.89	0.45
1:CA:2271:G:OP1	24:C0:18:ALA:HB1	2.16	0.45
1:CA:2412:A:H2'	1:CA:2413:G:O4'	2.16	0.45
2:CB:83:G:H5"	27:C3:52:HIS:CE1	2.52	0.45
2:CB:87:G:C2	2:CB:91:C:C2	3.04	0.45
3:CC:30:VAL:CG2	3:CC:31:LYS:N	2.78	0.45
8:CH:139:GLN:HG3	8:CH:140:LYS:N	2.32	0.45
34:DA:57:G:C2	34:DA:58:C:C2	3.05	0.45
34:DA:73:G:C6	34:DA:97:G:C6	3.04	0.45
34:DA:454:C:H3'	34:DA:455:C:C6	2.52	0.45
34:DA:623:C:C4	34:DA:624:C:C5	3.05	0.45
34:DA:945:G:C2	34:DA:1337:G:C2	3.04	0.45
34:DA:1168:A:H8	34:DA:1168:A:OP1	1.98	0.45
35:DB:71:VAL:HG12	35:DB:93:VAL:CG2	2.46	0.45
51:DR:56:THR:HB	51:DR:58:LEU:CD2	2.44	0.45
53:DT:43:LEU:HD13	53:DT:51:GLU:HB3	1.98	0.45
1:AA:217:A:OP1	13:AP:76:LYS:NZ	2.50	0.45
1:AA:646:A:OP2	13:AP:108:LYS:NZ	2.50	0.45
1:AA:1000:C:OP1	14:AQ:13:GLN:HA	2.17	0.45
1:AA:1044:C:P	18:AU:92:ARG:HH22	2.39	0.45
1:AA:1444:C:H2'	1:AA:1445:C:H6	1.82	0.45
1:AA:2298:A:OP1	30:A6:29:ASN:HB3	2.17	0.45
1:AA:2348:A:H61	24:A0:43:THR:CG2	2.29	0.45
3:AC:37:LYS:O	3:AC:38:PHE:HB3	2.17	0.45
5:AE:36:ARG:HH11	5:AE:85:ASN:ND2	2.14	0.45
16:AS:76:LYS:O	16:AS:80:LEU:HD13	2.17	0.45
18:AU:33:ARG:O	18:AU:37:GLU:HG3	2.16	0.45
31:A7:16:HIS:HB3	31:A7:44:PRO:HG2	1.97	0.45
33:A9:15:LYS:HD3	33:A9:26:ILE:HD11	1.98	0.45
34:BA:262:A:H2'	34:BA:263:A:C8	2.51	0.45
34:BA:373:A:C2	34:BA:482:A:C6	3.04	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:BA:604:G:C2	34:BA:635:G:C5	3.04	0.45
34:BA:642:A:N3	41:BH:113:SER:OG	2.39	0.45
34:BA:891:U:C2'	34:BA:892:A:H5'	2.45	0.45
34:BA:1026:G:H2'	34:BA:1026:G:N3	2.31	0.45
34:BA:1401:G:C2	34:BA:1402:C:H1'	2.51	0.45
42:BI:121:ARG:NH1	42:BI:122:ALA:O	2.49	0.45
46:BM:3:ARG:HG3	46:BM:4:ILE:H	1.81	0.45
51:BR:59:SER:H	51:BR:62:GLU:HG3	1.82	0.45
56:BX:31:G:C8	56:BX:32:5MC:HM53	2.50	0.45
57:BZ:115:GLU:O	57:BZ:118:SER:HB2	2.17	0.45
1:CA:723:G:H2'	1:CA:724:U:O4'	2.16	0.45
1:CA:1141:U:OP2	11:CN:63:THR:OG1	2.33	0.45
1:CA:1301:A:H2	1:CA:1626:G:N3	2.15	0.45
1:CA:2611:U:N3	29:C5:3:LYS:HG3	2.32	0.45
4:CD:68:LYS:C	4:CD:70:TRP:H	2.23	0.45
6:CF:123:LEU:HD12	6:CF:124:LEU:N	2.31	0.45
7:CG:2:PRO:HB2	7:CG:3:LEU:H	1.56	0.45
7:CG:64:THR:HG21	7:CG:92:VAL:HG11	1.97	0.45
7:CG:115:ARG:HB3	7:CG:115:ARG:CZ	2.47	0.45
7:CG:150:ASP:OD2	7:CG:153:ARG:NH1	2.49	0.45
10:CL:3:LYS:HE3	10:CL:3:LYS:HB3	1.78	0.45
10:CL:3:LYS:HE3	10:CL:29:GLN:HB3	1.99	0.45
22:CY:40:GLU:O	22:CY:42:VAL:HG23	2.17	0.45
22:CY:44:ILE:HA	22:CY:63:LYS:O	2.17	0.45
23:CZ:35:ARG:HA	23:CZ:35:ARG:HD2	1.69	0.45
34:DA:123:C:OP1	34:DA:311:C:O2'	2.30	0.45
34:DA:422:C:H4'	34:DA:423:G:C4	2.50	0.45
34:DA:878:G:C5'	41:DH:89:PRO:HG2	2.45	0.45
34:DA:964:A:N3	34:DA:969:A:O2'	2.49	0.45
34:DA:1192:C:OP2	36:DC:4:LYS:NZ	2.44	0.45
34:DA:1473:A:H2'	34:DA:1474:G:C8	2.51	0.45
38:DE:110:LEU:HB3	38:DE:115:VAL:HB	1.98	0.45
57:DZ:140:ASP:CG	62:DZ:704:GDP:HN21	2.25	0.45
1:AA:273:G:O2'	1:AA:274:U:H5"	2.17	0.45
1:AA:1474:C:O2'	1:AA:1475:G:H5'	2.16	0.45
1:AA:2074:G:H4'	5:AE:143:ASN:O	2.17	0.45
1:AA:2408:G:OP1	25:A1:25:LYS:NZ	2.26	0.45
3:AC:16:ASP:OD2	3:AC:19:LYS:HB2	2.17	0.45
14:AQ:43:THR:O	14:AQ:46:GLN:HB2	2.17	0.45
18:AU:104:GLN:O	18:AU:107:ALA:HB3	2.16	0.45
22:AY:6:HIS:H	22:AY:6:HIS:CD2	2.34	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:BA:49:U:O2'	34:BA:50:A:H2'	2.17	0.45
34:BA:100:C:H2'	34:BA:101:A:O4'	2.16	0.45
34:BA:153:C:N4	34:BA:169:C:H42	2.14	0.45
34:BA:453:A:C6	34:BA:454:C:C4	3.05	0.45
34:BA:738:C:C2	34:BA:739:C:C5	3.04	0.45
34:BA:1255:G:H2'	34:BA:1279:A:H62	1.82	0.45
34:BA:1260:C:O5'	34:BA:1284:C:H4'	2.16	0.45
34:BA:1316:G:O2'	47:BN:18:VAL:HG11	2.17	0.45
34:BA:1346:A:N6	34:BA:1375:A:OP2	2.45	0.45
34:BA:1346:A:C8	40:BG:10:ARG:NH2	2.84	0.45
34:BA:1392:G:N2	34:BA:1502:A:H8	2.14	0.45
35:BB:205:ASP:N	35:BB:205:ASP:OD1	2.47	0.45
37:BD:134:ASP:OD2	37:BD:135:LEU:HD13	2.16	0.45
39:BF:42:GLU:O	39:BF:44:GLY:N	2.49	0.45
42:BI:16:ARG:O	42:BI:64:THR:N	2.40	0.45
57:BZ:75:LYS:O	57:BZ:77:HIS:HD2	1.99	0.45
57:BZ:99:ARG:C	57:BZ:101:LEU:H	2.25	0.45
57:BZ:160:ARG:HD3	57:BZ:160:ARG:N	2.31	0.45
1:CA:118:A:O5'	1:CA:119:A:H5"	2.17	0.45
1:CA:1389:G:O2'	1:CA:1390:U:H5'	2.16	0.45
1:CA:1641:A:H2'	1:CA:1642:G:O4'	2.16	0.45
1:CA:2066:C:C2'	1:CA:2067:G:H5'	2.47	0.45
1:CA:2097:C:H2'	1:CA:2098:U:O4'	2.16	0.45
1:CA:2166:G:H3'	1:CA:2167:U:C5'	2.47	0.45
2:CB:114:C:H4'	16:CS:46:VAL:HG22	1.98	0.45
5:CE:135:HIS:NE2	63:CE:403:HOH:O	2.23	0.45
12:CO:25:LEU:HD12	12:CO:38:VAL:HG12	1.98	0.45
12:CO:111:PHE:O	12:CO:115:VAL:HG23	2.16	0.45
14:CQ:110:THR:HG23	14:CQ:113:GLN:HB2	1.98	0.45
19:CV:97:LYS:HD3	19:CV:97:LYS:HA	1.77	0.45
34:DA:303:A:H2'	34:DA:304:U:O4'	2.17	0.45
34:DA:690:G:H2'	34:DA:691:G:O4'	2.17	0.45
34:DA:939:G:H2'	34:DA:940:C:C6	2.52	0.45
39:DF:67:MET:HE1	39:DF:75:LEU:HG	1.99	0.45
48:DO:41:GLU:HA	48:DO:44:LYS:HD2	1.99	0.45
51:DR:33:ASP:OD2	51:DR:36:ASN:HB2	2.16	0.45
57:DZ:435:ASP:C	57:DZ:437:THR:H	2.25	0.45
1:AA:102:U:H3'	1:AA:103:C:H6	1.81	0.45
1:AA:459:A:N6	63:AA:4114:HOH:O	2.50	0.45
1:AA:669:A:H4'	1:AA:670:C:H5	1.82	0.45
1:AA:1322:A:C8	1:AA:1322:A:H5"	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:2094:G:H2'	1:AA:2095:C:O4'	2.16	0.45
1:AA:2227:G:O2'	1:AA:2228:G:OP1	2.31	0.45
1:AA:2283:G:OP1	24:A0:18:ALA:HB1	2.15	0.45
3:AC:7:ARG:HH22	3:AC:219:MET:HB2	1.82	0.45
5:AE:171:GLU:OE1	5:AE:185:LYS:NZ	2.47	0.45
7:AG:18:GLU:OE1	7:AG:22:ARG:HD3	2.17	0.45
16:AS:3:ARG:HD3	16:AS:4:LEU:H	1.81	0.45
16:AS:58:LEU:HD23	16:AS:58:LEU:HA	1.69	0.45
27:A3:5:LYS:HE3	27:A3:57:GLU:OE2	2.16	0.45
29:A5:58:LEU:HD23	29:A5:59:GLU:O	2.16	0.45
34:BA:402:G:C6	34:BA:403:C:C4	3.05	0.45
34:BA:432:A:C8	34:BA:433:C:C5	3.04	0.45
34:BA:944:G:C6	34:BA:1337:G:H2'	2.51	0.45
34:BA:1280:A:H5'	43:BJ:40:LEU:HD22	1.99	0.45
36:BC:60:ALA:HB3	36:BC:63:ASN:OD1	2.16	0.45
37:BD:12:CYS:SG	37:BD:19:LEU:HB2	2.57	0.45
57:BZ:-27:THR:O	57:BZ:-26:GLU:C	2.60	0.45
57:BZ:103:GLY:HA3	57:BZ:280:LEU:HD13	1.98	0.45
57:BZ:109:ASP:HB3	57:BZ:112:GLN:HB3	1.98	0.45
1:CA:385:C:O2'	1:CA:388:G:N2	2.49	0.45
1:CA:464:U:C2	1:CA:788:A:C6	3.05	0.45
1:CA:1449:A:N7	1:CA:1450:G:C8	2.84	0.45
1:CA:1851:U:C4	1:CA:1852:C:C4	3.05	0.45
1:CA:2544:G:H2'	1:CA:2545:G:O4'	2.16	0.45
1:CA:2718:G:C6	1:CA:2719:G:C5	3.05	0.45
3:CC:48:LEU:HD23	3:CC:59:VAL:HG21	1.98	0.45
8:CH:164:TYR:HB2	8:CH:167:GLU:HB2	1.99	0.45
23:CZ:144:LEU:HD11	23:CZ:150:LEU:HD23	1.99	0.45
34:DA:36:C:OP1	45:DL:123:LYS:NZ	2.49	0.45
34:DA:975:A:N6	43:DJ:48:THR:HB	2.32	0.45
34:DA:1316:G:N7	52:DS:7:LYS:NZ	2.65	0.45
38:DE:127:ASN:O	38:DE:131:ILE:HG12	2.16	0.45
44:DK:44:SER:H	44:DK:47:VAL:HB	1.82	0.45
47:DN:23:ARG:CZ	47:DN:30:ALA:HB2	2.47	0.45
50:DQ:9:VAL:HG21	50:DQ:84:LEU:HD13	1.98	0.45
57:DZ:-6:ARG:O	57:DZ:-2:ALA:HB3	2.16	0.45
57:DZ:147:TRP:CD1	57:DZ:147:TRP:H	2.32	0.45
1:AA:831:A:OP2	63:AA:3943:HOH:O	2.21	0.45
1:AA:1462:G:N1	1:AA:1629:C:N3	2.38	0.45
1:AA:1604:C:H2'	1:AA:1605:A:C2	2.52	0.45
1:AA:1839:U:O5'	1:AA:1839:U:H6	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:2036:A:H2'	1:AA:2037:A:C8	2.51	0.45
1:AA:2356:U:OP1	30:A6:37:ARG:HD3	2.17	0.45
1:AA:2444:A:C2	25:A1:33:LYS:HB3	2.52	0.45
1:AA:2619:G:H4'	63:AA:4509:HOH:O	2.16	0.45
4:AD:127:VAL:HA	4:AD:193:VAL:HG22	1.98	0.45
4:AD:260:ARG:CZ	4:AD:264:LYS:HD3	2.47	0.45
7:AG:3:LEU:HD13	28:A4:25:TYR:CZ	2.51	0.45
15:AR:36:THR:O	15:AR:111:LEU:HA	2.15	0.45
23:AZ:99:TYR:CZ	23:AZ:125:LEU:HD13	2.52	0.45
26:A2:56:GLN:O	26:A2:59:ARG:N	2.49	0.45
34:BA:243:A:C2	34:BA:246:A:C8	3.05	0.45
34:BA:438:G:H4'	37:BD:123:HIS:ND1	2.32	0.45
34:BA:900:A:H2'	34:BA:901:A:C8	2.52	0.45
34:BA:1005:A:N1	34:BA:1025:U:H1'	2.31	0.45
34:BA:1288:A:N1	34:BA:1371:G:H1'	2.32	0.45
35:BB:118:LEU:HD13	35:BB:142:LEU:HB2	1.99	0.45
35:BB:126:GLU:HB3	35:BB:127:ILE:H	1.63	0.45
40:BG:88:PRO:HG2	40:BG:152:ALA:HB2	1.98	0.45
41:BH:103:VAL:HG21	41:BH:109:ILE:C	2.41	0.45
42:BI:99:LEU:HB3	42:BI:101:PHE:CE1	2.52	0.45
43:BJ:31:GLY:HA2	43:BJ:32:ALA:HA	1.60	0.45
46:BM:95:GLY:O	46:BM:110:ARG:HG3	2.17	0.45
52:BS:50:ALA:HB1	52:BS:57:HIS:HB3	1.97	0.45
57:BZ:12:LEU:O	57:BZ:282:SER:HA	2.17	0.45
1:CA:242:G:N2	1:CA:254:G:H2'	2.31	0.45
1:CA:288:C:O2'	1:CA:289:A:H5'	2.17	0.45
1:CA:842:G:H2'	1:CA:843:G:O4'	2.17	0.45
1:CA:1384:A:N3	1:CA:1405:U:H1'	2.32	0.45
1:CA:2121:G:O4'	3:CC:168:LYS:CE	2.64	0.45
1:CA:2557:G:H2'	1:CA:2558:C:C6	2.52	0.45
1:CA:2698:U:H2'	1:CA:2699:C:C6	2.51	0.45
5:CE:32:PRO:HA	5:CE:90:THR:HA	1.98	0.45
6:CF:117:ARG:HD3	6:CF:117:ARG:HA	1.76	0.45
12:CO:71:ARG:HB2	12:CO:75:SER:O	2.16	0.45
34:DA:321:A:C2	34:DA:333:G:C2	3.05	0.45
34:DA:1316:G:H4'	47:DN:18:VAL:HG11	1.98	0.45
34:DA:1321:C:H4'	46:DM:87:TYR:CE2	2.51	0.45
35:DB:127:ILE:HG12	35:DB:128:GLU:H	1.82	0.45
35:DB:216:SER:C	35:DB:218:ALA:H	2.23	0.45
37:DD:155:LEU:HD23	37:DD:156:GLU:H	1.82	0.45
40:DG:104:LEU:HD13	40:DG:104:LEU:HA	1.85	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:DN:26:ARG:HD3	47:DN:43:CYS:SG	2.56	0.45
57:DZ:28:THR:O	57:DZ:32:ILE:HG13	2.17	0.45
57:DZ:238:THR:O	57:DZ:241:GLU:HG2	2.16	0.45
1:AA:580:U:O2	11:AN:45:ASN:HB2	2.17	0.45
1:AA:1258:A:N3	1:AA:1284:G:O2'	2.49	0.45
1:AA:2614:A:N6	63:AA:3996:HOH:O	2.35	0.45
1:AA:2711:C:O2'	1:AA:2712:C:H5'	2.17	0.45
1:AA:2765:C:O5'	1:AA:2765:C:H6	2.00	0.45
1:AA:2826:C:O3'	15:AR:99:LYS:NZ	2.50	0.45
4:AD:180:GLY:CA	4:AD:275:LYS:HD3	2.46	0.45
8:AH:9:ILE:HD12	8:AH:50:VAL:HG12	1.98	0.45
17:AT:128:GLU:O	17:AT:130:ALA:N	2.50	0.45
20:AW:55:ALA:O	20:AW:58:ALA:HB3	2.17	0.45
27:A3:23:LEU:HD12	27:A3:28:LEU:HD12	1.98	0.45
27:A3:28:LEU:HD21	27:A3:35:ARG:HB2	1.99	0.45
32:A8:34:TRP:CG	32:A8:35:GLN:N	2.84	0.45
34:BA:300:A:H1'	34:BA:565:U:O2	2.17	0.45
34:BA:582:U:C2	34:BA:760:G:C6	3.04	0.45
34:BA:626:U:C2	34:BA:627:G:C8	3.05	0.45
34:BA:983:A:H5'	34:BA:984:C:OP2	2.17	0.45
34:BA:1276:G:H8	34:BA:1276:G:O5'	1.99	0.45
34:BA:1323:G:H4'	34:BA:1363:C:C2	2.52	0.45
35:BB:18:GLY:HA3	35:BB:41:ILE:HA	1.97	0.45
35:BB:37:ASN:N	35:BB:37:ASN:OD1	2.50	0.45
35:BB:189:ASP:OD1	35:BB:189:ASP:N	2.45	0.45
37:BD:102:ASP:HB3	37:BD:121:VAL:HG21	1.98	0.45
38:BE:110:LEU:CD1	38:BE:118:ILE:HD13	2.46	0.45
42:BI:53:VAL:HG21	42:BI:92:TYR:CE1	2.52	0.45
43:BJ:17:ASP:O	43:BJ:21:GLN:HB2	2.17	0.45
51:BR:39:VAL:O	51:BR:42:ARG:HB2	2.16	0.45
57:BZ:-66:MET:N	57:BZ:-46:VAL:O	2.42	0.45
57:BZ:181:LEU:HD23	57:BZ:182:ARG:HG3	1.98	0.45
1:CA:42:G:C2	1:CA:43:A:H1'	2.52	0.45
1:CA:588:U:O4	1:CA:670:A:H1'	2.17	0.45
1:CA:1140:C:OP1	11:CN:24:GLY:N	2.45	0.45
1:CA:1428:C:C5	1:CA:1569:A:H5"	2.51	0.45
1:CA:1659:U:C4	1:CA:1660:C:C5	3.05	0.45
1:CA:2445:G:OP1	6:CF:74:ARG:NH2	2.48	0.45
3:CC:30:VAL:CG2	3:CC:31:LYS:H	2.27	0.45
18:CU:65:ILE:HG22	18:CU:76:TYR:HD2	1.82	0.45
19:CV:24:LYS:HA	19:CV:92:THR:OG1	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:CX:92:LEU:C	21:CX:94:GLY:N	2.72	0.45
23:CZ:99:TYR:CE1	23:CZ:125:LEU:HB2	2.51	0.45
33:C9:4:ARG:O	33:C9:36:GLN:HA	2.17	0.45
34:DA:401:C:OP2	37:DD:73:ARG:NH2	2.50	0.45
34:DA:547:A:N3	34:DA:548:G:H1'	2.32	0.45
34:DA:584:G:OP1	50:DQ:91:ARG:NH2	2.50	0.45
34:DA:1003:G:H2'	34:DA:1004:A:C4'	2.47	0.45
34:DA:1427:U:H2'	34:DA:1428:A:H8	1.80	0.45
35:DB:27:LYS:HG3	35:DB:194:PRO:CD	2.45	0.45
37:DD:72:GLU:O	37:DD:76:ARG:HB3	2.17	0.45
38:DE:50:GLU:HB2	38:DE:53:LEU:HD13	1.99	0.45
43:DJ:55:LYS:HE3	43:DJ:56:HIS:NE2	2.31	0.45
44:DK:59:TYR:CE2	44:DK:63:LEU:HD11	2.52	0.45
47:DN:29:ARG:NH1	47:DN:42:ILE:HD11	2.31	0.45
53:DT:44:ALA:HB3	53:DT:91:LEU:HD12	1.98	0.45
57:DZ:256:THR:O	57:DZ:258:VAL:HG23	2.17	0.45
57:DZ:608:VAL:O	57:DZ:644:ARG:HA	2.17	0.45
1:AA:762:G:C2	48:BO:56:LEU:HD21	2.52	0.45
1:AA:1888:G:O5'	1:AA:1888:G:H8	2.00	0.45
1:AA:1921:G:H2'	1:AA:1921:G:N3	2.32	0.45
1:AA:2098:U:OP2	1:AA:2250:G:N2	2.44	0.45
3:AC:48:LEU:HD23	3:AC:59:VAL:HG21	1.98	0.45
4:AD:65:ILE:HB	4:AD:67:PHE:CE2	2.52	0.45
9:AK:25:PHE:O	9:AK:85:ASP:N	2.46	0.45
10:AL:17:ALA:HB1	10:AL:38:VAL:HG22	1.99	0.45
10:AL:88:ALA:O	10:AL:90:LYS:N	2.50	0.45
17:AT:5:ALA:O	17:AT:6:LEU:C	2.60	0.45
23:AZ:5:LEU:HD22	23:AZ:6:LYS:O	2.17	0.45
25:A1:95:LEU:HD12	25:A1:98:LEU:CD1	2.47	0.45
34:BA:158:G:H2'	34:BA:159:G:C8	2.52	0.45
34:BA:357:G:C2	34:BA:358:U:C5	3.05	0.45
34:BA:918:A:H2'	34:BA:919:A:O4'	2.16	0.45
34:BA:1240:U:P	40:BG:116:ALA:H	2.40	0.45
35:BB:18:GLY:O	35:BB:19:HIS:HB3	2.15	0.45
36:BC:175:LEU:HD21	36:BC:201:TYR:CD2	2.52	0.45
43:BJ:47:PHE:CE1	47:BN:37:PHE:HE2	2.35	0.45
49:BP:69:THR:HA	49:BP:72:ARG:HB2	1.98	0.45
50:BQ:87:LYS:HD3	50:BQ:87:LYS:HA	1.70	0.45
56:BX:29:G:C2	56:BX:42:G:N3	2.85	0.45
56:BX:72:A:H2'	56:BX:73:A:O4'	2.17	0.45
57:BZ:24:GLY:O	57:BZ:25:LYS:C	2.60	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:82:G:N1	1:CA:103:A:OP2	2.36	0.45
1:CA:1591:G:C6	1:CA:1592:C:C4	3.05	0.45
1:CA:1813:G:H1'	4:CD:50:THR:OG1	2.17	0.45
1:CA:2177:C:H5'	3:CC:45:HIS:HB2	1.99	0.45
5:CE:108:SER:O	5:CE:162:ALA:HA	2.17	0.45
11:CN:39:ARG:HB3	11:CN:41:ASP:OD1	2.17	0.45
15:CR:18:LEU:O	15:CR:18:LEU:HD22	2.17	0.45
16:CS:61:ASN:O	16:CS:65:VAL:HG23	2.17	0.45
22:CY:43:ASN:C	22:CY:43:ASN:HD22	2.24	0.45
28:C4:41:PRO:HA	28:C4:44:THR:HG22	1.98	0.45
34:DA:394:G:H2'	34:DA:395:C:C6	2.52	0.45
34:DA:608:A:H2'	34:DA:609:A:O4'	2.16	0.45
34:DA:977:A:O2'	34:DA:979:C:OP2	2.33	0.45
34:DA:1289:A:H3'	34:DA:1290:G:H8	1.82	0.45
34:DA:1289:A:N1	34:DA:1371:G:O2'	2.38	0.45
35:DB:116:GLU:HA	35:DB:119:GLU:HB2	1.99	0.45
38:DE:78:HIS:HE2	38:DE:142:LEU:HD23	1.82	0.45
57:DZ:92:ILE:HG21	57:DZ:437:THR:CB	2.46	0.45
57:DZ:160:ARG:HG2	57:DZ:254:LYS:O	2.17	0.45
57:DZ:637:ARG:C	57:DZ:639:ASN:N	2.74	0.45
1:AA:81:G:H8	1:AA:81:G:O5'	2.00	0.45
1:AA:261:A:N1	1:AA:291:G:O2'	2.47	0.45
1:AA:475:A:H2'	1:AA:476:G:H5'	1.99	0.45
1:AA:880:U:O2	13:AP:55:ARG:NH2	2.50	0.45
1:AA:905:U:O2	1:AA:2280:A:H2'	2.17	0.45
1:AA:927:G:H8	1:AA:927:G:OP2	2.00	0.45
1:AA:2228:G:H2'	1:AA:2229:A:C2	2.52	0.45
1:AA:2331:G:N2	16:AS:3:ARG:HG2	2.32	0.45
4:AD:3:VAL:HG13	4:AD:17:THR:HB	1.99	0.45
5:AE:119:ARG:HG2	5:AE:160:TYR:CG	2.52	0.45
10:AL:55:VAL:CG2	10:AL:67:PHE:HB2	2.47	0.45
34:BA:345:C:H4'	34:BA:346:G:C2	2.52	0.45
34:BA:960:U:C5	34:BA:1225:A:C8	3.04	0.45
34:BA:1316:G:H4'	47:BN:18:VAL:HG13	1.97	0.45
37:BD:3:ARG:HH21	37:BD:118:ARG:HD3	1.82	0.45
37:BD:167:GLY:N	37:BD:168:ARG:HH12	2.07	0.45
44:BK:115:PRO:C	44:BK:117:ASN:H	2.25	0.45
48:BO:39:LEU:HD13	48:BO:56:LEU:HB2	1.98	0.45
49:BP:40:ASP:HA	49:BP:41:PRO:HD2	1.64	0.45
55:BV:17:U:O2'	55:BV:18:G:H5'	2.17	0.45
57:BZ:6:GLU:C	57:BZ:8:ASP:H	2.24	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:183:C:H1'	1:CA:433:C:H1'	1.98	0.45
1:CA:554:U:C4	1:CA:555:U:C4	3.05	0.45
1:CA:1046:A:H3'	1:CA:1047:G:C5'	2.46	0.45
1:CA:1465:G:N1	1:CA:1466:G:C5	2.85	0.45
1:CA:2290:G:C2	1:CA:2343:C:O2	2.70	0.45
3:CC:22:THR:HG23	3:CC:25:GLU:OE1	2.17	0.45
3:CC:176:VAL:O	3:CC:176:VAL:HG12	2.15	0.45
4:CD:125:ILE:HB	39:DF:81:ILE:HD11	1.99	0.45
7:CG:80:PHE:O	7:CG:82:LEU:N	2.50	0.45
11:CN:58:ASP:OD1	11:CN:125:GLY:N	2.48	0.45
15:CR:17:ARG:O	15:CR:20:LEU:HB3	2.17	0.45
26:C2:21:LEU:HB3	26:C2:64:LEU:HD23	1.99	0.45
34:DA:860:A:N6	34:DA:861:G:C2	2.85	0.45
34:DA:1065:U:H4'	34:DA:1066:C:H5'	1.99	0.45
34:DA:1183:A:H1'	34:DA:1184:G:OP1	2.17	0.45
34:DA:1252:A:H2'	34:DA:1253:G:O4'	2.16	0.45
41:DH:20:TYR:HD2	41:DH:65:TYR:CD2	2.35	0.45
42:DI:94:ALA:C	42:DI:96:LEU:H	2.25	0.45
43:DJ:6:ILE:HB	43:DJ:72:VAL:HG23	1.99	0.45
45:DL:28:LYS:N	45:DL:29:GLY:HA2	2.31	0.45
45:DL:114:LYS:NZ	45:DL:125:PRO:HG2	2.32	0.45
48:DO:53:HIS:O	48:DO:56:LEU:N	2.49	0.45
49:DP:66:PRO:HB2	49:DP:71:ARG:HB3	1.98	0.45
1:AA:610:C:OP2	13:AP:21:ARG:NH2	2.50	0.44
1:AA:973:G:H2'	1:AA:974:G:O4'	2.17	0.44
1:AA:1508:G:C5	1:AA:1509:C:C5	3.05	0.44
1:AA:1754:G:H2'	1:AA:1755:C:C6	2.52	0.44
1:AA:2149:G:H2'	1:AA:2150:C:C6	2.52	0.44
1:AA:2376:C:H2'	1:AA:2377:G:O4'	2.17	0.44
5:AE:116:VAL:HG13	5:AE:122:PHE:CB	2.47	0.44
6:AF:136:THR:HA	6:AF:166:ALA:O	2.17	0.44
6:AF:178:PRO:HB2	6:AF:201:VAL:CG2	2.47	0.44
10:AL:108:ALA:HB2	10:AL:127:ILE:HG13	2.00	0.44
12:AO:64:ARG:HD3	17:AT:70:VAL:HG11	1.99	0.44
13:AP:128:HIS:CD2	13:AP:148:LEU:HD21	2.52	0.44
34:BA:461:A:C5	34:BA:471:G:C6	3.04	0.44
34:BA:1015:A:H2'	34:BA:1016:A:H8	1.81	0.44
34:BA:1183:A:H3'	34:BA:1184:G:C5'	2.47	0.44
34:BA:1226:C:H2'	46:BM:103:THR:HB	1.97	0.44
35:BB:140:HIS:O	35:BB:144:ARG:HB3	2.17	0.44
38:BE:76:ILE:HD12	38:BE:93:PRO:HG3	1.97	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:BH:36:LEU:HD23	41:BH:36:LEU:HA	1.71	0.44
48:BO:31:LEU:HD23	48:BO:31:LEU:HA	1.66	0.44
57:BZ:-10:ARG:HB2	57:BZ:-10:ARG:NH1	2.31	0.44
57:BZ:2:LYS:O	57:BZ:6:GLU:HG3	2.16	0.44
1:CA:301:G:C4	1:CA:302:C:C5	3.05	0.44
1:CA:1312:U:H4'	1:CA:1313:U:O5'	2.16	0.44
1:CA:2056:G:H1	29:C5:3:LYS:HB3	1.82	0.44
1:CA:2584:U:H2'	1:CA:2585:U:H2'	1.99	0.44
1:CA:2632:A:O2'	1:CA:2811:G:O2'	2.15	0.44
1:CA:2815:C:H2'	1:CA:2816:C:O4'	2.17	0.44
2:CB:3:C:H2'	2:CB:4:C:C6	2.52	0.44
4:CD:8:PRO:HB3	4:CD:14:ARG:HB2	1.98	0.44
4:CD:16:MET:HE1	4:CD:208:LYS:HE2	1.98	0.44
4:CD:158:ALA:O	4:CD:161:THR:HG23	2.17	0.44
5:CE:170:LEU:HD23	5:CE:184:VAL:HG22	1.99	0.44
11:CN:128:HIS:HA	11:CN:129:PRO:HD3	1.69	0.44
17:CT:83:ILE:HD13	17:CT:86:ILE:HD11	1.98	0.44
17:CT:125:ARG:O	17:CT:129:ARG:HG3	2.17	0.44
34:DA:644:G:H4'	41:DH:92:ARG:NH2	2.32	0.44
34:DA:1095:U:OP1	34:DA:1108:G:N2	2.29	0.44
34:DA:1188:A:OP1	42:DI:114:TYR:HE2	2.00	0.44
36:DC:43:LEU:HD21	36:DC:91:LEU:HD13	1.98	0.44
42:DI:67:GLY:O	42:DI:73:GLN:NE2	2.37	0.44
42:DI:71:SER:HA	42:DI:74:ILE:HD12	1.98	0.44
50:DQ:29:HIS:CD2	50:DQ:30:PRO:HD2	2.52	0.44
50:DQ:45:HIS:HB3	50:DQ:72:ARG:HG3	2.00	0.44
57:DZ:356:LEU:HD12	57:DZ:365:GLU:HA	2.00	0.44
1:AA:25:U:H2'	1:AA:26:G:O4'	2.17	0.44
1:AA:1232:G:H5"	19:AV:81:TYR:CE1	2.52	0.44
3:AC:39:ASP:O	3:AC:178:LYS:HE3	2.17	0.44
5:AE:143:ASN:HD22	5:AE:147:PRO:CD	2.31	0.44
7:AG:116:ASP:N	7:AG:116:ASP:OD1	2.51	0.44
13:AP:114:ILE:O	13:AP:115:LEU:HD23	2.17	0.44
17:AT:28:VAL:O	17:AT:46:GLU:HA	2.17	0.44
27:A3:38:GLU:HB3	27:A3:40:THR:HG23	1.98	0.44
28:A4:59:PHE:HE1	52:BS:64:GLU:HB3	1.82	0.44
34:BA:108:G:C6	53:BT:15:ARG:HD2	2.52	0.44
34:BA:273:A:H2'	34:BA:274:A:O4'	2.17	0.44
34:BA:429:U:H3'	37:BD:9:CYS:SG	2.56	0.44
34:BA:515:G:C6	34:BA:516:U:N3	2.85	0.44
37:BD:15:GLU:HG3	37:BD:63:LYS:HD3	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:BE:79:GLU:H	38:BE:79:GLU:HG3	1.50	0.44
41:BH:81:HIS:HB2	41:BH:138:TRP:OXT	2.18	0.44
48:BO:35:ARG:NH2	48:BO:59:MET:HE2	2.33	0.44
49:BP:43:LYS:HG2	49:BP:48:TRP:CE2	2.52	0.44
57:BZ:132:ARG:H	57:BZ:132:ARG:HD2	1.82	0.44
57:BZ:165:GLN:HE21	57:BZ:260:LEU:HG	1.82	0.44
1:CA:72:U:OP2	21:CX:1:MET:N	2.50	0.44
1:CA:1143:A:N6	11:CN:28:THR:HG21	2.32	0.44
1:CA:1461:G:H2'	1:CA:1462:C:H6	1.82	0.44
1:CA:2228:G:C5	1:CA:2229:C:C4	3.05	0.44
1:CA:2461:C:C4	1:CA:2462:U:C4	3.06	0.44
1:CA:2522:U:C2	1:CA:2765:A:N7	2.86	0.44
2:CB:89:G:C6	2:CB:90:A:N6	2.86	0.44
3:CC:16:ASP:OD2	3:CC:19:LYS:HB2	2.17	0.44
4:CD:130:ALA:C	4:CD:131:LEU:HD12	2.42	0.44
5:CE:92:THR:O	5:CE:95:ILE:HG23	2.16	0.44
10:CL:72:PRO:HA	10:CL:73:PRO:HD3	1.88	0.44
15:CR:63:ARG:HA	15:CR:80:PHE:CZ	2.52	0.44
18:CU:76:TYR:C	18:CU:76:TYR:CD1	2.95	0.44
20:CW:34:ASN:ND2	29:C5:39:MET:HG3	2.33	0.44
21:CX:17:ALA:O	21:CX:20:GLY:N	2.37	0.44
32:C8:14:VAL:HG11	32:C8:58:ILE:HG21	1.99	0.44
34:DA:401:C:H1'	34:DA:622:A:H1'	1.98	0.44
34:DA:434:U:H2'	34:DA:435:C:C6	2.52	0.44
34:DA:920:U:C2	34:DA:921:U:C5	3.04	0.44
34:DA:1273:G:H3'	34:DA:1274:G:C8	2.52	0.44
38:DE:87:SER:HB3	38:DE:131:ILE:HD13	1.99	0.44
44:DK:34:ASP:HB2	44:DK:35:PRO:HD2	2.00	0.44
44:DK:93:GLN:O	44:DK:93:GLN:HG3	2.17	0.44
44:DK:120:ARG:HA	44:DK:121:PRO:HD3	1.77	0.44
48:DO:71:GLN:HB2	48:DO:78:TYR:CD2	2.52	0.44
51:DR:45:SER:HA	51:DR:51:LEU:HD21	2.00	0.44
53:DT:76:ALA:O	53:DT:80:ARG:HB2	2.17	0.44
57:DZ:31:ARG:O	57:DZ:34:TYR:HB3	2.17	0.44
1:AA:313:A:H2'	1:AA:314:G:O4'	2.17	0.44
1:AA:854:U:OP2	13:AP:41:ARG:NH2	2.50	0.44
1:AA:970:C:H2'	1:AA:971:C:C6	2.52	0.44
1:AA:1713:G:O2'	1:AA:1714:G:H5'	2.17	0.44
1:AA:2143:G:N2	3:AC:169:THR:CB	2.72	0.44
1:AA:2298:A:H2	30:A6:25:LYS:HB2	1.82	0.44
1:AA:2316:G:H22	1:AA:2324:U:H3	1.66	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:2483:C:H5'	1:AA:2484:G:OP2	2.17	0.44
1:AA:2507:G:O2'	14:AQ:83:MET:HE3	2.17	0.44
12:AO:120:GLU:OE2	17:AT:65:LYS:NZ	2.48	0.44
14:AQ:37:LEU:HD23	14:AQ:37:LEU:HA	1.75	0.44
23:AZ:111:VAL:C	23:AZ:113:ALA:N	2.75	0.44
27:A3:59:VAL:O	27:A3:60:GLU:HG2	2.17	0.44
29:A5:35:GLU:HG3	29:A5:51:TYR:CD2	2.53	0.44
32:A8:42:ARG:HD2	63:A8:5107:HOH:O	2.17	0.44
34:BA:189:G:H2'	34:BA:189(A):C:O4'	2.17	0.44
34:BA:397:A:H3'	34:BA:397:A:N3	2.32	0.44
34:BA:501:C:H1'	34:BA:549:C:H1'	1.99	0.44
34:BA:894:G:C6	34:BA:895:G:C5	3.05	0.44
34:BA:1127:G:H1'	34:BA:1280:A:C6	2.52	0.44
35:BB:81:VAL:HG12	35:BB:215:LEU:CD1	2.47	0.44
35:BB:185:ILE:HG23	35:BB:199:TYR:HB2	1.99	0.44
49:BP:49:LEU:HD12	49:BP:50:LYS:N	2.32	0.44
51:BR:38:GLU:OE2	51:BR:41:LYS:HD3	2.16	0.44
57:BZ:201:ILE:HG22	57:BZ:202:PRO:O	2.17	0.44
1:CA:2178:C:O2	3:CC:169:THR:HG21	2.18	0.44
1:CA:2839:G:C6	1:CA:2840:C:N3	2.85	0.44
3:CC:179:ALA:O	3:CC:180:SER:O	2.35	0.44
10:CL:3:LYS:HB3	10:CL:4:VAL:H	1.71	0.44
17:CT:6:LEU:HA	17:CT:6:LEU:HD13	1.68	0.44
17:CT:13:ARG:HB3	17:CT:13:ARG:NH1	2.32	0.44
21:CX:29:TRP:CZ3	21:CX:78:LYS:HD3	2.52	0.44
22:CY:76:CYS:SG	22:CY:99:CYS:HB2	2.58	0.44
23:CZ:109:ALA:N	23:CZ:144:LEU:O	2.51	0.44
25:C1:3:LYS:HB2	25:C1:61:ARG:HH11	1.82	0.44
34:DA:411:A:C5	34:DA:413:G:N3	2.86	0.44
34:DA:707:C:H2'	34:DA:708:C:C6	2.52	0.44
34:DA:1303:C:N4	34:DA:1304:G:C6	2.86	0.44
36:DC:182:ILE:HG12	36:DC:203:PHE:HD1	1.82	0.44
37:DD:146:ILE:N	37:DD:146:ILE:HD12	2.33	0.44
41:DH:26:VAL:HG22	41:DH:59:LEU:HB2	2.00	0.44
57:DZ:20:HIS:CE1	57:DZ:116:PRO:O	2.71	0.44
1:AA:594:A:O2'	19:AV:78:LYS:HE2	2.17	0.44
1:AA:2054:G:O2'	5:AE:145:LYS:HE2	2.16	0.44
1:AA:2377:G:O6	32:A8:39:LYS:HE3	2.17	0.44
1:AA:2880:C:H2'	1:AA:2881:C:O4'	2.18	0.44
3:AC:179:ALA:O	3:AC:180:SER:O	2.35	0.44
5:AE:54:GLN:NE2	5:AE:76:ARG:HG2	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:AH:140:LYS:HB2	8:AH:140:LYS:HE3	1.69	0.44
13:AP:81:GLN:OE1	13:AP:106:LEU:HD23	2.17	0.44
34:BA:542:G:P	37:BD:10:ARG:HH22	2.34	0.44
34:BA:580:U:H5"	48:BO:58:MET:HG2	1.99	0.44
38:BE:113:ALA:HB3	38:BE:115:VAL:HG23	1.99	0.44
42:BI:95:LYS:O	42:BI:96:LEU:HD23	2.17	0.44
48:BO:87:ILE:HG22	48:BO:88:ARG:N	2.32	0.44
57:BZ:-20:LEU:C	57:BZ:-18:ALA:H	2.25	0.44
57:BZ:24:GLY:HA2	62:BZ:801:GDP:PA	2.57	0.44
57:BZ:251:ILE:HG12	57:BZ:281:PRO:HG3	1.98	0.44
57:BZ:303:PRO:O	57:BZ:305:PRO:HD3	2.17	0.44
1:CA:963:U:H6	1:CA:963:U:O5'	2.00	0.44
1:CA:972:G:C6	1:CA:973:A:C6	3.06	0.44
1:CA:1471:A:H5'	1:CA:1472:A:OP2	2.17	0.44
1:CA:2792:G:C6	1:CA:2805:G:C6	3.05	0.44
2:CB:91:C:OP1	14:CQ:16:ARG:HG2	2.17	0.44
4:CD:37:LEU:HD13	4:CD:87:ASN:ND2	2.32	0.44
6:CF:196:LEU:HD23	6:CF:196:LEU:HA	1.83	0.44
7:CG:114:ILE:HG12	7:CG:136:ARG:HH22	1.82	0.44
19:CV:82:ARG:O	19:CV:83:ARG:HD3	2.17	0.44
20:CW:19:LEU:HB3	29:C5:25:LEU:HD11	2.00	0.44
20:CW:86:LEU:HD13	20:CW:96:ILE:HD11	2.00	0.44
23:CZ:117:LEU:HD12	23:CZ:174:VAL:HG22	1.99	0.44
34:DA:242:C:H2'	34:DA:243:A:H5'	2.00	0.44
37:DD:94:LEU:HD23	37:DD:94:LEU:HA	1.85	0.44
44:DK:32:ILE:O	44:DK:40:ILE:N	2.48	0.44
57:DZ:179:ASP:OD2	57:DZ:182:ARG:HD2	2.16	0.44
1:AA:501:U:H1'	1:AA:534:C:C2	2.52	0.44
1:AA:611:U:H2'	1:AA:612:C:H6	1.76	0.44
1:AA:756:U:H2'	1:AA:757:G:C8	2.53	0.44
1:AA:1446:G:H2'	1:AA:1447:G:C8	2.52	0.44
1:AA:2108:U:H2'	1:AA:2109:G:C8	2.53	0.44
1:AA:2575:U:O2'	1:AA:2577:A:N7	2.47	0.44
5:AE:96:PHE:O	5:AE:175:VAL:HG11	2.18	0.44
5:AE:144:ARG:HB3	5:AE:145:LYS:H	1.26	0.44
8:AH:15:VAL:HB	8:AH:27:LYS:O	2.17	0.44
10:AL:30:HIS:HB2	10:AL:32:ALA:HB2	1.99	0.44
31:A7:16:HIS:CB	31:A7:44:PRO:HG2	2.48	0.44
34:BA:153:C:H42	34:BA:169:C:N4	2.15	0.44
34:BA:973:G:OP1	43:BJ:57:LYS:HE3	2.16	0.44
34:BA:1286:A:H2'	34:BA:1287:A:H4'	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:BC:157:ILE:HG21	36:BC:164:ARG:HH12	1.83	0.44
38:BE:36:ASP:CG	38:BE:40:ARG:H	2.26	0.44
39:BF:10:LEU:HD21	39:BF:26:ILE:HD11	1.98	0.44
45:BL:70:ILE:HG12	45:BL:100:ILE:HD13	1.98	0.44
47:BN:27:CYS:HB3	47:BN:43:CYS:SG	2.57	0.44
49:BP:8:ARG:HG2	49:BP:9:PHE:N	2.31	0.44
52:BS:18:LYS:NZ	52:BS:31:ILE:HG23	2.32	0.44
57:BZ:-6:ARG:N	57:BZ:-6:ARG:HD2	2.32	0.44
1:CA:65:C:O2'	1:CA:456:C:N3	2.43	0.44
1:CA:196:A:H2'	1:CA:196:A:N3	2.32	0.44
1:CA:307:G:N2	1:CA:310:A:O5'	2.48	0.44
1:CA:322:A:H5'	1:CA:340:A:C1'	2.48	0.44
1:CA:574:C:N3	5:CE:145:LYS:NZ	2.59	0.44
1:CA:747:U:O2	1:CA:2014:A:H1'	2.16	0.44
1:CA:1319:G:C6	1:CA:1320:C:N4	2.85	0.44
1:CA:2394:C:OP2	32:C8:30:ARG:HD2	2.16	0.44
1:CA:2574:G:H2'	1:CA:2575:C:C6	2.52	0.44
5:CE:167:VAL:HG13	5:CE:170:LEU:HD13	1.99	0.44
10:CL:41:PHE:O	10:CL:45:THR:OG1	2.28	0.44
19:CV:61:VAL:HA	19:CV:94:LEU:HD23	2.00	0.44
28:C4:59:PHE:N	28:C4:60:GLN:HB2	2.32	0.44
34:DA:33:A:N3	45:DL:32:PHE:HE2	2.16	0.44
34:DA:517:G:N3	34:DA:531:U:H5'	2.33	0.44
34:DA:949:A:H2'	34:DA:950:U:O4'	2.16	0.44
34:DA:1170:A:H8	34:DA:1170:A:O5'	2.00	0.44
36:DC:84:ILE:O	36:DC:101:LEU:HD23	2.17	0.44
39:DF:78:GLU:O	39:DF:81:ILE:HG22	2.17	0.44
45:DL:7:ILE:HG22	50:DQ:34:LYS:HD2	1.99	0.44
53:DT:26:ASN:O	53:DT:30:LYS:HB2	2.18	0.44
57:DZ:138:LYS:HG2	62:DZ:704:GDP:C5	2.52	0.44
57:DZ:145:ASP:OD2	57:DZ:146:LEU:N	2.51	0.44
57:DZ:349:LYS:HB2	57:DZ:349:LYS:HE3	1.77	0.44
1:AA:603:C:OP1	1:AA:2040:G:H4'	2.17	0.44
1:AA:1128:U:O5'	1:AA:1128:U:H6	2.00	0.44
1:AA:2549:U:H2'	1:AA:2550:C:C6	2.53	0.44
1:AA:2589:A:H5'	29:A5:3:LYS:HD2	1.99	0.44
5:AE:143:ASN:HD22	5:AE:147:PRO:HD2	1.82	0.44
7:AG:39:ILE:HB	7:AG:92:VAL:HG12	1.99	0.44
7:AG:98:ARG:CZ	28:A4:1:MET:HE3	2.47	0.44
8:AH:103:LEU:HD12	8:AH:103:LEU:HA	1.58	0.44
9:AK:77:PRO:C	9:AK:79:ALA:H	2.24	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:AW:79:GLY:C	20:AW:100:THR:HG22	2.43	0.44
21:AX:35:THR:O	21:AX:39:ILE:HG13	2.18	0.44
23:AZ:183:LEU:HD12	23:AZ:183:LEU:HA	1.50	0.44
24:A0:2:ALA:N	63:A0:204:HOH:O	2.51	0.44
34:BA:384:G:H2'	34:BA:385:C:C6	2.53	0.44
34:BA:426:G:C6	34:BA:427:U:C4	3.06	0.44
34:BA:472:A:H4'	49:BP:80:PHE:O	2.17	0.44
34:BA:924:C:H2'	34:BA:925:G:C8	2.53	0.44
46:BM:50:GLU:HA	46:BM:53:VAL:HB	1.99	0.44
46:BM:67:GLU:OE2	46:BM:71:ARG:NH2	2.51	0.44
53:BT:24:LEU:HD13	53:BT:24:LEU:HA	1.76	0.44
57:BZ:19:ALA:O	57:BZ:25:LYS:HE2	2.17	0.44
57:BZ:29:THR:OG1	57:BZ:83:ASP:OD1	2.22	0.44
57:BZ:309:LEU:HD22	57:BZ:334:THR:O	2.18	0.44
1:CA:506:G:O3'	1:CA:507:A:H8	2.01	0.44
1:CA:881:G:C2	1:CA:897:C:N3	2.85	0.44
1:CA:1003:G:N2	1:CA:1153:C:C2	2.85	0.44
1:CA:1477:A:H2'	1:CA:1478:G:O4'	2.17	0.44
1:CA:1916:A:H2'	1:CA:1917:U:O4'	2.18	0.44
3:CC:39:ASP:O	3:CC:178:LYS:HE3	2.18	0.44
3:CC:194:ILE:HD11	3:CC:227:PRO:HB2	1.99	0.44
6:CF:170:LEU:HA	6:CF:171:PRO:HD3	1.84	0.44
7:CG:126:ASP:OD2	7:CG:130:ASN:ND2	2.26	0.44
32:C8:50:LEU:HD23	32:C8:50:LEU:HA	1.55	0.44
34:DA:188:C:N4	34:DA:189(L):G:H1	2.15	0.44
34:DA:399:G:H2'	34:DA:400:C:C6	2.53	0.44
34:DA:741:G:H5'	48:DO:39:LEU:HD11	2.00	0.44
35:DB:7:VAL:HG12	35:DB:8:LYS:HG2	2.00	0.44
35:DB:210:SER:OG	35:DB:211:ILE:HG13	2.18	0.44
38:DE:78:HIS:NE2	38:DE:142:LEU:HD23	2.32	0.44
38:DE:145:LYS:HB3	38:DE:145:LYS:HE2	1.67	0.44
41:DH:51:VAL:HG11	41:DH:60:ARG:NH1	2.18	0.44
41:DH:84:ARG:HH11	41:DH:86:ILE:HD11	1.82	0.44
44:DK:102:GLY:C	44:DK:103:LEU:HD22	2.42	0.44
55:DV:16:A:C6	55:DV:17:U:C4	3.06	0.44
57:DZ:116:PRO:HA	57:DZ:119:GLU:HG3	1.99	0.44
1:AA:278:G:H2'	1:AA:279:G:H5"	1.99	0.44
1:AA:505:A:N3	1:AA:507:G:H5"	2.32	0.44
1:AA:656:A:H1'	1:AA:2427:G:O2'	2.18	0.44
1:AA:2658:C:O5'	1:AA:2658:C:H6	2.00	0.44
1:AA:2736:C:OP2	5:AE:109:LYS:HE2	2.16	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:AC:22:THR:HG23	3:AC:25:GLU:OE1	2.17	0.44
3:AC:160:GLY:O	3:AC:161:ARG:C	2.61	0.44
4:AD:44:ASN:OD1	4:AD:46:GLN:HB2	2.17	0.44
4:AD:96:HIS:CD2	4:AD:102:LYS:HD3	2.52	0.44
4:AD:208:LYS:O	4:AD:209:ALA:C	2.60	0.44
5:AE:6:GLY:HA3	5:AE:28:ALA:HA	1.99	0.44
6:AF:106:ARG:H	6:AF:106:ARG:HG2	1.38	0.44
16:AS:8:GLU:O	16:AS:11:LYS:N	2.50	0.44
20:AW:14:PRO:HG2	20:AW:78:GLU:CD	2.43	0.44
20:AW:106:ILE:HD13	20:AW:106:ILE:HG21	1.63	0.44
21:AX:72:LYS:HE2	21:AX:73:ARG:O	2.17	0.44
34:BA:49:U:C2	34:BA:361:G:N2	2.85	0.44
34:BA:450:G:N7	34:BA:481:G:C6	2.86	0.44
34:BA:527:G:O2'	34:BA:535:A:N1	2.48	0.44
34:BA:701:C:O2	34:BA:703:G:N1	2.50	0.44
34:BA:857:C:H2'	34:BA:858:G:O4'	2.18	0.44
34:BA:1502:A:H5"	34:BA:1504:G:N7	2.31	0.44
35:BB:137:ARG:HB3	35:BB:137:ARG:NH1	2.32	0.44
42:BI:4:TYR:CE2	42:BI:88:TYR:HD1	2.35	0.44
46:BM:66:LEU:C	46:BM:70:LEU:HB2	2.43	0.44
48:BO:62:GLN:HA	48:BO:65:ARG:HH12	1.83	0.44
49:BP:26:ARG:HB3	49:BP:27:LYS:O	2.16	0.44
50:BQ:17:LYS:HA	50:BQ:49:GLU:HG2	2.00	0.44
53:BT:97:ALA:N	53:BT:98:PRO:HD3	2.32	0.44
57:BZ:335:LEU:HD13	57:BZ:335:LEU:HA	1.78	0.44
1:CA:249:C:O2'	13:CP:64:LYS:HE3	2.17	0.44
1:CA:271(M):G:H4'	1:CA:271(N):U:OP1	2.17	0.44
1:CA:284:U:H2'	1:CA:285:C:C6	2.52	0.44
1:CA:459:U:C5	1:CA:469:G:N2	2.86	0.44
1:CA:1021:A:C8	1:CA:1021:A:C3'	3.00	0.44
1:CA:1651:G:C5'	15:CR:39:PRO:HG2	2.48	0.44
1:CA:2177:C:O2	3:CC:171:ALA:HB2	2.10	0.44
1:CA:2415:G:O4'	13:CP:67:MET:HG2	2.18	0.44
1:CA:2543:G:H21	1:CA:2646:C:H5"	1.81	0.44
1:CA:2840:C:H4'	15:CR:53:HIS:CE1	2.53	0.44
6:CF:172:TRP:CD1	6:CF:172:TRP:H	2.36	0.44
17:CT:24:PRO:HG3	17:CT:52:ILE:HG13	1.99	0.44
22:CY:30:VAL:HG22	22:CY:37:VAL:HG12	2.00	0.44
27:C3:8:LEU:HD23	27:C3:54:VAL:HG23	1.99	0.44
34:DA:20:U:H2'	34:DA:21:G:O4'	2.18	0.44
34:DA:1057:G:H2'	34:DA:1058:G:O4'	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:DA:1333:A:H3'	34:DA:1334:G:H8	1.82	0.44
35:DB:155:LEU:HA	35:DB:155:LEU:HD23	1.67	0.44
37:DD:160:GLN:O	37:DD:163:GLU:N	2.46	0.44
44:DK:43:SER:OG	44:DK:44:SER:N	2.51	0.44
1:AA:383:A:H2'	1:AA:384:G:O4'	2.18	0.44
1:AA:517:A:H2'	1:AA:518:G:O4'	2.17	0.44
1:AA:739:C:O2'	1:AA:1400:A:O2'	2.31	0.44
1:AA:1068:G:N7	11:AN:66:LYS:HE2	2.33	0.44
1:AA:1088:G:H1	1:AA:1159:U:H3	1.65	0.44
1:AA:2803:A:H2'	1:AA:2803:A:N3	2.32	0.44
3:AC:194:ILE:HD11	3:AC:227:PRO:HB2	1.99	0.44
4:AD:164:GLN:NE2	4:AD:166:GLN:OE1	2.50	0.44
12:AO:71:ARG:HA	12:AO:72:PRO:HD3	1.85	0.44
14:AQ:133:ARG:HG2	14:AQ:134:ARG:N	2.30	0.44
17:AT:18:ASP:OD2	17:AT:18:ASP:N	2.51	0.44
17:AT:105:LEU:HB2	17:AT:110:ILE:CG1	2.45	0.44
34:BA:352:C:H42	34:BA:357:G:N2	2.16	0.44
34:BA:374:A:C6	34:BA:375:U:C4	3.06	0.44
34:BA:442:C:H42	34:BA:492:G:H1	1.66	0.44
34:BA:448:A:OP2	34:BA:485:G:N1	2.37	0.44
34:BA:564:C:HO2'	41:BH:91:ARG:HH22	1.55	0.44
34:BA:595:G:H22	34:BA:643:C:N4	2.16	0.44
34:BA:600:C:N3	34:BA:639:G:C2	2.86	0.44
34:BA:1225:A:H2'	34:BA:1226:C:C5	2.53	0.44
34:BA:1239:A:O2'	34:BA:1298:C:N4	2.44	0.44
36:BC:85:ARG:O	36:BC:89:GLU:HG2	2.18	0.44
44:BK:73:MET:HG2	44:BK:103:LEU:HD21	1.99	0.44
46:BM:53:VAL:HG12	46:BM:57:ARG:HH12	1.82	0.44
48:BO:26:GLU:H	48:BO:26:GLU:HG2	1.45	0.44
1:CA:515:A:H1'	1:CA:581:C:H1'	1.99	0.44
1:CA:608:A:H2'	1:CA:609:A:O4'	2.18	0.44
1:CA:1190:G:OP1	13:CP:32:THR:HA	2.17	0.44
1:CA:1834:U:H4'	1:CA:1969:A:C6	2.53	0.44
1:CA:1858:G:O6	63:CA:3751:HOH:O	2.19	0.44
1:CA:1902:C:H5'	4:CD:246:PRO:HD3	2.00	0.44
1:CA:2256:G:C5	1:CA:2257:U:C5	3.06	0.44
1:CA:2703:C:H2'	1:CA:2704:C:H6	1.83	0.44
63:CA:3912:HOH:O	6:CF:55:GLY:HA2	2.17	0.44
3:CC:211:ARG:HG2	3:CC:211:ARG:HH11	1.81	0.44
5:CE:9:VAL:CG2	17:CT:3:ARG:HG2	2.45	0.44
11:CN:91:LEU:HA	11:CN:95:PRO:HA	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:CX:32:PRO:O	21:CX:77:LYS:NZ	2.42	0.44
34:DA:357:G:N2	34:DA:358:U:C2	2.86	0.44
34:DA:517:G:C2	34:DA:531:U:H5'	2.53	0.44
34:DA:789:U:H2'	34:DA:791:G:OP2	2.18	0.44
34:DA:1076:C:C2	34:DA:1082:G:N2	2.86	0.44
34:DA:1153:C:N3	34:DA:1154:G:N2	2.66	0.44
34:DA:1318:A:O2'	52:DS:37:ARG:HB3	2.18	0.44
34:DA:1326:C:H5"	54:DU:18:TYR:O	2.17	0.44
34:DA:1413:A:C2	34:DA:1414:U:C2	3.06	0.44
34:DA:1466:C:H2'	34:DA:1467:G:O4'	2.17	0.44
35:DB:24:TRP:H	35:DB:24:TRP:CD1	2.36	0.44
41:DH:31:PHE:HZ	41:DH:134:ILE:CD1	2.30	0.44
48:DO:32:LEU:HD23	48:DO:32:LEU:HA	1.82	0.44
1:AA:207:A:C2	1:AA:224:U:H4'	2.53	0.44
1:AA:731:G:OP1	31:A7:16:HIS:ND1	2.46	0.44
1:AA:769:A:H2'	1:AA:770:G:O4'	2.18	0.44
1:AA:904:C:H4'	24:A0:23:VAL:HG21	2.00	0.44
1:AA:1733:C:H2'	1:AA:1734:G:O4'	2.17	0.44
1:AA:1836:U:O2	4:AD:50:THR:HB	2.18	0.44
1:AA:2368:C:H2'	1:AA:2369:U:O4'	2.17	0.44
1:AA:2418:U:C2	13:AP:72:PRO:HG2	2.52	0.44
8:AH:90:LYS:HD2	8:AH:163:TYR:CD1	2.53	0.44
9:AK:74:LEU:O	9:AK:76:GLY:N	2.46	0.44
13:AP:68:GLN:HG3	32:A8:12:LYS:HG2	1.99	0.44
13:AP:91:PHE:O	13:AP:123:LEU:HD21	2.17	0.44
18:AU:58:ARG:O	18:AU:62:ILE:HG13	2.18	0.44
34:BA:67:C:O2'	34:BA:171:A:H1'	2.18	0.44
34:BA:737:A:H2'	34:BA:738:C:C6	2.53	0.44
48:BO:60:VAL:O	48:BO:64:ARG:HB2	2.18	0.44
1:CA:143:G:H4'	21:CX:35:THR:HG21	1.99	0.44
1:CA:205:G:O2'	1:CA:206:U:P	2.76	0.44
1:CA:212:G:H2'	1:CA:213:A:O4'	2.17	0.44
1:CA:226:G:H21	1:CA:228:A:H62	1.66	0.44
1:CA:412:A:C8	1:CA:413:C:C5	3.05	0.44
1:CA:1011:G:C2	1:CA:1013:C:C2	3.06	0.44
1:CA:1344:G:H4'	1:CA:1384:A:N7	2.33	0.44
1:CA:1572:A:H2'	1:CA:1573:G:O4'	2.17	0.44
1:CA:1714:G:C2	1:CA:1717:G:C8	3.06	0.44
1:CA:1967:C:C2'	1:CA:1968:G:H5'	2.47	0.44
1:CA:2137:C:N4	1:CA:2154:G:H1	2.01	0.44
1:CA:2408:U:H2'	1:CA:2409:G:C8	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:2693:A:H2'	1:CA:2694:G:H8	1.83	0.44
3:CC:5:GLY:O	3:CC:6:LYS:C	2.61	0.44
3:CC:7:ARG:HH22	3:CC:219:MET:HB2	1.81	0.44
5:CE:51:PHE:O	5:CE:77:ILE:HG22	2.18	0.44
7:CG:117:PHE:HE1	7:CG:119:GLY:HA2	1.82	0.44
8:CH:44:VAL:HB	8:CH:51:ARG:HB2	1.99	0.44
11:CN:14:VAL:CG1	11:CN:138:LEU:HB2	2.47	0.44
12:CO:64:ARG:HB2	12:CO:83:ALA:HB3	1.98	0.44
14:CQ:109:VAL:HG22	14:CQ:113:GLN:OE1	2.18	0.44
16:CS:34:HIS:HB3	16:CS:35:ILE:H	1.43	0.44
20:CW:65:LEU:N	20:CW:109:GLU:OE1	2.41	0.44
34:DA:51:A:C6	34:DA:353:A:C2	3.06	0.44
34:DA:139:G:H2'	34:DA:140:A:C8	2.53	0.44
34:DA:818:G:O2'	34:DA:819:A:H5'	2.18	0.44
34:DA:1240:U:OP2	40:DG:116:ALA:N	2.49	0.44
34:DA:1427:U:H2'	34:DA:1428:A:C8	2.53	0.44
35:DB:158:LEU:HD23	35:DB:182:ILE:HD11	2.00	0.44
36:DC:50:ALA:HB2	36:DC:75:VAL:CB	2.48	0.44
37:DD:31:CYS:O	37:DD:35:ARG:HG3	2.18	0.44
39:DF:33:TYR:HB2	39:DF:75:LEU:HD23	2.00	0.44
42:DI:89:ASN:O	42:DI:92:TYR:HB2	2.18	0.44
46:DM:20:THR:HG22	46:DM:26:GLY:C	2.43	0.44
52:DS:63:THR:OG1	52:DS:64:GLU:N	2.50	0.44
53:DT:10:LEU:HD12	53:DT:10:LEU:HA	1.69	0.44
54:DU:12:LYS:HB3	54:DU:17:THR:O	2.18	0.44
57:DZ:341:VAL:HG12	57:DZ:391:GLY:HA2	2.00	0.44
1:AA:515:G:C6	1:AA:516:G:C5	3.06	0.43
1:AA:1891:G:H4'	3:AC:206:LYS:HD3	1.07	0.43
1:AA:2132:G:OP1	1:AA:2140:U:N3	2.51	0.43
1:AA:2439:C:H5"	1:AA:2440:G:OP1	2.17	0.43
1:AA:2701:U:C4	1:AA:2726:A:C2	3.06	0.43
3:AC:5:GLY:O	3:AC:6:LYS:C	2.61	0.43
3:AC:60:ARG:HG3	3:AC:165:ARG:HB2	2.01	0.43
4:AD:3:VAL:HG22	4:AD:18:VAL:O	2.17	0.43
4:AD:98:VAL:HG23	4:AD:99:ASP:N	2.33	0.43
5:AE:141:ILE:O	5:AE:150:VAL:HG22	2.17	0.43
7:AG:173:LEU:HD22	7:AG:178:PHE:CE1	2.52	0.43
11:AN:89:LYS:O	11:AN:93:THR:HG23	2.18	0.43
14:AQ:68:ILE:HD13	14:AQ:103:MET:HB3	1.99	0.43
17:AT:23:ARG:HG3	17:AT:120:ARG:NH1	2.33	0.43
34:BA:882:C:O2'	34:BA:883:C:H5'	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:BA:1437:C:H2'	34:BA:1438:G:H8	1.83	0.43
36:BC:175:LEU:HD21	36:BC:201:TYR:HD2	1.83	0.43
37:BD:94:LEU:HD23	37:BD:94:LEU:HA	1.89	0.43
37:BD:173:TRP:HB2	37:BD:187:ARG:O	2.18	0.43
40:BG:107:ALA:O	40:BG:111:ARG:HG3	2.18	0.43
41:BH:39:LEU:HD13	41:BH:39:LEU:HA	1.65	0.43
46:BM:4:ILE:HA	46:BM:5:ALA:HA	1.70	0.43
49:BP:70:ALA:O	49:BP:74:LEU:HB2	2.17	0.43
57:BZ:160:ARG:HE	57:BZ:254:LYS:HA	1.82	0.43
1:CA:265:A:H1'	1:CA:266:G:O4'	2.18	0.43
1:CA:847:U:H5'	63:CA:3711:HOH:O	2.17	0.43
1:CA:869:G:H5'	14:CQ:6:ARG:NH2	2.32	0.43
1:CA:1045:A:H62	1:CA:1111:A:H2'	1.81	0.43
1:CA:1155:A:OP1	18:CU:55:ARG:HD3	2.18	0.43
1:CA:2852:G:H2'	1:CA:2853:C:O4'	2.18	0.43
4:CD:244:ARG:HB2	4:CD:245:PRO:HD2	2.00	0.43
5:CE:4:ILE:HG22	5:CE:96:PHE:HE2	1.83	0.43
6:CF:106:ARG:O	6:CF:107:LYS:C	2.60	0.43
7:CG:39:ILE:N	7:CG:92:VAL:O	2.49	0.43
13:CP:55:ARG:HG2	13:CP:56:SER:O	2.17	0.43
14:CQ:42:ILE:HD13	14:CQ:97:VAL:HB	1.99	0.43
23:CZ:70:LEU:HD23	23:CZ:70:LEU:HA	1.66	0.43
34:DA:827:U:H5"	34:DA:828:A:OP2	2.18	0.43
34:DA:1274:G:N2	34:DA:1275:A:H62	2.16	0.43
36:DC:39:ILE:O	36:DC:43:LEU:HG	2.17	0.43
37:DD:105:VAL:HG21	37:DD:126:ILE:HD12	1.99	0.43
50:DQ:81:ARG:HE	50:DQ:84:LEU:HD11	1.83	0.43
57:DZ:85:PRO:HB2	57:DZ:90:PHE:HB3	2.00	0.43
57:DZ:152:THR:C	57:DZ:154:GLN:H	2.26	0.43
1:AA:236:G:H4'	1:AA:413:G:C6	2.52	0.43
1:AA:933:C:H4'	1:AA:933:C:OP1	2.17	0.43
1:AA:2087:C:H2'	1:AA:2088:C:C6	2.53	0.43
4:AD:16:MET:HB2	4:AD:207:GLY:HA3	2.00	0.43
6:AF:36:VAL:HA	6:AF:101:LEU:CD2	2.48	0.43
8:AH:33:LEU:HD23	8:AH:33:LEU:HA	1.76	0.43
10:AL:29:GLN:HE21	10:AL:29:GLN:HB3	1.60	0.43
12:AO:12:ASP:OD2	12:AO:85:VAL:HG13	2.19	0.43
18:AU:29:SER:O	18:AU:30:LYS:HD3	2.18	0.43
22:AY:79:CYS:SG	22:AY:81:LYS:HG3	2.59	0.43
23:AZ:8:TYR:CD1	23:AZ:8:TYR:N	2.85	0.43
34:BA:104:G:C2	34:BA:105:G:C8	3.06	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:BA:482:A:H3'	34:BA:483:C:C6	2.53	0.43
34:BA:909:A:H2'	34:BA:910:C:O4'	2.17	0.43
34:BA:926:G:H5"	34:BA:927:G:O5'	2.19	0.43
35:BB:223:ILE:C	35:BB:225:ALA:H	2.25	0.43
37:BD:104:VAL:O	37:BD:107:ARG:N	2.51	0.43
38:BE:129:ILE:HG22	38:BE:130:ASN:N	2.32	0.43
38:BE:152:ARG:HA	41:BH:64:LYS:NZ	2.33	0.43
40:BG:14:PRO:HB3	40:BG:19:GLY:O	2.18	0.43
41:BH:13:ILE:O	41:BH:17:THR:HG23	2.18	0.43
49:BP:55:ARG:C	49:BP:57:ARG:N	2.76	0.43
57:BZ:97:SER:O	57:BZ:101:LEU:HD12	2.18	0.43
1:CA:954:G:O2'	1:CA:2274:A:N1	2.43	0.43
1:CA:1487:G:N2	1:CA:1503:U:O2	2.51	0.43
1:CA:2011:U:OP1	20:CW:42:ARG:NH1	2.51	0.43
1:CA:2038:G:H2'	1:CA:2039:C:O4'	2.17	0.43
1:CA:2356:C:H2'	1:CA:2357:U:O4'	2.17	0.43
1:CA:2657:A:O3'	8:CH:160:LYS:NZ	2.52	0.43
4:CD:85:ASP:OD2	4:CD:88:ARG:NH1	2.48	0.43
5:CE:152:LYS:HB3	5:CE:152:LYS:HE3	1.68	0.43
8:CH:24:VAL:HG13	8:CH:37:VAL:HG21	2.00	0.43
14:CQ:21:THR:HG21	14:CQ:101:ARG:HH11	1.83	0.43
15:CR:30:THR:HG22	15:CR:31:HIS:CD2	2.53	0.43
16:CS:10:ARG:NE	16:CS:91:PRO:O	2.35	0.43
21:CX:44:GLU:O	21:CX:46:ALA:N	2.48	0.43
32:C8:63:PRO:HG2	32:C8:64:TYR:CD2	2.53	0.43
34:DA:126:G:OP1	34:DA:605:U:O2'	2.32	0.43
34:DA:255:G:H2'	34:DA:256:U:C6	2.53	0.43
34:DA:960:U:C4	34:DA:1225:A:C8	3.06	0.43
34:DA:1305:G:N2	34:DA:1331:G:H1'	2.32	0.43
34:DA:1446:U:N3	34:DA:1452:C:O2	2.51	0.43
40:DG:45:ASP:O	40:DG:117:ALA:HB1	2.18	0.43
41:DH:9:MET:SD	41:DH:26:VAL:HG21	2.58	0.43
41:DH:29:SER:HB3	41:DH:32:LYS:HE3	1.99	0.43
50:DQ:4:LYS:HD2	50:DQ:5:VAL:H	1.83	0.43
57:DZ:183:MET:SD	57:DZ:213:HIS:CD2	3.03	0.43
57:DZ:358:MET:HE1	57:DZ:363:ARG:HG2	2.00	0.43
1:AA:476:G:O6	63:AA:3941:HOH:O	2.21	0.43
1:AA:1548:C:H2'	1:AA:1549:U:C6	2.53	0.43
1:AA:1604:C:P	1:AA:1605:A:HO2'	2.36	0.43
1:AA:2383:G:H1'	30:A6:39:TYR:CD1	2.53	0.43
1:AA:2863:C:H2'	1:AA:2864:G:H8	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:AL:30:HIS:HA	10:AL:59:ILE:HG13	2.00	0.43
11:AN:75:TYR:CZ	11:AN:77:GLY:HA2	2.54	0.43
32:A8:62:LEU:HB3	32:A8:65:GLU:HG2	1.98	0.43
34:BA:620:C:H2'	34:BA:621:A:O4'	2.18	0.43
34:BA:865:A:C2	34:BA:918:A:H4'	2.52	0.43
34:BA:1142:G:H2'	34:BA:1143:G:O4'	2.18	0.43
34:BA:1343:G:H4'	42:BI:122:ALA:HB3	2.01	0.43
35:BB:98:LEU:HG	35:BB:101:MET:HE3	1.99	0.43
38:BE:95:ALA:HB1	38:BE:96:PRO:HD2	1.99	0.43
38:BE:131:ILE:HD13	38:BE:131:ILE:HA	1.70	0.43
45:BL:110:VAL:HG23	45:BL:120:TYR:HB3	2.00	0.43
50:BQ:53:LEU:HD12	50:BQ:53:LEU:HA	1.91	0.43
1:CA:521:G:H2'	1:CA:522:G:H8	1.83	0.43
1:CA:622:G:H2'	1:CA:623:G:C8	2.53	0.43
1:CA:720:C:H2'	1:CA:721:C:C6	2.54	0.43
1:CA:919:G:C6	1:CA:920:G:C5	3.06	0.43
1:CA:1153:C:H2'	1:CA:1154:G:C8	2.53	0.43
1:CA:1288:U:O2'	1:CA:1647:G:N2	2.52	0.43
1:CA:1317:A:H2'	1:CA:1318:C:C6	2.52	0.43
1:CA:1575:C:H2'	1:CA:1576:U:C6	2.53	0.43
1:CA:2386:C:H2'	1:CA:2387:U:C6	2.52	0.43
1:CA:2467:C:H4'	14:CQ:123:HIS:CG	2.53	0.43
1:CA:2626:C:H2'	1:CA:2627:G:C8	2.53	0.43
1:CA:2646:C:H6	1:CA:2646:C:O5'	2.01	0.43
1:CA:2848:G:N2	1:CA:2867:G:H1'	2.33	0.43
3:CC:31:LYS:H	3:CC:31:LYS:HG2	1.57	0.43
3:CC:160:GLY:O	3:CC:161:ARG:C	2.61	0.43
4:CD:164:GLN:NE2	4:CD:176:ARG:HH22	2.16	0.43
5:CE:187:ALA:O	63:CE:402:HOH:O	2.21	0.43
6:CF:187:VAL:HG13	13:CP:1:MET:O	2.19	0.43
7:CG:103:LEU:HA	7:CG:106:LEU:HB3	2.01	0.43
17:CT:119:LYS:O	17:CT:123:GLN:HG3	2.18	0.43
19:CV:18:LEU:O	19:CV:95:LEU:HD23	2.18	0.43
19:CV:25:LEU:HD23	19:CV:25:LEU:HA	1.49	0.43
21:CX:32:PRO:HA	21:CX:77:LYS:HB2	2.00	0.43
24:C0:40:GLN:HG3	24:C0:42:GLY:O	2.19	0.43
34:DA:28:G:O2'	34:DA:296:U:OP1	2.30	0.43
34:DA:264:U:H4'	50:DQ:63:ARG:HD3	1.99	0.43
34:DA:620:C:H2'	34:DA:621:A:O4'	2.18	0.43
34:DA:1022:G:H2'	34:DA:1023:G:C8	2.52	0.43
34:DA:1124:G:N7	34:DA:1145:C:O2'	2.44	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:DB:16:HIS:CD2	35:DB:17:PHE:N	2.82	0.43
35:DB:97:TRP:HZ3	35:DB:176:GLU:OE2	2.01	0.43
36:DC:31:HIS:C	36:DC:33:LEU:H	2.26	0.43
38:DE:123:LEU:HD23	38:DE:123:LEU:HA	1.60	0.43
41:DH:111:ILE:HG23	41:DH:135:CYS:SG	2.58	0.43
42:DI:50:LEU:HG	42:DI:81:ILE:HD11	2.00	0.43
45:DL:34:ARG:O	45:DL:61:THR:HG23	2.19	0.43
57:DZ:162:VAL:HG12	57:DZ:164:MET:SD	2.59	0.43
1:AA:540:A:C8	1:AA:541:C:C6	3.06	0.43
1:AA:925:A:H2'	1:AA:926:G:H5'	2.01	0.43
1:AA:1021:G:O2'	1:AA:1202:A:N1	2.37	0.43
1:AA:1040:C:OP2	18:AU:54:LYS:NZ	2.44	0.43
1:AA:1220:U:H1'	1:AA:1221:G:OP1	2.17	0.43
1:AA:2299:A:N3	1:AA:2301:G:C8	2.86	0.43
1:AA:2331:G:H1	16:AS:3:ARG:HA	1.84	0.43
1:AA:2868:C:H2'	1:AA:2869:G:O4'	2.18	0.43
5:AE:94:GLU:H	5:AE:94:GLU:HG2	1.57	0.43
13:AP:147:LEU:HD13	13:AP:148:LEU:O	2.18	0.43
14:AQ:82:ARG:H	24:A0:7:LEU:HD21	1.84	0.43
18:AU:18:LEU:O	18:AU:21:ALA:N	2.40	0.43
18:AU:66:ASN:O	18:AU:70:ARG:HG3	2.18	0.43
22:AY:6:HIS:HE1	22:AY:72:VAL:O	2.01	0.43
28:A4:17:GLY:C	28:A4:19:GLY:H	2.26	0.43
34:BA:106:C:H2'	34:BA:107:G:O4'	2.19	0.43
34:BA:147:G:C2	34:BA:148:G:C8	3.06	0.43
34:BA:439:A:C4	34:BA:496:A:C2	3.06	0.43
34:BA:613:C:H42	34:BA:627:G:H1	1.66	0.43
34:BA:918:A:H2'	34:BA:919:A:C8	2.53	0.43
34:BA:927:G:H4'	34:BA:927:G:OP2	2.17	0.43
34:BA:986:A:H1'	52:BS:55:LYS:HA	2.01	0.43
34:BA:1039:C:H2'	34:BA:1040:U:C6	2.52	0.43
34:BA:1226:C:O2'	46:BM:111:LYS:NZ	2.51	0.43
35:BB:108:ILE:HD13	35:BB:108:ILE:HA	1.86	0.43
37:BD:25:ARG:O	37:BD:28:SER:HB3	2.18	0.43
39:BF:61:LEU:HD12	39:BF:63:TYR:CZ	2.54	0.43
40:BG:150:ALA:HB2	44:BK:50:TYR:HE2	1.83	0.43
41:BH:49:GLU:HG2	41:BH:62:TYR:HE1	1.83	0.43
46:BM:108:ARG:HD3	46:BM:108:ARG:HA	1.82	0.43
57:BZ:88:VAL:HG23	57:BZ:89:ASP:OD2	2.18	0.43
1:CA:210:C:OP2	31:C7:29:LYS:HE3	2.18	0.43
1:CA:234:C:H2'	1:CA:235:U:C6	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:443:A:C5	6:CF:45:ARG:HD2	2.52	0.43
1:CA:753:C:H2'	1:CA:754:C:C6	2.52	0.43
1:CA:811:U:O3'	1:CA:1251:C:H5'	2.19	0.43
1:CA:1422:G:C4	1:CA:1423:G:C8	3.05	0.43
1:CA:1718:G:C2	1:CA:1719:G:C8	3.06	0.43
1:CA:1919:A:N1	34:DA:1495:U:O2'	2.50	0.43
1:CA:2037:G:C6	1:CA:2038:G:C6	3.07	0.43
1:CA:2059:A:O2'	6:CF:69:HIS:HD2	2.02	0.43
1:CA:2328:A:H2'	1:CA:2329:G:H8	1.83	0.43
1:CA:2774:C:H2'	1:CA:2775:A:O4'	2.18	0.43
2:CB:19:G:H2'	2:CB:20:C:O4'	2.19	0.43
3:CC:54:ARG:HE	3:CC:57:GLN:HG2	1.83	0.43
13:CP:21:ARG:HD3	13:CP:21:ARG:HA	1.85	0.43
18:CU:17:ILE:HD13	18:CU:20:LEU:HD12	2.01	0.43
30:C6:30:THR:O	30:C6:32:ASN:N	2.52	0.43
33:C9:19:ARG:HG2	33:C9:20:HIS:ND1	2.34	0.43
34:DA:456:C:H42	34:DA:475:G:H1	1.65	0.43
34:DA:586:C:N4	34:DA:755:G:H1	2.16	0.43
34:DA:586:C:O2'	34:DA:878:G:H4'	2.19	0.43
34:DA:1032:G:H2'	34:DA:1033:G:C8	2.53	0.43
35:DB:189:ASP:HB2	35:DB:190:THR:H	1.72	0.43
36:DC:35:GLU:O	36:DC:39:ILE:HG13	2.18	0.43
37:DD:8:VAL:O	37:DD:11:LEU:HB2	2.18	0.43
38:DE:8:GLU:OE2	38:DE:63:ARG:NH2	2.52	0.43
38:DE:47:LYS:HE2	38:DE:47:LYS:HB2	1.77	0.43
44:DK:47:VAL:HG12	44:DK:48:ILE:HD13	1.99	0.43
45:DL:27:LEU:HD13	45:DL:98:TYR:CE1	2.53	0.43
45:DL:59:ARG:HH21	57:DZ:422:GLU:H	1.66	0.43
52:DS:63:THR:HG22	52:DS:66:MET:HE3	1.99	0.43
57:DZ:-15:ARG:O	57:DZ:-12:ALA:HB3	2.19	0.43
1:AA:234:G:H2'	1:AA:235:C:H6	1.84	0.43
1:AA:1125:C:H4'	10:AL:132:ARG:HH22	1.83	0.43
1:AA:1321:A:H4'	1:AA:1322:A:OP1	2.18	0.43
1:AA:1679:A:C6	1:AA:1680:G:C6	3.07	0.43
1:AA:1706:U:H2'	1:AA:1707:C:O4'	2.18	0.43
1:AA:1807:G:N3	1:AA:1807:G:H2'	2.33	0.43
1:AA:2158:C:N4	1:AA:2177:G:H1	2.15	0.43
1:AA:2273:C:H1'	1:AA:2400:A:N3	2.34	0.43
1:AA:2402:U:O2'	1:AA:2403:G:H5'	2.18	0.43
4:AD:92:ILE:HD12	4:AD:104:TYR:CD1	2.53	0.43
5:AE:48:GLN:NE2	5:AE:78:LEU:HG	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:AF:167:ALA:O	6:AF:170:LEU:HD22	2.19	0.43
11:AN:91:LEU:HA	11:AN:91:LEU:HD23	1.53	0.43
12:AO:63:VAL:HG12	12:AO:106:LEU:HD11	1.99	0.43
14:AQ:30:GLY:HA2	14:AQ:107:ALA:HB2	2.00	0.43
15:AR:22:ARG:O	15:AR:26:LYS:HG3	2.18	0.43
20:AW:36:LEU:HD12	20:AW:48:ALA:HA	2.00	0.43
23:AZ:96:VAL:N	23:AZ:128:VAL:O	2.47	0.43
34:BA:264:U:H2'	34:BA:265:G:O4'	2.18	0.43
34:BA:413:G:H21	34:BA:428:G:H1'	1.83	0.43
34:BA:453:A:H62	34:BA:479:C:H42	1.65	0.43
34:BA:501:C:H2'	34:BA:502:G:H8	1.83	0.43
34:BA:663:A:H2'	34:BA:664:G:O4'	2.18	0.43
34:BA:696:A:N1	34:BA:797:C:O2'	2.50	0.43
34:BA:727:G:N2	34:BA:731:G:C4	2.86	0.43
34:BA:1285:A:H4'	34:BA:1286:A:O5'	2.18	0.43
35:BB:28:PHE:CD1	35:BB:190:THR:HG22	2.53	0.43
37:BD:62:GLN:OE1	37:BD:62:GLN:HA	2.18	0.43
37:BD:202:LEU:HA	37:BD:202:LEU:HD23	1.55	0.43
42:BI:11:LYS:C	42:BI:13:ALA:H	2.26	0.43
43:BJ:13:HIS:HA	43:BJ:16:LEU:HB3	2.01	0.43
45:BL:60:LEU:HD13	45:BL:60:LEU:HA	1.79	0.43
50:BQ:92:ARG:HD3	50:BQ:92:ARG:HA	1.57	0.43
54:BU:9:ARG:O	54:BU:13:ILE:HG13	2.19	0.43
57:BZ:211:GLU:C	57:BZ:213:HIS:H	2.25	0.43
57:BZ:358:MET:HE1	57:BZ:363:ARG:HG2	2.00	0.43
1:CA:483:A:N7	1:CA:497:A:H2	2.17	0.43
1:CA:1053:C:C2	1:CA:1107:G:N2	2.87	0.43
1:CA:1095:A:N7	1:CA:1096:A:C6	2.87	0.43
1:CA:1165:U:H2'	1:CA:1166:C:C6	2.53	0.43
3:CC:60:ARG:HG3	3:CC:165:ARG:HB2	2.01	0.43
11:CN:128:HIS:HE1	11:CN:135:PRO:HG2	1.83	0.43
17:CT:78:LEU:C	17:CT:79:HIS:HD2	2.26	0.43
17:CT:80:SER:HA	17:CT:81:PRO:HD2	1.78	0.43
22:CY:9:LYS:HA	22:CY:10:GLY:HA2	1.71	0.43
22:CY:99:CYS:SG	22:CY:101:LYS:N	2.91	0.43
28:C4:14:ILE:O	28:C4:21:VAL:HA	2.18	0.43
34:DA:418:C:H2'	34:DA:419:C:H6	1.82	0.43
34:DA:575:G:C6	34:DA:821:G:N7	2.86	0.43
34:DA:601:C:C2	34:DA:638:G:N2	2.86	0.43
34:DA:757:U:H2'	34:DA:758:G:O4'	2.18	0.43
34:DA:922:G:N1	34:DA:923:A:C2	2.86	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:DA:1040:U:O5'	34:DA:1040:U:H6	2.02	0.43
34:DA:1303:C:C4	34:DA:1304:G:C5	3.06	0.43
35:DB:30:ARG:HG3	35:DB:31:TYR:CD1	2.53	0.43
38:DE:139:LEU:C	38:DE:141:GLN:H	2.26	0.43
39:DF:76:ALA:O	39:DF:80:ARG:HG3	2.19	0.43
39:DF:98:LEU:HD23	51:DR:30:ASP:HA	1.99	0.43
42:DI:22:GLY:HA3	42:DI:60:ASP:CG	2.44	0.43
47:DN:27:CYS:SG	47:DN:29:ARG:N	2.91	0.43
49:DP:76:GLN:O	49:DP:76:GLN:HG3	2.16	0.43
50:DQ:92:ARG:HD3	50:DQ:92:ARG:HA	1.91	0.43
52:DS:50:ALA:HB1	52:DS:57:HIS:HB3	2.00	0.43
56:DX:18:G:C6	56:DX:57:A:C6	3.07	0.43
57:DZ:187:THR:HB	57:DZ:199:ILE:CD1	2.44	0.43
1:AA:489:G:N2	1:AA:492:A:OP2	2.49	0.43
1:AA:829:A:C2	4:AD:226:MET:HG2	2.54	0.43
1:AA:1676:G:H2'	1:AA:1677:C:C6	2.54	0.43
1:AA:1766:G:H5"	1:AA:1767:A:OP2	2.18	0.43
6:AF:36:VAL:O	6:AF:40:GLN:HG3	2.18	0.43
14:AQ:70:PRO:HA	14:AQ:95:ALA:HB2	2.00	0.43
16:AS:51:ALA:HB2	16:AS:73:LEU:HB2	2.01	0.43
34:BA:7:G:H5'	34:BA:298:A:O4'	2.18	0.43
34:BA:226:G:H2'	34:BA:227:G:O4'	2.17	0.43
34:BA:243:A:H4'	34:BA:244:U:O5'	2.18	0.43
34:BA:1316:G:N1	34:BA:1319:A:OP2	2.50	0.43
39:BF:19:LEU:HD11	39:BF:59:TYR:CE2	2.53	0.43
40:BG:30:ILE:HD13	40:BG:120:ILE:HD13	1.99	0.43
52:BS:15:LEU:O	52:BS:19:VAL:HG23	2.19	0.43
1:CA:252:G:OP1	13:CP:50:ARG:NH1	2.51	0.43
1:CA:994:C:H1'	19:CV:10:LYS:HE3	2.01	0.43
1:CA:1051:G:C2	1:CA:1052:C:C2	3.06	0.43
1:CA:1076:C:H2'	1:CA:1077:A:O4'	2.18	0.43
1:CA:1341:U:OP1	1:CA:1397:U:N3	2.31	0.43
1:CA:1666:G:C2'	1:CA:1667:G:H5'	2.49	0.43
1:CA:1882:C:H2'	1:CA:1883:G:O4'	2.19	0.43
1:CA:1967:C:C4	1:CA:1968:G:C5	3.07	0.43
1:CA:2070:G:OP2	63:CA:3759:HOH:O	2.21	0.43
1:CA:2756:U:H1'	1:CA:2757:A:H5"	2.01	0.43
2:CB:88:C:H2'	2:CB:89:G:O4'	2.19	0.43
4:CD:73:VAL:HG13	4:CD:120:GLY:CA	2.48	0.43
6:CF:154:VAL:HA	6:CF:191:ARG:HB2	2.00	0.43
13:CP:95:VAL:HA	13:CP:99:LEU:HD21	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:CP:127:ALA:HB3	13:CP:130:PHE:CE1	2.54	0.43
30:C6:34:LEU:HB2	30:C6:51:GLU:HB2	2.01	0.43
31:C7:10:ARG:O	31:C7:14:LYS:HB2	2.19	0.43
34:DA:9:G:H5'	38:DE:122:GLU:OE2	2.19	0.43
34:DA:300:A:H1'	34:DA:565:U:O2	2.19	0.43
34:DA:512:U:C2	34:DA:513:C:C5	3.06	0.43
34:DA:769:G:H4'	34:DA:1513:A:H4'	2.01	0.43
34:DA:1102:A:H5"	34:DA:1102:A:H8	1.83	0.43
34:DA:1168:A:C6	34:DA:1169:A:C6	3.07	0.43
37:DD:79:PHE:O	37:DD:82:ALA:HB3	2.19	0.43
37:DD:200:GLU:O	37:DD:204:ILE:HG12	2.18	0.43
40:DG:78:ARG:NH2	40:DG:79:ARG:HH22	2.17	0.43
44:DK:91:ARG:C	44:DK:93:GLN:H	2.25	0.43
52:DS:3:ARG:HH11	52:DS:7:LYS:HE2	1.84	0.43
57:DZ:-9:LEU:O	57:DZ:-6:ARG:HB2	2.18	0.43
57:DZ:13:ARG:NH1	57:DZ:77:HIS:CE1	2.85	0.43
1:AA:36:G:O2'	1:AA:476:G:H2'	2.19	0.43
1:AA:478:G:C4	1:AA:484:G:C6	3.06	0.43
1:AA:653:G:C6	1:AA:661:G:C2	3.06	0.43
1:AA:1698:G:H5'	15:AR:39:PRO:HG2	1.99	0.43
1:AA:2315:G:O2'	7:AG:132:ASN:HB2	2.19	0.43
4:AD:70:TRP:O	4:AD:70:TRP:HE3	2.02	0.43
7:AG:71:THR:N	7:AG:89:GLY:O	2.48	0.43
14:AQ:103:MET:HE1	14:AQ:125:LEU:HD13	2.01	0.43
17:AT:46:GLU:OE2	17:AT:89:VAL:HG11	2.18	0.43
18:AU:39:LEU:O	18:AU:42:ALA:HB3	2.18	0.43
20:AW:97:LYS:HE3	20:AW:99:ARG:NH2	2.34	0.43
25:A1:22:GLY:O	25:A1:32:LYS:NZ	2.52	0.43
33:A9:24:TYR:CE2	33:A9:35:ARG:HG3	2.53	0.43
34:BA:367:U:C6	34:BA:394:G:N2	2.86	0.43
34:BA:508:C:OP1	37:BD:209:ARG:NH2	2.52	0.43
34:BA:617:G:C6	34:BA:618:C:C5	3.07	0.43
34:BA:841:U:H6	34:BA:841:U:P	2.42	0.43
35:BB:83:MET:H	35:BB:83:MET:HG2	1.50	0.43
48:BO:82:ILE:O	48:BO:86:GLY:N	2.47	0.43
57:BZ:18:ALA:O	57:BZ:106:VAL:HA	2.19	0.43
1:CA:221:A:C4	1:CA:266:G:N7	2.86	0.43
1:CA:824:A:H1'	1:CA:2358:G:N7	2.34	0.43
1:CA:2454:G:H1'	63:CA:3802:HOH:O	2.18	0.43
4:CD:52:ARG:HH11	4:CD:52:ARG:HD3	1.67	0.43
6:CF:153:SER:OG	6:CF:190:GLU:N	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:CU:28:ARG:HD3	18:CU:38:THR:OG1	2.18	0.43
31:C7:14:LYS:HZ2	31:C7:14:LYS:HG2	1.68	0.43
34:DA:152:A:N6	34:DA:170:U:C2	2.87	0.43
34:DA:539:A:H2'	34:DA:540:G:C8	2.52	0.43
34:DA:602:A:H2'	34:DA:603:U:O4'	2.19	0.43
34:DA:697:U:C5	34:DA:698:G:C8	3.06	0.43
34:DA:1193:G:O2'	38:DE:25:ARG:NH2	2.50	0.43
36:DC:104:GLN:HE21	36:DC:104:GLN:HB3	1.72	0.43
37:DD:8:VAL:HG22	37:DD:21:LEU:HD13	2.00	0.43
37:DD:171:GLY:C	37:DD:173:TRP:N	2.76	0.43
42:DI:89:ASN:ND2	42:DI:91:ASP:H	2.17	0.43
1:AA:7:G:H2'	1:AA:8:A:O4'	2.18	0.43
1:AA:233:A:C2	1:AA:244:A:C4	3.07	0.43
1:AA:287:G:O6	1:AA:448:U:O2'	2.33	0.43
1:AA:921:G:N2	1:AA:950:C:C2	2.86	0.43
1:AA:1913:G:C6	1:AA:1914:C:N3	2.87	0.43
5:AE:14:ILE:C	5:AE:14:ILE:HD12	2.44	0.43
6:AF:53:THR:N	6:AF:56:GLU:OE2	2.47	0.43
7:AG:126:ASP:HB2	7:AG:130:ASN:H	1.83	0.43
8:AH:41:MET:HE3	8:AH:41:MET:HB3	1.70	0.43
12:AO:115:VAL:HG13	12:AO:121:VAL:HG21	2.01	0.43
14:AQ:56:ARG:HA	23:AZ:180:VAL:CG2	2.48	0.43
21:AX:35:THR:O	21:AX:38:GLU:HB3	2.18	0.43
24:A0:20:ARG:O	24:A0:24:LYS:NZ	2.44	0.43
31:A7:33:ARG:NH2	63:A7:202:HOH:O	2.50	0.43
34:BA:33:A:H2'	34:BA:34:C:H6	1.83	0.43
34:BA:840:C:H4'	34:BA:841:U:OP1	2.19	0.43
34:BA:1452:C:O2'	34:BA:1457:G:N7	2.51	0.43
43:BJ:43:ARG:HB2	43:BJ:67:THR:OG1	2.18	0.43
46:BM:70:LEU:O	46:BM:74:VAL:HG23	2.19	0.43
52:BS:44:MET:O	52:BS:47:HIS:HB2	2.18	0.43
57:BZ:127:LYS:O	57:BZ:128:TYR:CD2	2.71	0.43
1:CA:127:A:H5"	1:CA:128:C:C6	2.54	0.43
1:CA:543:C:H6	1:CA:543:C:O5'	2.01	0.43
1:CA:599:G:OP1	13:CP:9:ASN:ND2	2.52	0.43
1:CA:1614:A:P	1:CA:1614:A:H8	2.42	0.43
1:CA:2080:G:H2'	1:CA:2081:C:C6	2.52	0.43
1:CA:2461:C:N4	1:CA:2462:U:O4	2.51	0.43
4:CD:155:LEU:HD12	4:CD:155:LEU:HA	1.58	0.43
5:CE:21:VAL:HA	5:CE:22:PRO:HD2	1.87	0.43
17:CT:41:ARG:NH2	34:DA:345:C:H3'	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:CX:11:PRO:HB3	21:CX:92:LEU:HD21	2.01	0.43
34:DA:90:U:H2'	34:DA:91:C:H6	1.84	0.43
34:DA:270:A:H2'	34:DA:271:C:C6	2.53	0.43
34:DA:325:A:H2'	34:DA:326:G:O4'	2.18	0.43
34:DA:410:G:H5"	34:DA:411:A:OP1	2.19	0.43
34:DA:453:A:C5	34:DA:454:C:C4	3.06	0.43
34:DA:730:G:C5	34:DA:731:G:H1'	2.53	0.43
34:DA:883:C:O2'	34:DA:884:U:H5'	2.19	0.43
34:DA:1103:C:C2	34:DA:1104:G:C8	3.06	0.43
34:DA:1203:C:H2'	34:DA:1204:A:C8	2.54	0.43
34:DA:1262:C:H42	34:DA:1273:G:H1	1.64	0.43
34:DA:1298:C:H4'	34:DA:1299:A:C4	2.54	0.43
34:DA:1481:U:H2'	34:DA:1482:G:C8	2.54	0.43
35:DB:95:GLN:HB2	35:DB:148:TYR:HD1	1.84	0.43
35:DB:124:SER:OG	35:DB:125:PRO:HD3	2.18	0.43
44:DK:38:ASN:HA	44:DK:39:PRO:HD3	1.92	0.43
46:DM:19:LEU:HD13	46:DM:19:LEU:HA	1.76	0.43
56:DX:43:A:C2	56:DX:44:A:C5	3.07	0.43
57:DZ:-25:SER:O	57:DZ:-23:LEU:N	2.51	0.43
57:DZ:380:LEU:HA	57:DZ:380:LEU:HD12	1.61	0.43
1:AA:239:G:C6	1:AA:240:A:C6	3.07	0.43
1:AA:863:C:H2'	1:AA:864:C:O4'	2.18	0.43
1:AA:866:A:C4	1:AA:1234:A:C2	3.06	0.43
1:AA:1077:G:H21	33:A9:36:GLN:HE22	1.66	0.43
1:AA:1336:C:H2'	1:AA:1337:C:C6	2.54	0.43
1:AA:1781:G:N3	1:AA:2870:A:H2	2.17	0.43
1:AA:2584:A:N7	5:AE:144:ARG:HD2	2.34	0.43
1:AA:2860:A:C2	1:AA:2861:A:C4	3.07	0.43
8:AH:116:GLU:HG3	8:AH:117:PRO:HD2	2.01	0.43
16:AS:53:SER:OG	16:AS:54:LEU:N	2.52	0.43
21:AX:25:LYS:NZ	21:AX:82:GLN:HE21	2.17	0.43
23:AZ:183:LEU:O	23:AZ:185:GLU:N	2.51	0.43
25:A1:40:ARG:HE	25:A1:40:ARG:HB2	1.56	0.43
32:A8:51:ALA:O	32:A8:52:LYS:C	2.62	0.43
34:BA:116:A:C8	34:BA:116:A:OP2	2.72	0.43
34:BA:748:C:O5'	34:BA:748:C:H6	2.02	0.43
34:BA:912:C:O2'	34:BA:913:A:H5'	2.19	0.43
35:BB:54:THR:HG21	35:BB:201:ILE:HD11	2.00	0.43
38:BE:148:VAL:HG21	41:BH:107:LEU:HB3	2.00	0.43
53:BT:56:MET:HE3	53:BT:88:VAL:CB	2.48	0.43
57:BZ:87:HIS:HB3	57:BZ:90:PHE:HB2	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:30:G:H2'	1:CA:31:C:C6	2.53	0.43
1:CA:300:A:H1'	1:CA:319:C:C1'	2.49	0.43
1:CA:1049:C:H3'	1:CA:1050:A:C8	2.51	0.43
1:CA:1082:U:C4	1:CA:1083:U:H1'	2.54	0.43
1:CA:1364:G:OP2	25:C1:3:LYS:HG3	2.19	0.43
1:CA:2469:A:C2	1:CA:2470:G:H1'	2.54	0.43
3:CC:11:LEU:HD11	3:CC:35:THR:HG23	2.01	0.43
4:CD:275:LYS:HD3	4:CD:276:LYS:O	2.19	0.43
6:CF:56:GLU:OE1	6:CF:93:LYS:NZ	2.51	0.43
12:CO:9:GLU:O	12:CO:83:ALA:HA	2.19	0.43
14:CQ:137:TYR:CZ	23:CZ:83:PRO:HG3	2.54	0.43
16:CS:95:HIS:HA	16:CS:99:LYS:HD2	2.01	0.43
33:C9:7:VAL:HG12	33:C9:34:GLN:HB3	2.00	0.43
34:DA:279:A:N7	50:DQ:98:LEU:HD22	2.34	0.43
34:DA:666:G:H5'	34:DA:726:C:H1'	2.01	0.43
34:DA:814:A:H2'	34:DA:816:A:H5"	2.00	0.43
34:DA:931:C:H1'	34:DA:1387:G:N2	2.34	0.43
34:DA:1150:U:C4	34:DA:1151:A:N6	2.87	0.43
34:DA:1250:A:H2	34:DA:1370:G:H1'	1.83	0.43
34:DA:1263:C:H2'	34:DA:1264:C:H6	1.84	0.43
36:DC:148:GLY:HA3	36:DC:172:ARG:O	2.18	0.43
39:DF:33:TYR:CD1	39:DF:75:LEU:HD23	2.54	0.43
41:DH:75:ARG:HA	41:DH:76:PRO:HD2	1.65	0.43
48:DO:25:THR:CG2	48:DO:70:LEU:HD13	2.49	0.43
50:DQ:24:GLU:HB3	50:DQ:39:SER:HB3	2.00	0.43
50:DQ:29:HIS:CE1	50:DQ:32:TYR:CD2	3.07	0.43
57:DZ:-52:VAL:HG13	57:DZ:-51:GLY:N	2.34	0.43
57:DZ:18:ALA:HB1	57:DZ:121:VAL:HG21	2.00	0.43
57:DZ:168:ILE:HD13	57:DZ:202:PRO:HG3	1.99	0.43
1:AA:8:A:H2'	1:AA:9:U:H6	1.84	0.43
1:AA:12:U:O2	1:AA:12:U:H2'	2.19	0.43
1:AA:27:G:C2	1:AA:537:G:N3	2.87	0.43
1:AA:1640:G:H5'	63:AA:5196:HOH:O	2.18	0.43
3:AC:31:LYS:H	3:AC:31:LYS:HG2	1.57	0.43
4:AD:68:LYS:O	4:AD:69:ARG:HB2	2.19	0.43
5:AE:52:LEU:HA	5:AE:53:PRO:HD2	1.67	0.43
7:AG:62:LEU:O	7:AG:143:GLU:HG3	2.18	0.43
17:AT:119:LYS:HB2	34:BA:1442(A):G:N2	2.34	0.43
22:AY:75:ILE:HD13	22:AY:75:ILE:HA	1.78	0.43
32:A8:62:LEU:HB3	32:A8:65:GLU:CG	2.49	0.43
34:BA:924:C:H2'	34:BA:925:G:H8	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:BA:978:A:O2'	34:BA:1322:C:N3	2.45	0.43
34:BA:1268:A:C6	34:BA:1269:A:C6	3.07	0.43
35:BB:20:GLU:OE2	35:BB:21:ARG:NH2	2.51	0.43
35:BB:27:LYS:HE2	35:BB:193:ASP:OD1	2.19	0.43
38:BE:18:ARG:HG2	38:BE:25:ARG:O	2.19	0.43
39:BF:55:ASP:OD2	39:BF:86:ARG:NH1	2.52	0.43
48:BO:43:LEU:HD23	48:BO:43:LEU:HA	1.87	0.43
57:BZ:299:VAL:HG22	57:BZ:300:GLU:O	2.19	0.43
1:CA:854:G:H2'	1:CA:855:G:H8	1.84	0.43
1:CA:1171:G:N2	1:CA:1179:C:C2	2.81	0.43
1:CA:1266:G:O2'	1:CA:2012:G:O6	2.25	0.43
1:CA:1622:G:C2	1:CA:1623:G:C8	3.07	0.43
1:CA:1653:G:H4'	1:CA:1654:A:O5'	2.19	0.43
1:CA:1889:A:N1	1:CA:2234:G:H1'	2.34	0.43
1:CA:1913:A:H4'	1:CA:1914:C:C5'	2.38	0.43
1:CA:1956:U:C4	1:CA:1957:C:C5	3.07	0.43
1:CA:2256:G:C6	1:CA:2257:U:C4	3.06	0.43
1:CA:2543:G:H5'	1:CA:2767:C:OP1	2.19	0.43
5:CE:98:PRO:HG3	5:CE:174:ASP:HA	1.99	0.43
8:CH:29:PRO:HG2	8:CH:79:VAL:O	2.19	0.43
16:CS:3:ARG:CZ	16:CS:3:ARG:HB2	2.48	0.43
18:CU:17:ILE:HD13	18:CU:17:ILE:HA	1.79	0.43
19:CV:89:GLN:HA	19:CV:90:PRO:HD3	1.71	0.43
32:C8:54:GLU:OE1	32:C8:57:ARG:NH1	2.49	0.43
34:DA:130:A:H1'	34:DA:263:A:O2'	2.19	0.43
36:DC:112:SER:HB3	36:DC:115:LEU:HD22	2.01	0.43
39:DF:12:PRO:HG3	39:DF:57:GLN:O	2.19	0.43
40:DG:142:GLU:O	40:DG:145:ALA:HB3	2.19	0.43
46:DM:123:ALA:HB3	57:DZ:573:HIS:CB	2.49	0.43
48:DO:25:THR:O	48:DO:26:GLU:C	2.61	0.43
49:DP:55:ARG:O	49:DP:58:TYR:HB3	2.19	0.43
57:DZ:-50:GLN:HE21	57:DZ:-50:GLN:HB3	1.60	0.43
57:DZ:25:LYS:HE2	57:DZ:25:LYS:HB2	1.75	0.43
1:AA:91:G:H2'	1:AA:92:C:C6	2.54	0.42
1:AA:359:C:H2'	1:AA:360:C:H6	1.84	0.42
1:AA:755:C:O5'	1:AA:755:C:H6	2.01	0.42
1:AA:826:U:OP1	4:AD:49:ILE:HG13	2.19	0.42
1:AA:831:A:N6	4:AD:229:VAL:HG11	2.34	0.42
1:AA:1253:C:C4	1:AA:1254:G:N7	2.87	0.42
1:AA:1477:U:H2'	1:AA:1478:C:O4'	2.19	0.42
1:AA:1712:A:H2'	1:AA:1713:G:O4'	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1735:U:O2	1:AA:1747:A:H8	2.01	0.42
1:AA:1939:U:O2'	1:AA:1940:A:H5'	2.18	0.42
3:AC:195:ARG:HG3	3:AC:195:ARG:NH1	2.34	0.42
10:AL:55:VAL:HG22	10:AL:67:PHE:HB2	1.99	0.42
18:AU:17:ILE:HG13	18:AU:32:PHE:HE1	1.84	0.42
19:AV:22:VAL:HG23	19:AV:23:GLU:O	2.19	0.42
23:AZ:100:VAL:HG12	23:AZ:101:PRO:O	2.19	0.42
34:BA:41:G:N2	34:BA:42:G:C4	2.87	0.42
34:BA:302:G:C6	34:BA:303:A:C6	3.07	0.42
34:BA:302:G:O6	34:BA:303:A:C6	2.72	0.42
34:BA:1067:A:N3	34:BA:1068:G:H1'	2.34	0.42
34:BA:1097:C:H2'	34:BA:1098:C:H6	1.84	0.42
34:BA:1177:G:H2'	34:BA:1178:G:O4'	2.19	0.42
34:BA:1416:G:H2'	34:BA:1417:G:O4'	2.19	0.42
34:BA:1478:C:H2'	34:BA:1479:C:C6	2.54	0.42
35:BB:229:VAL:HG12	35:BB:230:VAL:H	1.83	0.42
41:BH:29:SER:OG	41:BH:32:LYS:HD2	2.18	0.42
41:BH:50:ARG:HA	41:BH:59:LEU:HD23	2.01	0.42
48:BO:9:GLN:O	48:BO:10:LYS:C	2.62	0.42
1:CA:511:U:H5"	1:CA:512:G:OP2	2.19	0.42
1:CA:647:G:H2'	1:CA:648:G:O4'	2.19	0.42
1:CA:788:A:OP1	1:CA:791:C:N4	2.44	0.42
1:CA:1588:C:H2'	1:CA:1589:C:H6	1.84	0.42
1:CA:1668:A:OP1	12:CO:5:GLN:HG2	2.19	0.42
1:CA:2256:G:O2'	1:CA:2257:U:H5'	2.18	0.42
3:CC:6:LYS:N	3:CC:9:ARG:HH12	2.17	0.42
4:CD:72:LYS:HG3	4:CD:103:ARG:NH2	2.33	0.42
4:CD:231:HIS:ND1	4:CD:232:PRO:HD2	2.34	0.42
6:CF:196:LEU:O	6:CF:199:TRP:HB3	2.19	0.42
18:CU:76:TYR:HH	18:CU:92:ARG:NH1	2.16	0.42
34:DA:232:G:H1'	34:DA:262:A:N1	2.33	0.42
34:DA:509:A:C8	34:DA:509:A:C3'	3.01	0.42
34:DA:837:G:H1	34:DA:849:C:N4	2.16	0.42
34:DA:1057:G:C5	34:DA:1204:A:C2	3.07	0.42
34:DA:1072:G:C6	34:DA:1073:U:C4	3.06	0.42
34:DA:1171:G:H8	34:DA:1171:G:OP2	2.00	0.42
34:DA:1317:C:O2	52:DS:37:ARG:NH1	2.52	0.42
34:DA:1338:G:C6	34:DA:1339:A:C6	3.07	0.42
39:DF:95:GLU:HA	39:DF:96:PRO:HD3	1.93	0.42
44:DK:69:ALA:O	44:DK:73:MET:HG2	2.19	0.42
51:DR:55:ARG:HE	51:DR:55:ARG:HB3	1.58	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1530:G:C2	1:AA:1552:C:C2	3.07	0.42
1:AA:1833:A:N1	1:AA:1853:G:H1'	2.34	0.42
1:AA:1864:U:H2'	1:AA:1865:U:H6	1.83	0.42
1:AA:2146:G:H2'	1:AA:2147:G:O4'	2.18	0.42
1:AA:2353:G:H2'	1:AA:2354:C:C6	2.53	0.42
1:AA:2710:U:H2'	1:AA:2711:C:C6	2.54	0.42
2:AB:6:C:H2'	2:AB:7:G:O4'	2.19	0.42
2:AB:29:A:C2	2:AB:30:C:C2	3.07	0.42
2:AB:85:G:H2'	2:AB:86:G:H5'	2.01	0.42
5:AE:170:LEU:HA	5:AE:170:LEU:HD12	1.84	0.42
8:AH:127:GLU:HG3	8:AH:130:ARG:HB2	2.01	0.42
12:AO:107:ARG:O	12:AO:110:GLY:N	2.44	0.42
12:AO:107:ARG:CZ	17:AT:36:GLU:HG2	2.49	0.42
13:AP:38:GLN:O	13:AP:44:GLY:HA2	2.19	0.42
14:AQ:48:GLU:O	14:AQ:52:VAL:HG23	2.19	0.42
17:AT:84:GLN:HG2	17:AT:85:LYS:HD3	2.01	0.42
26:A2:47:ASN:C	26:A2:49:LYS:H	2.27	0.42
34:BA:368:U:C4	57:BZ:354:ARG:NH1	2.79	0.42
34:BA:595:G:H22	34:BA:643:C:H41	1.66	0.42
34:BA:1527:C:O5'	34:BA:1527:C:H6	2.03	0.42
35:BB:44:LEU:HA	35:BB:47:THR:OG1	2.19	0.42
37:BD:162:LEU:CD1	37:BD:181:MET:HG2	2.49	0.42
48:BO:32:LEU:O	48:BO:33:THR:C	2.62	0.42
57:BZ:87:HIS:O	57:BZ:88:VAL:C	2.61	0.42
57:BZ:93:GLU:O	57:BZ:95:GLU:N	2.52	0.42
1:CA:275:G:H2'	1:CA:276:A:O4'	2.20	0.42
1:CA:706:A:H2'	1:CA:707:G:O4'	2.19	0.42
1:CA:754:C:H2'	1:CA:755:C:C6	2.54	0.42
1:CA:757:U:H2'	1:CA:758:C:O4'	2.19	0.42
1:CA:1021:A:OP2	11:CN:65:LYS:NZ	2.51	0.42
1:CA:1448:G:H1'	1:CA:1528:A:N1	2.33	0.42
1:CA:1857:G:O6	1:CA:1858:G:N1	2.52	0.42
1:CA:2370:G:C6	1:CA:2371:G:C6	3.07	0.42
1:CA:2406:U:H2'	1:CA:2406:U:OP2	2.19	0.42
1:CA:2600:A:H2'	1:CA:2601:C:C6	2.53	0.42
3:CC:195:ARG:HH11	3:CC:195:ARG:HG3	1.83	0.42
4:CD:29:PRO:HA	4:CD:83:GLU:OE1	2.19	0.42
4:CD:164:GLN:NE2	4:CD:176:ARG:HH12	2.17	0.42
5:CE:113:PHE:HA	5:CE:159:HIS:HD2	1.83	0.42
7:CG:43:LEU:HB3	7:CG:44:GLY:H	1.38	0.42
8:CH:7:LEU:HA	8:CH:8:PRO:HD3	1.90	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:CN:108:PRO:O	11:CN:113:GLY:HA3	2.19	0.42
17:CT:14:TYR:CD2	17:CT:14:TYR:N	2.87	0.42
18:CU:104:GLN:NE2	18:CU:105:VAL:HG23	2.34	0.42
32:C8:60:LEU:HD23	32:C8:60:LEU:HA	1.82	0.42
34:DA:622:A:C8	34:DA:623:C:C6	3.07	0.42
34:DA:904:C:H2'	34:DA:905:U:O4'	2.19	0.42
34:DA:1287:A:H2'	34:DA:1288:A:C8	2.54	0.42
34:DA:1318:A:H1'	52:DS:37:ARG:HD3	2.01	0.42
35:DB:175:ARG:HB3	35:DB:175:ARG:NH1	2.34	0.42
37:DD:129:ASN:ND2	37:DD:144:ASP:HA	2.24	0.42
38:DE:31:LEU:HD23	38:DE:31:LEU:HA	1.76	0.42
45:DL:93:LEU:HB3	45:DL:96:VAL:CG2	2.48	0.42
46:DM:20:THR:C	46:DM:22:ILE:H	2.27	0.42
46:DM:108:ARG:HD3	46:DM:108:ARG:HA	1.75	0.42
48:DO:29:VAL:HG11	48:DO:81:LEU:HD21	2.01	0.42
54:DU:6:ARG:HG2	54:DU:15:ARG:HD2	2.01	0.42
1:AA:400:U:O2	1:AA:450:A:H2	2.01	0.42
1:AA:820:U:H2'	1:AA:821:A:H5'	2.01	0.42
1:AA:891:C:C2'	1:AA:892:G:H5'	2.49	0.42
1:AA:1053:C:H5"	11:AN:35:ARG:HH11	1.84	0.42
1:AA:1389:G:H2'	1:AA:1430:A:C2	2.54	0.42
1:AA:1893:G:C2	1:AA:1903:C:C2	3.07	0.42
1:AA:2092:G:H2'	1:AA:2093:A:O4'	2.20	0.42
1:AA:2115:G:C6	1:AA:2237:A:C8	3.08	0.42
1:AA:2321:A:H8	1:AA:2321:A:O5'	2.02	0.42
1:AA:2639:G:O2'	1:AA:2794:A:N1	2.46	0.42
1:AA:2720:G:OP1	15:AR:68:ARG:HD3	2.19	0.42
2:AB:113:G:H2'	2:AB:114:C:C6	2.54	0.42
4:AD:148:GLU:CD	4:AD:151:LYS:HE3	2.44	0.42
4:AD:221:VAL:HG22	4:AD:226:MET:HE2	2.00	0.42
6:AF:53:THR:HG22	6:AF:55:GLY:H	1.82	0.42
11:AN:46:VAL:CG2	11:AN:48:MET:HG2	2.48	0.42
30:A6:10:LEU:HD23	30:A6:22:ALA:HB2	2.00	0.42
34:BA:406:G:H21	37:BD:119:GLN:NE2	2.15	0.42
34:BA:557:G:C6	34:BA:558:G:C6	3.07	0.42
34:BA:958:A:H8	34:BA:958:A:OP1	2.02	0.42
34:BA:1244:C:O2	34:BA:1294:G:N2	2.52	0.42
34:BA:1253:G:H2'	34:BA:1254:C:C6	2.54	0.42
35:BB:164:VAL:HB	35:BB:186:ALA:CB	2.49	0.42
48:BO:67:LEU:H	48:BO:67:LEU:HG	1.70	0.42
57:BZ:80:ASN:HD22	57:BZ:374:LEU:HB2	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:BZ:273:LEU:O	57:BZ:274:ASP:C	2.62	0.42
57:BZ:309:LEU:HG	57:BZ:391:GLY:H	1.84	0.42
1:CA:132:G:H2'	1:CA:133:C:C6	2.54	0.42
1:CA:627:A:C6	1:CA:637:A:C8	3.06	0.42
1:CA:1260:G:H2'	1:CA:1261:C:O4'	2.20	0.42
1:CA:1540:U:H2'	1:CA:1541:G:O4'	2.19	0.42
1:CA:1586:A:N6	1:CA:1587:A:C2	2.87	0.42
1:CA:2176:A:C3'	3:CC:45:HIS:CD2	3.02	0.42
1:CA:2470:G:C2	1:CA:2471:C:C6	3.07	0.42
2:CB:61:G:C6	2:CB:62:C:C4	3.07	0.42
6:CF:170:LEU:HA	6:CF:170:LEU:HD12	1.90	0.42
7:CG:117:PHE:CE1	7:CG:119:GLY:HA2	2.55	0.42
17:CT:118:ARG:HB3	34:DA:1442(A):G:C5	2.54	0.42
18:CU:44:ASN:ND2	19:CV:75:PHE:O	2.51	0.42
18:CU:92:ARG:HG2	18:CU:92:ARG:H	1.74	0.42
23:CZ:139:VAL:HG23	23:CZ:141:VAL:HG13	2.01	0.42
34:DA:131:C:H2'	34:DA:132:C:C6	2.54	0.42
34:DA:855:G:C2	34:DA:856:C:C2	3.06	0.42
34:DA:1198:G:H2'	34:DA:1199:U:C6	2.54	0.42
34:DA:1499:A:C1'	34:DA:1520:G:H5'	2.47	0.42
37:DD:12:CYS:O	37:DD:16:GLY:N	2.51	0.42
37:DD:86:LYS:HE3	37:DD:86:LYS:HB3	1.79	0.42
37:DD:200:GLU:OE2	37:DD:200:GLU:N	2.52	0.42
41:DH:33:GLU:HA	41:DH:36:LEU:HD12	2.00	0.42
45:DL:70:ILE:HD13	45:DL:77:LEU:HD12	2.01	0.42
49:DP:43:LYS:HG2	49:DP:48:TRP:CG	2.54	0.42
53:DT:81:LYS:HB2	53:DT:81:LYS:HE2	1.76	0.42
57:DZ:134:ALA:O	57:DZ:258:VAL:HA	2.17	0.42
57:DZ:341:VAL:HB	57:DZ:390:VAL:O	2.19	0.42
57:DZ:553:GLY:H	57:DZ:557:GLY:CA	2.24	0.42
1:AA:67:G:H2'	1:AA:68:C:O4'	2.20	0.42
1:AA:81:G:O2'	1:AA:82:G:H5'	2.19	0.42
1:AA:414:U:OP2	25:A1:20:ARG:NH1	2.48	0.42
1:AA:501:U:C4	1:AA:507:G:O6	2.72	0.42
1:AA:877:G:H5"	63:AA:4500:HOH:O	2.18	0.42
1:AA:1128:U:H5"	1:AA:1129:U:OP2	2.19	0.42
1:AA:1157:A:H2'	1:AA:1158:G:C1'	2.50	0.42
1:AA:1343:C:OP2	63:AA:3942:HOH:O	2.21	0.42
1:AA:1576:G:H2'	1:AA:1577:C:O4'	2.18	0.42
1:AA:1748:A:H2'	1:AA:1749:G:H5'	2.00	0.42
1:AA:1862:G:H1'	63:AA:5033:HOH:O	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:2116:G:C2	1:AA:2218:C:C2	3.08	0.42
1:AA:2638:C:H2'	1:AA:2639:G:H8	1.83	0.42
1:AA:2825:C:H2'	1:AA:2826:C:H6	1.84	0.42
2:AB:106:G:C5'	23:AZ:31:ARG:HB3	2.50	0.42
3:AC:20:VAL:O	3:AC:21:TYR:CB	2.58	0.42
4:AD:260:ARG:NH2	4:AD:264:LYS:HD3	2.35	0.42
5:AE:132:HIS:O	5:AE:133:LYS:HB2	2.20	0.42
8:AH:96:ALA:HB2	8:AH:105:LEU:HD12	2.00	0.42
10:AL:99:ILE:HG23	10:AL:103:GLN:HB3	2.00	0.42
17:AT:127:ALA:C	17:AT:129:ARG:H	2.27	0.42
23:AZ:124:ILE:HG12	23:AZ:125:LEU:H	1.85	0.42
23:AZ:180:VAL:O	23:AZ:183:LEU:HB2	2.19	0.42
28:A4:12:ALA:HA	28:A4:29:PRO:HA	2.01	0.42
34:BA:284:G:H2'	34:BA:285:G:C8	2.53	0.42
34:BA:619:U:O2	37:BD:133:VAL:HA	2.19	0.42
34:BA:1381:U:O4'	40:BG:79:ARG:NE	2.48	0.42
36:BC:6:HIS:CD2	36:BC:8:ILE:H	2.37	0.42
38:BE:31:LEU:HD23	38:BE:45:PHE:HB2	2.01	0.42
40:BG:16:LEU:HD12	42:BI:45:ALA:HB2	2.00	0.42
40:BG:73:MET:HG2	40:BG:145:ALA:HB1	2.00	0.42
41:BH:95:VAL:CG2	41:BH:100:ILE:HG12	2.49	0.42
50:BQ:45:HIS:HB3	50:BQ:72:ARG:HB3	2.01	0.42
50:BQ:86:GLU:C	50:BQ:88:TYR:H	2.28	0.42
1:CA:117:G:OP2	1:CA:119:A:O2'	2.26	0.42
1:CA:471:A:H8	1:CA:471:A:O5'	2.02	0.42
1:CA:829:A:N7	1:CA:2248:C:H5'	2.35	0.42
1:CA:2364:C:H2'	1:CA:2365:G:O4'	2.20	0.42
1:CA:2415:G:C6	1:CA:2416:C:C4	3.07	0.42
2:CB:72:G:O2'	2:CB:105:A:N6	2.52	0.42
3:CC:16:ASP:HA	3:CC:17:PRO:HD2	1.90	0.42
5:CE:117:MET:HB2	5:CE:136:ARG:HH21	1.84	0.42
6:CF:36:VAL:O	6:CF:40:GLN:HG3	2.18	0.42
13:CP:121:LYS:O	13:CP:123:LEU:N	2.53	0.42
16:CS:84:GLN:CA	16:CS:111:GLU:HB2	2.49	0.42
21:CX:57:LEU:HD11	21:CX:78:LYS:HE2	2.01	0.42
25:C1:8:SER:OG	25:C1:10:LYS:HB2	2.20	0.42
31:C7:35:ARG:HH11	31:C7:35:ARG:HD3	1.72	0.42
34:DA:633:G:H2'	34:DA:634:C:C6	2.54	0.42
34:DA:794:A:C5	34:DA:795:C:C4	3.08	0.42
34:DA:1103:C:H2'	34:DA:1104:G:O4'	2.18	0.42
34:DA:1126:U:H4'	34:DA:1281:U:H1'	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:DA:1315:U:H2'	34:DA:1316:G:O4'	2.19	0.42
34:DA:1357:A:HO2'	47:DN:34:TYR:HE2	1.65	0.42
37:DD:155:LEU:HD23	37:DD:156:GLU:N	2.34	0.42
43:DJ:45:ARG:HB3	43:DJ:65:LEU:HB3	2.01	0.42
46:DM:90:LEU:C	46:DM:92:HIS:H	2.26	0.42
57:DZ:191:ASP:OD1	57:DZ:267:LYS:NZ	2.52	0.42
57:DZ:303:PRO:O	57:DZ:305:PRO:HD3	2.18	0.42
1:AA:751:G:N3	1:AA:773:G:C2	2.88	0.42
1:AA:1018:A:O4'	1:AA:1233:U:C6	2.72	0.42
1:AA:1035:G:N7	27:A3:13:ILE:HG12	2.34	0.42
1:AA:1445:C:OP1	21:AX:25:LYS:NZ	2.53	0.42
1:AA:2143:G:C5'	3:AC:168:LYS:NZ	2.83	0.42
2:AB:9:G:OP1	16:AS:15:ARG:HD3	2.19	0.42
4:AD:221:VAL:HG22	4:AD:226:MET:CE	2.50	0.42
10:AL:38:VAL:O	10:AL:42:ASN:HB2	2.20	0.42
12:AO:1:MET:HE3	12:AO:32:TYR:CZ	2.55	0.42
12:AO:63:VAL:HG23	12:AO:64:ARG:HB2	2.01	0.42
14:AQ:61:GLY:HA3	23:AZ:177:PRO:O	2.19	0.42
15:AR:17:ARG:HH11	15:AR:17:ARG:HD2	1.71	0.42
34:BA:15:G:C6	34:BA:16:A:C5	3.08	0.42
34:BA:20:U:O2	34:BA:916:G:C2	2.72	0.42
34:BA:325:A:H2'	34:BA:326:G:O4'	2.19	0.42
34:BA:993:G:N3	34:BA:993:G:H2'	2.35	0.42
34:BA:1079:G:C6	34:BA:1080:A:N6	2.87	0.42
34:BA:1101:A:H4'	34:BA:1102:A:O5'	2.19	0.42
35:BB:15:VAL:O	35:BB:16:HIS:ND1	2.52	0.42
35:BB:82:ARG:NH1	35:BB:86:GLU:OE1	2.52	0.42
44:BK:40:ILE:HA	44:BK:40:ILE:HD13	1.74	0.42
49:BP:49:LEU:HD12	49:BP:50:LYS:H	1.83	0.42
52:BS:20:LEU:HD21	52:BS:43:GLU:OE2	2.18	0.42
57:BZ:-63:ILE:HB	57:BZ:-30:VAL:HG12	2.00	0.42
57:BZ:227:ILE:HG12	57:BZ:237:PRO:HB3	2.00	0.42
1:CA:84:A:H5'	22:CY:8:LYS:HG2	2.01	0.42
1:CA:221:A:N1	1:CA:265:A:O2'	2.51	0.42
1:CA:228:A:C8	1:CA:229:A:H5'	2.54	0.42
1:CA:231:C:H2'	1:CA:232:G:O4'	2.19	0.42
1:CA:448:U:O4	1:CA:583:G:H1'	2.19	0.42
1:CA:1446:C:N4	1:CA:1465:G:H1	2.07	0.42
1:CA:1906:G:C2	1:CA:1907:G:C8	3.08	0.42
1:CA:1908:C:O2	56:DX:12:G:H4'	2.19	0.42
1:CA:2331:G:O2'	1:CA:2336:A:N1	2.45	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:2349:G:OP1	63:CA:3758:HOH:O	2.21	0.42
1:CA:2813:A:C6	1:CA:2814:C:C4	3.08	0.42
2:CB:16:G:H2'	2:CB:17:C:C6	2.55	0.42
3:CC:225:ILE:O	3:CC:227:PRO:HD3	2.19	0.42
4:CD:77:ALA:HB2	4:CD:97:TYR:CD2	2.55	0.42
8:CH:124:GLU:HB2	8:CH:132:ARG:HB3	2.02	0.42
16:CS:19:LYS:H	16:CS:19:LYS:HG2	1.46	0.42
20:CW:20:VAL:O	20:CW:21:VAL:C	2.62	0.42
26:C2:62:THR:O	26:C2:66:GLU:HB2	2.20	0.42
34:DA:607:A:C2	49:DP:31:LYS:HG3	2.54	0.42
34:DA:1062:U:H2'	34:DA:1063:C:C6	2.55	0.42
36:DC:59:ARG:HG2	36:DC:64:VAL:HG13	2.02	0.42
41:DH:84:ARG:HG3	41:DH:136:GLU:HG2	2.00	0.42
48:DO:21:ASP:OD2	48:DO:24:SER:HB3	2.19	0.42
48:DO:63:ARG:O	48:DO:67:LEU:HB2	2.19	0.42
57:DZ:96:ARG:HB2	57:DZ:96:ARG:NH1	2.34	0.42
57:DZ:168:ILE:HB	57:DZ:176:GLY:CA	2.50	0.42
57:DZ:180:VAL:HG23	57:DZ:216:LEU:HD22	2.01	0.42
1:AA:20:C:OP1	18:AU:22:LYS:HE2	2.20	0.42
1:AA:127:C:H2'	1:AA:128:C:C6	2.54	0.42
1:AA:173:C:H2'	1:AA:174:U:H6	1.81	0.42
1:AA:311:C:H2'	1:AA:312:C:C6	2.53	0.42
1:AA:585:U:C4	1:AA:2058:C:O4'	2.73	0.42
1:AA:1127:U:O3'	10:AL:117:THR:HB	2.20	0.42
1:AA:1731:C:H2'	1:AA:1732:C:C6	2.55	0.42
1:AA:1748:A:C2'	1:AA:1749:G:H5'	2.50	0.42
1:AA:1828:C:C4	1:AA:1829:U:C5	3.07	0.42
1:AA:2216:G:H2'	1:AA:2217:C:O4'	2.19	0.42
1:AA:2330:G:H8	1:AA:2330:G:O5'	2.02	0.42
1:AA:2864:G:C2	1:AA:2865:C:C2	3.07	0.42
1:AA:2882:G:O2'	1:AA:2883:A:H5'	2.19	0.42
3:AC:195:ARG:HG3	3:AC:195:ARG:HH11	1.83	0.42
4:AD:213:ARG:HD2	4:AD:217:ARG:O	2.20	0.42
7:AG:142:PRO:HG2	7:AG:143:GLU:OE1	2.19	0.42
10:AL:5:VAL:HG12	10:AL:60:TYR:HA	2.00	0.42
10:AL:37:PHE:O	10:AL:41:PHE:HB3	2.18	0.42
12:AO:49:ARG:HH22	34:BA:1423:G:P	2.32	0.42
14:AQ:7:MET:HB2	14:AQ:7:MET:HE3	1.64	0.42
18:AU:109:LEU:HD23	18:AU:109:LEU:HA	1.68	0.42
19:AV:65:GLY:C	19:AV:66:ARG:HG3	2.44	0.42
21:AX:61:GLY:HA3	21:AX:73:ARG:O	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:AY:23:ARG:HG2	22:AY:42:VAL:HG22	2.00	0.42
23:AZ:18:LEU:HD12	23:AZ:18:LEU:HA	1.88	0.42
23:AZ:128:VAL:HG22	23:AZ:129:SER:N	2.35	0.42
29:A5:36:CYS:HB3	29:A5:49:CYS:HB3	2.02	0.42
34:BA:162:A:H3'	34:BA:163:C:O4'	2.19	0.42
34:BA:168:G:N2	34:BA:169:C:N3	2.67	0.42
34:BA:986:A:H1'	52:BS:54:GLY:O	2.20	0.42
34:BA:1197:G:OP2	63:BA:3311:HOH:O	2.22	0.42
34:BA:1323:G:H2'	34:BA:1324:A:C8	2.55	0.42
34:BA:1385:G:C6	34:BA:1386:G:C5	3.08	0.42
35:BB:87:ARG:CZ	35:BB:233:SER:HB3	2.50	0.42
35:BB:187:LEU:HA	35:BB:201:ILE:HB	2.01	0.42
37:BD:104:VAL:O	37:BD:105:VAL:C	2.63	0.42
39:BF:97:PHE:O	51:BR:31:LEU:HD23	2.19	0.42
40:BG:49:ILE:O	40:BG:53:LYS:HB3	2.20	0.42
52:BS:40:ILE:HG13	52:BS:69:HIS:O	2.20	0.42
53:BT:42:GLN:NE2	53:BT:42:GLN:O	2.53	0.42
57:BZ:276:VAL:O	57:BZ:280:LEU:HB2	2.19	0.42
1:CA:319:C:H2'	1:CA:320:A:O4'	2.20	0.42
1:CA:593:G:N2	1:CA:665:C:C2	2.88	0.42
1:CA:1071:G:C5	1:CA:1089:G:C2	3.07	0.42
1:CA:1274:A:N3	1:CA:1297:C:H1'	2.34	0.42
1:CA:2050:C:H2'	1:CA:2051:A:O4'	2.19	0.42
1:CA:2677:G:H2'	1:CA:2678:C:H6	1.84	0.42
1:CA:2787:C:H2'	1:CA:2788:C:C6	2.55	0.42
3:CC:195:ARG:HG3	3:CC:195:ARG:NH1	2.35	0.42
4:CD:148:GLU:CB	4:CD:151:LYS:HD2	2.48	0.42
5:CE:143:ASN:HD22	5:CE:147:PRO:HD3	1.84	0.42
8:CH:121:ILE:HD13	8:CH:121:ILE:HA	1.91	0.42
13:CP:57:THR:HG23	13:CP:60:MET:HB2	2.00	0.42
17:CT:65:LYS:O	17:CT:71:GLY:HA2	2.20	0.42
24:C0:33:ALA:HB2	24:C0:63:VAL:C	2.45	0.42
29:C5:51:TYR:CE1	29:C5:56:LYS:HD2	2.55	0.42
34:DA:409:G:H2'	34:DA:410:G:O4'	2.19	0.42
34:DA:592:G:C2	34:DA:648:A:C2	3.08	0.42
34:DA:986:A:H1'	52:DS:54:GLY:O	2.20	0.42
34:DA:1302:U:OP2	46:DM:21:TYR:OH	2.28	0.42
35:DB:98:LEU:HB2	35:DB:101:MET:HG3	2.02	0.42
35:DB:142:LEU:HD12	35:DB:142:LEU:HA	1.84	0.42
35:DB:187:LEU:HA	35:DB:201:ILE:HB	2.01	0.42
41:DH:20:TYR:HA	41:DH:65:TYR:CE2	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:DI:28:VAL:HA	42:DI:63:ILE:O	2.19	0.42
57:DZ:146:LEU:HG	57:DZ:260:LEU:HD23	2.01	0.42
1:AA:653:G:H2'	1:AA:654:G:C8	2.54	0.42
1:AA:1649:A:H5"	1:AA:1650:C:OP2	2.18	0.42
1:AA:1885:A:N1	1:AA:2109:G:O2'	2.37	0.42
1:AA:2073:A:H4'	5:AE:141:ILE:HG12	2.02	0.42
1:AA:2123:G:H1	1:AA:2210:C:H42	1.66	0.42
1:AA:2226:C:O2	1:AA:2232:G:C2	2.73	0.42
1:AA:2543:A:H5'	8:AH:157:TYR:CE1	2.54	0.42
1:AA:2576:A:H2'	1:AA:2577:A:C8	2.55	0.42
3:AC:11:LEU:HD11	3:AC:35:THR:HG23	2.01	0.42
4:AD:13:ARG:HA	4:AD:16:MET:HE3	2.02	0.42
5:AE:26:ILE:HB	5:AE:182:LEU:HB3	2.02	0.42
5:AE:63:LEU:O	5:AE:64:LYS:C	2.63	0.42
14:AQ:35:VAL:O	14:AQ:129:THR:HA	2.19	0.42
16:AS:99:LYS:O	16:AS:102:ALA:HB3	2.19	0.42
26:A2:61:LEU:HA	26:A2:61:LEU:HD23	1.65	0.42
26:A2:70:GLN:H	26:A2:70:GLN:HG3	1.61	0.42
31:A7:22:MET:HE3	31:A7:22:MET:HB3	1.83	0.42
34:BA:159:G:H2'	34:BA:161:A:OP2	2.19	0.42
34:BA:255:G:H1'	50:BQ:16:GLN:NE2	2.31	0.42
34:BA:260:G:H2'	34:BA:261:U:C6	2.54	0.42
34:BA:353:A:H5'	34:BA:353:A:H8	1.84	0.42
34:BA:827:U:H2'	34:BA:870:U:O4	2.19	0.42
34:BA:858:G:O6	34:BA:869:G:H3'	2.19	0.42
34:BA:929:G:N2	34:BA:1389:C:C2	2.88	0.42
34:BA:981:U:H2'	34:BA:982:U:C5	2.54	0.42
36:BC:122:GLU:O	36:BC:126:ARG:NH1	2.42	0.42
37:BD:108:LEU:HB3	37:BD:110:PHE:HE1	1.85	0.42
39:BF:71:ARG:HG2	39:BF:71:ARG:H	1.36	0.42
39:BF:100:ASN:HB2	51:BR:28:GLU:HA	2.01	0.42
46:BM:4:ILE:O	46:BM:22:ILE:HD11	2.20	0.42
57:BZ:99:ARG:HE	57:BZ:402:ILE:HD13	1.85	0.42
57:BZ:269:VAL:O	57:BZ:272:LEU:HB3	2.20	0.42
1:CA:1280:G:N2	1:CA:1291:C:C2	2.88	0.42
1:CA:1555:G:C2	1:CA:1556:C:C6	3.07	0.42
1:CA:2320:A:H2'	1:CA:2320:A:N3	2.34	0.42
1:CA:2748:A:H2'	1:CA:2749:A:C8	2.55	0.42
1:CA:2893:G:H5"	1:CA:2894:G:O4'	2.19	0.42
2:CB:21:G:H2'	2:CB:22:U:O4'	2.20	0.42
2:CB:89:G:C6	2:CB:90:A:C6	3.07	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:CD:133:LEU:HD23	4:CD:133:LEU:HA	1.88	0.42
14:CQ:77:LYS:HE3	14:CQ:82:ARG:O	2.20	0.42
14:CQ:85:LYS:NZ	63:CQ:301:HOH:O	2.52	0.42
17:CT:20:PRO:HB2	17:CT:21:GLU:H	1.44	0.42
21:CX:88:LYS:HB2	21:CX:88:LYS:HE2	1.89	0.42
28:C4:45:GLY:O	28:C4:47:GLN:N	2.52	0.42
34:DA:22:G:H4'	34:DA:885:G:C8	2.55	0.42
34:DA:1457:G:H2'	34:DA:1458:G:H8	1.84	0.42
38:DE:11:ILE:HG22	38:DE:31:LEU:HB3	2.01	0.42
38:DE:102:ALA:HB2	38:DE:120:THR:HG21	2.01	0.42
40:DG:92:SER:O	40:DG:95:ARG:N	2.53	0.42
41:DH:9:MET:HE1	41:DH:32:LYS:O	2.20	0.42
52:DS:41:VAL:HB	52:DS:44:MET:HG3	2.00	0.42
57:DZ:215:LYS:HA	57:DZ:218:GLU:CB	2.50	0.42
1:AA:858:U:C2	1:AA:1297:C:C5	3.08	0.42
1:AA:1128:U:H1'	10:AL:116:ASN:CG	2.45	0.42
1:AA:1358:U:H4'	1:AA:1359:U:O5'	2.20	0.42
1:AA:1522:G:H2'	1:AA:1523:C:H6	1.85	0.42
1:AA:2021:C:H2'	1:AA:2022:G:H8	1.85	0.42
1:AA:2086:C:H2'	1:AA:2087:C:C6	2.54	0.42
1:AA:2556:G:H1'	1:AA:2658:C:C4'	2.50	0.42
3:AC:6:LYS:N	3:AC:9:ARG:HH12	2.17	0.42
4:AD:181:GLU:HG3	4:AD:272:ALA:O	2.20	0.42
5:AE:7:VAL:HG23	5:AE:8:LYS:O	2.19	0.42
7:AG:77:ILE:N	7:AG:82:LEU:O	2.49	0.42
8:AH:41:MET:HE1	8:AH:65:HIS:HA	2.02	0.42
13:AP:47:ASP:OD1	13:AP:47:ASP:C	2.62	0.42
25:A1:70:VAL:O	25:A1:73:LEU:HB2	2.20	0.42
31:A7:23:ARG:O	31:A7:28:ARG:NH1	2.52	0.42
34:BA:323:U:O3'	53:BT:22:ARG:HD3	2.19	0.42
34:BA:396:G:P	57:BZ:349:LYS:NZ	2.93	0.42
34:BA:426:G:C2	34:BA:427:U:C2	3.08	0.42
34:BA:474:G:H2'	34:BA:475:G:C8	2.55	0.42
34:BA:485:G:O2'	34:BA:486:U:OP2	2.35	0.42
34:BA:540:G:H21	37:BD:42:GLN:NE2	2.17	0.42
35:BB:27:LYS:C	35:BB:29:ALA:H	2.26	0.42
36:BC:39:ILE:HD12	36:BC:57:ILE:HD13	2.02	0.42
38:BE:100:VAL:O	38:BE:107:ARG:NH2	2.41	0.42
38:BE:122:GLU:OE1	38:BE:131:ILE:HG13	2.20	0.42
40:BG:28:ASN:C	40:BG:31:MET:H	2.26	0.42
44:BK:19:ALA:N	44:BK:81:ASP:O	2.51	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:BM:81:LEU:O	46:BM:89:GLY:HA3	2.19	0.42
47:BN:4:LYS:O	47:BN:7:ILE:HG12	2.20	0.42
48:BO:24:SER:O	48:BO:28:GLN:HG3	2.20	0.42
57:BZ:271:LEU:HA	57:BZ:274:ASP:HB2	2.01	0.42
1:CA:143:G:C6	1:CA:143(A):C:N4	2.87	0.42
1:CA:583:G:OP2	18:CU:10:ARG:HD2	2.20	0.42
1:CA:742:G:H4'	1:CA:1676:A:H5'	2.02	0.42
1:CA:838:C:H2'	1:CA:839:U:C6	2.55	0.42
1:CA:1217:C:OP1	18:CU:15:LYS:HE3	2.20	0.42
1:CA:1912:A:C8	1:CA:1918:A:C2	3.08	0.42
1:CA:2123:G:N2	1:CA:2176:A:H1'	2.34	0.42
1:CA:2448:A:N6	63:CA:3911:HOH:O	2.50	0.42
2:CB:91:C:O2'	2:CB:92:C:H5'	2.19	0.42
3:CC:48:LEU:CD2	3:CC:59:VAL:HG21	2.50	0.42
3:CC:174:ALA:HA	3:CC:175:PRO:HD3	1.82	0.42
7:CG:14:GLU:C	7:CG:17:PRO:HD2	2.43	0.42
8:CH:149:ARG:HH12	8:CH:154:PRO:HG2	1.84	0.42
13:CP:58:THR:HG21	32:C8:54:GLU:HB3	2.02	0.42
19:CV:30:GLY:H	19:CV:61:VAL:HG13	1.84	0.42
34:DA:232:G:C6	34:DA:233:C:C4	3.08	0.42
34:DA:418:C:H1'	34:DA:540:G:O2'	2.18	0.42
34:DA:630:G:O2'	34:DA:631:G:H5'	2.19	0.42
34:DA:1060:C:OP1	47:DN:45:ARG:NH2	2.48	0.42
34:DA:1179:A:H4'	42:DI:103:THR:HA	2.01	0.42
34:DA:1319:A:H61	34:DA:1361:G:H21	1.66	0.42
38:DE:80:ILE:HD12	38:DE:80:ILE:HA	1.89	0.42
45:DL:96:VAL:H	45:DL:96:VAL:HG23	1.56	0.42
48:DO:24:SER:OG	48:DO:25:THR:N	2.49	0.42
48:DO:54:ARG:O	48:DO:58:MET:HG3	2.20	0.42
52:DS:40:ILE:HB	52:DS:67:VAL:O	2.20	0.42
56:DX:37:A:H5'	57:DZ:500:GLN:O	2.19	0.42
57:DZ:-52:VAL:C	57:DZ:-50:GLN:N	2.78	0.42
57:DZ:242:LEU:HD23	57:DZ:242:LEU:HA	1.72	0.42
1:AA:27:G:N2	1:AA:537:G:H1'	2.34	0.42
1:AA:296:U:H2'	1:AA:297:C:H6	1.85	0.42
1:AA:660:C:O5'	1:AA:660:C:H6	2.02	0.42
1:AA:1005:A:C8	1:AA:1007:G:C8	3.08	0.42
1:AA:1338:U:H2'	1:AA:1339:C:H6	1.79	0.42
1:AA:1522:G:H2'	1:AA:1523:C:C6	2.54	0.42
1:AA:1572:G:C2'	1:AA:1573:G:H5'	2.50	0.42
1:AA:2561:G:N7	63:AA:4005:HOH:O	2.37	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:2824:C:O2'	29:A5:29:THR:HG21	2.20	0.42
3:AC:54:ARG:HE	3:AC:57:GLN:HG2	1.83	0.42
3:AC:225:ILE:O	3:AC:227:PRO:HD3	2.19	0.42
6:AF:65:TRP:CH2	6:AF:72:ARG:CZ	3.02	0.42
11:AN:14:VAL:HA	11:AN:136:GLU:O	2.20	0.42
11:AN:91:LEU:O	11:AN:95:PRO:HG3	2.20	0.42
15:AR:70:LEU:HD12	15:AR:76:VAL:HG22	2.02	0.42
34:BA:254:G:OP1	50:BQ:67:LYS:O	2.37	0.42
34:BA:279:A:N6	50:BQ:98:LEU:O	2.52	0.42
34:BA:410:G:OP1	37:BD:30:LYS:NZ	2.49	0.42
34:BA:494:U:O5'	34:BA:494:U:H6	2.03	0.42
34:BA:515:G:N2	34:BA:537:G:C4	2.88	0.42
34:BA:533:A:O2'	34:BA:535:A:OP2	2.20	0.42
34:BA:609:A:H2'	34:BA:610:G:H5'	2.02	0.42
34:BA:625:G:H4'	49:BP:16:HIS:CG	2.55	0.42
34:BA:1005:A:H5"	34:BA:1006:C:OP2	2.19	0.42
34:BA:1316:G:N2	34:BA:1319:A:OP2	2.48	0.42
44:BK:103:LEU:HD23	44:BK:103:LEU:HA	1.79	0.42
45:BL:26:ALA:HB3	45:BL:98:TYR:OH	2.20	0.42
49:BP:4:ILE:HG12	49:BP:64:ALA:HB1	2.02	0.42
55:BV:12:A:H4'	55:BV:12:A:OP2	2.19	0.42
1:CA:18:C:H2'	1:CA:19:C:C6	2.55	0.42
1:CA:585:G:H2'	1:CA:1251:C:N4	2.35	0.42
1:CA:784:A:C8	1:CA:792:G:C5	3.08	0.42
1:CA:1221(A):C:C2	1:CA:1229:G:N2	2.87	0.42
1:CA:1359:A:C2	1:CA:1360:A:C8	3.08	0.42
1:CA:1509(A):A:C6	1:CA:1509(B):A:C5	3.08	0.42
1:CA:1816:G:H3'	4:CD:62:TYR:CE1	2.55	0.42
1:CA:1878:G:C6	1:CA:1879:C:C4	3.08	0.42
1:CA:1945:G:C6	1:CA:1946:U:C4	3.07	0.42
1:CA:2438:U:O2'	1:CA:2440:C:OP1	2.38	0.42
3:CC:41:THR:O	3:CC:42:VAL:CB	2.64	0.42
6:CF:129:PHE:HB3	6:CF:132:VAL:HG11	2.02	0.42
9:CK:4:LYS:HA	9:CK:5:ARG:HA	1.59	0.42
23:CZ:166:SER:O	23:CZ:169:GLU:HB3	2.20	0.42
34:DA:343:U:O3'	34:DA:344:A:H8	2.03	0.42
34:DA:523:A:H61	45:DL:53:ARG:NH1	2.17	0.42
34:DA:579:G:H2'	34:DA:580:U:C6	2.54	0.42
34:DA:1418:A:H5"	34:DA:1419:G:OP2	2.20	0.42
38:DE:33:VAL:HG13	38:DE:112:LEU:CD1	2.50	0.42
41:DH:82:HIS:CD2	41:DH:82:HIS:C	2.98	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:DI:49:PRO:HG2	42:DI:81:ILE:HG23	2.02	0.42
42:DI:106:ALA:O	42:DI:108:VAL:HG23	2.20	0.42
48:DO:3:ILE:H	48:DO:3:ILE:HG12	1.76	0.42
57:DZ:91:THR:O	57:DZ:92:ILE:HG22	2.19	0.42
57:DZ:208:GLN:HA	57:DZ:211:GLU:HB3	2.01	0.42
57:DZ:626:ALA:C	57:DZ:628:ARG:H	2.27	0.42
1:AA:194:G:O2'	1:AA:195:U:P	2.78	0.42
1:AA:231:G:C8	32:A8:5:LYS:HG3	2.55	0.42
1:AA:485:U:H5"	31:A7:40:TRP:CD2	2.55	0.42
1:AA:830:A:C5	1:AA:832:G:H1'	2.55	0.42
1:AA:1525:G:O2'	1:AA:1605:A:C2	2.72	0.42
1:AA:1530:G:N2	1:AA:1552:C:C2	2.88	0.42
1:AA:2074:G:C8	5:AE:141:ILE:HD11	2.55	0.42
1:AA:2154:U:H5	3:AC:6:LYS:HE3	1.85	0.42
1:AA:2835:C:H2'	1:AA:2836:A:O4'	2.20	0.42
4:AD:130:ALA:C	4:AD:131:LEU:HD12	2.45	0.42
8:AH:3:ARG:CZ	8:AH:5:GLY:H	2.33	0.42
14:AQ:10:ARG:CZ	14:AQ:10:ARG:HB2	2.47	0.42
14:AQ:51:ARG:HG3	14:AQ:66:ILE:HD11	2.01	0.42
17:AT:16:ARG:HD2	17:AT:18:ASP:OD2	2.20	0.42
23:AZ:111:VAL:O	23:AZ:113:ALA:N	2.53	0.42
23:AZ:150:LEU:HB3	23:AZ:171:ILE:HD11	2.01	0.42
25:A1:7:ILE:HD13	25:A1:7:ILE:HA	1.89	0.42
27:A3:4:LEU:HD23	27:A3:4:LEU:HA	1.71	0.42
34:BA:396:G:P	57:BZ:349:LYS:HZ1	2.42	0.42
34:BA:423:G:H3'	34:BA:423:G:N3	2.35	0.42
34:BA:866:C:C4	34:BA:867:G:H1'	2.55	0.42
38:BE:46:GLY:O	38:BE:54:ALA:HB1	2.20	0.42
49:BP:8:ARG:C	49:BP:9:PHE:HD1	2.28	0.42
52:BS:45:VAL:HG11	52:BS:64:GLU:HG2	2.01	0.42
57:BZ:6:GLU:C	57:BZ:8:ASP:N	2.78	0.42
1:CA:29:U:H2'	1:CA:30:G:C8	2.54	0.42
1:CA:450:G:OP1	63:CA:3760:HOH:O	2.22	0.42
1:CA:920:G:O2'	1:CA:921:G:H5'	2.20	0.42
1:CA:1141:U:P	11:CN:25:ARG:HH11	2.42	0.42
1:CA:1343:G:O2'	1:CA:1384:A:N1	2.50	0.42
1:CA:1359:A:C2	1:CA:1372:U:O4	2.73	0.42
1:CA:1580:A:H5'	1:CA:1581:G:OP2	2.20	0.42
1:CA:2143:C:O2	1:CA:2149:G:N2	2.53	0.42
1:CA:2529:G:O6	33:C9:31:LYS:NZ	2.53	0.42
2:CB:80:U:H2'	2:CB:81:G:H8	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:CG:41:GLN:HG2	7:CG:155:MET:HB3	2.02	0.42
12:CO:43:VAL:HG21	12:CO:56:ASP:HB2	2.01	0.42
20:CW:84:ARG:HG3	20:CW:98:LYS:HD2	2.00	0.42
34:DA:298:A:C6	34:DA:299:G:C2	3.08	0.42
34:DA:377:G:OP1	49:DP:3:LYS:HD2	2.19	0.42
34:DA:584:G:O6	63:DA:1811:HOH:O	2.21	0.42
34:DA:659:U:H2'	34:DA:660:G:O4'	2.20	0.42
35:DB:19:HIS:CD2	35:DB:204:ASN:HD21	2.37	0.42
36:DC:43:LEU:O	36:DC:47:LEU:HB2	2.20	0.42
37:DD:129:ASN:HD21	37:DD:145:GLU:H	1.67	0.42
38:DE:151:LEU:H	38:DE:151:LEU:HG	1.68	0.42
39:DF:97:PHE:O	51:DR:31:LEU:HB2	2.19	0.42
42:DI:128:ARG:NH1	56:DX:35:A:OP1	2.53	0.42
47:DN:58:LYS:HB3	47:DN:58:LYS:HE2	1.88	0.42
50:DQ:65:ILE:HD11	50:DQ:72:ARG:HD2	2.02	0.42
56:DX:67:C:H2'	56:DX:68:C:H5'	2.02	0.42
57:DZ:69:VAL:HG12	57:DZ:327:PHE:CD1	2.55	0.42
57:DZ:129:LYS:O	57:DZ:131:PRO:HD3	2.20	0.42
57:DZ:317:MET:O	57:DZ:319:ASP:N	2.53	0.42
1:AA:309:C:H2'	1:AA:310:C:H6	1.85	0.41
1:AA:624:C:O2'	1:AA:628:C:H5"	2.20	0.41
1:AA:864:C:H4'	1:AA:977:G:C6	2.55	0.41
1:AA:1520:G:C5	1:AA:1521:C:C5	3.08	0.41
1:AA:1671:C:H2'	1:AA:1672:G:O4'	2.20	0.41
1:AA:1751:G:O2'	1:AA:1752:G:H5'	2.20	0.41
1:AA:2470:G:H1'	1:AA:2471:A:N7	2.34	0.41
1:AA:2724:U:OP1	1:AA:2727:G:H4'	2.20	0.41
4:AD:248:SER:HB3	4:AD:252:TRP:CZ3	2.55	0.41
8:AH:121:ILE:HD13	8:AH:121:ILE:HA	1.88	0.41
8:AH:125:VAL:HG12	8:AH:127:GLU:O	2.20	0.41
9:AK:126:ALA:O	9:AK:130:THR:N	2.53	0.41
11:AN:4:TYR:CE2	18:AU:100:VAL:HG11	2.54	0.41
22:AY:56:PRO:C	22:AY:58:GLY:N	2.76	0.41
34:BA:7:G:H21	38:BE:121:LYS:HG2	1.85	0.41
34:BA:397:A:N6	34:BA:548:G:C8	2.88	0.41
34:BA:409:G:C4	34:BA:410:G:C8	3.08	0.41
34:BA:636:U:H2'	34:BA:637:G:H8	1.85	0.41
34:BA:834:C:C2	34:BA:853:G:C2	3.08	0.41
34:BA:1123:A:H5'	34:BA:1124:G:P	2.60	0.41
34:BA:1312:G:N7	52:BS:2:PRO:HG2	2.34	0.41
35:BB:64:ARG:HE	35:BB:64:ARG:HB2	1.60	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:BF:10:LEU:HB2	39:BF:59:TYR:HB3	2.02	0.41
42:BI:7:THR:O	42:BI:83:ARG:HD2	2.20	0.41
49:BP:22:THR:OG1	49:BP:23:ASP:N	2.53	0.41
51:BR:58:LEU:HA	51:BR:62:GLU:OE1	2.20	0.41
57:BZ:12:LEU:HD23	57:BZ:283:PRO:HG2	2.02	0.41
57:BZ:201:ILE:HB	57:BZ:206:LEU:HD13	2.01	0.41
1:CA:675:A:H2'	1:CA:676:A:O4'	2.20	0.41
1:CA:881:G:H2'	1:CA:882:G:C8	2.55	0.41
1:CA:1288:U:O4	15:CR:106:GLY:HA3	2.19	0.41
1:CA:1675:C:O5'	1:CA:1675:C:H6	2.03	0.41
1:CA:2176:A:H2'	1:CA:2177:C:C6	2.55	0.41
1:CA:2191:G:C6	1:CA:2192:G:C5	3.08	0.41
1:CA:2537:U:C4	1:CA:2538:C:N4	2.88	0.41
1:CA:2813:A:C2	1:CA:2814:C:C2	3.08	0.41
6:CF:150:GLY:HA2	6:CF:172:TRP:CD2	2.55	0.41
8:CH:9:ILE:HG12	8:CH:69:ARG:HD2	2.01	0.41
24:C0:10:THR:HG22	24:C0:12:ASN:N	2.28	0.41
24:C0:72:ARG:HB3	24:C0:75:LEU:HB2	2.01	0.41
27:C3:20:LYS:HE3	27:C3:20:LYS:HB2	1.63	0.41
34:DA:454:C:H3'	34:DA:455:C:C5	2.55	0.41
34:DA:982:U:H4'	34:DA:983:A:O5'	2.20	0.41
35:DB:71:VAL:HG21	35:DB:164:VAL:HG22	2.02	0.41
37:DD:155:LEU:O	37:DD:159:ARG:HG3	2.19	0.41
38:DE:66:MET:HB3	38:DE:66:MET:HE3	1.68	0.41
44:DK:97:ALA:O	44:DK:101:SER:HB3	2.20	0.41
45:DL:93:LEU:HA	45:DL:94:PRO:HD3	1.88	0.41
48:DO:61:GLY:O	48:DO:64:ARG:HB3	2.20	0.41
57:DZ:309:LEU:HB3	57:DZ:391:GLY:H	1.84	0.41
57:DZ:357:ARG:NH1	57:DZ:373:ASP:CG	2.76	0.41
1:AA:485:U:H4'	31:A7:40:TRP:CZ3	2.55	0.41
1:AA:895:G:N9	1:AA:978:A:H8	2.17	0.41
1:AA:1413:A:C5	1:AA:1414:G:H1'	2.55	0.41
1:AA:1537:G:C5	1:AA:1546:G:N2	2.88	0.41
1:AA:2375:C:H2'	1:AA:2376:C:C6	2.55	0.41
1:AA:2529:C:C6	1:AA:2554:A:N7	2.88	0.41
1:AA:2699:U:H2'	1:AA:2700:U:O4'	2.20	0.41
3:AC:48:LEU:CD2	3:AC:59:VAL:HG21	2.50	0.41
3:AC:60:ARG:NH2	3:AC:165:ARG:HH21	2.18	0.41
3:AC:167:ASP:OD1	3:AC:169:THR:OG1	2.38	0.41
4:AD:20:ASP:O	4:AD:22:SER:N	2.53	0.41
4:AD:142:VAL:HG13	4:AD:191:ALA:HB1	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:AE:7:VAL:HG12	5:AE:51:PHE:HE2	1.85	0.41
6:AF:95:ARG:HH11	6:AF:95:ARG:HD2	1.64	0.41
10:AL:119:ASP:OD1	10:AL:121:GLU:N	2.52	0.41
18:AU:29:SER:C	18:AU:30:LYS:HD3	2.45	0.41
19:AV:60:GLU:HB2	19:AV:97:LYS:HE2	2.02	0.41
19:AV:66:ARG:HH11	19:AV:66:ARG:HD3	1.72	0.41
21:AX:64:LYS:HA	21:AX:64:LYS:HD2	1.67	0.41
24:A0:36:ILE:N	24:A0:36:ILE:HD13	2.34	0.41
28:A4:57:GLU:HA	28:A4:58:ARG:HA	1.63	0.41
34:BA:133:U:H1'	34:BA:230:G:N2	2.35	0.41
34:BA:134:A:H1'	34:BA:325:A:C5	2.54	0.41
34:BA:351:G:H4'	34:BA:352:C:OP1	2.20	0.41
34:BA:402:G:O2'	34:BA:620:C:N3	2.52	0.41
34:BA:662:G:O2'	34:BA:836:G:H5'	2.19	0.41
34:BA:853:G:C6	34:BA:854:G:N7	2.88	0.41
34:BA:853:G:C5	34:BA:854:G:C8	3.08	0.41
34:BA:1188:A:H8	34:BA:1188:A:O5'	2.02	0.41
34:BA:1273:G:H3'	34:BA:1274:G:H8	1.85	0.41
34:BA:1311:G:H1	34:BA:1326:C:H42	1.68	0.41
34:BA:1356:G:H2'	34:BA:1357:A:C8	2.55	0.41
35:BB:96:ARG:HB2	35:BB:148:TYR:HE1	1.84	0.41
35:BB:156:LYS:HE2	35:BB:156:LYS:HB3	1.85	0.41
37:BD:78:LEU:HD23	37:BD:78:LEU:HA	1.80	0.41
53:BT:71:THR:HG22	53:BT:72:LEU:N	2.35	0.41
57:BZ:-18:ALA:O	57:BZ:-14:ALA:HB3	2.20	0.41
57:BZ:94:VAL:HG11	57:BZ:121:VAL:CG2	2.49	0.41
57:BZ:297:GLU:O	57:BZ:297:GLU:HG3	2.19	0.41
1:CA:245:G:O5'	13:CP:73:GLY:HA2	2.20	0.41
1:CA:518:G:H4'	20:CW:18:ARG:NH1	2.35	0.41
1:CA:675:A:N3	1:CA:2443:C:O2'	2.47	0.41
1:CA:1059:G:N9	10:CL:126:MET:HE2	2.35	0.41
1:CA:2360:A:H2'	1:CA:2361:A:O4'	2.19	0.41
1:CA:2488:A:H8	1:CA:2488:A:O5'	2.03	0.41
1:CA:2658:C:O3'	8:CH:158:HIS:CE1	2.69	0.41
1:CA:2833:G:H4'	1:CA:2834:G:OP2	2.20	0.41
5:CE:96:PHE:O	5:CE:175:VAL:HG11	2.20	0.41
23:CZ:153:SER:HA	23:CZ:167:PRO:HB3	2.01	0.41
27:C3:8:LEU:HD23	27:C3:8:LEU:HA	1.67	0.41
34:DA:127:G:N1	34:DA:128:G:C5	2.88	0.41
34:DA:144:G:H2'	34:DA:145:G:C8	2.54	0.41
34:DA:853:G:C4	34:DA:854:G:C8	3.08	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:DA:1173:G:H2'	34:DA:1174:G:H8	1.83	0.41
35:DB:155:LEU:HD22	35:DB:157:ARG:O	2.21	0.41
40:DG:26:PHE:CE1	40:DG:30:ILE:HD11	2.55	0.41
42:DI:46:ALA:HA	42:DI:78:LYS:HB2	2.02	0.41
49:DP:4:ILE:HB	49:DP:66:PRO:HA	2.01	0.41
49:DP:49:LEU:HD12	49:DP:50:LYS:N	2.35	0.41
53:DT:53:LEU:HA	53:DT:53:LEU:HD23	1.90	0.41
57:DZ:74:TRP:CH2	57:DZ:270:GLN:HG2	2.55	0.41
57:DZ:170:ARG:HH11	57:DZ:170:ARG:CG	2.34	0.41
57:DZ:251:ILE:HG21	57:DZ:285:ASP:HB3	2.02	0.41
57:DZ:290:LYS:HB2	57:DZ:291:GLY:H	1.53	0.41
1:AA:402:C:H2'	1:AA:403:C:C6	2.55	0.41
1:AA:668:A:O2'	1:AA:669:A:H5'	2.20	0.41
1:AA:902:G:H2'	1:AA:903:C:O4'	2.19	0.41
1:AA:1135:G:OP2	1:AA:1135:G:H2'	2.20	0.41
1:AA:1304:C:H2'	1:AA:1305:G:O4'	2.20	0.41
1:AA:1310:G:H8	1:AA:1310:G:O5'	2.03	0.41
1:AA:1541:A:H2'	1:AA:1542:A:C8	2.54	0.41
1:AA:1553:A:O2'	1:AA:1554:A:C8	2.73	0.41
1:AA:1932:G:O2'	1:AA:1933:U:H5'	2.20	0.41
1:AA:2099:A:H2'	1:AA:2100:C:C6	2.55	0.41
1:AA:2754:A:H2'	1:AA:2755:C:O4'	2.20	0.41
1:AA:2820:A:O3'	5:AE:61:ARG:HB2	2.20	0.41
1:AA:2855:G:O2'	1:AA:2856:G:H5'	2.21	0.41
1:AA:2897:U:H2'	1:AA:2898:C:H6	1.83	0.41
63:AA:3919:HOH:O	6:AF:104:LYS:HB2	2.20	0.41
7:AG:47:LYS:C	7:AG:86:MET:HE2	2.45	0.41
7:AG:75:LYS:HE3	7:AG:77:ILE:HD11	2.02	0.41
8:AH:158:HIS:O	8:AH:160:LYS:N	2.54	0.41
10:AL:51:ALA:HB2	10:AL:76:TYR:CE2	2.55	0.41
12:AO:80:ASP:CG	17:AT:71:GLY:HA3	2.46	0.41
14:AQ:38:GLU:HB2	14:AQ:39:PRO:HD2	2.02	0.41
14:AQ:134:ARG:CZ	14:AQ:134:ARG:HB3	2.50	0.41
16:AS:30:ARG:HB2	16:AS:35:ILE:HG13	2.01	0.41
30:A6:11:LEU:HD23	30:A6:11:LEU:HA	1.79	0.41
34:BA:427:U:H5'	37:BD:41:GLY:HA2	2.00	0.41
34:BA:461:A:C4	34:BA:471:G:C5	3.08	0.41
34:BA:872:A:C2	34:BA:874:G:C6	3.08	0.41
34:BA:1001:A:H2'	34:BA:1001(A):G:C8	2.55	0.41
34:BA:1084:G:C5	34:BA:1085:U:C4	3.08	0.41
34:BA:1279:A:N1	36:BC:26:LYS:NZ	2.63	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:BA:1370:G:C2	34:BA:1371:G:C8	3.09	0.41
34:BA:1412:C:H2'	34:BA:1413:A:H8	1.83	0.41
36:BC:6:HIS:HD2	36:BC:8:ILE:H	1.69	0.41
39:BF:97:PHE:HB2	51:BR:32:ARG:NH1	2.32	0.41
41:BH:96:GLY:O	41:BH:100:ILE:HG13	2.20	0.41
43:BJ:55:LYS:O	43:BJ:57:LYS:N	2.53	0.41
45:BL:113:ARG:C	45:BL:114:LYS:HD2	2.45	0.41
46:BM:11:ARG:NH1	46:BM:11:ARG:HB3	2.35	0.41
51:BR:32:ARG:HA	51:BR:69:THR:HG21	2.02	0.41
54:BU:5:ASP:O	54:BU:11:GLY:HA3	2.19	0.41
56:BX:75:C:H5"	56:BX:76:A:OP2	2.21	0.41
57:BZ:-55:LEU:HD22	57:BZ:-48:VAL:HG21	2.02	0.41
1:CA:270:A:H1'	1:CA:370:G:C2	2.55	0.41
1:CA:282:A:C8	1:CA:359:A:C6	3.08	0.41
1:CA:693:C:H1'	1:CA:1354:A:H1'	2.02	0.41
1:CA:848:G:C4	1:CA:933:A:C8	3.08	0.41
1:CA:1420:U:HO2'	1:CA:1421:G:P	2.43	0.41
1:CA:1604:C:OP1	63:CA:3761:HOH:O	2.22	0.41
1:CA:1902:C:H2'	1:CA:1903:G:O4'	2.20	0.41
1:CA:2074:U:H2'	1:CA:2075:U:C6	2.55	0.41
1:CA:2299:G:N1	1:CA:2318:G:N7	2.68	0.41
2:CB:8:U:OP1	16:CS:15:ARG:NH2	2.42	0.41
4:CD:3:VAL:HG13	4:CD:17:THR:HB	2.01	0.41
4:CD:26:LYS:HE2	4:CD:28:GLU:O	2.20	0.41
7:CG:41:GLN:NE2	7:CG:153:ARG:HB3	2.34	0.41
8:CH:10:PRO:HA	8:CH:49:VAL:HG23	2.02	0.41
9:CK:49:ALA:N	9:CK:90:ALA:HB1	2.35	0.41
13:CP:84:ASN:CG	13:CP:117:GLU:HB2	2.45	0.41
18:CU:14:HIS:CD2	18:CU:32:PHE:CE1	3.09	0.41
23:CZ:55:HIS:CE1	23:CZ:135:GLU:HB3	2.55	0.41
25:C1:83:GLU:HA	25:C1:84:GLY:HA2	1.64	0.41
33:C9:12:ASP:C	33:C9:13:LYS:HD2	2.45	0.41
33:C9:25:VAL:HB	33:C9:34:GLN:HB2	2.02	0.41
34:DA:297:G:O2'	34:DA:299:G:N7	2.41	0.41
34:DA:954:G:H2'	34:DA:955:U:C6	2.54	0.41
34:DA:1133:G:N2	34:DA:1141:C:O2	2.54	0.41
34:DA:1320:C:H1'	52:DS:73:GLU:HG2	2.02	0.41
36:DC:114:PRO:HA	36:DC:117:ALA:HB3	2.02	0.41
36:DC:137:ALA:HA	36:DC:140:ARG:HH11	1.85	0.41
38:DE:71:LEU:C	38:DE:72:GLN:HG2	2.46	0.41
42:DI:36:TYR:HD2	42:DI:37:PHE:CE2	2.38	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:DJ:47:PHE:CE2	47:DN:37:PHE:HZ	2.38	0.41
44:DK:48:ILE:HD13	44:DK:48:ILE:N	2.36	0.41
44:DK:112:THR:HA	44:DK:113:PRO:HD2	1.92	0.41
46:DM:60:VAL:HG23	46:DM:64:TRP:CZ3	2.55	0.41
48:DO:85:LEU:HB3	48:DO:87:ILE:HG13	2.02	0.41
51:DR:38:GLU:HA	51:DR:41:LYS:NZ	2.35	0.41
53:DT:26:ASN:HB3	53:DT:71:THR:HG23	2.02	0.41
1:AA:360:C:OP1	22:AY:84:ARG:HG2	2.20	0.41
1:AA:789:G:H4'	1:AA:1723:A:H5'	2.03	0.41
1:AA:873:U:H4'	13:AP:55:ARG:HB2	2.02	0.41
1:AA:932:C:N3	1:AA:937:A:N6	2.68	0.41
1:AA:1199:C:H2'	1:AA:1200:G:O4'	2.20	0.41
1:AA:2046:G:H1'	63:AA:4558:HOH:O	2.20	0.41
1:AA:2148:A:N7	1:AA:2185:C:H1'	2.36	0.41
5:AE:93:VAL:HB	5:AE:175:VAL:HG21	2.01	0.41
5:AE:104:VAL:O	5:AE:166:THR:HA	2.20	0.41
8:AH:29:PRO:HD2	8:AH:79:VAL:O	2.20	0.41
9:AK:18:GLU:C	9:AK:20:ALA:H	2.29	0.41
10:AL:80:LYS:HB3	10:AL:80:LYS:HE2	1.71	0.41
11:AN:99:LEU:HD23	11:AN:99:LEU:HA	1.81	0.41
14:AQ:18:LYS:HB2	14:AQ:18:LYS:HE3	1.37	0.41
14:AQ:63:LYS:HE2	23:AZ:175:VAL:HG21	2.01	0.41
15:AR:38:VAL:N	15:AR:39:PRO:CD	2.83	0.41
15:AR:96:ARG:CG	15:AR:115:GLU:HG2	2.51	0.41
17:AT:39:ARG:HH12	17:AT:41:ARG:HD3	1.86	0.41
23:AZ:73:GLN:HE21	23:AZ:73:GLN:HB3	1.60	0.41
34:BA:396:G:O2'	34:BA:398:C:OP1	2.34	0.41
34:BA:397:A:C6	34:BA:548:G:C8	3.09	0.41
34:BA:1244:C:C2	34:BA:1294:G:N2	2.88	0.41
34:BA:1318:A:H2'	34:BA:1319:A:H5"	2.03	0.41
34:BA:1429:C:H2'	34:BA:1430:C:H6	1.85	0.41
35:BB:122:PHE:CZ	35:BB:139:LYS:HB2	2.55	0.41
37:BD:190:ASP:H	37:BD:193:ASP:HB2	1.85	0.41
38:BE:87:SER:HB3	38:BE:131:ILE:HD13	2.02	0.41
41:BH:40:ALA:C	41:BH:42:GLU:H	2.28	0.41
43:BJ:5:ARG:HD3	43:BJ:71:LEU:HD11	2.02	0.41
50:BQ:84:LEU:HA	50:BQ:87:LYS:HB2	2.01	0.41
53:BT:18:GLN:O	53:BT:22:ARG:HG3	2.21	0.41
56:BX:8:4SU:H6	56:BX:8:4SU:O5'	2.20	0.41
56:BX:28:C:C2	56:BX:43:A:C2	3.09	0.41
56:BX:32:5MC:H2'	56:BX:33:U:H6	1.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:BZ:181:LEU:HD22	57:BZ:182:ARG:NH1	2.35	0.41
1:CA:262:A:C2	1:CA:430:G:N3	2.88	0.41
1:CA:1055:G:H5'	1:CA:1056:G:OP2	2.21	0.41
1:CA:1290:C:H2'	1:CA:1291:C:C6	2.56	0.41
1:CA:1316:U:H2'	1:CA:1317:A:C8	2.55	0.41
1:CA:1405:U:H2'	1:CA:1406:U:C6	2.55	0.41
1:CA:1485:G:H2'	1:CA:1486:A:O4'	2.20	0.41
1:CA:2650:U:H2'	1:CA:2651:C:C6	2.56	0.41
1:CA:2858:C:H6	1:CA:2858:C:O5'	2.03	0.41
4:CD:37:LEU:HD12	4:CD:62:TYR:HB2	2.01	0.41
4:CD:48:ARG:O	4:CD:49:ILE:C	2.62	0.41
7:CG:39:ILE:HG13	7:CG:157:ILE:HG23	2.02	0.41
14:CQ:52:VAL:HG22	23:CZ:183:LEU:HD11	2.02	0.41
21:CX:18:TYR:C	21:CX:20:GLY:N	2.78	0.41
23:CZ:158:PRO:O	23:CZ:161:VAL:HG12	2.20	0.41
34:DA:302:G:N3	34:DA:556:C:H4'	2.34	0.41
34:DA:435:C:H2'	34:DA:436:C:H6	1.82	0.41
34:DA:552:U:H5'	45:DL:86:ARG:HE	1.85	0.41
34:DA:728:A:H2'	34:DA:729:A:H8	1.79	0.41
35:DB:100:GLY:O	35:DB:104:ASN:N	2.42	0.41
35:DB:155:LEU:CD1	35:DB:159:PRO:HD3	2.49	0.41
37:DD:19:LEU:O	37:DD:21:LEU:N	2.51	0.41
57:DZ:284:LEU:C	57:DZ:286:ILE:H	2.29	0.41
1:AA:1717:C:H6	1:AA:1717:C:O5'	2.04	0.41
1:AA:1756:U:H1'	1:AA:2870:A:N3	2.35	0.41
1:AA:2383:G:H1'	30:A6:39:TYR:CE1	2.56	0.41
1:AA:2574:U:H1'	12:AO:23:ARG:NH1	2.36	0.41
1:AA:2807:C:H42	1:AA:2813:G:H1	1.69	0.41
3:AC:11:LEU:HD22	3:AC:11:LEU:H	1.86	0.41
23:AZ:139:VAL:HG22	23:AZ:155:LEU:HD12	2.02	0.41
34:BA:298:A:H2'	34:BA:299:G:O4'	2.21	0.41
34:BA:939:G:C6	34:BA:940:C:C4	3.09	0.41
34:BA:1412:C:C2	34:BA:1489:G:N2	2.88	0.41
34:BA:1460:A:H5"	34:BA:1461:G:OP2	2.20	0.41
40:BG:69:VAL:HG12	40:BG:69:VAL:O	2.20	0.41
48:BO:84:LYS:HD3	48:BO:84:LYS:O	2.20	0.41
57:BZ:125:ALA:HB1	57:BZ:132:ARG:HH21	1.85	0.41
57:BZ:129:LYS:HD2	57:BZ:253:LEU:HD22	2.03	0.41
57:BZ:349:LYS:HG2	57:BZ:350:GLU:N	2.34	0.41
1:CA:118:A:C8	1:CA:119:A:C8	3.09	0.41
1:CA:414:C:H4'	1:CA:1879:C:O2	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:673:C:H5”	6:CF:81:PRO:HD2	2.03	0.41
1:CA:838:C:H2’	1:CA:839:U:H6	1.85	0.41
1:CA:1019:U:OP1	1:CA:1035:U:O2’	2.30	0.41
1:CA:2064:C:O2	1:CA:2450:A:C6	2.73	0.41
1:CA:2507:C:H1’	1:CA:2583:G:N2	2.35	0.41
1:CA:2838:G:C6	1:CA:2839:G:C5	3.09	0.41
6:CF:108:LYS:HE3	6:CF:108:LYS:HB2	1.93	0.41
7:CG:39:ILE:HG23	7:CG:157:ILE:HG12	2.03	0.41
7:CG:136:ARG:NH1	7:CG:137:GLU:H	2.11	0.41
12:CO:48:PRO:HB3	34:DA:1422:G:H5’	2.02	0.41
14:CQ:116:GLU:CD	14:CQ:119:ARG:HH21	2.29	0.41
15:CR:38:VAL:HG23	15:CR:110:PRO:O	2.20	0.41
15:CR:67:LEU:CD1	15:CR:76:VAL:HG21	2.50	0.41
23:CZ:46:LYS:HE3	23:CZ:46:LYS:HB2	1.95	0.41
23:CZ:61:LEU:HB2	23:CZ:65:GLN:HB3	2.03	0.41
23:CZ:85:HIS:HE1	23:CZ:87:ASP:OD2	2.03	0.41
24:C0:82:ARG:HA	24:C0:83:PRO:HD3	1.86	0.41
28:C4:8:LYS:O	28:C4:27:THR:HA	2.21	0.41
34:DA:130:A:C8	50:DQ:63:ARG:HG3	2.54	0.41
34:DA:451:A:H61	34:DA:480:U:H2’	1.85	0.41
34:DA:832:C:N4	34:DA:833:U:C4	2.88	0.41
34:DA:1531:A:N7	34:DA:1532:U:C4	2.89	0.41
35:DB:204:ASN:OD1	35:DB:205:ASP:N	2.54	0.41
38:DE:41:VAL:HG22	38:DE:113:ALA:HB2	2.01	0.41
40:DG:126:ASP:HB3	40:DG:131:LYS:HB3	2.01	0.41
41:DH:85:ARG:NH2	41:DH:134:ILE:HG23	2.32	0.41
43:DJ:52:GLY:HA2	43:DJ:53:PRO:HD3	1.88	0.41
47:DN:22:THR:HB	47:DN:33:VAL:HB	2.01	0.41
55:DV:17:U:O2	57:DZ:502:GLY:O	2.37	0.41
57:DZ:170:ARG:HA	57:DZ:170:ARG:HD3	1.49	0.41
1:AA:160:G:O2’	1:AA:161:C:H5’	2.19	0.41
1:AA:332:G:C8	1:AA:526:A:O4’	2.73	0.41
1:AA:753:A:H2’	1:AA:754:G:O4’	2.20	0.41
1:AA:1109:G:H2’	1:AA:1110:C:O4’	2.21	0.41
1:AA:1857:G:H2’	1:AA:1858:C:O4’	2.21	0.41
1:AA:2562:G:C2	1:AA:2571:C:O2	2.73	0.41
6:AF:64:ILE:HG13	6:AF:65:TRP:N	2.35	0.41
8:AH:35:VAL:O	8:AH:37:VAL:HG23	2.21	0.41
13:AP:135:LEU:HD23	13:AP:135:LEU:HA	1.88	0.41
14:AQ:139:GLU:H	14:AQ:139:GLU:HG3	1.26	0.41
34:BA:120:A:C6	34:BA:122:G:C2	3.09	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:BA:224:C:OP1	53:BT:74:LYS:HE2	2.21	0.41
34:BA:341:C:O2'	34:BA:342:C:H5'	2.21	0.41
34:BA:407:G:O2'	37:BD:116:GLN:HA	2.20	0.41
34:BA:427:U:OP1	37:BD:13:ARG:NH2	2.54	0.41
34:BA:435:C:O5'	34:BA:435:C:H6	2.03	0.41
34:BA:581:G:N2	34:BA:582:U:C4	2.89	0.41
35:BB:15:VAL:HB	35:BB:209:ARG:HD3	2.02	0.41
35:BB:28:PHE:CD1	35:BB:190:THR:HA	2.56	0.41
35:BB:86:GLU:C	35:BB:88:ALA:N	2.78	0.41
35:BB:149:LEU:HD23	35:BB:149:LEU:HA	1.76	0.41
38:BE:98:THR:HB	38:BE:99:GLY:H	1.58	0.41
41:BH:134:ILE:HG12	41:BH:134:ILE:H	1.67	0.41
52:BS:12:ASP:C	52:BS:14:HIS:H	2.29	0.41
53:BT:63:ILE:HG22	53:BT:77:ALA:HB1	2.03	0.41
53:BT:100:ILE:HD13	53:BT:100:ILE:H	1.85	0.41
57:BZ:137:ASN:OD1	57:BZ:138:LYS:N	2.51	0.41
57:BZ:160:ARG:HE	57:BZ:255:ILE:N	2.18	0.41
57:BZ:165:GLN:HA	57:BZ:178:ILE:O	2.21	0.41
57:BZ:181:LEU:HD23	57:BZ:182:ARG:CG	2.50	0.41
1:CA:719:C:H2'	1:CA:720:C:C6	2.56	0.41
1:CA:1163:G:C2'	1:CA:1164:G:H5'	2.50	0.41
1:CA:1355:G:H8	1:CA:1355:G:O5'	2.04	0.41
1:CA:1570:A:H2'	1:CA:1571:A:C8	2.55	0.41
1:CA:1638:C:H2'	1:CA:1639:U:O4'	2.21	0.41
1:CA:2123:G:H21	3:CC:45:HIS:CE1	2.29	0.41
1:CA:2594:C:N3	1:CA:2600:A:C2	2.89	0.41
1:CA:2786:U:H4'	5:CE:65:GLY:C	2.45	0.41
4:CD:36:PRO:HA	4:CD:61:LEU:HD12	2.02	0.41
6:CF:148:LEU:HD22	6:CF:191:ARG:HD2	2.03	0.41
11:CN:20:GLY:HA2	11:CN:61:ARG:CZ	2.51	0.41
12:CO:71:ARG:NH2	12:CO:104:ARG:HB3	2.36	0.41
15:CR:8:ARG:O	15:CR:17:ARG:HD3	2.20	0.41
34:DA:902:G:C2	34:DA:903:G:C8	3.09	0.41
35:DB:115:LEU:O	35:DB:119:GLU:N	2.51	0.41
39:DF:72:VAL:O	39:DF:75:LEU:HB3	2.21	0.41
57:DZ:127:LYS:HG2	57:DZ:128:TYR:CE2	2.54	0.41
57:DZ:203:GLU:O	57:DZ:206:LEU:HB3	2.19	0.41
57:DZ:216:LEU:O	57:DZ:219:VAL:HG12	2.20	0.41
1:AA:504:A:C6	1:AA:506:A:C6	3.09	0.41
1:AA:1275:G:H2'	1:AA:1276:C:C6	2.56	0.41
1:AA:1438:A:C6	1:AA:1439:A:C6	3.09	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:2422:G:H2'	1:AA:2423:A:O4'	2.20	0.41
1:AA:2433:G:H5"	1:AA:2434:A:OP2	2.20	0.41
1:AA:2521:G:C2'	1:AA:2522:C:H5'	2.51	0.41
1:AA:2599:A:N6	1:AA:2620:G:O2'	2.53	0.41
1:AA:2736:C:O3'	15:AR:1:MET:HE1	2.20	0.41
3:AC:194:ILE:CD1	3:AC:227:PRO:CB	2.99	0.41
8:AH:143:GLN:HG3	8:AH:147:ASN:HD21	1.85	0.41
15:AR:53:HIS:O	15:AR:56:LYS:HB2	2.21	0.41
23:AZ:157:LEU:HD23	23:AZ:157:LEU:HA	1.90	0.41
28:A4:3:GLU:O	28:A4:5:ILE:N	2.54	0.41
34:BA:123:C:OP1	34:BA:311:C:O2'	2.32	0.41
34:BA:374:A:C4	34:BA:375:U:C5	3.08	0.41
34:BA:614:A:C2	34:BA:627:G:C2	3.09	0.41
34:BA:731:G:OP1	34:BA:766:A:H1'	2.20	0.41
34:BA:872:A:C4	34:BA:874:G:C8	3.09	0.41
34:BA:1248:A:C2	42:BI:70:LYS:HE2	2.55	0.41
34:BA:1433:A:C4	34:BA:1468:A:C2	3.09	0.41
36:BC:31:HIS:C	36:BC:33:LEU:N	2.78	0.41
36:BC:155:GLY:O	36:BC:157:ILE:HD12	2.20	0.41
47:BN:25:VAL:HG22	47:BN:38:GLY:O	2.19	0.41
52:BS:40:ILE:HG12	52:BS:71:LEU:HD12	2.03	0.41
56:BX:64:G:H2'	56:BX:65:C:C6	2.55	0.41
57:BZ:71:THR:HG22	57:BZ:80:ASN:OD1	2.20	0.41
57:BZ:127:LYS:HD3	57:BZ:128:TYR:CE2	2.55	0.41
57:BZ:317:MET:HE2	57:BZ:317:MET:HB3	1.78	0.41
1:CA:77:C:O2'	26:C2:14:ARG:NH2	2.50	0.41
1:CA:458:G:H8	31:C7:37:LYS:O	2.04	0.41
1:CA:534:U:H2'	1:CA:535:C:C6	2.56	0.41
1:CA:858:U:O2	1:CA:2268:A:H2'	2.21	0.41
1:CA:863:A:C2	1:CA:864:G:C4	3.09	0.41
1:CA:921:G:C6	1:CA:922:U:N3	2.89	0.41
1:CA:1055:G:H3'	1:CA:1056:G:C8	2.55	0.41
1:CA:1226:A:P	19:CV:84:LYS:HE2	2.60	0.41
1:CA:1355:G:P	4:CD:38:LYS:HE2	2.61	0.41
1:CA:1484:G:C6	1:CA:1485:G:C5	3.08	0.41
1:CA:2371:G:C2	1:CA:2372:G:C8	3.08	0.41
1:CA:2491:U:H1'	1:CA:2569:G:O3'	2.20	0.41
1:CA:2627:G:N2	1:CA:2777:G:OP2	2.53	0.41
1:CA:2723:C:P	5:CE:109:LYS:NZ	2.93	0.41
4:CD:106:ILE:HD12	4:CD:106:ILE:HG21	1.87	0.41
6:CF:148:LEU:HD13	6:CF:154:VAL:HG21	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:CH:71:LEU:HD12	8:CH:71:LEU:HA	1.83	0.41
13:CP:39:LYS:O	13:CP:39:LYS:HG2	2.19	0.41
18:CU:83:LEU:HG	18:CU:88:ILE:HB	2.02	0.41
21:CX:67:GLY:C	21:CX:69:TYR:H	2.28	0.41
23:CZ:108:PRO:HA	23:CZ:142:SER:HA	2.03	0.41
27:C3:4:LEU:HD23	27:C3:4:LEU:HA	1.76	0.41
34:DA:350:G:C6	34:DA:351:G:O6	2.73	0.41
34:DA:391:G:C5	34:DA:392:G:C8	3.09	0.41
34:DA:392:G:C2	34:DA:393:A:C4	3.08	0.41
34:DA:579:G:C5	34:DA:580:U:C5	3.09	0.41
34:DA:855:G:C6	34:DA:856:C:C4	3.09	0.41
34:DA:957:U:O2	34:DA:959:A:C8	2.74	0.41
34:DA:1053:G:H4'	34:DA:1054:C:H5'	2.01	0.41
35:DB:16:HIS:CG	35:DB:17:PHE:N	2.74	0.41
36:DC:182:ILE:HA	36:DC:202:ILE:O	2.21	0.41
43:DJ:48:THR:OG1	43:DJ:62:HIS:CE1	2.74	0.41
51:DR:58:LEU:HD13	51:DR:58:LEU:HA	1.85	0.41
57:DZ:-27:THR:O	57:DZ:-26:GLU:C	2.63	0.41
57:DZ:82:ILE:O	57:DZ:84:THR:HG23	2.21	0.41
57:DZ:185:ALA:HB3	57:DZ:200:PRO:O	2.20	0.41
1:AA:320:C:H2'	1:AA:321:C:H6	1.86	0.41
1:AA:771:U:H2'	1:AA:772:G:O4'	2.21	0.41
1:AA:779:C:H2'	1:AA:780:G:O4'	2.20	0.41
1:AA:791:G:OP1	63:AA:3944:HOH:O	2.22	0.41
1:AA:861:C:H4'	1:AA:1270:C:O2	2.20	0.41
1:AA:874:U:O2	1:AA:2258:G:H4'	2.21	0.41
1:AA:1114:G:O2'	1:AA:1142:A:O2'	2.35	0.41
1:AA:1856:A:OP1	4:AD:249:PRO:HD3	2.21	0.41
1:AA:2372:A:H2'	1:AA:2373:A:O4'	2.21	0.41
1:AA:2859:U:N3	1:AA:2877:G:O4'	2.53	0.41
2:AB:32:C:C2	2:AB:51:G:N2	2.88	0.41
4:AD:35:LYS:HB2	4:AD:36:PRO:HD2	2.01	0.41
4:AD:131:LEU:HB2	4:AD:136:ILE:HD11	2.03	0.41
5:AE:97:LYS:HE2	5:AE:97:LYS:HB3	1.92	0.41
7:AG:34:LEU:HD23	7:AG:161:THR:OG1	2.21	0.41
7:AG:61:ALA:O	28:A4:7:PRO:HG2	2.20	0.41
7:AG:121:ASN:HA	7:AG:122:PRO:HD3	1.85	0.41
8:AH:92:ILE:HD13	8:AH:92:ILE:HA	1.92	0.41
15:AR:16:HIS:O	15:AR:16:HIS:CD2	2.73	0.41
17:AT:27:THR:HB	17:AT:89:VAL:CG2	2.51	0.41
28:A4:61:ARG:HH21	52:BS:42:PRO:CD	2.34	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:BA:15:G:C4	34:BA:16:A:C8	3.09	0.41
34:BA:118:U:O4	34:BA:289:G:H4'	2.21	0.41
34:BA:244:U:O4	34:BA:906:G:H1'	2.21	0.41
34:BA:435:C:H2'	34:BA:436:C:C6	2.55	0.41
34:BA:1013:G:N2	34:BA:1016:A:OP2	2.51	0.41
34:BA:1418:A:O5'	34:BA:1418:A:H8	2.04	0.41
34:BA:1470:G:H2'	34:BA:1471:G:O4'	2.21	0.41
34:BA:1480:G:C6	34:BA:1481:U:C4	3.09	0.41
34:BA:1524:C:H2'	34:BA:1525:G:O4'	2.21	0.41
35:BB:86:GLU:C	35:BB:88:ALA:H	2.29	0.41
35:BB:186:ALA:N	35:BB:199:TYR:O	2.49	0.41
37:BD:125:HIS:O	37:BD:148:VAL:HG13	2.21	0.41
40:BG:113:GLU:HG3	40:BG:119:ARG:HA	2.02	0.41
53:BT:48:LYS:HA	53:BT:48:LYS:HD3	1.83	0.41
57:BZ:-20:LEU:HD22	57:BZ:-20:LEU:HA	1.85	0.41
57:BZ:180:VAL:O	57:BZ:213:HIS:CD2	2.74	0.41
57:BZ:230:LYS:HD2	57:BZ:235:GLU:CB	2.51	0.41
1:CA:185:U:C2	1:CA:212:G:N2	2.89	0.41
1:CA:309:G:O2'	1:CA:329:G:C8	2.71	0.41
1:CA:321:G:OP2	6:CF:135:LYS:HG3	2.21	0.41
1:CA:918:A:C5	1:CA:919:G:H1'	2.56	0.41
1:CA:950:G:H2'	1:CA:951:C:C6	2.55	0.41
1:CA:960:A:H2'	1:CA:962:G:H5'	2.02	0.41
1:CA:2016:U:C4	1:CA:2017:U:C4	3.09	0.41
1:CA:2206:G:H3'	1:CA:2207:G:N7	2.30	0.41
1:CA:2699:C:H2'	1:CA:2700:C:O4'	2.20	0.41
2:CB:14:U:H5'	2:CB:70:C:O2	2.21	0.41
7:CG:170:ARG:HD3	7:CG:170:ARG:HA	1.78	0.41
8:CH:143:GLN:O	8:CH:146:ALA:HB3	2.21	0.41
15:CR:28:LEU:HA	15:CR:28:LEU:HD23	1.84	0.41
16:CS:3:ARG:HE	16:CS:4:LEU:N	2.19	0.41
19:CV:72:VAL:O	19:CV:72:VAL:HG22	2.21	0.41
23:CZ:94:GLU:HA	23:CZ:95:PRO:HD2	1.90	0.41
26:C2:19:VAL:HA	26:C2:22:GLU:HG2	2.02	0.41
33:C9:29:ASN:HA	33:C9:30:PRO:HD3	1.88	0.41
34:DA:274:A:N3	34:DA:275:G:H1'	2.36	0.41
34:DA:729:A:H2'	34:DA:730:G:H8	1.85	0.41
34:DA:807:A:H2'	34:DA:808:C:H6	1.83	0.41
34:DA:1008:C:H2'	34:DA:1009:G:O4'	2.20	0.41
34:DA:1060:C:N3	34:DA:1198:G:N1	2.68	0.41
34:DA:1190:G:OP1	36:DC:5:ILE:N	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:DA:1305:G:H5'	54:DU:4:GLY:C	2.46	0.41
34:DA:1509:C:H2'	34:DA:1510:U:O4'	2.20	0.41
37:DD:15:GLU:HB3	37:DD:63:LYS:HG3	2.03	0.41
38:DE:36:ASP:C	38:DE:38:GLN:N	2.79	0.41
41:DH:12:ARG:HH11	41:DH:12:ARG:HD2	1.73	0.41
47:DN:24:CYS:O	47:DN:28:GLY:HA2	2.21	0.41
51:DR:51:LEU:HA	51:DR:51:LEU:HD23	1.82	0.41
57:DZ:140:ASP:HA	57:DZ:171:GLU:O	2.21	0.41
57:DZ:290:LYS:H	57:DZ:290:LYS:HG2	1.61	0.41
1:AA:701:A:H2	1:AA:702:A:C2	2.39	0.41
1:AA:874:U:H5'	1:AA:875:U:H5'	2.03	0.41
1:AA:1088:G:C6	1:AA:1089:C:C4	3.09	0.41
1:AA:1249:A:N1	1:AA:1287:A:N7	2.68	0.41
1:AA:1303:C:OP1	6:AF:75:HIS:NE2	2.42	0.41
1:AA:1558:G:H2'	1:AA:1559:C:O4'	2.21	0.41
1:AA:1785:C:H2'	1:AA:1786:A:O4'	2.21	0.41
1:AA:2105:G:O5'	1:AA:2105:G:H8	2.04	0.41
1:AA:2240:G:C6	1:AA:2241:C:C4	3.09	0.41
1:AA:2724:U:H5	1:AA:2728:C:OP1	2.04	0.41
2:AB:69:G:H2'	2:AB:70:C:C6	2.56	0.41
3:AC:44:VAL:HG23	3:AC:176:VAL:CG2	2.51	0.41
3:AC:189:ASN:O	3:AC:190:ILE:C	2.64	0.41
4:AD:16:MET:HE3	4:AD:16:MET:HB3	1.82	0.41
4:AD:20:ASP:C	4:AD:22:SER:N	2.79	0.41
4:AD:24:ILE:HG23	4:AD:83:GLU:HA	2.03	0.41
4:AD:178:PRO:C	4:AD:180:GLY:H	2.28	0.41
6:AF:150:GLY:HA2	6:AF:172:TRP:CD2	2.56	0.41
7:AG:6:ALA:HB3	7:AG:104:GLU:OE2	2.21	0.41
8:AH:23:ARG:CZ	8:AH:23:ARG:HB2	2.49	0.41
10:AL:40:ALA:HB3	10:AL:67:PHE:HZ	1.86	0.41
14:AQ:27:VAL:HG11	14:AQ:134:ARG:HG3	2.02	0.41
14:AQ:118:LEU:HB3	14:AQ:131:ILE:HG12	2.03	0.41
23:AZ:30:ASN:O	23:AZ:32:HIS:N	2.54	0.41
23:AZ:94:GLU:H	23:AZ:94:GLU:HG3	1.62	0.41
25:A1:73:LEU:HD12	25:A1:94:LEU:HB3	2.03	0.41
31:A7:33:ARG:HH11	31:A7:33:ARG:HD2	1.63	0.41
32:A8:31:HIS:CD2	32:A8:32:LEU:HD22	2.56	0.41
34:BA:28:G:O2'	34:BA:296:U:OP1	2.26	0.41
34:BA:437:U:O2'	37:BD:125:HIS:CE1	2.74	0.41
34:BA:828:A:OP2	41:BH:21:LYS:NZ	2.53	0.41
34:BA:949:A:H2'	34:BA:950:U:O4'	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:BA:1234:C:H2'	34:BA:1235:U:H6	1.82	0.41
34:BA:1396:A:H4'	34:BA:1397:C:O5'	2.20	0.41
34:BA:1438:G:H2'	34:BA:1439:C:H6	1.85	0.41
35:BB:80:ILE:HD11	35:BB:212:GLN:HA	2.03	0.41
35:BB:139:LYS:O	35:BB:143:GLU:HB2	2.21	0.41
37:BD:10:ARG:HA	37:BD:13:ARG:HG3	2.03	0.41
38:BE:43:LEU:CB	38:BE:136:MET:HE2	2.51	0.41
38:BE:66:MET:HB3	38:BE:66:MET:HE3	1.87	0.41
38:BE:123:LEU:HA	38:BE:123:LEU:HD23	1.70	0.41
39:BF:25:ILE:HD13	39:BF:25:ILE:HA	1.75	0.41
39:BF:38:GLU:HB2	39:BF:64:GLN:HG2	2.01	0.41
43:BJ:70:ARG:HA	43:BJ:70:ARG:HD3	1.87	0.41
45:BL:80:HIS:ND1	57:BZ:425:SER:HA	2.36	0.41
46:BM:11:ARG:HA	46:BM:45:VAL:HB	2.03	0.41
46:BM:15:VAL:HA	46:BM:18:ALA:HB3	2.02	0.41
46:BM:34:LEU:HD13	46:BM:41:PRO:HA	2.03	0.41
48:BO:43:LEU:HD13	48:BO:53:HIS:HD2	1.86	0.41
50:BQ:27:PHE:CE2	50:BQ:36:ILE:HD11	2.56	0.41
51:BR:47:THR:HG23	51:BR:49:LYS:HG3	2.02	0.41
52:BS:27:GLU:HB3	52:BS:28:LYS:HD2	2.02	0.41
53:BT:10:LEU:O	53:BT:13:LEU:HD11	2.21	0.41
57:BZ:-59:PRO:HD3	57:BZ:-52:VAL:HB	2.03	0.41
57:BZ:164:MET:SD	57:BZ:257:PRO:HB3	2.61	0.41
57:BZ:238:THR:OG1	57:BZ:241:GLU:HG2	2.21	0.41
57:BZ:305:PRO:HA	57:BZ:333:GLY:O	2.21	0.41
1:CA:176:G:O2'	1:CA:177:G:H5'	2.21	0.41
1:CA:251:A:C5	1:CA:252:G:H1'	2.56	0.41
1:CA:466:A:N1	1:CA:795:C:O2'	2.49	0.41
1:CA:620:G:H8	1:CA:622:G:O6	2.04	0.41
1:CA:729:G:C6	4:CD:208:LYS:HB2	2.55	0.41
1:CA:823:G:C6	1:CA:824:A:C6	3.08	0.41
1:CA:953:A:OP2	14:CQ:16:ARG:NE	2.54	0.41
1:CA:1067:A:O2'	57:DZ:633:GLY:HA2	2.21	0.41
1:CA:1102:C:H2'	1:CA:1103:A:H8	1.82	0.41
1:CA:1286:A:C6	1:CA:1289:C:C2	3.09	0.41
1:CA:1289:C:H2'	1:CA:1290:C:C6	2.56	0.41
1:CA:1305:C:C2	1:CA:1624:G:C2	3.09	0.41
1:CA:1309:G:P	31:C7:9:ARG:HD3	2.61	0.41
1:CA:1394:U:H2'	1:CA:1395:A:O4'	2.21	0.41
1:CA:1541:G:H3'	1:CA:1542:A:H2'	2.03	0.41
1:CA:1782:C:H1'	1:CA:2609:U:O4'	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1922:G:H2'	1:CA:1923:U:O4'	2.21	0.41
1:CA:2113:U:H2'	1:CA:2114:A:C8	2.51	0.41
1:CA:2390:U:P	32:C8:35:GLN:HE22	2.44	0.41
2:CB:38:C:H2'	2:CB:39:A:H8	1.85	0.41
3:CC:60:ARG:NH2	3:CC:165:ARG:HH21	2.18	0.41
5:CE:9:VAL:HG13	5:CE:25:VAL:HB	2.03	0.41
6:CF:101:LEU:O	6:CF:106:ARG:HD3	2.21	0.41
7:CG:86:MET:HA	7:CG:87:PRO:HD2	1.79	0.41
8:CH:38:SER:HA	8:CH:39:PRO:HD3	1.85	0.41
8:CH:101:ARG:NH2	8:CH:122:THR:HG23	2.36	0.41
10:CL:16:LYS:HB2	10:CL:16:LYS:HE3	1.78	0.41
10:CL:88:ALA:HB3	10:CL:134:MET:O	2.21	0.41
10:CL:100:THR:HB	10:CL:101:TRP:H	1.72	0.41
11:CN:20:GLY:HA2	11:CN:61:ARG:NE	2.36	0.41
11:CN:23:LEU:HA	11:CN:60:ILE:HD11	2.01	0.41
11:CN:39:ARG:HA	11:CN:40:PRO:HD2	1.94	0.41
14:CQ:1:MET:HB3	14:CQ:48:GLU:HG3	2.03	0.41
14:CQ:41:TRP:HB3	14:CQ:94:VAL:HB	2.02	0.41
14:CQ:111:GLU:HG3	14:CQ:112:GLU:N	2.33	0.41
18:CU:98:LEU:C	18:CU:100:VAL:H	2.29	0.41
19:CV:62:LEU:HB2	19:CV:93:GLU:O	2.21	0.41
21:CX:90:GLU:C	21:CX:92:LEU:H	2.29	0.41
23:CZ:180:VAL:O	23:CZ:183:LEU:HB3	2.21	0.41
25:C1:51:VAL:HG13	25:C1:53:VAL:HG23	2.03	0.41
26:C2:51:ARG:O	26:C2:55:ARG:HG3	2.20	0.41
30:C6:35:GLU:CD	30:C6:50:ARG:HH11	2.29	0.41
34:DA:34:C:H2'	34:DA:35:G:C8	2.56	0.41
34:DA:41:G:H2'	34:DA:42:G:C8	2.56	0.41
34:DA:149:A:H2'	34:DA:150:C:C6	2.55	0.41
34:DA:356:A:N3	34:DA:368:U:O2'	2.48	0.41
34:DA:491:G:H2'	34:DA:492:G:H8	1.86	0.41
34:DA:502:G:N1	34:DA:503:C:C2	2.89	0.41
34:DA:522:C:H41	45:DL:53:ARG:HH22	1.69	0.41
34:DA:831:U:H2'	34:DA:832:C:H6	1.86	0.41
34:DA:921:U:H2'	34:DA:922:G:O4'	2.20	0.41
34:DA:944:G:N1	34:DA:1338:G:OP2	2.47	0.41
34:DA:977:A:H2'	34:DA:978:A:H5"	2.02	0.41
34:DA:1051:C:H2'	34:DA:1052:U:C6	2.55	0.41
34:DA:1096:C:H2'	34:DA:1097:C:H6	1.85	0.41
34:DA:1121:U:C2'	34:DA:1122:U:H5'	2.51	0.41
34:DA:1344:C:H4'	42:DI:120:ARG:HB3	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:DA:1392:G:N2	34:DA:1502:A:H8	2.19	0.41
35:DB:56:ARG:HD2	35:DB:56:ARG:HA	1.73	0.41
35:DB:84:GLU:HA	35:DB:87:ARG:HD3	2.01	0.41
35:DB:178:ARG:NH1	35:DB:196:LEU:O	2.54	0.41
36:DC:19:GLU:HB3	36:DC:40:ARG:NH2	2.36	0.41
36:DC:125:GLU:HG2	36:DC:190:ARG:O	2.20	0.41
40:DG:50:ILE:HG22	40:DG:125:MET:HG3	2.03	0.41
40:DG:105:VAL:O	40:DG:108:ALA:HB3	2.20	0.41
46:DM:78:ILE:HG23	46:DM:92:HIS:CD2	2.55	0.41
48:DO:81:LEU:HA	48:DO:81:LEU:HD12	1.85	0.41
52:DS:20:LEU:C	52:DS:22:LEU:H	2.29	0.41
55:DV:16:A:C2	55:DV:17:U:C2	3.09	0.41
57:DZ:215:LYS:HA	57:DZ:218:GLU:HB2	2.02	0.41
57:DZ:503:GLY:C	57:DZ:505:GLY:N	2.79	0.41
1:AA:116:A:H3'	1:AA:117:A:C5'	2.51	0.41
1:AA:407:U:H4'	25:A1:16:ASN:O	2.21	0.41
1:AA:770:G:H2'	1:AA:771:U:O4'	2.21	0.41
1:AA:920:G:N2	1:AA:951:U:C2	2.89	0.41
1:AA:1133:G:C2	1:AA:1149:A:C2	3.09	0.41
1:AA:1188:A:C4	1:AA:1190:G:C8	3.09	0.41
1:AA:1404:G:O2'	1:AA:1405:A:H5"	2.20	0.41
1:AA:1405:A:H61	1:AA:1418:U:H3	1.69	0.41
1:AA:1773:C:H2'	1:AA:1774:C:C6	2.56	0.41
1:AA:2154:U:N1	3:AC:6:LYS:HB3	2.36	0.41
1:AA:2347:A:OP1	16:AS:13:ARG:HB2	2.21	0.41
1:AA:2653:G:H5"	1:AA:2653:G:C8	2.55	0.41
1:AA:2804:C:C5	1:AA:2902:G:C5	3.09	0.41
1:AA:2880:C:H5"	15:AR:65:LEU:HD21	2.03	0.41
7:AG:66:GLN:NE2	7:AG:93:THR:O	2.51	0.41
12:AO:8:LEU:N	12:AO:8:LEU:HD23	2.36	0.41
14:AQ:32:TYR:CE1	14:AQ:133:ARG:HB2	2.56	0.41
15:AR:100:LEU:HD12	15:AR:100:LEU:HA	1.83	0.41
18:AU:13:LYS:HB3	18:AU:13:LYS:HE3	1.49	0.41
32:A8:50:LEU:HD23	32:A8:50:LEU:HA	1.92	0.41
34:BA:124:G:C5	34:BA:125:U:C4	3.09	0.41
34:BA:368:U:N3	57:BZ:354:ARG:NH1	2.69	0.41
34:BA:403:C:H2'	34:BA:404:U:H6	1.86	0.41
34:BA:657:G:C2	34:BA:750:G:C5	3.08	0.41
34:BA:756:C:H2'	34:BA:757:U:O4'	2.21	0.41
34:BA:785:G:C2'	34:BA:786:G:H5'	2.51	0.41
34:BA:962:C:H42	34:BA:973:G:H1	1.68	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:BA:1333:A:C8	34:BA:1334:G:C8	3.09	0.41
35:BB:104:ASN:OD1	35:BB:107:THR:OG1	2.39	0.41
35:BB:120:ALA:O	35:BB:121:LEU:HD22	2.20	0.41
35:BB:137:ARG:HB3	35:BB:137:ARG:HH11	1.86	0.41
36:BC:143:GLU:C	36:BC:145:GLY:H	2.29	0.41
37:BD:176:LEU:HG	37:BD:178:VAL:HG22	2.03	0.41
38:BE:94:ALA:HB2	38:BE:119:LEU:HG	2.01	0.41
41:BH:39:LEU:HD12	41:BH:44:PHE:CB	2.51	0.41
43:BJ:90:LEU:HA	43:BJ:91:PRO:HD3	1.77	0.41
45:BL:44:THR:HA	45:BL:45:PRO:HD3	1.90	0.41
49:BP:69:THR:O	49:BP:69:THR:OG1	2.29	0.41
53:BT:47:GLY:HA2	53:BT:48:LYS:C	2.45	0.41
56:BX:23:C:H2'	56:BX:24:U:H6	1.84	0.41
57:BZ:78:ARG:NH1	57:BZ:357:ARG:NH2	2.69	0.41
1:CA:277:C:O2	1:CA:277:C:H2'	2.21	0.41
1:CA:678:C:H2'	1:CA:679:C:C6	2.55	0.41
1:CA:1164:G:H2'	1:CA:1165:U:C6	2.56	0.41
1:CA:1178:C:H2'	1:CA:1179:C:H6	1.86	0.41
1:CA:1958:C:C2'	1:CA:1959:G:H5'	2.50	0.41
1:CA:2031:A:C6	1:CA:2498:C:H1'	2.56	0.41
1:CA:2046:G:H2'	1:CA:2047:U:C6	2.56	0.41
1:CA:2363:C:O2	24:C0:39:ARG:NH2	2.53	0.41
1:CA:2450:A:C2	1:CA:2451:A:C4	3.09	0.41
1:CA:2570:G:C6	1:CA:2571:C:C4	3.09	0.41
1:CA:2685:G:H5'	12:CO:68:GLU:OE1	2.20	0.41
5:CE:170:LEU:HB3	5:CE:184:VAL:CG2	2.51	0.41
6:CF:140:LEU:O	6:CF:143:ALA:HB3	2.20	0.41
6:CF:200:GLU:O	6:CF:203:GLN:HB2	2.21	0.41
7:CG:98:ARG:H	7:CG:98:ARG:HG3	1.56	0.41
16:CS:95:HIS:C	16:CS:99:LYS:HB2	2.46	0.41
20:CW:86:LEU:HD23	20:CW:88:ARG:HD3	2.03	0.41
23:CZ:153:SER:HB3	23:CZ:167:PRO:O	2.20	0.41
25:C1:80:LEU:HB3	25:C1:82:LEU:HD21	2.03	0.41
34:DA:37:U:O2'	34:DA:38:G:H5'	2.21	0.41
34:DA:173:U:H5"	34:DA:197:A:O4'	2.21	0.41
34:DA:407:G:H1'	37:DD:119:GLN:OE1	2.21	0.41
34:DA:563:A:H2'	34:DA:567:G:C8	2.56	0.41
34:DA:657:G:H4'	48:DO:28:GLN:HG2	2.03	0.41
34:DA:841:U:H6	34:DA:841:U:OP2	2.04	0.41
34:DA:920:U:H2'	34:DA:921:U:H6	1.84	0.41
34:DA:973:G:O2'	47:DN:29:ARG:NH2	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:DA:1060:C:C5'	43:DJ:51:ARG:HB3	2.51	0.41
34:DA:1412:C:H2'	34:DA:1413:A:C8	2.56	0.41
36:DC:54:ARG:O	36:DC:69:HIS:ND1	2.50	0.41
46:DM:123:ALA:HB1	57:DZ:507:TYR:CB	2.51	0.41
1:AA:484:G:C8	31:A7:37:LYS:HG2	2.56	0.40
1:AA:486:A:H2'	1:AA:487:C:O4'	2.21	0.40
1:AA:856:G:O4'	1:AA:1300:A:H1'	2.21	0.40
1:AA:870:G:C2	1:AA:882:A:C2	3.08	0.40
1:AA:952:G:H2'	1:AA:953:U:O4'	2.22	0.40
1:AA:1091:A:C8	1:AA:1093:G:C2	3.10	0.40
1:AA:1440:U:H4'	1:AA:1649:A:H4'	2.02	0.40
1:AA:1569:U:H6	1:AA:1569:U:O5'	2.04	0.40
1:AA:1685:C:H4'	1:AA:2722:C:O2	2.20	0.40
1:AA:1879:A:H2'	1:AA:1880:G:C8	2.56	0.40
1:AA:1973:U:O2'	1:AA:1975:A:N7	2.40	0.40
1:AA:2556:G:O2'	1:AA:2557:G:H5'	2.21	0.40
1:AA:2623:U:H2'	29:A5:2:ALA:O	2.22	0.40
3:AC:165:ARG:C	3:AC:172:ILE:HD12	2.47	0.40
4:AD:53:PHE:HB3	4:AD:218:ARG:O	2.21	0.40
4:AD:162:SER:HB3	4:AD:195:ALA:CB	2.51	0.40
6:AF:112:MET:O	6:AF:115:ALA:HB3	2.21	0.40
12:AO:70:LYS:HE2	12:AO:70:LYS:HB3	1.61	0.40
12:AO:71:ARG:NH2	12:AO:77:ILE:HG21	2.36	0.40
16:AS:19:LYS:HG2	16:AS:19:LYS:H	1.74	0.40
16:AS:84:GLN:HG2	16:AS:111:GLU:OE2	2.20	0.40
19:AV:19:LYS:HA	19:AV:94:LEU:O	2.21	0.40
20:AW:65:LEU:O	20:AW:66:GLU:C	2.63	0.40
32:A8:44:LYS:O	32:A8:46:ARG:N	2.54	0.40
33:A9:17:ILE:HA	33:A9:17:ILE:HD12	1.78	0.40
34:BA:200:G:N2	34:BA:218:C:C2	2.89	0.40
34:BA:695:A:H2	34:BA:787:A:H1'	1.86	0.40
34:BA:695:A:H2'	34:BA:696:A:O4'	2.20	0.40
34:BA:987:G:H8	34:BA:987:G:O5'	2.04	0.40
34:BA:1157:A:C6	34:BA:1180:A:C6	3.08	0.40
34:BA:1346:A:N1	34:BA:1374:A:H5"	2.37	0.40
39:BF:8:ILE:HA	39:BF:87:ARG:O	2.21	0.40
46:BM:118:ALA:HB1	56:BX:28:C:H4'	2.03	0.40
49:BP:18:ARG:O	49:BP:20:VAL:HB	2.20	0.40
50:BQ:40:LYS:HD2	50:BQ:42:TYR:CZ	2.55	0.40
56:BX:32:5MC:H2'	56:BX:33:U:C6	2.56	0.40
57:BZ:13:ARG:HH12	57:BZ:247:ARG:NH1	2.14	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:BZ:122:TRP:CH2	57:BZ:132:ARG:HD3	2.56	0.40
57:BZ:168:ILE:HD13	57:BZ:168:ILE:HG21	1.87	0.40
57:BZ:325:LEU:HD23	57:BZ:325:LEU:HA	1.79	0.40
1:CA:41:C:H2'	1:CA:42:G:O4'	2.21	0.40
1:CA:280:C:H2'	1:CA:281:G:O4'	2.21	0.40
1:CA:510:C:C4	1:CA:511:U:C4	3.09	0.40
1:CA:624:C:O2'	1:CA:657:U:OP1	2.32	0.40
1:CA:647:G:H8	1:CA:647:G:O5'	2.04	0.40
1:CA:753:C:H2'	1:CA:754:C:H6	1.87	0.40
1:CA:857:C:H1'	24:C0:26:TYR:CE1	2.56	0.40
1:CA:869:G:H5'	14:CQ:6:ARG:HH21	1.86	0.40
1:CA:1647:G:H3'	1:CA:1647:G:OP2	2.20	0.40
1:CA:1647:G:H3'	1:CA:1647:G:P	2.61	0.40
1:CA:2660:A:H5"	1:CA:2661:G:OP2	2.21	0.40
4:CD:103:ARG:HB2	4:CD:104:TYR:H	1.71	0.40
4:CD:108:PRO:HG3	4:CD:143:HIS:CE1	2.56	0.40
5:CE:77:ILE:HA	5:CE:77:ILE:HD12	1.79	0.40
5:CE:78:LEU:C	5:CE:79:ARG:HG2	2.46	0.40
6:CF:64:ILE:HG21	6:CF:78:ILE:CG2	2.51	0.40
9:CK:29:TYR:H	9:CK:83:TYR:CB	2.33	0.40
13:CP:114:ILE:HG13	13:CP:125:VAL:HG21	2.02	0.40
16:CS:36:TYR:HE2	16:CS:54:LEU:HD22	1.85	0.40
17:CT:99:LEU:O	17:CT:100:TYR:C	2.63	0.40
20:CW:58:ALA:HB1	20:CW:69:LEU:HD21	2.03	0.40
21:CX:12:VAL:HG21	21:CX:27:THR:HG22	2.02	0.40
23:CZ:11:GLU:C	23:CZ:13:GLU:H	2.30	0.40
23:CZ:67:LEU:HD23	23:CZ:67:LEU:HA	1.96	0.40
24:C0:14:ARG:HH11	24:C0:14:ARG:HD2	1.69	0.40
25:C1:72:GLU:O	25:C1:76:ARG:HG3	2.21	0.40
28:C4:46:GLN:C	28:C4:48:ARG:H	2.30	0.40
34:DA:437:U:O2'	37:DD:123:HIS:HD2	2.04	0.40
34:DA:709:G:C4	34:DA:710:G:C8	3.09	0.40
34:DA:979:C:OP1	34:DA:1223:C:N4	2.54	0.40
34:DA:1061:G:C5	34:DA:1062:U:C5	3.09	0.40
34:DA:1527:C:H2'	34:DA:1528:U:C6	2.56	0.40
38:DE:74:GLY:O	38:DE:115:VAL:HG13	2.20	0.40
39:DF:99:ALA:O	51:DR:28:GLU:HA	2.21	0.40
40:DG:57:GLU:O	40:DG:61:VAL:HG23	2.20	0.40
40:DG:78:ARG:HG2	40:DG:79:ARG:H	1.85	0.40
40:DG:79:ARG:HB2	40:DG:80:VAL:H	1.44	0.40
46:DM:24:GLY:C	46:DM:25:ILE:HD12	2.46	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:DR:74:ARG:HA	51:DR:79:LEU:O	2.21	0.40
53:DT:12:ALA:HA	53:DT:15:ARG:HB2	2.03	0.40
57:DZ:-41:ALA:O	57:DZ:-36:LEU:HB2	2.21	0.40
57:DZ:-14:ALA:C	57:DZ:-12:ALA:N	2.80	0.40
1:AA:231:G:N2	1:AA:243:G:H2'	2.37	0.40
1:AA:733:G:H1	31:A7:16:HIS:CD2	2.40	0.40
1:AA:747:G:C6	1:AA:780:G:N2	2.89	0.40
1:AA:861:C:O2'	1:AA:1270:C:N3	2.54	0.40
1:AA:1097:G:C5	1:AA:1098:C:C4	3.10	0.40
1:AA:1973:U:H2'	1:AA:1975:A:OP2	2.22	0.40
1:AA:2024:G:OP1	15:AR:9:LYS:HE3	2.20	0.40
1:AA:2225:U:H4'	4:AD:151:LYS:HD3	2.03	0.40
1:AA:2375:C:H2'	1:AA:2376:C:H6	1.86	0.40
1:AA:2486:C:H5"	1:AA:2487:C:OP2	2.21	0.40
1:AA:2653:G:P	11:AN:74:ARG:HE	2.43	0.40
4:AD:242:ARG:HG2	4:AD:246:PRO:HG3	2.03	0.40
6:AF:17:ARG:HG2	6:AF:18:ARG:N	2.36	0.40
6:AF:52:LYS:HA	6:AF:56:GLU:OE2	2.20	0.40
6:AF:180:GLY:O	6:AF:181:LEU:C	2.65	0.40
6:AF:183:VAL:O	6:AF:184:TYR:C	2.63	0.40
7:AG:111:LEU:HA	7:AG:114:ILE:HG13	2.03	0.40
14:AQ:27:VAL:CG1	14:AQ:134:ARG:HG3	2.51	0.40
18:AU:112:ARG:H	18:AU:112:ARG:HG2	1.47	0.40
19:AV:10:LYS:NZ	19:AV:23:GLU:OE2	2.53	0.40
19:AV:43:GLU:OE1	19:AV:43:GLU:N	2.54	0.40
21:AX:39:ILE:O	21:AX:43:VAL:HG23	2.21	0.40
23:AZ:18:LEU:O	23:AZ:19:ARG:C	2.62	0.40
28:A4:15:ILE:HB	28:A4:32:TYR:CD2	2.57	0.40
34:BA:169:C:O2'	34:BA:170:U:H5'	2.20	0.40
34:BA:502:G:C2	34:BA:503:C:O2	2.74	0.40
34:BA:543:C:C2	34:BA:544:G:C8	3.09	0.40
34:BA:656:C:C2'	48:BO:28:GLN:HE22	2.32	0.40
34:BA:791:G:H2'	34:BA:792:A:H5'	2.02	0.40
34:BA:1168:A:H2'	34:BA:1169:A:O4'	2.20	0.40
34:BA:1252:A:H2'	34:BA:1253:G:O4'	2.21	0.40
34:BA:1255:G:C2	34:BA:1283:G:C2	3.09	0.40
34:BA:1513:A:H2'	34:BA:1514:C:C6	2.57	0.40
35:BB:16:HIS:HB2	35:BB:204:ASN:CB	2.47	0.40
35:BB:172:ILE:HB	35:BB:173:ALA:H	1.61	0.40
35:BB:201:ILE:O	35:BB:203:GLY:N	2.55	0.40
38:BE:91:LEU:HB3	38:BE:118:ILE:HD11	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:BI:9:ARG:HD3	42:BI:14:VAL:HG22	2.02	0.40
44:BK:33:THR:HB	44:BK:38:ASN:C	2.46	0.40
49:BP:65:GLN:HA	49:BP:66:PRO:HD3	1.85	0.40
50:BQ:29:HIS:HA	50:BQ:30:PRO:HD2	1.82	0.40
53:BT:53:LEU:O	53:BT:57:ARG:N	2.51	0.40
57:BZ:301:ILE:HG22	57:BZ:332:SER:HB3	2.03	0.40
1:CA:262:A:H2'	1:CA:263:C:O4'	2.22	0.40
1:CA:312:G:H4'	1:CA:331:A:N3	2.37	0.40
1:CA:346:A:C5	1:CA:347:A:C8	3.09	0.40
1:CA:637:A:H8	13:CP:117:GLU:HG3	1.86	0.40
1:CA:766:C:C4	1:CA:767:U:C4	3.09	0.40
1:CA:1216:G:C4	1:CA:1217:C:C5	3.09	0.40
1:CA:1255:U:C5	6:CF:73:ALA:HA	2.56	0.40
1:CA:1419:A:N6	1:CA:1494:A:N1	2.62	0.40
1:CA:1465:G:C4	1:CA:1466:G:C8	3.09	0.40
1:CA:1794:U:H2'	1:CA:1795:C:C6	2.56	0.40
1:CA:1859:A:H3'	3:CC:206:LYS:HD2	1.40	0.40
1:CA:2485:G:OP1	14:CQ:46:GLN:NE2	2.38	0.40
1:CA:2544:G:H1'	1:CA:2646:C:H4'	2.04	0.40
1:CA:2854:G:C6	1:CA:2855:C:C4	3.08	0.40
6:CF:94:PRO:O	6:CF:95:ARG:HB3	2.21	0.40
11:CN:13:TRP:CZ2	11:CN:51:PHE:CD2	3.09	0.40
13:CP:92:GLU:CD	13:CP:121:LYS:HZ2	2.30	0.40
15:CR:51:LEU:CD2	15:CR:66:VAL:HG22	2.52	0.40
18:CU:16:LYS:HB3	18:CU:16:LYS:HE2	1.72	0.40
20:CW:36:LEU:HD23	20:CW:36:LEU:HA	1.87	0.40
20:CW:96:ILE:HD13	20:CW:96:ILE:HG21	1.85	0.40
21:CX:84:ALA:O	21:CX:85:PRO:C	2.64	0.40
24:C0:19:LYS:HA	24:C0:19:LYS:HD3	1.80	0.40
34:DA:407:G:O2'	37:DD:116:GLN:HG3	2.20	0.40
34:DA:483:C:H3'	34:DA:484:G:H2'	2.02	0.40
34:DA:599:C:H2'	34:DA:600:C:C6	2.57	0.40
34:DA:791:G:H2'	34:DA:792:A:H5'	2.03	0.40
34:DA:1166:G:N2	34:DA:1170:A:OP2	2.49	0.40
40:DG:50:ILE:HD11	40:DG:58:PRO:HB3	2.03	0.40
40:DG:147:ALA:C	40:DG:149:ARG:H	2.30	0.40
42:DI:9:ARG:H	42:DI:79:LEU:HD23	1.86	0.40
53:DT:53:LEU:HA	53:DT:56:MET:HG2	2.02	0.40
57:DZ:129:LYS:HA	57:DZ:129:LYS:HD3	1.96	0.40
57:DZ:238:THR:HG23	57:DZ:241:GLU:H	1.85	0.40
1:AA:8:A:C5	1:AA:9:U:C5	3.10	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:160:G:N2	1:AA:161:C:C2	2.90	0.40
1:AA:475:A:H2'	1:AA:476:G:C5'	2.52	0.40
1:AA:889:G:H2'	1:AA:890:G:O4'	2.22	0.40
1:AA:1209:G:O2'	1:AA:1210:G:H5'	2.20	0.40
1:AA:1793:A:N1	63:AA:4002:HOH:O	2.37	0.40
1:AA:1870:G:C8	1:AA:1949:A:H1'	2.56	0.40
1:AA:2122:G:C2	1:AA:2212:G:C2	3.09	0.40
5:AE:116:VAL:HG13	5:AE:122:PHE:CG	2.57	0.40
7:AG:15:VAL:O	7:AG:16:ARG:C	2.63	0.40
10:AL:90:LYS:HE3	10:AL:90:LYS:HB3	1.89	0.40
13:AP:59:LEU:HD13	13:AP:60:MET:HE2	2.03	0.40
18:AU:50:ARG:O	18:AU:51:LYS:C	2.64	0.40
19:AV:4:ILE:HD13	19:AV:4:ILE:HG21	1.79	0.40
23:AZ:144:LEU:HD11	23:AZ:150:LEU:HD22	2.02	0.40
23:AZ:171:ILE:HD12	23:AZ:172:ALA:H	1.86	0.40
25:A1:35:THR:HG22	25:A1:35:THR:H	1.68	0.40
30:A6:9:LEU:HD21	30:A6:25:LYS:HB3	2.03	0.40
30:A6:40:CYS:HA	30:A6:41:PRO:HD3	1.82	0.40
31:A7:34:ARG:NH2	63:A7:201:HOH:O	2.46	0.40
34:BA:742:G:H5'	48:BO:58:MET:HE1	2.04	0.40
34:BA:1379:G:O6	40:BG:2:ALA:HB3	2.21	0.40
35:BB:196:LEU:HD12	35:BB:196:LEU:HA	1.97	0.40
36:BC:25:GLY:C	36:BC:27:LYS:H	2.28	0.40
36:BC:121:ALA:HB1	36:BC:189:ALA:HB2	2.03	0.40
37:BD:93:PHE:O	37:BD:97:LEU:N	2.51	0.40
39:BF:62:TRP:CD1	51:BR:35:ARG:CZ	3.04	0.40
40:BG:21:VAL:HG23	40:BG:22:LEU:H	1.85	0.40
40:BG:146:GLU:O	40:BG:149:ARG:HB2	2.21	0.40
41:BH:21:LYS:O	41:BH:63:LEU:HD23	2.21	0.40
50:BQ:32:TYR:O	50:BQ:34:LYS:N	2.52	0.40
52:BS:18:LYS:CE	52:BS:31:ILE:HG23	2.52	0.40
57:BZ:94:VAL:O	57:BZ:98:MET:HG2	2.21	0.40
57:BZ:110:SER:OG	57:BZ:136:ALA:HB1	2.22	0.40
1:CA:763:G:C4	1:CA:765:G:C8	3.09	0.40
1:CA:866:A:O5'	1:CA:866:A:C8	2.75	0.40
1:CA:1116:C:H2'	1:CA:1117:G:C8	2.50	0.40
1:CA:1505:C:H2'	1:CA:1506:C:C6	2.56	0.40
1:CA:1597:A:H5"	1:CA:1598:C:OP1	2.21	0.40
1:CA:1614:A:H62	20:CW:91:GLY:HA2	1.86	0.40
1:CA:1860:G:C6	1:CA:1883:G:N2	2.90	0.40
1:CA:2113:U:O4	1:CA:2170:A:N6	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:2542:A:H4'	1:CA:2543:G:C8	2.54	0.40
1:CA:2854:G:H2'	1:CA:2855:C:C6	2.56	0.40
2:CB:16:G:H1	2:CB:68:C:H42	1.68	0.40
2:CB:16:G:C6	2:CB:69:G:C2	3.10	0.40
3:CC:194:ILE:CD1	3:CC:227:PRO:CB	2.99	0.40
5:CE:141:ILE:HG13	5:CE:150:VAL:CG2	2.52	0.40
6:CF:184:TYR:O	6:CF:188:ARG:HB2	2.21	0.40
8:CH:157:TYR:CE1	8:CH:172:LYS:HG2	2.56	0.40
11:CN:119:ARG:HH11	11:CN:119:ARG:HD3	1.77	0.40
11:CN:120:LEU:HD22	11:CN:122:VAL:HG23	2.03	0.40
14:CQ:16:ARG:NH2	14:CQ:18:LYS:HD3	2.35	0.40
14:CQ:63:LYS:HG2	23:CZ:178:GLU:HG2	2.03	0.40
15:CR:50:HIS:O	15:CR:54:LEU:HD13	2.21	0.40
15:CR:57:ARG:NE	15:CR:59:ASP:OD1	2.30	0.40
18:CU:86:ALA:O	19:CV:49:THR:HG23	2.21	0.40
22:CY:90:LEU:HB2	22:CY:92:ASN:HB3	2.02	0.40
34:DA:130:A:O2'	34:DA:131:C:O5'	2.33	0.40
34:DA:1040:U:C2	34:DA:1041:A:C8	3.09	0.40
34:DA:1168:A:C2	34:DA:1169:A:C4	3.10	0.40
34:DA:1254:C:OP1	43:DJ:45:ARG:HA	2.21	0.40
48:DO:70:LEU:HD23	48:DO:78:TYR:HA	2.02	0.40
57:DZ:280:LEU:HD23	57:DZ:281:PRO:HD2	2.04	0.40
1:AA:83:A:H5"	22:AY:8:LYS:HD2	2.01	0.40
1:AA:815:G:H2'	1:AA:816:G:O4'	2.22	0.40
1:AA:866:A:N3	1:AA:1234:A:C2	2.89	0.40
1:AA:950:C:H2'	1:AA:951:U:C6	2.56	0.40
1:AA:1067:A:H61	1:AA:1188:A:H61	1.69	0.40
1:AA:1097:G:C6	1:AA:1098:C:N3	2.90	0.40
1:AA:1331:G:C5	1:AA:1375:U:C4	3.10	0.40
1:AA:1374:G:O2'	1:AA:1375:U:H2'	2.22	0.40
1:AA:1462:G:O2'	1:AA:1463:C:H5	2.04	0.40
1:AA:1790:A:H1'	1:AA:2723:A:C2	2.56	0.40
1:AA:2021:C:H2'	1:AA:2022:G:C8	2.56	0.40
1:AA:2108:U:H2'	1:AA:2109:G:H8	1.86	0.40
1:AA:2119:C:H2'	1:AA:2120:U:C6	2.57	0.40
1:AA:2149:G:N2	1:AA:2195:A:H1'	2.36	0.40
1:AA:2453:C:OP2	1:AA:2598:C:O2'	2.38	0.40
1:AA:2556:G:H2'	1:AA:2557:G:O4'	2.22	0.40
1:AA:2897:U:O5'	1:AA:2897:U:H6	2.05	0.40
11:AN:99:LEU:O	11:AN:103:VAL:HG23	2.21	0.40
13:AP:126:VAL:HG12	13:AP:148:LEU:HD13	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:AR:96:ARG:O	15:AR:96:ARG:HG3	2.20	0.40
18:AU:41:ALA:O	18:AU:42:ALA:C	2.64	0.40
23:AZ:92:SER:OG	23:AZ:94:GLU:HG3	2.22	0.40
25:A1:3:LYS:HZ3	25:A1:3:LYS:HG3	1.66	0.40
25:A1:80:LEU:HB3	25:A1:82:LEU:HG	2.02	0.40
28:A4:47:GLN:HG2	28:A4:49:PHE:H	1.87	0.40
34:BA:583:A:H2'	34:BA:584:G:O4'	2.22	0.40
34:BA:715:A:H5"	34:BA:805:C:C1'	2.51	0.40
34:BA:1321:C:H6	34:BA:1322:C:H2'	1.86	0.40
34:BA:1438:G:H2'	34:BA:1439:C:C6	2.56	0.40
35:BB:172:ILE:H	35:BB:172:ILE:HG13	1.47	0.40
44:BK:40:ILE:HG23	44:BK:75:TYR:CD2	2.55	0.40
44:BK:79:SER:OG	44:BK:106:LYS:HD2	2.21	0.40
50:BQ:3:LYS:HD2	50:BQ:60:ILE:HD11	2.04	0.40
57:BZ:236:GLU:HG3	57:BZ:236:GLU:O	2.21	0.40
1:CA:118:A:H3'	1:CA:119:A:C5'	2.51	0.40
1:CA:359:A:H2'	1:CA:360:G:O4'	2.21	0.40
1:CA:428:A:H3'	1:CA:429:A:H8	1.86	0.40
1:CA:433:C:C4	1:CA:434:U:O4	2.75	0.40
1:CA:621:A:H3'	1:CA:622:G:H8	1.86	0.40
1:CA:1142:U:O5'	1:CA:1142:U:H6	2.04	0.40
1:CA:1152:C:H2'	1:CA:1153:C:C6	2.55	0.40
1:CA:1309:G:OP1	31:C7:9:ARG:HD3	2.22	0.40
1:CA:1426:G:H5"	1:CA:1427:A:OP2	2.20	0.40
1:CA:1815:A:OP1	1:CA:1815:A:H8	2.04	0.40
1:CA:2309:A:N6	1:CA:2310:A:C6	2.89	0.40
1:CA:2687:U:H2'	1:CA:2688:U:O4'	2.22	0.40
2:CB:38:C:H2'	2:CB:39:A:C8	2.56	0.40
3:CC:54:ARG:CZ	3:CC:55:SER:O	2.69	0.40
4:CD:159:ALA:HB1	4:CD:198:ASN:O	2.21	0.40
4:CD:222:ARG:O	4:CD:226:MET:HG3	2.20	0.40
5:CE:201:THR:HG23	5:CE:203:LYS:H	1.86	0.40
8:CH:35:VAL:HA	8:CH:36:PRO:HD2	1.81	0.40
10:CL:69:THR:C	10:CL:70:LYS:HD2	2.46	0.40
15:CR:67:LEU:HD12	15:CR:67:LEU:HA	1.95	0.40
16:CS:10:ARG:O	16:CS:14:VAL:HG22	2.22	0.40
17:CT:64:ARG:NH1	17:CT:103:ARG:HA	2.37	0.40
26:C2:26:ARG:CZ	26:C2:26:ARG:HB2	2.50	0.40
27:C3:34:GLU:O	27:C3:35:ARG:HG3	2.22	0.40
28:C4:16:CYS:SG	28:C4:17:GLY:N	2.95	0.40
34:DA:304:U:H2'	34:DA:305:G:C8	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:DA:625:G:OP1	49:DP:9:PHE:HB3	2.21	0.40
34:DA:866:C:C5	34:DA:867:G:H1'	2.56	0.40
34:DA:1135:U:H4'	34:DA:1136:U:H5	1.86	0.40
34:DA:1281:U:H5"	34:DA:1282:C:C5	2.55	0.40
36:DC:11:ARG:HG2	36:DC:178:LEU:HD12	2.03	0.40
45:DL:124:LYS:HA	45:DL:125:PRO:HD3	1.90	0.40
47:DN:15:LYS:HE2	47:DN:15:LYS:HB3	1.88	0.40
1:AA:252:C:H1'	1:AA:457:G:N3	2.36	0.40
1:AA:354:A:C2	1:AA:1255:A:O2'	2.64	0.40
1:AA:776:G:N7	4:AD:209:ALA:HB3	2.37	0.40
1:AA:793:A:H2'	1:AA:2624:C:H5"	2.04	0.40
1:AA:1386:U:OP1	21:AX:16:LYS:NZ	2.52	0.40
1:AA:1588:G:H3'	1:AA:1589:A:H2'	2.02	0.40
1:AA:1753:U:OP1	63:AA:3947:HOH:O	2.22	0.40
1:AA:1858:C:O2'	1:AA:1992:A:N3	2.53	0.40
1:AA:1911:A:H2'	1:AA:1912:A:C8	2.57	0.40
1:AA:2039:U:H5"	1:AA:2040:G:P	2.62	0.40
1:AA:2367:C:O3'	24:A0:24:LYS:HE3	2.22	0.40
1:AA:2672:A:C2'	1:AA:2673:G:H5'	2.52	0.40
2:AB:1:U:O2	2:AB:1:U:H2'	2.21	0.40
4:AD:16:MET:HB2	4:AD:16:MET:HE2	1.82	0.40
4:AD:67:PHE:HD1	4:AD:153:ALA:HB3	1.85	0.40
4:AD:223:GLY:HA3	4:AD:231:HIS:NE2	2.36	0.40
5:AE:47:VAL:HB	5:AE:49:LEU:HD13	2.03	0.40
13:AP:49:ARG:HD2	32:A8:60:LEU:HB2	2.04	0.40
14:AQ:135:ASP:N	14:AQ:138:ASP:OD2	2.48	0.40
18:AU:33:ARG:O	18:AU:36:ARG:HB3	2.22	0.40
19:AV:85:LYS:HZ3	19:AV:85:LYS:HG3	1.72	0.40
33:A9:10:ILE:HG22	33:A9:32:HIS:CE1	2.57	0.40
33:A9:18:ARG:NH2	33:A9:21:GLY:HA2	2.37	0.40
34:BA:124:G:H4'	34:BA:291:C:O2'	2.21	0.40
34:BA:153:C:H42	34:BA:168:G:H22	1.69	0.40
34:BA:434:U:H2'	34:BA:435:C:O4'	2.22	0.40
34:BA:641:U:O2'	34:BA:642:A:OP2	2.35	0.40
34:BA:1290:G:C4	34:BA:1291:G:C8	3.10	0.40
36:BC:71:ALA:C	36:BC:73:PRO:HD3	2.47	0.40
37:BD:194:LEU:HD12	37:BD:195:ALA:N	2.32	0.40
38:BE:76:ILE:H	38:BE:76:ILE:HG13	1.74	0.40
48:BO:32:LEU:HD23	48:BO:32:LEU:HA	1.69	0.40
57:BZ:183:MET:CG	57:BZ:213:HIS:HD2	2.35	0.40
57:BZ:289:ILE:HD11	57:BZ:331:TYR:CD2	2.57	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:BZ:637:ARG:O	57:BZ:639:ASN:N	2.54	0.40
1:CA:309:G:C5	1:CA:330:A:N6	2.90	0.40
1:CA:479:A:C2	1:CA:480:A:C5	3.10	0.40
1:CA:562:U:C4	1:CA:2036:C:O4'	2.74	0.40
1:CA:652(C):G:H5"	1:CA:652(D):C:OP2	2.21	0.40
1:CA:862:G:H2'	1:CA:863:A:O4'	2.21	0.40
1:CA:904:C:H2'	1:CA:905:U:C6	2.57	0.40
1:CA:990:A:H5"	1:CA:991:C:OP1	2.22	0.40
1:CA:1488:G:C6	1:CA:1489:U:C2	3.10	0.40
1:CA:1688:U:H1'	1:CA:1701:A:C6	2.56	0.40
1:CA:2012:G:H8	1:CA:2012:G:O5'	2.04	0.40
1:CA:2403:C:OP2	63:CA:3762:HOH:O	2.22	0.40
6:CF:157:VAL:HG11	6:CF:181:LEU:CD1	2.51	0.40
9:CK:24:PHE:HA	9:CK:87:VAL:H	1.87	0.40
15:CR:59:ASP:OD2	15:CR:61:HIS:HB3	2.20	0.40
23:CZ:100:VAL:HA	23:CZ:101:PRO:HD3	1.87	0.40
26:C2:32:LEU:HD22	26:C2:32:LEU:O	2.22	0.40
26:C2:52:ASP:O	26:C2:56:GLN:HG3	2.22	0.40
34:DA:45:U:H2'	34:DA:46:G:C8	2.57	0.40
34:DA:255:G:O3'	50:DQ:17:LYS:HD2	2.22	0.40
34:DA:391:G:O6	34:DA:392:G:C6	2.75	0.40
34:DA:559:A:H5'	34:DA:559:A:N3	2.36	0.40
34:DA:814:A:H2'	34:DA:816:A:H5'	2.02	0.40
34:DA:1143:G:C2	34:DA:1144:G:C5	3.10	0.40
34:DA:1504:G:H4'	34:DA:1505:G:C4	2.57	0.40
38:DE:60:TYR:CD1	38:DE:60:TYR:C	2.99	0.40
41:DH:103:VAL:HG21	41:DH:110:ALA:HB2	2.03	0.40
46:DM:84:ILE:HB	52:DS:66:MET:HE2	2.03	0.40
48:DO:28:GLN:NE2	48:DO:66:LEU:HD21	2.36	0.40

There are no symmetry-related clashes.

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
3	AC	133/228 (58%)	90 (68%)	25 (19%)	18 (14%)	0 0
3	CC	133/228 (58%)	90 (68%)	25 (19%)	18 (14%)	0 0
4	AD	273/276 (99%)	239 (88%)	28 (10%)	6 (2%)	5 19
4	CD	273/276 (99%)	234 (86%)	35 (13%)	4 (2%)	8 28
5	AE	202/206 (98%)	181 (90%)	19 (9%)	2 (1%)	12 38
5	CE	202/206 (98%)	178 (88%)	20 (10%)	4 (2%)	6 21
6	AF	201/210 (96%)	182 (90%)	15 (8%)	4 (2%)	6 21
6	CF	201/210 (96%)	181 (90%)	14 (7%)	6 (3%)	3 12
7	AG	179/182 (98%)	152 (85%)	19 (11%)	8 (4%)	2 7
7	CG	179/182 (98%)	148 (83%)	21 (12%)	10 (6%)	1 4
8	AH	172/180 (96%)	152 (88%)	17 (10%)	3 (2%)	7 25
8	CH	172/180 (96%)	149 (87%)	20 (12%)	3 (2%)	7 25
9	AK	128/173 (74%)	66 (52%)	31 (24%)	31 (24%)	0 0
9	CK	128/173 (74%)	77 (60%)	29 (23%)	22 (17%)	0 0
10	AL	137/147 (93%)	105 (77%)	24 (18%)	8 (6%)	1 4
10	CL	137/147 (93%)	97 (71%)	35 (26%)	5 (4%)	2 10
11	AN	138/140 (99%)	127 (92%)	10 (7%)	1 (1%)	18 47
11	CN	138/140 (99%)	127 (92%)	9 (6%)	2 (1%)	9 30
12	AO	120/122 (98%)	106 (88%)	13 (11%)	1 (1%)	16 44
12	CO	120/122 (98%)	108 (90%)	9 (8%)	3 (2%)	4 16
13	AP	147/150 (98%)	133 (90%)	10 (7%)	4 (3%)	4 15
13	CP	147/150 (98%)	124 (84%)	18 (12%)	5 (3%)	3 11
14	AQ	139/141 (99%)	126 (91%)	11 (8%)	2 (1%)	9 30
14	CQ	139/141 (99%)	124 (89%)	12 (9%)	3 (2%)	5 19
15	AR	116/118 (98%)	105 (90%)	9 (8%)	2 (2%)	7 25
15	CR	116/118 (98%)	100 (86%)	14 (12%)	2 (2%)	7 25
16	AS	108/112 (96%)	92 (85%)	12 (11%)	4 (4%)	2 9
16	CS	108/112 (96%)	91 (84%)	13 (12%)	4 (4%)	2 9
17	AT	129/146 (88%)	115 (89%)	13 (10%)	1 (1%)	16 44
17	CT	129/146 (88%)	118 (92%)	9 (7%)	2 (2%)	7 27
18	AU	114/118 (97%)	106 (93%)	6 (5%)	2 (2%)	6 23
18	CU	114/118 (97%)	102 (90%)	11 (10%)	1 (1%)	14 41

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
19	AV	99/101 (98%)	90 (91%)	6 (6%)	3 (3%)	3 12
19	CV	99/101 (98%)	85 (86%)	9 (9%)	5 (5%)	1 5
20	AW	110/113 (97%)	99 (90%)	9 (8%)	2 (2%)	6 23
20	CW	110/113 (97%)	97 (88%)	11 (10%)	2 (2%)	6 23
21	AX	93/96 (97%)	83 (89%)	9 (10%)	1 (1%)	11 36
21	CX	93/96 (97%)	75 (81%)	14 (15%)	4 (4%)	2 7
22	AY	105/110 (96%)	90 (86%)	11 (10%)	4 (4%)	2 9
22	CY	105/110 (96%)	82 (78%)	21 (20%)	2 (2%)	6 22
23	AZ	183/206 (89%)	147 (80%)	23 (13%)	13 (7%)	1 2
23	CZ	183/206 (89%)	147 (80%)	24 (13%)	12 (7%)	1 3
24	A0	81/85 (95%)	72 (89%)	7 (9%)	2 (2%)	4 16
24	C0	81/85 (95%)	73 (90%)	7 (9%)	1 (1%)	10 34
25	A1	95/98 (97%)	90 (95%)	3 (3%)	2 (2%)	5 20
25	C1	95/98 (97%)	88 (93%)	4 (4%)	3 (3%)	3 11
26	A2	68/72 (94%)	59 (87%)	9 (13%)	0	100 100
26	C2	68/72 (94%)	60 (88%)	7 (10%)	1 (2%)	8 28
27	A3	57/60 (95%)	55 (96%)	2 (4%)	0	100 100
27	C3	57/60 (95%)	54 (95%)	3 (5%)	0	100 100
28	A4	67/71 (94%)	45 (67%)	15 (22%)	7 (10%)	0 1
28	C4	67/71 (94%)	52 (78%)	10 (15%)	5 (8%)	1 2
29	A5	57/60 (95%)	53 (93%)	4 (7%)	0	100 100
29	C5	57/60 (95%)	51 (90%)	6 (10%)	0	100 100
30	A6	51/54 (94%)	47 (92%)	4 (8%)	0	100 100
30	C6	51/54 (94%)	44 (86%)	6 (12%)	1 (2%)	6 21
31	A7	46/49 (94%)	41 (89%)	5 (11%)	0	100 100
31	C7	46/49 (94%)	39 (85%)	6 (13%)	1 (2%)	5 19
32	A8	62/65 (95%)	54 (87%)	5 (8%)	3 (5%)	2 6
32	C8	62/65 (95%)	58 (94%)	4 (6%)	0	100 100
33	A9	35/37 (95%)	34 (97%)	0	1 (3%)	3 13
33	C9	35/37 (95%)	33 (94%)	2 (6%)	0	100 100
35	BB	229/256 (90%)	174 (76%)	42 (18%)	13 (6%)	1 4

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
35	DB	229/256 (90%)	176 (77%)	40 (18%)	13 (6%)	1 4
36	BC	204/239 (85%)	165 (81%)	32 (16%)	7 (3%)	3 11
36	DC	204/239 (85%)	172 (84%)	30 (15%)	2 (1%)	12 38
37	BD	206/209 (99%)	150 (73%)	42 (20%)	14 (7%)	1 2
37	DD	206/209 (99%)	165 (80%)	30 (15%)	11 (5%)	1 5
38	BE	146/162 (90%)	123 (84%)	17 (12%)	6 (4%)	2 8
38	DE	146/162 (90%)	122 (84%)	19 (13%)	5 (3%)	3 11
39	BF	98/101 (97%)	84 (86%)	10 (10%)	4 (4%)	2 8
39	DF	98/101 (97%)	86 (88%)	12 (12%)	0	100 100
40	BG	153/156 (98%)	127 (83%)	20 (13%)	6 (4%)	2 8
40	DG	153/156 (98%)	127 (83%)	19 (12%)	7 (5%)	2 6
41	BH	135/138 (98%)	111 (82%)	17 (13%)	7 (5%)	1 5
41	DH	135/138 (98%)	120 (89%)	13 (10%)	2 (2%)	8 28
42	BI	125/128 (98%)	105 (84%)	14 (11%)	6 (5%)	2 6
42	DI	125/128 (98%)	109 (87%)	15 (12%)	1 (1%)	16 44
43	BJ	95/105 (90%)	80 (84%)	12 (13%)	3 (3%)	3 11
43	DJ	94/105 (90%)	76 (81%)	9 (10%)	9 (10%)	0 1
44	BK	112/129 (87%)	94 (84%)	16 (14%)	2 (2%)	6 23
44	DK	112/129 (87%)	93 (83%)	15 (13%)	4 (4%)	2 10
45	BL	120/132 (91%)	108 (90%)	12 (10%)	0	100 100
45	DL	120/132 (91%)	109 (91%)	9 (8%)	2 (2%)	7 25
46	BM	115/126 (91%)	97 (84%)	15 (13%)	3 (3%)	4 15
46	DM	120/126 (95%)	96 (80%)	18 (15%)	6 (5%)	1 5
47	BN	58/61 (95%)	46 (79%)	10 (17%)	2 (3%)	3 11
47	DN	58/61 (95%)	56 (97%)	2 (3%)	0	100 100
48	BO	86/89 (97%)	71 (83%)	15 (17%)	0	100 100
48	DO	86/89 (97%)	72 (84%)	10 (12%)	4 (5%)	2 6
49	BP	80/88 (91%)	55 (69%)	19 (24%)	6 (8%)	1 2
49	DP	80/88 (91%)	67 (84%)	10 (12%)	3 (4%)	2 9
50	BQ	97/105 (92%)	87 (90%)	8 (8%)	2 (2%)	5 20
50	DQ	97/105 (92%)	88 (91%)	9 (9%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
51	BR	66/88 (75%)	57 (86%)	9 (14%)	0	100 100
51	DR	66/88 (75%)	56 (85%)	9 (14%)	1 (2%)	8 28
52	BS	82/93 (88%)	71 (87%)	10 (12%)	1 (1%)	10 34
52	DS	81/93 (87%)	69 (85%)	8 (10%)	4 (5%)	1 6
53	BT	94/106 (89%)	81 (86%)	5 (5%)	8 (8%)	0 1
53	DT	94/106 (89%)	80 (85%)	10 (11%)	4 (4%)	2 7
54	BU	21/27 (78%)	20 (95%)	1 (5%)	0	100 100
54	DU	21/27 (78%)	18 (86%)	2 (10%)	1 (5%)	2 6
57	BZ	726/758 (96%)	561 (77%)	115 (16%)	50 (7%)	1 2
57	DZ	726/758 (96%)	558 (77%)	113 (16%)	55 (8%)	1 2
All	All	13389/14444 (93%)	11204 (84%)	1645 (12%)	540 (4%)	2 8

All (540) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	AC	42	VAL
3	AC	47	LYS
3	AC	68	GLY
3	AC	180	SER
3	AC	181	PHE
4	AD	99	ASP
6	AF	130	ALA
7	AG	47	LYS
9	AK	29	TYR
9	AK	30	GLN
9	AK	33	PRO
9	AK	40	LEU
9	AK	47	ASN
9	AK	71	LEU
9	AK	74	LEU
9	AK	77	PRO
9	AK	80	VAL
9	AK	104	ILE
9	AK	105	PRO
9	AK	107	VAL
9	AK	128	LEU
10	AL	16	LYS
15	AR	2	ARG

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Mol	Chain	Res	Type
16	AS	59	LYS
19	AV	31	ALA
23	AZ	136	PHE
23	AZ	154	ASP
28	A4	34	GLU
28	A4	59	PHE
32	A8	45	GLY
35	BB	10	LEU
35	BB	17	PHE
35	BB	125	PRO
36	BC	26	LYS
36	BC	65	ALA
37	BD	5	ILE
37	BD	42	GLN
37	BD	105	VAL
39	BF	70	ASP
40	BG	79	ARG
40	BG	80	VAL
42	BI	41	VAL
44	BK	49	GLY
47	BN	52	GLN
49	BP	24	ALA
49	BP	56	ALA
53	BT	10	LEU
57	BZ	-33	GLY
57	BZ	88	VAL
57	BZ	100	VAL
57	BZ	171	GLU
57	BZ	182	ARG
57	BZ	183	MET
57	BZ	253	LEU
57	BZ	274	ASP
57	BZ	400	GLU
57	BZ	402	ILE
57	BZ	404	VAL
57	BZ	446	THR
57	BZ	469	GLU
57	BZ	504	ARG
3	CC	42	VAL
3	CC	47	LYS
3	CC	68	GLY
3	CC	180	SER

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Mol	Chain	Res	Type
3	CC	181	PHE
4	CD	239	ARG
6	CF	21	ALA
6	CF	130	ALA
6	CF	132	VAL
7	CG	47	LYS
7	CG	181	ARG
8	CH	126	PRO
9	CK	33	PRO
9	CK	68	LEU
9	CK	69	PRO
9	CK	74	LEU
9	CK	77	PRO
9	CK	80	VAL
9	CK	100	ASN
9	CK	107	VAL
9	CK	128	LEU
10	CL	89	HIS
10	CL	115	LEU
12	CO	117	LEU
14	CQ	28	ALA
19	CV	79	VAL
23	CZ	154	ASP
23	CZ	182	LYS
23	CZ	184	ALA
25	C1	85	LEU
31	C7	46	VAL
35	DB	10	LEU
35	DB	17	PHE
35	DB	21	ARG
35	DB	74	LYS
40	DG	80	VAL
42	DI	54	ASP
43	DJ	29	ARG
43	DJ	56	HIS
48	DO	19	PRO
51	DR	52	PRO
52	DS	30	LEU
53	DT	100	ILE
57	DZ	-65	LYS
57	DZ	-57	GLU
57	DZ	-25	SER

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Mol	Chain	Res	Type
57	DZ	-23	LEU
57	DZ	89	ASP
57	DZ	92	ILE
57	DZ	93	GLU
57	DZ	160	ARG
57	DZ	183	MET
57	DZ	290	LYS
57	DZ	303	PRO
57	DZ	402	ILE
57	DZ	416	LYS
57	DZ	472	VAL
57	DZ	528	ALA
3	AC	53	ARG
3	AC	161	ARG
3	AC	179	ALA
4	AD	111	LEU
4	AD	209	ALA
4	AD	274	ARG
5	AE	135	HIS
7	AG	24	GLY
7	AG	74	LYS
8	AH	126	PRO
9	AK	84	GLU
9	AK	91	LYS
9	AK	119	ALA
9	AK	120	LYS
9	AK	132	ASP
10	AL	13	PRO
13	AP	4	SER
13	AP	36	LYS
16	AS	70	GLY
16	AS	82	ILE
16	AS	96	GLY
17	AT	118	ARG
18	AU	51	LYS
20	AW	58	ALA
20	AW	111	HIS
21	AX	94	GLY
22	AY	54	LYS
23	AZ	137	ILE
23	AZ	184	ALA
24	A0	74	ARG

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Mol	Chain	Res	Type
25	A1	10	LYS
28	A4	4	GLY
28	A4	45	GLY
32	A8	53	PRO
35	BB	21	ARG
36	BC	66	VAL
36	BC	107	GLN
37	BD	48	ALA
37	BD	101	LEU
37	BD	109	GLY
37	BD	178	VAL
37	BD	179	GLU
38	BE	98	THR
38	BE	140	ARG
39	BF	43	LEU
39	BF	71	ARG
41	BH	51	VAL
41	BH	83	ILE
41	BH	133	LEU
42	BI	43	ALA
42	BI	44	VAL
42	BI	54	ASP
43	BJ	31	GLY
43	BJ	56	HIS
46	BM	67	GLU
47	BN	4	LYS
49	BP	78	GLY
50	BQ	49	GLU
53	BT	47	GLY
53	BT	100	ILE
57	BZ	-57	GLU
57	BZ	-25	SER
57	BZ	-23	LEU
57	BZ	-8	ALA
57	BZ	-4	ALA
57	BZ	39	ILE
57	BZ	170	ARG
57	BZ	235	GLU
57	BZ	277	VAL
57	BZ	416	LYS
57	BZ	418	LYS
57	BZ	468	ARG

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Mol	Chain	Res	Type
57	BZ	472	VAL
57	BZ	656	ALA
57	BZ	671	MET
3	CC	53	ARG
3	CC	161	ARG
3	CC	179	ALA
4	CD	3	VAL
6	CF	133	ASN
7	CG	14	GLU
7	CG	32	PRO
7	CG	51	ARG
7	CG	84	LYS
7	CG	164	GLU
9	CK	20	ALA
9	CK	30	GLN
9	CK	75	GLN
9	CK	90	ALA
9	CK	93	LEU
9	CK	119	ALA
10	CL	13	PRO
13	CP	122	PRO
14	CQ	88	GLY
15	CR	58	GLY
16	CS	35	ILE
17	CT	20	PRO
17	CT	100	TYR
19	CV	29	PRO
19	CV	43	GLU
21	CX	94	GLY
23	CZ	119	GLU
23	CZ	161	VAL
23	CZ	183	LEU
25	C1	10	LYS
28	C4	46	GLN
37	DD	5	ILE
37	DD	10	ARG
37	DD	129	ASN
37	DD	171	GLY
37	DD	182	LYS
40	DG	55	GLY
40	DG	114	ARG
43	DJ	36	GLY

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Mol	Chain	Res	Type
43	DJ	55	LYS
43	DJ	75	ILE
43	DJ	77	PRO
43	DJ	79	ARG
44	DK	49	GLY
44	DK	106	LYS
46	DM	67	GLU
46	DM	108	ARG
49	DP	78	GLY
52	DS	12	ASP
57	DZ	-32	LEU
57	DZ	-24	ASN
57	DZ	-13	GLN
57	DZ	-12	ALA
57	DZ	39	ILE
57	DZ	85	PRO
57	DZ	88	VAL
57	DZ	154	GLN
57	DZ	318	ALA
57	DZ	324	ARG
57	DZ	446	THR
57	DZ	456	GLU
57	DZ	468	ARG
57	DZ	533	VAL
3	AC	30	VAL
3	AC	43	GLU
3	AC	52	PRO
3	AC	69	LEU
3	AC	184	GLU
3	AC	202	PRO
3	AC	209	PHE
7	AG	43	LEU
7	AG	123	ASN
9	AK	22	GLY
9	AK	49	ALA
9	AK	73	GLY
9	AK	75	GLN
9	AK	93	LEU
9	AK	123	GLU
13	AP	29	LYS
18	AU	50	ARG
22	AY	11	ASP

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Mol	Chain	Res	Type
22	AY	94	LYS
23	AZ	155	LEU
23	AZ	178	GLU
23	AZ	183	LEU
25	A1	96	LYS
28	A4	49	PHE
28	A4	62	ARG
36	BC	3	ASN
36	BC	81	GLY
37	BD	31	CYS
40	BG	144	MET
41	BH	132	GLU
43	BJ	75	ILE
49	BP	66	PRO
53	BT	23	ARG
57	BZ	85	PRO
57	BZ	486	THR
57	BZ	521	SER
57	BZ	638	GLY
3	CC	30	VAL
3	CC	43	GLU
3	CC	52	PRO
3	CC	69	LEU
3	CC	184	GLU
3	CC	202	PRO
3	CC	209	PHE
5	CE	74	PRO
6	CF	200	GLU
7	CG	81	LYS
8	CH	152	ARG
9	CK	101	PRO
9	CK	129	PRO
10	CL	50	ASP
10	CL	72	PRO
13	CP	45	LEU
14	CQ	59	ARG
15	CR	73	VAL
16	CS	89	ARG
21	CX	44	GLU
23	CZ	155	LEU
23	CZ	157	LEU
23	CZ	178	GLU

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Mol	Chain	Res	Type
26	C2	54	LYS
28	C4	45	GLY
30	C6	27	LYS
35	DB	20	GLU
35	DB	125	PRO
35	DB	232	PRO
37	DD	47	ARG
38	DE	73	ASN
40	DG	79	ARG
40	DG	118	VAL
40	DG	140	ASP
46	DM	106	ASN
48	DO	24	SER
48	DO	88	ARG
57	DZ	9	LEU
57	DZ	115	GLU
57	DZ	144	ALA
57	DZ	158	GLY
57	DZ	170	ARG
57	DZ	247	ARG
57	DZ	403	GLU
57	DZ	404	VAL
57	DZ	444	PRO
57	DZ	457	LEU
57	DZ	636	PRO
57	DZ	671	MET
3	AC	16	ASP
5	AE	52	LEU
6	AF	141	ALA
6	AF	142	TRP
7	AG	126	ASP
8	AH	159	GLU
9	AK	5	ARG
9	AK	125	LEU
10	AL	21	PRO
10	AL	89	HIS
10	AL	139	VAL
14	AQ	40	ALA
14	AQ	60	ARG
19	AV	67	GLY
22	AY	57	GLN
23	AZ	161	VAL

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Mol	Chain	Res	Type
24	A0	6	GLY
28	A4	63	TYR
33	A9	33	LYS
35	BB	13	ALA
35	BB	16	HIS
35	BB	28	PHE
35	BB	106	LYS
35	BB	204	ASN
35	BB	212	GLN
35	BB	231	GLU
36	BC	160	ALA
37	BD	177	ASP
38	BE	69	VAL
40	BG	4	ARG
41	BH	46	LYS
42	BI	29	ASN
52	BS	81	ARG
53	BT	102	GLY
57	BZ	37	GLY
57	BZ	112	GLN
57	BZ	114	VAL
57	BZ	199	ILE
57	BZ	206	LEU
57	BZ	269	VAL
57	BZ	332	SER
57	BZ	473	ASP
57	BZ	500	GLN
57	BZ	640	ALA
3	CC	16	ASP
5	CE	52	LEU
5	CE	69	LYS
6	CF	66	PRO
7	CG	30	GLU
7	CG	126	ASP
8	CH	169	VAL
9	CK	23	SER
9	CK	53	VAL
9	CK	104	ILE
11	CN	2	LYS
12	CO	116	SER
13	CP	140	ALA
16	CS	90	GLY

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Mol	Chain	Res	Type
19	CV	53	GLU
20	CW	57	ASN
21	CX	91	ALA
22	CY	57	GLN
22	CY	78	ALA
28	C4	68	ARG
35	DB	134	GLU
35	DB	189	ASP
37	DD	136	PRO
37	DD	168	ARG
38	DE	146	ALA
41	DH	51	VAL
43	DJ	37	PRO
43	DJ	78	ASN
45	DL	125	PRO
46	DM	6	GLY
48	DO	23	GLY
53	DT	61	SER
53	DT	95	ALA
53	DT	102	GLY
54	DU	7	ARG
57	DZ	237	PRO
57	DZ	380	LEU
57	DZ	640	ALA
57	DZ	656	ALA
3	AC	21	TYR
4	AD	79	VAL
4	AD	275	LYS
7	AG	32	PRO
7	AG	87	PRO
12	AO	5	GLN
19	AV	79	VAL
23	AZ	157	LEU
35	BB	37	ASN
37	BD	3	ARG
37	BD	104	VAL
37	BD	189	PRO
38	BE	68	GLU
38	BE	129	ILE
40	BG	93	PRO
44	BK	106	LYS
46	BM	93	ARG

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Mol	Chain	Res	Type
46	BM	113	PRO
49	BP	39	TYR
50	BQ	30	PRO
53	BT	71	THR
57	BZ	75	LYS
57	BZ	239	GLU
57	BZ	395	PRO
57	BZ	444	PRO
3	CC	21	TYR
4	CD	21	PHE
9	CK	85	ASP
9	CK	114	GLY
12	CO	26	LYS
13	CP	29	LYS
16	CS	84	GLN
19	CV	61	VAL
21	CX	45	THR
25	C1	3	LYS
28	C4	11	PRO
35	DB	124	SER
35	DB	131	PRO
35	DB	227	GLY
36	DC	156	ARG
37	DD	56	VAL
37	DD	100	ARG
38	DE	27	ARG
46	DM	5	ALA
46	DM	21	TYR
52	DS	29	ARG
57	DZ	-1	GLU
57	DZ	153	MET
57	DZ	257	PRO
57	DZ	532	GLY
3	AC	221	PRO
6	AF	168	ARG
8	AH	55	PRO
9	AK	78	SER
9	AK	86	PRO
10	AL	51	ALA
15	AR	71	GLN
23	AZ	177	PRO
35	BB	159	PRO

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Mol	Chain	Res	Type
37	BD	142	PRO
39	BF	89	MET
41	BH	9	MET
42	BI	97	LYS
53	BT	9	ASN
53	BT	96	GLY
57	BZ	115	GLU
3	CC	221	PRO
4	CD	191	ALA
5	CE	144	ARG
18	CU	6	THR
20	CW	22	ASP
23	CZ	101	PRO
23	CZ	136	PHE
24	C0	73	GLY
28	C4	54	GLY
35	DB	217	ARG
37	DD	167	GLY
49	DP	46	PRO
49	DP	53	VAL
57	DZ	575	VAL
57	DZ	637	ARG
9	AK	101	PRO
10	AL	24	GLY
13	AP	122	PRO
23	AZ	120	ILE
32	A8	52	LYS
41	BH	13	ILE
57	BZ	94	VAL
23	CZ	115	GLY
44	DK	105	VAL
45	DL	83	VAL
52	DS	42	PRO
57	DZ	502	GLY
23	AZ	68	PRO
23	AZ	159	PRO
38	BE	109	ILE
49	BP	19	ILE
36	DC	99	VAL
44	DK	39	PRO
40	BG	130	GLY
11	CN	64	GLY

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Mol	Chain	Res	Type
13	CP	142	GLY
40	DG	19	GLY
41	DH	73	ASP
9	AK	53	VAL
9	AK	68	LEU
11	AN	129	PRO
57	BZ	347	GLY
38	DE	11	ILE
38	DE	22	GLY
57	DZ	-52	VAL
57	DZ	32	ILE
57	DZ	638	GLY
10	AL	113	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
3	AC	111/180 (62%)	100 (90%)	11 (10%)	7 24
3	CC	111/180 (62%)	100 (90%)	11 (10%)	7 24
4	AD	215/218 (99%)	174 (81%)	41 (19%)	1 5
4	CD	216/218 (99%)	176 (82%)	40 (18%)	1 6
5	AE	164/166 (99%)	125 (76%)	39 (24%)	1 3
5	CE	164/166 (99%)	133 (81%)	31 (19%)	1 5
6	AF	160/166 (96%)	121 (76%)	39 (24%)	1 2
6	CF	159/166 (96%)	126 (79%)	33 (21%)	1 4
7	AG	143/156 (92%)	110 (77%)	33 (23%)	1 3
7	CG	142/156 (91%)	108 (76%)	34 (24%)	1 3
8	AH	144/148 (97%)	122 (85%)	22 (15%)	3 10
8	CH	144/148 (97%)	118 (82%)	26 (18%)	2 6
10	AL	104/111 (94%)	85 (82%)	19 (18%)	2 6
10	CL	104/111 (94%)	79 (76%)	25 (24%)	1 2

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
11	AN	118/119 (99%)	89 (75%)	29 (25%)	1 2
11	CN	118/119 (99%)	93 (79%)	25 (21%)	1 4
12	AO	100/100 (100%)	82 (82%)	18 (18%)	2 6
12	CO	100/100 (100%)	81 (81%)	19 (19%)	1 5
13	AP	116/116 (100%)	89 (77%)	27 (23%)	1 3
13	CP	115/116 (99%)	93 (81%)	22 (19%)	1 5
14	AQ	111/111 (100%)	90 (81%)	21 (19%)	1 5
14	CQ	111/111 (100%)	92 (83%)	19 (17%)	2 7
15	AR	101/101 (100%)	82 (81%)	19 (19%)	1 5
15	CR	101/101 (100%)	78 (77%)	23 (23%)	1 3
16	AS	87/88 (99%)	71 (82%)	16 (18%)	1 6
16	CS	85/88 (97%)	63 (74%)	22 (26%)	0 2
17	AT	115/127 (91%)	95 (83%)	20 (17%)	2 7
17	CT	113/127 (89%)	83 (74%)	30 (26%)	0 2
18	AU	93/94 (99%)	79 (85%)	14 (15%)	3 10
18	CU	93/94 (99%)	75 (81%)	18 (19%)	1 5
19	AV	80/82 (98%)	61 (76%)	19 (24%)	1 3
19	CV	80/82 (98%)	65 (81%)	15 (19%)	1 5
20	AW	90/92 (98%)	72 (80%)	18 (20%)	1 4
20	CW	90/92 (98%)	74 (82%)	16 (18%)	2 6
21	AX	77/78 (99%)	67 (87%)	10 (13%)	4 14
21	CX	77/78 (99%)	65 (84%)	12 (16%)	2 9
22	AY	85/91 (93%)	69 (81%)	16 (19%)	1 5
22	CY	85/91 (93%)	62 (73%)	23 (27%)	0 1
23	AZ	156/179 (87%)	120 (77%)	36 (23%)	1 3
23	CZ	156/179 (87%)	131 (84%)	25 (16%)	2 9
24	A0	65/67 (97%)	59 (91%)	6 (9%)	8 27
24	C0	65/67 (97%)	59 (91%)	6 (9%)	8 27
25	A1	80/83 (96%)	64 (80%)	16 (20%)	1 4
25	C1	80/83 (96%)	69 (86%)	11 (14%)	3 12
26	A2	65/67 (97%)	53 (82%)	12 (18%)	1 6

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
26	C2	65/67 (97%)	55 (85%)	10 (15%)	2 10
27	A3	51/52 (98%)	40 (78%)	11 (22%)	1 3
27	C3	50/52 (96%)	37 (74%)	13 (26%)	0 2
28	A4	60/63 (95%)	51 (85%)	9 (15%)	3 10
28	C4	53/63 (84%)	39 (74%)	14 (26%)	0 2
29	A5	50/52 (96%)	42 (84%)	8 (16%)	2 9
29	C5	50/52 (96%)	38 (76%)	12 (24%)	1 2
30	A6	51/52 (98%)	38 (74%)	13 (26%)	0 2
30	C6	50/52 (96%)	40 (80%)	10 (20%)	1 4
31	A7	41/42 (98%)	36 (88%)	5 (12%)	5 16
31	C7	41/42 (98%)	30 (73%)	11 (27%)	0 1
32	A8	54/55 (98%)	43 (80%)	11 (20%)	1 4
32	C8	54/55 (98%)	47 (87%)	7 (13%)	4 14
33	A9	34/34 (100%)	32 (94%)	2 (6%)	18 48
33	C9	34/34 (100%)	30 (88%)	4 (12%)	5 17
35	BB	192/220 (87%)	148 (77%)	44 (23%)	1 3
35	DB	187/220 (85%)	153 (82%)	34 (18%)	2 6
36	BC	143/188 (76%)	129 (90%)	14 (10%)	7 25
36	DC	141/188 (75%)	111 (79%)	30 (21%)	1 4
37	BD	170/181 (94%)	137 (81%)	33 (19%)	1 5
37	DD	174/181 (96%)	137 (79%)	37 (21%)	1 4
38	BE	113/123 (92%)	96 (85%)	17 (15%)	3 10
38	DE	114/123 (93%)	91 (80%)	23 (20%)	1 4
39	BF	84/90 (93%)	69 (82%)	15 (18%)	2 6
39	DF	86/90 (96%)	75 (87%)	11 (13%)	4 15
40	BG	119/127 (94%)	95 (80%)	24 (20%)	1 4
40	DG	120/127 (94%)	106 (88%)	14 (12%)	5 18
41	BH	114/119 (96%)	86 (75%)	28 (25%)	1 2
41	DH	114/119 (96%)	94 (82%)	20 (18%)	2 7
42	BI	91/99 (92%)	73 (80%)	18 (20%)	1 5
42	DI	89/99 (90%)	73 (82%)	16 (18%)	2 6

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
43	BJ	66/92 (72%)	58 (88%)	8 (12%)	5 16
43	DJ	69/92 (75%)	65 (94%)	4 (6%)	18 49
44	BK	83/99 (84%)	71 (86%)	12 (14%)	3 11
44	DK	83/99 (84%)	72 (87%)	11 (13%)	4 14
45	BL	97/109 (89%)	80 (82%)	17 (18%)	2 7
45	DL	97/109 (89%)	79 (81%)	18 (19%)	1 5
46	BM	91/101 (90%)	75 (82%)	16 (18%)	2 7
46	DM	92/101 (91%)	80 (87%)	12 (13%)	4 14
47	BN	49/50 (98%)	37 (76%)	12 (24%)	1 2
47	DN	49/50 (98%)	41 (84%)	8 (16%)	2 8
48	BO	78/80 (98%)	67 (86%)	11 (14%)	3 12
48	DO	78/80 (98%)	63 (81%)	15 (19%)	1 5
49	BP	69/74 (93%)	54 (78%)	15 (22%)	1 3
49	DP	68/74 (92%)	55 (81%)	13 (19%)	1 5
50	BQ	94/97 (97%)	79 (84%)	15 (16%)	2 9
50	DQ	94/97 (97%)	86 (92%)	8 (8%)	10 31
51	BR	59/77 (77%)	50 (85%)	9 (15%)	3 10
51	DR	59/77 (77%)	45 (76%)	14 (24%)	1 3
52	BS	70/80 (88%)	62 (89%)	8 (11%)	5 19
52	DS	67/80 (84%)	57 (85%)	10 (15%)	3 10
53	BT	70/82 (85%)	52 (74%)	18 (26%)	0 2
53	DT	71/82 (87%)	62 (87%)	9 (13%)	4 15
54	BU	18/22 (82%)	16 (89%)	2 (11%)	6 20
54	DU	18/22 (82%)	18 (100%)	0	100 100
57	BZ	369/636 (58%)	260 (70%)	109 (30%)	0 1
57	DZ	370/636 (58%)	266 (72%)	104 (28%)	0 1
All	All	10306/11672 (88%)	8323 (81%)	1983 (19%)	1 5

All (1983) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	AC	28	ARG
3	AC	29	LEU

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Mol	Chain	Res	Type
3	AC	32	GLU
3	AC	48	LEU
3	AC	50	ILE
3	AC	54	ARG
3	AC	63	VAL
3	AC	184	GLU
3	AC	203	GLU
3	AC	206	LYS
3	AC	208	THR
4	AD	3	VAL
4	AD	12	SER
4	AD	18	VAL
4	AD	38	LYS
4	AD	52	ARG
4	AD	61	LEU
4	AD	75	ILE
4	AD	78	LYS
4	AD	94	LEU
4	AD	99	ASP
4	AD	103	ARG
4	AD	106	ILE
4	AD	111	LEU
4	AD	113	VAL
4	AD	116	GLN
4	AD	126	GLN
4	AD	127	VAL
4	AD	136	ILE
4	AD	138	VAL
4	AD	140	THR
4	AD	141	VAL
4	AD	142	VAL
4	AD	147	LEU
4	AD	155	LEU
4	AD	165	ILE
4	AD	173	VAL
4	AD	175	LEU
4	AD	183	ARG
4	AD	193	VAL
4	AD	200	ASP
4	AD	211	ARG
4	AD	217	ARG
4	AD	221	VAL

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Mol	Chain	Res	Type
4	AD	228	PRO
4	AD	229	VAL
4	AD	242	ARG
4	AD	253	GLN
4	AD	257	LEU
4	AD	259	THR
4	AD	265	PRO
4	AD	273	ARG
5	AE	1	MET
5	AE	2	LYS
5	AE	7	VAL
5	AE	9	VAL
5	AE	21	VAL
5	AE	33	VAL
5	AE	34	VAL
5	AE	38	THR
5	AE	39	PRO
5	AE	40	GLU
5	AE	47	VAL
5	AE	49	LEU
5	AE	59	VAL
5	AE	72	VAL
5	AE	75	VAL
5	AE	77	ILE
5	AE	78	LEU
5	AE	82	ARG
5	AE	89	ASP
5	AE	93	VAL
5	AE	97	LYS
5	AE	105	THR
5	AE	109	LYS
5	AE	111	ARG
5	AE	116	VAL
5	AE	119	ARG
5	AE	121	ASN
5	AE	144	ARG
5	AE	154	LYS
5	AE	163	GLU
5	AE	167	VAL
5	AE	170	LEU
5	AE	175	VAL
5	AE	178	GLU

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Mol	Chain	Res	Type
5	AE	179	GLU
5	AE	181	LEU
5	AE	184	VAL
5	AE	185	LYS
5	AE	188	VAL
6	AF	8	GLN
6	AF	12	LEU
6	AF	15	SER
6	AF	19	GLU
6	AF	20	LEU
6	AF	24	LEU
6	AF	27	GLU
6	AF	28	ILE
6	AF	33	LEU
6	AF	38	ARG
6	AF	44	ARG
6	AF	53	THR
6	AF	57	VAL
6	AF	74	ARG
6	AF	78	ILE
6	AF	88	VAL
6	AF	89	VAL
6	AF	93	LYS
6	AF	95	ARG
6	AF	106	ARG
6	AF	110	LEU
6	AF	119	ARG
6	AF	125	LEU
6	AF	127	GLU
6	AF	132	VAL
6	AF	133	ASN
6	AF	137	LYS
6	AF	140	LEU
6	AF	151	SER
6	AF	157	VAL
6	AF	162	LEU
6	AF	165	ARG
6	AF	168	ARG
6	AF	170	LEU
6	AF	183	VAL
6	AF	191	ARG
6	AF	192	LEU

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Mol	Chain	Res	Type
6	AF	200	GLU
6	AF	201	VAL
7	AG	3	LEU
7	AG	5	VAL
7	AG	7	LEU
7	AG	20	ILE
7	AG	28	VAL
7	AG	31	VAL
7	AG	41	GLN
7	AG	43	LEU
7	AG	45	GLU
7	AG	58	GLN
7	AG	60	LEU
7	AG	77	ILE
7	AG	79	ASN
7	AG	82	LEU
7	AG	86	MET
7	AG	91	ARG
7	AG	103	LEU
7	AG	116	ASP
7	AG	123	ASN
7	AG	126	ASP
7	AG	128	ARG
7	AG	136	ARG
7	AG	137	GLU
7	AG	138	GLN
7	AG	140	ILE
7	AG	143	GLU
7	AG	153	ARG
7	AG	157	ILE
7	AG	159	VAL
7	AG	161	THR
7	AG	162	THR
7	AG	170	ARG
7	AG	175	LEU
8	AH	6	ARG
8	AH	13	LYS
8	AH	24	VAL
8	AH	34	GLU
8	AH	35	VAL
8	AH	36	PRO
8	AH	50	VAL

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Mol	Chain	Res	Type
8	AH	69	ARG
8	AH	71	LEU
8	AH	84	SER
8	AH	85	LYS
8	AH	88	LEU
8	AH	98	LEU
8	AH	107	VAL
8	AH	119	GLU
8	AH	122	THR
8	AH	127	GLU
8	AH	136	ILE
8	AH	139	GLN
8	AH	153	LYS
8	AH	172	LYS
8	AH	175	LYS
10	AL	2	LYS
10	AL	3	LYS
10	AL	4	VAL
10	AL	7	VAL
10	AL	23	VAL
10	AL	34	ILE
10	AL	35	MET
10	AL	45	THR
10	AL	50	ASP
10	AL	52	ILE
10	AL	58	THR
10	AL	59	ILE
10	AL	70	LYS
10	AL	85	GLU
10	AL	86	LYS
10	AL	93	ARG
10	AL	96	VAL
10	AL	104	VAL
10	AL	136	VAL
11	AN	14	VAL
11	AN	15	LEU
11	AN	28	THR
11	AN	33	LEU
11	AN	34	LEU
11	AN	39	ARG
11	AN	48	MET
11	AN	54	VAL

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Mol	Chain	Res	Type
11	AN	58	ASP
11	AN	60	ILE
11	AN	61	ARG
11	AN	62	VAL
11	AN	65	LYS
11	AN	73	THR
11	AN	79	PRO
11	AN	84	LYS
11	AN	85	ILE
11	AN	87	LEU
11	AN	89	LYS
11	AN	90	MET
11	AN	91	LEU
11	AN	97	ARG
11	AN	99	LEU
11	AN	112	LEU
11	AN	119	ARG
11	AN	120	LEU
11	AN	133	GLN
11	AN	137	LYS
11	AN	140	VAL
12	AO	1	MET
12	AO	3	GLN
12	AO	8	LEU
12	AO	10	VAL
12	AO	18	LYS
12	AO	22	ILE
12	AO	24	VAL
12	AO	28	SER
12	AO	59	LYS
12	AO	69	ILE
12	AO	77	ILE
12	AO	91	LEU
12	AO	94	ARG
12	AO	98	VAL
12	AO	105	GLU
12	AO	108	GLU
12	AO	113	LYS
12	AO	114	ILE
13	AP	2	LYS
13	AP	16	ARG
13	AP	21	ARG

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Mol	Chain	Res	Type
13	AP	42	SER
13	AP	55	ARG
13	AP	59	LEU
13	AP	68	GLN
13	AP	70	GLN
13	AP	72	PRO
13	AP	76	LYS
13	AP	77	ARG
13	AP	83	VAL
13	AP	95	VAL
13	AP	99	LEU
13	AP	101	VAL
13	AP	105	LEU
13	AP	106	LEU
13	AP	112	LEU
13	AP	114	ILE
13	AP	117	GLU
13	AP	119	GLU
13	AP	121	LYS
13	AP	125	VAL
13	AP	126	VAL
13	AP	133	SER
13	AP	148	LEU
13	AP	149	GLU
14	AQ	1	MET
14	AQ	2	LEU
14	AQ	3	MET
14	AQ	5	ARG
14	AQ	7	MET
14	AQ	8	LYS
14	AQ	10	ARG
14	AQ	14	ARG
14	AQ	16	ARG
14	AQ	18	LYS
14	AQ	21	THR
14	AQ	35	VAL
14	AQ	45	GLN
14	AQ	55	VAL
14	AQ	56	ARG
14	AQ	75	THR
14	AQ	106	VAL
14	AQ	109	VAL

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Mol	Chain	Res	Type
14	AQ	110	THR
14	AQ	133	ARG
14	AQ	139	GLU
15	AR	6	SER
15	AR	18	LEU
15	AR	28	LEU
15	AR	29	LEU
15	AR	33	ARG
15	AR	36	THR
15	AR	44	LEU
15	AR	54	LEU
15	AR	60	LEU
15	AR	65	LEU
15	AR	67	LEU
15	AR	75	LEU
15	AR	79	LEU
15	AR	100	LEU
15	AR	102	GLU
15	AR	111	LEU
15	AR	113	LEU
15	AR	114	VAL
15	AR	117	VAL
16	AS	3	ARG
16	AS	11	LYS
16	AS	14	VAL
16	AS	19	LYS
16	AS	27	SER
16	AS	32	LEU
16	AS	38	GLN
16	AS	43	GLU
16	AS	46	VAL
16	AS	50	SER
16	AS	65	VAL
16	AS	69	VAL
16	AS	73	LEU
16	AS	78	LEU
16	AS	83	LYS
16	AS	110	LEU
17	AT	6	LEU
17	AT	8	LYS
17	AT	16	ARG
17	AT	17	THR

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Mol	Chain	Res	Type
17	AT	23	ARG
17	AT	27	THR
17	AT	28	VAL
17	AT	39	ARG
17	AT	49	VAL
17	AT	59	THR
17	AT	72	VAL
17	AT	78	LEU
17	AT	84	GLN
17	AT	85	LYS
17	AT	104	ASN
17	AT	111	ARG
17	AT	114	LEU
17	AT	115	ARG
17	AT	118	ARG
17	AT	128	GLU
18	AU	13	LYS
18	AU	19	LYS
18	AU	59	ARG
18	AU	60	LEU
18	AU	74	LEU
18	AU	77	SER
18	AU	80	ILE
18	AU	83	LEU
18	AU	84	LYS
18	AU	92	ARG
18	AU	95	LEU
18	AU	104	GLN
18	AU	108	GLU
18	AU	112	ARG
19	AV	15	GLU
19	AV	18	LEU
19	AV	21	ARG
19	AV	28	GLU
19	AV	32	THR
19	AV	35	LEU
19	AV	43	GLU
19	AV	46	VAL
19	AV	51	VAL
19	AV	52	VAL
19	AV	61	VAL
19	AV	62	LEU

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Mol	Chain	Res	Type
19	AV	69	LYS
19	AV	72	VAL
19	AV	73	SER
19	AV	79	VAL
19	AV	92	THR
19	AV	95	LEU
19	AV	100	ARG
20	AW	4	LYS
20	AW	11	ARG
20	AW	12	ILE
20	AW	13	SER
20	AW	15	ARG
20	AW	17	VAL
20	AW	19	LEU
20	AW	23	LEU
20	AW	24	ILE
20	AW	31	GLU
20	AW	41	LYS
20	AW	42	ARG
20	AW	51	LEU
20	AW	62	HIS
20	AW	67	ASP
20	AW	96	ILE
20	AW	98	LYS
20	AW	100	THR
21	AX	33	LYS
21	AX	35	THR
21	AX	45	THR
21	AX	52	VAL
21	AX	57	LEU
21	AX	65	ARG
21	AX	70	LEU
21	AX	72	LYS
21	AX	76	ARG
21	AX	92	LEU
22	AY	2	ARG
22	AY	7	VAL
22	AY	9	LYS
22	AY	11	ASP
22	AY	21	LYS
22	AY	23	ARG
22	AY	29	GLU

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Mol	Chain	Res	Type
22	AY	40	GLU
22	AY	47	LYS
22	AY	55	TYR
22	AY	73	ARG
22	AY	75	ILE
22	AY	85	VAL
22	AY	88	LYS
22	AY	90	LEU
22	AY	91	GLU
23	AZ	5	LEU
23	AZ	8	TYR
23	AZ	18	LEU
23	AZ	19	ARG
23	AZ	24	LEU
23	AZ	31	ARG
23	AZ	33	LEU
23	AZ	41	LEU
23	AZ	42	VAL
23	AZ	49	ARG
23	AZ	52	SER
23	AZ	65	GLN
23	AZ	66	SER
23	AZ	72	ARG
23	AZ	73	GLN
23	AZ	77	ASP
23	AZ	78	LYS
23	AZ	82	ARG
23	AZ	86	VAL
23	AZ	91	LEU
23	AZ	92	SER
23	AZ	119	GLU
23	AZ	124	ILE
23	AZ	126	VAL
23	AZ	129	SER
23	AZ	136	PHE
23	AZ	137	ILE
23	AZ	155	LEU
23	AZ	156	LYS
23	AZ	157	LEU
23	AZ	162	GLU
23	AZ	170	THR
23	AZ	180	VAL

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Mol	Chain	Res	Type
23	AZ	182	LYS
23	AZ	183	LEU
23	AZ	185	GLU
24	A0	7	LEU
24	A0	20	ARG
24	A0	36	ILE
24	A0	43	THR
24	A0	55	ARG
24	A0	67	VAL
25	A1	21	ARG
25	A1	26	ARG
25	A1	30	VAL
25	A1	32	LYS
25	A1	33	LYS
25	A1	37	ILE
25	A1	40	ARG
25	A1	46	LEU
25	A1	51	VAL
25	A1	73	LEU
25	A1	74	VAL
25	A1	75	GLU
25	A1	80	LEU
25	A1	89	GLU
25	A1	95	LEU
25	A1	98	LEU
26	A2	8	LYS
26	A2	28	LYS
26	A2	30	ARG
26	A2	32	LEU
26	A2	52	ASP
26	A2	53	LEU
26	A2	62	THR
26	A2	64	LEU
26	A2	66	GLU
26	A2	67	LYS
26	A2	69	ARG
26	A2	70	GLN
27	A3	3	ARG
27	A3	6	VAL
27	A3	8	LEU
27	A3	10	LYS
27	A3	17	LYS

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Mol	Chain	Res	Type
27	A3	23	LEU
27	A3	29	ARG
27	A3	37	LEU
27	A3	54	VAL
27	A3	58	VAL
27	A3	60	GLU
28	A4	1	MET
28	A4	10	VAL
28	A4	33	VAL
28	A4	34	GLU
28	A4	35	VAL
28	A4	46	GLN
28	A4	49	PHE
28	A4	50	VAL
28	A4	58	ARG
29	A5	6	VAL
29	A5	9	LYS
29	A5	29	THR
29	A5	40	LYS
29	A5	55	ARG
29	A5	56	LYS
29	A5	57	VAL
29	A5	60	VAL
30	A6	4	GLU
30	A6	7	ILE
30	A6	9	LEU
30	A6	14	THR
30	A6	24	GLU
30	A6	33	LYS
30	A6	35	GLU
30	A6	44	ARG
30	A6	47	THR
30	A6	48	VAL
30	A6	50	ARG
30	A6	52	VAL
30	A6	54	ILE
31	A7	1	MET
31	A7	9	ARG
31	A7	24	THR
31	A7	43	THR
31	A7	46	VAL
32	A8	13	ARG

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Mol	Chain	Res	Type
32	A8	14	VAL
32	A8	15	LYS
32	A8	21	LYS
32	A8	23	VAL
32	A8	26	LYS
32	A8	30	ARG
32	A8	32	LEU
32	A8	41	ILE
32	A8	52	LYS
32	A8	59	LYS
33	A9	4	ARG
33	A9	17	ILE
35	BB	7	VAL
35	BB	8	LYS
35	BB	11	LEU
35	BB	15	VAL
35	BB	16	HIS
35	BB	17	PHE
35	BB	20	GLU
35	BB	21	ARG
35	BB	37	ASN
35	BB	39	ILE
35	BB	47	THR
35	BB	48	MET
35	BB	49	GLU
35	BB	76	GLN
35	BB	78	GLN
35	BB	80	ILE
35	BB	83	MET
35	BB	87	ARG
35	BB	96	ARG
35	BB	107	THR
35	BB	111	ARG
35	BB	112	VAL
35	BB	119	GLU
35	BB	127	ILE
35	BB	142	LEU
35	BB	144	ARG
35	BB	145	LEU
35	BB	149	LEU
35	BB	150	SER
35	BB	156	LYS

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Mol	Chain	Res	Type
35	BB	160	ASP
35	BB	168	THR
35	BB	169	LYS
35	BB	172	ILE
35	BB	178	ARG
35	BB	187	LEU
35	BB	200	ILE
35	BB	215	LEU
35	BB	217	ARG
35	BB	221	LEU
35	BB	223	ILE
35	BB	224	GLN
35	BB	229	VAL
35	BB	235	SER
36	BC	5	ILE
36	BC	28	GLN
36	BC	45	LYS
36	BC	52	LEU
36	BC	115	LEU
36	BC	123	GLN
36	BC	150	LYS
36	BC	157	ILE
36	BC	178	LEU
36	BC	188	LEU
36	BC	192	THR
36	BC	196	LEU
36	BC	206	GLU
36	BC	207	VAL
37	BD	5	ILE
37	BD	13	ARG
37	BD	15	GLU
37	BD	31	CYS
37	BD	46	LYS
37	BD	47	ARG
37	BD	49	ARG
37	BD	58	LEU
37	BD	61	LYS
37	BD	76	ARG
37	BD	78	LEU
37	BD	83	SER
37	BD	97	LEU
37	BD	101	LEU

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Mol	Chain	Res	Type
37	BD	107	ARG
37	BD	119	GLN
37	BD	120	LEU
37	BD	121	VAL
37	BD	126	ILE
37	BD	127	THR
37	BD	134	ASP
37	BD	135	LEU
37	BD	140	VAL
37	BD	155	LEU
37	BD	158	ILE
37	BD	168	ARG
37	BD	178	VAL
37	BD	186	LEU
37	BD	188	LEU
37	BD	193	ASP
37	BD	196	LEU
37	BD	200	GLU
37	BD	203	VAL
38	BE	10	MET
38	BE	11	ILE
38	BE	31	LEU
38	BE	38	GLN
38	BE	41	VAL
38	BE	47	LYS
38	BE	56	GLN
38	BE	73	ASN
38	BE	75	THR
38	BE	79	GLU
38	BE	91	LEU
38	BE	111	GLU
38	BE	121	LYS
38	BE	131	ILE
38	BE	140	ARG
38	BE	143	ARG
38	BE	147	ASP
39	BF	1	MET
39	BF	25	ILE
39	BF	30	LEU
39	BF	37	VAL
39	BF	40	VAL
39	BF	43	LEU

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Mol	Chain	Res	Type
39	BF	54	LYS
39	BF	64	GLN
39	BF	66	GLU
39	BF	69	GLU
39	BF	71	ARG
39	BF	72	VAL
39	BF	73	ASN
39	BF	82	ARG
39	BF	92	LYS
40	BG	8	GLU
40	BG	12	LEU
40	BG	15	ASP
40	BG	16	LEU
40	BG	21	VAL
40	BG	29	LYS
40	BG	38	LEU
40	BG	41	ARG
40	BG	51	GLN
40	BG	52	GLU
40	BG	56	GLN
40	BG	61	VAL
40	BG	66	VAL
40	BG	73	MET
40	BG	75	VAL
40	BG	76	ARG
40	BG	78	ARG
40	BG	104	LEU
40	BG	111	ARG
40	BG	113	GLU
40	BG	114	ARG
40	BG	115	ARG
40	BG	131	LYS
40	BG	138	LYS
41	BH	2	LEU
41	BH	10	LEU
41	BH	13	ILE
41	BH	18	ARG
41	BH	19	VAL
41	BH	24	THR
41	BH	25	ASP
41	BH	26	VAL
41	BH	38	ILE

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Mol	Chain	Res	Type
41	BH	39	LEU
41	BH	50	ARG
41	BH	51	VAL
41	BH	52	ASP
41	BH	53	VAL
41	BH	60	ARG
41	BH	63	LEU
41	BH	75	ARG
41	BH	78	GLN
41	BH	83	ILE
41	BH	91	ARG
41	BH	95	VAL
41	BH	109	ILE
41	BH	111	ILE
41	BH	112	LEU
41	BH	123	GLU
41	BH	133	LEU
41	BH	134	ILE
41	BH	137	VAL
42	BI	23	ASN
42	BI	25	LYS
42	BI	27	THR
42	BI	29	ASN
42	BI	31	GLN
42	BI	53	VAL
42	BI	64	THR
42	BI	65	VAL
42	BI	70	LYS
42	BI	81	ILE
42	BI	93	ARG
42	BI	102	LEU
42	BI	104	ARG
42	BI	107	ARG
42	BI	108	VAL
42	BI	113	LYS
42	BI	127	LYS
42	BI	128	ARG
43	BJ	5	ARG
43	BJ	16	LEU
43	BJ	21	GLN
43	BJ	46	ARG
43	BJ	49	VAL

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Mol	Chain	Res	Type
43	BJ	65	LEU
43	BJ	92	THR
43	BJ	94	VAL
44	BK	14	VAL
44	BK	18	ARG
44	BK	25	TYR
44	BK	33	THR
44	BK	40	ILE
44	BK	48	ILE
44	BK	51	LYS
44	BK	83	ILE
44	BK	96	ARG
44	BK	104	GLN
44	BK	109	VAL
44	BK	114	VAL
45	BL	18	VAL
45	BL	23	LYS
45	BL	27	LEU
45	BL	36	VAL
45	BL	46	LYS
45	BL	53	ARG
45	BL	55	VAL
45	BL	57	LYS
45	BL	60	LEU
45	BL	67	THR
45	BL	83	VAL
45	BL	91	LYS
45	BL	96	VAL
45	BL	97	ARG
45	BL	100	ILE
45	BL	110	VAL
45	BL	116	SER
46	BM	3	ARG
46	BM	4	ILE
46	BM	15	VAL
46	BM	16	ASP
46	BM	17	VAL
46	BM	32	GLU
46	BM	56	LEU
46	BM	64	TRP
46	BM	66	LEU
46	BM	70	LEU

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Mol	Chain	Res	Type
46	BM	82	MET
46	BM	84	ILE
46	BM	103	THR
46	BM	110	ARG
46	BM	114	ARG
46	BM	116	THR
47	BN	3	ARG
47	BN	4	LYS
47	BN	7	ILE
47	BN	8	GLU
47	BN	15	LYS
47	BN	18	VAL
47	BN	22	THR
47	BN	23	ARG
47	BN	33	VAL
47	BN	41	ARG
47	BN	44	LEU
47	BN	49	HIS
48	BO	3	ILE
48	BO	5	LYS
48	BO	6	GLU
48	BO	26	GLU
48	BO	39	LEU
48	BO	41	GLU
48	BO	66	LEU
48	BO	71	GLN
48	BO	72	ARG
48	BO	76	GLU
48	BO	87	ILE
49	BP	2	VAL
49	BP	4	ILE
49	BP	11	SER
49	BP	16	HIS
49	BP	18	ARG
49	BP	19	ILE
49	BP	21	VAL
49	BP	33	ILE
49	BP	49	LEU
49	BP	50	LYS
49	BP	54	GLU
49	BP	69	THR
49	BP	72	ARG

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Mol	Chain	Res	Type
49	BP	74	LEU
49	BP	76	GLN
50	BQ	9	VAL
50	BQ	16	GLN
50	BQ	36	ILE
50	BQ	49	GLU
50	BQ	52	LYS
50	BQ	60	ILE
50	BQ	62	SER
50	BQ	65	ILE
50	BQ	72	ARG
50	BQ	74	LEU
50	BQ	77	VAL
50	BQ	78	GLU
50	BQ	91	ARG
50	BQ	92	ARG
50	BQ	94	ASN
51	BR	26	LEU
51	BR	29	PHE
51	BR	35	ARG
51	BR	37	VAL
51	BR	41	LYS
51	BR	65	ILE
51	BR	68	LYS
51	BR	70	ILE
51	BR	76	LEU
52	BS	9	VAL
52	BS	28	LYS
52	BS	38	SER
52	BS	49	ILE
52	BS	65	ASN
52	BS	66	MET
52	BS	78	ARG
52	BS	83	HIS
53	BT	8	ARG
53	BT	13	LEU
53	BT	20	LEU
53	BT	24	LEU
53	BT	31	SER
53	BT	37	SER
53	BT	38	LYS
53	BT	45	GLN

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Mol	Chain	Res	Type
53	BT	56	MET
53	BT	58	LYS
53	BT	60	GLU
53	BT	62	LEU
53	BT	70	SER
53	BT	75	ASN
53	BT	81	LYS
53	BT	84	LEU
53	BT	93	GLU
53	BT	100	ILE
54	BU	12	LYS
54	BU	15	ARG
57	BZ	-66	MET
57	BZ	-64	VAL
57	BZ	-58	LEU
57	BZ	-56	ASN
57	BZ	-49	VAL
57	BZ	-47	ASP
57	BZ	-45	LYS
57	BZ	-36	LEU
57	BZ	-30	VAL
57	BZ	-24	ASN
57	BZ	-22	LYS
57	BZ	-20	LEU
57	BZ	-10	ARG
57	BZ	-6	ARG
57	BZ	-3	GLU
57	BZ	0	ARG
57	BZ	1	LEU
57	BZ	2	LYS
57	BZ	4	ILE
57	BZ	8	ASP
57	BZ	13	ARG
57	BZ	21	ILE
57	BZ	25	LYS
57	BZ	28	THR
57	BZ	30	GLU
57	BZ	39	ILE
57	BZ	40	HIS
57	BZ	75	LYS
57	BZ	79	ILE
57	BZ	81	ILE

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Mol	Chain	Res	Type
57	BZ	83	ASP
57	BZ	84	THR
57	BZ	88	VAL
57	BZ	92	ILE
57	BZ	97	SER
57	BZ	102	ASP
57	BZ	117	GLN
57	BZ	121	VAL
57	BZ	130	VAL
57	BZ	132	ARG
57	BZ	139	MET
57	BZ	146	LEU
57	BZ	150	ILE
57	BZ	152	THR
57	BZ	154	GLN
57	BZ	155	GLU
57	BZ	156	ARG
57	BZ	157	LEU
57	BZ	160	ARG
57	BZ	163	VAL
57	BZ	164	MET
57	BZ	166	LEU
57	BZ	172	ASP
57	BZ	173	THR
57	BZ	180	VAL
57	BZ	181	LEU
57	BZ	183	MET
57	BZ	187	THR
57	BZ	196	ILE
57	BZ	198	GLU
57	BZ	199	ILE
57	BZ	204	GLU
57	BZ	207	ASP
57	BZ	210	ARG
57	BZ	213	HIS
57	BZ	215	LYS
57	BZ	216	LEU
57	BZ	225	GLU
57	BZ	236	GLU
57	BZ	238	THR
57	BZ	240	GLU
57	BZ	252	ASP

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Mol	Chain	Res	Type
57	BZ	254	LYS
57	BZ	255	ILE
57	BZ	260	LEU
57	BZ	269	VAL
57	BZ	271	LEU
57	BZ	280	LEU
57	BZ	284	LEU
57	BZ	286	ILE
57	BZ	289	ILE
57	BZ	292	THR
57	BZ	297	GLU
57	BZ	298	VAL
57	BZ	301	ILE
57	BZ	309	LEU
57	BZ	312	LEU
57	BZ	315	LYS
57	BZ	316	ILE
57	BZ	325	LEU
57	BZ	328	ILE
57	BZ	329	ARG
57	BZ	335	LEU
57	BZ	350	GLU
57	BZ	352	VAL
57	BZ	354	ARG
57	BZ	356	LEU
57	BZ	361	ASN
57	BZ	363	ARG
57	BZ	367	GLU
57	BZ	377	VAL
57	BZ	378	VAL
57	BZ	384	ILE
57	BZ	385	THR
57	BZ	392	GLU
57	BZ	393	ASP
57	BZ	396	ARG
57	BZ	399	LEU
57	BZ	651	GLU
3	CC	28	ARG
3	CC	29	LEU
3	CC	32	GLU
3	CC	48	LEU
3	CC	50	ILE

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Mol	Chain	Res	Type
3	CC	54	ARG
3	CC	63	VAL
3	CC	184	GLU
3	CC	203	GLU
3	CC	206	LYS
3	CC	208	THR
4	CD	3	VAL
4	CD	4	LYS
4	CD	12	SER
4	CD	37	LEU
4	CD	46	GLN
4	CD	49	ILE
4	CD	61	LEU
4	CD	68	LYS
4	CD	71	ASP
4	CD	79	VAL
4	CD	94	LEU
4	CD	98	VAL
4	CD	99	ASP
4	CD	101	GLU
4	CD	103	ARG
4	CD	105	ILE
4	CD	106	ILE
4	CD	111	LEU
4	CD	126	GLN
4	CD	134	ARG
4	CD	136	ILE
4	CD	142	VAL
4	CD	147	LEU
4	CD	154	LYS
4	CD	155	LEU
4	CD	165	ILE
4	CD	173	VAL
4	CD	193	VAL
4	CD	211	ARG
4	CD	217	ARG
4	CD	221	VAL
4	CD	229	VAL
4	CD	253	GLN
4	CD	254	THR
4	CD	257	LEU
4	CD	259	THR

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Mol	Chain	Res	Type
4	CD	260	ARG
4	CD	262	ARG
4	CD	270	ILE
4	CD	274	ARG
5	CE	9	VAL
5	CE	12	THR
5	CE	14	ILE
5	CE	24	THR
5	CE	33	VAL
5	CE	34	VAL
5	CE	38	THR
5	CE	40	GLU
5	CE	52	LEU
5	CE	73	GLU
5	CE	74	PRO
5	CE	75	VAL
5	CE	76	ARG
5	CE	79	ARG
5	CE	82	ARG
5	CE	85	ASN
5	CE	94	GLU
5	CE	105	THR
5	CE	111	ARG
5	CE	116	VAL
5	CE	119	ARG
5	CE	141	ILE
5	CE	144	ARG
5	CE	154	LYS
5	CE	175	VAL
5	CE	181	LEU
5	CE	182	LEU
5	CE	185	LYS
5	CE	188	VAL
5	CE	195	LEU
5	CE	202	LYS
6	CF	19	GLU
6	CF	20	LEU
6	CF	24	LEU
6	CF	27	GLU
6	CF	28	ILE
6	CF	43	LYS
6	CF	50	SER

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Mol	Chain	Res	Type
6	CF	53	THR
6	CF	57	VAL
6	CF	62	ARG
6	CF	70	THR
6	CF	74	ARG
6	CF	88	VAL
6	CF	102	PRO
6	CF	106	ARG
6	CF	119	ARG
6	CF	120	GLU
6	CF	126	VAL
6	CF	135	LYS
6	CF	137	LYS
6	CF	140	LEU
6	CF	154	VAL
6	CF	157	VAL
6	CF	158	THR
6	CF	162	LEU
6	CF	169	ASN
6	CF	170	LEU
6	CF	175	THR
6	CF	181	LEU
6	CF	183	VAL
6	CF	192	LEU
6	CF	195	ASP
6	CF	201	VAL
7	CG	3	LEU
7	CG	5	VAL
7	CG	7	LEU
7	CG	9	ARG
7	CG	16	ARG
7	CG	20	ILE
7	CG	21	ARG
7	CG	32	PRO
7	CG	33	ARG
7	CG	38	VAL
7	CG	43	LEU
7	CG	47	LYS
7	CG	60	LEU
7	CG	63	ILE
7	CG	70	VAL
7	CG	71	THR

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Mol	Chain	Res	Type
7	CG	75	LYS
7	CG	98	ARG
7	CG	115	ARG
7	CG	126	ASP
7	CG	133	LEU
7	CG	135	LEU
7	CG	136	ARG
7	CG	140	ILE
7	CG	143	GLU
7	CG	145	THR
7	CG	148	MET
7	CG	150	ASP
7	CG	159	VAL
7	CG	164	GLU
7	CG	165	THR
7	CG	170	ARG
7	CG	173	LEU
7	CG	175	LEU
8	CH	3	ARG
8	CH	4	ILE
8	CH	7	LEU
8	CH	25	LYS
8	CH	33	LEU
8	CH	37	VAL
8	CH	41	MET
8	CH	43	VAL
8	CH	49	VAL
8	CH	59	ARG
8	CH	69	ARG
8	CH	71	LEU
8	CH	79	VAL
8	CH	81	GLU
8	CH	92	ILE
8	CH	104	GLU
8	CH	106	THR
8	CH	110	SER
8	CH	115	VAL
8	CH	122	THR
8	CH	125	VAL
8	CH	133	VAL
8	CH	136	ILE
8	CH	139	GLN

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Mol	Chain	Res	Type
8	CH	171	LEU
8	CH	172	LYS
10	CL	2	LYS
10	CL	4	VAL
10	CL	8	VAL
10	CL	11	GLN
10	CL	29	GLN
10	CL	30	HIS
10	CL	38	VAL
10	CL	47	ASN
10	CL	57	ILE
10	CL	59	ILE
10	CL	65	PHE
10	CL	77	LEU
10	CL	86	LYS
10	CL	93	ARG
10	CL	95	LYS
10	CL	96	VAL
10	CL	102	GLU
10	CL	105	LEU
10	CL	111	LYS
10	CL	117	THR
10	CL	118	THR
10	CL	127	ILE
10	CL	133	SER
10	CL	134	MET
10	CL	136	VAL
11	CN	5	VAL
11	CN	10	GLU
11	CN	16	ILE
11	CN	28	THR
11	CN	33	LEU
11	CN	34	LEU
11	CN	46	VAL
11	CN	48	MET
11	CN	58	ASP
11	CN	59	LYS
11	CN	61	ARG
11	CN	63	THR
11	CN	73	THR
11	CN	83	LYS
11	CN	84	LYS

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Mol	Chain	Res	Type
11	CN	87	LEU
11	CN	97	ARG
11	CN	99	LEU
11	CN	109	LYS
11	CN	120	LEU
11	CN	121	LYS
11	CN	127	ASP
11	CN	133	GLN
11	CN	137	LYS
11	CN	138	LEU
12	CO	5	GLN
12	CO	8	LEU
12	CO	10	VAL
12	CO	18	LYS
12	CO	23	ARG
12	CO	24	VAL
12	CO	28	SER
12	CO	38	VAL
12	CO	49	ARG
12	CO	65	THR
12	CO	69	ILE
12	CO	75	SER
12	CO	78	ARG
12	CO	94	ARG
12	CO	98	VAL
12	CO	102	VAL
12	CO	108	GLU
12	CO	113	LYS
12	CO	116	SER
13	CP	3	LEU
13	CP	16	ARG
13	CP	21	ARG
13	CP	40	SER
13	CP	45	LEU
13	CP	55	ARG
13	CP	57	THR
13	CP	58	THR
13	CP	59	LEU
13	CP	64	LYS
13	CP	65	ARG
13	CP	83	VAL
13	CP	92	GLU

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Mol	Chain	Res	Type
13	CP	98	GLU
13	CP	100	LEU
13	CP	101	VAL
13	CP	106	LEU
13	CP	112	LEU
13	CP	121	LYS
13	CP	125	VAL
13	CP	147	LEU
13	CP	148	LEU
14	CQ	1	MET
14	CQ	5	ARG
14	CQ	16	ARG
14	CQ	21	THR
14	CQ	35	VAL
14	CQ	45	GLN
14	CQ	46	GLN
14	CQ	48	GLU
14	CQ	63	LYS
14	CQ	75	THR
14	CQ	97	VAL
14	CQ	109	VAL
14	CQ	110	THR
14	CQ	111	GLU
14	CQ	112	GLU
14	CQ	113	GLN
14	CQ	128	LYS
14	CQ	131	ILE
14	CQ	133	ARG
15	CR	1	MET
15	CR	6	SER
15	CR	8	ARG
15	CR	9	LYS
15	CR	18	LEU
15	CR	24	GLN
15	CR	28	LEU
15	CR	29	LEU
15	CR	33	ARG
15	CR	44	LEU
15	CR	60	LEU
15	CR	63	ARG
15	CR	65	LEU
15	CR	67	LEU

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Mol	Chain	Res	Type
15	CR	70	LEU
15	CR	73	VAL
15	CR	75	LEU
15	CR	79	LEU
15	CR	96	ARG
15	CR	100	LEU
15	CR	104	ARG
15	CR	111	LEU
15	CR	114	VAL
16	CS	3	ARG
16	CS	13	ARG
16	CS	19	LYS
16	CS	20	ARG
16	CS	35	ILE
16	CS	38	GLN
16	CS	40	ILE
16	CS	46	VAL
16	CS	49	VAL
16	CS	50	SER
16	CS	52	SER
16	CS	53	SER
16	CS	54	LEU
16	CS	57	LYS
16	CS	62	LYS
16	CS	63	THR
16	CS	67	ARG
16	CS	76	LYS
16	CS	85	VAL
16	CS	98	VAL
16	CS	110	LEU
16	CS	111	GLU
17	CT	6	LEU
17	CT	8	LYS
17	CT	10	VAL
17	CT	13	ARG
17	CT	17	THR
17	CT	18	ASP
17	CT	19	LEU
17	CT	23	ARG
17	CT	28	VAL
17	CT	30	VAL
17	CT	39	ARG

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Mol	Chain	Res	Type
17	CT	40	THR
17	CT	42	ILE
17	CT	49	VAL
17	CT	51	ARG
17	CT	53	ARG
17	CT	59	THR
17	CT	65	LYS
17	CT	74	ARG
17	CT	75	ILE
17	CT	78	LEU
17	CT	85	LYS
17	CT	89	VAL
17	CT	96	ARG
17	CT	98	LYS
17	CT	105	LEU
17	CT	110	ILE
17	CT	113	LYS
17	CT	115	ARG
17	CT	118	ARG
18	CU	6	THR
18	CU	8	VAL
18	CU	15	LYS
18	CU	17	ILE
18	CU	31	SER
18	CU	33	ARG
18	CU	52	ARG
18	CU	60	LEU
18	CU	65	ILE
18	CU	69	CYS
18	CU	74	LEU
18	CU	83	LEU
18	CU	92	ARG
18	CU	93	LYS
18	CU	95	LEU
18	CU	100	VAL
18	CU	104	GLN
18	CU	108	GLU
19	CV	6	LYS
19	CV	15	GLU
19	CV	18	LEU
19	CV	21	ARG
19	CV	24	LYS

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Mol	Chain	Res	Type
19	CV	32	THR
19	CV	35	LEU
19	CV	46	VAL
19	CV	51	VAL
19	CV	52	VAL
19	CV	61	VAL
19	CV	62	LEU
19	CV	72	VAL
19	CV	79	VAL
19	CV	95	LEU
20	CW	4	LYS
20	CW	6	ILE
20	CW	10	VAL
20	CW	11	ARG
20	CW	17	VAL
20	CW	19	LEU
20	CW	23	LEU
20	CW	24	ILE
20	CW	35	ILE
20	CW	37	ARG
20	CW	50	VAL
20	CW	51	LEU
20	CW	60	ASN
20	CW	100	THR
20	CW	107	LEU
20	CW	111	HIS
21	CX	9	LEU
21	CX	14	SER
21	CX	23	GLU
21	CX	37	THR
21	CX	57	LEU
21	CX	64	LYS
21	CX	65	ARG
21	CX	70	LEU
21	CX	72	LYS
21	CX	76	ARG
21	CX	81	VAL
21	CX	82	GLN
22	CY	3	VAL
22	CY	7	VAL
22	CY	9	LYS
22	CY	12	THR

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Mol	Chain	Res	Type
22	CY	14	LEU
22	CY	21	LYS
22	CY	37	VAL
22	CY	38	ILE
22	CY	40	GLU
22	CY	42	VAL
22	CY	43	ASN
22	CY	47	LYS
22	CY	49	VAL
22	CY	64	GLU
22	CY	66	PRO
22	CY	67	LEU
22	CY	72	VAL
22	CY	75	ILE
22	CY	85	VAL
22	CY	88	LYS
22	CY	91	GLU
22	CY	95	LYS
22	CY	96	ILE
23	CZ	5	LEU
23	CZ	16	SER
23	CZ	18	LEU
23	CZ	32	HIS
23	CZ	33	LEU
23	CZ	37	VAL
23	CZ	39	VAL
23	CZ	41	LEU
23	CZ	61	LEU
23	CZ	76	LEU
23	CZ	78	LYS
23	CZ	86	VAL
23	CZ	91	LEU
23	CZ	107	THR
23	CZ	111	VAL
23	CZ	126	VAL
23	CZ	136	PHE
23	CZ	139	VAL
23	CZ	142	SER
23	CZ	149	SER
23	CZ	150	LEU
23	CZ	155	LEU
23	CZ	156	LYS

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Mol	Chain	Res	Type
23	CZ	161	VAL
23	CZ	170	THR
24	C0	3	HIS
24	C0	9	SER
24	C0	11	ARG
24	C0	20	ARG
24	C0	67	VAL
24	C0	74	ARG
25	C1	3	LYS
25	C1	4	VAL
25	C1	30	VAL
25	C1	37	ILE
25	C1	39	LYS
25	C1	40	ARG
25	C1	51	VAL
25	C1	59	THR
25	C1	80	LEU
25	C1	94	LEU
25	C1	95	LEU
26	C2	14	ARG
26	C2	28	LYS
26	C2	32	LEU
26	C2	35	LEU
26	C2	41	ILE
26	C2	43	GLN
26	C2	45	SER
26	C2	53	LEU
26	C2	60	LEU
26	C2	70	GLN
27	C3	6	VAL
27	C3	8	LEU
27	C3	9	VAL
27	C3	18	ASP
27	C3	23	LEU
27	C3	24	LYS
27	C3	30	ARG
27	C3	31	LEU
27	C3	32	GLN
27	C3	36	VAL
27	C3	49	LYS
27	C3	54	VAL
27	C3	56	VAL

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Mol	Chain	Res	Type
28	C4	5	ILE
28	C4	10	VAL
28	C4	33	VAL
28	C4	34	GLU
28	C4	35	VAL
28	C4	50	VAL
28	C4	56	VAL
28	C4	58	ARG
28	C4	59	PHE
28	C4	61	ARG
28	C4	63	TYR
28	C4	67	TYR
28	C4	68	ARG
28	C4	69	LYS
29	C5	6	VAL
29	C5	16	ARG
29	C5	20	ARG
29	C5	21	SER
29	C5	26	THR
29	C5	29	THR
29	C5	31	VAL
29	C5	33	CYS
29	C5	36	CYS
29	C5	40	LYS
29	C5	57	VAL
29	C5	59	GLU
30	C6	6	ARG
30	C6	14	THR
30	C6	20	ASN
30	C6	23	THR
30	C6	27	LYS
30	C6	34	LEU
30	C6	38	LYS
30	C6	44	ARG
30	C6	48	VAL
30	C6	53	LYS
31	C7	4	THR
31	C7	9	ARG
31	C7	10	ARG
31	C7	14	LYS
31	C7	23	ARG
31	C7	29	LYS

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Mol	Chain	Res	Type
31	C7	32	LYS
31	C7	35	ARG
31	C7	41	ARG
31	C7	43	THR
31	C7	47	ARG
32	C8	3	LYS
32	C8	4	MET
32	C8	12	LYS
32	C8	14	VAL
32	C8	23	VAL
32	C8	27	THR
32	C8	30	ARG
33	C9	4	ARG
33	C9	26	ILE
33	C9	27	CYS
33	C9	35	ARG
35	DB	7	VAL
35	DB	23	ARG
35	DB	44	LEU
35	DB	47	THR
35	DB	51	LEU
35	DB	53	ARG
35	DB	56	ARG
35	DB	58	ILE
35	DB	80	ILE
35	DB	93	VAL
35	DB	94	ASN
35	DB	98	LEU
35	DB	102	LEU
35	DB	107	THR
35	DB	110	GLN
35	DB	115	LEU
35	DB	117	GLU
35	DB	119	GLU
35	DB	144	ARG
35	DB	149	LEU
35	DB	154	LEU
35	DB	157	ARG
35	DB	169	LYS
35	DB	170	GLU
35	DB	179	LYS
35	DB	180	LEU

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Mol	Chain	Res	Type
35	DB	185	ILE
35	DB	187	LEU
35	DB	189	ASP
35	DB	213	LEU
35	DB	217	ARG
35	DB	224	GLN
35	DB	229	VAL
35	DB	230	VAL
36	DC	3	ASN
36	DC	4	LYS
36	DC	5	ILE
36	DC	8	ILE
36	DC	15	THR
36	DC	26	LYS
36	DC	30	ARG
36	DC	43	LEU
36	DC	45	LYS
36	DC	47	LEU
36	DC	52	LEU
36	DC	57	ILE
36	DC	64	VAL
36	DC	67	THR
36	DC	102	ASN
36	DC	104	GLN
36	DC	105	GLU
36	DC	108	ASN
36	DC	116	VAL
36	DC	120	VAL
36	DC	130	VAL
36	DC	131	ARG
36	DC	152	ILE
36	DC	164	ARG
36	DC	178	LEU
36	DC	188	LEU
36	DC	190	ARG
36	DC	191	THR
36	DC	195	VAL
36	DC	202	ILE
37	DD	5	ILE
37	DD	8	VAL
37	DD	13	ARG
37	DD	19	LEU

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Mol	Chain	Res	Type
37	DD	28	SER
37	DD	31	CYS
37	DD	34	GLU
37	DD	47	ARG
37	DD	58	LEU
37	DD	61	LYS
37	DD	67	ILE
37	DD	76	ARG
37	DD	85	LYS
37	DD	86	LYS
37	DD	96	LEU
37	DD	97	LEU
37	DD	103	ASN
37	DD	108	LEU
37	DD	115	ARG
37	DD	119	GLN
37	DD	120	LEU
37	DD	126	ILE
37	DD	127	THR
37	DD	129	ASN
37	DD	132	ARG
37	DD	135	LEU
37	DD	150	GLU
37	DD	153	ARG
37	DD	160	GLN
37	DD	162	LEU
37	DD	163	GLU
37	DD	170	VAL
37	DD	187	ARG
37	DD	188	LEU
37	DD	194	LEU
37	DD	202	LEU
37	DD	208	SER
38	DE	11	ILE
38	DE	12	LEU
38	DE	13	ILE
38	DE	25	ARG
38	DE	31	LEU
38	DE	41	VAL
38	DE	47	LYS
38	DE	66	MET
38	DE	68	GLU

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Mol	Chain	Res	Type
38	DE	71	LEU
38	DE	78	HIS
38	DE	81	GLU
38	DE	90	VAL
38	DE	91	LEU
38	DE	96	PRO
38	DE	107	ARG
38	DE	116	THR
38	DE	120	THR
38	DE	135	THR
38	DE	137	GLU
38	DE	147	ASP
38	DE	150	ARG
38	DE	151	LEU
39	DF	27	GLN
39	DF	28	ARG
39	DF	37	VAL
39	DF	48	LEU
39	DF	67	MET
39	DF	69	GLU
39	DF	72	VAL
39	DF	86	ARG
39	DF	87	ARG
39	DF	91	VAL
39	DF	92	LYS
40	DG	4	ARG
40	DG	8	GLU
40	DG	24	THR
40	DG	32	ARG
40	DG	57	GLU
40	DG	73	MET
40	DG	75	VAL
40	DG	76	ARG
40	DG	85	TYR
40	DG	87	VAL
40	DG	104	LEU
40	DG	137	LYS
40	DG	140	ASP
40	DG	155	ARG
41	DH	2	LEU
41	DH	3	THR
41	DH	24	THR

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Mol	Chain	Res	Type
41	DH	26	VAL
41	DH	35	ILE
41	DH	51	VAL
41	DH	52	ASP
41	DH	63	LEU
41	DH	78	GLN
41	DH	80	ILE
41	DH	84	ARG
41	DH	85	ARG
41	DH	91	ARG
41	DH	98	LYS
41	DH	99	GLU
41	DH	104	ARG
41	DH	111	ILE
41	DH	112	LEU
41	DH	120	THR
41	DH	133	LEU
42	DI	7	THR
42	DI	17	VAL
42	DI	23	ASN
42	DI	27	THR
42	DI	41	VAL
42	DI	53	VAL
42	DI	64	THR
42	DI	65	VAL
42	DI	81	ILE
42	DI	83	ARG
42	DI	92	TYR
42	DI	96	LEU
42	DI	102	LEU
42	DI	108	VAL
42	DI	109	VAL
42	DI	124	GLN
43	DJ	38	ILE
43	DJ	58	ASP
43	DJ	59	SER
43	DJ	67	THR
44	DK	30	VAL
44	DK	33	THR
44	DK	38	ASN
44	DK	47	VAL
44	DK	92	GLU

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Mol	Chain	Res	Type
44	DK	96	ARG
44	DK	109	VAL
44	DK	114	VAL
44	DK	117	ASN
44	DK	120	ARG
44	DK	126	ARG
45	DL	6	THR
45	DL	8	ASN
45	DL	10	LEU
45	DL	24	VAL
45	DL	27	LEU
45	DL	33	ARG
45	DL	39	VAL
45	DL	52	LEU
45	DL	53	ARG
45	DL	55	VAL
45	DL	82	VAL
45	DL	83	VAL
45	DL	84	LEU
45	DL	85	ILE
45	DL	96	VAL
45	DL	97	ARG
45	DL	104	VAL
45	DL	114	LYS
46	DM	12	ASN
46	DM	15	VAL
46	DM	17	VAL
46	DM	19	LEU
46	DM	29	ARG
46	DM	56	LEU
46	DM	66	LEU
46	DM	70	LEU
46	DM	73	GLU
46	DM	106	ASN
46	DM	110	ARG
46	DM	114	ARG
47	DN	3	ARG
47	DN	12	ARG
47	DN	22	THR
47	DN	33	VAL
47	DN	42	ILE
47	DN	43	CYS

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Mol	Chain	Res	Type
47	DN	44	LEU
47	DN	46	GLU
48	DO	3	ILE
48	DO	4	THR
48	DO	5	LYS
48	DO	7	GLU
48	DO	10	LYS
48	DO	22	THR
48	DO	26	GLU
48	DO	33	THR
48	DO	38	ARG
48	DO	39	LEU
48	DO	41	GLU
48	DO	48	LYS
48	DO	66	LEU
48	DO	68	ARG
48	DO	87	ILE
49	DP	2	VAL
49	DP	4	ILE
49	DP	5	ARG
49	DP	8	ARG
49	DP	20	VAL
49	DP	21	VAL
49	DP	25	ARG
49	DP	27	LYS
49	DP	35	LYS
49	DP	38	TYR
49	DP	60	LEU
49	DP	62	VAL
49	DP	69	THR
50	DQ	37	LYS
50	DQ	50	LYS
50	DQ	65	ILE
50	DQ	72	ARG
50	DQ	74	LEU
50	DQ	76	LEU
50	DQ	77	VAL
50	DQ	98	LEU
51	DR	21	LYS
51	DR	25	THR
51	DR	31	LEU
51	DR	32	ARG

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Mol	Chain	Res	Type
51	DR	37	VAL
51	DR	41	LYS
51	DR	53	ARG
51	DR	55	ARG
51	DR	58	LEU
51	DR	69	THR
51	DR	70	ILE
51	DR	76	LEU
51	DR	84	LYS
51	DR	86	VAL
52	DS	3	ARG
52	DS	12	ASP
52	DS	15	LEU
52	DS	16	LEU
52	DS	28	LYS
52	DS	33	THR
52	DS	38	SER
52	DS	43	GLU
52	DS	77	THR
52	DS	78	ARG
53	DT	23	ARG
53	DT	24	LEU
53	DT	36	LEU
53	DT	56	MET
53	DT	62	LEU
53	DT	72	LEU
53	DT	80	ARG
53	DT	84	LEU
53	DT	89	ARG
57	DZ	-65	LYS
57	DZ	-63	ILE
57	DZ	-62	LEU
57	DZ	-58	LEU
57	DZ	-52	VAL
57	DZ	-50	GLN
57	DZ	-30	VAL
57	DZ	-29	LEU
57	DZ	-27	THR
57	DZ	-23	LEU
57	DZ	-22	LYS
57	DZ	-20	LEU
57	DZ	-19	GLU

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Mol	Chain	Res	Type
57	DZ	-6	ARG
57	DZ	1	LEU
57	DZ	6	GLU
57	DZ	9	LEU
57	DZ	10	LYS
57	DZ	12	LEU
57	DZ	15	ILE
57	DZ	17	ILE
57	DZ	21	ILE
57	DZ	22	ASP
57	DZ	25	LYS
57	DZ	26	THR
57	DZ	28	THR
57	DZ	38	ARG
57	DZ	39	ILE
57	DZ	75	LYS
57	DZ	79	ILE
57	DZ	81	ILE
57	DZ	87	HIS
57	DZ	92	ILE
57	DZ	100	VAL
57	DZ	105	ILE
57	DZ	112	GLN
57	DZ	114	VAL
57	DZ	115	GLU
57	DZ	118	SER
57	DZ	130	VAL
57	DZ	133	ILE
57	DZ	141	LYS
57	DZ	142	THR
57	DZ	146	LEU
57	DZ	151	ARG
57	DZ	152	THR
57	DZ	155	GLU
57	DZ	157	LEU
57	DZ	162	VAL
57	DZ	163	VAL
57	DZ	170	ARG
57	DZ	180	VAL
57	DZ	181	LEU
57	DZ	182	ARG
57	DZ	184	LYS

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Mol	Chain	Res	Type
57	DZ	187	THR
57	DZ	192	LEU
57	DZ	201	ILE
57	DZ	203	GLU
57	DZ	204	GLU
57	DZ	207	ASP
57	DZ	214	GLU
57	DZ	215	LYS
57	DZ	217	VAL
57	DZ	219	VAL
57	DZ	222	ASP
57	DZ	227	ILE
57	DZ	228	MET
57	DZ	236	GLU
57	DZ	240	GLU
57	DZ	242	LEU
57	DZ	243	VAL
57	DZ	253	LEU
57	DZ	255	ILE
57	DZ	265	LYS
57	DZ	277	VAL
57	DZ	284	LEU
57	DZ	285	ASP
57	DZ	290	LYS
57	DZ	292	THR
57	DZ	297	GLU
57	DZ	298	VAL
57	DZ	299	VAL
57	DZ	302	HIS
57	DZ	312	LEU
57	DZ	315	LYS
57	DZ	322	VAL
57	DZ	328	ILE
57	DZ	352	VAL
57	DZ	355	LEU
57	DZ	356	LEU
57	DZ	361	ASN
57	DZ	363	ARG
57	DZ	364	GLU
57	DZ	368	GLU
57	DZ	369	LEU
57	DZ	377	VAL

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Mol	Chain	Res	Type
57	DZ	380	LEU
57	DZ	381	LYS
57	DZ	385	THR
57	DZ	392	GLU
57	DZ	396	ARG
57	DZ	402	ILE
57	DZ	661	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (209) such sidechains are listed below:

Mol	Chain	Res	Type
3	AC	18	ASN
3	AC	67	HIS
3	AC	173	HIS
3	AC	189	ASN
3	AC	200	HIS
4	AD	87	ASN
4	AD	253	GLN
5	AE	85	ASN
5	AE	121	ASN
5	AE	143	ASN
6	AF	69	HIS
6	AF	169	ASN
6	AF	203	GLN
7	AG	26	GLN
7	AG	41	GLN
7	AG	58	GLN
7	AG	138	GLN
8	AH	147	ASN
10	AL	29	GLN
10	AL	30	HIS
11	AN	101	HIS
11	AN	131	GLN
13	AP	38	GLN
13	AP	70	GLN
15	AR	11	ASN
15	AR	13	HIS
15	AR	71	GLN
16	AS	95	HIS
17	AT	43	GLN
17	AT	123	GLN
19	AV	80	GLN

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Mol	Chain	Res	Type
20	AW	40	ASN
20	AW	60	ASN
20	AW	111	HIS
21	AX	31	HIS
21	AX	82	GLN
22	AY	6	HIS
22	AY	92	ASN
23	AZ	34	ASN
23	AZ	50	GLN
23	AZ	55	HIS
23	AZ	121	HIS
26	A2	46	GLN
26	A2	65	ASN
28	A4	46	GLN
29	A5	4	HIS
30	A6	20	ASN
32	A8	35	GLN
33	A9	36	GLN
35	BB	40	HIS
35	BB	45	GLN
35	BB	76	GLN
35	BB	212	GLN
36	BC	28	GLN
36	BC	37	GLN
36	BC	98	ASN
36	BC	104	GLN
36	BC	136	GLN
36	BC	181	ASN
37	BD	42	GLN
37	BD	45	GLN
37	BD	77	ASN
37	BD	123	HIS
37	BD	125	HIS
37	BD	161	ASN
38	BE	38	GLN
38	BE	56	GLN
38	BE	73	ASN
38	BE	141	GLN
39	BF	7	ASN
40	BG	13	GLN
40	BG	28	ASN
40	BG	56	GLN

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Mol	Chain	Res	Type
40	BG	109	ASN
41	BH	78	GLN
42	BI	23	ASN
42	BI	31	GLN
42	BI	34	ASN
42	BI	73	GLN
42	BI	124	GLN
43	BJ	21	GLN
43	BJ	62	HIS
44	BK	93	GLN
44	BK	99	GLN
45	BL	78	GLN
45	BL	99	HIS
46	BM	40	ASN
46	BM	92	HIS
47	BN	49	HIS
48	BO	9	GLN
48	BO	13	GLN
48	BO	28	GLN
48	BO	62	GLN
50	BQ	16	GLN
50	BQ	26	GLN
50	BQ	94	ASN
52	BS	65	ASN
52	BS	69	HIS
52	BS	83	HIS
53	BT	26	ASN
53	BT	42	GLN
53	BT	45	GLN
57	BZ	-50	GLN
57	BZ	7	ASN
57	BZ	77	HIS
57	BZ	154	GLN
57	BZ	165	GLN
57	BZ	213	HIS
57	BZ	362	HIS
3	CC	18	ASN
3	CC	67	HIS
3	CC	189	ASN
3	CC	200	HIS
4	CD	87	ASN
4	CD	96	HIS

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Mol	Chain	Res	Type
4	CD	116	GLN
4	CD	143	HIS
4	CD	164	GLN
4	CD	253	GLN
5	CE	48	GLN
5	CE	66	HIS
6	CF	29	ASN
6	CF	69	HIS
6	CF	75	HIS
7	CG	108	ASN
8	CH	147	ASN
8	CH	158	HIS
10	CL	29	GLN
10	CL	30	HIS
10	CL	33	ASN
10	CL	103	GLN
11	CN	56	ASN
11	CN	69	GLN
11	CN	101	HIS
11	CN	128	HIS
11	CN	133	GLN
13	CP	38	GLN
13	CP	84	ASN
14	CQ	13	GLN
14	CQ	57	HIS
14	CQ	123	HIS
15	CR	50	HIS
16	CS	68	GLN
17	CT	38	ASN
17	CT	79	HIS
17	CT	123	GLN
18	CU	72	HIS
18	CU	94	ASN
18	CU	104	GLN
20	CW	60	ASN
21	CX	31	HIS
22	CY	43	ASN
23	CZ	55	HIS
23	CZ	65	GLN
26	C2	38	GLN
26	C2	65	ASN
26	C2	70	GLN

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Mol	Chain	Res	Type
27	C3	33	GLN
28	C4	60	GLN
30	C6	20	ASN
30	C6	32	ASN
31	C7	36	GLN
32	C8	35	GLN
32	C8	43	GLN
33	C9	29	ASN
33	C9	36	GLN
35	DB	16	HIS
35	DB	19	HIS
35	DB	45	GLN
35	DB	76	GLN
35	DB	94	ASN
35	DB	135	GLN
35	DB	146	GLN
35	DB	224	GLN
36	DC	28	GLN
36	DC	31	HIS
36	DC	63	ASN
36	DC	104	GLN
36	DC	110	ASN
37	DD	74	GLN
37	DD	77	ASN
37	DD	123	HIS
37	DD	129	ASN
37	DD	160	GLN
38	DE	73	ASN
38	DE	130	ASN
39	DF	7	ASN
40	DG	28	ASN
40	DG	51	GLN
40	DG	109	ASN
40	DG	148	ASN
42	DI	89	ASN
43	DJ	68	HIS
44	DK	93	GLN
45	DL	9	GLN
45	DL	49	ASN
45	DL	75	HIS
45	DL	78	GLN
46	DM	77	ASN

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Mol	Chain	Res	Type
48	DO	13	GLN
48	DO	28	GLN
49	DP	13	HIS
50	DQ	16	GLN
52	DS	83	HIS
57	DZ	-50	GLN
57	DZ	77	HIS
57	DZ	117	GLN
57	DZ	154	GLN
57	DZ	213	HIS

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	2845/2915 (97%)	568 (19%)	43 (1%)
1	CA	2839/2915 (97%)	584 (20%)	33 (1%)
2	AB	119/121 (98%)	25 (21%)	1 (0%)
2	CB	119/121 (98%)	23 (19%)	0
34	BA	1491/1521 (98%)	300 (20%)	18 (1%)
34	DA	1498/1521 (98%)	297 (19%)	20 (1%)
55	BV	12/24 (50%)	7 (58%)	0
55	DV	5/24 (20%)	1 (20%)	0
56	BX	75/77 (97%)	15 (20%)	1 (1%)
56	DX	75/77 (97%)	11 (14%)	0
All	All	9078/9316 (97%)	1831 (20%)	116 (1%)

All (1831) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	12	U
1	AA	13	A
1	AA	17	G
1	AA	34	C
1	AA	36	G
1	AA	45	C
1	AA	57	G
1	AA	63	A
1	AA	70	A
1	AA	73	A
1	AA	74	G
1	AA	83	A

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Mol	Chain	Res	Type
1	AA	87	G
1	AA	89	U
1	AA	94	G
1	AA	95	G
1	AA	116	A
1	AA	117	A
1	AA	118	U
1	AA	119	G
1	AA	120	G
1	AA	121	G
1	AA	123	G
1	AA	131	C
1	AA	149	A
1	AA	162	G
1	AA	170	A
1	AA	171	A
1	AA	185	A
1	AA	188	A
1	AA	189	U
1	AA	190	C
1	AA	194	G
1	AA	203	G
1	AA	204	G
1	AA	205	A
1	AA	210	A
1	AA	211	A
1	AA	213	G
1	AA	214	A
1	AA	217	A
1	AA	218	A
1	AA	222	A
1	AA	237	G
1	AA	239	G
1	AA	250	G
1	AA	253	C
1	AA	255	G
1	AA	269	G
1	AA	271	U
1	AA	272	U
1	AA	273	G
1	AA	274	U
1	AA	279	G

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Mol	Chain	Res	Type
1	AA	282	G
1	AA	289	G
1	AA	299	G
1	AA	303	C
1	AA	307	A
1	AA	311	C
1	AA	335	A
1	AA	336	G
1	AA	341	G
1	AA	349	G
1	AA	353	G
1	AA	354	A
1	AA	358	C
1	AA	366	G
1	AA	370	A
1	AA	376	G
1	AA	387	G
1	AA	391	G
1	AA	397	G
1	AA	413	G
1	AA	416	G
1	AA	434	G
1	AA	438	G
1	AA	449	A
1	AA	455	A
1	AA	469	A
1	AA	470	C
1	AA	474	U
1	AA	477	C
1	AA	483	A
1	AA	489	G
1	AA	496	A
1	AA	497	A
1	AA	499	G
1	AA	501	U
1	AA	507	G
1	AA	519	G
1	AA	528	A
1	AA	529	U
1	AA	530	A
1	AA	533	G
1	AA	534	C

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Mol	Chain	Res	Type
1	AA	537	G
1	AA	553	A
1	AA	554	A
1	AA	555	G
1	AA	556	C
1	AA	557	A
1	AA	558	G
1	AA	573	G
1	AA	574	G
1	AA	586	G
1	AA	596	G
1	AA	598	A
1	AA	607	C
1	AA	609	A
1	AA	625	G
1	AA	626	A
1	AA	627	G
1	AA	630	U
1	AA	631	A
1	AA	638	U
1	AA	639	G
1	AA	640	A
1	AA	641	G
1	AA	643	C
1	AA	659	C
1	AA	662	A
1	AA	670	C
1	AA	671	A
1	AA	697	C
1	AA	716	G
1	AA	733	G
1	AA	746	A
1	AA	764	G
1	AA	777	C
1	AA	787	U
1	AA	804	U
1	AA	809	U
1	AA	811	A
1	AA	812	G
1	AA	821	A
1	AA	822	G
1	AA	823	G

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Mol	Chain	Res	Type
1	AA	829	A
1	AA	830	A
1	AA	831	A
1	AA	832	G
1	AA	836	A
1	AA	837	C
1	AA	839	G
1	AA	845	G
1	AA	852	G
1	AA	859	C
1	AA	874	U
1	AA	875	U
1	AA	880	U
1	AA	897	C
1	AA	906	G
1	AA	913	A
1	AA	914	C
1	AA	924	U
1	AA	927	G
1	AA	929	G
1	AA	932	C
1	AA	933	C
1	AA	934	A
1	AA	935	C
1	AA	936	C
1	AA	937	A
1	AA	938	G
1	AA	939	C
1	AA	940	C
1	AA	942	A
1	AA	943	C
1	AA	945	A
1	AA	953	U
1	AA	956	A
1	AA	957	A
1	AA	960	C
1	AA	968	U
1	AA	977	G
1	AA	986	A
1	AA	990	A
1	AA	991	G
1	AA	992	G

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Mol	Chain	Res	Type
1	AA	1004	A
1	AA	1006	C
1	AA	1019	G
1	AA	1020	C
1	AA	1029	A
1	AA	1031	C
1	AA	1037	C
1	AA	1042	A
1	AA	1051	C
1	AA	1052	C
1	AA	1054	C
1	AA	1058	U
1	AA	1059	C
1	AA	1068	G
1	AA	1069	U
1	AA	1072	U
1	AA	1079	U
1	AA	1080	G
1	AA	1082	G
1	AA	1084	C
1	AA	1087	C
1	AA	1093	G
1	AA	1097	G
1	AA	1099	C
1	AA	1100	A
1	AA	1105	G
1	AA	1107	U
1	AA	1108	G
1	AA	1112	U
1	AA	1114	G
1	AA	1116	A
1	AA	1119	A
1	AA	1120	G
1	AA	1121	C
1	AA	1122	C
1	AA	1128	U
1	AA	1129	U
1	AA	1134	A
1	AA	1135	G
1	AA	1141	A
1	AA	1142	A
1	AA	1144	A

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Mol	Chain	Res	Type
1	AA	1147	U
1	AA	1155	C
1	AA	1156	G
1	AA	1158	G
1	AA	1164	C
1	AA	1188	A
1	AA	1189	A
1	AA	1210	G
1	AA	1217	G
1	AA	1218	G
1	AA	1219	A
1	AA	1220	U
1	AA	1221	G
1	AA	1222	A
1	AA	1223	C
1	AA	1255	A
1	AA	1256	U
1	AA	1290	G
1	AA	1299	A
1	AA	1302	G
1	AA	1317	G
1	AA	1318	A
1	AA	1319	U
1	AA	1329	G
1	AA	1338	U
1	AA	1339	C
1	AA	1340	U
1	AA	1343	C
1	AA	1346	U
1	AA	1347	A
1	AA	1352	C
1	AA	1364	C
1	AA	1367	A
1	AA	1372	U
1	AA	1380	G
1	AA	1393	G
1	AA	1395	A
1	AA	1398	U
1	AA	1405	A
1	AA	1406	A
1	AA	1411	A
1	AA	1416	C

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Mol	Chain	Res	Type
1	AA	1423	G
1	AA	1424	A
1	AA	1425	A
1	AA	1430	A
1	AA	1431	G
1	AA	1432	C
1	AA	1436	U
1	AA	1437	U
1	AA	1441	A
1	AA	1453	C
1	AA	1460	G
1	AA	1462	G
1	AA	1463	C
1	AA	1466	U
1	AA	1467	G
1	AA	1468	G
1	AA	1469	G
1	AA	1474	C
1	AA	1476	C
1	AA	1479	U
1	AA	1485	A
1	AA	1491	A
1	AA	1493	C
1	AA	1496	A
1	AA	1497	G
1	AA	1506	G
1	AA	1508	G
1	AA	1514	C
1	AA	1518	A
1	AA	1525	G
1	AA	1529	G
1	AA	1539	C
1	AA	1540	A
1	AA	1554	A
1	AA	1555	C
1	AA	1556	A
1	AA	1571	G
1	AA	1576	G
1	AA	1579	C
1	AA	1589	A
1	AA	1590	C
1	AA	1605	A

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Mol	Chain	Res	Type
1	AA	1607	G
1	AA	1608	G
1	AA	1613	A
1	AA	1616	A
1	AA	1625	U
1	AA	1628	G
1	AA	1630	A
1	AA	1631	C
1	AA	1632	A
1	AA	1651	C
1	AA	1654	A
1	AA	1655	A
1	AA	1656	A
1	AA	1663	C
1	AA	1670	G
1	AA	1680	G
1	AA	1686	U
1	AA	1694	G
1	AA	1695	C
1	AA	1700	G
1	AA	1701	A
1	AA	1706	U
1	AA	1721	G
1	AA	1722	C
1	AA	1729	G
1	AA	1743	G
1	AA	1745	A
1	AA	1747	A
1	AA	1748	A
1	AA	1752	G
1	AA	1766	G
1	AA	1767	A
1	AA	1768	U
1	AA	1769	G
1	AA	1775	C
1	AA	1776	G
1	AA	1779	G
1	AA	1787	G
1	AA	1793	A
1	AA	1794	G
1	AA	1795	G
1	AA	1804	A

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Mol	Chain	Res	Type
1	AA	1811	A
1	AA	1813	C
1	AA	1822	A
1	AA	1831	C
1	AA	1832	G
1	AA	1833	A
1	AA	1847	G
1	AA	1859	G
1	AA	1860	A
1	AA	1870	G
1	AA	1878	A
1	AA	1889	G
1	AA	1892	G
1	AA	1893	G
1	AA	1900	G
1	AA	1911	A
1	AA	1922	A
1	AA	1928	G
1	AA	1937	U
1	AA	1945	U
1	AA	1951	G
1	AA	1952	G
1	AA	1954	A
1	AA	1959	A
1	AA	1960	A
1	AA	1977	U
1	AA	1984	C
1	AA	1985	U
1	AA	1989	C
1	AA	1992	A
1	AA	1993	A
1	AA	1994	A
1	AA	1995	G
1	AA	2003	A
1	AA	2008	A
1	AA	2014	G
1	AA	2015	U
1	AA	2019	G
1	AA	2039	U
1	AA	2042	A
1	AA	2045	G
1	AA	2052	A

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Mol	Chain	Res	Type
1	AA	2053	A
1	AA	2055	A
1	AA	2065	C
1	AA	2069	U
1	AA	2071	G
1	AA	2073	A
1	AA	2077	C
1	AA	2078	G
1	AA	2082	A
1	AA	2083	G
1	AA	2084	A
1	AA	2085	C
1	AA	2091	G
1	AA	2102	G
1	AA	2115	G
1	AA	2120	U
1	AA	2133	C
1	AA	2134	G
1	AA	2137	G
1	AA	2139	A
1	AA	2141	A
1	AA	2149	G
1	AA	2151	C
1	AA	2154	U
1	AA	2156	A
1	AA	2157	A
1	AA	2158	C
1	AA	2160	C
1	AA	2163	G
1	AA	2164	C
1	AA	2167	C
1	AA	2168	C
1	AA	2169	G
1	AA	2172	U
1	AA	2173	G
1	AA	2175	G
1	AA	2178	G
1	AA	2179	G
1	AA	2180	A
1	AA	2181	G
1	AA	2188	G
1	AA	2189	U

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Mol	Chain	Res	Type
1	AA	2190	G
1	AA	2191	A
1	AA	2192	A
1	AA	2194	U
1	AA	2195	A
1	AA	2197	C
1	AA	2204	G
1	AA	2206	G
1	AA	2210	C
1	AA	2211	U
1	AA	2213	G
1	AA	2214	G
1	AA	2217	C
1	AA	2220	A
1	AA	2221	A
1	AA	2227	G
1	AA	2228	G
1	AA	2229	A
1	AA	2230	U
1	AA	2237	A
1	AA	2250	G
1	AA	2251	G
1	AA	2254	G
1	AA	2261	U
1	AA	2271	G
1	AA	2280	A
1	AA	2281	A
1	AA	2287	C
1	AA	2288	G
1	AA	2295	C
1	AA	2299	A
1	AA	2317	A
1	AA	2319	G
1	AA	2320	G
1	AA	2332	A
1	AA	2337	G
1	AA	2338	C
1	AA	2339	A
1	AA	2347	A
1	AA	2348	A
1	AA	2355	C
1	AA	2358	A

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Mol	Chain	Res	Type
1	AA	2359	C
1	AA	2362	C
1	AA	2378	A
1	AA	2384	G
1	AA	2385	G
1	AA	2395	G
1	AA	2397	C
1	AA	2418	U
1	AA	2419	G
1	AA	2434	A
1	AA	2435	U
1	AA	2436	C
1	AA	2437	A
1	AA	2441	G
1	AA	2442	A
1	AA	2443	U
1	AA	2447	A
1	AA	2451	A
1	AA	2452	C
1	AA	2453	C
1	AA	2457	G
1	AA	2459	G
1	AA	2460	A
1	AA	2461	U
1	AA	2480	G
1	AA	2488	A
1	AA	2490	A
1	AA	2491	G
1	AA	2509	A
1	AA	2514	G
1	AA	2517	G
1	AA	2518	U
1	AA	2519	C
1	AA	2522	C
1	AA	2530	A
1	AA	2532	C
1	AA	2537	G
1	AA	2541	G
1	AA	2566	U
1	AA	2578	A
1	AA	2579	G
1	AA	2584	A

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Mol	Chain	Res	Type
1	AA	2585	C
1	AA	2590	G
1	AA	2594	G
1	AA	2597	U
1	AA	2598	C
1	AA	2600	G
1	AA	2613	C
1	AA	2614	A
1	AA	2621	U
1	AA	2622	C
1	AA	2623	U
1	AA	2624	C
1	AA	2642	G
1	AA	2673	G
1	AA	2674	A
1	AA	2685	G
1	AA	2701	U
1	AA	2702	C
1	AA	2714	U
1	AA	2715	C
1	AA	2719	G
1	AA	2725	A
1	AA	2726	A
1	AA	2727	G
1	AA	2739	U
1	AA	2740	G
1	AA	2746	A
1	AA	2757	G
1	AA	2768	C
1	AA	2770	A
1	AA	2771	A
1	AA	2773	C
1	AA	2778	A
1	AA	2779	G
1	AA	2791	A
1	AA	2794	A
1	AA	2803	A
1	AA	2804	C
1	AA	2807	C
1	AA	2813	G
1	AA	2830	A
1	AA	2831	A

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Mol	Chain	Res	Type
1	AA	2839	C
1	AA	2843	G
1	AA	2845	A
1	AA	2846	U
1	AA	2849	G
1	AA	2871	G
1	AA	2881	C
1	AA	2882	G
1	AA	2902	G
1	AA	2903	G
2	AB	2	C
2	AB	12	C
2	AB	13	A
2	AB	23	G
2	AB	26	A
2	AB	31	C
2	AB	32	C
2	AB	44	G
2	AB	45	A
2	AB	47	C
2	AB	50	G
2	AB	52	A
2	AB	56	G
2	AB	58	A
2	AB	63	G
2	AB	73	A
2	AB	85	G
2	AB	90	A
2	AB	93	G
2	AB	94	C
2	AB	95	C
2	AB	108	U
2	AB	110	G
2	AB	113	G
2	AB	118	G
34	BA	5	U
34	BA	7	G
34	BA	8	A
34	BA	9	G
34	BA	11	G
34	BA	32	A
34	BA	39	G

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Mol	Chain	Res	Type
34	BA	43	C
34	BA	44	G
34	BA	47	C
34	BA	48	C
34	BA	50	A
34	BA	51	A
34	BA	61	G
34	BA	66	G
34	BA	77	G
34	BA	78	G
34	BA	79	G
34	BA	97	G
34	BA	101	A
34	BA	115	G
34	BA	116	A
34	BA	121	C
34	BA	127	G
34	BA	131	C
34	BA	137	C
34	BA	160	A
34	BA	163	C
34	BA	164	U
34	BA	174	C
34	BA	182	U
34	BA	189(F)	U
34	BA	189(J)	G
34	BA	195	A
34	BA	197	A
34	BA	199	G
34	BA	202	U
34	BA	204	U
34	BA	216	G
34	BA	231	G
34	BA	243	A
34	BA	247	G
34	BA	251	G
34	BA	266	G
34	BA	267	C
34	BA	270	A
34	BA	281	G
34	BA	286	G
34	BA	289	G

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Mol	Chain	Res	Type
34	BA	305	G
34	BA	306	G
34	BA	318	G
34	BA	320	C
34	BA	328	C
34	BA	329	A
34	BA	330	C
34	BA	331	G
34	BA	332	G
34	BA	343	U
34	BA	346	G
34	BA	347	G
34	BA	348	G
34	BA	351	G
34	BA	352	C
34	BA	353	A
34	BA	354	G
34	BA	355	C
34	BA	356	A
34	BA	367	U
34	BA	370	C
34	BA	372	C
34	BA	373	A
34	BA	384	G
34	BA	397	A
34	BA	398	C
34	BA	406	G
34	BA	412	A
34	BA	413	G
34	BA	422	C
34	BA	424	G
34	BA	429	U
34	BA	439	A
34	BA	442	C
34	BA	446	G
34	BA	452	A
34	BA	470	C
34	BA	485	G
34	BA	496	A
34	BA	498	U
34	BA	505	G
34	BA	509	A

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Mol	Chain	Res	Type
34	BA	510	A
34	BA	511	C
34	BA	518	C
34	BA	521	G
34	BA	526	C
34	BA	527	G
34	BA	531	U
34	BA	532	A
34	BA	533	A
34	BA	547	A
34	BA	549	C
34	BA	559	A
34	BA	561	U
34	BA	572	A
34	BA	573	A
34	BA	574	A
34	BA	576	G
34	BA	577	G
34	BA	581	G
34	BA	618	C
34	BA	630	G
34	BA	631	G
34	BA	633	G
34	BA	634	C
34	BA	649	G
34	BA	653	A
34	BA	665	A
34	BA	671	G
34	BA	687	A
34	BA	688	G
34	BA	693	G
34	BA	694	A
34	BA	695	A
34	BA	702	A
34	BA	717	C
34	BA	723	U
34	BA	724	G
34	BA	731	G
34	BA	734	G
34	BA	749	C
34	BA	755	G
34	BA	759	A

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Mol	Chain	Res	Type
34	BA	766	A
34	BA	774	G
34	BA	777	A
34	BA	787	A
34	BA	792	A
34	BA	793	U
34	BA	794	A
34	BA	796	C
34	BA	799	G
34	BA	806	C
34	BA	815	A
34	BA	817	C
34	BA	828	A
34	BA	829	G
34	BA	836	G
34	BA	840	C
34	BA	841	U
34	BA	848	C
34	BA	850	U
34	BA	851	G
34	BA	853	G
34	BA	859	A
34	BA	870	U
34	BA	872	A
34	BA	874	G
34	BA	875	C
34	BA	892	A
34	BA	896	C
34	BA	902	G
34	BA	913	A
34	BA	914	A
34	BA	922	G
34	BA	926	G
34	BA	927	G
34	BA	932	C
34	BA	934	C
34	BA	935	A
34	BA	942	G
34	BA	960	U
34	BA	961	U
34	BA	964	A
34	BA	966	G

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Mol	Chain	Res	Type
34	BA	968	A
34	BA	969	A
34	BA	971	G
34	BA	972	C
34	BA	974	A
34	BA	975	A
34	BA	976	G
34	BA	977	A
34	BA	992	U
34	BA	993	G
34	BA	1003	G
34	BA	1004	A
34	BA	1005	A
34	BA	1009	G
34	BA	1011	G
34	BA	1016	A
34	BA	1019	C
34	BA	1021	G
34	BA	1022	G
34	BA	1023	G
34	BA	1025	U
34	BA	1026	G
34	BA	1028	C
34	BA	1029	C
34	BA	1030	C
34	BA	1030(A)	G
34	BA	1030(C)	G
34	BA	1031	G
34	BA	1045	C
34	BA	1053	G
34	BA	1054	C
34	BA	1065	U
34	BA	1066	C
34	BA	1068	G
34	BA	1075	C
34	BA	1076	C
34	BA	1081	G
34	BA	1094	G
34	BA	1095	U
34	BA	1101	A
34	BA	1118	C
34	BA	1123	A

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Mol	Chain	Res	Type
34	BA	1124	G
34	BA	1125	U
34	BA	1126	U
34	BA	1130	A
34	BA	1136	U
34	BA	1137	C
34	BA	1139	G
34	BA	1140	C
34	BA	1141	C
34	BA	1146	A
34	BA	1152	A
34	BA	1157	A
34	BA	1159	U
34	BA	1165	C
34	BA	1166	G
34	BA	1169	A
34	BA	1183	A
34	BA	1184	G
34	BA	1190	G
34	BA	1196	U
34	BA	1197	G
34	BA	1200	C
34	BA	1201	A
34	BA	1202	G
34	BA	1213	A
34	BA	1214	C
34	BA	1227	A
34	BA	1236	A
34	BA	1238	A
34	BA	1239	A
34	BA	1240	U
34	BA	1241	G
34	BA	1253	G
34	BA	1256	A
34	BA	1257	U
34	BA	1258	G
34	BA	1260	C
34	BA	1261	A
34	BA	1270	C
34	BA	1278	U
34	BA	1279	A
34	BA	1280	A

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Mol	Chain	Res	Type
34	BA	1286	A
34	BA	1287	A
34	BA	1299	A
34	BA	1300	G
34	BA	1305	G
34	BA	1317	C
34	BA	1322	C
34	BA	1338	G
34	BA	1340	A
34	BA	1344	C
34	BA	1346	A
34	BA	1347	G
34	BA	1353	G
34	BA	1360	A
34	BA	1363	C
34	BA	1370	G
34	BA	1397	C
34	BA	1400	C
34	BA	1402	C
34	BA	1403	C
34	BA	1419	G
34	BA	1442	G
34	BA	1442(A)	G
34	BA	1446	U
34	BA	1447	A
34	BA	1452	C
34	BA	1460	A
34	BA	1475	G
34	BA	1478	C
34	BA	1487	G
34	BA	1488	G
34	BA	1497	G
34	BA	1499	A
34	BA	1502	A
34	BA	1504	G
34	BA	1506	U
34	BA	1508	G
34	BA	1517	G
34	BA	1529	G
34	BA	1530	G
34	BA	1531	A
55	BV	13	A

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Mol	Chain	Res	Type
55	BV	14	A
55	BV	17	U
55	BV	18	G
55	BV	19	U
55	BV	23	A
55	BV	24	A
56	BX	6	G
56	BX	9	G
56	BX	13	C
56	BX	19	G
56	BX	20	U
56	BX	21	A
56	BX	25	C
56	BX	31	G
56	BX	34	C
56	BX	42	G
56	BX	47	U
56	BX	56	C
56	BX	58	A
56	BX	68	C
56	BX	76	A
1	CA	12	U
1	CA	13	A
1	CA	15	G
1	CA	34	C
1	CA	35	G
1	CA	36	G
1	CA	45	C
1	CA	71	A
1	CA	74	A
1	CA	75	G
1	CA	78	A
1	CA	84	A
1	CA	90	U
1	CA	100	G
1	CA	102	G
1	CA	107	C
1	CA	118	A
1	CA	119	A
1	CA	120	U
1	CA	131	G
1	CA	139(A)	G

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Mol	Chain	Res	Type
1	CA	141	A
1	CA	154(A)	C
1	CA	157	U
1	CA	181	A
1	CA	196	A
1	CA	199	A
1	CA	200	U
1	CA	205	G
1	CA	214	G
1	CA	215	G
1	CA	216	A
1	CA	221	A
1	CA	222	A
1	CA	228	A
1	CA	229	A
1	CA	231	C
1	CA	232	G
1	CA	233	A
1	CA	235	U
1	CA	237	C
1	CA	245	G
1	CA	248	G
1	CA	249	C
1	CA	250	G
1	CA	271(I)	G
1	CA	271(K)	U
1	CA	271(L)	U
1	CA	271(M)	G
1	CA	271(O)	C
1	CA	272	G
1	CA	272(A)	U
1	CA	272(B)	G
1	CA	272(J)	C
1	CA	277	C
1	CA	278	A
1	CA	286	C
1	CA	289	A
1	CA	294	A
1	CA	298	G
1	CA	299	A
1	CA	302	C
1	CA	308	G

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Mol	Chain	Res	Type
1	CA	310	A
1	CA	311	A
1	CA	317	G
1	CA	327	G
1	CA	329	G
1	CA	330	A
1	CA	331	A
1	CA	333	G
1	CA	338	G
1	CA	352	G
1	CA	362	U
1	CA	363	G
1	CA	363(B)	G
1	CA	363(C)	G
1	CA	386	G
1	CA	396	G
1	CA	405	U
1	CA	406	G
1	CA	407	G
1	CA	411	G
1	CA	412	A
1	CA	416	C
1	CA	419	C
1	CA	422	A
1	CA	428	A
1	CA	438	G
1	CA	443	A
1	CA	444	C
1	CA	449	A
1	CA	455	C
1	CA	456	C
1	CA	457	A
1	CA	467	G
1	CA	470	A
1	CA	479	A
1	CA	481	G
1	CA	504	U
1	CA	505	A
1	CA	509	C
1	CA	528	A
1	CA	529	A
1	CA	530	G

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Mol	Chain	Res	Type
1	CA	531	C
1	CA	532	A
1	CA	533	G
1	CA	545	G
1	CA	563	G
1	CA	573	G
1	CA	575	A
1	CA	586	A
1	CA	588	U
1	CA	603	A
1	CA	604	G
1	CA	605	C
1	CA	606	U
1	CA	607	U
1	CA	614(A)	U
1	CA	615	G
1	CA	616	G
1	CA	627	A
1	CA	631	A
1	CA	637	A
1	CA	641	C
1	CA	645	C
1	CA	646	A
1	CA	652(B)	A
1	CA	652(C)	G
1	CA	652(U)	G
1	CA	668	G
1	CA	669	G
1	CA	685	A
1	CA	686	G
1	CA	696	G
1	CA	730	C
1	CA	746	A
1	CA	747	U
1	CA	751	A
1	CA	755	C
1	CA	762	U
1	CA	764	A
1	CA	765	G
1	CA	774	A
1	CA	775	G
1	CA	776	G

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Mol	Chain	Res	Type
1	CA	777	A
1	CA	782	A
1	CA	784	A
1	CA	785	G
1	CA	790	C
1	CA	792	G
1	CA	794	G
1	CA	802	A
1	CA	805	G
1	CA	812	C
1	CA	819	A
1	CA	827	U
1	CA	828	U
1	CA	830	G
1	CA	847	U
1	CA	857	C
1	CA	859	G
1	CA	866	A
1	CA	867	C
1	CA	879	G
1	CA	880	G
1	CA	884	C
1	CA	886	C
1	CA	887	A
1	CA	888	C
1	CA	889	C
1	CA	890	A
1	CA	893	C
1	CA	896	A
1	CA	897	C
1	CA	898	C
1	CA	900	A
1	CA	901	A
1	CA	902	C
1	CA	907	U
1	CA	910	A
1	CA	915	C
1	CA	917	A
1	CA	932	G
1	CA	933	A
1	CA	938	G
1	CA	941	A

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Mol	Chain	Res	Type
1	CA	945	A
1	CA	946	G
1	CA	958	U
1	CA	959	A
1	CA	961	C
1	CA	971	C
1	CA	974	G
1	CA	975	C
1	CA	980	A
1	CA	983	A
1	CA	996	A
1	CA	1002	G
1	CA	1012	U
1	CA	1013	C
1	CA	1022	G
1	CA	1025	G
1	CA	1027	A
1	CA	1033	U
1	CA	1038	C
1	CA	1039	G
1	CA	1041	C
1	CA	1042	G
1	CA	1046	A
1	CA	1047	G
1	CA	1048	A
1	CA	1050	A
1	CA	1055	G
1	CA	1057	A
1	CA	1058	G
1	CA	1060	U
1	CA	1061	U
1	CA	1062	G
1	CA	1070	A
1	CA	1071	G
1	CA	1073	A
1	CA	1075	C
1	CA	1076	C
1	CA	1079	C
1	CA	1083	U
1	CA	1088	A
1	CA	1090	U
1	CA	1101	U

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Mol	Chain	Res	Type
1	CA	1103	A
1	CA	1106	G
1	CA	1109	C
1	CA	1110	G
1	CA	1111	A
1	CA	1112	G
1	CA	1113	U
1	CA	1142	U
1	CA	1164	G
1	CA	1171	G
1	CA	1191	G
1	CA	1205	U
1	CA	1211	U
1	CA	1220	A
1	CA	1230	C
1	CA	1236	G
1	CA	1244	G
1	CA	1246	A
1	CA	1248	G
1	CA	1250	G
1	CA	1253	A
1	CA	1256	G
1	CA	1271	G
1	CA	1272	A
1	CA	1273	U
1	CA	1283	G
1	CA	1300	U
1	CA	1301	A
1	CA	1314	C
1	CA	1319	G
1	CA	1321	A
1	CA	1335	U
1	CA	1338	G
1	CA	1345	C
1	CA	1349	A
1	CA	1359	A
1	CA	1360	A
1	CA	1365	A
1	CA	1368	G
1	CA	1370	C
1	CA	1380	G
1	CA	1384	A

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Mol	Chain	Res	Type
1	CA	1385	G
1	CA	1388	G
1	CA	1390	U
1	CA	1395	A
1	CA	1416	G
1	CA	1417	C
1	CA	1419	A
1	CA	1420	U
1	CA	1421	G
1	CA	1427	A
1	CA	1428	C
1	CA	1445	A
1	CA	1449	A
1	CA	1450	G
1	CA	1455	G
1	CA	1459	G
1	CA	1460	A
1	CA	1467	C
1	CA	1471	A
1	CA	1472	A
1	CA	1482	G
1	CA	1489	U
1	CA	1490	A
1	CA	1493	C
1	CA	1495	A
1	CA	1496	A
1	CA	1497	U
1	CA	1498	C
1	CA	1502	C
1	CA	1509	C
1	CA	1509(A)	A
1	CA	1529	G
1	CA	1533	G
1	CA	1543	C
1	CA	1547	C
1	CA	1558	A
1	CA	1559	G
1	CA	1560	G
1	CA	1569	A
1	CA	1575	C
1	CA	1578	U
1	CA	1580	A

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Mol	Chain	Res	Type
1	CA	1583	A
1	CA	1584	C
1	CA	1586	A
1	CA	1608	A
1	CA	1609	A
1	CA	1610	A
1	CA	1612	C
1	CA	1616	A
1	CA	1618	A
1	CA	1633	G
1	CA	1640	C
1	CA	1646	C
1	CA	1647	G
1	CA	1648	C
1	CA	1651	G
1	CA	1654	A
1	CA	1655	A
1	CA	1672	C
1	CA	1673	U
1	CA	1674	G
1	CA	1696	G
1	CA	1700	A
1	CA	1701	A
1	CA	1703	G
1	CA	1721	G
1	CA	1722	A
1	CA	1742	G
1	CA	1746	G
1	CA	1756	G
1	CA	1758	G
1	CA	1762	A
1	CA	1763	G
1	CA	1764	G
1	CA	1769	G
1	CA	1773	A
1	CA	1774	C
1	CA	1780	A
1	CA	1782	C
1	CA	1786	A
1	CA	1791	A
1	CA	1800	C
1	CA	1801	G

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Mol	Chain	Res	Type
1	CA	1808	U
1	CA	1811	G
1	CA	1812	A
1	CA	1816	G
1	CA	1823	G
1	CA	1829	A
1	CA	1835	G
1	CA	1839	G
1	CA	1847	A
1	CA	1848	A
1	CA	1877	A
1	CA	1878	G
1	CA	1884	A
1	CA	1889	A
1	CA	1896	G
1	CA	1900	A
1	CA	1906	G
1	CA	1913	A
1	CA	1914	C
1	CA	1926	U
1	CA	1929	G
1	CA	1930	G
1	CA	1937	A
1	CA	1938	A
1	CA	1952	A
1	CA	1955	U
1	CA	1959	G
1	CA	1960	A
1	CA	1962	C
1	CA	1963	U
1	CA	1964	G
1	CA	1966	A
1	CA	1967	C
1	CA	1970	A
1	CA	1971	A
1	CA	1972	A
1	CA	1983	C
1	CA	1992	G
1	CA	1993	U
1	CA	1996	C
1	CA	1997	G
1	CA	2005	A

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Mol	Chain	Res	Type
1	CA	2009	G
1	CA	2020	A
1	CA	2023	G
1	CA	2027	G
1	CA	2031	A
1	CA	2032	G
1	CA	2033	A
1	CA	2038	G
1	CA	2043	C
1	CA	2046	G
1	CA	2047	U
1	CA	2055	C
1	CA	2056	G
1	CA	2060	A
1	CA	2061	G
1	CA	2062	A
1	CA	2067	G
1	CA	2069	G
1	CA	2082	A
1	CA	2099	U
1	CA	2102	U
1	CA	2105	C
1	CA	2106	G
1	CA	2110	G
1	CA	2111	C
1	CA	2113	U
1	CA	2115	G
1	CA	2116	G
1	CA	2117	A
1	CA	2119	A
1	CA	2122	U
1	CA	2126	A
1	CA	2127	G
1	CA	2129	C
1	CA	2130	U
1	CA	2131	G
1	CA	2132	U
1	CA	2133	G
1	CA	2134	A
1	CA	2135	A
1	CA	2136	C
1	CA	2137	C

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Mol	Chain	Res	Type
1	CA	2141	G
1	CA	2142	C
1	CA	2144	U
1	CA	2146	C
1	CA	2150	U
1	CA	2153	G
1	CA	2154	G
1	CA	2157	G
1	CA	2162	G
1	CA	2164	C
1	CA	2165	G
1	CA	2167	U
1	CA	2168	G
1	CA	2169	A
1	CA	2172	U
1	CA	2178	C
1	CA	2181	G
1	CA	2186	G
1	CA	2188	C
1	CA	2189	U
1	CA	2190	G
1	CA	2192	G
1	CA	2198	A
1	CA	2206	G
1	CA	2207	G
1	CA	2208	A
1	CA	2225	A
1	CA	2238	G
1	CA	2258	C
1	CA	2259	G
1	CA	2268	A
1	CA	2275	C
1	CA	2283	C
1	CA	2287	A
1	CA	2288	A
1	CA	2305	A
1	CA	2308	G
1	CA	2311	A
1	CA	2312	U
1	CA	2318	G
1	CA	2319	G
1	CA	2320	A

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Mol	Chain	Res	Type
1	CA	2325	G
1	CA	2327	A
1	CA	2336	A
1	CA	2343	C
1	CA	2347	C
1	CA	2350	C
1	CA	2354	G
1	CA	2355	C
1	CA	2379	G
1	CA	2383	G
1	CA	2385	C
1	CA	2400	G
1	CA	2406	U
1	CA	2407	G
1	CA	2410	G
1	CA	2418	A
1	CA	2422	A
1	CA	2425	A
1	CA	2428	G
1	CA	2429	G
1	CA	2430	A
1	CA	2434	A
1	CA	2435	A
1	CA	2439	A
1	CA	2441	C
1	CA	2448	A
1	CA	2460	U
1	CA	2468	G
1	CA	2474	C
1	CA	2476	A
1	CA	2487	G
1	CA	2490	G
1	CA	2494	G
1	CA	2502	G
1	CA	2505	G
1	CA	2506	U
1	CA	2518	A
1	CA	2525	G
1	CA	2529	G
1	CA	2543	G
1	CA	2549	G
1	CA	2554	U

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Mol	Chain	Res	Type
1	CA	2555	U
1	CA	2566	A
1	CA	2567	G
1	CA	2573	C
1	CA	2574	G
1	CA	2602	A
1	CA	2608	G
1	CA	2609	U
1	CA	2611	U
1	CA	2612	C
1	CA	2630	G
1	CA	2632	A
1	CA	2654	A
1	CA	2660	A
1	CA	2663	G
1	CA	2681	C
1	CA	2683	C
1	CA	2684	U
1	CA	2689	U
1	CA	2690	C
1	CA	2691	C
1	CA	2702	U
1	CA	2703	C
1	CA	2712(A)	A
1	CA	2713	A
1	CA	2714	G
1	CA	2721	A
1	CA	2726	U
1	CA	2733	A
1	CA	2748	A
1	CA	2757	A
1	CA	2758	A
1	CA	2760	C
1	CA	2765	A
1	CA	2766	G
1	CA	2767	C
1	CA	2778	A
1	CA	2780	G
1	CA	2785	C
1	CA	2794	C
1	CA	2802	G
1	CA	2803	C

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Mol	Chain	Res	Type
1	CA	2818	G
1	CA	2820	A
1	CA	2821	A
1	CA	2833	G
1	CA	2835	A
1	CA	2836	U
1	CA	2839	G
1	CA	2872	G
1	CA	2874	C
1	CA	2875	C
1	CA	2877	G
1	CA	2879	C
1	CA	2892	A
1	CA	2893	G
1	CA	2894	G
1	CA	2896	C
1	CA	2897	U
2	CB	2	C
2	CB	7	G
2	CB	9	G
2	CB	13	A
2	CB	15	A
2	CB	20	C
2	CB	21	G
2	CB	24	G
2	CB	25	A
2	CB	32	C
2	CB	34	U
2	CB	42	C
2	CB	45	A
2	CB	52	A
2	CB	56	G
2	CB	58	A
2	CB	67	G
2	CB	73	A
2	CB	85	G
2	CB	106	G
2	CB	110	G
2	CB	116	G
2	CB	118	G
34	DA	5	U
34	DA	6	G

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Mol	Chain	Res	Type
34	DA	9	G
34	DA	29	G
34	DA	30	U
34	DA	32	A
34	DA	39	G
34	DA	47	C
34	DA	48	C
34	DA	51	A
34	DA	54	C
34	DA	69	G
34	DA	73	G
34	DA	80	G
34	DA	97	G
34	DA	101	A
34	DA	111	G
34	DA	115	G
34	DA	116	A
34	DA	121	C
34	DA	131	C
34	DA	143	A
34	DA	163	C
34	DA	174	C
34	DA	182	U
34	DA	189(E)	U
34	DA	189(G)	G
34	DA	189(H)	G
34	DA	189(K)	U
34	DA	195	A
34	DA	197	A
34	DA	201	C
34	DA	203	U
34	DA	204	U
34	DA	216	G
34	DA	220	G
34	DA	240	C
34	DA	243	A
34	DA	247	G
34	DA	251	G
34	DA	258	G
34	DA	261	U
34	DA	266	G
34	DA	267	C

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Mol	Chain	Res	Type
34	DA	269	C
34	DA	281	G
34	DA	289	G
34	DA	290	C
34	DA	298	A
34	DA	299	G
34	DA	301	G
34	DA	308	C
34	DA	309	G
34	DA	318	G
34	DA	321	A
34	DA	328	C
34	DA	332	G
34	DA	339	C
34	DA	342	C
34	DA	343	U
34	DA	344	A
34	DA	346	G
34	DA	347	G
34	DA	352	C
34	DA	353	A
34	DA	354	G
34	DA	367	U
34	DA	372	C
34	DA	373	A
34	DA	382	A
34	DA	384	G
34	DA	388	G
34	DA	398	C
34	DA	406	G
34	DA	412	A
34	DA	413	G
34	DA	424	G
34	DA	429	U
34	DA	430	A
34	DA	439	A
34	DA	442	C
34	DA	443	C
34	DA	452	A
34	DA	485	G
34	DA	496	A
34	DA	498	U

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Mol	Chain	Res	Type
34	DA	505	G
34	DA	509	A
34	DA	510	A
34	DA	511	C
34	DA	518	C
34	DA	521	G
34	DA	527	G
34	DA	531	U
34	DA	532	A
34	DA	533	A
34	DA	545	C
34	DA	547	A
34	DA	559	A
34	DA	560	U
34	DA	561	U
34	DA	562	C
34	DA	563	A
34	DA	564	C
34	DA	571	U
34	DA	572	A
34	DA	573	A
34	DA	576	G
34	DA	592	G
34	DA	596	C
34	DA	601	C
34	DA	610	G
34	DA	620	C
34	DA	628	G
34	DA	630	G
34	DA	632	A
34	DA	653	A
34	DA	665	A
34	DA	687	A
34	DA	688	G
34	DA	693	G
34	DA	695	A
34	DA	702	A
34	DA	717	C
34	DA	721	G
34	DA	723	U
34	DA	728	A
34	DA	731	G

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Mol	Chain	Res	Type
34	DA	734	G
34	DA	749	C
34	DA	753	A
34	DA	755	G
34	DA	756	C
34	DA	759	A
34	DA	774	G
34	DA	777	A
34	DA	788	U
34	DA	792	A
34	DA	793	U
34	DA	794	A
34	DA	817	C
34	DA	821	G
34	DA	825	G
34	DA	827	U
34	DA	828	A
34	DA	829	G
34	DA	840	C
34	DA	841	U
34	DA	848	C
34	DA	851	G
34	DA	859	A
34	DA	874	G
34	DA	880	C
34	DA	884	U
34	DA	902	G
34	DA	908	A
34	DA	914	A
34	DA	916	G
34	DA	922	G
34	DA	926	G
34	DA	927	G
34	DA	934	C
34	DA	936	C
34	DA	960	U
34	DA	961	U
34	DA	966	G
34	DA	968	A
34	DA	969	A
34	DA	971	G
34	DA	974	A

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Mol	Chain	Res	Type
34	DA	975	A
34	DA	976	G
34	DA	977	A
34	DA	978	A
34	DA	989	C
34	DA	992	U
34	DA	993	G
34	DA	1003	G
34	DA	1005	A
34	DA	1006	C
34	DA	1007	C
34	DA	1016	A
34	DA	1022	G
34	DA	1025	U
34	DA	1026	G
34	DA	1027	C
34	DA	1028	C
34	DA	1030	C
34	DA	1030(A)	G
34	DA	1030(B)	C
34	DA	1031	G
34	DA	1033	G
34	DA	1046	A
34	DA	1065	U
34	DA	1066	C
34	DA	1067	A
34	DA	1081	G
34	DA	1094	G
34	DA	1095	U
34	DA	1100	C
34	DA	1101	A
34	DA	1105	A
34	DA	1117	G
34	DA	1121	U
34	DA	1122	U
34	DA	1124	G
34	DA	1125	U
34	DA	1127	G
34	DA	1130	A
34	DA	1136	U
34	DA	1137	C
34	DA	1138	G

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Mol	Chain	Res	Type
34	DA	1139	G
34	DA	1146	A
34	DA	1152	A
34	DA	1154	G
34	DA	1159	U
34	DA	1161	C
34	DA	1164	G
34	DA	1166	G
34	DA	1170	A
34	DA	1181	G
34	DA	1183	A
34	DA	1184	G
34	DA	1190	G
34	DA	1196	U
34	DA	1197	G
34	DA	1202	G
34	DA	1211	U
34	DA	1212	U
34	DA	1220	G
34	DA	1225	A
34	DA	1227	A
34	DA	1228	C
34	DA	1236	A
34	DA	1238	A
34	DA	1240	U
34	DA	1241	G
34	DA	1249	C
34	DA	1253	G
34	DA	1254	C
34	DA	1256	A
34	DA	1257	U
34	DA	1258	G
34	DA	1260	C
34	DA	1261	A
34	DA	1279	A
34	DA	1280	A
34	DA	1281	U
34	DA	1282	C
34	DA	1285	A
34	DA	1286	A
34	DA	1287	A
34	DA	1301	U

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Mol	Chain	Res	Type
34	DA	1305	G
34	DA	1322	C
34	DA	1326	C
34	DA	1332	A
34	DA	1347	G
34	DA	1358	U
34	DA	1360	A
34	DA	1363	C
34	DA	1363(A)	A
34	DA	1364	U
34	DA	1368	G
34	DA	1397	C
34	DA	1398	A
34	DA	1401	G
34	DA	1419	G
34	DA	1437	C
34	DA	1442	G
34	DA	1442(A)	G
34	DA	1442(B)	A
34	DA	1445	C
34	DA	1446	U
34	DA	1447	A
34	DA	1452	C
34	DA	1456	G
34	DA	1467	G
34	DA	1469	G
34	DA	1473	A
34	DA	1487	G
34	DA	1495	U
34	DA	1496	C
34	DA	1497	G
34	DA	1502	A
34	DA	1503	A
34	DA	1504	G
34	DA	1506	U
34	DA	1507	A
34	DA	1517	G
34	DA	1519	A
34	DA	1520	G
34	DA	1529	G
34	DA	1530	G
34	DA	1531	A

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Mol	Chain	Res	Type
34	DA	1532	U
55	DV	14	A
56	DX	6	G
56	DX	13	C
56	DX	18	G
56	DX	19	G
56	DX	20	U
56	DX	21	A
56	DX	22	G
56	DX	47	U
56	DX	48	C
56	DX	68	C
56	DX	76	A

All (116) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	AA	184	A
1	AA	188	A
1	AA	271	U
1	AA	302	A
1	AA	334	A
1	AA	555	G
1	AA	572	A
1	AA	716	G
1	AA	793	A
1	AA	811	A
1	AA	821	A
1	AA	906	G
1	AA	1098	C
1	AA	1154	U
1	AA	1188	A
1	AA	1219	A
1	AA	1220	U
1	AA	1221	G
1	AA	1255	A
1	AA	1431	G
1	AA	1466	U
1	AA	1654	A
1	AA	1655	A
1	AA	1700	G
1	AA	1721	G

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Mol	Chain	Res	Type
1	AA	1793	A
1	AA	1859	G
1	AA	1935	A
1	AA	2014	G
1	AA	2019	G
1	AA	2084	A
1	AA	2203	G
1	AA	2209	G
1	AA	2287	C
1	AA	2403	G
1	AA	2418	U
1	AA	2434	A
1	AA	2442	A
1	AA	2451	A
1	AA	2623	U
1	AA	2701	U
1	AA	2769	U
1	AA	2902	G
2	AB	109	C
34	BA	115	G
34	BA	266	G
34	BA	347	G
34	BA	509	A
34	BA	532	A
34	BA	560	U
34	BA	687	A
34	BA	748	C
34	BA	793	U
34	BA	839	U
34	BA	913	A
34	BA	991	U
34	BA	1065	U
34	BA	1067	A
34	BA	1165	C
34	BA	1201	A
34	BA	1285	A
34	BA	1442	G
56	BX	19	G
1	CA	195	A
1	CA	199	A
1	CA	249	C
1	CA	277	C

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Mol	Chain	Res	Type
1	CA	310	A
1	CA	685	A
1	CA	746	A
1	CA	764	A
1	CA	774	A
1	CA	856	C
1	CA	900	A
1	CA	1026	U
1	CA	1057	A
1	CA	1300	U
1	CA	1379	A
1	CA	1420	U
1	CA	1427	A
1	CA	1497	U
1	CA	1608	A
1	CA	1653	G
1	CA	1913	A
1	CA	1939	U
1	CA	1992	G
1	CA	1996	C
1	CA	2081	C
1	CA	2110	G
1	CA	2250	G
1	CA	2318	G
1	CA	2406	U
1	CA	2439	A
1	CA	2689	U
1	CA	2726	U
1	CA	2756	U
34	DA	115	G
34	DA	173	U
34	DA	266	G
34	DA	428	G
34	DA	429	U
34	DA	509	A
34	DA	510	A
34	DA	560	U
34	DA	687	A
34	DA	748	C
34	DA	840	C
34	DA	913	A
34	DA	991	U

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Mol	Chain	Res	Type
34	DA	1064	G
34	DA	1065	U
34	DA	1183	A
34	DA	1201	A
34	DA	1279	A
34	DA	1442	G
34	DA	1530	G

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

8 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	$\#\|Z\| > 2$
56	PSU	DX	55	56	18,21,22	1.41	2 (11%)	21,30,33	1.93	4 (19%)
56	5MU	DX	54	56	19,22,23	1.38	5 (26%)	27,32,35	2.19	8 (29%)
56	PSU	BX	55	56	18,21,22	1.35	1 (5%)	21,30,33	2.22	4 (19%)
56	4SU	DX	8	56	18,21,22	1.72	4 (22%)	25,30,33	2.08	7 (28%)
56	5MC	DX	32	56	19,22,23	2.18	2 (10%)	26,32,35	1.27	4 (15%)
56	4SU	BX	8	56	18,21,22	1.82	5 (27%)	25,30,33	2.55	7 (28%)
56	5MC	BX	32	56	19,22,23	1.41	3 (15%)	26,32,35	1.13	2 (7%)
56	5MU	BX	54	58,56	19,22,23	1.59	6 (31%)	27,32,35	1.96	7 (25%)

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
56	PSU	DX	55	56	-	0/7/25/26	0/2/2/2
56	5MU	DX	54	56	-	0/7/25/26	0/2/2/2
56	PSU	BX	55	56	-	0/7/25/26	0/2/2/2
56	4SU	DX	8	56	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
56	5MC	DX	32	56	-	0/7/25/26	0/2/2/2
56	4SU	BX	8	56	-	0/7/25/26	0/2/2/2
56	5MC	BX	32	56	-	0/7/25/26	0/2/2/2
56	5MU	BX	54	58,56	-	0/7/25/26	0/2/2/2

All (28) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
56	DX	32	5MC	C5-C4	8.29	1.50	1.44
56	BX	8	4SU	C4-S4	-5.02	1.59	1.68
56	BX	55	PSU	C6-C5	4.52	1.40	1.35
56	DX	8	4SU	C4-S4	-4.50	1.60	1.68
56	BX	32	5MC	C5-C4	4.28	1.47	1.44
56	DX	55	PSU	C6-C5	3.97	1.39	1.35
56	DX	32	5MC	C6-C5	3.48	1.40	1.34
56	BX	54	5MU	C4-C5	3.48	1.50	1.44
56	DX	8	4SU	C2-N1	3.19	1.43	1.38
56	BX	32	5MC	C6-C5	3.18	1.39	1.34
56	BX	8	4SU	C2-N3	-3.01	1.32	1.38
56	BX	54	5MU	C6-C5	2.85	1.39	1.34
56	DX	54	5MU	C2-N1	2.77	1.42	1.38
56	DX	8	4SU	C4-N3	-2.76	1.34	1.37
56	BX	8	4SU	C4-N3	-2.75	1.34	1.37
56	BX	54	5MU	C2-N1	2.63	1.42	1.38
56	BX	54	5MU	C4-N3	-2.45	1.34	1.38
56	BX	32	5MC	C6-N1	-2.44	1.33	1.38
56	BX	8	4SU	C5-C4	-2.43	1.39	1.42
56	BX	8	4SU	C2-N1	2.39	1.42	1.38
56	DX	54	5MU	C4-N3	-2.35	1.34	1.38
56	DX	54	5MU	C6-C5	2.28	1.38	1.34
56	DX	8	4SU	C6-C5	2.23	1.40	1.35
56	DX	54	5MU	C4-C5	2.22	1.48	1.44
56	DX	54	5MU	C6-N1	-2.20	1.34	1.38
56	BX	54	5MU	C6-N1	-2.15	1.34	1.38
56	DX	55	PSU	C4-N3	-2.14	1.34	1.38
56	BX	54	5MU	C2-N3	-2.01	1.34	1.38

All (43) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
56	BX	8	4SU	C4-N3-C2	-7.02	120.58	127.31
56	BX	8	4SU	C5-C4-N3	6.72	121.00	114.75

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
56	BX	55	PSU	N1-C2-N3	6.20	121.71	115.17
56	DX	8	4SU	C4-N3-C2	-6.07	121.50	127.31
56	DX	55	PSU	N1-C2-N3	5.87	121.36	115.17
56	BX	55	PSU	O2-C2-N1	-5.03	117.60	122.79
56	DX	54	5MU	C4-N3-C2	-5.02	120.76	127.34
56	DX	8	4SU	N3-C2-N1	4.79	121.13	114.89
56	DX	54	5MU	O4-C4-C5	-4.73	119.50	124.92
56	BX	54	5MU	C4-N3-C2	-4.71	121.17	127.34
56	DX	54	5MU	C5-C4-N3	4.70	119.41	115.32
56	DX	8	4SU	C5-C4-N3	4.62	119.05	114.75
56	BX	54	5MU	N3-C2-N1	4.44	120.67	114.89
56	BX	54	5MU	C5-C4-N3	4.31	119.07	115.32
56	BX	55	PSU	C4-N3-C2	-4.19	120.61	126.37
56	BX	8	4SU	N3-C2-N1	4.17	120.32	114.89
56	BX	8	4SU	C5-C4-S4	-4.12	119.60	124.31
56	DX	54	5MU	N3-C2-N1	4.10	120.23	114.89
56	DX	54	5MU	C5-C6-N1	-3.77	119.22	123.31
56	DX	32	5MC	C5-C6-N1	-3.70	119.29	123.31
56	DX	55	PSU	C4-N3-C2	-3.69	121.29	126.37
56	BX	8	4SU	C1'-N1-C2	3.60	124.06	117.59
56	BX	54	5MU	C5-C6-N1	-3.49	119.52	123.31
56	BX	32	5MC	C5-C4-N3	-3.25	118.43	121.75
56	DX	32	5MC	C5-C4-N3	-3.18	118.49	121.75
56	BX	54	5MU	C5M-C5-C4	3.04	122.03	118.78
56	DX	55	PSU	O2-C2-N1	-3.01	119.68	122.79
56	DX	8	4SU	C6-N1-C2	-2.67	117.75	121.00
56	DX	54	5MU	C1'-N1-C6	-2.63	116.82	121.15
56	BX	8	4SU	O2-C2-N3	-2.55	116.78	121.49
56	BX	32	5MC	C5-C6-N1	-2.48	120.62	123.31
56	BX	54	5MU	O4-C4-C5	-2.43	122.13	124.92
56	DX	8	4SU	O2-C2-N3	-2.38	117.10	121.49
56	BX	55	PSU	O4-C4-C5	-2.37	118.11	124.01
56	DX	55	PSU	C5-C6-N1	-2.35	118.87	122.14
56	DX	32	5MC	O2-C2-N3	-2.25	118.78	122.33
56	DX	54	5MU	C1'-N1-C2	2.20	121.55	117.59
56	BX	54	5MU	C5M-C5-C6	-2.19	119.89	122.85
56	DX	54	5MU	C5M-C5-C4	2.14	121.07	118.78
56	DX	8	4SU	C1'-N1-C2	2.04	121.27	117.59
56	DX	32	5MC	CM5-C5-C6	-2.03	120.10	122.85
56	DX	8	4SU	C5-C4-S4	-2.02	122.00	124.31
56	BX	8	4SU	C1'-N1-C6	-2.02	116.47	120.78

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
56	DX	55	PSU	1	0
56	DX	8	4SU	1	0
56	BX	8	4SU	1	0
56	BX	32	5MC	3	0

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 2062 ligands modelled in this entry, 2058 are monoatomic - leaving 4 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	$\#\|Z\| > 2$
62	GDP	DZ	704	58	29,30,30	1.33	5 (17%)	45,47,47	1.78	9 (20%)
62	GDP	BZ	801	58	29,30,30	1.23	4 (13%)	45,47,47	1.78	6 (13%)
61	SF4	DD	501	37	0,12,12	-	-	-		
61	SF4	BD	501	37	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
61	SF4	BD	501	37	-	-	0/6/5/5
61	SF4	DD	501	37	-	-	0/6/5/5
62	GDP	BZ	801	58	-	5/16/32/32	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
62	GDP	DZ	704	58	-	4/16/32/32	0/3/3/3

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
62	DZ	704	GDP	C5-C4	2.96	1.46	1.38
62	DZ	704	GDP	PA-O3A	2.91	1.62	1.59
62	BZ	801	GDP	C5-C4	2.83	1.46	1.38
62	BZ	801	GDP	C5-N7	-2.62	1.33	1.39
62	DZ	704	GDP	C4-N9	-2.58	1.31	1.38
62	DZ	704	GDP	C6-N1	-2.49	1.34	1.38
62	BZ	801	GDP	C4-N9	-2.31	1.32	1.38
62	DZ	704	GDP	C5-N7	-2.21	1.34	1.39
62	BZ	801	GDP	C6-N1	-2.14	1.34	1.38

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
62	BZ	801	GDP	C5-C4-N3	-5.74	119.25	128.39
62	DZ	704	GDP	C5-C4-N3	-5.50	119.64	128.39
62	BZ	801	GDP	C2-N3-C4	4.97	120.86	112.30
62	DZ	704	GDP	C2-N3-C4	4.44	119.95	112.30
62	DZ	704	GDP	N9-C4-N3	3.98	133.90	125.95
62	BZ	801	GDP	N9-C4-N3	3.96	133.87	125.95
62	DZ	704	GDP	C2'-C1'-N9	-3.67	103.04	113.25
62	BZ	801	GDP	C6-C5-N7	3.59	136.83	130.29
62	DZ	704	GDP	C6-C5-N7	3.16	136.05	130.29
62	BZ	801	GDP	C4-C5-N7	-2.74	106.33	110.67
62	DZ	704	GDP	O2B-PB-O3A	2.48	112.94	104.64
62	BZ	801	GDP	O2B-PB-O3A	2.47	112.91	104.64
62	DZ	704	GDP	C4-C5-N7	-2.46	106.77	110.67
62	DZ	704	GDP	O6-C6-C5	-2.02	121.19	126.53
62	DZ	704	GDP	C3'-C2'-C1'	2.01	105.27	101.46

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
62	DZ	704	GDP	C5'-O5'-PA-O3A
62	DZ	704	GDP	C5'-O5'-PA-O2A
62	DZ	704	GDP	O4'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
62	DZ	704	GDP	C3'-C4'-C5'-O5'
62	BZ	801	GDP	O4'-C4'-C5'-O5'
62	BZ	801	GDP	C3'-C4'-C5'-O5'
62	BZ	801	GDP	C5'-O5'-PA-O3A
62	BZ	801	GDP	C5'-O5'-PA-O1A
62	BZ	801	GDP	C5'-O5'-PA-O2A

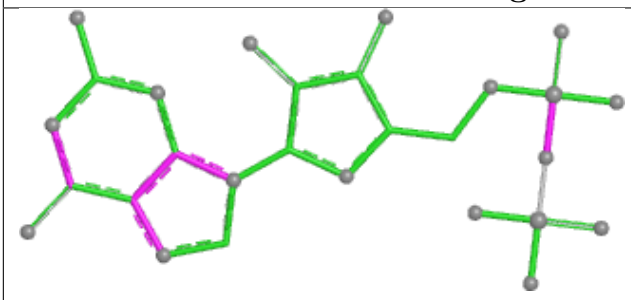
There are no ring outliers.

2 monomers are involved in 11 short contacts:

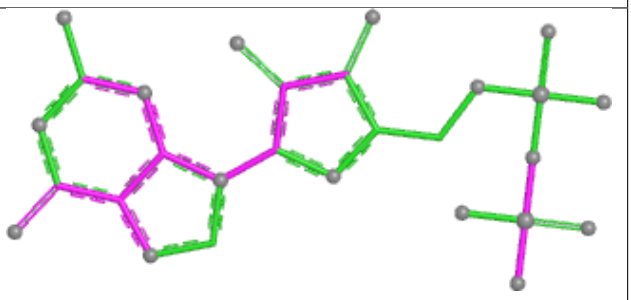
Mol	Chain	Res	Type	Clashes	Symm-Clashes
62	DZ	704	GDP	7	0
62	BZ	801	GDP	4	0

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

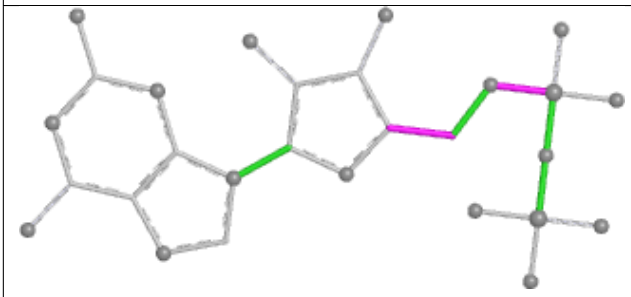
Ligand GDP DZ 704



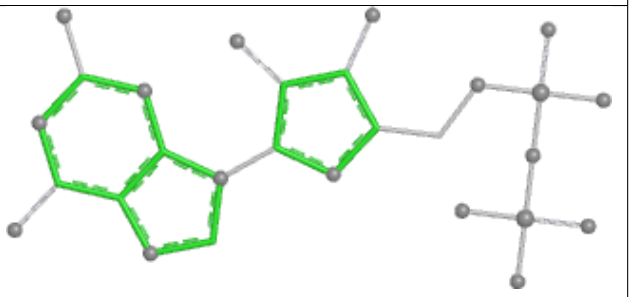
Bond lengths



Bond angles

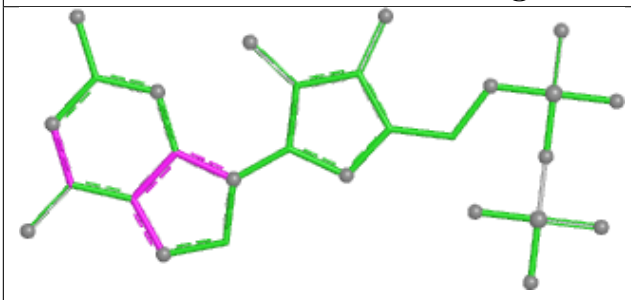


Torsions

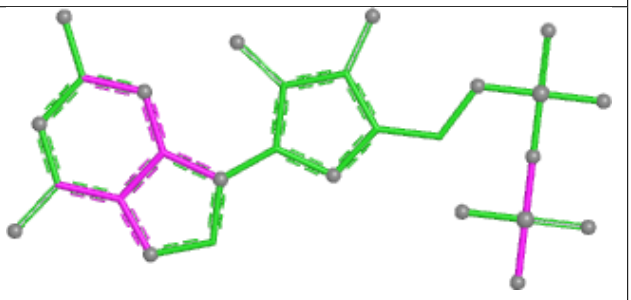


Rings

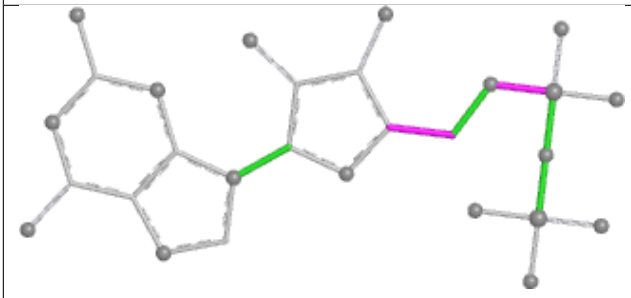
Ligand GDP BZ 801



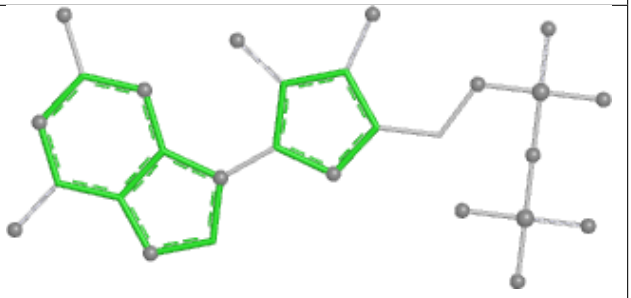
Bond lengths



Bond angles



Torsions



Rings

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

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	AA	2852/2915 (97%)	-0.45	117 (4%) 41 33	14, 34, 140, 350	0
1	CA	2848/2915 (97%)	0.16	197 (6%) 23 16	27, 57, 179, 341	0
2	AB	120/121 (99%)	-0.18	1 (0%) 82 75	23, 50, 72, 108	0
2	CB	120/121 (99%)	0.93	5 (4%) 40 32	64, 91, 118, 166	0
3	AC	137/228 (60%)	3.49	125 (91%) 0 0	132, 205, 251, 280	0
3	CC	137/228 (60%)	3.16	116 (84%) 0 0	144, 214, 251, 276	0
4	AD	275/276 (99%)	-0.35	3 (1%) 78 70	12, 34, 59, 136	0
4	CD	275/276 (99%)	-0.01	4 (1%) 72 63	23, 47, 73, 128	0
5	AE	204/206 (99%)	-0.42	1 (0%) 87 82	5, 33, 57, 80	0
5	CE	204/206 (99%)	0.43	11 (5%) 31 24	20, 62, 106, 135	0
6	AF	203/210 (96%)	-0.28	2 (0%) 79 72	11, 35, 77, 171	0
6	CF	203/210 (96%)	0.35	5 (2%) 58 48	21, 62, 105, 154	0
7	AG	181/182 (99%)	1.03	32 (17%) 4 3	36, 76, 134, 205	0
7	CG	181/182 (99%)	1.77	70 (38%) 1 0	72, 111, 173, 199	0
8	AH	174/180 (96%)	0.00	4 (2%) 61 51	25, 45, 68, 110	0
8	CH	174/180 (96%)	1.63	53 (30%) 1 1	63, 112, 161, 197	0
9	AK	130/173 (75%)	1.97	55 (42%) 0 0	46, 103, 172, 216	0
9	CK	130/173 (75%)	2.91	98 (75%) 0 0	74, 159, 199, 218	0
10	AL	139/147 (94%)	2.57	101 (72%) 0 0	96, 170, 224, 247	0
10	CL	139/147 (94%)	3.39	118 (84%) 0 0	126, 194, 241, 274	0
11	AN	140/140 (100%)	-0.40	0 100 100	14, 27, 59, 93	0
11	CN	140/140 (100%)	0.74	9 (6%) 25 18	32, 70, 108, 151	0
12	AO	122/122 (100%)	-0.39	0 100 100	18, 36, 61, 77	0
12	CO	122/122 (100%)	0.27	3 (2%) 58 48	36, 57, 84, 107	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
13	AP	149/150 (99%)	-0.01	3 (2%) 65 56	11, 42, 80, 108	0
13	CP	149/150 (99%)	0.61	7 (4%) 36 29	30, 67, 115, 135	0
14	AQ	141/141 (100%)	-0.29	2 (1%) 73 64	12, 33, 54, 82	0
14	CQ	141/141 (100%)	0.73	7 (4%) 34 26	37, 69, 99, 119	0
15	AR	118/118 (100%)	-0.51	0 100 100	16, 29, 45, 54	0
15	CR	118/118 (100%)	0.33	1 (0%) 82 75	33, 55, 89, 103	0
16	AS	110/112 (98%)	0.05	0 100 100	30, 50, 80, 92	0
16	CS	110/112 (98%)	1.21	15 (13%) 7 5	46, 85, 120, 150	0
17	AT	131/146 (89%)	-0.05	4 (3%) 51 41	23, 40, 90, 169	0
17	CT	131/146 (89%)	0.59	6 (4%) 37 29	42, 65, 106, 141	0
18	AU	116/118 (98%)	-0.58	0 100 100	9, 22, 39, 87	0
18	CU	116/118 (98%)	0.62	1 (0%) 81 74	27, 65, 92, 105	0
19	AV	101/101 (100%)	-0.68	0 100 100	9, 28, 49, 73	0
19	CV	101/101 (100%)	0.59	6 (5%) 28 21	35, 78, 111, 165	0
20	AW	112/113 (99%)	-0.49	0 100 100	13, 25, 43, 110	0
20	CW	112/113 (99%)	0.15	1 (0%) 81 74	28, 49, 80, 117	0
21	AX	95/96 (98%)	-0.21	2 (2%) 63 54	15, 34, 68, 98	0
21	CX	95/96 (98%)	0.44	3 (3%) 50 40	38, 60, 85, 105	0
22	AY	107/110 (97%)	0.06	2 (1%) 66 57	23, 44, 84, 162	0
22	CY	107/110 (97%)	0.93	11 (10%) 12 9	45, 74, 115, 169	0
23	AZ	185/206 (89%)	0.36	7 (3%) 44 35	28, 56, 91, 145	0
23	CZ	185/206 (89%)	1.59	54 (29%) 1 1	61, 104, 149, 210	0
24	A0	83/85 (97%)	0.12	7 (8%) 17 12	12, 35, 83, 218	0
24	C0	83/85 (97%)	1.11	15 (18%) 3 3	42, 66, 119, 223	0
25	A1	97/98 (98%)	0.00	2 (2%) 63 54	20, 43, 78, 101	0
25	C1	97/98 (98%)	0.26	4 (4%) 41 33	30, 51, 89, 127	0
26	A2	70/72 (97%)	-0.01	2 (2%) 53 43	24, 43, 70, 121	0
26	C2	70/72 (97%)	0.82	9 (12%) 7 6	47, 71, 100, 116	0
27	A3	59/60 (98%)	-0.39	0 100 100	15, 29, 54, 99	0
27	C3	59/60 (98%)	0.94	3 (5%) 33 25	45, 72, 111, 147	0
28	A4	69/71 (97%)	1.58	24 (34%) 1 0	60, 117, 203, 232	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
28	C4	69/71 (97%)	1.89	27 (39%) 1 0	80, 157, 202, 217	0
29	A5	59/60 (98%)	-0.63	0 100 100	9, 25, 40, 52	0
29	C5	59/60 (98%)	0.04	0 100 100	26, 51, 89, 104	0
30	A6	53/54 (98%)	-0.41	0 100 100	22, 40, 54, 74	0
30	C6	53/54 (98%)	0.31	0 100 100	40, 59, 79, 105	0
31	A7	48/49 (97%)	-0.26	2 (4%) 40 32	13, 24, 68, 133	0
31	C7	48/49 (97%)	-0.02	4 (8%) 17 12	26, 39, 95, 118	0
32	A8	64/65 (98%)	-0.40	0 100 100	15, 28, 45, 65	0
32	C8	64/65 (98%)	0.13	0 100 100	37, 51, 71, 85	0
33	A9	37/37 (100%)	-0.27	0 100 100	23, 35, 56, 66	0
33	C9	37/37 (100%)	1.15	8 (21%) 2 2	45, 77, 95, 127	0
34	BA	1495/1521 (98%)	0.81	159 (10%) 11 8	31, 83, 186, 328	0
34	DA	1501/1521 (98%)	0.85	184 (12%) 8 6	38, 89, 195, 331	0
35	BB	231/256 (90%)	1.43	53 (22%) 2 1	42, 104, 170, 215	0
35	DB	231/256 (90%)	1.68	70 (30%) 1 1	70, 123, 177, 208	0
36	BC	206/239 (86%)	1.65	59 (28%) 1 1	56, 117, 174, 195	0
36	DC	206/239 (86%)	1.86	83 (40%) 0 0	68, 136, 180, 209	0
37	BD	208/209 (99%)	1.28	41 (19%) 3 2	44, 86, 137, 185	0
37	DD	208/209 (99%)	1.16	34 (16%) 4 4	58, 85, 135, 197	0
38	BE	148/162 (91%)	0.62	7 (4%) 36 29	34, 72, 104, 126	0
38	DE	148/162 (91%)	0.88	10 (6%) 23 17	49, 79, 116, 178	0
39	BF	100/101 (99%)	0.89	4 (4%) 42 33	55, 85, 116, 135	0
39	DF	100/101 (99%)	0.76	1 (1%) 79 72	47, 86, 117, 133	0
40	BG	155/156 (99%)	1.55	44 (28%) 1 1	67, 112, 179, 223	0
40	DG	155/156 (99%)	1.76	61 (39%) 1 0	69, 131, 189, 215	0
41	BH	137/138 (99%)	0.60	2 (1%) 72 63	47, 72, 99, 118	0
41	DH	137/138 (99%)	0.92	13 (9%) 14 10	56, 80, 109, 141	0
42	BI	127/128 (99%)	2.29	70 (55%) 0 0	64, 124, 167, 195	0
42	DI	127/128 (99%)	2.58	79 (62%) 0 0	88, 143, 190, 213	0
43	BJ	97/105 (92%)	2.20	49 (50%) 0 0	80, 129, 183, 210	0
43	DJ	96/105 (91%)	2.44	58 (60%) 0 0	90, 150, 196, 218	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
44	BK	114/129 (88%)	0.83	14 (12%) 8 6	35, 78, 125, 148	0
44	DK	114/129 (88%)	0.93	13 (11%) 10 7	50, 89, 115, 170	0
45	BL	122/132 (92%)	0.36	4 (3%) 49 39	36, 58, 77, 111	0
45	DL	122/132 (92%)	0.74	10 (8%) 17 13	46, 70, 94, 115	0
46	BM	117/126 (92%)	2.32	57 (48%) 0 0	76, 135, 181, 201	0
46	DM	122/126 (96%)	2.47	64 (52%) 0 0	93, 150, 196, 255	0
47	BN	60/61 (98%)	2.30	34 (56%) 0 0	65, 111, 146, 169	0
47	DN	60/61 (98%)	2.94	48 (80%) 0 0	97, 138, 173, 193	0
48	BO	88/89 (98%)	0.74	4 (4%) 38 30	36, 70, 106, 119	0
48	DO	88/89 (98%)	0.79	9 (10%) 12 9	46, 70, 105, 153	0
49	BP	82/88 (93%)	1.38	12 (14%) 6 4	49, 79, 118, 168	0
49	DP	82/88 (93%)	1.12	9 (10%) 10 8	53, 77, 112, 154	0
50	BQ	99/105 (94%)	0.80	7 (7%) 22 16	44, 71, 98, 124	0
50	DQ	99/105 (94%)	0.98	13 (13%) 7 6	43, 77, 104, 115	0
51	BR	68/88 (77%)	0.84	5 (7%) 20 15	41, 79, 122, 133	0
51	DR	68/88 (77%)	0.75	4 (5%) 28 21	52, 82, 127, 143	0
52	BS	84/93 (90%)	2.56	51 (60%) 0 0	95, 144, 193, 207	0
52	DS	83/93 (89%)	2.87	60 (72%) 0 0	90, 164, 211, 224	0
53	BT	96/106 (90%)	1.50	28 (29%) 1 1	60, 83, 123, 164	0
53	DT	96/106 (90%)	1.27	23 (23%) 2 1	56, 85, 134, 156	0
54	BU	23/27 (85%)	2.90	20 (86%) 0 0	62, 116, 154, 180	0
54	DU	23/27 (85%)	2.75	14 (60%) 0 0	90, 134, 171, 184	0
55	BV	13/24 (54%)	2.63	10 (76%) 0 0	48, 85, 170, 176	0
55	DV	6/24 (25%)	2.72	3 (50%) 0 0	62, 78, 169, 197	0
56	BX	72/77 (93%)	0.62	3 (4%) 40 32	33, 76, 123, 186	0
56	DX	72/77 (93%)	0.81	7 (9%) 13 10	40, 99, 147, 161	0
57	BZ	730/758 (96%)	1.57	241 (33%) 1 1	34, 77, 135, 187	0
57	DZ	730/758 (96%)	2.01	336 (46%) 0 0	36, 100, 165, 220	0
All	All	22704/23760 (95%)	0.69	3553 (15%) 5 4	5, 70, 179, 350	0

All (3553) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
10	CL	127	ILE	12.3
46	DM	123	ALA	8.9
9	CK	57	THR	8.8
10	AL	10	LEU	8.6
57	BZ	572	TYR	8.6
10	CL	9	LYS	8.2
57	BZ	538	TYR	8.0
3	AC	30	VAL	7.9
3	AC	26	ALA	7.7
46	DM	98	VAL	7.7
57	DZ	576	ASP	7.7
42	DI	64	THR	7.5
52	BS	2	PRO	7.4
3	AC	210	LEU	7.3
10	CL	107	ILE	7.3
10	CL	12	LEU	7.2
3	CC	215	VAL	7.1
46	DM	124	PRO	7.1
57	DZ	501	THR	7.0
57	BZ	504	ARG	6.8
3	AC	190	ILE	6.8
9	CK	85	ASP	6.8
38	DE	22	GLY	6.8
57	BZ	434	GLU	6.7
57	DZ	507	TYR	6.7
52	DS	2	PRO	6.7
57	BZ	401	SER	6.6
3	CC	164	PHE	6.6
57	DZ	86	GLY	6.6
57	BZ	527	ASN	6.6
10	CL	10	LEU	6.6
8	AH	2	SER	6.6
10	CL	11	GLN	6.5
57	BZ	454	MET	6.4
42	DI	66	ARG	6.4
57	DZ	656	ALA	6.4
10	CL	130	SER	6.4
57	DZ	89	ASP	6.3
24	C0	2	ALA	6.3
10	CL	57	ILE	6.2
10	CL	78	ILE	6.2
53	BT	9	ASN	6.2
42	DI	106	ALA	6.2

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Mol	Chain	Res	Type	RSRZ
52	DS	4	SER	6.2
57	DZ	419	ALA	6.2
24	C0	3	HIS	6.1
57	BZ	91	THR	6.1
57	DZ	572	TYR	6.1
46	DM	122	LYS	6.1
3	CC	190	ILE	6.1
46	BM	100	GLY	6.1
52	BS	71	LEU	6.1
57	DZ	426	GLN	6.1
57	DZ	578	SER	6.1
24	C0	7	LEU	6.1
53	DT	9	ASN	6.0
3	CC	194	ILE	6.0
10	CL	113	PRO	6.0
3	AC	33	LEU	6.0
9	CK	58	LEU	6.0
57	DZ	502	GLY	6.0
46	BM	98	VAL	6.0
57	DZ	255	ILE	6.0
57	DZ	613	PRO	6.0
52	BS	68	GLY	6.0
3	CC	59	VAL	6.0
57	DZ	574	GLU	5.9
10	CL	19	PRO	5.9
3	CC	15	VAL	5.9
3	CC	210	LEU	5.9
46	BM	63	THR	5.9
10	CL	96	VAL	5.9
3	CC	221	PRO	5.9
52	DS	71	LEU	5.9
24	A0	7	LEU	5.8
34	DA	1202	G	5.8
42	DI	105	ASP	5.8
54	BU	18	TYR	5.8
10	CL	13	PRO	5.8
52	BS	11	VAL	5.8
57	DZ	411	VAL	5.8
57	BZ	420	ASP	5.8
10	CL	8	VAL	5.7
10	CL	136	VAL	5.7
46	DM	87	TYR	5.7

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Mol	Chain	Res	Type	RSRZ
8	CH	63	SER	5.7
24	A0	8	GLY	5.7
3	AC	215	VAL	5.7
10	CL	55	VAL	5.7
1	CA	652(B)	A	5.7
3	CC	223	VAL	5.7
57	BZ	530	VAL	5.7
10	CL	123	ALA	5.7
24	A0	3	HIS	5.6
57	DZ	570	GLY	5.6
1	CA	2124	G	5.6
34	BA	1447	A	5.6
3	CC	213	VAL	5.6
47	DN	2	ALA	5.6
43	DJ	59	SER	5.6
46	BM	23	TYR	5.6
3	AC	164	PHE	5.6
35	BB	136	VAL	5.6
9	CK	89	ALA	5.6
57	DZ	531	GLY	5.6
54	DU	4	GLY	5.5
7	CG	77	ILE	5.5
57	DZ	457	LEU	5.5
47	DN	7	ILE	5.5
57	DZ	504	ARG	5.5
36	BC	171	GLY	5.5
46	BM	24	GLY	5.5
3	AC	44	VAL	5.5
9	CK	53	VAL	5.4
42	BI	37	PHE	5.4
57	DZ	463	VAL	5.4
1	AA	2139	A	5.4
10	CL	74	ALA	5.4
10	CL	21	PRO	5.4
57	DZ	237	PRO	5.4
57	DZ	506	GLN	5.4
3	CC	222	SER	5.4
10	CL	114	ASP	5.4
37	DD	23	GLY	5.4
3	AC	12	LEU	5.4
3	AC	166	ASN	5.4
42	BI	106	ALA	5.4

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Mol	Chain	Res	Type	RSRZ
57	DZ	643	ILE	5.4
47	DN	22	THR	5.4
9	CK	39	ALA	5.4
57	DZ	461	ILE	5.4
40	BG	80	VAL	5.3
40	BG	34	GLY	5.3
3	AC	194	ILE	5.3
1	AA	2137	G	5.3
47	BN	20	ALA	5.3
52	DS	79	THR	5.3
24	A0	6	GLY	5.3
57	BZ	457	LEU	5.3
9	CK	83	TYR	5.3
10	AL	22	PRO	5.3
57	DZ	582	PHE	5.2
35	DB	222	ILE	5.2
43	DJ	6	ILE	5.2
3	CC	20	VAL	5.2
37	BD	3	ARG	5.2
10	CL	20	ALA	5.2
46	DM	78	ILE	5.2
57	DZ	429	ALA	5.2
57	DZ	473	ASP	5.2
47	DN	6	LEU	5.2
1	CA	2123	G	5.2
3	AC	61	GLY	5.2
57	DZ	532	GLY	5.2
3	AC	69	LEU	5.2
57	DZ	577	SER	5.2
57	DZ	432	ALA	5.1
3	AC	227	PRO	5.1
46	BM	94	ARG	5.1
3	AC	167	ASP	5.1
24	C0	8	GLY	5.1
57	DZ	462	ILE	5.1
1	CA	1533	G	5.1
57	DZ	454	MET	5.1
57	DZ	497	PHE	5.1
35	BB	12	GLU	5.1
40	DG	83	ALA	5.1
57	DZ	420	ASP	5.1
47	DN	39	LEU	5.1

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Mol	Chain	Res	Type	RSRZ
46	BM	6	GLY	5.1
55	BV	24	A	5.1
9	CK	49	ALA	5.1
22	AY	1	MET	5.1
43	DJ	47	PHE	5.0
10	CL	34	ILE	5.0
40	DG	37	ASN	5.0
3	CC	179	ALA	5.0
54	DU	14	TRP	5.0
1	CA	2117	A	5.0
3	AC	197	LEU	5.0
52	DS	31	ILE	5.0
3	AC	55	SER	5.0
57	BZ	411	VAL	5.0
3	AC	65	LEU	5.0
10	CL	115	LEU	5.0
3	AC	162	ILE	5.0
57	DZ	437	THR	5.0
22	CY	1	MET	5.0
3	AC	175	PRO	5.0
3	AC	37	LYS	5.0
52	DS	45	VAL	5.0
46	DM	118	ALA	5.0
13	CP	76	LYS	5.0
3	CC	8	TYR	5.0
3	AC	186	LEU	5.0
3	CC	44	VAL	5.0
10	AL	11	GLN	4.9
57	DZ	537	GLU	4.9
36	DC	168	ALA	4.9
52	DS	76	PRO	4.9
1	AA	2138	G	4.9
1	CA	1087	G	4.9
52	DS	9	VAL	4.9
52	BS	10	PHE	4.9
10	CL	23	VAL	4.9
57	BZ	529	ILE	4.9
57	BZ	570	GLY	4.9
47	DN	34	TYR	4.9
17	AT	131	ALA	4.8
25	C1	2	SER	4.8
36	DC	154	SER	4.8

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Mol	Chain	Res	Type	RSRZ
43	BJ	72	VAL	4.8
3	AC	54	ARG	4.8
36	DC	159	GLY	4.8
57	BZ	83	ASP	4.8
3	AC	208	THR	4.8
10	CL	126	MET	4.8
57	BZ	94	VAL	4.8
52	BS	78	ARG	4.8
1	CA	1536	C	4.8
36	DC	189	ALA	4.8
47	DN	38	GLY	4.8
43	BJ	77	PRO	4.8
52	BS	12	ASP	4.8
57	BZ	464	ASP	4.8
43	BJ	40	LEU	4.8
10	CL	68	VAL	4.8
57	DZ	401	SER	4.8
47	BN	12	ARG	4.8
36	BC	37	GLN	4.8
43	DJ	37	PRO	4.8
54	BU	17	THR	4.8
7	CG	75	LYS	4.8
3	AC	59	VAL	4.8
57	DZ	425	SER	4.8
3	AC	27	ALA	4.8
57	BZ	86	GLY	4.8
52	DS	80	TYR	4.8
52	BS	9	VAL	4.7
57	DZ	530	VAL	4.7
3	AC	57	GLN	4.7
57	BZ	515	GLU	4.7
42	DI	125	TYR	4.7
1	CA	2116	G	4.7
47	BN	3	ARG	4.7
54	DU	17	THR	4.7
52	BS	4	SER	4.7
47	BN	6	LEU	4.7
52	BS	5	LEU	4.7
52	DS	75	ALA	4.7
54	DU	18	TYR	4.7
57	BZ	39	ILE	4.7
46	DM	120	LYS	4.7

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Mol	Chain	Res	Type	RSRZ
47	BN	4	LYS	4.7
3	CC	10	ALA	4.7
43	DJ	40	LEU	4.7
3	AC	213	VAL	4.7
9	CK	63	LEU	4.7
57	DZ	216	LEU	4.7
9	CK	6	ASN	4.7
36	BC	2	GLY	4.7
3	CC	30	VAL	4.7
57	DZ	493	VAL	4.7
44	DK	75	TYR	4.6
57	BZ	576	ASP	4.6
57	DZ	102	ASP	4.6
10	CL	26	ALA	4.6
43	BJ	46	ARG	4.6
57	BZ	422	GLU	4.6
42	DI	14	VAL	4.6
42	DI	7	THR	4.6
57	DZ	614	GLU	4.6
9	CK	55	LYS	4.6
10	CL	69	THR	4.6
34	DA	1092	A	4.6
3	CC	4	HIS	4.6
24	A0	2	ALA	4.6
57	BZ	495	GLY	4.6
3	CC	12	LEU	4.6
9	CK	54	ALA	4.6
10	AL	124	ALA	4.6
46	DM	113	PRO	4.6
45	DL	18	VAL	4.6
57	DZ	476	VAL	4.6
42	BI	11	LYS	4.6
43	DJ	38	ILE	4.5
7	CG	65	GLY	4.5
43	DJ	39	PRO	4.5
57	DZ	85	PRO	4.5
57	DZ	422	GLU	4.5
3	CC	63	VAL	4.5
57	BZ	475	ASN	4.5
3	CC	48	LEU	4.5
3	CC	186	LEU	4.5
9	CK	38	HIS	4.5

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Mol	Chain	Res	Type	RSRZ
46	BM	95	GLY	4.5
57	BZ	562	ASP	4.5
57	DZ	88	VAL	4.5
1	CA	1048	A	4.5
55	DV	14	A	4.5
9	AK	6	ASN	4.5
43	BJ	47	PHE	4.5
10	CL	52	ILE	4.5
9	CK	62	ALA	4.5
46	DM	97	PRO	4.5
57	BZ	541	ALA	4.5
42	BI	6	GLY	4.5
9	CK	7	VAL	4.5
10	AL	136	VAL	4.5
42	DI	102	LEU	4.5
57	BZ	497	PHE	4.5
16	CS	61	ASN	4.5
1	CA	1072	C	4.5
57	BZ	268	GLY	4.5
57	BZ	533	VAL	4.5
26	A2	70	GLN	4.5
57	DZ	464	ASP	4.5
3	AC	11	LEU	4.5
4	CD	276	LYS	4.4
3	AC	171	ALA	4.4
10	CL	72	PRO	4.4
10	CL	73	PRO	4.4
46	BM	28	ALA	4.4
1	AA	2182	G	4.4
24	C0	4	LYS	4.4
1	CA	1067	A	4.4
34	DA	977	A	4.4
35	DB	111	ARG	4.4
42	DI	11	LYS	4.4
42	DI	113	LYS	4.4
1	CA	2148	G	4.4
52	DS	42	PRO	4.4
10	CL	7	VAL	4.4
10	CL	120	LEU	4.4
31	A7	47	ARG	4.4
4	AD	275	LYS	4.4
7	CG	76	SER	4.4

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Mol	Chain	Res	Type	RSRZ
37	DD	154	ASN	4.4
7	CG	127	GLY	4.4
9	AK	53	VAL	4.4
46	BM	87	TYR	4.4
57	DZ	538	TYR	4.4
57	DZ	448	GLN	4.4
3	CC	33	LEU	4.4
9	CK	51	LEU	4.4
42	BI	19	LEU	4.4
46	DM	102	ARG	4.4
54	BU	15	ARG	4.4
42	DI	18	PHE	4.4
57	DZ	573	HIS	4.4
57	DZ	427	ALA	4.3
47	DN	13	THR	4.3
57	BZ	575	VAL	4.3
10	AL	15	GLY	4.3
3	AC	214	TYR	4.3
37	BD	153	ARG	4.3
49	BP	82	GLN	4.3
57	DZ	500	GLN	4.3
1	CA	2160	G	4.3
28	C4	49	PHE	4.3
55	BV	23	A	4.3
57	BZ	458	HIS	4.3
3	AC	20	VAL	4.3
42	DI	65	VAL	4.3
34	BA	532	A	4.3
55	BV	14	A	4.3
55	DV	13	A	4.3
57	DZ	472	VAL	4.3
3	AC	204	GLY	4.3
7	AG	48	GLU	4.3
9	CK	40	LEU	4.3
36	DC	34	LEU	4.3
42	DI	27	THR	4.3
57	DZ	157	LEU	4.3
42	BI	126	SER	4.3
3	CC	162	ILE	4.3
43	DJ	74	ILE	4.3
52	DS	40	ILE	4.3
42	DI	117	HIS	4.3

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Mol	Chain	Res	Type	RSRZ
34	DA	1363(A)	A	4.3
57	BZ	419	ALA	4.3
57	DZ	491	VAL	4.3
57	DZ	575	VAL	4.3
1	CA	1058	G	4.3
47	DN	27	CYS	4.3
1	CA	1026	U	4.3
56	BX	47	U	4.3
3	AC	221	PRO	4.3
9	AK	49	ALA	4.3
42	BI	14	VAL	4.3
52	BS	13	ASP	4.3
9	AK	74	LEU	4.3
3	CC	41	THR	4.2
46	BM	103	THR	4.2
57	DZ	442	THR	4.2
33	C9	17	ILE	4.2
42	DI	62	TYR	4.2
52	BS	14	HIS	4.2
3	AC	182	PRO	4.2
9	CK	77	PRO	4.2
9	CK	86	PRO	4.2
35	BB	133	LYS	4.2
57	BZ	432	ALA	4.2
22	CY	107	ASP	4.2
57	BZ	473	ASP	4.2
54	BU	4	GLY	4.2
57	DZ	84	THR	4.2
43	BJ	54	PHE	4.2
52	DS	10	PHE	4.2
57	DZ	639	ASN	4.2
57	DZ	443	HIS	4.2
45	BL	89	ARG	4.2
37	BD	2	GLY	4.2
36	DC	162	GLN	4.2
4	AD	276	LYS	4.2
46	DM	99	ARG	4.2
57	BZ	160	ARG	4.2
43	DJ	49	VAL	4.2
9	CK	79	ALA	4.2
7	CG	42	GLY	4.2
1	CA	34	C	4.2

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Mol	Chain	Res	Type	RSRZ
1	CA	2147	G	4.2
3	AC	35	THR	4.2
10	CL	67	PHE	4.2
8	CH	175	LYS	4.2
9	AK	35	LYS	4.2
28	C4	63	TYR	4.2
10	AL	96	VAL	4.2
57	BZ	407	PRO	4.2
40	BG	83	ALA	4.2
49	BP	68	ASP	4.2
52	DS	77	THR	4.1
57	DZ	641	GLN	4.1
1	CA	1047	G	4.1
52	BS	37	ARG	4.1
57	DZ	455	GLY	4.1
57	DZ	503	GLY	4.1
4	CD	262	ARG	4.1
34	BA	1362	C	4.1
3	AC	29	LEU	4.1
43	DJ	65	LEU	4.1
52	BS	76	PRO	4.1
57	BZ	683	VAL	4.1
46	BM	33	ALA	4.1
52	BS	75	ALA	4.1
6	CF	207	GLY	4.1
3	AC	198	GLU	4.1
42	BI	2	GLU	4.1
57	DZ	660	ARG	4.1
3	AC	200	HIS	4.1
57	DZ	87	HIS	4.1
8	CH	43	VAL	4.1
3	CC	227	PRO	4.1
9	CK	67	GLY	4.1
47	DN	51	GLY	4.1
28	A4	62	ARG	4.1
3	AC	169	THR	4.1
34	BA	1286	A	4.1
57	BZ	417	THR	4.1
43	BJ	85	LEU	4.1
57	DZ	408	VAL	4.1
10	CL	22	PRO	4.1
42	DI	49	PRO	4.1

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Mol	Chain	Res	Type	RSRZ
35	BB	97	TRP	4.1
44	BK	89	ALA	4.1
47	DN	21	TYR	4.1
48	BO	89	GLY	4.1
52	DS	66	MET	4.1
43	BJ	35	SER	4.1
1	CA	2115	G	4.1
34	BA	630	G	4.1
36	BC	192	THR	4.0
39	BF	83	ASP	4.0
1	CA	2169	A	4.0
35	BB	7	VAL	4.0
9	CK	34	ALA	4.0
35	DB	48	MET	4.0
40	BG	156	TRP	4.0
42	BI	78	LYS	4.0
10	AL	60	TYR	4.0
10	AL	78	ILE	4.0
10	AL	132	ARG	4.0
42	DI	10	ARG	4.0
57	BZ	468	ARG	4.0
57	BZ	421	GLN	4.0
9	AK	51	LEU	4.0
3	CC	208	THR	4.0
52	DS	33	THR	4.0
46	BM	7	VAL	4.0
57	DZ	562	ASP	4.0
1	CA	1057	A	4.0
57	DZ	498	ILE	4.0
8	CH	174	GLY	4.0
40	BG	4	ARG	4.0
57	BZ	90	PHE	4.0
3	CC	11	LEU	4.0
36	BC	207	VAL	4.0
43	DJ	72	VAL	4.0
3	CC	17	PRO	4.0
43	DJ	41	PRO	4.0
57	BZ	89	ASP	4.0
17	CT	130	ALA	4.0
42	DI	45	ALA	4.0
3	CC	70	GLY	4.0
35	DB	99	GLY	4.0

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Mol	Chain	Res	Type	RSRZ
42	BI	72	GLY	4.0
1	CA	1847	A	4.0
34	DA	1183	A	4.0
57	DZ	403	GLU	4.0
42	DI	33	PHE	4.0
5	CE	195	LEU	4.0
42	BI	102	LEU	4.0
57	DZ	440	VAL	4.0
1	CA	1060	U	4.0
3	AC	62	THR	4.0
42	BI	64	THR	4.0
57	DZ	566	THR	4.0
38	BE	85	GLY	4.0
47	DN	31	ARG	4.0
52	DS	82	GLY	4.0
10	AL	12	LEU	4.0
46	BM	96	LEU	4.0
1	AA	2163	G	4.0
1	AA	2188	G	4.0
1	CA	2120	G	4.0
1	CA	2133	G	4.0
10	AL	55	VAL	4.0
47	DN	25	VAL	4.0
42	BI	117	HIS	4.0
53	BT	73	HIS	4.0
57	DZ	634	MET	4.0
10	CL	124	ALA	3.9
10	CL	128	ALA	3.9
46	DM	107	ALA	3.9
42	DI	9	ARG	3.9
57	BZ	597	GLY	3.9
57	BZ	537	GLU	3.9
3	CC	197	LEU	3.9
42	BI	41	VAL	3.9
10	AL	13	PRO	3.9
3	CC	26	ALA	3.9
36	BC	14	ILE	3.9
46	BM	4	ILE	3.9
1	CA	1171	G	3.9
37	DD	2	GLY	3.9
42	BI	30	GLY	3.9
57	DZ	623	ASP	3.9

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Mol	Chain	Res	Type	RSRZ
3	CC	209	PHE	3.9
23	CZ	162	GLU	3.9
36	BC	206	GLU	3.9
22	CY	55	TYR	3.9
42	BI	5	TYR	3.9
46	BM	21	TYR	3.9
57	BZ	507	TYR	3.9
42	DI	73	GLN	3.9
42	DI	108	VAL	3.9
3	AC	52	PRO	3.9
9	CK	78	SER	3.9
57	BZ	636	PRO	3.9
3	AC	23	ILE	3.9
57	DZ	39	ILE	3.9
10	CL	71	THR	3.9
10	CL	108	ALA	3.9
43	DJ	43	ARG	3.9
40	DG	82	GLY	3.9
9	CK	56	ASN	3.9
43	BJ	69	ASN	3.9
1	AA	2197	C	3.9
3	AC	66	PRO	3.9
42	BI	98	PRO	3.9
3	AC	179	ALA	3.9
47	DN	19	ARG	3.9
10	CL	27	LEU	3.9
36	BC	94	LEU	3.9
36	DC	87	LEU	3.9
37	BD	24	GLU	3.9
43	BJ	65	LEU	3.9
57	DZ	434	GLU	3.9
42	DI	5	TYR	3.9
46	DM	60	VAL	3.9
1	CA	2833	G	3.9
34	DA	1002	G	3.9
46	DM	92	HIS	3.9
46	DM	88	ARG	3.9
57	BZ	436	PRO	3.9
57	DZ	246	ILE	3.9
1	AA	2196	C	3.9
3	CC	35	THR	3.9
36	DC	192	THR	3.9

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Mol	Chain	Res	Type	RSRZ
57	BZ	452	SER	3.9
57	DZ	238	THR	3.9
10	AL	16	LYS	3.8
46	DM	119	GLY	3.8
40	BG	90	GLU	3.8
57	DZ	492	ASP	3.8
43	BJ	34	VAL	3.8
3	CC	225	ILE	3.8
3	AC	199	ALA	3.8
9	AK	88	ALA	3.8
46	DM	28	ALA	3.8
1	AA	2143	G	3.8
1	CA	1093	G	3.8
34	DA	1032	G	3.8
47	BN	15	LYS	3.8
57	BZ	449	THR	3.8
9	CK	125	LEU	3.8
10	AL	92	GLY	3.8
50	BQ	98	LEU	3.8
1	CA	2174	C	3.8
3	CC	203	GLU	3.8
34	BA	1363	C	3.8
57	BZ	574	GLU	3.8
57	DZ	438	PHE	3.8
57	DZ	435	ASP	3.8
1	CA	1103	A	3.8
36	BC	162	GLN	3.8
57	DZ	664	GLN	3.8
36	DC	3	ASN	3.8
46	DM	106	ASN	3.8
3	AC	205	ALA	3.8
9	CK	43	ALA	3.8
3	AC	41	THR	3.8
42	DI	30	GLY	3.8
46	DM	6	GLY	3.8
57	BZ	501	THR	3.8
1	AA	2200	C	3.8
34	BA	723	U	3.8
46	BM	97	PRO	3.8
3	AC	8	TYR	3.8
9	CK	97	ALA	3.8
10	CL	37	PHE	3.8

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Mol	Chain	Res	Type	RSRZ
57	DZ	441	SER	3.8
57	DZ	94	VAL	3.8
52	DS	49	ILE	3.8
1	CA	2162	G	3.8
34	DA	1365	G	3.8
52	DS	56	GLN	3.8
3	AC	4	HIS	3.8
46	DM	5	ALA	3.8
7	CG	135	LEU	3.8
3	AC	70	GLY	3.8
36	DC	155	GLY	3.8
36	DC	158	GLY	3.8
36	DC	191	THR	3.8
3	AC	25	GLU	3.7
41	DH	99	GLU	3.7
42	BI	12	GLU	3.7
28	C4	66	SER	3.7
57	DZ	661	SER	3.7
3	CC	42	VAL	3.7
8	CH	97	ARG	3.7
36	DC	207	VAL	3.7
42	DI	109	VAL	3.7
43	BJ	24	VAL	3.7
47	BN	19	ARG	3.7
23	CZ	68	PRO	3.7
57	BZ	535	PRO	3.7
57	DZ	405	PRO	3.7
57	DZ	543	GLN	3.7
17	AT	130	ALA	3.7
23	CZ	21	ALA	3.7
1	CA	2150	U	3.7
34	BA	1320	C	3.7
34	DA	1363	C	3.7
37	BD	154	ASN	3.7
37	BD	159	ARG	3.7
45	BL	18	VAL	3.7
3	AC	17	PRO	3.7
9	CK	105	PRO	3.7
23	CZ	95	PRO	3.7
54	DU	23	PRO	3.7
57	DZ	179	ASP	3.7
40	DG	38	LEU	3.7

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Mol	Chain	Res	Type	RSRZ
46	BM	90	LEU	3.7
57	DZ	626	ALA	3.7
28	C4	67	TYR	3.7
1	AA	2201	C	3.7
43	DJ	54	PHE	3.7
40	DG	4	ARG	3.7
46	DM	104	ARG	3.7
57	BZ	442	THR	3.7
1	CA	2110	G	3.7
34	DA	1224	G	3.7
57	BZ	82	ILE	3.7
57	DZ	533	VAL	3.7
3	CC	182	PRO	3.7
35	BB	131	PRO	3.7
48	BO	2	PRO	3.7
3	CC	65	LEU	3.7
3	AC	181	PHE	3.7
57	DZ	90	PHE	3.7
57	DZ	665	GLY	3.7
57	BZ	524	GLU	3.7
3	AC	71	LYS	3.7
9	CK	98	LYS	3.7
57	DZ	496	LYS	3.7
7	CG	39	ILE	3.7
9	CK	104	ILE	3.7
10	AL	7	VAL	3.7
10	CL	104	VAL	3.7
1	CA	1059	G	3.7
8	CH	2	SER	3.7
57	DZ	648	PRO	3.7
3	AC	67	HIS	3.7
57	BZ	588	MET	3.7
57	DZ	650	ALA	3.7
57	DZ	619	ASP	3.7
57	DZ	674	ASP	3.7
3	CC	214	TYR	3.7
10	CL	76	TYR	3.7
43	DJ	46	ARG	3.7
37	BD	179	GLU	3.7
57	BZ	579	GLU	3.7
3	CC	50	ILE	3.7
8	CH	4	ILE	3.7

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Mol	Chain	Res	Type	RSRZ
1	CA	2111	C	3.6
1	CA	2146	C	3.6
1	CA	2161	C	3.6
35	DB	232	PRO	3.6
57	BZ	540	PRO	3.6
5	CE	78	LEU	3.6
7	CG	152	LEU	3.6
9	CK	44	LEU	3.6
10	CL	105	LEU	3.6
35	DB	140	HIS	3.6
52	DS	20	LEU	3.6
40	BG	77	SER	3.6
46	BM	30	ALA	3.6
47	BN	2	ALA	3.6
3	AC	193	PHE	3.6
40	DG	115	ARG	3.6
46	BM	13	LYS	3.6
47	DN	15	LYS	3.6
49	BP	81	ARG	3.6
57	DZ	470	PHE	3.6
3	CC	166	ASN	3.6
35	DB	165	VAL	3.6
10	AL	66	THR	3.6
43	BJ	71	LEU	3.6
52	BS	22	LEU	3.6
57	DZ	407	PRO	3.6
7	AG	76	SER	3.6
33	C9	6	SER	3.6
42	BI	15	ALA	3.6
1	CA	1118	C	3.6
1	CA	1069	A	3.6
3	AC	224	ARG	3.6
23	CZ	156	LYS	3.6
42	BI	20	ARG	3.6
47	BN	17	LYS	3.6
7	CG	80	PHE	3.6
10	CL	15	GLY	3.6
35	DB	163	PHE	3.6
3	AC	225	ILE	3.6
57	BZ	433	GLU	3.6
57	DZ	227	ILE	3.6
1	CA	2112	G	3.6

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Mol	Chain	Res	Type	RSRZ
34	BA	1331	G	3.6
40	DG	80	VAL	3.6
3	AC	216	THR	3.6
3	CC	66	PRO	3.6
3	CC	69	LEU	3.6
10	CL	25	PRO	3.6
34	BA	202	U	3.6
55	BV	22	U	3.6
57	DZ	659	LEU	3.6
52	DS	69	HIS	3.6
9	CK	30	GLN	3.6
10	CL	111	LYS	3.6
42	DI	118	LYS	3.6
13	CP	15	ARG	3.6
28	A4	54	GLY	3.6
36	BC	158	GLY	3.6
46	DM	112	GLY	3.6
9	CK	121	ASP	3.6
42	DI	75	ASP	3.6
3	AC	42	VAL	3.6
8	CH	37	VAL	3.6
10	CL	134	MET	3.6
42	BI	79	LEU	3.6
1	AA	2123	G	3.6
1	AA	2181	G	3.6
1	CA	2121	G	3.6
3	CC	37	LYS	3.6
28	A4	60	GLN	3.6
47	DN	20	ALA	3.6
52	BS	56	GLN	3.6
52	DS	78	ARG	3.6
57	DZ	99	ARG	3.6
3	AC	209	PHE	3.6
3	CC	5	GLY	3.6
10	AL	107	ILE	3.6
10	AL	68	VAL	3.6
35	DB	136	VAL	3.6
42	BI	53	VAL	3.6
57	DZ	460	GLU	3.6
1	AA	2183	C	3.6
1	CA	1104	C	3.6
9	CK	37	THR	3.6

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Mol	Chain	Res	Type	RSRZ
42	DI	103	THR	3.6
9	CK	129	PRO	3.6
42	DI	123	PRO	3.6
47	BN	14	PRO	3.6
40	DG	117	ALA	3.5
42	BI	82	ALA	3.5
52	DS	37	ARG	3.5
3	CC	193	PHE	3.5
34	DA	1190	G	3.5
3	AC	50	ILE	3.5
42	DI	86	VAL	3.5
57	BZ	561	VAL	3.5
57	BZ	609	GLU	3.5
57	DZ	217	VAL	3.5
57	DZ	433	GLU	3.5
10	CL	112	MET	3.5
28	A4	43	TYR	3.5
57	DZ	417	THR	3.5
1	CA	1049	C	3.5
34	DA	1447	A	3.5
3	AC	159	ALA	3.5
40	DG	32	ARG	3.5
43	DJ	18	ALA	3.5
53	DT	25	ARG	3.5
9	CK	106	GLN	3.5
57	BZ	412	ALA	3.5
57	DZ	275	ALA	3.5
1	AA	271	U	3.5
57	BZ	438	PHE	3.5
3	AC	172	ILE	3.5
46	DM	4	ILE	3.5
35	DB	7	VAL	3.5
57	BZ	408	VAL	3.5
57	DZ	635	GLU	3.5
34	BA	1190	G	3.5
57	DZ	580	MET	3.5
57	DZ	423	LYS	3.5
42	BI	114	TYR	3.5
10	CL	116	ASN	3.5
28	A4	52	THR	3.5
57	DZ	527	ASN	3.5
42	BI	66	ARG	3.5

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Mol	Chain	Res	Type	RSRZ
57	DZ	458	HIS	3.5
36	DC	129	ALA	3.5
1	CA	2175	C	3.5
34	BA	342	C	3.5
55	BV	21	C	3.5
10	AL	52	ILE	3.5
43	BJ	36	GLY	3.5
9	AK	7	VAL	3.5
46	DM	117	VAL	3.5
52	DS	51	VAL	3.5
57	BZ	472	VAL	3.5
7	AG	35	GLU	3.5
9	CK	109	SER	3.5
57	BZ	571	SER	3.5
47	DN	4	LYS	3.5
9	AK	86	PRO	3.5
17	AT	107	ASP	3.5
57	DZ	202	PRO	3.5
43	BJ	5	ARG	3.5
43	DJ	42	THR	3.5
46	DM	62	ASN	3.5
57	BZ	639	ASN	3.5
8	CH	96	ALA	3.5
57	DZ	640	ALA	3.5
10	AL	37	PHE	3.5
40	BG	26	PHE	3.5
46	BM	25	ILE	3.5
57	BZ	462	ILE	3.5
1	CA	2179	C	3.5
10	CL	87	GLY	3.5
34	DA	975	A	3.5
34	DA	980	C	3.5
34	DA	1320	C	3.5
57	DZ	379	GLY	3.5
49	BP	62	VAL	3.5
57	BZ	536	LYS	3.5
3	CC	212	SER	3.5
54	BU	14	TRP	3.5
57	DZ	444	PRO	3.5
43	DJ	87	THR	3.5
40	BG	37	ASN	3.5
47	DN	10	ALA	3.5

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Mol	Chain	Res	Type	RSRZ
9	CK	25	PHE	3.4
52	BS	74	PHE	3.4
1	AA	2173	G	3.4
10	CL	135	GLY	3.4
31	A7	48	LYS	3.4
40	DG	22	LEU	3.4
40	DG	101	LEU	3.4
45	DL	47	LYS	3.4
57	DZ	243	VAL	3.4
23	CZ	169	GLU	3.4
34	DA	994	A	3.4
1	AA	2151	C	3.4
1	CA	271(K)	U	3.4
35	DB	144	ARG	3.4
52	DS	3	ARG	3.4
57	BZ	499	ARG	3.4
10	AL	64	SER	3.4
10	CL	75	SER	3.4
40	DG	112	PRO	3.4
57	BZ	577	SER	3.4
57	DZ	257	PRO	3.4
3	AC	196	ALA	3.4
3	AC	217	THR	3.4
28	A4	63	TYR	3.4
36	BC	193	TYR	3.4
36	DC	149	ALA	3.4
37	DD	20	TYR	3.4
52	DS	63	THR	3.4
43	BJ	76	ASN	3.4
43	DJ	50	ILE	3.4
4	CD	275	LYS	3.4
16	CS	60	GLY	3.4
9	CK	17	LEU	3.4
9	CK	74	LEU	3.4
24	C0	84	LEU	3.4
28	C4	56	VAL	3.4
23	AZ	168	GLU	3.4
57	BZ	494	GLU	3.4
26	C2	7	ARG	3.4
42	DI	42	ARG	3.4
43	DJ	70	ARG	3.4
1	CA	2118	U	3.4

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Mol	Chain	Res	Type	RSRZ
1	AA	2136	A	3.4
10	AL	25	PRO	3.4
57	BZ	648	PRO	3.4
34	BA	979	C	3.4
37	BD	113	SER	3.4
47	DN	59	ALA	3.4
57	DZ	541	ALA	3.4
3	AC	51	ASP	3.4
36	BC	184	TYR	3.4
43	BJ	81	THR	3.4
52	DS	13	ASP	3.4
57	DZ	83	ASP	3.4
36	DC	182	ILE	3.4
43	BJ	74	ILE	3.4
10	AL	70	LYS	3.4
52	DS	44	MET	3.4
7	CG	62	LEU	3.4
37	BD	124	GLY	3.4
42	DI	17	VAL	3.4
52	DS	5	LEU	3.4
57	BZ	386	GLY	3.4
35	DB	134	GLU	3.4
57	DZ	406	GLU	3.4
9	CK	50	ARG	3.4
47	DN	41	ARG	3.4
57	DZ	430	ARG	3.4
9	AK	105	PRO	3.4
1	AA	2135	U	3.4
1	CA	2113	U	3.4
1	AA	2145	G	3.4
1	CA	1044	G	3.4
1	CA	1170	G	3.4
57	DZ	509	HIS	3.4
1	CA	2128	C	3.4
3	CC	39	ASP	3.4
3	CC	167	ASP	3.4
7	AG	146	TYR	3.4
33	C9	12	ASP	3.4
43	DJ	73	ASP	3.4
48	DO	3	ILE	3.4
49	DP	19	ILE	3.4
46	DM	121	LYS	3.4

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Mol	Chain	Res	Type	RSRZ
47	BN	16	PHE	3.4
7	CG	44	GLY	3.4
10	AL	8	VAL	3.4
57	BZ	466	LEU	3.4
46	DM	100	GLY	3.4
23	CZ	97	GLU	3.4
54	BU	23	PRO	3.4
35	BB	140	HIS	3.4
34	DA	1364	U	3.4
40	DG	36	LYS	3.4
52	DS	35	SER	3.4
10	CL	101	TRP	3.4
43	DJ	100	THR	3.4
10	CL	62	ASP	3.4
46	BM	16	ASP	3.4
47	DN	36	PHE	3.4
34	DA	1531	A	3.4
40	DG	16	LEU	3.3
1	CA	2100	G	3.3
1	CA	2182	G	3.3
3	AC	176	VAL	3.3
46	BM	45	VAL	3.3
34	DA	1234	C	3.3
37	BD	23	GLY	3.3
28	A4	55	ARG	3.3
53	BT	23	ARG	3.3
3	CC	175	PRO	3.3
46	BM	10	PRO	3.3
9	CK	102	LYS	3.3
10	AL	9	LYS	3.3
24	A0	5	LYS	3.3
36	DC	163	ALA	3.3
42	BI	97	LYS	3.3
57	DZ	136	ALA	3.3
38	DE	10	MET	3.3
1	CA	1090	U	3.3
3	AC	180	SER	3.3
28	C4	44	THR	3.3
35	DB	11	LEU	3.3
40	BG	12	LEU	3.3
10	AL	114	ASP	3.3
36	DC	55	VAL	3.3

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Mol	Chain	Res	Type	RSRZ
57	BZ	88	VAL	3.3
57	DZ	569	ASP	3.3
54	DU	11	GLY	3.3
57	BZ	532	GLY	3.3
1	AA	1219	A	3.3
13	AP	98	GLU	3.3
1	CA	2183	C	3.3
1	CA	2127	G	3.3
1	CA	2166	G	3.3
34	BA	976	G	3.3
34	DA	1001(A)	G	3.3
10	AL	112	MET	3.3
47	DN	5	ALA	3.3
57	DZ	593	ALA	3.3
35	DB	196	LEU	3.3
46	DM	19	LEU	3.3
49	DP	82	GLN	3.3
57	DZ	624	LEU	3.3
5	CE	58	ARG	3.3
9	AK	50	ARG	3.3
37	DD	118	ARG	3.3
3	AC	58	ASN	3.3
10	AL	116	ASN	3.3
43	DJ	69	ASN	3.3
52	BS	53	ASN	3.3
23	CZ	11	GLU	3.3
42	DI	110	GLU	3.3
57	BZ	469	GLU	3.3
57	DZ	615	GLU	3.3
1	AA	2141	A	3.3
1	CA	1913	A	3.3
27	C3	2	PRO	3.3
34	DA	1110	A	3.3
55	BV	13	A	3.3
1	CA	2105	C	3.3
1	CA	2129	C	3.3
34	BA	1368	G	3.3
35	BB	61	LEU	3.3
40	DG	99	LEU	3.3
42	DI	96	LEU	3.3
8	CH	3	ARG	3.3
10	CL	58	THR	3.3

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Mol	Chain	Res	Type	RSRZ
10	CL	118	THR	3.3
28	A4	61	ARG	3.3
37	BD	100	ARG	3.3
42	BI	120	ARG	3.3
42	DI	120	ARG	3.3
46	BM	102	ARG	3.3
52	DS	41	VAL	3.3
57	DZ	180	VAL	3.3
3	AC	222	SER	3.3
8	AH	174	GLY	3.3
10	CL	92	GLY	3.3
36	BC	41	GLY	3.3
37	DD	152	SER	3.3
42	DI	67	GLY	3.3
53	BT	11	SER	3.3
9	CK	28	ASN	3.3
57	DZ	226	ASN	3.3
9	CK	35	LYS	3.3
35	DB	133	LYS	3.3
7	CG	2	PRO	3.3
9	AK	104	ILE	3.3
55	DV	15	A	3.3
9	CK	11	ALA	3.3
10	CL	44	ALA	3.3
10	CL	81	ALA	3.3
1	AA	2130	C	3.3
57	BZ	684	GLN	3.3
8	CH	66	GLY	3.3
10	AL	87	GLY	3.3
23	AZ	114	GLY	3.3
34	BA	1323	G	3.3
35	DB	97	TRP	3.3
35	DB	227	GLY	3.3
52	DS	34	TRP	3.3
9	AK	99	SER	3.3
3	CC	56	ASP	3.2
34	BA	1364	U	3.2
39	BF	54	LYS	3.2
50	DQ	100	LYS	3.2
3	CC	226	ASN	3.2
53	BT	75	ASN	3.2
10	AL	73	PRO	3.2

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Mol	Chain	Res	Type	RSRZ
42	DI	82	ALA	3.2
57	BZ	429	ALA	3.2
57	BZ	589	ALA	3.2
46	DM	66	LEU	3.2
57	DZ	459	LEU	3.2
8	CH	95	ARG	3.2
9	CK	24	PHE	3.2
34	DA	532	A	3.2
35	DB	70	PHE	3.2
47	BN	29	ARG	3.2
57	DZ	514	VAL	3.2
1	AA	2199	C	3.2
52	BS	8	GLY	3.2
52	BS	33	THR	3.2
52	DS	68	GLY	3.2
9	AK	109	SER	3.2
9	AK	123	GLU	3.2
57	DZ	186	TYR	3.2
3	AC	226	ASN	3.2
43	BJ	98	ILE	3.2
40	DG	2	ALA	3.2
53	BT	95	ALA	3.2
57	BZ	585	ALA	3.2
28	A4	58	ARG	3.2
46	DM	80	ARG	3.2
54	DU	15	ARG	3.2
57	DZ	439	ARG	3.2
31	C7	46	VAL	3.2
57	BZ	463	VAL	3.2
57	DZ	404	VAL	3.2
1	CA	2173	A	3.2
9	AK	102	LYS	3.2
10	CL	18	THR	3.2
37	DD	6	GLY	3.2
9	CK	65	GLU	3.2
47	DN	46	GLU	3.2
1	CA	2108	C	3.2
34	DA	1116	C	3.2
34	DA	1270	C	3.2
49	BP	38	TYR	3.2
3	CC	172	ILE	3.2
36	DC	152	ILE	3.2

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Mol	Chain	Res	Type	RSRZ
54	DU	5	ASP	3.2
1	CA	1066	U	3.2
35	DB	21	ARG	3.2
36	BC	129	ALA	3.2
47	DN	29	ARG	3.2
1	AA	2203	G	3.2
1	CA	2106	G	3.2
1	CA	2318	G	3.2
3	AC	15	VAL	3.2
9	AK	87	VAL	3.2
10	CL	5	VAL	3.2
40	DG	17	VAL	3.2
47	BN	18	VAL	3.2
57	DZ	679	VAL	3.2
43	DJ	55	LYS	3.2
36	DC	148	GLY	3.2
57	DZ	633	GLY	3.2
46	DM	63	THR	3.2
34	BA	977	A	3.2
10	CL	54	PRO	3.2
46	DM	86	CYS	3.2
9	AK	83	TYR	3.2
23	CZ	99	TYR	3.2
36	BC	201	TYR	3.2
3	CC	9	ARG	3.2
14	CQ	60	ARG	3.2
34	BA	1352	C	3.2
36	DC	47	LEU	3.2
52	BS	69	HIS	3.2
52	DS	14	HIS	3.2
55	BV	20	U	3.2
46	BM	117	VAL	3.2
1	AA	2190	G	3.2
1	CA	2149	G	3.2
34	DA	1185	G	3.2
35	DB	228	GLY	3.2
42	BI	67	GLY	3.2
57	BZ	502	GLY	3.2
57	DZ	453	GLY	3.2
9	AK	92	THR	3.2
9	CK	12	THR	3.2
57	DZ	612	THR	3.2

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Mol	Chain	Res	Type	RSRZ
5	CE	73	GLU	3.2
9	CK	84	GLU	3.2
23	CZ	60	GLU	3.2
3	AC	202	PRO	3.2
10	CL	99	ILE	3.2
57	BZ	92	ILE	3.2
57	BZ	546	ILE	3.2
57	BZ	590	ILE	3.2
57	DZ	82	ILE	3.2
34	BA	1360	A	3.1
14	CQ	10	ARG	3.1
42	DI	104	ARG	3.1
57	BZ	666	ARG	3.1
10	AL	61	ALA	3.1
40	DG	84	ASN	3.1
35	DB	132	LYS	3.1
1	AA	1122	C	3.1
1	CA	2122	U	3.1
10	AL	23	VAL	3.1
34	BA	1049	U	3.1
36	DC	130	VAL	3.1
47	BN	33	VAL	3.1
57	BZ	514	VAL	3.1
3	CC	204	GLY	3.1
40	BG	82	GLY	3.1
23	CZ	2	GLU	3.1
42	DI	12	GLU	3.1
57	DZ	456	GLU	3.1
57	DZ	494	GLU	3.1
57	DZ	199	ILE	3.1
3	CC	29	LEU	3.1
10	AL	79	ARG	3.1
34	DA	963	G	3.1
34	DA	1371	G	3.1
35	BB	144	ARG	3.1
36	DC	172	ARG	3.1
47	DN	57	ARG	3.1
54	BU	10	ARG	3.1
54	DU	6	ARG	3.1
47	BN	21	TYR	3.1
35	DB	225	ALA	3.1
1	AA	218	A	3.1

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Mol	Chain	Res	Type	RSRZ
1	CA	1050	A	3.1
3	AC	56	ASP	3.1
3	AC	188	ASP	3.1
55	BV	12	A	3.1
57	BZ	573	HIS	3.1
3	AC	38	PHE	3.1
3	CC	176	VAL	3.1
1	AA	2152	U	3.1
1	CA	1081	U	3.1
1	AA	2129	C	3.1
1	CA	2137	C	3.1
3	CC	220	GLY	3.1
9	CK	76	GLY	3.1
34	BA	163	C	3.1
34	DA	1038	C	3.1
42	DI	115	GLY	3.1
10	AL	56	GLU	3.1
10	AL	69	THR	3.1
42	DI	2	GLU	3.1
10	CL	91	PRO	3.1
57	DZ	516	PRO	3.1
10	AL	93	ARG	3.1
43	DJ	45	ARG	3.1
57	DZ	229	LEU	3.1
7	CG	146	TYR	3.1
37	BD	149	ALA	3.1
57	DZ	245	ALA	3.1
10	AL	30	HIS	3.1
10	AL	67	PHE	3.1
1	AA	2187	G	3.1
1	CA	1062	G	3.1
9	CK	27	VAL	3.1
10	AL	138	VAL	3.1
10	CL	119	ASP	3.1
10	CL	138	VAL	3.1
35	DB	152	PHE	3.1
34	BA	1001(A)	G	3.1
52	BS	60	VAL	3.1
52	BS	65	ASN	3.1
57	BZ	569	ASP	3.1
1	AA	572	A	3.1
1	CA	1085	A	3.1

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Mol	Chain	Res	Type	RSRZ
1	CA	1095	A	3.1
1	CA	2135	A	3.1
40	BG	89	MET	3.1
1	CA	1083	U	3.1
3	CC	49	GLY	3.1
10	AL	57	ILE	3.1
43	BJ	83	GLU	3.1
53	BT	100	ILE	3.1
57	BZ	547	GLU	3.1
57	BZ	592	GLU	3.1
1	CA	2164	C	3.1
1	CA	2188	C	3.1
9	CK	33	PRO	3.1
34	DA	1029	C	3.1
36	DC	165	THR	3.1
43	DJ	71	LEU	3.1
46	BM	34	LEU	3.1
52	BS	48	THR	3.1
57	BZ	465	ARG	3.1
10	CL	70	LYS	3.1
3	CC	159	ALA	3.1
7	CG	159	VAL	3.1
42	BI	86	VAL	3.1
10	AL	62	ASP	3.1
22	CY	57	GLN	3.1
42	DI	68	GLY	3.1
52	BS	84	GLY	3.1
57	DZ	234	GLY	3.1
34	BA	160	A	3.1
10	AL	34	ILE	3.1
10	AL	127	ILE	3.1
43	DJ	96	ILE	3.1
3	AC	203	GLU	3.1
9	CK	41	ARG	3.1
37	BD	118	ARG	3.1
37	DD	3	ARG	3.1
53	BT	8	ARG	3.1
54	BU	9	ARG	3.1
3	AC	201	LYS	3.1
8	CH	21	PRO	3.1
9	CK	32	LEU	3.1
10	AL	120	LEU	3.1

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Mol	Chain	Res	Type	RSRZ
46	BM	113	PRO	3.1
57	BZ	405	PRO	3.1
3	AC	218	THR	3.1
1	CA	1080	C	3.1
10	CL	17	ALA	3.0
10	CL	40	ALA	3.0
10	CL	122	ALA	3.0
34	BA	1328	C	3.1
34	DA	1149	C	3.1
36	DC	160	ALA	3.0
42	BI	61	ALA	3.0
11	CN	140	VAL	3.0
28	A4	59	PHE	3.0
57	BZ	217	VAL	3.0
37	BD	77	ASN	3.0
44	BK	16	SER	3.0
42	BI	87	GLN	3.0
43	DJ	10	GLY	3.0
35	DB	36	ARG	3.0
36	BC	79	ARG	3.0
40	DG	5	ARG	3.0
42	BI	42	ARG	3.0
57	BZ	170	ARG	3.0
7	CG	81	LYS	3.0
23	AZ	135	GLU	3.0
43	BJ	99	LYS	3.0
35	DB	234	PRO	3.0
46	BM	32	GLU	3.0
57	BZ	202	PRO	3.0
57	DZ	445	GLU	3.0
57	DZ	579	GLU	3.0
1	AA	1123	A	3.0
36	BC	191	THR	3.0
1	AA	2171	G	3.0
1	CA	652(C)	G	3.0
1	CA	2101	G	3.0
34	DA	1182	G	3.0
10	AL	26	ALA	3.0
22	CY	105	ALA	3.0
3	CC	200	HIS	3.0
8	CH	52	VAL	3.0
28	C4	10	VAL	3.0

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Mol	Chain	Res	Type	RSRZ
46	DM	64	TRP	3.0
57	BZ	617	MET	3.0
1	CA	2136	C	3.0
1	CA	2138	C	3.0
3	AC	21	TYR	3.0
16	CS	36	TYR	3.0
9	CK	100	ASN	3.0
40	DG	109	ASN	3.0
54	BU	5	ASP	3.0
57	BZ	619	ASP	3.0
23	CZ	114	GLY	3.0
9	CK	14	LYS	3.0
36	DC	8	ILE	3.0
47	DN	11	LYS	3.0
53	BT	55	ILE	3.0
54	BU	6	ARG	3.0
57	BZ	450	ILE	3.0
10	CL	77	LEU	3.0
42	DI	50	LEU	3.0
43	DJ	8	LEU	3.0
53	BT	62	LEU	3.0
10	AL	21	PRO	3.0
37	BD	163	GLU	3.0
57	BZ	456	GLU	3.0
1	CA	1061	U	3.0
54	DU	8	THR	3.0
1	CA	2310	A	3.0
27	C3	51	ALA	3.0
34	BA	1183	A	3.0
36	DC	24	ALA	3.0
57	DZ	220	ALA	3.0
3	AC	223	VAL	3.0
7	CG	160	VAL	3.0
34	BA	1002	G	3.0
34	BA	1276	G	3.0
34	BA	1312	G	3.0
34	BA	1353	G	3.0
34	DA	1347	G	3.0
47	DN	61	TRP	3.0
1	CA	1043	C	3.0
1	CA	1076	C	3.0
3	AC	14	LYS	3.0

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Mol	Chain	Res	Type	RSRZ
3	AC	168	LYS	3.0
3	CC	57	GLN	3.0
13	CP	109	GLY	3.0
53	BT	58	LYS	3.0
57	BZ	416	LYS	3.0
36	BC	181	ASN	3.0
45	DL	116	SER	3.0
52	DS	65	ASN	3.0
57	BZ	557	GLY	3.0
57	DZ	551	GLN	3.0
52	BS	15	LEU	3.0
57	DZ	424	LEU	3.0
23	CZ	159	PRO	3.0
57	BZ	566	THR	3.0
3	AC	174	ALA	3.0
40	BG	2	ALA	3.0
57	DZ	528	ALA	3.0
10	CL	4	VAL	3.0
42	BI	108	VAL	3.0
47	DN	18	VAL	3.0
1	CA	6	A	3.0
1	CA	2134	A	3.0
42	DI	112	LYS	3.0
47	DN	17	LYS	3.0
50	BQ	87	LYS	3.0
9	CK	117	LEU	3.0
35	BB	154	LEU	3.0
42	BI	3	GLN	3.0
47	BN	55	GLY	3.0
53	DT	99	LEU	3.0
57	BZ	229	LEU	3.0
1	AA	2134	G	3.0
1	CA	2159	G	3.0
1	CA	2319	G	3.0
34	DA	1368	G	3.0
3	AC	64	SER	3.0
3	CC	55	SER	3.0
1	CA	1109	C	3.0
1	CA	2145	C	3.0
8	CH	36	PRO	3.0
57	DZ	636	PRO	3.0
10	CL	117	THR	3.0

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Mol	Chain	Res	Type	RSRZ
36	DC	60	ALA	3.0
43	BJ	42	THR	3.0
52	BS	41	VAL	3.0
1	AA	2172	U	3.0
34	DA	1236	A	2.9
40	BG	85	TYR	2.9
43	DJ	88	LEU	2.9
9	AK	106	GLN	2.9
57	DZ	630	GLN	2.9
11	CN	68	GLU	2.9
17	AT	38	ASN	2.9
23	CZ	30	ASN	2.9
37	BD	150	GLU	2.9
52	BS	59	PRO	2.9
57	BZ	435	ASP	2.9
57	DZ	469	GLU	2.9
1	CA	2104	G	2.9
1	CA	2190	G	2.9
34	DA	1033	G	2.9
43	DJ	86	MET	2.9
1	CA	2178	C	2.9
3	AC	10	ALA	2.9
7	CG	6	ALA	2.9
35	BB	34	ALA	2.9
35	DB	177	ALA	2.9
40	DG	25	ALA	2.9
36	BC	138	VAL	2.9
37	DD	148	VAL	2.9
40	DG	62	PHE	2.9
40	DG	91	VAL	2.9
43	DJ	63	PHE	2.9
57	BZ	84	THR	2.9
57	DZ	610	VAL	2.9
57	DZ	675	HIS	2.9
57	BZ	467	LYS	2.9
16	CS	3	ARG	2.9
43	BJ	50	ILE	2.9
57	BZ	409	ILE	2.9
9	AK	40	LEU	2.9
35	DB	61	LEU	2.9
57	BZ	216	LEU	2.9
57	BZ	424	LEU	2.9

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Mol	Chain	Res	Type	RSRZ
38	DE	20	GLN	2.9
52	BS	80	TYR	2.9
52	DS	52	TYR	2.9
57	BZ	641	GLN	2.9
1	AA	2198	A	2.9
37	DD	37	PRO	2.9
3	CC	43	GLU	2.9
9	CK	15	GLU	2.9
26	C2	12	GLU	2.9
50	BQ	96	GLU	2.9
57	BZ	460	GLU	2.9
57	BZ	678	GLU	2.9
3	CC	16	ASP	2.9
7	AG	49	ASP	2.9
10	CL	50	ASP	2.9
26	C2	52	ASP	2.9
52	DS	53	ASN	2.9
37	BD	208	SER	2.9
57	DZ	588	MET	2.9
8	CH	113	VAL	2.9
9	CK	94	VAL	2.9
10	AL	4	VAL	2.9
44	BK	65	ALA	2.9
57	BZ	474	ALA	2.9
57	BZ	626	ALA	2.9
10	AL	71	THR	2.9
57	BZ	223	PHE	2.9
57	BZ	486	THR	2.9
57	DZ	184	LYS	2.9
10	CL	30	HIS	2.9
57	DZ	611	THR	2.9
1	AA	2167	C	2.9
3	AC	165	ARG	2.9
34	BA	1045	C	2.9
46	BM	91	ARG	2.9
1	CA	1117	G	2.9
1	CA	2125	G	2.9
1	CA	2152	G	2.9
34	BA	1224	G	2.9
34	DA	1036	G	2.9
34	DA	1316	G	2.9
7	CG	144	ILE	2.9

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Mol	Chain	Res	Type	RSRZ
36	DC	77	ILE	2.9
57	BZ	227	ILE	2.9
57	DZ	601	ILE	2.9
7	CG	133	LEU	2.9
10	AL	115	LEU	2.9
35	DB	155	LEU	2.9
43	BJ	8	LEU	2.9
53	BT	20	LEU	2.9
28	C4	45	GLY	2.9
9	AK	113	GLN	2.9
52	BS	42	PRO	2.9
57	BZ	490	PRO	2.9
57	DZ	415	PRO	2.9
3	CC	219	MET	2.9
35	DB	231	GLU	2.9
44	BK	92	GLU	2.9
1	CA	2309	A	2.9
28	A4	51	ASP	2.9
28	C4	65	ASP	2.9
43	BJ	73	ASP	2.9
9	CK	99	SER	2.9
8	CH	141	VAL	2.9
10	CL	86	LYS	2.9
35	BB	93	VAL	2.9
53	BT	97	ALA	2.9
57	DZ	564	LYS	2.9
9	AK	118	THR	2.9
37	DD	132	ARG	2.9
57	DZ	446	THR	2.9
57	BZ	-29	LEU	2.9
1	AA	1555	C	2.9
1	CA	277	C	2.9
34	DA	1314	C	2.9
2	CB	1	U	2.9
34	DA	1351	U	2.9
36	DC	41	GLY	2.9
57	DZ	505	GLY	2.9
57	DZ	508	GLY	2.9
1	AA	1221	G	2.9
1	CA	1071	G	2.9
34	DA	971	G	2.9
35	BB	95	GLN	2.9

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Mol	Chain	Res	Type	RSRZ
43	BJ	33	GLN	2.9
35	BB	31	TYR	2.9
35	BB	125	PRO	2.9
25	C1	75	GLU	2.9
36	BC	166	GLU	2.9
57	BZ	382	GLU	2.9
3	CC	14	LYS	2.9
9	CK	64	LYS	2.9
36	BC	26	LYS	2.9
43	DJ	99	LYS	2.9
3	AC	34	ALA	2.9
17	CT	131	ALA	2.9
35	BB	229	VAL	2.9
35	DB	197	VAL	2.9
40	BG	43	PHE	2.9
46	DM	91	ARG	2.9
47	BN	32	SER	2.9
49	DP	9	PHE	2.9
47	BN	35	ARG	2.9
53	BT	22	ARG	2.9
57	BZ	578	SER	2.9
1	CA	1073	A	2.9
34	DA	974	A	2.9
8	CH	129	THR	2.9
57	BZ	437	THR	2.9
3	CC	23	ILE	2.9
7	AG	53	LEU	2.9
7	CG	157	ILE	2.9
36	DC	124	ILE	2.9
42	BI	81	ILE	2.9
49	BP	60	LEU	2.9
52	DS	30	LEU	2.9
57	DZ	431	LEU	2.9
4	CD	194	GLY	2.8
28	C4	54	GLY	2.8
54	BU	11	GLY	2.8
35	DB	101	MET	2.8
1	AA	1121	C	2.8
1	AA	2168	C	2.8
34	DA	1223	C	2.8
14	CQ	128	LYS	2.8
24	A0	4	LYS	2.8

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Mol	Chain	Res	Type	RSRZ
36	DC	23	TYR	2.8
42	DI	4	TYR	2.8
46	DM	27	LYS	2.8
1	AA	2204	G	2.8
1	CA	100	G	2.8
3	CC	46	ALA	2.8
3	CC	192	ALA	2.8
34	DA	1106	G	2.8
34	DA	1117	G	2.8
34	DA	1233	G	2.8
5	CE	19	ARG	2.8
9	AK	90	ALA	2.8
42	BI	17	VAL	2.8
57	BZ	404	VAL	2.8
52	BS	29	ARG	2.8
6	CF	23	ASP	2.8
3	AC	45	HIS	2.8
9	AK	23	SER	2.8
47	BN	13	THR	2.8
57	DZ	271	LEU	2.8
1	CA	1045	A	2.8
1	CA	1086	A	2.8
1	CA	1098	A	2.8
34	BA	1252	A	2.8
34	DA	1350	A	2.8
3	CC	177	GLY	2.8
10	CL	24	GLY	2.8
57	BZ	586	GLY	2.8
7	AG	142	PRO	2.8
38	BE	52	PRO	2.8
57	BZ	682	GLN	2.8
57	DZ	131	PRO	2.8
57	DZ	682	GLN	2.8
52	DS	7	LYS	2.8
57	DZ	418	LYS	2.8
57	DZ	536	LYS	2.8
3	CC	163	GLU	2.8
9	AK	127	GLU	2.8
1	AA	2154	U	2.8
1	AA	2133	C	2.8
1	CA	2103	C	2.8
1	CA	2143	C	2.8

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Mol	Chain	Res	Type	RSRZ
9	AK	81	VAL	2.8
10	AL	17	ALA	2.8
31	C7	23	ARG	2.8
34	BA	1223	C	2.8
36	DC	137	ALA	2.8
42	BI	13	ALA	2.8
42	DI	43	ALA	2.8
46	BM	80	ARG	2.8
57	BZ	476	VAL	2.8
57	DZ	647	VAL	2.8
7	AG	77	ILE	2.8
7	CG	43	LEU	2.8
9	AK	93	LEU	2.8
36	BC	152	ILE	2.8
36	DC	94	LEU	2.8
36	DC	188	LEU	2.8
40	BG	38	LEU	2.8
43	DJ	75	ILE	2.8
52	BS	62	ILE	2.8
10	AL	75	SER	2.8
1	CA	1074	G	2.8
1	CA	1091	G	2.8
1	CA	1110	G	2.8
3	CC	217	THR	2.8
9	AK	130	THR	2.8
34	DA	1030(A)	G	2.8
46	DM	43	THR	2.8
57	DZ	91	THR	2.8
1	AA	2191	A	2.8
3	AC	207	GLY	2.8
33	C9	37	GLY	2.8
37	DD	87	GLY	2.8
54	BU	16	GLY	2.8
10	CL	90	LYS	2.8
42	BI	127	LYS	2.8
57	BZ	596	LYS	2.8
3	CC	202	PRO	2.8
57	DZ	294	PRO	2.8
23	CZ	178	GLU	2.8
35	DB	170	GLU	2.8
3	CC	21	TYR	2.8
40	DG	44	TYR	2.8

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Mol	Chain	Res	Type	RSRZ
57	BZ	439	ARG	2.8
1	AA	1107	U	2.8
34	BA	170	U	2.8
34	DA	1212	U	2.8
9	CK	52	PHE	2.8
35	DB	122	PHE	2.8
57	DZ	221	ALA	2.8
36	BC	188	LEU	2.8
36	DC	6	HIS	2.8
1	AA	34	C	2.8
1	AA	2162	C	2.8
7	CG	4	ASP	2.8
34	DA	995	C	2.8
34	DA	1030	C	2.8
57	DZ	222	ASP	2.8
43	BJ	100	THR	2.8
57	DZ	552	SER	2.8
35	BB	22	LYS	2.8
28	C4	17	GLY	2.8
36	DC	74	GLY	2.8
57	BZ	453	GLY	2.8
1	AA	2128	G	2.8
1	AA	2170	G	2.8
10	AL	113	PRO	2.8
34	BA	1309	G	2.8
42	DI	21	PRO	2.8
57	BZ	415	PRO	2.8
57	BZ	613	PRO	2.8
57	DZ	208	GLN	2.8
28	A4	57	GLU	2.8
34	BA	1275	A	2.8
34	DA	1357	A	2.8
53	BT	51	GLU	2.8
54	DU	10	ARG	2.8
35	DB	230	VAL	2.8
36	BC	151	VAL	2.8
10	CL	65	PHE	2.8
28	A4	67	TYR	2.8
35	BB	237	ALA	2.8
35	DB	105	PHE	2.8
53	BT	94	ALA	2.8
57	DZ	483	TYR	2.8

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Mol	Chain	Res	Type	RSRZ
57	DZ	645	ALA	2.8
7	AG	144	ILE	2.8
23	CZ	33	LEU	2.8
39	BF	10	LEU	2.8
40	BG	101	LEU	2.8
42	DI	63	ILE	2.8
52	DS	16	LEU	2.8
57	DZ	466	LEU	2.8
57	DZ	546	ILE	2.8
7	CG	155	MET	2.8
10	AL	90	LYS	2.8
24	C0	5	LYS	2.8
57	DZ	250	THR	2.8
1	AA	696	C	2.8
1	AA	2165	C	2.8
2	CB	20	C	2.8
2	CB	31	C	2.8
9	AK	78	SER	2.8
34	BA	1397	C	2.8
34	DA	1039	C	2.8
7	CG	129	GLY	2.8
8	CH	5	GLY	2.8
46	BM	89	GLY	2.8
3	CC	52	PRO	2.8
28	C4	29	PRO	2.8
9	CK	42	GLN	2.7
36	DC	37	GLN	2.7
3	CC	7	ARG	2.7
7	AG	51	ARG	2.7
9	AK	5	ARG	2.7
9	CK	18	GLU	2.7
42	DI	107	ARG	2.7
57	DZ	465	ARG	2.7
43	DJ	34	VAL	2.7
52	DS	19	VAL	2.7
57	BZ	491	VAL	2.7
3	CC	34	ALA	2.7
17	CT	126	ALA	2.7
1	AA	2142	G	2.7
1	CA	1056	G	2.7
9	AK	25	PHE	2.7
34	BA	994	A	2.7

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Mol	Chain	Res	Type	RSRZ
34	BA	996	A	2.7
40	BG	134	ALA	2.7
43	BJ	20	ALA	2.7
9	CK	29	TYR	2.7
35	BB	11	LEU	2.7
42	BI	74	ILE	2.7
42	DI	77	ILE	2.7
42	DI	81	ILE	2.7
47	BN	34	TYR	2.7
57	DZ	632	LEU	2.7
10	CL	89	HIS	2.7
1	AA	2144	U	2.7
1	CA	2130	U	2.7
34	DA	1313	U	2.7
10	AL	86	LYS	2.7
43	BJ	7	LYS	2.7
53	DT	34	LYS	2.7
48	DO	22	THR	2.7
57	BZ	410	ASP	2.7
57	BZ	623	ASP	2.7
40	BG	130	GLY	2.7
57	BZ	85	PRO	2.7
4	AD	262	ARG	2.7
25	C1	26	ARG	2.7
26	C2	69	ARG	2.7
37	DD	49	ARG	2.7
46	BM	110	ARG	2.7
57	BZ	484	ARG	2.7
57	DZ	124	GLN	2.7
57	DZ	644	ARG	2.7
57	DZ	666	ARG	2.7
1	CA	1079	C	2.7
26	C2	66	GLU	2.7
57	DZ	515	GLU	2.7
9	AK	27	VAL	2.7
11	CN	9	VAL	2.7
57	BZ	670	VAL	2.7
57	DZ	162	VAL	2.7
10	AL	74	ALA	2.7
28	A4	49	PHE	2.7
35	BB	17	PHE	2.7
48	BO	87	ILE	2.7

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Mol	Chain	Res	Type	RSRZ
53	DT	72	LEU	2.7
57	DZ	19	ALA	2.7
7	CG	131	TYR	2.7
40	BG	44	TYR	2.7
42	BI	92	TYR	2.7
42	DI	114	TYR	2.7
54	BU	21	TYR	2.7
1	CA	1088	A	2.7
1	CA	2170	A	2.7
3	AC	6	LYS	2.7
10	AL	35	MET	2.7
34	BA	1201	A	2.7
42	BI	95	LYS	2.7
43	BJ	14	LYS	2.7
57	BZ	418	LYS	2.7
57	BZ	681	LYS	2.7
1	CA	2165	G	2.7
34	BA	1011	G	2.7
34	BA	1047	G	2.7
34	BA	1253	G	2.7
3	AC	68	GLY	2.7
3	CC	207	GLY	2.7
9	AK	103	GLY	2.7
10	AL	50	ASP	2.7
10	CL	31	GLY	2.7
28	A4	64	GLY	2.7
54	DU	16	GLY	2.7
57	BZ	492	ASP	2.7
57	DZ	622	GLY	2.7
35	DB	226	ARG	2.7
43	BJ	37	PRO	2.7
44	DK	13	GLN	2.7
47	BN	25	VAL	2.7
57	DZ	269	VAL	2.7
7	AG	82	LEU	2.7
8	CH	33	LEU	2.7
25	A1	98	LEU	2.7
34	BA	1270	C	2.7
34	BA	1452	C	2.7
34	DA	1214	C	2.7
35	BB	138	LEU	2.7
36	BC	91	LEU	2.7

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Mol	Chain	Res	Type	RSRZ
46	BM	9	ILE	2.7
47	DN	37	PHE	2.7
50	DQ	36	ILE	2.7
53	DT	40	ALA	2.7
57	DZ	92	ILE	2.7
57	DZ	413	ILE	2.7
57	DZ	563	ILE	2.7
42	BI	125	TYR	2.7
57	DZ	550	MET	2.7
1	AA	1935	A	2.7
42	BI	29	ASN	2.7
3	AC	160	GLY	2.7
21	CX	60	ARG	2.7
35	DB	65	GLY	2.7
37	DD	73	ARG	2.7
46	BM	26	GLY	2.7
46	DM	3	ARG	2.7
47	DN	35	ARG	2.7
51	BR	47	THR	2.7
52	BS	3	ARG	2.7
7	CG	116	ASP	2.7
57	DZ	200	PRO	2.7
1	CA	1107	G	2.7
34	DA	630	G	2.7
36	DC	173	VAL	2.7
42	DI	26	VAL	2.7
43	BJ	44	VAL	2.7
46	BM	60	VAL	2.7
47	DN	8	GLU	2.7
57	DZ	670	VAL	2.7
3	AC	48	LEU	2.7
7	CG	73	ALA	2.7
10	CL	82	ALA	2.7
23	CZ	53	ILE	2.7
35	DB	221	LEU	2.7
40	DG	59	LEU	2.7
43	BJ	88	LEU	2.7
42	DI	101	PHE	2.7
43	BJ	6	ILE	2.7
57	BZ	459	LEU	2.7
47	BN	36	PHE	2.7
57	DZ	402	ILE	2.7

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Mol	Chain	Res	Type	RSRZ
57	DZ	556	ILE	2.7
3	CC	178	LYS	2.7
10	AL	80	LYS	2.7
28	C4	69	LYS	2.7
36	DC	135	LYS	2.7
40	BG	70	LYS	2.7
46	DM	82	MET	2.7
10	AL	101	TRP	2.7
33	C9	20	HIS	2.7
1	CA	2107	C	2.7
34	BA	1008	C	2.7
40	DG	154	TYR	2.7
57	DZ	568	TYR	2.7
37	BD	65	ARG	2.7
47	BN	23	ARG	2.7
53	DT	86	ARG	2.7
7	CG	161	THR	2.7
40	BG	84	ASN	2.7
46	BM	62	ASN	2.7
50	DQ	2	PRO	2.7
52	DS	39	THR	2.7
34	DA	1188	A	2.7
34	DA	1261	A	2.7
7	CG	147	ASP	2.7
57	DZ	224	ASP	2.7
10	CL	29	GLN	2.7
10	AL	5	VAL	2.7
38	BE	50	GLU	2.7
47	DN	56	VAL	2.7
57	DZ	603	GLU	2.7
7	CG	78	SER	2.7
23	CZ	16	SER	2.7
35	DB	41	ILE	2.6
36	DC	196	LEU	2.7
37	DD	188	LEU	2.7
42	DI	56	LEU	2.7
52	BS	35	SER	2.7
57	BZ	521	SER	2.7
50	DQ	37	LYS	2.6
10	AL	14	ALA	2.6
42	BI	84	ALA	2.6
57	BZ	673	PHE	2.6

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Mol	Chain	Res	Type	RSRZ
57	DZ	558	PHE	2.6
57	DZ	581	ALA	2.6
57	DZ	672	PHE	2.6
1	AA	299	G	2.6
1	AA	2132	G	2.6
1	CA	1106	G	2.6
34	BA	631	G	2.6
34	BA	1365	G	2.6
34	DA	976	G	2.6
57	BZ	580	MET	2.6
57	BZ	509	HIS	2.6
34	BA	1262	C	2.6
34	DA	1114	C	2.6
3	AC	183	PRO	2.6
8	CH	112	PRO	2.6
9	CK	69	PRO	2.6
23	CZ	62	PRO	2.6
38	DE	99	GLY	2.6
40	DG	81	GLY	2.6
41	BH	5	PRO	2.6
42	BI	80	GLY	2.6
54	BU	2	GLY	2.6
46	BM	109	THR	2.6
3	CC	58	ASN	2.6
5	CE	121	ASN	2.6
1	AA	1124	U	2.6
1	CA	1420	U	2.6
3	AC	39	ASP	2.6
3	AC	163	GLU	2.6
8	CH	7	LEU	2.6
8	CH	137	ASP	2.6
9	CK	21	GLN	2.6
9	CK	75	GLN	2.6
10	AL	110	GLN	2.6
13	CP	92	GLU	2.6
34	BA	65	U	2.6
40	BG	13	GLN	2.6
40	DG	21	VAL	2.6
46	BM	69	GLU	2.6
52	DS	64	GLU	2.6
57	BZ	-48	VAL	2.6
57	DZ	232	LEU	2.6

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Mol	Chain	Res	Type	RSRZ
1	CA	896	A	2.6
34	BA	1363(A)	A	2.6
34	DA	1046	A	2.6
35	BB	222	ILE	2.6
47	BN	7	ILE	2.6
9	AK	126	ALA	2.6
10	AL	133	SER	2.6
24	C0	9	SER	2.6
44	BK	53	SER	2.6
50	BQ	99	SER	2.6
1	AA	1108	G	2.6
9	CK	60	ARG	2.6
34	DA	1491	G	2.6
53	DT	8	ARG	2.6
54	BU	7	ARG	2.6
57	BZ	676	TYR	2.6
10	AL	91	PRO	2.6
14	CQ	100	GLY	2.6
46	BM	41	PRO	2.6
57	BZ	455	GLY	2.6
57	BZ	654	GLY	2.6
24	C0	43	THR	2.6
1	AA	1579	C	2.6
1	CA	652(D)	C	2.6
3	CC	6	LYS	2.6
10	AL	47	ASN	2.6
28	C4	38	LYS	2.6
3	AC	13	GLU	2.6
8	CH	26	VAL	2.6
9	CK	115	GLN	2.6
28	A4	56	VAL	2.6
34	DA	1030(B)	C	2.6
34	DA	1260	C	2.6
34	DA	1267	C	2.6
40	BG	91	VAL	2.6
40	DG	66	VAL	2.6
42	BI	47	LEU	2.6
43	DJ	76	ASN	2.6
52	DS	70	LYS	2.6
35	BB	165	VAL	2.6
52	DS	22	LEU	2.6
57	DZ	428	LEU	2.6

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Mol	Chain	Res	Type	RSRZ
43	DJ	64	GLU	2.6
57	DZ	30	GLU	2.6
57	DZ	201	ILE	2.6
36	BC	62	ASP	2.6
41	DH	54	ASP	2.6
3	AC	187	ALA	2.6
3	CC	38	PHE	2.6
3	CC	181	PHE	2.6
9	CK	96	PHE	2.6
51	BR	20	ALA	2.6
57	DZ	159	ALA	2.6
1	CA	229	A	2.6
3	AC	212	SER	2.6
34	DA	1286	A	2.6
42	DI	126	SER	2.6
50	DQ	97	SER	2.6
37	BD	132	ARG	2.6
3	CC	160	GLY	2.6
33	C9	30	PRO	2.6
10	CL	2	LYS	2.6
45	DL	126	LYS	2.6
1	AA	2228	G	2.6
3	CC	62	THR	2.6
8	CH	19	VAL	2.6
8	CH	72	ILE	2.6
23	CZ	161	VAL	2.6
34	DA	1310	G	2.6
34	DA	1456	G	2.6
37	BD	21	LEU	2.6
42	BI	28	VAL	2.6
47	BN	56	VAL	2.6
52	BS	40	ILE	2.6
52	BS	51	VAL	2.6
56	DX	46	G	2.6
57	DZ	-48	VAL	2.6
9	AK	75	GLN	2.6
10	AL	29	GLN	2.6
23	AZ	2	GLU	2.6
57	BZ	615	GLU	2.6
3	CC	196	ALA	2.6
7	AG	50	ALA	2.6
9	AK	89	ALA	2.6

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Mol	Chain	Res	Type	RSRZ
42	BI	33	PHE	2.6
42	DI	15	ALA	2.6
57	DZ	482	ALA	2.6
34	DA	970	C	2.6
34	DA	1115	C	2.6
34	DA	1195	C	2.6
23	CZ	166	SER	2.6
36	BC	154	SER	2.6
52	DS	83	HIS	2.6
57	DZ	668	SER	2.6
3	AC	53	ARG	2.6
40	BG	78	ARG	2.6
46	DM	94	ARG	2.6
1	CA	2119	A	2.6
1	CA	2602	A	2.6
34	BA	1324	A	2.6
34	DA	949	A	2.6
7	CG	25	TYR	2.6
35	BB	202	PRO	2.6
43	BJ	55	LYS	2.6
44	BK	51	LYS	2.6
53	BT	14	LYS	2.6
57	BZ	559	PRO	2.6
23	CZ	144	LEU	2.6
57	DZ	181	LEU	2.6
3	AC	22	THR	2.6
23	CZ	98	MET	2.6
35	DB	229	VAL	2.6
36	BC	195	VAL	2.6
40	DG	27	ILE	2.6
46	DM	7	VAL	2.6
57	BZ	451	ILE	2.6
57	BZ	594	VAL	2.6
57	DZ	529	ILE	2.6
3	CC	187	ALA	2.6
9	AK	28	ASN	2.6
10	AL	44	ALA	2.6
10	CL	51	ALA	2.6
35	BB	28	PHE	2.6
36	BC	200	ALA	2.6
40	BG	28	ASN	2.6
42	DI	29	ASN	2.6

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Mol	Chain	Res	Type	RSRZ
46	BM	107	ALA	2.6
57	BZ	-2	ALA	2.6
57	DZ	475	ASN	2.6
1	AA	2147	G	2.5
1	CA	549	G	2.5
1	CA	2157	G	2.5
42	BI	105	ASP	2.6
1	AA	2166	U	2.5
1	CA	2132	U	2.5
9	CK	5	ARG	2.5
17	CT	125	ARG	2.5
1	AA	2164	C	2.5
1	CA	645	C	2.5
3	CC	64	SER	2.5
34	DA	940	C	2.5
34	DA	1097	C	2.5
34	DA	1210	C	2.5
34	DA	1367	C	2.5
42	DI	71	SER	2.5
9	CK	45	LYS	2.5
42	DI	95	LYS	2.5
1	CA	1054	A	2.5
1	CA	1077	A	2.5
3	CC	183	PRO	2.5
8	CH	168	PRO	2.5
9	AK	77	PRO	2.5
34	BA	983	A	2.5
34	DA	1180	A	2.5
34	DA	1319	A	2.5
41	DH	71	GLY	2.5
42	DI	19	LEU	2.5
42	DI	69	GLY	2.5
57	DZ	540	PRO	2.5
7	CG	3	LEU	2.5
7	CG	19	LEU	2.5
10	AL	76	TYR	2.5
35	BB	33	TYR	2.5
35	DB	44	LEU	2.5
57	DZ	212	TYR	2.5
7	CG	15	VAL	2.5
35	DB	112	VAL	2.5
35	DB	164	VAL	2.5

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Mol	Chain	Res	Type	RSRZ
57	DZ	605	ILE	2.5
57	DZ	671	MET	2.5
10	CL	36	GLU	2.5
23	CZ	94	GLU	2.5
36	DC	95	THR	2.5
47	BN	52	GLN	2.5
50	DQ	49	GLU	2.5
52	DS	48	THR	2.5
57	BZ	685	GLU	2.5
7	CG	57	ALA	2.5
43	BJ	32	ALA	2.5
57	BZ	244	ALA	2.5
44	DK	117	ASN	2.5
7	AG	116	ASP	2.5
7	CG	21	ARG	2.5
35	BB	137	ARG	2.5
36	BC	172	ARG	2.5
36	DC	190	ARG	2.5
47	DN	26	ARG	2.5
52	BS	36	ARG	2.5
53	DT	23	ARG	2.5
57	BZ	393	ASP	2.5
1	AA	1466	U	2.5
3	CC	71	LYS	2.5
28	C4	37	SER	2.5
40	DG	92	SER	2.5
57	DZ	118	SER	2.5
57	DZ	587	SER	2.5
1	AA	2126	G	2.5
1	CA	1055	G	2.5
1	CA	2186	G	2.5
34	BA	951	G	2.5
34	DA	1031	G	2.5
34	DA	1042	G	2.5
3	CC	61	GLY	2.5
9	CK	66	LEU	2.5
10	AL	27	LEU	2.5
16	CS	58	LEU	2.5
35	DB	121	LEU	2.5
37	BD	37	PRO	2.5
37	DD	39	PRO	2.5
57	DZ	535	PRO	2.5

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Mol	Chain	Res	Type	RSRZ
28	A4	45	GLY	2.5
57	DZ	158	GLY	2.5
9	AK	131	MET	2.5
10	CL	48	MET	2.5
9	CK	122	VAL	2.5
36	BC	29	TYR	2.5
36	DC	103	VAL	2.5
36	DC	193	TYR	2.5
46	DM	17	VAL	2.5
54	BU	13	ILE	2.5
57	DZ	481	VAL	2.5
57	DZ	510	VAL	2.5
1	AA	2322	A	2.5
34	BA	149	A	2.5
34	BA	1531	A	2.5
34	DA	978	A	2.5
34	DA	1201	A	2.5
3	CC	218	THR	2.5
9	AK	12	THR	2.5
9	CK	8	GLU	2.5
9	CK	130	THR	2.5
36	DC	166	GLU	2.5
10	AL	65	PHE	2.5
40	DG	110	GLN	2.5
57	BZ	523	PHE	2.5
57	BZ	582	PHE	2.5
3	AC	36	ALA	2.5
3	CC	27	ALA	2.5
9	AK	124	ALA	2.5
35	BB	171	ALA	2.5
36	BC	168	ALA	2.5
41	DH	16	ALA	2.5
42	BI	119	ALA	2.5
57	BZ	310	ALA	2.5
57	BZ	482	ALA	2.5
3	CC	18	ASN	2.5
8	CH	101	ARG	2.5
35	BB	23	ARG	2.5
36	BC	30	ARG	2.5
42	BI	128	ARG	2.5
3	AC	173	HIS	2.5
42	BI	75	ASP	2.5

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Mol	Chain	Res	Type	RSRZ
46	DM	16	ASP	2.5
16	CS	31	SER	2.5
34	DA	992	U	2.5
57	BZ	441	SER	2.5
57	DZ	175	SER	2.5
6	CF	14	PRO	2.5
7	CG	139	LEU	2.5
10	AL	84	LEU	2.5
28	C4	11	PRO	2.5
36	DC	174	PRO	2.5
41	BH	133	LEU	2.5
42	DI	85	LEU	2.5
36	DC	13	GLY	2.5
44	DK	77	MET	2.5
57	DZ	308	PRO	2.5
10	AL	83	GLY	2.5
16	CS	96	GLY	2.5
44	BK	95	ILE	2.5
52	DS	72	GLY	2.5
57	DZ	539	ILE	2.5
40	DG	156	TRP	2.5
44	DK	14	VAL	2.5
46	BM	15	VAL	2.5
49	DP	48	TRP	2.5
57	BZ	493	VAL	2.5
1	AA	2150	C	2.5
1	AA	2210	C	2.5
1	CA	1102	C	2.5
34	DA	1066	C	2.5
34	DA	1113	C	2.5
1	CA	171	G	2.5
1	CA	2751	G	2.5
34	BA	79	G	2.5
34	DA	1124	G	2.5
34	DA	1139	G	2.5
34	DA	1312	G	2.5
36	DC	184	TYR	2.5
57	DZ	616	TYR	2.5
7	AG	167	GLU	2.5
46	DM	49	THR	2.5
47	DN	16	PHE	2.5
57	BZ	406	GLU	2.5

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Mol	Chain	Res	Type	RSRZ
3	CC	174	ALA	2.5
7	CG	158	ALA	2.5
43	DJ	27	ALA	2.5
43	DJ	32	ALA	2.5
57	DZ	67	ALA	2.5
57	DZ	486	THR	2.5
34	DA	1225	A	2.5
38	BE	24	ARG	2.5
40	BG	79	ARG	2.5
28	C4	18	CYS	2.5
54	DU	3	LYS	2.5
23	CZ	32	HIS	2.5
57	DZ	40	HIS	2.5
43	DJ	89	ASP	2.5
37	DD	176	LEU	2.5
46	BM	19	LEU	2.5
52	BS	30	LEU	2.5
10	AL	54	PRO	2.5
57	DZ	153	MET	2.5
40	BG	81	GLY	2.5
40	DG	77	SER	2.5
57	DZ	288	PRO	2.5
1	AA	12	U	2.5
14	CQ	23	GLY	2.5
46	DM	95	GLY	2.5
53	BT	69	GLY	2.5
53	BT	101	GLY	2.5
8	CH	44	VAL	2.5
35	DB	184	VAL	2.5
44	DK	82	VAL	2.5
52	DS	67	VAL	2.5
57	DZ	163	VAL	2.5
7	AG	45	GLU	2.5
23	CZ	9	TYR	2.5
36	BC	90	GLU	2.5
57	DZ	279	TYR	2.5
57	DZ	669	PHE	2.5
10	AL	51	ALA	2.5
12	CO	103	ALA	2.5
37	BD	47	ARG	2.5
42	BI	9	ARG	2.5
42	BI	46	ALA	2.5

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Mol	Chain	Res	Type	RSRZ
43	BJ	45	ARG	2.5
48	DO	68	ARG	2.5
57	DZ	468	ARG	2.5
1	CA	1509	C	2.5
34	DA	1096	C	2.5
47	BN	11	LYS	2.5
52	BS	70	LYS	2.5
1	CA	274	G	2.5
1	CA	1051	G	2.5
1	CA	1099	G	2.5
1	CA	2168	G	2.5
1	CA	2187	G	2.5
34	BA	64	G	2.5
1	CA	2114	A	2.5
49	DP	13	HIS	2.5
14	CQ	7	MET	2.4
19	CV	71	LEU	2.4
35	BB	10	LEU	2.4
36	DC	175	LEU	2.4
46	BM	83	ASP	2.4
10	AL	19	PRO	2.4
57	BZ	255	ILE	2.4
57	BZ	487	ILE	2.4
9	CK	103	GLY	2.4
3	CC	180	SER	2.4
9	CK	23	SER	2.4
15	CR	73	VAL	2.4
35	BB	66	GLY	2.4
43	DJ	36	GLY	2.4
46	DM	54	VAL	2.4
57	BZ	633	GLY	2.4
57	BZ	638	GLY	2.4
57	DZ	189	GLY	2.4
47	DN	60	SER	2.4
57	DZ	452	SER	2.4
1	CA	2180	U	2.4
34	BA	343	U	2.4
34	BA	1126	U	2.4
34	DA	1281	U	2.4
8	CH	123	PHE	2.4
26	C2	11	GLU	2.4
26	C2	51	ARG	2.4

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Mol	Chain	Res	Type	RSRZ
36	DC	167	TRP	2.4
37	BD	49	ARG	2.4
37	DD	163	GLU	2.4
42	DI	16	ARG	2.4
43	BJ	43	ARG	2.4
57	DZ	414	GLU	2.4
8	CH	94	TYR	2.4
9	AK	79	ALA	2.4
10	AL	123	ALA	2.4
10	CL	6	ALA	2.4
36	DC	29	TYR	2.4
40	BG	154	TYR	2.4
40	DG	65	ALA	2.4
42	BI	118	LYS	2.4
43	DJ	57	LYS	2.4
46	BM	59	TYR	2.4
46	DM	111	LYS	2.4
57	DZ	165	GLN	2.4
57	DZ	589	ALA	2.4
57	DZ	595	GLN	2.4
57	DZ	655	TYR	2.4
43	DJ	13	HIS	2.4
57	BZ	40	HIS	2.4
1	AA	670	C	2.4
1	CA	1053	C	2.4
1	CA	2789	C	2.4
34	BA	218	C	2.4
34	BA	1244	C	2.4
34	DA	1359	C	2.4
3	AC	189	ASN	2.4
7	CG	34	LEU	2.4
9	AK	112	LEU	2.4
36	BC	87	LEU	2.4
36	DC	91	LEU	2.4
43	BJ	86	MET	2.4
57	BZ	431	LEU	2.4
57	DZ	228	MET	2.4
1	AA	1507	A	2.4
1	CA	1084	A	2.4
34	BA	1227	A	2.4
34	BA	1332	A	2.4
7	AG	112	PRO	2.4

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Mol	Chain	Res	Type	RSRZ
34	BA	306	G	2.4
34	BA	1003	G	2.4
34	BA	1021	G	2.4
35	BB	195	ASP	2.4
42	BI	21	PRO	2.4
57	DZ	534	ILE	2.4
5	CE	33	VAL	2.4
10	AL	31	GLY	2.4
23	CZ	37	VAL	2.4
57	BZ	610	VAL	2.4
10	CL	133	SER	2.4
23	CZ	131	ARG	2.4
24	C0	82	ARG	2.4
35	DB	233	SER	2.4
47	BN	41	ARG	2.4
7	AG	30	GLU	2.4
9	CK	123	GLU	2.4
34	DA	1150	U	2.4
34	DA	1315	U	2.4
37	DD	156	GLU	2.4
52	DS	43	GLU	2.4
57	DZ	223	PHE	2.4
3	CC	205	ALA	2.4
10	CL	110	GLN	2.4
23	CZ	184	ALA	2.4
31	C7	45	ALA	2.4
40	BG	56	GLN	2.4
46	DM	76	ALA	2.4
42	BI	4	TYR	2.4
38	DE	144	THR	2.4
7	AG	62	LEU	2.4
7	CG	90	LEU	2.4
40	BG	59	LEU	2.4
42	DI	47	LEU	2.4
5	AE	77	ILE	2.4
34	BA	980	C	2.4
34	BA	1243	C	2.4
34	BA	1282	C	2.4
34	DA	979	C	2.4
43	DJ	53	PRO	2.4
3	AC	24	ASP	2.4
3	AC	170	GLY	2.4

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Mol	Chain	Res	Type	RSRZ
8	CH	15	VAL	2.4
9	CK	22	GLY	2.4
9	CK	110	GLY	2.4
19	CV	42	GLY	2.4
28	A4	17	GLY	2.4
49	DP	68	ASP	2.4
52	BS	67	VAL	2.4
1	CA	2126	A	2.4
34	BA	1001	A	2.4
34	DA	1044	A	2.4
34	DA	1360	A	2.4
3	CC	211	ARG	2.4
7	AG	55	LYS	2.4
9	AK	98	LYS	2.4
10	CL	3	LYS	2.4
16	CS	11	LYS	2.4
35	BB	147	LYS	2.4
36	DC	54	ARG	2.4
37	DD	35	ARG	2.4
43	DJ	14	LYS	2.4
46	DM	13	LYS	2.4
50	DQ	14	LYS	2.4
52	DS	6	LYS	2.4
57	BZ	324	ARG	2.4
1	AA	691	G	2.4
1	AA	2155	G	2.4
1	CA	2181	G	2.4
7	CG	167	GLU	2.4
34	DA	1160	G	2.4
34	DA	1353	G	2.4
35	DB	57	PHE	2.4
40	DG	43	PHE	2.4
57	BZ	470	PHE	2.4
9	CK	119	ALA	2.4
40	BG	7	ALA	2.4
47	DN	48	ALA	2.4
56	DX	47	U	2.4
44	DK	25	TYR	2.4
10	AL	58	THR	2.4
46	DM	20	THR	2.4
52	BS	39	THR	2.4
40	BG	153	HIS	2.4

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Mol	Chain	Res	Type	RSRZ
16	CS	56	LEU	2.4
35	BB	180	LEU	2.4
46	DM	90	LEU	2.4
22	CY	44	ILE	2.4
40	BG	42	ILE	2.4
46	DM	9	ILE	2.4
7	CG	112	PRO	2.4
53	DT	98	PRO	2.4
3	CC	168	LYS	2.4
23	CZ	143	GLY	2.4
23	CZ	160	GLY	2.4
28	C4	4	GLY	2.4
33	C9	16	VAL	2.4
42	DI	6	GLY	2.4
46	BM	74	VAL	2.4
52	BS	45	VAL	2.4
53	BT	102	GLY	2.4
1	AA	2159	C	2.4
1	AA	2205	C	2.4
34	BA	479	C	2.4
34	BA	1030(B)	C	2.4
34	DA	972	C	2.4
34	DA	1112	C	2.4
34	DA	1366	C	2.4
1	CA	2062	A	2.4
10	CL	85	GLU	2.4
34	BA	958	A	2.4
34	BA	1289	A	2.4
42	BI	35	GLU	2.4
3	CC	171	ALA	2.4
57	BZ	528	ALA	2.4
11	CN	8	GLN	2.4
28	A4	66	SER	2.4
35	BB	110	GLN	2.4
57	BZ	448	GLN	2.4
57	BZ	595	GLN	2.4
57	DZ	122	TRP	2.4
1	CA	614(B)	G	2.4
1	CA	2184	G	2.4
34	BA	102	G	2.4
34	BA	346	G	2.4
34	BA	384	G	2.4

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Mol	Chain	Res	Type	RSRZ
34	BA	933	G	2.4
34	BA	993	G	2.4
34	BA	1000	U	2.4
34	DA	1090	U	2.4
34	DA	1094	G	2.4
34	DA	1194	U	2.4
37	DD	27	TYR	2.4
57	DZ	657	THR	2.4
37	BD	194	LEU	2.4
40	DG	153	HIS	2.4
51	BR	85	LEU	2.4
7	CG	140	ILE	2.4
42	BI	63	ILE	2.4
41	DH	72	PRO	2.4
43	BJ	41	PRO	2.4
57	DZ	436	PRO	2.4
7	CG	38	VAL	2.3
7	CG	70	VAL	2.3
10	AL	53	VAL	2.3
14	CQ	22	LYS	2.3
23	CZ	74	VAL	2.3
24	C0	46	LYS	2.3
3	AC	49	GLY	2.3
6	CF	150	GLY	2.3
7	AG	119	GLY	2.3
8	CH	51	ARG	2.3
28	A4	68	ARG	2.3
36	BC	135	LYS	2.3
37	BD	170	VAL	2.3
38	DE	27	ARG	2.3
45	BL	20	LYS	2.3
46	BM	106	ASN	2.3
52	BS	6	LYS	2.3
57	DZ	160	ARG	2.3
57	DZ	542	VAL	2.3
57	DZ	600	VAL	2.3
46	DM	68	GLY	2.3
57	DZ	557	GLY	2.3
3	CC	51	ASP	2.3
7	AG	150	ASP	2.3
9	AK	24	PHE	2.3
23	CZ	136	PHE	2.3

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Mol	Chain	Res	Type	RSRZ
44	DK	36	ASP	2.3
7	AG	54	GLU	2.3
28	C4	23	GLU	2.3
35	DB	62	ALA	2.3
43	DJ	20	ALA	2.3
47	BN	59	ALA	2.3
50	BQ	86	GLU	2.3
52	BS	73	GLU	2.3
57	BZ	214	GLU	2.3
57	DZ	209	ALA	2.3
57	DZ	310	ALA	2.3
1	AA	270	C	2.3
1	AA	1118	C	2.3
1	AA	2125	C	2.3
1	AA	2158	C	2.3
1	AA	2186	C	2.3
34	BA	990	C	2.3
34	BA	1030	C	2.3
34	DA	1043	C	2.3
57	DZ	677	GLN	2.3
3	AC	219	MET	2.3
34	DA	1030(D)	A	2.3
55	BV	15	A	2.3
3	CC	216	THR	2.3
9	CK	10	LEU	2.3
9	CK	61	LEU	2.3
43	BJ	62	HIS	2.3
46	BM	92	HIS	2.3
47	DN	49	HIS	2.3
57	BZ	602	LEU	2.3
57	BZ	616	TYR	2.3
57	DZ	166	LEU	2.3
57	DZ	205	TYR	2.3
1	CA	958	U	2.3
1	CA	1078	U	2.3
34	BA	1446	U	2.3
34	DA	1065	U	2.3
34	DA	1211	U	2.3
7	AG	140	ILE	2.3
16	CS	35	ILE	2.3
36	DC	134	ILE	2.3
37	DD	5	ILE	2.3

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Mol	Chain	Res	Type	RSRZ
43	BJ	96	ILE	2.3
16	CS	62	LYS	2.3
22	CY	63	LYS	2.3
36	BC	174	PRO	2.3
1	AA	2146	G	2.3
1	CA	652(U)	G	2.3
3	AC	7	ARG	2.3
7	CG	118	ARG	2.3
33	C9	22	ARG	2.3
34	BA	1310	G	2.3
34	DA	945	G	2.3
40	BG	41	ARG	2.3
42	BI	65	VAL	2.3
53	DT	57	ARG	2.3
57	BZ	565	VAL	2.3
57	BZ	600	VAL	2.3
3	CC	189	ASN	2.3
19	CV	54	GLY	2.3
37	BD	103	ASN	2.3
37	DD	167	GLY	2.3
40	BG	55	GLY	2.3
44	DK	17	GLY	2.3
36	DC	203	PHE	2.3
57	BZ	672	PHE	2.3
3	CC	198	GLU	2.3
9	AK	62	ALA	2.3
9	CK	90	ALA	2.3
10	AL	88	ALA	2.3
10	AL	122	ALA	2.3
10	CL	102	GLU	2.3
37	DD	179	GLU	2.3
40	BG	129	GLU	2.3
57	BZ	220	ALA	2.3
57	BZ	403	GLU	2.3
57	DZ	204	GLU	2.3
57	DZ	252	ASP	2.3
57	DZ	410	ASP	2.3
40	DG	152	ALA	2.3
42	DI	61	ALA	2.3
43	BJ	27	ALA	2.3
47	DN	30	ALA	2.3
6	CF	8	GLN	2.3

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Mol	Chain	Res	Type	RSRZ
7	CG	26	GLN	2.3
36	DC	170	GLN	2.3
57	DZ	12	LEU	2.3
57	DZ	567	LEU	2.3
1	AA	1138	C	2.3
1	CA	888	C	2.3
34	BA	165	C	2.3
34	BA	999	C	2.3
34	BA	1039	C	2.3
34	BA	1137	C	2.3
34	BA	1336	C	2.3
34	DA	154	C	2.3
34	DA	1118	C	2.3
36	DC	69	HIS	2.3
36	DC	157	ILE	2.3
40	DG	18	TYR	2.3
42	BI	77	ILE	2.3
43	DJ	15	THR	2.3
43	DJ	23	ILE	2.3
43	DJ	98	ILE	2.3
47	BN	22	THR	2.3
57	BZ	231	TYR	2.3
57	BZ	385	THR	2.3
57	BZ	611	THR	2.3
34	DA	996	A	2.3
34	DA	1256	A	2.3
40	DG	29	LYS	2.3
40	DG	35	LYS	2.3
45	DL	115	LYS	2.3
57	DZ	478	LYS	2.3
1	CA	272(A)	U	2.3
1	CA	2109	U	2.3
3	CC	165	ARG	2.3
7	AG	153	ARG	2.3
10	CL	132	ARG	2.3
23	CZ	80	ARG	2.3
35	DB	157	ARG	2.3
36	DC	11	ARG	2.3
40	BG	102	ARG	2.3
40	DG	76	ARG	2.3
47	BN	31	ARG	2.3
49	BP	25	ARG	2.3

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Mol	Chain	Res	Type	RSRZ
52	DS	81	ARG	2.3
23	CZ	56	VAL	2.3
23	CZ	115	GLY	2.3
37	BD	130	GLY	2.3
37	BD	180	GLY	2.3
48	DO	89	GLY	2.3
42	BI	18	PHE	2.3
1	AA	2149	G	2.3
1	CA	1524	G	2.3
3	AC	32	GLU	2.3
7	CG	61	ALA	2.3
23	CZ	145	GLU	2.3
34	BA	1124	G	2.3
34	BA	1182	G	2.3
34	BA	1361	G	2.3
46	DM	35	GLU	2.3
46	DM	51	ALA	2.3
51	DR	24	ALA	2.3
57	BZ	651	GLU	2.3
57	DZ	412	ALA	2.3
57	DZ	651	GLU	2.3
57	BZ	98	MET	2.3
40	BG	16	LEU	2.3
53	BT	13	LEU	2.3
53	DT	90	GLN	2.3
10	CL	16	LYS	2.3
35	BB	127	ILE	2.3
35	BB	200	ILE	2.3
35	DB	16	HIS	2.3
53	DT	70	SER	2.3
57	DZ	248	LYS	2.3
35	BB	67	THR	2.3
54	BU	8	THR	2.3
14	AQ	60	ARG	2.3
35	DB	114	ARG	2.3
36	BC	131	ARG	2.3
38	DE	24	ARG	2.3
42	BI	104	ARG	2.3
42	BI	121	ARG	2.3
49	DP	81	ARG	2.3
53	BT	25	ARG	2.3
57	DZ	676	TYR	2.3

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Mol	Chain	Res	Type	RSRZ
1	AA	2156	A	2.3
1	CA	652(V)	C	2.3
8	CH	35	VAL	2.3
8	CH	107	VAL	2.3
10	AL	104	VAL	2.3
23	CZ	177	PRO	2.3
34	BA	1043	C	2.3
1	CA	2102	U	2.3
34	BA	1188	A	2.3
34	BA	1317	C	2.3
34	BA	1357	A	2.3
34	DA	983	A	2.3
34	DA	1203	C	2.3
34	DA	1196	U	2.3
10	CL	28	GLY	2.3
10	CL	97	GLY	2.3
36	DC	171	GLY	2.3
42	DI	39	GLY	2.3
44	BK	49	GLY	2.3
16	CS	29	PHE	2.3
42	DI	37	PHE	2.3
49	BP	80	PHE	2.3
7	CG	164	GLU	2.3
9	CK	131	MET	2.3
10	CL	43	ALA	2.3
10	CL	121	GLU	2.3
36	BC	61	ALA	2.3
36	DC	90	GLU	2.3
38	DE	81	GLU	2.3
41	DH	22	GLU	2.3
47	BN	10	ALA	2.3
53	DT	52	ALA	2.3
7	CG	126	ASP	2.3
8	CH	88	LEU	2.3
9	CK	68	LEU	2.3
11	CN	138	LEU	2.3
23	CZ	41	LEU	2.3
36	BC	101	LEU	2.3
49	BP	76	GLN	2.3
57	DZ	335	LEU	2.3
57	DZ	658	ASP	2.3
47	DN	58	LYS	2.3

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Mol	Chain	Res	Type	RSRZ
49	BP	27	LYS	2.3
57	BZ	591	LYS	2.3
1	AA	927	G	2.3
1	AA	1217	G	2.3
1	AA	2843	G	2.3
1	CA	1068	G	2.3
1	CA	2151	G	2.3
1	CA	2206	G	2.3
1	CA	2308	G	2.3
34	BA	971	G	2.3
34	BA	1117	G	2.3
34	DA	1026	G	2.3
34	DA	1047	G	2.3
34	DA	1053	G	2.3
56	DX	2	G	2.3
56	DX	19	G	2.3
3	AC	191	ARG	2.3
8	CH	42	ARG	2.3
43	DJ	66	ARG	2.3
57	DZ	97	SER	2.3
7	AG	160	VAL	2.3
10	AL	72	PRO	2.3
10	CL	60	TYR	2.3
57	BZ	212	TYR	2.3
57	DZ	231	TYR	2.3
36	BC	76	VAL	2.3
40	DG	105	VAL	2.3
57	DZ	642	VAL	2.3
7	AG	42	GLY	2.3
25	C1	84	GLY	2.3
50	DQ	54	GLY	2.3
57	BZ	447	GLY	2.3
1	AA	2124	U	2.3
1	AA	2131	U	2.3
1	CA	1097	U	2.3
34	BA	1307	U	2.3
1	AA	155	C	2.2
1	AA	2157	A	2.2
1	AA	2614	A	2.2
1	CA	1075	C	2.2
9	CK	82	PHE	2.2
10	CL	41	PHE	2.2

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Mol	Chain	Res	Type	RSRZ
34	BA	217	C	2.2
34	BA	1306	A	2.2
34	DA	219	C	2.2
34	DA	1027	C	2.2
34	DA	1037	C	2.2
10	CL	35	MET	2.2
37	BD	165	MET	2.2
10	AL	46	ALA	2.2
35	BB	37	ASN	2.2
37	DD	150	GLU	2.2
53	DT	49	ALA	2.2
9	AK	10	LEU	2.2
36	DC	32	LEU	2.2
47	DN	47	LEU	2.2
57	BZ	1	LEU	2.2
57	DZ	148	LEU	2.2
7	AG	182	LYS	2.2
7	CG	84	LYS	2.2
8	CH	27	LYS	2.2
35	DB	135	GLN	2.2
46	BM	27	LYS	2.2
57	BZ	506	GLN	2.2
57	DZ	684	GLN	2.2
57	DZ	195	ASP	2.2
35	DB	127	ILE	2.2
46	DM	84	ILE	2.2
31	C7	47	ARG	2.2
5	CE	56	PRO	2.2
17	CT	17	THR	2.2
28	C4	27	THR	2.2
36	BC	177	THR	2.2
36	DC	7	PRO	2.2
40	BG	24	THR	2.2
41	DH	3	THR	2.2
19	CV	72	VAL	2.2
36	DC	153	VAL	2.2
44	BK	14	VAL	2.2
44	DK	107	SER	2.2
47	DN	14	PRO	2.2
44	BK	25	TYR	2.2
45	DL	69	TYR	2.2
57	BZ	97	SER	2.2

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Mol	Chain	Res	Type	RSRZ
1	AA	2174	G	2.2
1	AA	2206	G	2.2
1	AA	2212	G	2.2
34	BA	139	G	2.2
34	BA	973	G	2.2
34	BA	1185	G	2.2
34	BA	1370	G	2.2
34	DA	306	G	2.2
34	DA	1003	G	2.2
34	DA	1138	G	2.2
34	DA	1370	G	2.2
56	BX	46	G	2.2
10	CL	83	GLY	2.2
24	C0	6	GLY	2.2
38	BE	22	GLY	2.2
42	DI	72	GLY	2.2
45	DL	103	GLY	2.2
47	DN	55	GLY	2.2
10	AL	134	MET	2.2
23	CZ	44	PHE	2.2
36	DC	10	PHE	2.2
1	AA	2202	U	2.2
1	CA	1105	U	2.2
34	BA	991	U	2.2
34	BA	1302	U	2.2
34	DA	1232	U	2.2
7	CG	69	ALA	2.2
42	DI	119	ALA	2.2
49	DP	54	GLU	2.2
57	DZ	18	ALA	2.2
10	CL	84	LEU	2.2
17	CT	114	LEU	2.2
1	CA	2163	C	2.2
3	CC	47	LYS	2.2
3	CC	206	LYS	2.2
7	CG	79	ASN	2.2
22	AY	92	ASN	2.2
34	BA	995	C	2.2
34	BA	1248	A	2.2
37	DD	157	LEU	2.2
52	DS	25	LYS	2.2
53	BT	74	LYS	2.2

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Mol	Chain	Res	Type	RSRZ
57	BZ	206	LEU	2.2
57	BZ	215	LYS	2.2
57	BZ	428	LEU	2.2
34	BA	1354	C	2.2
34	DA	89	C	2.2
34	DA	848	C	2.2
34	DA	999	C	2.2
34	DA	1137	C	2.2
34	DA	1147	C	2.2
37	BD	160	GLN	2.2
40	DG	42	ILE	2.2
40	DG	97	GLN	2.2
3	AC	16	ASP	2.2
3	AC	161	ARG	2.2
3	AC	195	ARG	2.2
24	C0	44	ARG	2.2
35	BB	178	ARG	2.2
35	DB	137	ARG	2.2
36	BC	6	HIS	2.2
57	DZ	182	ARG	2.2
57	DZ	628	ARG	2.2
9	CK	81	VAL	2.2
23	AZ	159	PRO	2.2
35	BB	24	TRP	2.2
41	DH	79	VAL	2.2
43	DJ	48	THR	2.2
57	BZ	488	THR	2.2
57	DZ	565	VAL	2.2
7	CG	12	TYR	2.2
40	DG	85	TYR	2.2
42	DI	92	TYR	2.2
46	DM	59	TYR	2.2
35	BB	100	GLY	2.2
35	DB	38	GLY	2.2
36	DC	80	GLY	2.2
37	DD	180	GLY	2.2
57	DZ	477	GLY	2.2
57	DZ	553	GLY	2.2
57	DZ	652	MET	2.2
40	BG	62	PHE	2.2
40	DG	26	PHE	2.2
57	BZ	525	PHE	2.2

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Mol	Chain	Res	Type	RSRZ
3	AC	178	LYS	2.2
7	CG	8	LYS	2.2
11	CN	118	LYS	2.2
1	CA	1089	G	2.2
1	CA	2141	G	2.2
9	CK	36	GLU	2.2
13	AP	99	LEU	2.2
36	BC	149	ALA	2.2
36	DC	199	LYS	2.2
36	DC	204	LEU	2.2
42	DI	79	LEU	2.2
42	DI	122	ALA	2.2
50	DQ	87	LYS	2.2
34	BA	1030(A)	G	2.2
34	BA	1220	G	2.2
34	BA	1290	G	2.2
34	DA	1087	G	2.2
34	DA	1186	G	2.2
34	DA	1221	G	2.2
46	DM	61	GLU	2.2
51	BR	60	ALA	2.2
53	BT	60	GLU	2.2
57	BZ	548	GLU	2.2
1	AA	1220	U	2.2
34	DA	202	U	2.2
34	DA	1532	U	2.2
9	CK	16	ASN	2.2
10	AL	33	ASN	2.2
10	CL	42	ASN	2.2
7	AG	136	ARG	2.2
7	CG	138	GLN	2.2
8	CH	6	ARG	2.2
8	CH	92	ILE	2.2
11	CN	115	ARG	2.2
26	C2	43	GLN	2.2
43	BJ	38	ILE	2.2
57	DZ	13	ARG	2.2
1	CA	653	A	2.2
34	BA	161	A	2.2
34	BA	975	A	2.2
34	BA	1280	A	2.2
34	BA	1287	A	2.2

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Mol	Chain	Res	Type	RSRZ
34	DA	965	A	2.2
34	DA	1151	A	2.2
34	DA	1213	A	2.2
1	CA	271(J)	C	2.2
1	CA	2139	C	2.2
34	BA	1149	C	2.2
34	BA	1297	C	2.2
34	DA	1045	C	2.2
34	DA	1321	C	2.2
43	DJ	56	HIS	2.2
23	CZ	140	ASP	2.2
36	DC	62	ASP	2.2
7	CG	142	PRO	2.2
36	DC	68	VAL	2.2
40	DG	93	PRO	2.2
46	DM	41	PRO	2.2
57	BZ	510	VAL	2.2
57	BZ	608	VAL	2.2
57	DZ	526	VAL	2.2
10	CL	100	THR	2.2
21	CX	1	MET	2.2
37	BD	87	GLY	2.2
37	DD	124	GLY	2.2
40	DG	73	MET	2.2
52	DS	26	GLY	2.2
57	DZ	495	GLY	2.2
57	DZ	513	LYS	2.2
57	DZ	583	LYS	2.2
3	CC	32	GLU	2.2
7	AG	46	ALA	2.2
8	AH	32	GLU	2.2
10	CL	32	ALA	2.2
10	CL	131	ALA	2.2
35	DB	186	ALA	2.2
38	BE	95	ALA	2.2
47	BN	5	ALA	2.2
51	DR	20	ALA	2.2
57	DZ	171	GLU	2.2
3	CC	53	ARG	2.2
16	CS	13	ARG	2.2
44	DK	126	ARG	2.2
45	DL	70	ILE	2.2

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Mol	Chain	Res	Type	RSRZ
48	DO	88	ARG	2.2
50	DQ	92	ARG	2.2
57	BZ	430	ARG	2.2
57	DZ	21	ILE	2.2
10	CL	103	GLN	2.2
23	CZ	34	ASN	2.2
26	C2	65	ASN	2.2
34	DA	1302	U	2.2
40	DG	11	GLN	2.2
41	DH	15	ASN	2.2
44	BK	117	ASN	2.2
57	DZ	421	GLN	2.2
1	AA	2176	G	2.2
1	CA	2155	G	2.2
34	BA	1031	G	2.2
34	BA	1042	G	2.2
34	BA	1291	G	2.2
34	DA	942	G	2.2
36	DC	31	HIS	2.2
1	AA	90	A	2.2
1	AA	1222	A	2.2
1	CA	1460	A	2.2
2	CB	120	A	2.2
7	CG	97	ASP	2.2
23	AZ	177	PRO	2.2
23	CZ	86	VAL	2.2
35	DB	79	ASP	2.2
37	DD	140	VAL	2.2
40	DG	9	VAL	2.2
42	BI	109	VAL	2.2
57	BZ	518	PRO	2.2
57	DZ	-59	PRO	2.2
57	DZ	116	PRO	2.2
1	AA	1087	C	2.2
1	CA	2177	C	2.2
34	BA	1113	C	2.2
34	BA	1369	C	2.2
34	DA	1018	C	2.2
34	DA	1192	C	2.2
7	CG	162	THR	2.2
10	AL	18	THR	2.2
28	C4	52	THR	2.2

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Mol	Chain	Res	Type	RSRZ
35	DB	168	THR	2.2
5	CE	71	GLY	2.2
8	AH	175	LYS	2.2
22	CY	4	LYS	2.2
35	BB	72	GLY	2.2
36	DC	185	GLY	2.2
37	BD	167	GLY	2.2
41	DH	113	SER	2.2
43	DJ	11	PHE	2.2
46	DM	23	TYR	2.2
47	DN	43	CYS	2.2
53	DT	54	LYS	2.2
57	BZ	544	LYS	2.2
52	BS	52	TYR	2.2
9	AK	26	LEU	2.2
10	AL	130	SER	2.2
52	BS	38	SER	2.2
52	DS	74	PHE	2.2
43	DJ	85	LEU	2.2
47	BN	39	LEU	2.2
57	BZ	567	LEU	2.2
9	AK	54	ALA	2.2
10	CL	61	ALA	2.2
35	BB	62	ALA	2.2
35	DB	143	GLU	2.2
37	BD	156	GLU	2.2
38	DE	94	ALA	2.2
39	BF	69	GLU	2.2
43	BJ	64	GLU	2.2
46	BM	2	ALA	2.2
46	BM	5	ALA	2.2
52	BS	43	GLU	2.2
28	C4	61	ARG	2.1
37	DD	139	ARG	2.1
40	BG	5	ARG	2.1
43	BJ	66	ARG	2.1
46	BM	99	ARG	2.1
47	DN	42	ILE	2.1
48	DO	77	ARG	2.1
49	BP	19	ILE	2.1
52	DS	29	ARG	2.1
53	BT	83	ARG	2.1

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Mol	Chain	Res	Type	RSRZ
57	BZ	11	ARG	2.1
57	DZ	450	ILE	2.1
7	AG	26	GLN	2.1
2	AB	1	U	2.1
57	DZ	625	ASN	2.1
3	AC	63	VAL	2.1
28	A4	35	VAL	2.1
57	BZ	604	PRO	2.1
57	BZ	647	VAL	2.1
57	DZ	276	VAL	2.1
9	CK	132	ASP	2.1
23	CZ	93	ASP	2.1
35	DB	83	MET	2.1
37	BD	144	ASP	2.1
44	DK	67	ASP	2.1
1	AA	1134	A	2.1
1	AA	1878	A	2.1
1	AA	2184	G	2.1
1	CA	655	A	2.1
1	CA	2631	G	2.1
9	AK	48	GLY	2.1
34	BA	1010	G	2.1
34	BA	1030(D)	A	2.1
34	BA	1138	G	2.1
34	BA	1491	G	2.1
34	DA	941	G	2.1
34	DA	1266	G	2.1
36	DC	4	LYS	2.1
50	BQ	100	LYS	2.1
57	DZ	449	THR	2.1
57	DZ	488	THR	2.1
57	DZ	662	LYS	2.1
34	DA	1324	A	2.1
51	DR	57	GLY	2.1
1	AA	1155	C	2.1
7	AG	139	LEU	2.1
9	AK	52	PHE	2.1
22	CY	90	LEU	2.1
24	C0	59	LEU	2.1
8	CH	164	TYR	2.1
9	AK	29	TYR	2.1
34	BA	100	C	2.1

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Mol	Chain	Res	Type	RSRZ
34	BA	436	C	2.1
34	BA	1254	C	2.1
34	DA	422	C	2.1
34	DA	1054	C	2.1
34	DA	1242	C	2.1
34	DA	1262	C	2.1
34	DA	1322	C	2.1
35	BB	163	PHE	2.1
44	BK	125	PHE	2.1
53	DT	13	LEU	2.1
57	DZ	646	PHE	2.1
35	DB	236	TYR	2.1
9	CK	126	ALA	2.1
10	AL	43	ALA	2.1
25	A1	2	SER	2.1
37	BD	152	SER	2.1
3	AC	28	ARG	2.1
3	CC	54	ARG	2.1
20	CW	30	GLU	2.1
21	AX	68	ARG	2.1
26	A2	11	GLU	2.1
36	BC	54	ARG	2.1
46	BM	108	ARG	2.1
53	BT	17	ARG	2.1
57	DZ	235	GLU	2.1
57	DZ	241	GLU	2.1
35	BB	185	ILE	2.1
35	BB	214	ILE	2.1
36	DC	5	ILE	2.1
57	DZ	451	ILE	2.1
51	BR	63	GLN	2.1
57	BZ	664	GLN	2.1
43	BJ	68	HIS	2.1
57	BZ	87	HIS	2.1
1	AA	1003	U	2.1
40	BG	31	MET	2.1
46	DM	10	PRO	2.1
47	DN	33	VAL	2.1
57	DZ	219	VAL	2.1
57	DZ	608	VAL	2.1
3	AC	31	LYS	2.1
10	CL	80	LYS	2.1

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Mol	Chain	Res	Type	RSRZ
16	CS	93	LYS	2.1
23	CZ	127	LYS	2.1
46	DM	65	LYS	2.1
53	DT	14	LYS	2.1
53	DT	74	LYS	2.1
57	BZ	423	LYS	2.1
57	DZ	10	LYS	2.1
57	DZ	75	LYS	2.1
23	CZ	179	ASP	2.1
57	DZ	598	ASP	2.1
7	AG	145	THR	2.1
7	CG	119	GLY	2.1
10	AL	135	GLY	2.1
10	CL	66	THR	2.1
38	BE	98	THR	2.1
53	DT	69	GLY	2.1
57	BZ	391	GLY	2.1
57	BZ	505	GLY	2.1
57	DZ	545	GLY	2.1
7	CG	125	PHE	2.1
7	CG	178	PHE	2.1
22	CY	31	LEU	2.1
35	DB	55	PHE	2.1
36	DC	43	LEU	2.1
42	DI	99	LEU	2.1
52	DS	15	LEU	2.1
57	DZ	174	PHE	2.1
1	AA	2195	A	2.1
3	AC	46	ALA	2.1
6	AF	143	ALA	2.1
10	AL	20	ALA	2.1
10	AL	128	ALA	2.1
10	CL	88	ALA	2.1
14	AQ	10	ARG	2.1
34	BA	152	A	2.1
34	DA	1001	A	2.1
34	DA	1179	A	2.1
35	DB	148	TYR	2.1
37	DD	209	ARG	2.1
40	DG	7	ALA	2.1
42	BI	83	ARG	2.1
46	DM	42	ALA	2.1

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Mol	Chain	Res	Type	RSRZ
54	DU	7	ARG	2.1
57	DZ	156	ARG	2.1
1	CA	2191	G	2.1
1	CA	2300	G	2.1
9	AK	8	GLU	2.1
9	CK	70	GLU	2.1
10	AL	106	GLU	2.1
23	CZ	84	GLU	2.1
28	C4	34	GLU	2.1
34	BA	77	G	2.1
34	BA	1030(C)	G	2.1
34	BA	1033	G	2.1
34	BA	1215	G	2.1
34	BA	1221	G	2.1
34	DA	1013	G	2.1
34	DA	1030(C)	G	2.1
34	DA	1184	G	2.1
34	DA	1193	G	2.1
35	DB	150	SER	2.1
38	DE	68	GLU	2.1
40	DG	49	ILE	2.1
43	DJ	61	GLU	2.1
46	BM	8	GLU	2.1
57	BZ	199	ILE	2.1
57	BZ	461	ILE	2.1
57	BZ	614	GLU	2.1
2	CB	88	C	2.1
34	BA	176	C	2.1
34	BA	1217	C	2.1
34	DA	1119	C	2.1
34	DA	1317	C	2.1
57	BZ	661	SER	2.1
57	BZ	630	GLN	2.1
10	AL	38	VAL	2.1
10	CL	38	VAL	2.1
36	BC	68	VAL	2.1
36	DC	109	PRO	2.1
40	DG	48	LYS	2.1
40	DG	89	MET	2.1
41	DH	19	VAL	2.1
46	BM	111	LYS	2.1
48	DO	2	PRO	2.1

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Mol	Chain	Res	Type	RSRZ
50	DQ	52	LYS	2.1
52	BS	85	LYS	2.1
52	DS	18	LYS	2.1
57	BZ	-59	PRO	2.1
57	BZ	513	LYS	2.1
57	DZ	-56	ASN	2.1
57	DZ	594	VAL	2.1
57	DZ	320	PRO	2.1
57	DZ	680	PRO	2.1
34	BA	204	U	2.1
34	BA	1125	U	2.1
34	BA	1247	U	2.1
9	CK	71	LEU	2.1
10	AL	105	LEU	2.1
5	CE	96	PHE	2.1
13	CP	47	ASP	2.1
19	CV	26	ASP	2.1
23	CZ	64	GLY	2.1
36	BC	17	ASP	2.1
36	BC	80	GLY	2.1
36	BC	96	GLY	2.1
53	BT	24	LEU	2.1
57	BZ	166	LEU	2.1
57	DZ	253	LEU	2.1
42	BI	103	THR	2.1
3	AC	211	ARG	2.1
3	CC	224	ARG	2.1
36	BC	167	TRP	2.1
37	BD	115	ARG	2.1
37	BD	122	ARG	2.1
44	BK	126	ARG	2.1
49	DP	59	TRP	2.1
52	BS	34	TRP	2.1
23	CZ	51	ALA	2.1
36	DC	39	ILE	2.1
37	BD	158	ILE	2.1
37	DD	126	ILE	2.1
40	DG	147	ALA	2.1
8	CH	34	GLU	2.1
8	CH	86	GLU	2.1
23	AZ	162	GLU	2.1
28	C4	25	TYR	2.1

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Mol	Chain	Res	Type	RSRZ
39	DF	95	GLU	2.1
43	BJ	23	ILE	2.1
57	BZ	205	TYR	2.1
1	AA	1119	A	2.1
1	CA	1070	A	2.1
34	BA	1041	A	2.1
34	BA	1044	A	2.1
34	BA	1251	A	2.1
34	BA	1288	A	2.1
34	DA	1289	A	2.1
37	BD	137	SER	2.1
56	DX	76	A	2.1
35	DB	95	GLN	2.1
43	DJ	33	GLN	2.1
1	AA	1631	C	2.1
8	CH	65	HIS	2.1
1	CA	1037	G	2.1
1	CA	1414	G	2.1
10	AL	2	LYS	2.1
13	AP	1	MET	2.1
34	BA	216	G	2.1
34	BA	1106	G	2.1
34	BA	1335	C	2.1
43	DJ	62	HIS	2.1
34	DA	951	G	2.1
34	DA	1154	G	2.1
34	DA	1253	G	2.1
35	BB	15	VAL	2.1
36	BC	173	VAL	2.1
36	DC	151	VAL	2.1
53	BT	38	LYS	2.1
8	CH	8	PRO	2.1
48	BO	75	PRO	2.1
57	BZ	131	PRO	2.1
57	DZ	518	PRO	2.1
8	CH	67	LEU	2.1
23	CZ	183	LEU	2.1
35	DB	98	LEU	2.1
48	DO	81	LEU	2.1
51	DR	58	LEU	2.1
1	CA	614(A)	U	2.1
1	CA	1082	U	2.1

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Mol	Chain	Res	Type	RSRZ
12	CO	110	GLY	2.1
35	BB	122	PHE	2.1
37	DD	183	GLY	2.1
45	DL	121	GLY	2.1
54	BU	19	GLY	2.1
55	BV	19	U	2.1
3	AC	60	ARG	2.1
3	CC	161	ARG	2.1
8	CH	68	THR	2.1
36	DC	83	ARG	2.1
40	BG	32	ARG	2.1
40	DG	10	ARG	2.1
42	DI	121	ARG	2.1
47	DN	12	ARG	2.1
50	DQ	13	ASP	2.1
52	DS	12	ASP	2.1
54	BU	22	ARG	2.1
7	CG	29	TRP	2.1
7	CG	46	ALA	2.1
13	CP	140	ALA	2.1
35	DB	200	ILE	2.1
36	BC	24	ALA	2.1
36	BC	50	ALA	2.1
42	DI	94	ALA	2.1
44	BK	74	ALA	2.1
53	DT	41	ILE	2.1
57	BZ	549	ALA	2.1
57	BZ	640	ALA	2.1
57	DZ	474	ALA	2.1
37	BD	200	GLU	2.1
46	DM	50	GLU	2.1
52	DS	73	GLU	2.1
21	AX	69	TYR	2.1
21	CX	69	TYR	2.1
23	CZ	8	TYR	2.1
28	C4	32	TYR	2.1
8	CH	38	SER	2.0
10	AL	48	MET	2.0
28	C4	8	LYS	2.0
35	BB	132	LYS	2.0
40	DG	51	GLN	2.0
42	BI	70	LYS	2.0

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Mol	Chain	Res	Type	RSRZ
44	DK	62	GLN	2.0
46	BM	36	LYS	2.0
54	BU	3	LYS	2.0
57	DZ	164	MET	2.0
57	DZ	471	LYS	2.0
3	CC	173	HIS	2.0
34	DA	968	A	2.0
34	DA	1152	A	2.0
43	BJ	49	VAL	2.0
43	DJ	44	VAL	2.0
8	CH	12	PRO	2.0
8	CH	118	PRO	2.0
40	DG	14	PRO	2.0
41	DH	57	PRO	2.0
45	BL	48	PRO	2.0
49	BP	66	PRO	2.0
57	DZ	554	PRO	2.0
1	AA	932	C	2.0
1	AA	2161	C	2.0
1	CA	1092	C	2.0
7	CG	132	ASN	2.0
7	CG	175	LEU	2.0
8	CH	98	LEU	2.0
34	BA	435	C	2.0
34	DA	962	C	2.0
34	DA	1145	C	2.0
42	DI	23	ASN	2.0
50	DQ	98	LEU	2.0
56	BX	69	C	2.0
1	AA	2175	G	2.0
1	AA	2227	G	2.0
3	CC	170	GLY	2.0
10	CL	125	ARG	2.0
11	CN	61	ARG	2.0
28	A4	48	ARG	2.0
28	C4	59	PHE	2.0
34	BA	1023	G	2.0
34	BA	1026	G	2.0
34	BA	1193	G	2.0
34	BA	1216	G	2.0
34	DA	993	G	2.0
34	DA	1206	G	2.0

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Mol	Chain	Res	Type	RSRZ
34	DA	1255	G	2.0
34	DA	1276	G	2.0
35	BB	226	ARG	2.0
42	BI	93	ARG	2.0
47	DN	23	ARG	2.0
48	DO	18	PHE	2.0
56	DX	70	G	2.0
57	BZ	522	GLY	2.0
1	CA	999	U	2.0
1	CA	1101	U	2.0
23	CZ	146	ILE	2.0
34	BA	90	U	2.0
34	DA	1049	U	2.0
42	BI	7	THR	2.0
57	BZ	663	THR	2.0
16	CS	79	ALA	2.0
35	DB	237	ALA	2.0
57	DZ	353	ALA	2.0
10	AL	94	GLU	2.0
10	CL	56	GLU	2.0
36	BC	44	GLU	2.0
57	BZ	-26	GLU	2.0
57	DZ	524	GLU	2.0
10	AL	3	LYS	2.0
13	CP	110	TYR	2.0
19	CV	85	LYS	2.0
28	A4	28	LYS	2.0
57	BZ	248	LYS	2.0
57	DZ	591	LYS	2.0
23	CZ	1	MET	2.0
8	CH	114	VAL	2.0
9	CK	95	GLN	2.0
22	CY	42	VAL	2.0
23	CZ	149	SER	2.0
27	C3	56	VAL	2.0
35	DB	224	GLN	2.0
36	DC	104	GLN	2.0
42	DI	31	GLN	2.0
45	DL	55	VAL	2.0
50	BQ	35	VAL	2.0
53	DT	11	SER	2.0
57	BZ	219	VAL	2.0

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Mol	Chain	Res	Type	RSRZ
5	CE	62	PRO	2.0
11	CN	11	PRO	2.0
35	BB	194	PRO	2.0
57	BZ	599	PRO	2.0
1	CA	1111	A	2.0
1	CA	1445	A	2.0
1	CA	2311	A	2.0
7	CG	106	LEU	2.0
34	DA	1332	A	2.0
36	DC	42	LEU	2.0
57	DZ	146	LEU	2.0
8	CH	147	ASN	2.0
10	AL	98	ARG	2.0
24	C0	11	ARG	2.0
36	BC	127	ARG	2.0
36	BC	132	ARG	2.0
37	BD	73	ARG	2.0
41	DH	75	ARG	2.0
46	BM	14	ARG	2.0
57	DZ	247	ARG	2.0
3	AC	5	GLY	2.0
6	AF	131	GLY	2.0
9	CK	114	GLY	2.0
18	CU	106	PHE	2.0
35	BB	105	PHE	2.0
57	BZ	653	PHE	2.0
57	DZ	347	GLY	2.0
1	AA	935	C	2.0
1	CA	1038	C	2.0
1	CA	2142	C	2.0
1	CA	2313	C	2.0
7	CG	63	ILE	2.0
10	CL	59	ILE	2.0
34	BA	1325	C	2.0
34	DA	1019	C	2.0
34	DA	1153	C	2.0
34	DA	1243	C	2.0
36	BC	77	ILE	2.0
36	BC	124	ILE	2.0
52	BS	49	ILE	2.0
57	BZ	498	ILE	2.0
37	DD	127	THR	2.0

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Mol	Chain	Res	Type	RSRZ
53	DT	12	ALA	2.0
57	BZ	-12	ALA	2.0
57	BZ	650	ALA	2.0
1	AA	1218	G	2.0
1	CA	11	G	2.0
7	CG	48	GLU	2.0
12	CO	108	GLU	2.0
28	A4	53	GLU	2.0
34	BA	1211	U	2.0
34	DA	84	U	2.0
34	DA	1088	G	2.0
34	DA	1216	G	2.0
34	DA	1271	G	2.0
34	DA	1355	G	2.0
35	DB	12	GLU	2.0
40	DG	139	GLU	2.0
40	DG	140	ASP	2.0
57	BZ	252	ASP	2.0
56	DX	63	G	2.0
36	DC	18	TRP	2.0
57	DZ	617	MET	2.0
36	BC	48	TYR	2.0
57	DZ	35	TYR	2.0
9	AK	122	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
56	5MC	DX	32	21/22	0.83	0.14	86,86,86,86	0
56	PSU	DX	55	20/21	0.84	0.13	95,95,95,95	0
56	5MU	DX	54	21/22	0.88	0.13	108,108,108,108	0
56	4SU	DX	8	20/21	0.89	0.12	96,96,96,96	0
56	5MU	BX	54	21/22	0.90	0.13	85,85,85,85	0
56	PSU	BX	55	20/21	0.90	0.10	74,74,74,74	0
56	5MC	BX	32	21/22	0.93	0.13	65,65,65,65	0
56	4SU	BX	8	20/21	0.94	0.10	70,70,70,70	1

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
58	MG	DA	1624	1/1	0.28	0.21	115,115,115,115	0
58	MG	DZ	701	1/1	0.29	0.19	112,112,112,112	0
58	MG	CA	3140	1/1	0.39	0.34	122,122,122,122	0
58	MG	DA	1753	1/1	0.43	0.21	83,83,83,83	0
58	MG	CA	3296	1/1	0.53	0.19	80,80,80,80	0
58	MG	BA	3025	1/1	0.53	0.20	88,88,88,88	0
58	MG	BA	3169	1/1	0.55	0.26	130,130,130,130	0
58	MG	CA	3494	1/1	0.55	0.27	88,88,88,88	0
58	MG	CB	3013	1/1	0.55	0.21	96,96,96,96	0
58	MG	CA	3002	1/1	0.56	0.37	112,112,112,112	0
58	MG	BA	3203	1/1	0.56	0.20	83,83,83,83	0
58	MG	CA	3238	1/1	0.56	0.19	85,85,85,85	0
58	MG	CA	3209	1/1	0.57	0.19	82,82,82,82	0
58	MG	CA	3509	1/1	0.58	0.14	96,96,96,96	0
58	MG	DA	1752	1/1	0.58	0.20	79,79,79,79	0
58	MG	AA	3026	1/1	0.58	0.14	83,83,83,83	0
58	MG	DA	1602	1/1	0.58	0.31	95,95,95,95	0
58	MG	BA	3035	1/1	0.59	0.38	99,99,99,99	0
58	MG	BA	3052	1/1	0.59	0.29	102,102,102,102	0
58	MG	BA	3106	1/1	0.59	0.19	93,93,93,93	0
58	MG	BA	3155	1/1	0.60	0.09	96,96,96,96	0
58	MG	CA	3553	1/1	0.62	0.15	88,88,88,88	0
58	MG	DA	1734	1/1	0.64	0.13	78,78,78,78	0
58	MG	AA	3614	1/1	0.64	0.16	103,103,103,103	0
58	MG	CA	3072	1/1	0.64	0.38	93,93,93,93	0
58	MG	DK	5001	1/1	0.64	0.15	101,101,101,101	0
58	MG	DA	1729	1/1	0.64	0.36	79,79,79,79	0
58	MG	BA	3173	1/1	0.66	0.34	113,113,113,113	0
58	MG	CA	3081	1/1	0.66	0.32	85,85,85,85	0
58	MG	DA	1714	1/1	0.66	0.12	78,78,78,78	0
58	MG	BA	3017	1/1	0.67	0.16	133,133,133,133	0
58	MG	DE	202	1/1	0.67	0.17	93,93,93,93	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	DA	1690	1/1	0.67	0.15	85,85,85,85	0
58	MG	CA	3576	1/1	0.67	0.11	71,71,71,71	0
58	MG	BA	3103	1/1	0.68	0.25	85,85,85,85	0
58	MG	CA	3149	1/1	0.68	0.20	63,63,63,63	0
58	MG	CA	3046	1/1	0.68	0.31	113,113,113,113	0
58	MG	BL	3001	1/1	0.69	0.33	80,80,80,80	0
58	MG	CA	3141	1/1	0.69	0.24	97,97,97,97	0
58	MG	CA	3592	1/1	0.69	0.14	93,93,93,93	0
58	MG	AA	3784	1/1	0.69	0.29	73,73,73,73	0
58	MG	CA	3008	1/1	0.69	0.39	98,98,98,98	0
58	MG	AA	3679	1/1	0.70	0.12	64,64,64,64	0
58	MG	BA	3110	1/1	0.70	0.29	103,103,103,103	0
58	MG	CA	3482	1/1	0.70	0.10	89,89,89,89	0
58	MG	BA	3088	1/1	0.70	0.22	68,68,68,68	0
58	MG	AA	3752	1/1	0.70	0.15	64,64,64,64	1
58	MG	CA	3292	1/1	0.71	0.29	75,75,75,75	0
58	MG	BA	3048	1/1	0.71	0.11	75,75,75,75	0
58	MG	CA	3297	1/1	0.72	0.19	83,83,83,83	0
58	MG	CA	3305	1/1	0.72	0.13	90,90,90,90	0
58	MG	CA	3645	1/1	0.72	0.39	79,79,79,79	0
58	MG	BA	3140	1/1	0.73	0.14	91,91,91,91	0
58	MG	DA	1659	1/1	0.73	0.15	87,87,87,87	0
58	MG	AA	3690	1/1	0.73	0.16	69,69,69,69	0
58	MG	AA	3745	1/1	0.73	0.18	84,84,84,84	0
58	MG	AA	3611	1/1	0.73	0.12	55,55,55,55	0
58	MG	BA	3069	1/1	0.73	0.21	82,82,82,82	0
58	MG	CA	3619	1/1	0.73	0.18	79,79,79,79	0
58	MG	CA	3623	1/1	0.73	0.17	69,69,69,69	0
58	MG	CA	3114	1/1	0.73	0.26	94,94,94,94	0
58	MG	BA	3119	1/1	0.73	0.15	79,79,79,79	0
58	MG	BX	107	1/1	0.73	0.10	67,67,67,67	0
58	MG	CA	3541	1/1	0.74	0.24	71,71,71,71	0
58	MG	CA	3067	1/1	0.74	0.30	83,83,83,83	0
58	MG	BA	3160	1/1	0.74	0.14	61,61,61,61	0
58	MG	BA	3117	1/1	0.74	0.12	65,65,65,65	0
58	MG	AA	3248	1/1	0.74	0.32	72,72,72,72	0
58	MG	AA	3711	1/1	0.75	0.22	74,74,74,74	0
58	MG	AA	3274	1/1	0.75	0.22	88,88,88,88	0
58	MG	BA	3033	1/1	0.75	0.20	52,52,52,52	0
58	MG	CA	3057	1/1	0.75	0.14	84,84,84,84	0
58	MG	DZ	702	1/1	0.75	0.16	61,61,61,61	0
58	MG	CA	3587	1/1	0.76	0.18	81,81,81,81	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	CA	3628	1/1	0.76	0.23	76,76,76,76	0
58	MG	CA	3510	1/1	0.76	0.15	93,93,93,93	0
58	MG	CA	3648	1/1	0.76	0.14	77,77,77,77	0
58	MG	CA	3616	1/1	0.76	0.20	71,71,71,71	0
58	MG	BA	3059	1/1	0.76	0.29	76,76,76,76	0
58	MG	DA	1675	1/1	0.77	0.09	77,77,77,77	0
58	MG	BA	3081	1/1	0.77	0.36	82,82,82,82	0
58	MG	CA	3555	1/1	0.77	0.14	80,80,80,80	0
58	MG	CA	3031	1/1	0.77	0.16	74,74,74,74	0
58	MG	CA	3106	1/1	0.77	0.11	79,79,79,79	0
58	MG	CB	3006	1/1	0.77	0.12	82,82,82,82	0
58	MG	AA	3017	1/1	0.77	0.22	78,78,78,78	0
58	MG	DA	1764	1/1	0.77	0.20	72,72,72,72	0
58	MG	CA	3596	1/1	0.77	0.17	77,77,77,77	0
58	MG	BA	3179	1/1	0.77	0.18	78,78,78,78	0
58	MG	DA	1635	1/1	0.77	0.14	89,89,89,89	0
58	MG	BA	3196	1/1	0.77	0.18	84,84,84,84	0
58	MG	BA	3112	1/1	0.78	0.29	70,70,70,70	0
58	MG	CA	3527	1/1	0.78	0.15	81,81,81,81	0
58	MG	CA	3071	1/1	0.78	0.41	84,84,84,84	0
58	MG	DA	1749	1/1	0.78	0.20	80,80,80,80	0
58	MG	DA	1615	1/1	0.78	0.28	85,85,85,85	0
58	MG	CA	3545	1/1	0.78	0.24	61,61,61,61	0
58	MG	BA	3158	1/1	0.78	0.19	63,63,63,63	0
58	MG	AA	3246	1/1	0.78	0.34	98,98,98,98	0
58	MG	DJ	5001	1/1	0.78	0.15	105,105,105,105	0
58	MG	AA	3633	1/1	0.78	0.24	75,75,75,75	0
58	MG	AA	3270	1/1	0.78	0.20	80,80,80,80	0
58	MG	DA	1704	1/1	0.78	0.26	128,128,128,128	0
58	MG	CA	3124	1/1	0.79	0.29	87,87,87,87	0
58	MG	CA	3034	1/1	0.79	0.22	100,100,100,100	0
58	MG	CA	3043	1/1	0.79	0.35	101,101,101,101	0
58	MG	BA	3187	1/1	0.79	0.11	59,59,59,59	0
58	MG	CA	3647	1/1	0.79	0.28	82,82,82,82	0
58	MG	BA	3095	1/1	0.79	0.14	99,99,99,99	0
58	MG	AZ	301	1/1	0.79	0.19	98,98,98,98	0
58	MG	CA	3275	1/1	0.79	0.17	67,67,67,67	0
58	MG	A4	502	1/1	0.79	0.14	120,120,120,120	0
58	MG	AA	3680	1/1	0.79	0.14	58,58,58,58	0
58	MG	AA	3196	1/1	0.79	0.16	50,50,50,50	0
58	MG	AA	3778	1/1	0.79	0.13	55,55,55,55	0
58	MG	CA	3455	1/1	0.79	0.13	78,78,78,78	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	AA	3201	1/1	0.79	0.19	91,91,91,91	0
58	MG	DA	1673	1/1	0.80	0.15	61,61,61,61	0
58	MG	BA	3188	1/1	0.80	0.11	86,86,86,86	0
58	MG	DA	1685	1/1	0.80	0.13	52,52,52,52	0
58	MG	DA	1686	1/1	0.80	0.16	101,101,101,101	0
58	MG	AA	3109	1/1	0.80	0.50	124,124,124,124	0
58	MG	BA	3030	1/1	0.80	0.18	62,62,62,62	0
58	MG	BA	3092	1/1	0.80	0.22	86,86,86,86	0
58	MG	CB	3001	1/1	0.80	0.20	96,96,96,96	0
58	MG	CA	3094	1/1	0.80	0.41	83,83,83,83	0
58	MG	CA	3074	1/1	0.81	0.21	91,91,91,91	0
58	MG	BA	3071	1/1	0.81	0.28	93,93,93,93	0
58	MG	BA	3199	1/1	0.81	0.12	68,68,68,68	0
58	MG	CA	3583	1/1	0.81	0.15	78,78,78,78	0
58	MG	BA	3177	1/1	0.81	0.14	73,73,73,73	0
58	MG	AA	3354	1/1	0.81	0.18	58,58,58,58	0
58	MG	CA	3377	1/1	0.81	0.10	64,64,64,64	0
58	MG	CA	3049	1/1	0.81	0.11	78,78,78,78	0
58	MG	CA	3461	1/1	0.81	0.21	107,107,107,107	0
58	MG	DA	1707	1/1	0.81	0.21	69,69,69,69	0
58	MG	BA	3182	1/1	0.81	0.13	80,80,80,80	0
58	MG	CA	3490	1/1	0.81	0.30	78,78,78,78	0
58	MG	DA	1733	1/1	0.81	0.23	81,81,81,81	0
58	MG	CA	3059	1/1	0.81	0.26	76,76,76,76	0
58	MG	BX	108	1/1	0.81	0.13	78,78,78,78	0
58	MG	CA	3154	1/1	0.81	0.17	77,77,77,77	0
58	MG	CA	3650	1/1	0.81	0.11	67,67,67,67	0
58	MG	AA	3122	1/1	0.81	0.26	67,67,67,67	0
58	MG	CA	3535	1/1	0.81	0.16	79,79,79,79	0
58	MG	CB	3008	1/1	0.81	0.09	58,58,58,58	0
58	MG	CA	3539	1/1	0.81	0.22	77,77,77,77	0
58	MG	BA	3007	1/1	0.81	0.21	75,75,75,75	0
58	MG	CA	3241	1/1	0.81	0.22	74,74,74,74	0
58	MG	BN	503	1/1	0.82	0.24	66,66,66,66	0
58	MG	CA	3239	1/1	0.82	0.16	74,74,74,74	0
58	MG	AA	3442	1/1	0.82	0.20	64,64,64,64	0
58	MG	BA	3002	1/1	0.82	0.13	91,91,91,91	0
58	MG	DA	1641	1/1	0.82	0.10	79,79,79,79	0
58	MG	DA	1656	1/1	0.82	0.20	91,91,91,91	0
58	MG	BA	3054	1/1	0.82	0.15	77,77,77,77	0
58	MG	DA	1670	1/1	0.82	0.17	81,81,81,81	0
58	MG	AA	3237	1/1	0.82	0.18	63,63,63,63	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	CA	3100	1/1	0.82	0.11	90,90,90,90	0
58	MG	BA	3060	1/1	0.82	0.24	82,82,82,82	0
58	MG	CA	3315	1/1	0.82	0.26	76,76,76,76	0
58	MG	CA	3324	1/1	0.82	0.12	66,66,66,66	0
58	MG	DA	1695	1/1	0.82	0.17	88,88,88,88	0
58	MG	CA	3610	1/1	0.82	0.24	98,98,98,98	0
58	MG	AA	3775	1/1	0.82	0.14	45,45,45,45	0
58	MG	CA	3119	1/1	0.82	0.08	55,55,55,55	0
58	MG	AA	3689	1/1	0.82	0.12	55,55,55,55	0
58	MG	CA	3624	1/1	0.82	0.16	72,72,72,72	0
58	MG	CA	3481	1/1	0.82	0.16	55,55,55,55	0
58	MG	DA	1744	1/1	0.82	0.27	90,90,90,90	0
58	MG	CA	3644	1/1	0.82	0.13	66,66,66,66	0
58	MG	AA	3641	1/1	0.82	0.39	76,76,76,76	0
58	MG	AN	3001	1/1	0.82	0.28	83,83,83,83	0
58	MG	CA	3143	1/1	0.82	0.15	69,69,69,69	0
58	MG	CA	3500	1/1	0.82	0.11	82,82,82,82	0
58	MG	BA	3090	1/1	0.82	0.18	90,90,90,90	0
58	MG	AA	3658	1/1	0.82	0.15	60,60,60,60	0
58	MG	BL	3003	1/1	0.82	0.12	79,79,79,79	0
58	MG	CA	3225	1/1	0.82	0.27	79,79,79,79	0
58	MG	CA	3200	1/1	0.83	0.21	72,72,72,72	0
58	MG	CA	3351	1/1	0.83	0.10	83,83,83,83	0
58	MG	AA	3099	1/1	0.83	0.10	57,57,57,57	0
58	MG	CA	3429	1/1	0.83	0.21	62,62,62,62	1
58	MG	CA	3216	1/1	0.83	0.17	74,74,74,74	0
58	MG	DA	1699	1/1	0.83	0.21	123,123,123,123	0
58	MG	CA	3663	1/1	0.83	0.16	73,73,73,73	0
58	MG	AA	3364	1/1	0.83	0.25	79,79,79,79	0
58	MG	CA	3475	1/1	0.83	0.25	75,75,75,75	0
58	MG	A8	5001	1/1	0.83	0.21	57,57,57,57	0
58	MG	BA	3093	1/1	0.83	0.16	65,65,65,65	0
58	MG	AA	3616	1/1	0.83	0.12	37,37,37,37	1
58	MG	DA	1603	1/1	0.83	0.12	81,81,81,81	0
58	MG	BA	3055	1/1	0.83	0.10	54,54,54,54	0
58	MG	AA	3729	1/1	0.83	0.15	58,58,58,58	0
58	MG	AA	3806	1/1	0.83	0.12	60,60,60,60	0
58	MG	AB	3014	1/1	0.83	0.14	67,67,67,67	0
58	MG	AB	3017	1/1	0.83	0.15	76,76,76,76	0
58	MG	CA	3627	1/1	0.83	0.25	101,101,101,101	0
58	MG	AA	3095	1/1	0.83	0.51	110,110,110,110	0
58	MG	DA	1672	1/1	0.83	0.25	100,100,100,100	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	CA	3638	1/1	0.83	0.18	78,78,78,78	0
58	MG	AA	3461	1/1	0.84	0.14	64,64,64,64	0
58	MG	AA	3476	1/1	0.84	0.16	68,68,68,68	0
58	MG	DA	1642	1/1	0.84	0.13	76,76,76,76	0
58	MG	BA	3200	1/1	0.84	0.10	63,63,63,63	0
58	MG	CA	3379	1/1	0.84	0.18	86,86,86,86	0
58	MG	AA	3608	1/1	0.84	0.09	29,29,29,29	0
58	MG	CA	3173	1/1	0.84	0.27	81,81,81,81	0
58	MG	CA	3195	1/1	0.84	0.21	69,69,69,69	0
58	MG	CA	3466	1/1	0.84	0.14	65,65,65,65	0
58	MG	AA	3794	1/1	0.84	0.26	68,68,68,68	0
58	MG	AA	3803	1/1	0.84	0.11	62,62,62,62	0
58	MG	AA	3652	1/1	0.84	0.12	74,74,74,74	0
58	MG	CA	3486	1/1	0.84	0.25	81,81,81,81	0
58	MG	AA	3727	1/1	0.84	0.14	66,66,66,66	0
58	MG	CA	3086	1/1	0.84	0.15	63,63,63,63	0
58	MG	AA	3344	1/1	0.84	0.17	85,85,85,85	0
58	MG	DA	1709	1/1	0.84	0.10	44,44,44,44	0
58	MG	AB	3023	1/1	0.84	0.28	74,74,74,74	0
58	MG	CA	3242	1/1	0.84	0.11	63,63,63,63	0
58	MG	DA	1732	1/1	0.84	0.10	80,80,80,80	0
58	MG	CA	3245	1/1	0.84	0.23	77,77,77,77	0
58	MG	CA	3274	1/1	0.84	0.21	73,73,73,73	0
58	MG	DA	1742	1/1	0.84	0.12	77,77,77,77	0
58	MG	AD	308	1/1	0.84	0.13	70,70,70,70	0
58	MG	AA	3664	1/1	0.84	0.14	55,55,55,55	0
58	MG	CA	3116	1/1	0.84	0.17	75,75,75,75	0
58	MG	CE	307	1/1	0.84	0.09	65,65,65,65	0
58	MG	DA	1761	1/1	0.84	0.11	75,75,75,75	0
58	MG	AA	3100	1/1	0.84	0.13	60,60,60,60	0
58	MG	AA	3766	1/1	0.84	0.10	70,70,70,70	0
58	MG	DA	1607	1/1	0.84	0.34	82,82,82,82	0
58	MG	BA	3195	1/1	0.84	0.16	73,73,73,73	0
58	MG	CA	3577	1/1	0.84	0.14	43,43,43,43	1
58	MG	DA	1629	1/1	0.84	0.16	73,73,73,73	0
58	MG	AA	3640	1/1	0.85	0.12	74,74,74,74	0
58	MG	CA	3537	1/1	0.85	0.20	67,67,67,67	0
58	MG	CA	3077	1/1	0.85	0.12	81,81,81,81	0
58	MG	DA	1628	1/1	0.85	0.07	69,69,69,69	0
58	MG	AA	3310	1/1	0.85	0.10	57,57,57,57	0
58	MG	DA	1634	1/1	0.85	0.17	71,71,71,71	0
58	MG	CA	3543	1/1	0.85	0.11	70,70,70,70	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	BA	3154	1/1	0.85	0.12	94,94,94,94	0
58	MG	CA	3255	1/1	0.85	0.18	95,95,95,95	0
58	MG	BA	3082	1/1	0.85	0.15	69,69,69,69	0
58	MG	CA	3099	1/1	0.85	0.27	82,82,82,82	0
58	MG	BV	101	1/1	0.85	0.20	110,110,110,110	0
58	MG	BX	101	1/1	0.85	0.09	78,78,78,78	0
58	MG	AA	3683	1/1	0.85	0.23	65,65,65,65	0
58	MG	CA	3588	1/1	0.85	0.13	68,68,68,68	0
58	MG	DA	1683	1/1	0.85	0.27	70,70,70,70	0
58	MG	AA	3491	1/1	0.85	0.13	33,33,33,33	0
58	MG	CA	3118	1/1	0.85	0.19	67,67,67,67	0
58	MG	BA	3163	1/1	0.85	0.12	52,52,52,52	0
58	MG	CA	3611	1/1	0.85	0.17	58,58,58,58	0
58	MG	CA	3337	1/1	0.85	0.19	68,68,68,68	0
58	MG	AA	3762	1/1	0.85	0.10	58,58,58,58	0
58	MG	DA	1705	1/1	0.85	0.20	86,86,86,86	0
58	MG	AB	3001	1/1	0.85	0.32	85,85,85,85	0
58	MG	AB	3004	1/1	0.85	0.26	87,87,87,87	0
58	MG	CA	3412	1/1	0.85	0.12	58,58,58,58	0
58	MG	DA	1728	1/1	0.85	0.16	85,85,85,85	0
58	MG	BA	3096	1/1	0.85	0.12	64,64,64,64	0
58	MG	CA	3437	1/1	0.85	0.14	74,74,74,74	0
58	MG	BA	3101	1/1	0.85	0.21	60,60,60,60	0
58	MG	CA	3151	1/1	0.85	0.12	54,54,54,54	0
58	MG	BA	3006	1/1	0.85	0.12	71,71,71,71	0
58	MG	CA	3156	1/1	0.85	0.11	84,84,84,84	0
58	MG	BA	3104	1/1	0.85	0.16	76,76,76,76	0
58	MG	DA	1751	1/1	0.85	0.14	69,69,69,69	0
58	MG	CA	3181	1/1	0.85	0.31	108,108,108,108	0
58	MG	AA	3539	1/1	0.85	0.22	63,63,63,63	0
58	MG	CA	3060	1/1	0.85	0.16	60,60,60,60	0
58	MG	BA	3010	1/1	0.85	0.14	68,68,68,68	0
58	MG	CA	3210	1/1	0.85	0.32	93,93,93,93	0
58	MG	CA	3068	1/1	0.85	0.20	72,72,72,72	0
58	MG	CF	301	1/1	0.85	0.18	62,62,62,62	0
58	MG	BA	3062	1/1	0.85	0.48	81,81,81,81	0
58	MG	AA	3106	1/1	0.85	0.14	80,80,80,80	0
58	MG	DA	1620	1/1	0.86	0.10	69,69,69,69	0
58	MG	CA	3246	1/1	0.86	0.33	77,77,77,77	0
58	MG	AA	3264	1/1	0.86	0.17	77,77,77,77	0
58	MG	CA	3004	1/1	0.86	0.28	64,64,64,64	0
58	MG	AA	3001	1/1	0.86	0.10	36,36,36,36	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	CA	3546	1/1	0.86	0.07	79,79,79,79	0
58	MG	BA	3039	1/1	0.86	0.30	78,78,78,78	0
58	MG	BA	3176	1/1	0.86	0.10	61,61,61,61	0
58	MG	CA	3563	1/1	0.86	0.16	92,92,92,92	0
58	MG	CA	3042	1/1	0.86	0.43	96,96,96,96	0
58	MG	DA	1668	1/1	0.86	0.15	82,82,82,82	0
58	MG	CA	3129	1/1	0.86	0.14	69,69,69,69	0
58	MG	CA	3579	1/1	0.86	0.12	83,83,83,83	0
58	MG	BA	3045	1/1	0.86	0.21	75,75,75,75	0
58	MG	AA	3113	1/1	0.86	0.31	97,97,97,97	0
58	MG	CA	3048	1/1	0.86	0.23	85,85,85,85	0
58	MG	DA	1684	1/1	0.86	0.19	63,63,63,63	0
58	MG	CA	3341	1/1	0.86	0.10	48,48,48,48	0
58	MG	CA	3146	1/1	0.86	0.22	80,80,80,80	0
58	MG	AA	3057	1/1	0.86	0.10	56,56,56,56	0
58	MG	AA	3148	1/1	0.86	0.16	68,68,68,68	0
58	MG	CA	3153	1/1	0.86	0.16	55,55,55,55	0
58	MG	CA	3413	1/1	0.86	0.18	79,79,79,79	0
58	MG	A7	103	1/1	0.86	0.25	48,48,48,48	0
58	MG	BA	3056	1/1	0.86	0.22	67,67,67,67	0
58	MG	CA	3448	1/1	0.86	0.16	78,78,78,78	0
58	MG	CA	3169	1/1	0.86	0.19	55,55,55,55	0
58	MG	DA	1718	1/1	0.86	0.19	72,72,72,72	0
58	MG	DA	1720	1/1	0.86	0.14	64,64,64,64	0
58	MG	BA	3107	1/1	0.86	0.11	59,59,59,59	0
58	MG	BA	3057	1/1	0.86	0.17	89,89,89,89	0
58	MG	CA	3468	1/1	0.86	0.29	80,80,80,80	0
58	MG	CA	3190	1/1	0.86	0.19	68,68,68,68	0
58	MG	AA	3538	1/1	0.86	0.13	91,91,91,91	0
58	MG	AA	3192	1/1	0.86	0.14	41,41,41,41	0
58	MG	AA	3649	1/1	0.86	0.16	90,90,90,90	0
58	MG	AA	3651	1/1	0.86	0.12	49,49,49,49	0
58	MG	CA	3078	1/1	0.86	0.12	66,66,66,66	0
58	MG	CA	3498	1/1	0.86	0.19	71,71,71,71	0
58	MG	AB	3002	1/1	0.86	0.17	58,58,58,58	0
58	MG	DA	1754	1/1	0.86	0.10	66,66,66,66	0
58	MG	AA	3590	1/1	0.86	0.22	23,23,23,23	1
58	MG	CA	3090	1/1	0.86	0.16	79,79,79,79	0
58	MG	CQ	204	1/1	0.86	0.16	79,79,79,79	0
58	MG	CA	3515	1/1	0.86	0.16	73,73,73,73	0
58	MG	AA	3598	1/1	0.86	0.09	61,61,61,61	0
58	MG	AA	3756	1/1	0.86	0.14	61,61,61,61	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	BA	3161	1/1	0.86	0.17	87,87,87,87	0
58	MG	CA	3285	1/1	0.87	0.20	59,59,59,59	0
58	MG	AA	3695	1/1	0.87	0.11	44,44,44,44	0
58	MG	BA	3074	1/1	0.87	0.09	66,66,66,66	0
58	MG	CA	3127	1/1	0.87	0.20	94,94,94,94	0
58	MG	AA	3807	1/1	0.87	0.12	65,65,65,65	0
58	MG	DA	1640	1/1	0.87	0.22	74,74,74,74	0
58	MG	CA	3308	1/1	0.87	0.13	50,50,50,50	0
58	MG	CA	3557	1/1	0.87	0.24	82,82,82,82	0
58	MG	DA	1648	1/1	0.87	0.21	90,90,90,90	0
58	MG	CA	3135	1/1	0.87	0.27	84,84,84,84	0
58	MG	DA	1657	1/1	0.87	0.17	72,72,72,72	0
58	MG	BA	3014	1/1	0.87	0.11	97,97,97,97	0
58	MG	CA	3045	1/1	0.87	0.27	65,65,65,65	0
58	MG	AA	3813	1/1	0.87	0.12	57,57,57,57	0
58	MG	BA	3089	1/1	0.87	0.27	89,89,89,89	0
58	MG	CA	3375	1/1	0.87	0.12	74,74,74,74	0
58	MG	AA	3635	1/1	0.87	0.17	60,60,60,60	0
58	MG	AA	3375	1/1	0.87	0.17	57,57,57,57	0
58	MG	CA	3593	1/1	0.87	0.11	82,82,82,82	0
58	MG	CA	3407	1/1	0.87	0.10	70,70,70,70	0
58	MG	AA	3423	1/1	0.87	0.12	65,65,65,65	0
58	MG	DA	1688	1/1	0.87	0.12	57,57,57,57	0
58	MG	AA	3740	1/1	0.87	0.21	92,92,92,92	0
58	MG	CA	3066	1/1	0.87	0.11	50,50,50,50	0
58	MG	AA	3580	1/1	0.87	0.13	39,39,39,39	0
58	MG	BA	3191	1/1	0.87	0.12	74,74,74,74	0
58	MG	AB	3018	1/1	0.87	0.14	81,81,81,81	0
58	MG	CA	3189	1/1	0.87	0.22	58,58,58,58	0
58	MG	BA	3047	1/1	0.87	0.24	71,71,71,71	0
58	MG	AA	3437	1/1	0.87	0.10	55,55,55,55	0
58	MG	BA	3051	1/1	0.87	0.20	71,71,71,71	0
58	MG	AA	3441	1/1	0.87	0.14	46,46,46,46	0
58	MG	BA	3109	1/1	0.87	0.13	79,79,79,79	0
58	MG	CA	3082	1/1	0.87	0.15	66,66,66,66	0
58	MG	CA	3487	1/1	0.87	0.19	68,68,68,68	0
58	MG	CA	3223	1/1	0.87	0.27	75,75,75,75	0
58	MG	AF	304	1/1	0.87	0.09	41,41,41,41	0
58	MG	DA	1739	1/1	0.87	0.15	76,76,76,76	0
58	MG	CA	3495	1/1	0.87	0.22	62,62,62,62	0
58	MG	AA	3601	1/1	0.87	0.09	59,59,59,59	0
58	MG	CB	3012	1/1	0.87	0.23	74,74,74,74	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	AA	3206	1/1	0.87	0.19	62,62,62,62	0
58	MG	CA	3098	1/1	0.87	0.11	79,79,79,79	0
58	MG	AA	3200	1/1	0.87	0.11	52,52,52,52	0
58	MG	CG	3001	1/1	0.87	0.22	81,81,81,81	0
58	MG	DA	1760	1/1	0.87	0.08	71,71,71,71	0
58	MG	BA	3136	1/1	0.87	0.14	70,70,70,70	0
58	MG	CA	3523	1/1	0.87	0.17	62,62,62,62	0
58	MG	AA	3239	1/1	0.87	0.13	69,69,69,69	0
58	MG	AA	3193	1/1	0.87	0.27	72,72,72,72	0
58	MG	AA	3627	1/1	0.87	0.22	72,72,72,72	0
58	MG	AA	3527	1/1	0.87	0.08	21,21,21,21	0
58	MG	DA	1621	1/1	0.87	0.07	58,58,58,58	0
58	MG	AA	3222	1/1	0.88	0.22	61,61,61,61	0
58	MG	AA	3478	1/1	0.88	0.11	40,40,40,40	0
58	MG	BA	3115	1/1	0.88	0.21	86,86,86,86	0
58	MG	AA	3612	1/1	0.88	0.20	49,49,49,49	0
58	MG	AA	3360	1/1	0.88	0.19	111,111,111,111	0
58	MG	AA	3027	1/1	0.88	0.30	77,77,77,77	0
58	MG	AA	3621	1/1	0.88	0.17	39,39,39,39	0
58	MG	DA	1650	1/1	0.88	0.17	57,57,57,57	0
58	MG	CA	3389	1/1	0.88	0.17	81,81,81,81	0
58	MG	CA	3390	1/1	0.88	0.15	74,74,74,74	0
58	MG	AA	3709	1/1	0.88	0.15	53,53,53,53	0
58	MG	DA	1663	1/1	0.88	0.15	63,63,63,63	0
58	MG	AA	3622	1/1	0.88	0.18	46,46,46,46	0
58	MG	BA	3157	1/1	0.88	0.15	67,67,67,67	0
58	MG	DA	1671	1/1	0.88	0.26	72,72,72,72	0
58	MG	CA	3606	1/1	0.88	0.11	51,51,51,51	0
58	MG	CA	3608	1/1	0.88	0.15	70,70,70,70	0
58	MG	BA	3058	1/1	0.88	0.23	69,69,69,69	0
58	MG	DA	1676	1/1	0.88	0.10	75,75,75,75	0
58	MG	CA	3159	1/1	0.88	0.15	68,68,68,68	0
58	MG	AA	3159	1/1	0.88	0.26	97,97,97,97	0
58	MG	CA	3617	1/1	0.88	0.21	52,52,52,52	0
58	MG	AA	3321	1/1	0.88	0.12	69,69,69,69	0
58	MG	AA	3634	1/1	0.88	0.11	57,57,57,57	1
58	MG	AA	3562	1/1	0.88	0.10	57,57,57,57	0
58	MG	DA	1691	1/1	0.88	0.17	74,74,74,74	0
58	MG	CA	3063	1/1	0.88	0.20	66,66,66,66	0
58	MG	BA	3170	1/1	0.88	0.08	71,71,71,71	0
58	MG	DA	1700	1/1	0.88	0.12	62,62,62,62	0
58	MG	CA	3479	1/1	0.88	0.11	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	AZ	302	1/1	0.88	0.19	66,66,66,66	0
58	MG	BA	3073	1/1	0.88	0.27	74,74,74,74	0
58	MG	AA	3579	1/1	0.88	0.15	53,53,53,53	0
58	MG	AA	3753	1/1	0.88	0.16	72,72,72,72	0
58	MG	AA	3336	1/1	0.88	0.11	53,53,53,53	0
58	MG	AA	3758	1/1	0.88	0.24	81,81,81,81	0
58	MG	DA	1724	1/1	0.88	0.11	77,77,77,77	0
58	MG	AA	3647	1/1	0.88	0.16	71,71,71,71	0
58	MG	AA	3266	1/1	0.88	0.21	74,74,74,74	0
58	MG	AA	3774	1/1	0.88	0.22	78,78,78,78	0
58	MG	AA	3592	1/1	0.88	0.10	63,63,63,63	0
58	MG	BA	3197	1/1	0.88	0.08	75,75,75,75	0
58	MG	DA	1737	1/1	0.88	0.24	78,78,78,78	0
58	MG	CD	301	1/1	0.88	0.24	79,79,79,79	0
58	MG	CE	304	1/1	0.88	0.14	65,65,65,65	0
58	MG	BA	3016	1/1	0.88	0.09	73,73,73,73	0
58	MG	AA	3593	1/1	0.88	0.13	51,51,51,51	0
58	MG	AA	3345	1/1	0.88	0.09	67,67,67,67	0
58	MG	CO	201	1/1	0.88	0.11	61,61,61,61	0
58	MG	BA	3205	1/1	0.88	0.07	68,68,68,68	0
58	MG	AA	3347	1/1	0.88	0.12	40,40,40,40	0
58	MG	AA	3668	1/1	0.88	0.09	38,38,38,38	0
58	MG	DA	1606	1/1	0.88	0.10	72,72,72,72	0
58	MG	DA	1763	1/1	0.88	0.17	94,94,94,94	0
58	MG	BN	502	1/1	0.88	0.07	64,64,64,64	0
58	MG	DA	1765	1/1	0.88	0.09	64,64,64,64	0
58	MG	AA	3804	1/1	0.88	0.12	65,65,65,65	0
58	MG	AA	3672	1/1	0.88	0.22	32,32,32,32	1
58	MG	BA	3108	1/1	0.88	0.11	49,49,49,49	0
58	MG	CA	3548	1/1	0.88	0.11	116,116,116,116	0
58	MG	AA	3674	1/1	0.88	0.16	74,74,74,74	0
58	MG	CA	3564	1/1	0.89	0.11	75,75,75,75	0
58	MG	CA	3570	1/1	0.89	0.09	41,41,41,41	0
58	MG	CA	3070	1/1	0.89	0.26	82,82,82,82	0
58	MG	CA	3166	1/1	0.89	0.19	61,61,61,61	0
58	MG	CA	3387	1/1	0.89	0.15	62,62,62,62	0
58	MG	CA	3580	1/1	0.89	0.13	79,79,79,79	0
58	MG	BA	3075	1/1	0.89	0.20	56,56,56,56	0
58	MG	BA	3137	1/1	0.89	0.09	73,73,73,73	0
58	MG	CA	3400	1/1	0.89	0.11	73,73,73,73	0
58	MG	CA	3406	1/1	0.89	0.19	89,89,89,89	0
58	MG	CA	3174	1/1	0.89	0.18	65,65,65,65	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	DA	1664	1/1	0.89	0.19	59,59,59,59	0
58	MG	DA	1665	1/1	0.89	0.10	64,64,64,64	0
58	MG	AA	3443	1/1	0.89	0.09	61,61,61,61	0
58	MG	CA	3185	1/1	0.89	0.13	66,66,66,66	0
58	MG	CA	3607	1/1	0.89	0.08	67,67,67,67	0
58	MG	A7	101	1/1	0.89	0.28	64,64,64,64	0
58	MG	AA	3760	1/1	0.89	0.07	27,27,27,27	0
58	MG	AA	3444	1/1	0.89	0.15	73,73,73,73	0
58	MG	CA	3613	1/1	0.89	0.24	96,96,96,96	0
58	MG	AA	3660	1/1	0.89	0.16	68,68,68,68	0
58	MG	CA	3204	1/1	0.89	0.08	58,58,58,58	0
58	MG	CA	3205	1/1	0.89	0.10	71,71,71,71	0
58	MG	BA	3004	1/1	0.89	0.17	64,64,64,64	0
58	MG	BX	103	1/1	0.89	0.26	87,87,87,87	0
58	MG	BA	3053	1/1	0.89	0.15	69,69,69,69	0
58	MG	BA	3094	1/1	0.89	0.09	78,78,78,78	0
58	MG	CA	3631	1/1	0.89	0.20	66,66,66,66	0
58	MG	BX	109	1/1	0.89	0.13	78,78,78,78	0
58	MG	CA	3229	1/1	0.89	0.24	61,61,61,61	0
58	MG	BA	3164	1/1	0.89	0.09	60,60,60,60	0
58	MG	BA	3167	1/1	0.89	0.11	85,85,85,85	0
58	MG	CA	3108	1/1	0.89	0.27	106,106,106,106	0
58	MG	AA	3455	1/1	0.89	0.12	56,56,56,56	0
58	MG	CA	3013	1/1	0.89	0.20	61,61,61,61	0
58	MG	CA	3499	1/1	0.89	0.10	65,65,65,65	0
58	MG	DA	1719	1/1	0.89	0.15	66,66,66,66	0
58	MG	AA	3335	1/1	0.89	0.09	40,40,40,40	0
58	MG	DA	1723	1/1	0.89	0.07	68,68,68,68	0
58	MG	CB	3007	1/1	0.89	0.25	64,64,64,64	0
58	MG	CA	3504	1/1	0.89	0.16	69,69,69,69	0
58	MG	CB	3009	1/1	0.89	0.12	64,64,64,64	0
58	MG	AA	3362	1/1	0.89	0.14	67,67,67,67	0
58	MG	CA	3271	1/1	0.89	0.19	84,84,84,84	0
58	MG	BA	3013	1/1	0.89	0.14	75,75,75,75	0
58	MG	AA	3119	1/1	0.89	0.15	62,62,62,62	0
58	MG	CA	3279	1/1	0.89	0.11	89,89,89,89	0
58	MG	CA	3530	1/1	0.89	0.17	78,78,78,78	0
58	MG	AD	302	1/1	0.89	0.16	46,46,46,46	0
58	MG	CN	5001	1/1	0.89	0.12	76,76,76,76	0
58	MG	AA	3675	1/1	0.89	0.12	40,40,40,40	0
58	MG	BA	3184	1/1	0.89	0.07	49,49,49,49	0
58	MG	CA	3540	1/1	0.89	0.11	70,70,70,70	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	AA	3481	1/1	0.89	0.08	50,50,50,50	0
58	MG	DA	1604	1/1	0.89	0.08	72,72,72,72	0
58	MG	BA	3065	1/1	0.89	0.15	57,57,57,57	0
58	MG	AA	3249	1/1	0.89	0.13	62,62,62,62	0
58	MG	CA	3148	1/1	0.89	0.24	77,77,77,77	0
58	MG	BA	3070	1/1	0.89	0.12	72,72,72,72	0
58	MG	AA	3681	1/1	0.89	0.11	63,63,63,63	0
58	MG	AA	3518	1/1	0.89	0.08	19,19,19,19	0
58	MG	BA	3037	1/1	0.89	0.12	64,64,64,64	0
58	MG	DL	3001	1/1	0.89	0.12	57,57,57,57	0
58	MG	BA	3131	1/1	0.89	0.09	76,76,76,76	0
58	MG	DA	1632	1/1	0.89	0.17	69,69,69,69	0
58	MG	CA	3237	1/1	0.90	0.27	75,75,75,75	0
58	MG	AA	3631	1/1	0.90	0.21	68,68,68,68	0
58	MG	CA	3506	1/1	0.90	0.07	61,61,61,61	0
58	MG	BA	3149	1/1	0.90	0.18	82,82,82,82	0
58	MG	BA	3028	1/1	0.90	0.20	90,90,90,90	0
58	MG	CA	3511	1/1	0.90	0.11	74,74,74,74	0
58	MG	CA	3514	1/1	0.90	0.11	63,63,63,63	0
58	MG	BA	3077	1/1	0.90	0.28	86,86,86,86	0
58	MG	CA	3516	1/1	0.90	0.20	105,105,105,105	0
58	MG	BX	104	1/1	0.90	0.08	69,69,69,69	0
58	MG	CA	3526	1/1	0.90	0.09	75,75,75,75	0
58	MG	AA	3272	1/1	0.90	0.22	69,69,69,69	0
58	MG	CA	3248	1/1	0.90	0.10	58,58,58,58	0
58	MG	DA	1626	1/1	0.90	0.28	72,72,72,72	0
58	MG	CA	3532	1/1	0.90	0.10	58,58,58,58	0
58	MG	AA	3488	1/1	0.90	0.09	23,23,23,23	0
58	MG	CA	3260	1/1	0.90	0.13	69,69,69,69	0
58	MG	AA	3060	1/1	0.90	0.20	64,64,64,64	0
58	MG	AA	3761	1/1	0.90	0.09	48,48,48,48	0
58	MG	DA	1637	1/1	0.90	0.20	67,67,67,67	0
58	MG	AA	3029	1/1	0.90	0.16	50,50,50,50	0
58	MG	AA	3107	1/1	0.90	0.20	48,48,48,48	0
58	MG	CA	3128	1/1	0.90	0.23	60,60,60,60	0
58	MG	AH	3002	1/1	0.90	0.17	77,77,77,77	0
58	MG	CA	3130	1/1	0.90	0.14	68,68,68,68	0
58	MG	DA	1651	1/1	0.90	0.11	70,70,70,70	0
58	MG	DA	1655	1/1	0.90	0.27	73,73,73,73	0
58	MG	CA	3549	1/1	0.90	0.13	61,61,61,61	0
58	MG	CA	3024	1/1	0.90	0.25	87,87,87,87	0
58	MG	CA	3139	1/1	0.90	0.10	63,63,63,63	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	DA	1661	1/1	0.90	0.07	62,62,62,62	0
58	MG	DA	1662	1/1	0.90	0.15	70,70,70,70	0
58	MG	CA	3025	1/1	0.90	0.22	75,75,75,75	0
58	MG	AA	3773	1/1	0.90	0.31	36,36,36,36	0
58	MG	AA	3349	1/1	0.90	0.25	39,39,39,39	0
58	MG	CA	3565	1/1	0.90	0.09	90,90,90,90	0
58	MG	AA	3431	1/1	0.90	0.13	56,56,56,56	0
58	MG	CA	3573	1/1	0.90	0.18	64,64,64,64	0
58	MG	CA	3339	1/1	0.90	0.15	62,62,62,62	0
58	MG	AA	3547	1/1	0.90	0.09	30,30,30,30	0
58	MG	AA	3699	1/1	0.90	0.18	38,38,38,38	1
58	MG	CA	3358	1/1	0.90	0.15	78,78,78,78	0
58	MG	DA	1677	1/1	0.90	0.22	80,80,80,80	0
58	MG	CA	3582	1/1	0.90	0.09	96,96,96,96	0
58	MG	CA	3374	1/1	0.90	0.16	56,56,56,56	0
58	MG	AA	3015	1/1	0.90	0.20	62,62,62,62	0
58	MG	BA	3181	1/1	0.90	0.08	47,47,47,47	0
58	MG	DA	1687	1/1	0.90	0.11	66,66,66,66	0
58	MG	AA	3801	1/1	0.90	0.09	89,89,89,89	0
58	MG	AA	3653	1/1	0.90	0.09	67,67,67,67	0
58	MG	BA	3186	1/1	0.90	0.16	67,67,67,67	0
58	MG	CA	3160	1/1	0.90	0.30	74,74,74,74	0
58	MG	CA	3396	1/1	0.90	0.24	64,64,64,64	0
58	MG	AA	3717	1/1	0.90	0.08	56,56,56,56	0
58	MG	BA	3005	1/1	0.90	0.26	64,64,64,64	0
58	MG	CA	3172	1/1	0.90	0.09	53,53,53,53	0
58	MG	DA	1706	1/1	0.90	0.12	85,85,85,85	0
58	MG	CA	3408	1/1	0.90	0.10	54,54,54,54	0
58	MG	AA	3574	1/1	0.90	0.09	47,47,47,47	0
58	MG	BA	3194	1/1	0.90	0.08	60,60,60,60	0
58	MG	CA	3424	1/1	0.90	0.14	51,51,51,51	0
58	MG	CA	3175	1/1	0.90	0.24	60,60,60,60	0
58	MG	AA	3577	1/1	0.90	0.13	36,36,36,36	0
58	MG	CA	3445	1/1	0.90	0.20	91,91,91,91	0
58	MG	AA	3737	1/1	0.90	0.12	75,75,75,75	0
58	MG	CA	3629	1/1	0.90	0.20	73,73,73,73	0
58	MG	BA	3116	1/1	0.90	0.14	82,82,82,82	0
58	MG	CA	3634	1/1	0.90	0.10	75,75,75,75	0
58	MG	AA	3821	1/1	0.90	0.13	58,58,58,58	0
58	MG	CA	3639	1/1	0.90	0.28	79,79,79,79	0
58	MG	DA	1736	1/1	0.90	0.13	78,78,78,78	0
58	MG	AA	3477	1/1	0.90	0.10	57,57,57,57	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	DA	1738	1/1	0.90	0.11	78,78,78,78	0
58	MG	CA	3196	1/1	0.90	0.14	58,58,58,58	0
58	MG	DA	1740	1/1	0.90	0.12	79,79,79,79	0
58	MG	CA	3198	1/1	0.90	0.18	62,62,62,62	0
58	MG	BA	3125	1/1	0.90	0.14	63,63,63,63	0
58	MG	AA	3440	1/1	0.90	0.15	51,51,51,51	0
58	MG	CA	3652	1/1	0.90	0.14	84,84,84,84	0
58	MG	CA	3657	1/1	0.90	0.13	62,62,62,62	0
58	MG	BA	3210	1/1	0.90	0.11	68,68,68,68	0
58	MG	CA	3483	1/1	0.90	0.16	68,68,68,68	0
58	MG	CB	3003	1/1	0.90	0.12	76,76,76,76	0
58	MG	CA	3484	1/1	0.90	0.16	67,67,67,67	0
58	MG	CA	3485	1/1	0.90	0.10	74,74,74,74	0
58	MG	BA	3135	1/1	0.90	0.28	80,80,80,80	0
58	MG	BA	3072	1/1	0.90	0.28	75,75,75,75	0
58	MG	DA	1766	1/1	0.90	0.13	53,53,53,53	0
58	MG	CA	3088	1/1	0.90	0.13	65,65,65,65	0
58	MG	CA	3493	1/1	0.90	0.29	105,105,105,105	0
58	MG	CA	3089	1/1	0.90	0.22	73,73,73,73	0
58	MG	BL	3004	1/1	0.90	0.18	67,67,67,67	0
58	MG	CA	3227	1/1	0.90	0.29	68,68,68,68	0
58	MG	AA	3629	1/1	0.90	0.20	74,74,74,74	0
58	MG	AA	3234	1/1	0.91	0.21	77,77,77,77	0
58	MG	AA	3553	1/1	0.91	0.15	60,60,60,60	0
58	MG	CA	3473	1/1	0.91	0.20	70,70,70,70	0
58	MG	AA	3181	1/1	0.91	0.24	94,94,94,94	0
58	MG	CA	3478	1/1	0.91	0.14	73,73,73,73	0
58	MG	BA	3031	1/1	0.91	0.09	61,61,61,61	0
58	MG	AA	3186	1/1	0.91	0.18	41,41,41,41	0
58	MG	CE	306	1/1	0.91	0.25	99,99,99,99	0
58	MG	BA	3034	1/1	0.91	0.13	61,61,61,61	0
58	MG	CA	3020	1/1	0.91	0.10	61,61,61,61	0
58	MG	CA	3179	1/1	0.91	0.13	55,55,55,55	0
58	MG	AA	3703	1/1	0.91	0.13	41,41,41,41	1
58	MG	BA	3124	1/1	0.91	0.09	71,71,71,71	0
58	MG	CQ	202	1/1	0.91	0.10	66,66,66,66	0
58	MG	AA	3816	1/1	0.91	0.14	91,91,91,91	0
58	MG	CA	3488	1/1	0.91	0.09	69,69,69,69	0
58	MG	CA	3489	1/1	0.91	0.09	53,53,53,53	0
58	MG	BA	3126	1/1	0.91	0.11	59,59,59,59	0
58	MG	DA	1605	1/1	0.91	0.20	75,75,75,75	0
58	MG	CA	3038	1/1	0.91	0.07	46,46,46,46	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	AA	3705	1/1	0.91	0.11	57,57,57,57	0
58	MG	AA	3576	1/1	0.91	0.11	69,69,69,69	0
58	MG	CA	3199	1/1	0.91	0.07	36,36,36,36	0
58	MG	BA	3046	1/1	0.91	0.15	60,60,60,60	0
58	MG	AA	3036	1/1	0.91	0.10	49,49,49,49	0
58	MG	AA	3713	1/1	0.91	0.11	47,47,47,47	0
58	MG	CA	3206	1/1	0.91	0.16	104,104,104,104	0
58	MG	BA	3144	1/1	0.91	0.10	53,53,53,53	0
58	MG	CA	3051	1/1	0.91	0.40	64,64,64,64	0
58	MG	CA	3211	1/1	0.91	0.20	72,72,72,72	0
58	MG	CA	3053	1/1	0.91	0.17	57,57,57,57	0
58	MG	AB	3006	1/1	0.91	0.18	70,70,70,70	0
58	MG	AA	3452	1/1	0.91	0.14	67,67,67,67	0
58	MG	CA	3520	1/1	0.91	0.25	83,83,83,83	0
58	MG	AA	3721	1/1	0.91	0.13	76,76,76,76	0
58	MG	AA	3071	1/1	0.91	0.14	59,59,59,59	0
58	MG	CA	3232	1/1	0.91	0.23	65,65,65,65	0
58	MG	AB	3019	1/1	0.91	0.11	64,64,64,64	0
58	MG	AA	3645	1/1	0.91	0.23	78,78,78,78	0
58	MG	AA	3736	1/1	0.91	0.09	35,35,35,35	0
58	MG	AD	307	1/1	0.91	0.10	56,56,56,56	0
58	MG	AA	3083	1/1	0.91	0.10	27,27,27,27	1
58	MG	CA	3243	1/1	0.91	0.29	110,110,110,110	0
58	MG	BA	3166	1/1	0.91	0.07	58,58,58,58	0
58	MG	AD	309	1/1	0.91	0.12	37,37,37,37	0
58	MG	CA	3247	1/1	0.91	0.15	55,55,55,55	0
58	MG	AD	311	1/1	0.91	0.12	55,55,55,55	0
58	MG	CA	3547	1/1	0.91	0.10	66,66,66,66	0
58	MG	CA	3249	1/1	0.91	0.19	64,64,64,64	0
58	MG	BA	3064	1/1	0.91	0.09	78,78,78,78	0
58	MG	CA	3257	1/1	0.91	0.16	65,65,65,65	0
58	MG	AD	312	1/1	0.91	0.38	58,58,58,58	0
58	MG	BA	3067	1/1	0.91	0.19	73,73,73,73	0
58	MG	CA	3083	1/1	0.91	0.09	70,70,70,70	0
58	MG	BA	3068	1/1	0.91	0.11	87,87,87,87	0
58	MG	AA	3111	1/1	0.91	0.18	79,79,79,79	0
58	MG	CA	3569	1/1	0.91	0.10	54,54,54,54	0
58	MG	AA	3359	1/1	0.91	0.09	49,49,49,49	0
58	MG	CA	3286	1/1	0.91	0.19	90,90,90,90	0
58	MG	AA	3112	1/1	0.91	0.10	46,46,46,46	0
58	MG	AU	203	1/1	0.91	0.18	56,56,56,56	0
58	MG	DA	1689	1/1	0.91	0.12	80,80,80,80	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	CA	3096	1/1	0.91	0.20	63,63,63,63	0
58	MG	BA	3185	1/1	0.91	0.20	111,111,111,111	0
58	MG	AA	3600	1/1	0.91	0.15	57,57,57,57	0
58	MG	DA	1697	1/1	0.91	0.20	65,65,65,65	0
58	MG	AA	3480	1/1	0.91	0.12	54,54,54,54	0
58	MG	CA	3585	1/1	0.91	0.09	80,80,80,80	0
58	MG	CA	3101	1/1	0.91	0.34	77,77,77,77	0
58	MG	AA	3607	1/1	0.91	0.21	59,59,59,59	0
58	MG	CA	3591	1/1	0.91	0.15	77,77,77,77	0
58	MG	A5	104	1/1	0.91	0.10	60,60,60,60	0
58	MG	BA	3080	1/1	0.91	0.08	52,52,52,52	0
58	MG	DA	1710	1/1	0.91	0.09	79,79,79,79	0
58	MG	DA	1711	1/1	0.91	0.12	70,70,70,70	0
58	MG	CA	3344	1/1	0.91	0.09	36,36,36,36	0
58	MG	AA	3759	1/1	0.91	0.12	63,63,63,63	0
58	MG	AA	3172	1/1	0.91	0.39	32,32,32,32	0
58	MG	BA	3083	1/1	0.91	0.22	68,68,68,68	0
58	MG	A7	104	1/1	0.91	0.16	44,44,44,44	1
58	MG	CA	3376	1/1	0.91	0.16	70,70,70,70	0
58	MG	CA	3126	1/1	0.91	0.24	71,71,71,71	0
58	MG	AA	3216	1/1	0.91	0.08	36,36,36,36	0
58	MG	DA	1730	1/1	0.91	0.12	75,75,75,75	0
58	MG	A9	502	1/1	0.91	0.21	58,58,58,58	0
58	MG	AA	3174	1/1	0.91	0.33	62,62,62,62	0
58	MG	BA	3209	1/1	0.91	0.12	79,79,79,79	0
58	MG	CA	3392	1/1	0.91	0.08	63,63,63,63	0
58	MG	CA	3394	1/1	0.91	0.06	84,84,84,84	0
58	MG	AA	3673	1/1	0.91	0.14	66,66,66,66	0
58	MG	CA	3136	1/1	0.91	0.22	64,64,64,64	0
58	MG	CA	3403	1/1	0.91	0.14	70,70,70,70	0
58	MG	BA	3212	1/1	0.91	0.16	73,73,73,73	0
58	MG	CA	3635	1/1	0.91	0.11	79,79,79,79	0
58	MG	CA	3636	1/1	0.91	0.17	65,65,65,65	0
58	MG	BD	502	1/1	0.91	0.22	80,80,80,80	0
58	MG	AA	3767	1/1	0.91	0.13	66,66,66,66	0
58	MG	AA	3292	1/1	0.91	0.18	71,71,71,71	0
58	MG	AA	3223	1/1	0.91	0.19	54,54,54,54	0
58	MG	CA	3646	1/1	0.91	0.08	75,75,75,75	0
58	MG	CA	3422	1/1	0.91	0.19	74,74,74,74	0
58	MG	BA	3098	1/1	0.91	0.14	78,78,78,78	0
58	MG	CA	3649	1/1	0.91	0.12	94,94,94,94	0
58	MG	AA	3319	1/1	0.91	0.11	66,66,66,66	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	CA	3433	1/1	0.91	0.20	61,61,61,61	0
58	MG	CA	3656	1/1	0.91	0.24	96,96,96,96	0
58	MG	AA	3232	1/1	0.91	0.20	79,79,79,79	0
58	MG	AA	3624	1/1	0.91	0.15	70,70,70,70	0
58	MG	BA	3015	1/1	0.91	0.23	87,87,87,87	0
58	MG	AA	3626	1/1	0.91	0.09	58,58,58,58	0
58	MG	AA	3688	1/1	0.91	0.09	29,29,29,29	0
62	GDP	DZ	704	28/28	0.91	0.10	80,80,80,80	0
58	MG	AA	3513	1/1	0.92	0.09	58,58,58,58	0
58	MG	CA	3654	1/1	0.92	0.07	29,29,29,29	0
58	MG	BA	3099	1/1	0.92	0.25	70,70,70,70	0
58	MG	BT	3001	1/1	0.92	0.23	60,60,60,60	0
58	MG	CA	3417	1/1	0.92	0.09	48,48,48,48	0
58	MG	BA	3100	1/1	0.92	0.21	74,74,74,74	0
58	MG	AA	3243	1/1	0.92	0.10	66,66,66,66	0
58	MG	CB	3004	1/1	0.92	0.15	67,67,67,67	0
58	MG	BA	3008	1/1	0.92	0.13	61,61,61,61	0
58	MG	CA	3432	1/1	0.92	0.18	96,96,96,96	0
58	MG	AA	3519	1/1	0.92	0.09	32,32,32,32	0
58	MG	BA	3105	1/1	0.92	0.12	60,60,60,60	0
58	MG	BA	3011	1/1	0.92	0.07	76,76,76,76	0
58	MG	CA	3167	1/1	0.92	0.17	43,43,43,43	0
58	MG	AA	3244	1/1	0.92	0.21	69,69,69,69	0
58	MG	AA	3129	1/1	0.92	0.19	57,57,57,57	0
58	MG	AA	3358	1/1	0.92	0.10	61,61,61,61	0
58	MG	AA	3137	1/1	0.92	0.06	49,49,49,49	0
58	MG	CA	3472	1/1	0.92	0.12	45,45,45,45	0
58	MG	AA	3655	1/1	0.92	0.09	59,59,59,59	0
58	MG	CA	3017	1/1	0.92	0.09	45,45,45,45	0
58	MG	BA	3020	1/1	0.92	0.07	51,51,51,51	0
58	MG	CO	202	1/1	0.92	0.12	52,52,52,52	0
58	MG	CQ	201	1/1	0.92	0.17	63,63,63,63	0
58	MG	BA	3021	1/1	0.92	0.08	37,37,37,37	0
58	MG	CA	3187	1/1	0.92	0.14	67,67,67,67	0
58	MG	BA	3022	1/1	0.92	0.06	46,46,46,46	0
58	MG	CA	3026	1/1	0.92	0.16	79,79,79,79	0
58	MG	CA	3194	1/1	0.92	0.11	61,61,61,61	0
58	MG	AA	3199	1/1	0.92	0.12	55,55,55,55	0
58	MG	BA	3027	1/1	0.92	0.12	75,75,75,75	0
58	MG	AA	3785	1/1	0.92	0.13	70,70,70,70	0
58	MG	DA	1611	1/1	0.92	0.11	74,74,74,74	0
58	MG	AA	3793	1/1	0.92	0.10	60,60,60,60	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	DA	1617	1/1	0.92	0.11	63,63,63,63	0
58	MG	AA	3024	1/1	0.92	0.18	55,55,55,55	0
58	MG	CA	3201	1/1	0.92	0.17	52,52,52,52	0
58	MG	AA	3796	1/1	0.92	0.14	19,19,19,19	1
58	MG	AA	3564	1/1	0.92	0.11	48,48,48,48	0
58	MG	AA	3802	1/1	0.92	0.11	54,54,54,54	0
58	MG	AA	3363	1/1	0.92	0.07	28,28,28,28	0
58	MG	DA	1630	1/1	0.92	0.12	56,56,56,56	0
58	MG	DA	1631	1/1	0.92	0.15	59,59,59,59	0
58	MG	CA	3050	1/1	0.92	0.07	43,43,43,43	0
58	MG	AA	3669	1/1	0.92	0.07	34,34,34,34	0
58	MG	CA	3215	1/1	0.92	0.16	39,39,39,39	0
58	MG	BA	3148	1/1	0.92	0.10	67,67,67,67	0
58	MG	DA	1639	1/1	0.92	0.29	83,83,83,83	0
58	MG	CA	3055	1/1	0.92	0.21	37,37,37,37	0
58	MG	AA	3265	1/1	0.92	0.16	60,60,60,60	0
58	MG	CA	3058	1/1	0.92	0.08	48,48,48,48	0
58	MG	AA	3149	1/1	0.92	0.15	67,67,67,67	0
58	MG	AA	3381	1/1	0.92	0.09	26,26,26,26	0
58	MG	AA	3404	1/1	0.92	0.10	43,43,43,43	0
58	MG	DA	1652	1/1	0.92	0.10	58,58,58,58	0
58	MG	AA	3414	1/1	0.92	0.07	55,55,55,55	0
58	MG	AA	3421	1/1	0.92	0.12	70,70,70,70	0
58	MG	CA	3240	1/1	0.92	0.09	58,58,58,58	0
58	MG	AA	3269	1/1	0.92	0.25	84,84,84,84	0
58	MG	AA	3596	1/1	0.92	0.07	54,54,54,54	0
58	MG	CA	3531	1/1	0.92	0.10	58,58,58,58	0
58	MG	AA	3597	1/1	0.92	0.14	40,40,40,40	0
58	MG	CA	3534	1/1	0.92	0.12	79,79,79,79	0
58	MG	AA	3202	1/1	0.92	0.09	63,63,63,63	0
58	MG	AA	3435	1/1	0.92	0.09	37,37,37,37	0
58	MG	CA	3538	1/1	0.92	0.12	69,69,69,69	0
58	MG	AA	3156	1/1	0.92	0.18	63,63,63,63	0
58	MG	AA	3605	1/1	0.92	0.10	40,40,40,40	1
58	MG	CA	3080	1/1	0.92	0.17	56,56,56,56	0
58	MG	DA	1674	1/1	0.92	0.11	72,72,72,72	0
58	MG	CA	3250	1/1	0.92	0.13	76,76,76,76	0
58	MG	CA	3253	1/1	0.92	0.10	56,56,56,56	0
58	MG	AB	3022	1/1	0.92	0.07	56,56,56,56	0
58	MG	BA	3174	1/1	0.92	0.07	69,69,69,69	0
58	MG	AA	3606	1/1	0.92	0.15	64,64,64,64	0
58	MG	AA	3273	1/1	0.92	0.17	52,52,52,52	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	AA	3211	1/1	0.92	0.28	86,86,86,86	0
58	MG	AA	3277	1/1	0.92	0.32	78,78,78,78	0
58	MG	AA	3285	1/1	0.92	0.09	44,44,44,44	0
58	MG	AA	3002	1/1	0.92	0.11	54,54,54,54	0
58	MG	AA	3718	1/1	0.92	0.12	47,47,47,47	0
58	MG	CA	3287	1/1	0.92	0.10	55,55,55,55	0
58	MG	CA	3566	1/1	0.92	0.12	41,41,41,41	1
58	MG	DA	1696	1/1	0.92	0.19	64,64,64,64	0
58	MG	CA	3288	1/1	0.92	0.12	63,63,63,63	0
58	MG	CA	3097	1/1	0.92	0.17	65,65,65,65	0
58	MG	CA	3293	1/1	0.92	0.07	26,26,26,26	0
58	MG	CA	3294	1/1	0.92	0.15	71,71,71,71	0
58	MG	AA	3719	1/1	0.92	0.12	41,41,41,41	0
58	MG	AF	307	1/1	0.92	0.13	61,61,61,61	0
58	MG	AA	3019	1/1	0.92	0.10	57,57,57,57	0
58	MG	DA	1708	1/1	0.92	0.17	68,68,68,68	0
58	MG	AA	3618	1/1	0.92	0.10	49,49,49,49	0
58	MG	CA	3311	1/1	0.92	0.09	48,48,48,48	0
58	MG	CA	3102	1/1	0.92	0.16	76,76,76,76	0
58	MG	BA	3192	1/1	0.92	0.09	65,65,65,65	0
58	MG	CA	3334	1/1	0.92	0.19	72,72,72,72	0
58	MG	CA	3590	1/1	0.92	0.12	62,62,62,62	0
58	MG	AQ	202	1/1	0.92	0.06	29,29,29,29	0
58	MG	BA	3076	1/1	0.92	0.10	42,42,42,42	0
58	MG	AA	3316	1/1	0.92	0.16	59,59,59,59	0
58	MG	DA	1725	1/1	0.92	0.13	64,64,64,64	0
58	MG	DA	1726	1/1	0.92	0.08	61,61,61,61	0
58	MG	AA	3028	1/1	0.92	0.16	55,55,55,55	0
58	MG	CA	3598	1/1	0.92	0.10	66,66,66,66	0
58	MG	CA	3600	1/1	0.92	0.06	39,39,39,39	0
58	MG	CA	3349	1/1	0.92	0.14	54,54,54,54	0
58	MG	BA	3198	1/1	0.92	0.20	68,68,68,68	0
58	MG	AA	3229	1/1	0.92	0.10	54,54,54,54	0
58	MG	CA	3359	1/1	0.92	0.10	44,44,44,44	0
58	MG	CA	3361	1/1	0.92	0.11	48,48,48,48	0
58	MG	CA	3366	1/1	0.92	0.10	47,47,47,47	0
58	MG	CA	3367	1/1	0.92	0.20	59,59,59,59	0
58	MG	CA	3125	1/1	0.92	0.12	47,47,47,47	0
58	MG	AA	3330	1/1	0.92	0.11	66,66,66,66	0
58	MG	CA	3622	1/1	0.92	0.20	51,51,51,51	0
58	MG	DA	1746	1/1	0.92	0.11	77,77,77,77	0
58	MG	AA	3068	1/1	0.92	0.13	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	AA	3748	1/1	0.92	0.11	56,56,56,56	0
58	MG	CA	3378	1/1	0.92	0.08	78,78,78,78	0
58	MG	BA	3208	1/1	0.92	0.10	81,81,81,81	0
58	MG	CA	3380	1/1	0.92	0.14	63,63,63,63	0
58	MG	CA	3385	1/1	0.92	0.14	70,70,70,70	0
58	MG	AA	3185	1/1	0.92	0.17	65,65,65,65	0
58	MG	CA	3134	1/1	0.92	0.20	69,69,69,69	0
58	MG	AA	3341	1/1	0.92	0.08	15,15,15,15	0
58	MG	BA	3211	1/1	0.92	0.10	59,59,59,59	0
58	MG	CA	3138	1/1	0.92	0.27	70,70,70,70	0
58	MG	CA	3395	1/1	0.92	0.07	53,53,53,53	0
58	MG	AA	3101	1/1	0.92	0.16	51,51,51,51	0
58	MG	CA	3397	1/1	0.92	0.08	59,59,59,59	0
58	MG	AA	3757	1/1	0.92	0.12	43,43,43,43	0
58	MG	DT	3001	1/1	0.92	0.20	66,66,66,66	0
58	MG	AA	3069	1/1	0.92	0.10	63,63,63,63	0
58	MG	AA	3492	1/1	0.92	0.08	61,61,61,61	0
58	MG	DZ	703	1/1	0.92	0.08	56,56,56,56	0
59	K	AA	3818	1/1	0.92	0.13	87,87,87,87	0
58	MG	AA	3493	1/1	0.92	0.17	44,44,44,44	0
58	MG	CA	3069	1/1	0.93	0.12	56,56,56,56	0
58	MG	CA	3228	1/1	0.93	0.20	51,51,51,51	0
58	MG	AA	3051	1/1	0.93	0.19	34,34,34,34	0
58	MG	BA	3172	1/1	0.93	0.09	55,55,55,55	0
58	MG	CD	302	1/1	0.93	0.07	76,76,76,76	0
58	MG	CA	3235	1/1	0.93	0.30	70,70,70,70	0
58	MG	AA	3754	1/1	0.93	0.06	40,40,40,40	0
58	MG	AA	3453	1/1	0.93	0.13	54,54,54,54	0
58	MG	AA	3134	1/1	0.93	0.18	67,67,67,67	0
58	MG	AA	3079	1/1	0.93	0.29	63,63,63,63	0
58	MG	AA	3464	1/1	0.93	0.14	59,59,59,59	0
58	MG	AA	3284	1/1	0.93	0.16	43,43,43,43	0
58	MG	AV	205	1/1	0.93	0.07	37,37,37,37	0
58	MG	AA	3145	1/1	0.93	0.05	38,38,38,38	0
58	MG	CA	3496	1/1	0.93	0.17	64,64,64,64	0
58	MG	AA	3018	1/1	0.93	0.31	75,75,75,75	0
58	MG	CU	3001	1/1	0.93	0.22	91,91,91,91	0
58	MG	A1	101	1/1	0.93	0.10	54,54,54,54	0
58	MG	A2	3001	1/1	0.93	0.07	50,50,50,50	0
58	MG	CA	3501	1/1	0.93	0.09	63,63,63,63	0
58	MG	AA	3373	1/1	0.93	0.17	57,57,57,57	0
58	MG	AA	3088	1/1	0.93	0.21	73,73,73,73	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	CA	3508	1/1	0.93	0.10	57,57,57,57	0
58	MG	DA	1609	1/1	0.93	0.09	45,45,45,45	0
58	MG	BA	3078	1/1	0.93	0.19	66,66,66,66	0
58	MG	DA	1613	1/1	0.93	0.27	70,70,70,70	0
58	MG	AA	3771	1/1	0.93	0.18	38,38,38,38	1
58	MG	AA	3482	1/1	0.93	0.10	64,64,64,64	0
58	MG	AA	3110	1/1	0.93	0.06	50,50,50,50	0
58	MG	AA	3609	1/1	0.93	0.08	71,71,71,71	0
58	MG	BA	3085	1/1	0.93	0.18	49,49,49,49	0
58	MG	CA	3517	1/1	0.93	0.10	77,77,77,77	0
58	MG	CA	3518	1/1	0.93	0.06	61,61,61,61	0
58	MG	CA	3519	1/1	0.93	0.15	62,62,62,62	0
58	MG	AA	3399	1/1	0.93	0.13	39,39,39,39	0
58	MG	CA	3521	1/1	0.93	0.16	77,77,77,77	0
58	MG	CA	3522	1/1	0.93	0.09	59,59,59,59	0
58	MG	CA	3103	1/1	0.93	0.15	55,55,55,55	0
58	MG	BA	3001	1/1	0.93	0.09	55,55,55,55	0
58	MG	BA	3202	1/1	0.93	0.09	62,62,62,62	0
58	MG	DA	1638	1/1	0.93	0.10	74,74,74,74	0
58	MG	AA	3780	1/1	0.93	0.08	41,41,41,41	0
58	MG	AA	3093	1/1	0.93	0.30	52,52,52,52	0
58	MG	CA	3290	1/1	0.93	0.10	53,53,53,53	0
58	MG	CA	3117	1/1	0.93	0.30	73,73,73,73	0
58	MG	DA	1643	1/1	0.93	0.10	55,55,55,55	0
58	MG	BA	3206	1/1	0.93	0.12	62,62,62,62	0
58	MG	CA	3536	1/1	0.93	0.10	75,75,75,75	0
58	MG	AA	3165	1/1	0.93	0.08	56,56,56,56	0
58	MG	CA	3121	1/1	0.93	0.23	60,60,60,60	0
58	MG	AA	3788	1/1	0.93	0.18	60,60,60,60	0
58	MG	CA	3300	1/1	0.93	0.14	66,66,66,66	0
58	MG	AA	3789	1/1	0.93	0.16	52,52,52,52	0
58	MG	DA	1658	1/1	0.93	0.06	63,63,63,63	0
58	MG	CA	3542	1/1	0.93	0.09	82,82,82,82	0
58	MG	DA	1660	1/1	0.93	0.10	70,70,70,70	0
58	MG	AA	3416	1/1	0.93	0.09	25,25,25,25	0
58	MG	AA	3209	1/1	0.93	0.15	59,59,59,59	0
58	MG	AA	3422	1/1	0.93	0.07	23,23,23,23	0
58	MG	AA	3332	1/1	0.93	0.10	44,44,44,44	0
58	MG	CA	3332	1/1	0.93	0.11	50,50,50,50	0
58	MG	AA	3253	1/1	0.93	0.11	65,65,65,65	0
58	MG	CA	3551	1/1	0.93	0.07	57,57,57,57	0
58	MG	AA	3625	1/1	0.93	0.10	63,63,63,63	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	AA	3030	1/1	0.93	0.14	31,31,31,31	1
58	MG	CA	3556	1/1	0.93	0.19	66,66,66,66	0
58	MG	AA	3543	1/1	0.93	0.12	62,62,62,62	0
58	MG	CA	3342	1/1	0.93	0.11	69,69,69,69	0
58	MG	BA	3018	1/1	0.93	0.08	72,72,72,72	0
58	MG	AA	3213	1/1	0.93	0.14	50,50,50,50	1
58	MG	DA	1680	1/1	0.93	0.15	56,56,56,56	0
58	MG	AA	3808	1/1	0.93	0.15	33,33,33,33	1
58	MG	CA	3352	1/1	0.93	0.08	46,46,46,46	0
58	MG	CA	3357	1/1	0.93	0.15	57,57,57,57	0
58	MG	BX	102	1/1	0.93	0.15	67,67,67,67	0
58	MG	AA	3811	1/1	0.93	0.10	53,53,53,53	0
58	MG	BA	3023	1/1	0.93	0.28	75,75,75,75	0
58	MG	CA	3362	1/1	0.93	0.16	57,57,57,57	0
58	MG	CA	3364	1/1	0.93	0.10	65,65,65,65	0
58	MG	BX	105	1/1	0.93	0.11	78,78,78,78	0
58	MG	AA	3630	1/1	0.93	0.10	58,58,58,58	0
58	MG	CA	3369	1/1	0.93	0.09	58,58,58,58	0
58	MG	AA	3714	1/1	0.93	0.16	55,55,55,55	1
58	MG	AA	3819	1/1	0.93	0.08	44,44,44,44	0
58	MG	AA	3096	1/1	0.93	0.21	81,81,81,81	0
58	MG	CA	3155	1/1	0.93	0.24	69,69,69,69	0
58	MG	AA	3268	1/1	0.93	0.29	61,61,61,61	0
58	MG	CA	3157	1/1	0.93	0.18	68,68,68,68	0
58	MG	CA	3595	1/1	0.93	0.07	69,69,69,69	0
58	MG	BA	3120	1/1	0.93	0.16	78,78,78,78	0
58	MG	AA	3016	1/1	0.93	0.19	57,57,57,57	0
58	MG	AA	3041	1/1	0.93	0.33	75,75,75,75	0
58	MG	CA	3601	1/1	0.93	0.08	73,73,73,73	0
58	MG	CA	3605	1/1	0.93	0.12	63,63,63,63	0
58	MG	DA	1716	1/1	0.93	0.10	75,75,75,75	0
58	MG	DA	1717	1/1	0.93	0.13	74,74,74,74	0
58	MG	CA	3388	1/1	0.93	0.12	68,68,68,68	0
58	MG	CA	3018	1/1	0.93	0.14	62,62,62,62	0
58	MG	CA	3168	1/1	0.93	0.14	58,58,58,58	0
58	MG	CA	3609	1/1	0.93	0.12	64,64,64,64	0
58	MG	AB	3005	1/1	0.93	0.16	67,67,67,67	0
58	MG	BA	3128	1/1	0.93	0.11	47,47,47,47	0
58	MG	BA	3130	1/1	0.93	0.07	49,49,49,49	0
58	MG	BA	3036	1/1	0.93	0.24	72,72,72,72	0
58	MG	AA	3726	1/1	0.93	0.08	37,37,37,37	0
58	MG	CA	3033	1/1	0.93	0.20	88,88,88,88	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	DA	1731	1/1	0.93	0.14	82,82,82,82	0
58	MG	CA	3180	1/1	0.93	0.29	74,74,74,74	0
58	MG	BA	3038	1/1	0.93	0.08	65,65,65,65	0
58	MG	AB	3008	1/1	0.93	0.16	51,51,51,51	0
58	MG	CA	3625	1/1	0.93	0.13	53,53,53,53	0
58	MG	BA	3043	1/1	0.93	0.18	65,65,65,65	0
58	MG	CA	3410	1/1	0.93	0.11	40,40,40,40	0
58	MG	AA	3638	1/1	0.93	0.08	45,45,45,45	0
58	MG	CA	3044	1/1	0.93	0.10	52,52,52,52	0
58	MG	BA	3147	1/1	0.93	0.09	84,84,84,84	0
58	MG	CA	3420	1/1	0.93	0.10	58,58,58,58	0
58	MG	AB	3016	1/1	0.93	0.09	33,33,33,33	0
58	MG	DA	1747	1/1	0.93	0.20	78,78,78,78	0
58	MG	AA	3226	1/1	0.93	0.20	73,73,73,73	0
58	MG	CA	3428	1/1	0.93	0.08	55,55,55,55	0
58	MG	BA	3150	1/1	0.93	0.11	47,47,47,47	0
58	MG	CA	3430	1/1	0.93	0.16	71,71,71,71	0
58	MG	AA	3732	1/1	0.93	0.13	41,41,41,41	0
58	MG	DA	1755	1/1	0.93	0.19	71,71,71,71	0
58	MG	DA	1757	1/1	0.93	0.12	73,73,73,73	0
58	MG	DA	1759	1/1	0.93	0.07	64,64,64,64	0
58	MG	AA	3448	1/1	0.93	0.06	17,17,17,17	0
58	MG	AB	3020	1/1	0.93	0.11	53,53,53,53	0
58	MG	CA	3203	1/1	0.93	0.29	76,76,76,76	0
58	MG	AB	3021	1/1	0.93	0.17	60,60,60,60	0
58	MG	AA	3643	1/1	0.93	0.09	47,47,47,47	0
58	MG	CA	3457	1/1	0.93	0.15	58,58,58,58	0
58	MG	DE	201	1/1	0.93	0.12	82,82,82,82	0
58	MG	AA	3738	1/1	0.93	0.11	28,28,28,28	0
58	MG	BA	3162	1/1	0.93	0.09	54,54,54,54	0
58	MG	AA	3449	1/1	0.93	0.13	53,53,53,53	0
58	MG	CA	3665	1/1	0.93	0.15	55,55,55,55	0
58	MG	AA	3451	1/1	0.93	0.11	53,53,53,53	1
58	MG	CA	3064	1/1	0.93	0.12	51,51,51,51	0
58	MG	AA	3747	1/1	0.93	0.13	62,62,62,62	0
58	MG	CA	3476	1/1	0.93	0.12	54,54,54,54	0
58	MG	AA	3583	1/1	0.93	0.16	64,64,64,64	0
60	ZN	C4	501	1/1	0.93	0.06	192,192,192,192	0
58	MG	AA	3588	1/1	0.93	0.18	54,54,54,54	0
58	MG	AA	3236	1/1	0.94	0.22	37,37,37,37	1
58	MG	CA	3402	1/1	0.94	0.14	67,67,67,67	0
58	MG	CA	3150	1/1	0.94	0.13	63,63,63,63	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	AE	302	1/1	0.94	0.15	68,68,68,68	0
58	MG	CA	3651	1/1	0.94	0.14	51,51,51,51	0
58	MG	AF	302	1/1	0.94	0.21	31,31,31,31	1
58	MG	BB	3001	1/1	0.94	0.23	76,76,76,76	0
58	MG	AA	3615	1/1	0.94	0.06	55,55,55,55	0
58	MG	AA	3462	1/1	0.94	0.12	70,70,70,70	0
58	MG	CA	3659	1/1	0.94	0.22	104,104,104,104	0
58	MG	AG	202	1/1	0.94	0.07	73,73,73,73	0
58	MG	CA	3414	1/1	0.94	0.07	39,39,39,39	0
58	MG	CA	3666	1/1	0.94	0.22	62,62,62,62	0
58	MG	CA	3415	1/1	0.94	0.09	52,52,52,52	0
58	MG	CB	3002	1/1	0.94	0.07	64,64,64,64	0
58	MG	AH	3001	1/1	0.94	0.18	50,50,50,50	0
58	MG	AA	3177	1/1	0.94	0.13	51,51,51,51	0
58	MG	AA	3179	1/1	0.94	0.17	78,78,78,78	0
58	MG	CA	3423	1/1	0.94	0.12	54,54,54,54	0
58	MG	AP	201	1/1	0.94	0.16	66,66,66,66	0
58	MG	AP	203	1/1	0.94	0.10	41,41,41,41	0
58	MG	CB	3010	1/1	0.94	0.09	53,53,53,53	0
58	MG	AA	3116	1/1	0.94	0.16	75,75,75,75	0
58	MG	AU	201	1/1	0.94	0.11	44,44,44,44	0
58	MG	CA	3431	1/1	0.94	0.20	51,51,51,51	0
58	MG	AA	3743	1/1	0.94	0.13	80,80,80,80	0
58	MG	CE	303	1/1	0.94	0.17	53,53,53,53	0
58	MG	AV	204	1/1	0.94	0.17	37,37,37,37	0
58	MG	CA	3435	1/1	0.94	0.07	28,28,28,28	0
58	MG	AA	3184	1/1	0.94	0.07	36,36,36,36	0
58	MG	AW	3001	1/1	0.94	0.20	50,50,50,50	0
58	MG	CF	303	1/1	0.94	0.10	50,50,50,50	0
58	MG	AW	3004	1/1	0.94	0.21	64,64,64,64	0
58	MG	AA	3004	1/1	0.94	0.10	24,24,24,24	0
58	MG	CA	3183	1/1	0.94	0.11	25,25,25,25	0
58	MG	CA	3184	1/1	0.94	0.28	85,85,85,85	0
58	MG	CA	3001	1/1	0.94	0.20	71,71,71,71	0
58	MG	CA	3467	1/1	0.94	0.08	54,54,54,54	0
58	MG	CQ	203	1/1	0.94	0.08	59,59,59,59	0
58	MG	BA	3097	1/1	0.94	0.17	66,66,66,66	0
58	MG	CA	3470	1/1	0.94	0.13	69,69,69,69	0
58	MG	CV	202	1/1	0.94	0.18	85,85,85,85	0
58	MG	AA	3014	1/1	0.94	0.12	44,44,44,44	0
58	MG	CA	3006	1/1	0.94	0.08	65,65,65,65	0
58	MG	AA	3125	1/1	0.94	0.16	63,63,63,63	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	AA	3128	1/1	0.94	0.16	71,71,71,71	0
58	MG	AA	3489	1/1	0.94	0.07	63,63,63,63	0
58	MG	CA	3197	1/1	0.94	0.23	63,63,63,63	0
58	MG	DA	1608	1/1	0.94	0.11	58,58,58,58	0
58	MG	A5	101	1/1	0.94	0.10	43,43,43,43	1
58	MG	AA	3262	1/1	0.94	0.14	49,49,49,49	0
58	MG	AA	3632	1/1	0.94	0.07	45,45,45,45	0
58	MG	AA	3194	1/1	0.94	0.17	60,60,60,60	0
58	MG	DA	1616	1/1	0.94	0.08	51,51,51,51	0
58	MG	AA	3082	1/1	0.94	0.08	38,38,38,38	0
58	MG	AA	3496	1/1	0.94	0.07	58,58,58,58	0
58	MG	CA	3032	1/1	0.94	0.24	67,67,67,67	0
58	MG	AA	3637	1/1	0.94	0.17	64,64,64,64	0
58	MG	CA	3208	1/1	0.94	0.16	69,69,69,69	0
58	MG	AA	3500	1/1	0.94	0.09	55,55,55,55	0
58	MG	CA	3491	1/1	0.94	0.12	65,65,65,65	0
58	MG	CA	3035	1/1	0.94	0.16	58,58,58,58	0
58	MG	AA	3765	1/1	0.94	0.13	61,61,61,61	0
58	MG	CA	3213	1/1	0.94	0.12	68,68,68,68	0
58	MG	CA	3214	1/1	0.94	0.16	43,43,43,43	0
58	MG	CA	3039	1/1	0.94	0.18	69,69,69,69	0
58	MG	BA	3113	1/1	0.94	0.13	60,60,60,60	0
58	MG	CA	3218	1/1	0.94	0.10	50,50,50,50	0
58	MG	CA	3222	1/1	0.94	0.10	53,53,53,53	0
58	MG	AA	3639	1/1	0.94	0.17	71,71,71,71	0
58	MG	CA	3224	1/1	0.94	0.14	64,64,64,64	0
58	MG	AA	3509	1/1	0.94	0.14	48,48,48,48	0
58	MG	AA	3769	1/1	0.94	0.16	56,56,56,56	0
58	MG	DA	1644	1/1	0.94	0.17	64,64,64,64	0
58	MG	DA	1646	1/1	0.94	0.16	57,57,57,57	0
58	MG	AA	3770	1/1	0.94	0.32	39,39,39,39	0
58	MG	AA	3511	1/1	0.94	0.21	56,56,56,56	0
58	MG	BA	3121	1/1	0.94	0.07	59,59,59,59	0
58	MG	CA	3233	1/1	0.94	0.14	56,56,56,56	0
58	MG	DA	1654	1/1	0.94	0.17	57,57,57,57	0
58	MG	AA	3365	1/1	0.94	0.11	54,54,54,54	0
58	MG	AA	3372	1/1	0.94	0.18	61,61,61,61	0
58	MG	AA	3197	1/1	0.94	0.17	49,49,49,49	0
58	MG	AA	3103	1/1	0.94	0.19	48,48,48,48	0
58	MG	CA	3056	1/1	0.94	0.14	61,61,61,61	0
58	MG	AA	3529	1/1	0.94	0.09	28,28,28,28	0
58	MG	AA	3783	1/1	0.94	0.10	52,52,52,52	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	BA	3132	1/1	0.94	0.12	61,61,61,61	0
58	MG	BA	3133	1/1	0.94	0.09	68,68,68,68	0
58	MG	AA	3062	1/1	0.94	0.28	66,66,66,66	0
58	MG	AA	3385	1/1	0.94	0.08	28,28,28,28	0
58	MG	DA	1667	1/1	0.94	0.25	61,61,61,61	0
58	MG	BA	3019	1/1	0.94	0.14	55,55,55,55	0
58	MG	AA	3144	1/1	0.94	0.15	47,47,47,47	0
58	MG	BA	3143	1/1	0.94	0.14	79,79,79,79	0
58	MG	AA	3544	1/1	0.94	0.12	52,52,52,52	0
58	MG	AA	3546	1/1	0.94	0.08	53,53,53,53	1
58	MG	AA	3661	1/1	0.94	0.20	43,43,43,43	0
58	MG	CA	3258	1/1	0.94	0.12	40,40,40,40	0
58	MG	AA	3271	1/1	0.94	0.10	55,55,55,55	0
58	MG	CA	3261	1/1	0.94	0.11	47,47,47,47	0
58	MG	BA	3026	1/1	0.94	0.20	57,57,57,57	0
58	MG	CA	3076	1/1	0.94	0.26	69,69,69,69	0
58	MG	AA	3799	1/1	0.94	0.13	48,48,48,48	0
58	MG	CA	3544	1/1	0.94	0.09	66,66,66,66	0
58	MG	CA	3278	1/1	0.94	0.07	48,48,48,48	0
58	MG	AA	3665	1/1	0.94	0.14	83,83,83,83	0
58	MG	CA	3282	1/1	0.94	0.07	31,31,31,31	0
58	MG	CA	3284	1/1	0.94	0.07	48,48,48,48	0
58	MG	AA	3085	1/1	0.94	0.10	30,30,30,30	0
58	MG	AA	3204	1/1	0.94	0.12	55,55,55,55	0
58	MG	DA	1694	1/1	0.94	0.19	65,65,65,65	0
58	MG	BA	3032	1/1	0.94	0.09	47,47,47,47	0
58	MG	AA	3419	1/1	0.94	0.12	26,26,26,26	0
58	MG	AA	3572	1/1	0.94	0.10	49,49,49,49	0
58	MG	AA	3108	1/1	0.94	0.12	74,74,74,74	0
58	MG	CA	3559	1/1	0.94	0.07	75,75,75,75	0
58	MG	DA	1701	1/1	0.94	0.17	64,64,64,64	0
58	MG	AA	3063	1/1	0.94	0.27	66,66,66,66	0
58	MG	AA	3809	1/1	0.94	0.16	60,60,60,60	0
58	MG	CA	3295	1/1	0.94	0.08	69,69,69,69	0
58	MG	CA	3091	1/1	0.94	0.20	63,63,63,63	0
58	MG	CA	3567	1/1	0.94	0.15	49,49,49,49	0
58	MG	CA	3092	1/1	0.94	0.27	107,107,107,107	0
58	MG	CA	3299	1/1	0.94	0.21	54,54,54,54	0
58	MG	CA	3093	1/1	0.94	0.12	68,68,68,68	0
58	MG	DA	1712	1/1	0.94	0.08	51,51,51,51	0
58	MG	DA	1713	1/1	0.94	0.15	74,74,74,74	0
58	MG	CA	3575	1/1	0.94	0.07	78,78,78,78	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	AA	3278	1/1	0.94	0.07	35,35,35,35	0
58	MG	AA	3429	1/1	0.94	0.17	42,42,42,42	0
58	MG	BA	3042	1/1	0.94	0.09	69,69,69,69	0
58	MG	AA	3089	1/1	0.94	0.07	33,33,33,33	0
58	MG	AA	3064	1/1	0.94	0.06	35,35,35,35	0
58	MG	CA	3331	1/1	0.94	0.13	43,43,43,43	0
58	MG	AA	3436	1/1	0.94	0.08	52,52,52,52	0
58	MG	BA	3175	1/1	0.94	0.14	78,78,78,78	0
58	MG	AA	3215	1/1	0.94	0.08	56,56,56,56	0
58	MG	AA	3438	1/1	0.94	0.05	19,19,19,19	0
58	MG	CA	3105	1/1	0.94	0.13	45,45,45,45	0
58	MG	BA	3049	1/1	0.94	0.07	36,36,36,36	0
58	MG	BA	3050	1/1	0.94	0.21	67,67,67,67	0
58	MG	CA	3345	1/1	0.94	0.14	87,87,87,87	0
58	MG	CA	3113	1/1	0.94	0.13	60,60,60,60	0
58	MG	AA	3298	1/1	0.94	0.10	57,57,57,57	0
58	MG	AA	3698	1/1	0.94	0.10	62,62,62,62	0
58	MG	CA	3355	1/1	0.94	0.11	59,59,59,59	0
58	MG	CA	3602	1/1	0.94	0.09	78,78,78,78	0
58	MG	CA	3604	1/1	0.94	0.07	74,74,74,74	0
58	MG	AA	3160	1/1	0.94	0.19	50,50,50,50	0
58	MG	DA	1741	1/1	0.94	0.19	68,68,68,68	0
58	MG	AA	3700	1/1	0.94	0.14	48,48,48,48	0
58	MG	AA	3052	1/1	0.94	0.28	63,63,63,63	0
58	MG	CA	3120	1/1	0.94	0.17	127,127,127,127	0
58	MG	AA	3704	1/1	0.94	0.08	76,76,76,76	0
58	MG	BA	3190	1/1	0.94	0.17	89,89,89,89	0
58	MG	AA	3317	1/1	0.94	0.13	57,57,57,57	0
58	MG	CA	3612	1/1	0.94	0.19	74,74,74,74	0
58	MG	AA	3168	1/1	0.94	0.10	64,64,64,64	0
58	MG	CA	3368	1/1	0.94	0.18	64,64,64,64	0
58	MG	BA	3193	1/1	0.94	0.10	70,70,70,70	0
58	MG	AA	3447	1/1	0.94	0.23	75,75,75,75	0
58	MG	AA	3171	1/1	0.94	0.11	53,53,53,53	0
58	MG	BA	3061	1/1	0.94	0.22	67,67,67,67	0
58	MG	CA	3131	1/1	0.94	0.25	70,70,70,70	0
58	MG	CA	3132	1/1	0.94	0.14	61,61,61,61	0
58	MG	CA	3626	1/1	0.94	0.08	62,62,62,62	0
58	MG	AA	3325	1/1	0.94	0.07	65,65,65,65	0
58	MG	BA	3063	1/1	0.94	0.19	51,51,51,51	0
58	MG	DD	502	1/1	0.94	0.16	61,61,61,61	0
58	MG	AA	3715	1/1	0.94	0.15	54,54,54,54	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	AA	3056	1/1	0.94	0.12	61,61,61,61	0
58	MG	CA	3633	1/1	0.94	0.07	61,61,61,61	0
58	MG	AA	3231	1/1	0.94	0.15	41,41,41,41	0
58	MG	AD	303	1/1	0.94	0.13	70,70,70,70	0
58	MG	DL	3002	1/1	0.94	0.08	74,74,74,74	0
58	MG	AA	3115	1/1	0.94	0.09	15,15,15,15	0
58	MG	CA	3637	1/1	0.94	0.09	79,79,79,79	0
58	MG	CA	3142	1/1	0.94	0.17	54,54,54,54	0
58	MG	AA	3610	1/1	0.94	0.09	51,51,51,51	0
58	MG	CA	3145	1/1	0.94	0.20	66,66,66,66	0
58	MG	AA	3175	1/1	0.94	0.21	60,60,60,60	0
58	MG	AA	3460	1/1	0.94	0.10	71,71,71,71	0
58	MG	AA	3303	1/1	0.95	0.09	53,53,53,53	0
58	MG	CB	3011	1/1	0.95	0.21	51,51,51,51	0
58	MG	AA	3730	1/1	0.95	0.07	38,38,38,38	0
58	MG	CA	3471	1/1	0.95	0.09	69,69,69,69	0
58	MG	AA	3523	1/1	0.95	0.12	27,27,27,27	0
58	MG	AA	3733	1/1	0.95	0.08	66,66,66,66	0
58	MG	CD	303	1/1	0.95	0.07	35,35,35,35	0
58	MG	CA	3226	1/1	0.95	0.18	64,64,64,64	0
58	MG	AA	3734	1/1	0.95	0.16	65,65,65,65	0
58	MG	CE	305	1/1	0.95	0.09	41,41,41,41	0
58	MG	BA	3165	1/1	0.95	0.07	61,61,61,61	0
58	MG	AA	3735	1/1	0.95	0.11	21,21,21,21	0
58	MG	CA	3073	1/1	0.95	0.11	53,53,53,53	0
58	MG	CF	302	1/1	0.95	0.22	63,63,63,63	0
58	MG	AA	3189	1/1	0.95	0.06	11,11,11,11	0
58	MG	CA	3234	1/1	0.95	0.13	58,58,58,58	0
58	MG	AA	3430	1/1	0.95	0.08	25,25,25,25	0
58	MG	CA	3236	1/1	0.95	0.10	52,52,52,52	0
58	MG	AA	3531	1/1	0.95	0.06	52,52,52,52	0
58	MG	AD	310	1/1	0.95	0.13	44,44,44,44	0
58	MG	AA	3739	1/1	0.95	0.17	74,74,74,74	0
58	MG	AA	3191	1/1	0.95	0.14	44,44,44,44	0
58	MG	AA	3741	1/1	0.95	0.09	45,45,45,45	0
58	MG	AE	305	1/1	0.95	0.07	29,29,29,29	0
58	MG	CU	3002	1/1	0.95	0.15	63,63,63,63	0
58	MG	CA	3492	1/1	0.95	0.09	52,52,52,52	0
58	MG	C0	101	1/1	0.95	0.10	64,64,64,64	0
58	MG	C8	5001	1/1	0.95	0.17	48,48,48,48	0
58	MG	DA	1601	1/1	0.95	0.14	59,59,59,59	0
58	MG	AA	3154	1/1	0.95	0.14	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	AA	3155	1/1	0.95	0.19	48,48,48,48	0
58	MG	AA	3080	1/1	0.95	0.13	33,33,33,33	0
58	MG	AG	201	1/1	0.95	0.09	49,49,49,49	0
58	MG	AA	3324	1/1	0.95	0.06	32,32,32,32	0
58	MG	BA	3066	1/1	0.95	0.17	53,53,53,53	0
58	MG	AA	3750	1/1	0.95	0.06	14,14,14,14	0
58	MG	AA	3158	1/1	0.95	0.09	35,35,35,35	0
58	MG	CA	3503	1/1	0.95	0.11	49,49,49,49	1
58	MG	AA	3552	1/1	0.95	0.12	51,51,51,51	0
58	MG	DA	1614	1/1	0.95	0.18	70,70,70,70	0
58	MG	CA	3505	1/1	0.95	0.07	60,60,60,60	0
58	MG	AA	3328	1/1	0.95	0.05	17,17,17,17	0
58	MG	AA	3045	1/1	0.95	0.44	43,43,43,43	0
58	MG	CA	3259	1/1	0.95	0.20	56,56,56,56	0
58	MG	AQ	201	1/1	0.95	0.28	51,51,51,51	0
58	MG	DA	1622	1/1	0.95	0.06	42,42,42,42	0
58	MG	DA	1623	1/1	0.95	0.26	77,77,77,77	0
58	MG	AA	3023	1/1	0.95	0.09	37,37,37,37	0
58	MG	CA	3512	1/1	0.95	0.07	64,64,64,64	0
58	MG	DA	1627	1/1	0.95	0.21	48,48,48,48	0
58	MG	CA	3264	1/1	0.95	0.06	60,60,60,60	0
58	MG	CA	3269	1/1	0.95	0.11	54,54,54,54	0
58	MG	AA	3164	1/1	0.95	0.16	37,37,37,37	0
58	MG	CA	3273	1/1	0.95	0.11	54,54,54,54	0
58	MG	AA	3445	1/1	0.95	0.09	59,59,59,59	0
58	MG	AA	3250	1/1	0.95	0.11	62,62,62,62	0
58	MG	AA	3252	1/1	0.95	0.09	46,46,46,46	0
58	MG	AA	3032	1/1	0.95	0.12	37,37,37,37	0
58	MG	AA	3764	1/1	0.95	0.10	54,54,54,54	0
58	MG	CA	3112	1/1	0.95	0.08	70,70,70,70	0
58	MG	AX	101	1/1	0.95	0.23	72,72,72,72	0
58	MG	BA	3201	1/1	0.95	0.11	68,68,68,68	0
58	MG	AA	3167	1/1	0.95	0.18	29,29,29,29	0
58	MG	AA	3581	1/1	0.95	0.07	27,27,27,27	0
58	MG	AA	3662	1/1	0.95	0.15	58,58,58,58	0
58	MG	DA	1645	1/1	0.95	0.18	61,61,61,61	0
58	MG	BA	3086	1/1	0.95	0.23	51,51,51,51	0
58	MG	BA	3087	1/1	0.95	0.11	70,70,70,70	0
58	MG	DA	1649	1/1	0.95	0.10	60,60,60,60	0
58	MG	AA	3263	1/1	0.95	0.32	71,71,71,71	0
58	MG	CA	3122	1/1	0.95	0.10	43,43,43,43	0
58	MG	AA	3587	1/1	0.95	0.08	59,59,59,59	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	AA	3203	1/1	0.95	0.15	46,46,46,46	0
58	MG	BA	3091	1/1	0.95	0.24	72,72,72,72	0
58	MG	AA	3127	1/1	0.95	0.16	52,52,52,52	0
58	MG	CA	3302	1/1	0.95	0.09	84,84,84,84	0
58	MG	A6	101	1/1	0.95	0.10	64,64,64,64	0
58	MG	AA	3670	1/1	0.95	0.08	31,31,31,31	0
58	MG	AA	3458	1/1	0.95	0.07	70,70,70,70	0
58	MG	AA	3169	1/1	0.95	0.21	61,61,61,61	0
58	MG	CA	3317	1/1	0.95	0.06	51,51,51,51	0
58	MG	AA	3267	1/1	0.95	0.10	49,49,49,49	0
58	MG	CA	3326	1/1	0.95	0.07	39,39,39,39	0
58	MG	CA	3328	1/1	0.95	0.13	52,52,52,52	0
58	MG	DA	1666	1/1	0.95	0.15	47,47,47,47	0
58	MG	CA	3329	1/1	0.95	0.07	57,57,57,57	0
58	MG	AA	3208	1/1	0.95	0.14	26,26,26,26	1
58	MG	DA	1669	1/1	0.95	0.07	73,73,73,73	0
58	MG	AA	3676	1/1	0.95	0.13	64,64,64,64	0
58	MG	AA	3055	1/1	0.95	0.13	34,34,34,34	0
58	MG	CA	3137	1/1	0.95	0.09	51,51,51,51	0
58	MG	AA	3599	1/1	0.95	0.10	52,52,52,52	0
58	MG	AA	3468	1/1	0.95	0.11	51,51,51,51	0
58	MG	AA	3790	1/1	0.95	0.09	48,48,48,48	0
58	MG	AA	3792	1/1	0.95	0.09	27,27,27,27	0
58	MG	AA	3474	1/1	0.95	0.08	50,50,50,50	0
58	MG	CA	3347	1/1	0.95	0.07	33,33,33,33	0
58	MG	BX	106	1/1	0.95	0.07	55,55,55,55	0
58	MG	CA	3572	1/1	0.95	0.18	76,76,76,76	0
58	MG	CA	3144	1/1	0.95	0.25	56,56,56,56	0
58	MG	BA	3009	1/1	0.95	0.18	58,58,58,58	0
58	MG	CA	3354	1/1	0.95	0.07	46,46,46,46	0
58	MG	AA	3685	1/1	0.95	0.09	47,47,47,47	0
58	MG	CA	3147	1/1	0.95	0.15	58,58,58,58	0
58	MG	AA	3603	1/1	0.95	0.07	35,35,35,35	0
58	MG	BX	110	1/1	0.95	0.08	57,57,57,57	0
58	MG	AA	3797	1/1	0.95	0.08	39,39,39,39	0
58	MG	AA	3033	1/1	0.95	0.29	34,34,34,34	0
58	MG	CA	3003	1/1	0.95	0.21	44,44,44,44	0
58	MG	AA	3020	1/1	0.95	0.07	23,23,23,23	0
58	MG	CA	3005	1/1	0.95	0.22	56,56,56,56	0
58	MG	BA	3114	1/1	0.95	0.21	55,55,55,55	0
58	MG	AA	3693	1/1	0.95	0.17	60,60,60,60	0
58	MG	DA	1702	1/1	0.95	0.14	73,73,73,73	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	CA	3010	1/1	0.95	0.09	40,40,40,40	0
58	MG	AA	3094	1/1	0.95	0.09	29,29,29,29	0
58	MG	CA	3162	1/1	0.95	0.17	63,63,63,63	0
58	MG	CA	3597	1/1	0.95	0.11	51,51,51,51	0
58	MG	CA	3165	1/1	0.95	0.12	41,41,41,41	0
58	MG	CA	3599	1/1	0.95	0.10	69,69,69,69	0
58	MG	CA	3014	1/1	0.95	0.14	62,62,62,62	0
58	MG	CA	3016	1/1	0.95	0.18	79,79,79,79	0
58	MG	AA	3696	1/1	0.95	0.21	76,76,76,76	0
58	MG	CA	3603	1/1	0.95	0.05	48,48,48,48	0
58	MG	AA	3805	1/1	0.95	0.18	40,40,40,40	1
58	MG	AA	3697	1/1	0.95	0.12	69,69,69,69	0
58	MG	AA	3366	1/1	0.95	0.06	52,52,52,52	0
58	MG	AA	3367	1/1	0.95	0.08	50,50,50,50	0
58	MG	AA	3176	1/1	0.95	0.09	49,49,49,49	0
58	MG	CA	3391	1/1	0.95	0.04	61,61,61,61	0
58	MG	DA	1721	1/1	0.95	0.10	65,65,65,65	0
58	MG	DA	1722	1/1	0.95	0.07	58,58,58,58	0
58	MG	CA	3178	1/1	0.95	0.10	34,34,34,34	0
58	MG	CA	3393	1/1	0.95	0.07	35,35,35,35	0
58	MG	BA	3024	1/1	0.95	0.23	63,63,63,63	0
58	MG	BA	3127	1/1	0.95	0.11	50,50,50,50	0
58	MG	CA	3615	1/1	0.95	0.19	65,65,65,65	0
58	MG	AA	3484	1/1	0.95	0.12	35,35,35,35	0
58	MG	CA	3182	1/1	0.95	0.10	47,47,47,47	0
58	MG	CA	3399	1/1	0.95	0.09	63,63,63,63	0
58	MG	CA	3621	1/1	0.95	0.20	65,65,65,65	0
58	MG	AA	3138	1/1	0.95	0.09	54,54,54,54	0
58	MG	CA	3401	1/1	0.95	0.14	60,60,60,60	0
58	MG	DA	1735	1/1	0.95	0.09	70,70,70,70	0
58	MG	AA	3140	1/1	0.95	0.05	56,56,56,56	0
58	MG	CA	3036	1/1	0.95	0.08	42,42,42,42	0
58	MG	CA	3037	1/1	0.95	0.10	57,57,57,57	0
58	MG	AA	3817	1/1	0.95	0.21	57,57,57,57	0
58	MG	AA	3707	1/1	0.95	0.16	31,31,31,31	1
58	MG	CA	3191	1/1	0.95	0.14	84,84,84,84	0
58	MG	AA	3490	1/1	0.95	0.06	50,50,50,50	0
58	MG	AA	3225	1/1	0.95	0.10	34,34,34,34	0
58	MG	DA	1745	1/1	0.95	0.09	69,69,69,69	0
58	MG	AA	3280	1/1	0.95	0.09	46,46,46,46	0
58	MG	BA	3138	1/1	0.95	0.14	62,62,62,62	0
58	MG	DA	1748	1/1	0.95	0.18	66,66,66,66	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	AA	3281	1/1	0.95	0.21	60,60,60,60	0
58	MG	DA	1750	1/1	0.95	0.08	71,71,71,71	0
58	MG	CA	3418	1/1	0.95	0.10	39,39,39,39	0
58	MG	BA	3141	1/1	0.95	0.08	49,49,49,49	0
58	MG	AA	3282	1/1	0.95	0.14	39,39,39,39	0
58	MG	AA	3716	1/1	0.95	0.06	63,63,63,63	0
58	MG	BA	3146	1/1	0.95	0.13	65,65,65,65	0
58	MG	CA	3052	1/1	0.95	0.24	69,69,69,69	0
58	MG	DA	1758	1/1	0.95	0.13	64,64,64,64	0
58	MG	AA	3623	1/1	0.95	0.06	43,43,43,43	0
58	MG	CA	3054	1/1	0.95	0.19	68,68,68,68	0
58	MG	CA	3207	1/1	0.95	0.21	55,55,55,55	0
58	MG	AB	3010	1/1	0.95	0.11	51,51,51,51	1
58	MG	AA	3074	1/1	0.95	0.16	59,59,59,59	0
58	MG	CA	3434	1/1	0.95	0.10	68,68,68,68	0
58	MG	AA	3078	1/1	0.95	0.14	49,49,49,49	0
58	MG	CA	3436	1/1	0.95	0.06	53,53,53,53	0
58	MG	AA	3286	1/1	0.95	0.07	53,53,53,53	0
58	MG	CA	3443	1/1	0.95	0.18	66,66,66,66	0
58	MG	BA	3044	1/1	0.95	0.09	56,56,56,56	0
58	MG	BA	3156	1/1	0.95	0.09	36,36,36,36	0
58	MG	CA	3062	1/1	0.95	0.27	65,65,65,65	0
58	MG	CA	3456	1/1	0.95	0.07	46,46,46,46	0
58	MG	AA	3097	1/1	0.95	0.12	61,61,61,61	0
58	MG	CA	3459	1/1	0.95	0.06	48,48,48,48	0
58	MG	CA	3217	1/1	0.95	0.10	66,66,66,66	0
58	MG	CA	3463	1/1	0.95	0.08	50,50,50,50	0
58	MG	CA	3464	1/1	0.95	0.15	47,47,47,47	0
58	MG	AA	3021	1/1	0.95	0.10	39,39,39,39	0
60	ZN	DN	501	1/1	0.95	0.07	127,127,127,127	0
58	MG	CA	3221	1/1	0.95	0.10	76,76,76,76	0
58	MG	AA	3131	1/1	0.96	0.10	36,36,36,36	0
58	MG	CA	3664	1/1	0.96	0.13	55,55,55,55	0
58	MG	BA	3111	1/1	0.96	0.32	72,72,72,72	0
58	MG	AA	3276	1/1	0.96	0.26	50,50,50,50	0
58	MG	CA	3202	1/1	0.96	0.20	58,58,58,58	0
58	MG	AA	3132	1/1	0.96	0.14	53,53,53,53	0
58	MG	A0	103	1/1	0.96	0.09	54,54,54,54	0
58	MG	A0	105	1/1	0.96	0.07	36,36,36,36	0
58	MG	CB	3005	1/1	0.96	0.24	61,61,61,61	0
58	MG	AA	3195	1/1	0.96	0.10	43,43,43,43	0
58	MG	CA	3041	1/1	0.96	0.18	31,31,31,31	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	CA	3441	1/1	0.96	0.18	56,56,56,56	0
58	MG	CA	3442	1/1	0.96	0.19	75,75,75,75	0
58	MG	AA	3751	1/1	0.96	0.05	26,26,26,26	0
58	MG	AA	3279	1/1	0.96	0.10	51,51,51,51	0
58	MG	AA	3081	1/1	0.96	0.08	56,56,56,56	0
58	MG	CA	3449	1/1	0.96	0.08	42,42,42,42	0
58	MG	CA	3451	1/1	0.96	0.05	47,47,47,47	0
58	MG	CA	3452	1/1	0.96	0.07	62,62,62,62	0
58	MG	CA	3453	1/1	0.96	0.15	59,59,59,59	0
58	MG	CA	3454	1/1	0.96	0.07	38,38,38,38	0
58	MG	AA	3370	1/1	0.96	0.12	57,57,57,57	0
58	MG	BA	3122	1/1	0.96	0.07	58,58,58,58	0
58	MG	BA	3123	1/1	0.96	0.07	54,54,54,54	0
58	MG	CA	3458	1/1	0.96	0.12	46,46,46,46	0
58	MG	AA	3371	1/1	0.96	0.11	59,59,59,59	0
58	MG	AA	3235	1/1	0.96	0.10	54,54,54,54	0
58	MG	AA	3136	1/1	0.96	0.21	66,66,66,66	0
58	MG	AA	3494	1/1	0.96	0.07	33,33,33,33	1
58	MG	AA	3283	1/1	0.96	0.18	59,59,59,59	0
58	MG	AA	3379	1/1	0.96	0.06	30,30,30,30	0
58	MG	AA	3198	1/1	0.96	0.07	36,36,36,36	0
58	MG	CA	3469	1/1	0.96	0.08	61,61,61,61	0
58	MG	AA	3763	1/1	0.96	0.14	62,62,62,62	0
58	MG	AA	3382	1/1	0.96	0.07	38,38,38,38	1
58	MG	AA	3238	1/1	0.96	0.15	55,55,55,55	0
58	MG	CR	201	1/1	0.96	0.06	51,51,51,51	0
58	MG	AA	3515	1/1	0.96	0.05	18,18,18,18	0
58	MG	AA	3517	1/1	0.96	0.09	18,18,18,18	0
58	MG	CA	3061	1/1	0.96	0.24	74,74,74,74	0
58	MG	CA	3477	1/1	0.96	0.10	54,54,54,54	0
58	MG	C1	101	1/1	0.96	0.09	67,67,67,67	0
58	MG	C7	101	1/1	0.96	0.07	47,47,47,47	0
58	MG	AA	3642	1/1	0.96	0.10	41,41,41,41	0
58	MG	AA	3394	1/1	0.96	0.05	18,18,18,18	0
58	MG	CA	3480	1/1	0.96	0.09	44,44,44,44	0
58	MG	AA	3034	1/1	0.96	0.14	56,56,56,56	0
58	MG	AA	3646	1/1	0.96	0.11	57,57,57,57	0
58	MG	BA	3012	1/1	0.96	0.05	29,29,29,29	0
58	MG	AA	3401	1/1	0.96	0.10	33,33,33,33	0
58	MG	AA	3241	1/1	0.96	0.15	64,64,64,64	0
58	MG	AA	3777	1/1	0.96	0.05	20,20,20,20	0
58	MG	AA	3405	1/1	0.96	0.06	54,54,54,54	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	DA	1610	1/1	0.96	0.10	45,45,45,45	0
58	MG	AA	3779	1/1	0.96	0.12	61,61,61,61	0
58	MG	DA	1612	1/1	0.96	0.07	38,38,38,38	0
58	MG	AA	3411	1/1	0.96	0.06	41,41,41,41	0
58	MG	AA	3532	1/1	0.96	0.12	60,60,60,60	0
58	MG	CA	3075	1/1	0.96	0.09	52,52,52,52	0
58	MG	AA	3654	1/1	0.96	0.13	65,65,65,65	0
58	MG	AA	3296	1/1	0.96	0.06	18,18,18,18	0
58	MG	DA	1618	1/1	0.96	0.10	47,47,47,47	0
58	MG	DA	1619	1/1	0.96	0.18	62,62,62,62	0
58	MG	AA	3787	1/1	0.96	0.14	50,50,50,50	0
58	MG	AA	3297	1/1	0.96	0.05	20,20,20,20	0
58	MG	AA	3542	1/1	0.96	0.06	45,45,45,45	0
58	MG	CA	3251	1/1	0.96	0.07	47,47,47,47	0
58	MG	AA	3035	1/1	0.96	0.12	59,59,59,59	0
58	MG	CA	3254	1/1	0.96	0.17	63,63,63,63	0
58	MG	AA	3139	1/1	0.96	0.11	49,49,49,49	0
58	MG	AA	3305	1/1	0.96	0.12	53,53,53,53	0
58	MG	CA	3087	1/1	0.96	0.14	35,35,35,35	0
58	MG	AA	3309	1/1	0.96	0.10	44,44,44,44	0
58	MG	BA	3029	1/1	0.96	0.08	54,54,54,54	0
58	MG	CA	3507	1/1	0.96	0.09	71,71,71,71	0
58	MG	DA	1633	1/1	0.96	0.19	60,60,60,60	0
58	MG	AA	3666	1/1	0.96	0.14	62,62,62,62	0
58	MG	AA	3667	1/1	0.96	0.12	29,29,29,29	0
58	MG	DA	1636	1/1	0.96	0.17	64,64,64,64	0
58	MG	CA	3265	1/1	0.96	0.12	55,55,55,55	0
58	MG	CA	3266	1/1	0.96	0.09	58,58,58,58	0
58	MG	AA	3548	1/1	0.96	0.05	29,29,29,29	0
58	MG	CA	3513	1/1	0.96	0.13	66,66,66,66	0
58	MG	AA	3550	1/1	0.96	0.07	52,52,52,52	0
58	MG	CA	3272	1/1	0.96	0.06	34,34,34,34	0
58	MG	AA	3428	1/1	0.96	0.12	41,41,41,41	0
58	MG	AA	3671	1/1	0.96	0.10	57,57,57,57	0
58	MG	AA	3047	1/1	0.96	0.05	31,31,31,31	0
58	MG	CA	3276	1/1	0.96	0.07	51,51,51,51	0
58	MG	DA	1647	1/1	0.96	0.07	49,49,49,49	0
58	MG	CA	3277	1/1	0.96	0.07	42,42,42,42	0
58	MG	AA	3554	1/1	0.96	0.07	40,40,40,40	0
58	MG	AA	3555	1/1	0.96	0.06	49,49,49,49	0
58	MG	BA	3178	1/1	0.96	0.09	63,63,63,63	0
58	MG	CA	3524	1/1	0.96	0.10	54,54,54,54	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	DA	1653	1/1	0.96	0.05	29,29,29,29	0
58	MG	CA	3525	1/1	0.96	0.12	40,40,40,40	0
58	MG	AA	3560	1/1	0.96	0.08	39,39,39,39	0
58	MG	BA	3180	1/1	0.96	0.06	41,41,41,41	0
58	MG	AA	3311	1/1	0.96	0.09	34,34,34,34	0
58	MG	CA	3104	1/1	0.96	0.13	60,60,60,60	0
58	MG	AA	3677	1/1	0.96	0.04	40,40,40,40	0
58	MG	CA	3289	1/1	0.96	0.14	51,51,51,51	0
58	MG	AA	3810	1/1	0.96	0.15	62,62,62,62	0
58	MG	CA	3107	1/1	0.96	0.07	54,54,54,54	0
58	MG	AA	3563	1/1	0.96	0.11	49,49,49,49	1
58	MG	CA	3109	1/1	0.96	0.15	59,59,59,59	0
58	MG	CA	3111	1/1	0.96	0.12	62,62,62,62	0
58	MG	AA	3812	1/1	0.96	0.08	57,57,57,57	0
58	MG	AA	3247	1/1	0.96	0.34	68,68,68,68	0
58	MG	AA	3814	1/1	0.96	0.11	43,43,43,43	0
58	MG	CA	3115	1/1	0.96	0.19	37,37,37,37	0
58	MG	BA	3189	1/1	0.96	0.08	66,66,66,66	0
58	MG	CA	3303	1/1	0.96	0.08	45,45,45,45	0
58	MG	AA	3565	1/1	0.96	0.07	17,17,17,17	0
58	MG	AA	3682	1/1	0.96	0.05	51,51,51,51	0
58	MG	AA	3569	1/1	0.96	0.06	15,15,15,15	0
58	MG	CA	3314	1/1	0.96	0.11	50,50,50,50	0
58	MG	AA	3173	1/1	0.96	0.22	71,71,71,71	0
58	MG	CA	3552	1/1	0.96	0.06	34,34,34,34	0
58	MG	DA	1679	1/1	0.96	0.10	60,60,60,60	0
58	MG	CA	3316	1/1	0.96	0.05	60,60,60,60	0
58	MG	DA	1681	1/1	0.96	0.15	46,46,46,46	0
58	MG	DA	1682	1/1	0.96	0.11	52,52,52,52	0
58	MG	AA	3142	1/1	0.96	0.06	41,41,41,41	0
58	MG	CA	3320	1/1	0.96	0.08	66,66,66,66	0
58	MG	CA	3323	1/1	0.96	0.08	45,45,45,45	0
58	MG	AA	3575	1/1	0.96	0.10	30,30,30,30	0
58	MG	CA	3560	1/1	0.96	0.17	56,56,56,56	0
58	MG	AA	3205	1/1	0.96	0.12	56,56,56,56	0
58	MG	AA	3691	1/1	0.96	0.17	87,87,87,87	0
58	MG	AA	3692	1/1	0.96	0.09	51,51,51,51	0
58	MG	AA	3143	1/1	0.96	0.12	28,28,28,28	0
58	MG	DA	1692	1/1	0.96	0.09	53,53,53,53	0
58	MG	DA	1693	1/1	0.96	0.08	60,60,60,60	0
58	MG	AA	3207	1/1	0.96	0.19	37,37,37,37	0
58	MG	AA	3254	1/1	0.96	0.12	35,35,35,35	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	CA	3336	1/1	0.96	0.08	60,60,60,60	0
58	MG	CA	3571	1/1	0.96	0.08	77,77,77,77	0
58	MG	AB	3015	1/1	0.96	0.04	38,38,38,38	0
58	MG	AA	3261	1/1	0.96	0.27	69,69,69,69	0
58	MG	AA	3582	1/1	0.96	0.06	37,37,37,37	0
58	MG	CA	3133	1/1	0.96	0.05	29,29,29,29	0
58	MG	AA	3058	1/1	0.96	0.13	35,35,35,35	0
58	MG	CA	3578	1/1	0.96	0.13	38,38,38,38	0
58	MG	BA	3207	1/1	0.96	0.09	66,66,66,66	0
58	MG	CA	3346	1/1	0.96	0.06	40,40,40,40	0
58	MG	CA	3581	1/1	0.96	0.08	51,51,51,51	0
58	MG	AA	3585	1/1	0.96	0.09	63,63,63,63	0
58	MG	AA	3701	1/1	0.96	0.09	33,33,33,33	0
58	MG	CA	3584	1/1	0.96	0.08	43,43,43,43	0
58	MG	AA	3586	1/1	0.96	0.10	65,65,65,65	0
58	MG	CA	3586	1/1	0.96	0.06	46,46,46,46	0
58	MG	AA	3333	1/1	0.96	0.09	66,66,66,66	0
58	MG	AA	3334	1/1	0.96	0.07	58,58,58,58	0
58	MG	AA	3706	1/1	0.96	0.18	29,29,29,29	1
58	MG	AA	3446	1/1	0.96	0.06	59,59,59,59	0
58	MG	BF	3001	1/1	0.96	0.23	71,71,71,71	0
58	MG	AD	306	1/1	0.96	0.09	41,41,41,41	0
58	MG	CA	3594	1/1	0.96	0.17	74,74,74,74	0
58	MG	BL	3002	1/1	0.96	0.07	49,49,49,49	0
58	MG	AA	3591	1/1	0.96	0.09	66,66,66,66	0
58	MG	AA	3104	1/1	0.96	0.05	13,13,13,13	0
58	MG	AA	3210	1/1	0.96	0.18	63,63,63,63	0
58	MG	AA	3338	1/1	0.96	0.05	29,29,29,29	0
58	MG	DA	1727	1/1	0.96	0.06	57,57,57,57	0
58	MG	AA	3121	1/1	0.96	0.11	46,46,46,46	0
58	MG	AA	3342	1/1	0.96	0.07	4,4,4,4	0
58	MG	BA	3079	1/1	0.96	0.05	35,35,35,35	0
58	MG	AE	301	1/1	0.96	0.06	19,19,19,19	0
58	MG	AA	3073	1/1	0.96	0.07	25,25,25,25	0
58	MG	AE	304	1/1	0.96	0.07	40,40,40,40	0
58	MG	AA	3153	1/1	0.96	0.12	67,67,67,67	0
58	MG	CA	3158	1/1	0.96	0.09	54,54,54,54	0
58	MG	AA	3456	1/1	0.96	0.05	32,32,32,32	0
58	MG	CA	3381	1/1	0.96	0.10	68,68,68,68	0
58	MG	AF	303	1/1	0.96	0.10	43,43,43,43	0
58	MG	CA	3386	1/1	0.96	0.18	63,63,63,63	0
58	MG	AA	3602	1/1	0.96	0.20	47,47,47,47	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	CA	3163	1/1	0.96	0.12	45,45,45,45	0
58	MG	AF	306	1/1	0.96	0.18	48,48,48,48	0
58	MG	AA	3457	1/1	0.96	0.13	65,65,65,65	0
58	MG	AF	308	1/1	0.96	0.07	55,55,55,55	0
58	MG	CA	3618	1/1	0.96	0.09	37,37,37,37	0
58	MG	AA	3048	1/1	0.96	0.10	33,33,33,33	0
58	MG	AA	3728	1/1	0.96	0.08	48,48,48,48	0
58	MG	CA	3171	1/1	0.96	0.10	45,45,45,45	0
58	MG	AA	3061	1/1	0.96	0.05	26,26,26,26	0
58	MG	AA	3350	1/1	0.96	0.08	32,32,32,32	0
58	MG	AA	3351	1/1	0.96	0.07	29,29,29,29	0
58	MG	CA	3398	1/1	0.96	0.06	58,58,58,58	0
58	MG	AN	3003	1/1	0.96	0.07	45,45,45,45	0
58	MG	AA	3463	1/1	0.96	0.10	46,46,46,46	0
58	MG	CA	3012	1/1	0.96	0.09	58,58,58,58	0
58	MG	AA	3353	1/1	0.96	0.12	75,75,75,75	0
58	MG	AA	3466	1/1	0.96	0.07	59,59,59,59	0
58	MG	CA	3015	1/1	0.96	0.17	82,82,82,82	0
58	MG	AA	3007	1/1	0.96	0.08	20,20,20,20	0
58	MG	AQ	203	1/1	0.96	0.13	40,40,40,40	0
58	MG	AR	5001	1/1	0.96	0.06	32,32,32,32	0
58	MG	AA	3470	1/1	0.96	0.07	28,28,28,28	0
58	MG	CA	3021	1/1	0.96	0.09	27,27,27,27	0
58	MG	CA	3022	1/1	0.96	0.06	35,35,35,35	0
58	MG	AA	3355	1/1	0.96	0.05	57,57,57,57	0
58	MG	CA	3416	1/1	0.96	0.07	34,34,34,34	0
58	MG	CA	3192	1/1	0.96	0.22	65,65,65,65	0
58	MG	CA	3193	1/1	0.96	0.10	57,57,57,57	0
58	MG	CA	3419	1/1	0.96	0.13	40,40,40,40	0
58	MG	AA	3224	1/1	0.96	0.10	26,26,26,26	0
58	MG	CA	3421	1/1	0.96	0.14	69,69,69,69	0
58	MG	AA	3040	1/1	0.96	0.17	45,45,45,45	0
58	MG	CA	3653	1/1	0.96	0.12	25,25,25,25	0
58	MG	CA	3028	1/1	0.96	0.08	42,42,42,42	0
58	MG	AA	3619	1/1	0.96	0.09	37,37,37,37	0
60	ZN	A4	501	1/1	0.96	0.06	133,133,133,133	0
58	MG	CA	3425	1/1	0.96	0.11	54,54,54,54	0
58	MG	AA	3130	1/1	0.96	0.16	70,70,70,70	0
62	GDP	BZ	801	28/28	0.96	0.07	52,52,52,52	0
58	MG	CA	3661	1/1	0.96	0.13	60,60,60,60	0
58	MG	BA	3040	1/1	0.97	0.10	48,48,48,48	0
58	MG	BA	3041	1/1	0.97	0.07	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	AA	3098	1/1	0.97	0.06	24,24,24,24	0
58	MG	CE	301	1/1	0.97	0.14	64,64,64,64	0
58	MG	AA	3467	1/1	0.97	0.07	44,44,44,44	0
58	MG	CA	3256	1/1	0.97	0.12	40,40,40,40	0
58	MG	CA	3095	1/1	0.97	0.15	86,86,86,86	0
58	MG	AA	3702	1/1	0.97	0.17	46,46,46,46	1
58	MG	AA	3123	1/1	0.97	0.07	53,53,53,53	0
58	MG	CA	3474	1/1	0.97	0.05	52,52,52,52	0
58	MG	AA	3124	1/1	0.97	0.20	43,43,43,43	0
58	MG	AB	3009	1/1	0.97	0.08	55,55,55,55	0
58	MG	CA	3262	1/1	0.97	0.13	64,64,64,64	0
58	MG	CA	3263	1/1	0.97	0.10	29,29,29,29	0
58	MG	AA	3012	1/1	0.97	0.15	34,34,34,34	0
58	MG	AB	3012	1/1	0.97	0.06	30,30,30,30	1
58	MG	AA	3240	1/1	0.97	0.20	60,60,60,60	0
58	MG	CA	3268	1/1	0.97	0.12	69,69,69,69	0
58	MG	AA	3287	1/1	0.97	0.12	46,46,46,46	0
58	MG	CA	3270	1/1	0.97	0.18	66,66,66,66	0
58	MG	AA	3289	1/1	0.97	0.07	26,26,26,26	0
58	MG	AA	3479	1/1	0.97	0.07	53,53,53,53	0
58	MG	AA	3290	1/1	0.97	0.20	63,63,63,63	0
58	MG	AA	3291	1/1	0.97	0.08	44,44,44,44	0
58	MG	CY	502	1/1	0.97	0.11	54,54,54,54	0
58	MG	AA	3025	1/1	0.97	0.16	41,41,41,41	0
58	MG	AA	3483	1/1	0.97	0.04	44,44,44,44	0
58	MG	C3	101	1/1	0.97	0.07	69,69,69,69	0
58	MG	CA	3110	1/1	0.97	0.10	51,51,51,51	0
58	MG	AA	3293	1/1	0.97	0.12	32,32,32,32	0
58	MG	AA	3295	1/1	0.97	0.12	46,46,46,46	0
58	MG	CA	3280	1/1	0.97	0.10	38,38,38,38	0
58	MG	CA	3281	1/1	0.97	0.05	34,34,34,34	0
58	MG	AD	301	1/1	0.97	0.23	44,44,44,44	0
58	MG	CA	3497	1/1	0.97	0.08	63,63,63,63	0
58	MG	CA	3283	1/1	0.97	0.08	49,49,49,49	0
58	MG	AA	3613	1/1	0.97	0.06	54,54,54,54	0
58	MG	AA	3376	1/1	0.97	0.06	18,18,18,18	0
58	MG	AD	304	1/1	0.97	0.07	18,18,18,18	0
58	MG	CA	3502	1/1	0.97	0.07	69,69,69,69	0
58	MG	AD	305	1/1	0.97	0.21	64,64,64,64	0
58	MG	BA	3204	1/1	0.97	0.10	68,68,68,68	0
58	MG	AA	3723	1/1	0.97	0.06	19,19,19,19	0
58	MG	AA	3377	1/1	0.97	0.04	20,20,20,20	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	AA	3378	1/1	0.97	0.07	18,18,18,18	0
58	MG	AA	3617	1/1	0.97	0.12	30,30,30,30	0
58	MG	CA	3123	1/1	0.97	0.14	66,66,66,66	0
58	MG	AA	3042	1/1	0.97	0.06	36,36,36,36	0
58	MG	AA	3102	1/1	0.97	0.13	50,50,50,50	0
58	MG	AA	3731	1/1	0.97	0.13	31,31,31,31	0
58	MG	AA	3166	1/1	0.97	0.13	57,57,57,57	0
58	MG	AA	3299	1/1	0.97	0.08	21,21,21,21	0
58	MG	CA	3301	1/1	0.97	0.07	58,58,58,58	0
58	MG	AA	3498	1/1	0.97	0.05	45,45,45,45	0
58	MG	BE	3001	1/1	0.97	0.04	59,59,59,59	0
58	MG	CA	3304	1/1	0.97	0.06	53,53,53,53	0
58	MG	AA	3390	1/1	0.97	0.07	47,47,47,47	0
58	MG	BK	201	1/1	0.97	0.12	56,56,56,56	0
58	MG	AA	3505	1/1	0.97	0.07	55,55,55,55	0
58	MG	CA	3312	1/1	0.97	0.07	49,49,49,49	0
58	MG	CA	3313	1/1	0.97	0.07	51,51,51,51	0
58	MG	AA	3507	1/1	0.97	0.10	31,31,31,31	0
58	MG	AA	3391	1/1	0.97	0.05	42,42,42,42	0
58	MG	AA	3628	1/1	0.97	0.11	53,53,53,53	0
58	MG	AA	3301	1/1	0.97	0.05	22,22,22,22	0
58	MG	CA	3529	1/1	0.97	0.09	79,79,79,79	0
58	MG	CA	3318	1/1	0.97	0.04	45,45,45,45	0
58	MG	AA	3043	1/1	0.97	0.12	32,32,32,32	0
58	MG	CA	3322	1/1	0.97	0.05	32,32,32,32	0
58	MG	AA	3059	1/1	0.97	0.12	49,49,49,49	0
58	MG	AA	3744	1/1	0.97	0.11	77,77,77,77	0
58	MG	CA	3325	1/1	0.97	0.13	39,39,39,39	0
58	MG	AA	3403	1/1	0.97	0.04	18,18,18,18	0
58	MG	CA	3327	1/1	0.97	0.06	33,33,33,33	0
58	MG	AA	3306	1/1	0.97	0.06	47,47,47,47	0
58	MG	AA	3307	1/1	0.97	0.10	6,6,6,6	0
58	MG	AA	3749	1/1	0.97	0.14	55,55,55,55	0
58	MG	AO	5001	1/1	0.97	0.05	53,53,53,53	0
58	MG	CA	3333	1/1	0.97	0.07	41,41,41,41	0
58	MG	AA	3520	1/1	0.97	0.08	23,23,23,23	0
58	MG	CA	3335	1/1	0.97	0.10	43,43,43,43	0
58	MG	AA	3636	1/1	0.97	0.07	24,24,24,24	0
58	MG	AA	3522	1/1	0.97	0.05	30,30,30,30	0
58	MG	AA	3410	1/1	0.97	0.10	46,46,46,46	0
58	MG	AA	3526	1/1	0.97	0.15	38,38,38,38	0
58	MG	AA	3105	1/1	0.97	0.19	31,31,31,31	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	AA	3413	1/1	0.97	0.09	36,36,36,36	0
58	MG	AU	202	1/1	0.97	0.24	44,44,44,44	0
58	MG	AA	3044	1/1	0.97	0.13	34,34,34,34	0
58	MG	AV	201	1/1	0.97	0.15	19,19,19,19	0
58	MG	CA	3348	1/1	0.97	0.09	58,58,58,58	0
58	MG	CA	3558	1/1	0.97	0.04	47,47,47,47	0
58	MG	AA	3006	1/1	0.97	0.13	52,52,52,52	0
58	MG	CA	3350	1/1	0.97	0.13	39,39,39,39	0
58	MG	CA	3561	1/1	0.97	0.07	55,55,55,55	1
58	MG	AA	3536	1/1	0.97	0.07	15,15,15,15	0
58	MG	CA	3009	1/1	0.97	0.16	67,67,67,67	0
58	MG	CA	3353	1/1	0.97	0.05	66,66,66,66	0
58	MG	BA	3102	1/1	0.97	0.25	56,56,56,56	0
58	MG	CA	3011	1/1	0.97	0.07	46,46,46,46	0
58	MG	CA	3356	1/1	0.97	0.05	41,41,41,41	0
58	MG	AA	3313	1/1	0.97	0.08	33,33,33,33	0
58	MG	CA	3164	1/1	0.97	0.12	38,38,38,38	0
58	MG	AW	3002	1/1	0.97	0.06	52,52,52,52	0
58	MG	CA	3360	1/1	0.97	0.10	43,43,43,43	0
58	MG	AW	3003	1/1	0.97	0.10	55,55,55,55	0
58	MG	DA	1678	1/1	0.97	0.10	57,57,57,57	0
58	MG	AA	3315	1/1	0.97	0.09	34,34,34,34	0
58	MG	AA	3648	1/1	0.97	0.10	38,38,38,38	0
58	MG	CA	3365	1/1	0.97	0.14	29,29,29,29	0
58	MG	AA	3540	1/1	0.97	0.04	29,29,29,29	0
58	MG	AA	3005	1/1	0.97	0.09	61,61,61,61	0
58	MG	A0	101	1/1	0.97	0.12	51,51,51,51	0
58	MG	A0	102	1/1	0.97	0.09	43,43,43,43	0
58	MG	CA	3370	1/1	0.97	0.07	56,56,56,56	0
58	MG	AA	3010	1/1	0.97	0.22	66,66,66,66	0
58	MG	CA	3023	1/1	0.97	0.08	45,45,45,45	0
58	MG	A0	104	1/1	0.97	0.08	41,41,41,41	0
58	MG	AA	3425	1/1	0.97	0.06	49,49,49,49	0
58	MG	AA	3768	1/1	0.97	0.13	96,96,96,96	0
58	MG	CA	3027	1/1	0.97	0.09	47,47,47,47	0
58	MG	AA	3318	1/1	0.97	0.19	53,53,53,53	0
58	MG	CA	3030	1/1	0.97	0.07	57,57,57,57	0
58	MG	AA	3257	1/1	0.97	0.06	26,26,26,26	0
58	MG	AA	3258	1/1	0.97	0.04	13,13,13,13	0
58	MG	CA	3186	1/1	0.97	0.26	58,58,58,58	0
58	MG	A5	102	1/1	0.97	0.10	47,47,47,47	0
58	MG	AA	3259	1/1	0.97	0.06	20,20,20,20	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	AA	3260	1/1	0.97	0.12	23,23,23,23	0
58	MG	AA	3086	1/1	0.97	0.11	53,53,53,53	0
58	MG	AA	3663	1/1	0.97	0.15	60,60,60,60	0
58	MG	AA	3049	1/1	0.97	0.08	51,51,51,51	0
58	MG	AA	3065	1/1	0.97	0.07	28,28,28,28	0
58	MG	CA	3040	1/1	0.97	0.14	64,64,64,64	0
58	MG	AA	3556	1/1	0.97	0.07	37,37,37,37	0
58	MG	AA	3781	1/1	0.97	0.17	52,52,52,52	1
58	MG	AA	3782	1/1	0.97	0.12	72,72,72,72	0
58	MG	BA	3003	1/1	0.97	0.05	51,51,51,51	0
58	MG	AA	3439	1/1	0.97	0.10	33,33,33,33	0
58	MG	AA	3178	1/1	0.97	0.19	61,61,61,61	0
58	MG	CA	3047	1/1	0.97	0.09	60,60,60,60	0
58	MG	DA	1715	1/1	0.97	0.08	49,49,49,49	0
58	MG	BA	3134	1/1	0.97	0.15	62,62,62,62	0
58	MG	CA	3404	1/1	0.97	0.06	86,86,86,86	0
58	MG	CA	3405	1/1	0.97	0.06	53,53,53,53	0
58	MG	CA	3614	1/1	0.97	0.18	89,89,89,89	0
58	MG	AA	3066	1/1	0.97	0.07	48,48,48,48	0
58	MG	AA	3786	1/1	0.97	0.11	57,57,57,57	0
58	MG	AA	3011	1/1	0.97	0.13	39,39,39,39	0
58	MG	CA	3409	1/1	0.97	0.16	61,61,61,61	0
58	MG	AA	3218	1/1	0.97	0.16	49,49,49,49	0
58	MG	CA	3620	1/1	0.97	0.07	34,34,34,34	0
58	MG	BA	3139	1/1	0.97	0.07	54,54,54,54	0
58	MG	AA	3337	1/1	0.97	0.05	10,10,10,10	0
58	MG	AA	3570	1/1	0.97	0.06	18,18,18,18	0
58	MG	AA	3221	1/1	0.97	0.12	55,55,55,55	0
58	MG	CA	3212	1/1	0.97	0.07	37,37,37,37	0
58	MG	AA	3339	1/1	0.97	0.08	41,41,41,41	0
58	MG	AA	3037	1/1	0.97	0.09	44,44,44,44	0
58	MG	AA	3795	1/1	0.97	0.06	49,49,49,49	0
58	MG	AA	3146	1/1	0.97	0.06	34,34,34,34	0
58	MG	AA	3678	1/1	0.97	0.12	32,32,32,32	0
58	MG	CA	3632	1/1	0.97	0.12	54,54,54,54	0
58	MG	AA	3798	1/1	0.97	0.07	32,32,32,32	0
58	MG	CA	3219	1/1	0.97	0.24	52,52,52,52	0
58	MG	CA	3220	1/1	0.97	0.09	30,30,30,30	0
58	MG	BA	3151	1/1	0.97	0.11	63,63,63,63	0
58	MG	CA	3427	1/1	0.97	0.15	53,53,53,53	0
58	MG	BA	3152	1/1	0.97	0.08	58,58,58,58	0
58	MG	CA	3065	1/1	0.97	0.04	41,41,41,41	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	CA	3640	1/1	0.97	0.12	57,57,57,57	0
58	MG	CA	3641	1/1	0.97	0.08	54,54,54,54	0
58	MG	CA	3643	1/1	0.97	0.05	57,57,57,57	0
58	MG	AA	3117	1/1	0.97	0.11	50,50,50,50	0
58	MG	AA	3450	1/1	0.97	0.07	48,48,48,48	0
58	MG	AA	3187	1/1	0.97	0.06	36,36,36,36	0
58	MG	AA	3346	1/1	0.97	0.06	45,45,45,45	0
58	MG	AA	3188	1/1	0.97	0.05	31,31,31,31	0
58	MG	BA	3159	1/1	0.97	0.04	55,55,55,55	0
58	MG	CA	3231	1/1	0.97	0.22	50,50,50,50	0
58	MG	AA	3684	1/1	0.97	0.05	28,28,28,28	0
58	MG	CA	3438	1/1	0.97	0.06	49,49,49,49	0
58	MG	AA	3228	1/1	0.97	0.08	55,55,55,55	0
58	MG	AA	3686	1/1	0.97	0.12	70,70,70,70	0
58	MG	AA	3687	1/1	0.97	0.05	46,46,46,46	0
58	MG	AA	3584	1/1	0.97	0.05	14,14,14,14	0
58	MG	DA	1762	1/1	0.97	0.05	53,53,53,53	0
58	MG	CA	3658	1/1	0.97	0.16	50,50,50,50	0
58	MG	CA	3446	1/1	0.97	0.10	39,39,39,39	0
58	MG	CA	3660	1/1	0.97	0.09	38,38,38,38	0
58	MG	AA	3275	1/1	0.97	0.11	56,56,56,56	0
58	MG	AA	3053	1/1	0.97	0.05	13,13,13,13	0
58	MG	CA	3450	1/1	0.97	0.07	66,66,66,66	0
58	MG	CA	3079	1/1	0.97	0.05	46,46,46,46	0
58	MG	DF	3001	1/1	0.97	0.07	49,49,49,49	0
58	MG	AA	3352	1/1	0.97	0.08	51,51,51,51	0
58	MG	AA	3230	1/1	0.97	0.16	49,49,49,49	0
58	MG	AA	3190	1/1	0.97	0.14	40,40,40,40	0
58	MG	AA	3815	1/1	0.97	0.18	53,53,53,53	0
58	MG	CA	3244	1/1	0.97	0.07	40,40,40,40	0
58	MG	CA	3084	1/1	0.97	0.22	86,86,86,86	0
58	MG	AA	3152	1/1	0.97	0.07	49,49,49,49	0
58	MG	AA	3120	1/1	0.97	0.09	43,43,43,43	0
58	MG	CA	3460	1/1	0.97	0.09	49,49,49,49	0
58	MG	AA	3072	1/1	0.97	0.20	40,40,40,40	0
58	MG	CA	3462	1/1	0.97	0.13	43,43,43,43	0
58	MG	AA	3595	1/1	0.97	0.07	42,42,42,42	0
61	SF4	DD	501	8/8	0.97	0.06	90,90,90,90	0
58	MG	AA	3465	1/1	0.97	0.05	40,40,40,40	0
58	MG	CA	3465	1/1	0.97	0.07	46,46,46,46	0
58	MG	AA	3545	1/1	0.98	0.06	15,15,15,15	0
58	MG	AA	3161	1/1	0.98	0.05	54,54,54,54	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	AA	3162	1/1	0.98	0.08	58,58,58,58	0
58	MG	AA	3046	1/1	0.98	0.09	35,35,35,35	0
58	MG	AA	3549	1/1	0.98	0.10	58,58,58,58	0
58	MG	AA	3300	1/1	0.98	0.08	51,51,51,51	0
58	MG	AA	3551	1/1	0.98	0.04	46,46,46,46	0
58	MG	CA	3372	1/1	0.98	0.06	53,53,53,53	0
58	MG	BA	3153	1/1	0.98	0.06	48,48,48,48	0
58	MG	AA	3356	1/1	0.98	0.05	33,33,33,33	0
58	MG	AA	3090	1/1	0.98	0.09	50,50,50,50	0
58	MG	AA	3302	1/1	0.98	0.15	56,56,56,56	0
58	MG	AA	3091	1/1	0.98	0.10	34,34,34,34	0
58	MG	AA	3361	1/1	0.98	0.12	28,28,28,28	0
58	MG	AA	3557	1/1	0.98	0.06	39,39,39,39	0
58	MG	AA	3559	1/1	0.98	0.10	50,50,50,50	0
58	MG	CA	3554	1/1	0.98	0.04	67,67,67,67	0
58	MG	AA	3092	1/1	0.98	0.06	43,43,43,43	0
58	MG	AA	3561	1/1	0.98	0.06	56,56,56,56	0
58	MG	DA	1625	1/1	0.98	0.04	42,42,42,42	0
58	MG	AA	3227	1/1	0.98	0.17	31,31,31,31	0
58	MG	AA	3008	1/1	0.98	0.05	18,18,18,18	0
58	MG	AA	3070	1/1	0.98	0.16	33,33,33,33	0
58	MG	AA	3170	1/1	0.98	0.08	39,39,39,39	0
58	MG	AA	3567	1/1	0.98	0.08	26,26,26,26	0
58	MG	AA	3568	1/1	0.98	0.06	51,51,51,51	0
58	MG	AA	3013	1/1	0.98	0.13	34,34,34,34	0
58	MG	AA	3368	1/1	0.98	0.05	39,39,39,39	0
58	MG	AA	3369	1/1	0.98	0.07	27,27,27,27	0
58	MG	AA	3573	1/1	0.98	0.05	31,31,31,31	0
58	MG	AA	3312	1/1	0.98	0.09	52,52,52,52	0
58	MG	AA	3126	1/1	0.98	0.24	26,26,26,26	0
58	MG	CA	3230	1/1	0.98	0.07	50,50,50,50	0
58	MG	AA	3820	1/1	0.98	0.13	30,30,30,30	1
58	MG	AA	3314	1/1	0.98	0.08	28,28,28,28	0
58	MG	CA	3574	1/1	0.98	0.05	53,53,53,53	0
58	MG	AA	3233	1/1	0.98	0.09	51,51,51,51	0
58	MG	CA	3085	1/1	0.98	0.13	62,62,62,62	0
58	MG	AA	3147	1/1	0.98	0.33	37,37,37,37	0
58	MG	AB	3003	1/1	0.98	0.12	50,50,50,50	0
58	MG	AA	3694	1/1	0.98	0.05	47,47,47,47	0
58	MG	BA	3183	1/1	0.98	0.04	60,60,60,60	0
58	MG	AA	3031	1/1	0.98	0.11	22,22,22,22	1
58	MG	AA	3050	1/1	0.98	0.15	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	AB	3007	1/1	0.98	0.09	45,45,45,45	0
58	MG	CA	3411	1/1	0.98	0.07	31,31,31,31	0
58	MG	AA	3150	1/1	0.98	0.07	62,62,62,62	0
58	MG	AA	3151	1/1	0.98	0.05	14,14,14,14	0
58	MG	AA	3322	1/1	0.98	0.05	33,33,33,33	0
58	MG	AB	3011	1/1	0.98	0.05	31,31,31,31	0
58	MG	AA	3323	1/1	0.98	0.03	21,21,21,21	0
58	MG	AB	3013	1/1	0.98	0.08	53,53,53,53	0
58	MG	AA	3469	1/1	0.98	0.05	42,42,42,42	0
58	MG	AA	3383	1/1	0.98	0.09	34,34,34,34	0
58	MG	AA	3473	1/1	0.98	0.04	17,17,17,17	0
58	MG	AA	3589	1/1	0.98	0.08	38,38,38,38	0
58	MG	AA	3084	1/1	0.98	0.15	41,41,41,41	0
58	MG	AA	3475	1/1	0.98	0.05	60,60,60,60	0
58	MG	AA	3388	1/1	0.98	0.06	17,17,17,17	0
58	MG	AA	3708	1/1	0.98	0.11	32,32,32,32	1
58	MG	CA	3426	1/1	0.98	0.07	51,51,51,51	0
58	MG	AA	3067	1/1	0.98	0.05	50,50,50,50	0
58	MG	AA	3710	1/1	0.98	0.16	32,32,32,32	1
58	MG	AA	3594	1/1	0.98	0.11	27,27,27,27	0
58	MG	AA	3712	1/1	0.98	0.13	36,36,36,36	1
58	MG	AA	3326	1/1	0.98	0.05	59,59,59,59	0
58	MG	AA	3327	1/1	0.98	0.04	13,13,13,13	0
58	MG	AA	3395	1/1	0.98	0.06	22,22,22,22	0
58	MG	AA	3396	1/1	0.98	0.07	16,16,16,16	0
58	MG	AA	3397	1/1	0.98	0.03	15,15,15,15	0
58	MG	AA	3398	1/1	0.98	0.05	17,17,17,17	0
58	MG	CA	3267	1/1	0.98	0.07	39,39,39,39	0
58	MG	AA	3180	1/1	0.98	0.10	72,72,72,72	0
58	MG	CA	3439	1/1	0.98	0.04	46,46,46,46	0
58	MG	CA	3440	1/1	0.98	0.06	39,39,39,39	0
58	MG	AA	3485	1/1	0.98	0.04	15,15,15,15	0
58	MG	AA	3722	1/1	0.98	0.05	11,11,11,11	0
58	MG	AA	3486	1/1	0.98	0.08	28,28,28,28	0
58	MG	CA	3444	1/1	0.98	0.03	37,37,37,37	0
58	MG	AA	3725	1/1	0.98	0.11	39,39,39,39	0
58	MG	AA	3604	1/1	0.98	0.06	65,65,65,65	0
58	MG	CA	3447	1/1	0.98	0.09	62,62,62,62	0
58	MG	AA	3487	1/1	0.98	0.06	39,39,39,39	0
58	MG	AA	3400	1/1	0.98	0.09	33,33,33,33	0
58	MG	AF	301	1/1	0.98	0.10	43,43,43,43	0
58	MG	AA	3329	1/1	0.98	0.04	17,17,17,17	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	AA	3402	1/1	0.98	0.05	27,27,27,27	0
58	MG	AA	3242	1/1	0.98	0.06	28,28,28,28	0
58	MG	AF	305	1/1	0.98	0.09	40,40,40,40	0
58	MG	AA	3331	1/1	0.98	0.15	34,34,34,34	0
58	MG	CA	3630	1/1	0.98	0.09	61,61,61,61	0
58	MG	BA	3084	1/1	0.98	0.06	80,80,80,80	0
58	MG	AA	3114	1/1	0.98	0.11	62,62,62,62	0
58	MG	AA	3408	1/1	0.98	0.06	44,44,44,44	0
58	MG	AA	3495	1/1	0.98	0.12	50,50,50,50	0
58	MG	AA	3409	1/1	0.98	0.07	30,30,30,30	0
58	MG	DA	1703	1/1	0.98	0.04	68,68,68,68	0
58	MG	AA	3497	1/1	0.98	0.09	51,51,51,51	0
58	MG	AA	3182	1/1	0.98	0.05	23,23,23,23	1
58	MG	AA	3499	1/1	0.98	0.04	35,35,35,35	0
58	MG	AA	3245	1/1	0.98	0.06	28,28,28,28	1
58	MG	AA	3501	1/1	0.98	0.06	48,48,48,48	0
58	MG	AA	3742	1/1	0.98	0.10	39,39,39,39	1
58	MG	CA	3642	1/1	0.98	0.09	53,53,53,53	0
58	MG	BZ	800	1/1	0.98	0.09	44,44,44,44	0
58	MG	AP	202	1/1	0.98	0.16	31,31,31,31	0
58	MG	AA	3620	1/1	0.98	0.05	42,42,42,42	0
58	MG	AA	3502	1/1	0.98	0.05	24,24,24,24	0
58	MG	CA	3298	1/1	0.98	0.09	42,42,42,42	0
58	MG	AA	3503	1/1	0.98	0.05	52,52,52,52	0
58	MG	AA	3746	1/1	0.98	0.05	28,28,28,28	0
58	MG	AA	3504	1/1	0.98	0.08	62,62,62,62	0
58	MG	CA	3007	1/1	0.98	0.06	27,27,27,27	0
58	MG	AR	5002	1/1	0.98	0.20	40,40,40,40	0
58	MG	AA	3183	1/1	0.98	0.08	75,75,75,75	0
58	MG	CA	3152	1/1	0.98	0.06	49,49,49,49	0
58	MG	CA	3306	1/1	0.98	0.05	61,61,61,61	0
58	MG	AA	3506	1/1	0.98	0.04	32,32,32,32	0
58	MG	CA	3309	1/1	0.98	0.04	40,40,40,40	0
58	MG	AA	3075	1/1	0.98	0.04	13,13,13,13	0
58	MG	AA	3415	1/1	0.98	0.07	30,30,30,30	0
58	MG	AA	3510	1/1	0.98	0.08	47,47,47,47	0
58	MG	AA	3087	1/1	0.98	0.14	49,49,49,49	0
58	MG	AA	3512	1/1	0.98	0.06	11,11,11,11	0
58	MG	AA	3418	1/1	0.98	0.09	30,30,30,30	0
58	MG	AA	3214	1/1	0.98	0.21	39,39,39,39	1
58	MG	CA	3161	1/1	0.98	0.05	40,40,40,40	0
58	MG	CA	3319	1/1	0.98	0.06	33,33,33,33	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	AA	3420	1/1	0.98	0.08	12,12,12,12	0
58	MG	CA	3321	1/1	0.98	0.05	30,30,30,30	0
58	MG	CA	3019	1/1	0.98	0.05	27,27,27,27	0
58	MG	AA	3135	1/1	0.98	0.18	62,62,62,62	0
58	MG	AA	3340	1/1	0.98	0.13	58,58,58,58	0
58	MG	AA	3288	1/1	0.98	0.05	25,25,25,25	0
58	MG	AA	3521	1/1	0.98	0.05	37,37,37,37	0
58	MG	AA	3424	1/1	0.98	0.05	17,17,17,17	0
58	MG	DA	1743	1/1	0.98	0.11	60,60,60,60	0
58	MG	AA	3251	1/1	0.98	0.08	33,33,33,33	1
58	MG	CA	3170	1/1	0.98	0.08	32,32,32,32	0
58	MG	CA	3330	1/1	0.98	0.06	29,29,29,29	0
58	MG	AA	3525	1/1	0.98	0.07	26,26,26,26	0
58	MG	AA	3427	1/1	0.98	0.07	34,34,34,34	0
58	MG	AA	3343	1/1	0.98	0.13	65,65,65,65	0
58	MG	CA	3029	1/1	0.98	0.05	32,32,32,32	0
58	MG	CE	302	1/1	0.98	0.09	46,46,46,46	0
58	MG	AA	3528	1/1	0.98	0.06	25,25,25,25	0
58	MG	CA	3176	1/1	0.98	0.05	41,41,41,41	0
58	MG	CA	3177	1/1	0.98	0.11	50,50,50,50	0
58	MG	CA	3338	1/1	0.98	0.05	41,41,41,41	0
58	MG	DA	1756	1/1	0.98	0.15	68,68,68,68	0
58	MG	AA	3644	1/1	0.98	0.06	49,49,49,49	0
58	MG	CA	3340	1/1	0.98	0.03	35,35,35,35	0
58	MG	AA	3077	1/1	0.98	0.09	92,92,92,92	0
58	MG	AA	3530	1/1	0.98	0.06	15,15,15,15	0
58	MG	CF	304	1/1	0.98	0.05	54,54,54,54	0
58	MG	CA	3343	1/1	0.98	0.07	46,46,46,46	0
58	MG	AA	3217	1/1	0.98	0.09	46,46,46,46	0
58	MG	AA	3118	1/1	0.98	0.17	36,36,36,36	1
58	MG	AA	3534	1/1	0.98	0.05	22,22,22,22	0
58	MG	BA	3129	1/1	0.98	0.10	52,52,52,52	0
58	MG	AA	3650	1/1	0.98	0.06	59,59,59,59	0
58	MG	AA	3432	1/1	0.98	0.06	28,28,28,28	0
58	MG	A7	105	1/1	0.98	0.07	44,44,44,44	0
58	MG	AA	3537	1/1	0.98	0.05	35,35,35,35	0
58	MG	A8	5002	1/1	0.98	0.05	30,30,30,30	0
58	MG	AA	3433	1/1	0.98	0.06	18,18,18,18	0
58	MG	CV	201	1/1	0.98	0.04	69,69,69,69	0
58	MG	AA	3434	1/1	0.98	0.07	22,22,22,22	0
58	MG	AA	3255	1/1	0.98	0.16	40,40,40,40	0
58	MG	AA	3656	1/1	0.98	0.09	55,55,55,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	CA	3528	1/1	0.98	0.03	38,38,38,38	0
58	MG	AA	3657	1/1	0.98	0.09	51,51,51,51	1
58	MG	AA	3541	1/1	0.98	0.04	29,29,29,29	0
58	MG	AA	3294	1/1	0.98	0.06	65,65,65,65	0
60	ZN	BN	501	1/1	0.98	0.04	121,121,121,121	0
58	MG	BA	3142	1/1	0.98	0.04	47,47,47,47	0
58	MG	CA	3533	1/1	0.98	0.08	52,52,52,52	0
61	SF4	BD	501	8/8	0.98	0.04	79,79,79,79	0
58	MG	AA	3256	1/1	0.98	0.08	54,54,54,54	0
58	MG	AA	3220	1/1	0.98	0.04	34,34,34,34	0
58	MG	CA	3363	1/1	0.98	0.07	42,42,42,42	0
58	MG	AA	3791	1/1	0.99	0.08	15,15,15,15	0
58	MG	AV	202	1/1	0.99	0.03	40,40,40,40	0
58	MG	AV	203	1/1	0.99	0.07	34,34,34,34	1
58	MG	AA	3133	1/1	0.99	0.06	30,30,30,30	0
58	MG	AA	3459	1/1	0.99	0.06	18,18,18,18	0
58	MG	AA	3571	1/1	0.99	0.05	14,14,14,14	0
58	MG	CA	3550	1/1	0.99	0.03	54,54,54,54	1
58	MG	CA	3291	1/1	0.99	0.10	40,40,40,40	0
58	MG	AA	3374	1/1	0.99	0.10	17,17,17,17	0
58	MG	AA	3357	1/1	0.99	0.06	27,27,27,27	0
58	MG	AA	3022	1/1	0.99	0.08	9,9,9,9	0
58	MG	AA	3533	1/1	0.99	0.08	24,24,24,24	0
58	MG	AA	3219	1/1	0.99	0.04	4,4,4,4	0
58	MG	AA	3535	1/1	0.99	0.06	27,27,27,27	0
58	MG	AA	3578	1/1	0.99	0.04	34,34,34,34	0
58	MG	AA	3163	1/1	0.99	0.15	45,45,45,45	0
58	MG	AA	3755	1/1	0.99	0.09	29,29,29,29	0
58	MG	AA	3038	1/1	0.99	0.09	10,10,10,10	0
58	MG	AA	3380	1/1	0.99	0.04	15,15,15,15	0
58	MG	AA	3406	1/1	0.99	0.08	50,50,50,50	0
58	MG	CA	3188	1/1	0.99	0.02	36,36,36,36	0
58	MG	AA	3407	1/1	0.99	0.03	19,19,19,19	0
58	MG	BA	3145	1/1	0.99	0.03	37,37,37,37	0
58	MG	CA	3568	1/1	0.99	0.03	40,40,40,40	0
58	MG	CA	3307	1/1	0.99	0.04	39,39,39,39	0
58	MG	AA	3054	1/1	0.99	0.08	38,38,38,38	0
58	MG	AA	3039	1/1	0.99	0.06	44,44,44,44	0
58	MG	CA	3371	1/1	0.99	0.11	46,46,46,46	0
58	MG	CA	3310	1/1	0.99	0.06	29,29,29,29	0
58	MG	CA	3373	1/1	0.99	0.07	42,42,42,42	0
58	MG	AE	303	1/1	0.99	0.02	17,17,17,17	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	AA	3471	1/1	0.99	0.03	34,34,34,34	0
58	MG	CA	3252	1/1	0.99	0.05	51,51,51,51	0
58	MG	AA	3472	1/1	0.99	0.03	25,25,25,25	0
58	MG	AA	3003	1/1	0.99	0.02	19,19,19,19	0
58	MG	A7	102	1/1	0.99	0.07	39,39,39,39	0
58	MG	AA	3384	1/1	0.99	0.04	28,28,28,28	0
58	MG	AA	3720	1/1	0.99	0.04	59,59,59,59	0
58	MG	CA	3382	1/1	0.99	0.02	37,37,37,37	0
58	MG	CA	3383	1/1	0.99	0.04	40,40,40,40	0
58	MG	CA	3384	1/1	0.99	0.10	44,44,44,44	0
58	MG	CA	3655	1/1	0.99	0.10	52,52,52,52	0
58	MG	AA	3508	1/1	0.99	0.07	13,13,13,13	0
58	MG	AA	3348	1/1	0.99	0.08	31,31,31,31	0
58	MG	AA	3386	1/1	0.99	0.04	18,18,18,18	0
58	MG	CA	3589	1/1	0.99	0.03	35,35,35,35	0
58	MG	AA	3387	1/1	0.99	0.04	24,24,24,24	0
58	MG	AA	3212	1/1	0.99	0.07	31,31,31,31	1
58	MG	CA	3662	1/1	0.99	0.13	48,48,48,48	0
58	MG	AA	3772	1/1	0.99	0.07	22,22,22,22	1
58	MG	AA	3417	1/1	0.99	0.10	42,42,42,42	0
58	MG	AA	3514	1/1	0.99	0.10	35,35,35,35	0
58	MG	AA	3389	1/1	0.99	0.09	34,34,34,34	0
58	MG	AA	3516	1/1	0.99	0.04	20,20,20,20	0
58	MG	DA	1698	1/1	0.99	0.08	76,76,76,76	0
58	MG	AN	3002	1/1	0.99	0.03	26,26,26,26	0
58	MG	AA	3304	1/1	0.99	0.05	30,30,30,30	0
58	MG	AA	3320	1/1	0.99	0.09	23,23,23,23	0
58	MG	BA	3168	1/1	0.99	0.03	57,57,57,57	0
58	MG	AA	3558	1/1	0.99	0.07	18,18,18,18	0
58	MG	AA	3392	1/1	0.99	0.06	21,21,21,21	0
58	MG	BA	3171	1/1	0.99	0.08	61,61,61,61	0
58	MG	AA	3393	1/1	0.99	0.06	26,26,26,26	0
58	MG	AA	3157	1/1	0.99	0.12	40,40,40,40	1
58	MG	BA	3118	1/1	0.99	0.05	43,43,43,43	0
60	ZN	A9	501	1/1	0.99	0.03	41,41,41,41	0
58	MG	AA	3009	1/1	0.99	0.04	23,23,23,23	0
58	MG	AA	3454	1/1	0.99	0.05	49,49,49,49	0
60	ZN	C6	501	1/1	0.99	0.02	60,60,60,60	0
60	ZN	C9	501	1/1	0.99	0.07	93,93,93,93	0
58	MG	AA	3524	1/1	0.99	0.12	29,29,29,29	0
58	MG	AA	3076	1/1	0.99	0.03	8,8,8,8	0
58	MG	AA	3566	1/1	0.99	0.05	28,28,28,28	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	AA	3426	1/1	0.99	0.06	33,33,33,33	0
58	MG	AA	3141	1/1	0.99	0.05	51,51,51,51	0
58	MG	AA	3800	1/1	1.00	0.04	30,30,30,30	0
58	MG	AA	3308	1/1	1.00	0.04	28,28,28,28	0
60	ZN	CY	501	1/1	1.00	0.02	92,92,92,92	0
58	MG	AA	3776	1/1	1.00	0.03	40,40,40,40	0
60	ZN	C5	101	1/1	1.00	0.04	66,66,66,66	0
58	MG	AA	3724	1/1	1.00	0.04	22,22,22,22	0
58	MG	AA	3412	1/1	1.00	0.07	20,20,20,20	0
58	MG	CA	3562	1/1	1.00	0.04	36,36,36,36	0
60	ZN	AY	501	1/1	1.00	0.02	63,63,63,63	0
58	MG	AA	3659	1/1	1.00	0.04	14,14,14,14	0
60	ZN	A5	103	1/1	1.00	0.01	36,36,36,36	0
60	ZN	A6	102	1/1	1.00	0.02	46,46,46,46	0

6.5 Other polymers (i)

There are no such residues in this entry.