Full wwPDB X-ray Structure Validation Report (i)

Apr 19, 2026 – 08:46 AM UTC

PDB ID	:	7RQE / pdb_00007rqe
Title	:	Crystal structure of the Thermus thermophilus 70S ribosome in complex with protein Y, A-site deacylated tRNA analog CACCA, P-site MAI-tripeptidyl-tRNA analog ACCA-IAM, and chloramphenicol at 2.40A resolution
Authors	:	Syroegin, E.A.; Flemmich, L.; Klepacki, D.; Vazquez-Laslop, N.; Micura, R.; Polikanov, Y.S.
Deposited on	:	2021-08-06
Resolution	:	2.40 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 (1)) were used in the production of this report:

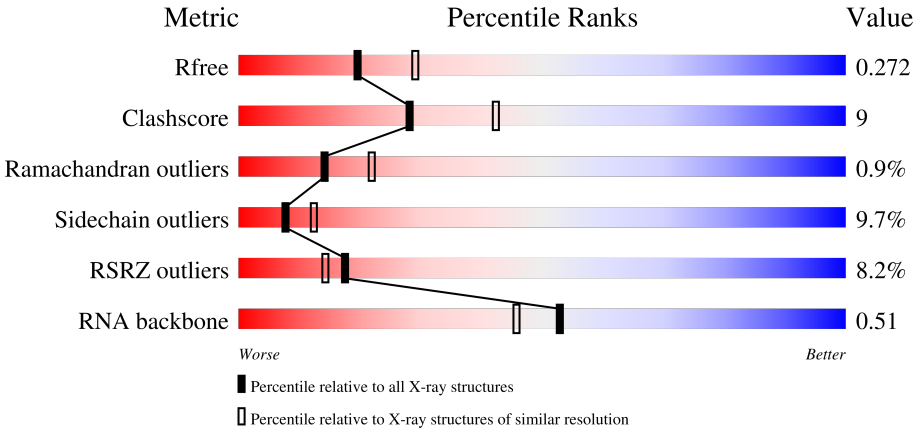
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal 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 2.40 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	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)
RNA backbone	3983	1155 (2.70-2.10)

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	1A	2915	5% 65% 28% 6%
1	2A	2915	5% 59% 32% 7%
2	1B	121	2% 69% 26%
2	2B	121	3% 55% 40% 5%

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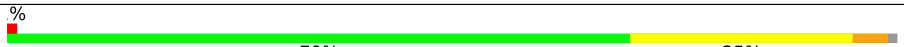
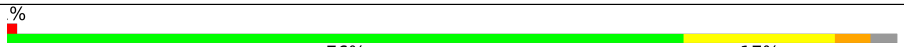
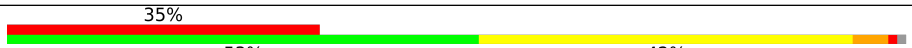
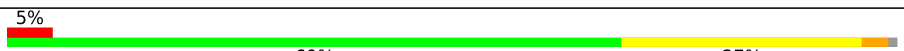
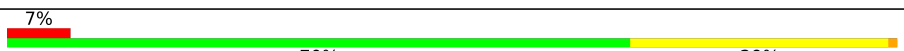
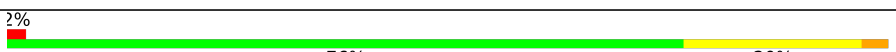
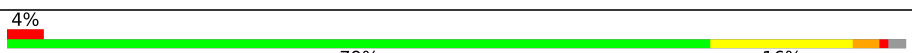
Mol	Chain	Length	Quality of chain
3	1D	276	
3	2D	276	
4	1E	206	
4	2E	206	
5	1F	210	
5	2F	210	
6	1G	182	
6	2G	182	
7	1H	180	
7	2H	180	
8	1I	148	
8	2I	148	
9	1N	140	
9	2N	140	
10	1O	122	
10	2O	122	
11	1P	150	
11	2P	150	
12	1Q	141	
12	2Q	141	
13	1R	118	
13	2R	118	
14	1S	112	
14	2S	112	
15	1T	146	

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Mol	Chain	Length	Quality of chain
15	2T	146	2% 64% 23% 10%
16	1U	118	% 81% 15%
16	2U	118	3% 70% 25%
17	1V	101	% 78% 19%
17	2V	101	4% 64% 29% 6%
18	1W	113	% 81% 17%
18	2W	113	3% 78% 20%
19	1X	96	2% 77% 21%
19	2X	96	8% 77% 21%
20	1Y	110	2% 72% 23%
20	2Y	110	11% 56% 33% 8%
21	1Z	206	2% 72% 23%
21	2Z	206	15% 62% 31% 5%
22	10	85	7% 79% 16%
22	20	85	9% 74% 22%
23	11	98	% 73% 22%
23	21	98	% 58% 35% 6%
24	12	72	3% 68% 28%
24	22	72	8% 68% 26%
25	13	60	67% 28%
25	23	60	5% 67% 30%
26	14	71	24% 54% 35% 8%
26	24	71	54% 42% 44% 10%
27	15	60	2% 72% 22% 5%
27	25	60	2% 80% 15%

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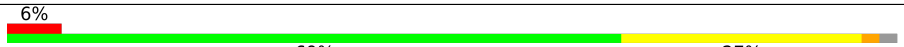
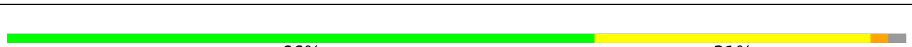
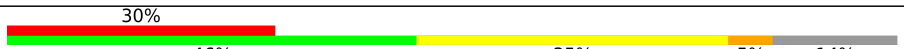
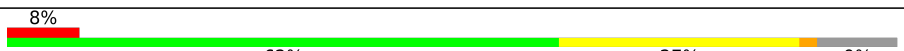
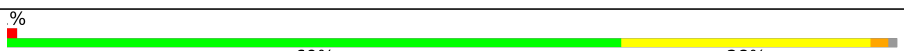
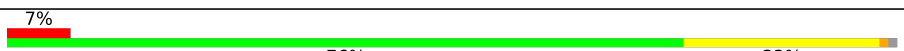
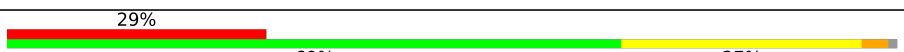
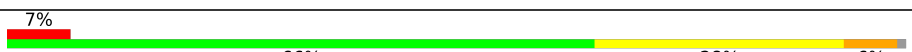
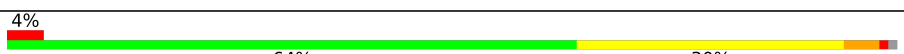
Mol	Chain	Length	Quality of chain
28	16	54	
28	26	54	
29	17	49	
29	27	49	
30	18	65	
30	28	65	
31	19	37	
31	29	37	
32	1a	1521	
32	2a	1521	
33	1b	256	
33	2b	256	
34	1c	239	
34	2c	239	
35	1d	209	
35	2d	209	
36	1e	162	
36	2e	162	
37	1f	101	
37	2f	101	
38	1g	156	
38	2g	156	
39	1h	138	
39	2h	138	
40	1i	128	

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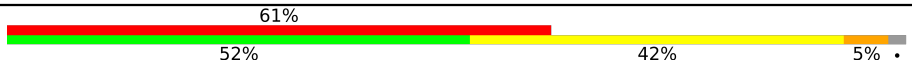
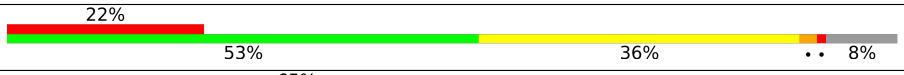
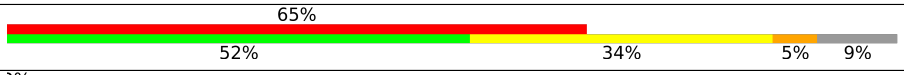
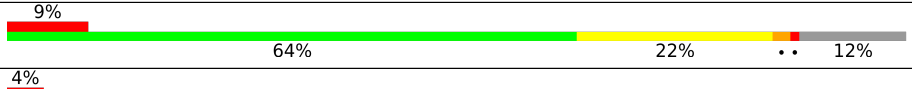
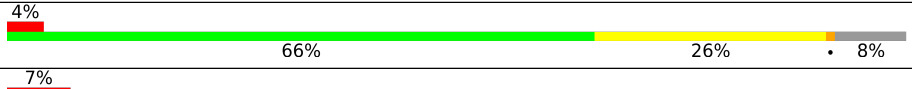
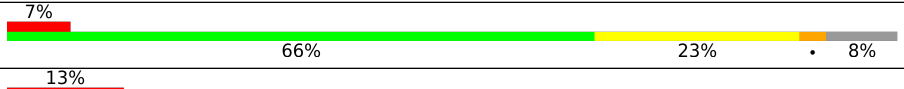
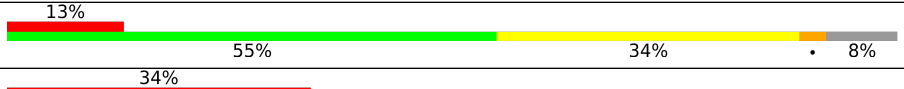
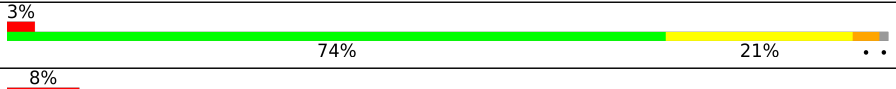
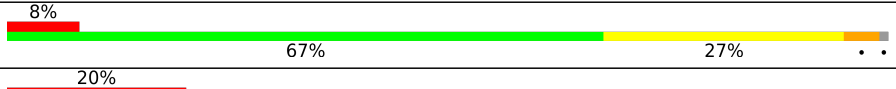
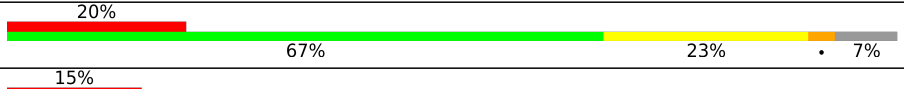
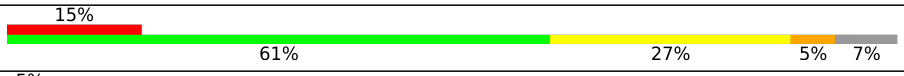
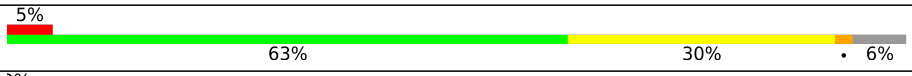
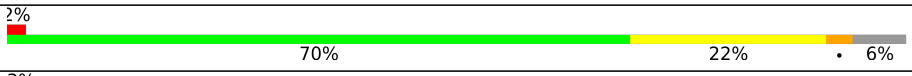
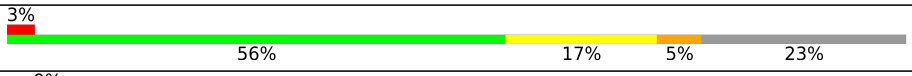
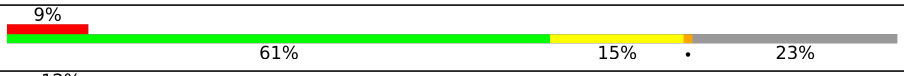
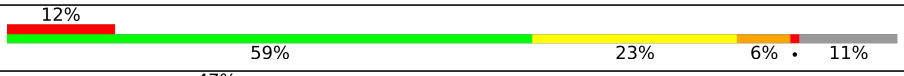
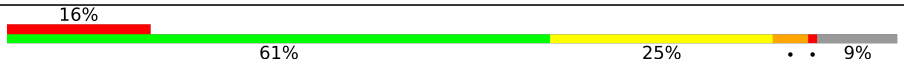
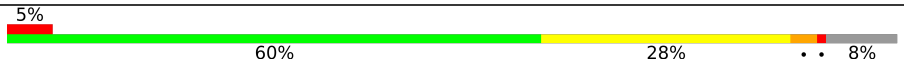
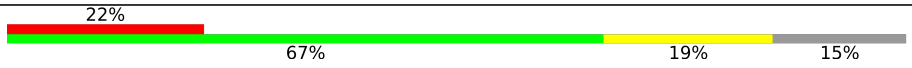
Mol	Chain	Length	Quality of chain
40	2i	128	
41	1j	105	
41	2j	105	
42	1k	129	
42	2k	129	
43	1l	132	
43	2l	132	
44	1m	126	
44	2m	126	
45	1n	61	
45	2n	61	
46	1o	89	
46	2o	89	
47	1p	88	
47	2p	88	
48	1q	105	
48	2q	105	
49	1r	88	
49	2r	88	
50	1s	93	
50	2s	93	
51	1t	106	
51	2t	106	
52	1u	27	
52	2u	27	

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Mol	Chain	Length	Quality of chain
53	1y	113	5% 65% 20% 14%
53	2y	113	61% 49% 32% 15%
54	1w	5	80% 20%
54	2w	5	80% 20%
55	1x	4	25% 75% 25%
55	2x	4	25% 75% 25%
56	1v	3	67% 33%
56	2v	3	100%

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
57	MG	1A	3323	-	-	-	X
57	MG	2a	3050	-	-	-	X

2 Entry composition (i)

There are 63 unique types of molecules in this entry. The entry contains 297868 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	1A	2872	Total	C	N	O	P	0	0	0
			61869	27540	11574	19884	2871			
1	2A	2867	Total	C	N	O	P	0	0	0
			61758	27491	11552	19850	2865			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	1B	120	Total	C	N	O	P	0	0	0
			2572	1145	476	832	119			
2	2B	120	Total	C	N	O	P	0	0	0
			2573	1146	476	832	119			

- Molecule 3 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	1D	275	Total	C	N	O	S	0	0	0
			2131	1346	422	360	3			
3	2D	275	Total	C	N	O	S	0	0	0
			2136	1349	423	361	3			

- Molecule 4 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	1E	204	Total	C	N	O	S	0	0	0
			1559	985	298	270	6			
4	2E	204	Total	C	N	O	S	0	0	0
			1559	985	298	270	6			

- Molecule 5 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	1F	203	Total	C	N	O	S	0	0	1
			1584	1009	298	275	2			
5	2F	203	Total	C	N	O	S	0	0	1
			1580	1007	297	274	2			

- Molecule 6 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	1G	181	Total	C	N	O	S	0	0	0
			1426	916	253	253	4			
6	2G	181	Total	C	N	O	S	0	0	0
			1424	912	259	249	4			

- Molecule 7 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	1H	174	Total	C	N	O	S	0	0	0
			1330	845	248	236	1			
7	2H	173	Total	C	N	O	S	0	0	0
			1324	842	247	234	1			

- Molecule 8 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	1I	147	Total	C	N	O	S	0	0	0
			1094	699	191	203	1			
8	2I	146	Total	C	N	O	S	0	0	0
			1076	687	186	202	1			

- Molecule 9 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	1N	140	Total	C	N	O	S	0	0	0
			1121	722	208	187	4			
9	2N	140	Total	C	N	O	S	0	0	0
			1117	719	207	187	4			

- Molecule 10 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	1O	122	Total	C	N	O	S	0	0	0
			933	588	171	170	4			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	2O	122	Total 933	C 588	N 171	O 170	S 4	0	0	0

- Molecule 11 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	1P	149	Total 1135	C 706	N 230	O 196	S 3	0	0	0
11	2P	149	Total 1135	C 706	N 230	O 196	S 3	0	0	0

- Molecule 12 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	1Q	141	Total 1122	C 715	N 212	O 188	S 7	0	0	0
12	2Q	141	Total 1122	C 715	N 212	O 188	S 7	0	0	0

- Molecule 13 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	1R	118	Total 968	C 604	N 203	O 160	S 1	0	0	0
13	2R	118	Total 968	C 604	N 203	O 160	S 1	0	0	0

- Molecule 14 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
14	1S	110	Total 877	C 553	N 175	O 149	0	0	0
14	2S	110	Total 870	C 549	N 173	O 148	0	0	0

- Molecule 15 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
15	1T	131	Total 1091	C 680	N 225	O 185	S 1	0	0	0
15	2T	131	Total 1083	C 675	N 224	O 183	S 1	0	0	0

- Molecule 16 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
16	1U	116	Total	C	N	O	S	0	0	0
			959	608	201	149	1			
16	2U	116	Total	C	N	O	S	0	0	0
			959	608	201	149	1			

- Molecule 17 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
17	1V	101	Total	C	N	O	S	0	0	0
			775	498	141	135	1			
17	2V	101	Total	C	N	O	S	0	0	0
			771	495	140	135	1			

- Molecule 18 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
18	1W	112	Total	C	N	O	S	0	0	0
			886	557	174	153	2			
18	2W	112	Total	C	N	O	S	0	0	0
			886	557	174	153	2			

- Molecule 19 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	1X	95	Total	C	N	O	S	0	0	0
			750	488	135	126	1			
19	2X	95	Total	C	N	O	S	0	0	0
			750	488	135	126	1			

- Molecule 20 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	1Y	107	Total	C	N	O	S	0	0	0
			810	520	153	131	6			
20	2Y	107	Total	C	N	O	S	0	0	0
			810	519	153	132	6			

- Molecule 21 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
21	1Z	203	Total	C	N	O	S	0	0	0
			1587	1011	282	292	2			
21	2Z	201	Total	C	N	O	S	0	0	0
			1557	995	274	286	2			

- Molecule 22 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	10	83	Total	C	N	O	S	0	0	0
			653	404	139	109	1			
22	20	83	Total	C	N	O	S	0	0	0
			650	401	139	109	1			

- Molecule 23 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
23	11	97	Total	C	N	O	S	0	0	0
			754	475	148	130	1			
23	21	97	Total	C	N	O	S	0	0	0
			759	478	149	131	1			

- Molecule 24 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
24	12	70	Total	C	N	O	S	0	0	0
			588	365	118	103	2			
24	22	70	Total	C	N	O	S	0	0	0
			592	368	119	103	2			

- Molecule 25 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
25	13	59	Total	C	N	O	0	0	0
			469	298	90	81			
25	23	59	Total	C	N	O	0	0	0
			464	296	90	78			

- Molecule 26 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	14	69	Total	C	N	O	S	0	0	0
			546	346	96	99	5			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	24	69	Total	C	N	O	S	0	0	0
			536	342	98	91	5			

- Molecule 27 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
27	15	59	Total	C	N	O	S	0	0	0
			459	288	90	76	5			
27	25	59	Total	C	N	O	S	0	0	0
			455	285	89	76	5			

- Molecule 28 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
28	16	53	Total	C	N	O	S	0	0	0
			453	281	91	77	4			
28	26	53	Total	C	N	O	S	0	0	0
			449	279	91	75	4			

- Molecule 29 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
29	17	48	Total	C	N	O	S	0	0	0
			418	257	104	55	2			
29	27	48	Total	C	N	O	S	0	0	0
			418	257	104	55	2			

- Molecule 30 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
30	18	64	Total	C	N	O	S	0	0	0
			517	331	102	82	2			
30	28	64	Total	C	N	O	S	0	0	0
			517	331	102	82	2			

- Molecule 31 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
31	19	37	Total	C	N	O	S	0	0	0
			307	188	68	47	4			
31	29	37	Total	C	N	O	S	0	0	0
			307	188	68	47	4			

- Molecule 32 is a RNA chain called 16S Ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
32	1a	1500	Total	C	N	O	P	0	0	0
			32246	14358	5975	10413	1500			
32	2a	1504	Total	C	N	O	P	0	0	0
			32331	14396	5990	10441	1504			

- Molecule 33 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
33	1b	231	Total	C	N	O	S	0	0	0
			1842	1175	330	332	5			
33	2b	231	Total	C	N	O	S	0	0	0
			1825	1167	326	327	5			

- Molecule 34 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
34	1c	206	Total	C	N	O	S	0	0	0
			1558	979	305	273	1			
34	2c	206	Total	C	N	O	S	0	0	0
			1542	968	300	273	1			

- Molecule 35 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
35	1d	208	Total	C	N	O	S	0	0	0
			1665	1043	329	286	7			
35	2d	208	Total	C	N	O	S	0	0	0
			1668	1047	330	284	7			

- Molecule 36 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
36	1e	148	Total	C	N	O	S	0	0	0
			1133	716	214	199	4			
36	2e	148	Total	C	N	O	S	0	0	0
			1133	716	214	199	4			

- Molecule 37 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
37	1f	100	Total	C	N	O	S	0	0	0
			814	516	144	151	3			
37	2f	100	Total	C	N	O	S	0	0	0
			816	516	146	151	3			

- Molecule 38 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
38	1g	155	Total	C	N	O	S	0	0	0
			1235	769	244	216	6			
38	2g	155	Total	C	N	O	S	0	0	0
			1229	766	241	216	6			

- Molecule 39 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
39	1h	137	Total	C	N	O	S	0	0	0
			1098	694	210	192	2			
39	2h	137	Total	C	N	O	S	0	0	0
			1088	689	206	191	2			

- Molecule 40 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
40	1i	127	Total	C	N	O	0	0	0
			986	625	193	168			
40	2i	126	Total	C	N	O	0	0	0
			966	613	186	167			

- Molecule 41 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
41	1j	97	Total	C	N	O	0	0	0
			719	446	142	131			
41	2j	96	Total	C	N	O	0	0	0
			710	442	137	131			

- Molecule 42 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
42	1k	114	Total	C	N	O	S	0	0	0
			834	520	156	155	3			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
42	2k	114	Total	C	N	O	S	0	0	0
			833	519	156	155	3			

- Molecule 43 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
43	1l	122	Total	C	N	O	S	0	0	0
			932	586	185	159	2			
43	2l	122	Total	C	N	O	S	0	0	0
			932	586	185	159	2			

- Molecule 44 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
44	1m	116	Total	C	N	O	S	0	0	0
			914	564	189	159	2			
44	2m	114	Total	C	N	O	S	0	0	0
			895	550	186	157	2			

- Molecule 45 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
45	1n	60	Total	C	N	O	S	0	0	0
			492	312	104	72	4			
45	2n	60	Total	C	N	O	S	0	0	0
			492	312	104	72	4			

- Molecule 46 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
46	1o	88	Total	C	N	O	S	0	0	0
			728	456	144	126	2			
46	2o	88	Total	C	N	O	S	0	0	0
			728	456	144	126	2			

- Molecule 47 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
47	1p	82	Total	C	N	O	S	0	0	0
			681	433	134	113	1			
47	2p	82	Total	C	N	O	S	0	0	0
			677	430	133	113	1			

- Molecule 48 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
48	1q	99	Total	C	N	O	S	0	0	0
			823	528	151	142	2			
48	2q	99	Total	C	N	O	S	0	0	0
			823	528	151	142	2			

- Molecule 49 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
49	1r	68	Total	C	N	O	0	0	0
			555	355	108	92			
49	2r	68	Total	C	N	O	0	0	0
			555	355	108	92			

- Molecule 50 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
50	1s	83	Total	C	N	O	S	0	0	0
			648	415	120	111	2			
50	2s	83	Total	C	N	O	S	0	0	0
			645	410	118	115	2			

- Molecule 51 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
51	1t	96	Total	C	N	O	S	0	0	0
			732	449	157	124	2			
51	2t	98	Total	C	N	O	S	0	0	0
			733	451	154	126	2			

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
52	1u	23	Total	C	N	O	0	0	0
			199	122	48	29			
52	2u	23	Total	C	N	O	0	0	0
			199	122	48	29			

- Molecule 53 is a protein called Ribosome-associated inhibitor A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
53	1y	97	Total	C	N	O	S	0	0	0
			764	478	144	139	3			
53	2y	96	Total	C	N	O	S	0	0	0
			749	468	141	137	3			

- Molecule 54 is a RNA chain called A-site Deacylated tRNA Analog.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
54	1w	4	Total	C	N	O	P	0	0	1
			63	28	11	21	3			
54	2w	4	Total	C	N	O	P	0	0	1
			63	28	11	21	3			

- Molecule 55 is a RNA chain called P-site Peptidyl-tRNA Analog RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
55	1x	4	Total	C	N	O	P	0	0	1
			63	28	12	20	3			
55	2x	4	Total	C	N	O	P	0	0	1
			63	28	12	20	3			

- Molecule 56 is a protein called P-site Peptidyl-tRNA Analog Peptide.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
56	1v	3	Total	C	N	O	S	0	0	0
			21	14	3	3	1			
56	2v	3	Total	C	N	O	S	0	0	0
			21	14	3	3	1			

- Molecule 57 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
57	1A	1016	Total	Mg	0	0
			1016	1016		
57	1B	30	Total	Mg	0	0
			30	30		
57	1D	21	Total	Mg	0	0
			21	21		
57	1E	8	Total	Mg	0	0
			8	8		
57	1F	18	Total	Mg	0	0
			18	18		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
57	1G	4	Total Mg 4 4	0	0
57	1H	2	Total Mg 2 2	0	0
57	1N	4	Total Mg 4 4	0	0
57	1O	1	Total Mg 1 1	0	0
57	1P	5	Total Mg 5 5	0	0
57	1Q	5	Total Mg 5 5	0	0
57	1R	5	Total Mg 5 5	0	0
57	1T	7	Total Mg 7 7	0	0
57	1U	6	Total Mg 6 6	0	0
57	1V	7	Total Mg 7 7	0	0
57	1W	3	Total Mg 3 3	0	0
57	1X	1	Total Mg 1 1	0	0
57	1Y	2	Total Mg 2 2	0	0
57	1Z	1	Total Mg 1 1	0	0
57	10	8	Total Mg 8 8	0	0
57	11	5	Total Mg 5 5	0	0
57	13	3	Total Mg 3 3	0	0
57	15	7	Total Mg 7 7	0	0
57	17	5	Total Mg 5 5	0	0
57	18	3	Total Mg 3 3	0	0
57	19	3	Total Mg 3 3	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
57	1a	266	Total Mg 266 266	0	0
57	1b	1	Total Mg 1 1	0	0
57	1d	4	Total Mg 4 4	0	0
57	1e	2	Total Mg 2 2	0	0
57	1f	2	Total Mg 2 2	0	0
57	1g	2	Total Mg 2 2	0	0
57	1h	2	Total Mg 2 2	0	0
57	1i	1	Total Mg 1 1	0	0
57	1l	2	Total Mg 2 2	0	0
57	1m	1	Total Mg 1 1	0	0
57	1n	3	Total Mg 3 3	0	0
57	1o	2	Total Mg 2 2	0	0
57	1t	2	Total Mg 2 2	0	0
57	1y	2	Total Mg 2 2	0	0
57	1x	2	Total Mg 2 2	0	0
57	2A	746	Total Mg 746 746	0	0
57	2B	19	Total Mg 19 19	0	0
57	2D	8	Total Mg 8 8	0	0
57	2E	8	Total Mg 8 8	0	0
57	2F	4	Total Mg 4 4	0	0
57	2G	3	Total Mg 3 3	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
57	2I	1	Total Mg 1 1	0	0
57	2N	1	Total Mg 1 1	0	0
57	2O	2	Total Mg 2 2	0	0
57	2P	2	Total Mg 2 2	0	0
57	2Q	3	Total Mg 3 3	0	0
57	2R	2	Total Mg 2 2	0	0
57	2T	4	Total Mg 4 4	0	0
57	2U	1	Total Mg 1 1	0	0
57	2V	3	Total Mg 3 3	0	0
57	2W	3	Total Mg 3 3	0	0
57	2X	1	Total Mg 1 1	0	0
57	2Y	1	Total Mg 1 1	0	0
57	20	2	Total Mg 2 2	0	0
57	21	1	Total Mg 1 1	0	0
57	23	1	Total Mg 1 1	0	0
57	25	3	Total Mg 3 3	0	0
57	27	1	Total Mg 1 1	0	0
57	28	2	Total Mg 2 2	0	0
57	2a	190	Total Mg 190 190	0	0
57	2e	1	Total Mg 1 1	0	0
57	2f	1	Total Mg 1 1	0	0

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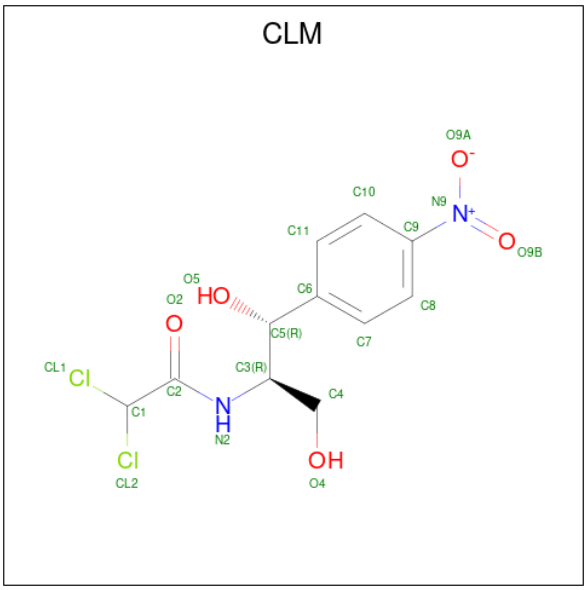
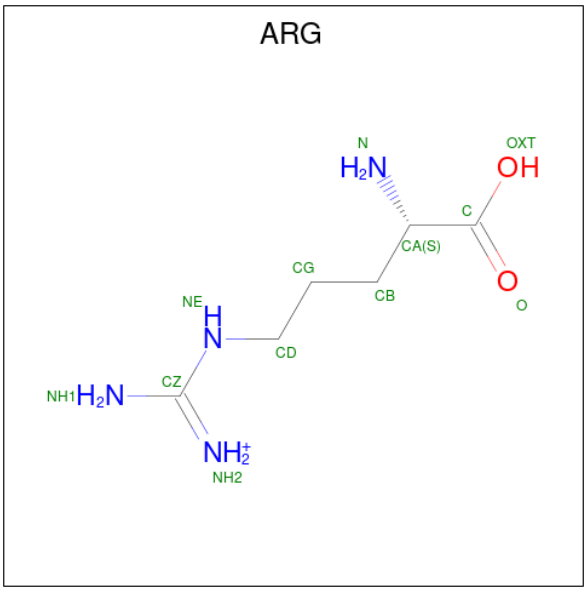
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
57	2j	2	Total Mg 2 2	0	0
57	2r	1	Total Mg 1 1	0	0
57	2t	1	Total Mg 1 1	0	0
57	2x	1	Total Mg 1 1	0	0

- Molecule 58 is CHLORAMPHENICOL (CCD ID: CLM) (formula: $C_{11}H_{12}Cl_2N_2O_5$).



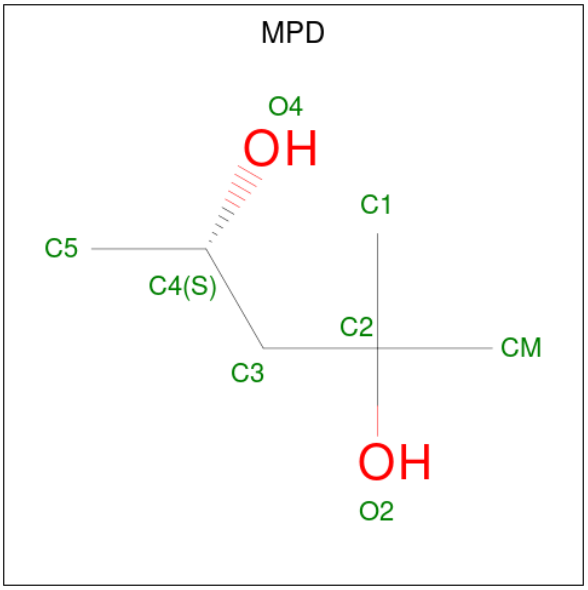
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
58	1A	1	Total C Cl N O 20 11 2 2 5	0	0
58	2A	1	Total C Cl N O 20 11 2 2 5	0	0

- Molecule 59 is ARGININE (CCD ID: ARG) (formula: $C_6H_{15}N_4O_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
59	1A	1	Total C N O 12 6 4 2	0	0
59	1B	1	Total C N O 12 6 4 2	0	0

- Molecule 60 is (4S)-2-METHYL-2,4-PENTANEDIOL (CCD ID: MPD) (formula: $C_6H_{14}O_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
60	1A	1	Total C O 8 6 2	0	0
60	1T	1	Total C O 8 6 2	0	0

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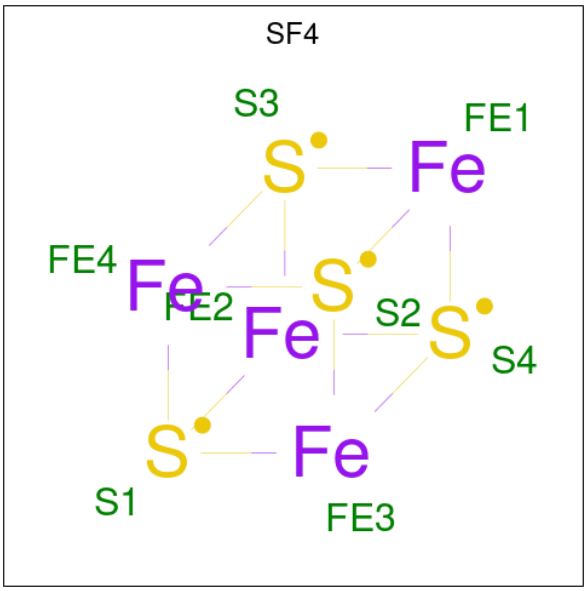
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
60	18	1	Total C O 8 6 2	0	0
60	1a	1	Total C O 8 6 2	0	0
60	2A	1	Total C O 8 6 2	0	0
60	2B	1	Total C O 8 6 2	0	0

- Molecule 61 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
61	1Y	1	Total Zn 1 1	0	0
61	14	1	Total Zn 1 1	0	0
61	15	1	Total Zn 1 1	0	0
61	16	1	Total Zn 1 1	0	0
61	19	1	Total Zn 1 1	0	0
61	1n	1	Total Zn 1 1	0	0
61	2Y	1	Total Zn 1 1	0	0
61	24	1	Total Zn 1 1	0	0
61	25	1	Total Zn 1 1	0	0
61	26	1	Total Zn 1 1	0	0
61	29	1	Total Zn 1 1	0	0
61	2n	1	Total Zn 1 1	0	0

- Molecule 62 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe_4S_4).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
62	1d	1	Total Fe S 8 4 4	0	0
62	2d	1	Total Fe S 8 4 4	0	0

- Molecule 63 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
63	1A	4023	Total O 4023 4023	0	0
63	1B	93	Total O 93 93	0	0
63	1D	112	Total O 112 112	0	0
63	1E	81	Total O 81 81	0	0
63	1F	61	Total O 61 61	0	0
63	1G	20	Total O 20 20	0	0
63	1H	12	Total O 12 12	0	0
63	1I	6	Total O 6 6	0	0
63	1N	51	Total O 51 51	0	0
63	1O	24	Total O 24 24	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
63	1P	71	Total O 71 71	0	0
63	1Q	41	Total O 41 41	0	0
63	1R	33	Total O 33 33	0	0
63	1S	16	Total O 16 16	0	0
63	1T	34	Total O 34 34	0	0
63	1U	54	Total O 54 54	0	0
63	1V	42	Total O 42 42	0	0
63	1W	29	Total O 29 29	0	0
63	1X	23	Total O 23 23	0	0
63	1Y	16	Total O 16 16	0	0
63	1Z	12	Total O 12 12	0	0
63	10	25	Total O 25 25	0	0
63	11	22	Total O 22 22	0	0
63	12	13	Total O 13 13	0	0
63	13	21	Total O 21 21	0	0
63	14	2	Total O 2 2	0	0
63	15	26	Total O 26 26	0	0
63	16	20	Total O 20 20	0	0
63	17	16	Total O 16 16	0	0
63	18	30	Total O 30 30	0	0
63	19	6	Total O 6 6	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
63	1a	378	Total O 378 378	0	0
63	1b	1	Total O 1 1	0	0
63	1d	3	Total O 3 3	0	0
63	1e	3	Total O 3 3	0	0
63	1f	2	Total O 2 2	0	0
63	1h	1	Total O 1 1	0	0
63	1j	1	Total O 1 1	0	0
63	1l	6	Total O 6 6	0	0
63	1o	2	Total O 2 2	0	0
63	1p	3	Total O 3 3	0	0
63	1t	1	Total O 1 1	0	0
63	1y	2	Total O 2 2	0	0
63	1w	5	Total O 5 5	0	0
63	1x	3	Total O 3 3	0	0
63	2A	2284	Total O 2284 2284	0	0
63	2B	46	Total O 46 46	0	0
63	2D	57	Total O 57 57	0	0
63	2E	32	Total O 32 32	0	0
63	2F	27	Total O 27 27	0	0
63	2G	6	Total O 6 6	0	0
63	2H	3	Total O 3 3	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
63	2I	4	Total O 4 4	0	0
63	2N	6	Total O 6 6	0	0
63	2O	21	Total O 21 21	0	0
63	2P	24	Total O 24 24	0	0
63	2Q	17	Total O 17 17	0	0
63	2R	16	Total O 16 16	0	0
63	2S	5	Total O 5 5	0	0
63	2T	13	Total O 13 13	0	0
63	2U	16	Total O 16 16	0	0
63	2V	5	Total O 5 5	0	0
63	2W	17	Total O 17 17	0	0
63	2X	8	Total O 8 8	0	0
63	2Y	5	Total O 5 5	0	0
63	2Z	11	Total O 11 11	0	0
63	20	11	Total O 11 11	0	0
63	21	20	Total O 20 20	0	0
63	22	1	Total O 1 1	0	0
63	23	3	Total O 3 3	0	0
63	25	13	Total O 13 13	0	0
63	26	5	Total O 5 5	0	0
63	27	9	Total O 9 9	0	0

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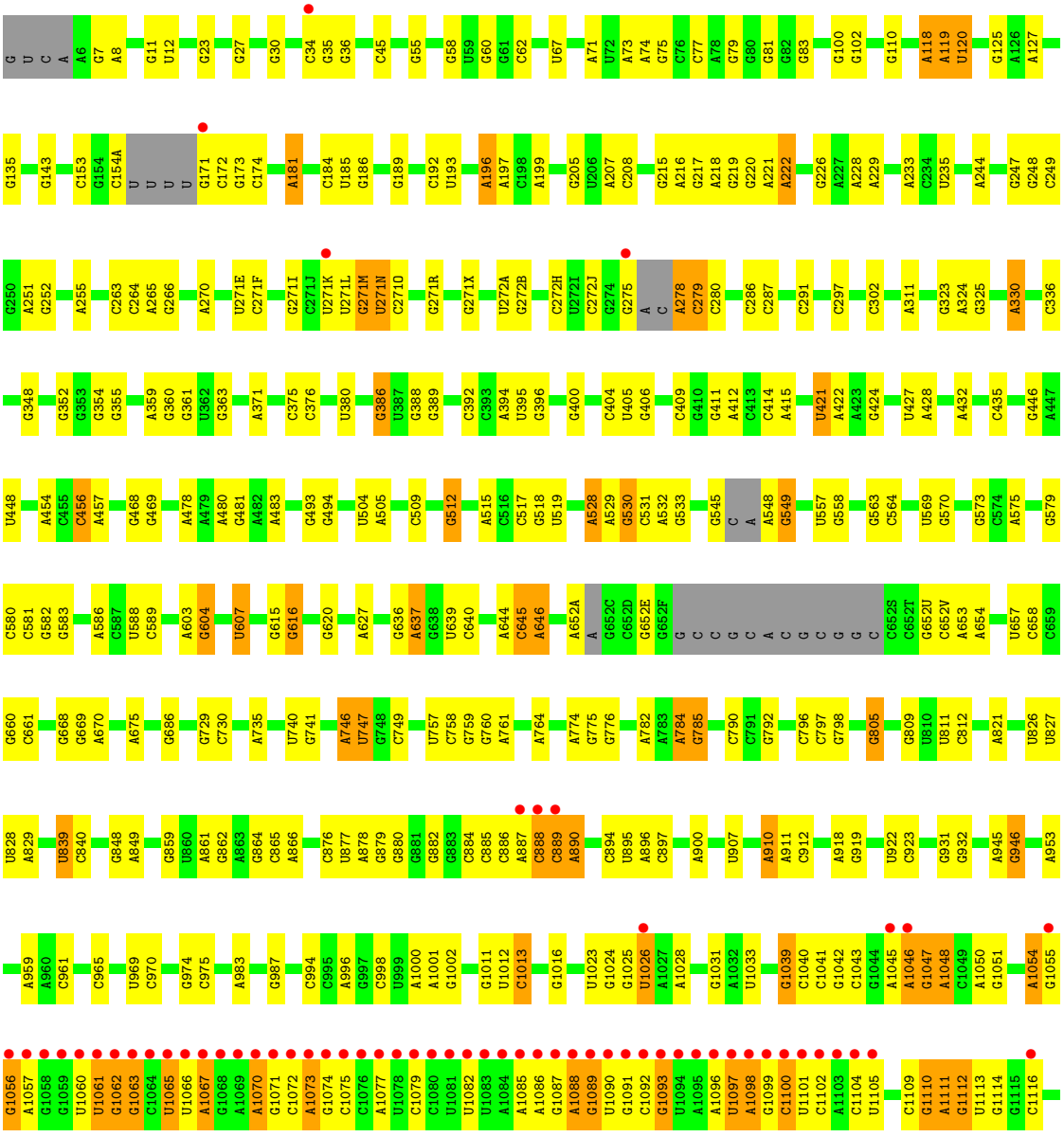
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
63	28	11	Total O 11 11	0	0
63	29	2	Total O 2 2	0	0
63	2a	317	Total O 317 317	0	0
63	2d	2	Total O 2 2	0	0
63	2e	1	Total O 1 1	0	0
63	2f	3	Total O 3 3	0	0
63	2j	2	Total O 2 2	0	0
63	2l	2	Total O 2 2	0	0
63	2n	2	Total O 2 2	0	0
63	2o	4	Total O 4 4	0	0
63	2p	2	Total O 2 2	0	0
63	2r	3	Total O 3 3	0	0
63	2t	2	Total O 2 2	0	0
63	2y	3	Total O 3 3	0	0
63	2w	3	Total O 3 3	0	0
63	2x	3	Total O 3 3	0	0

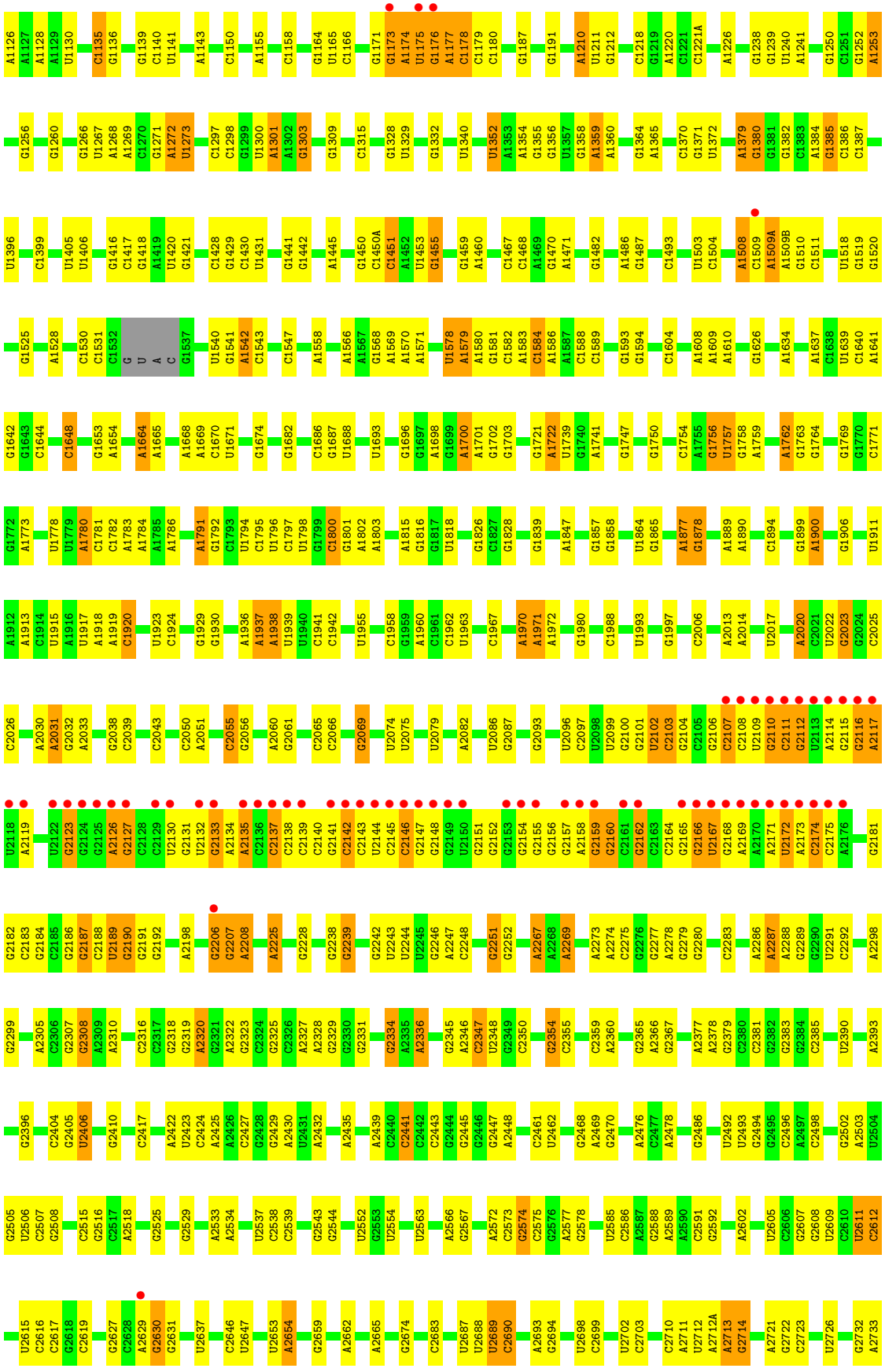
3 Residue-property plots (i)

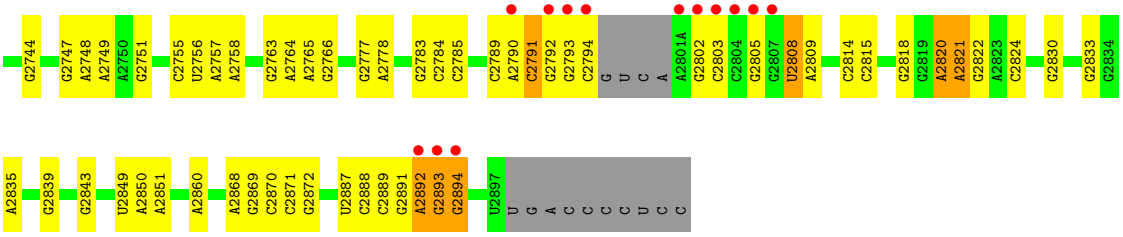
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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 1A:

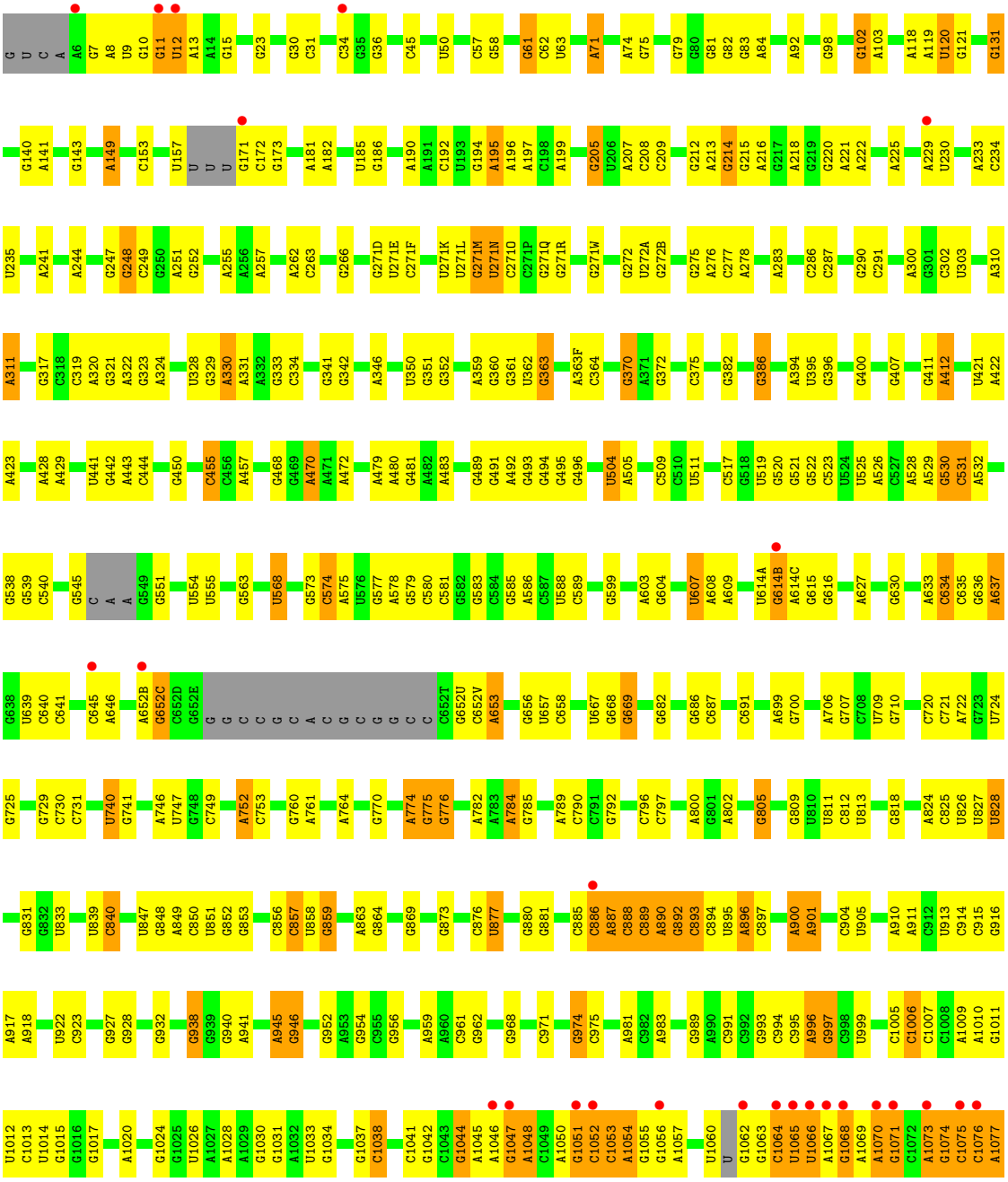


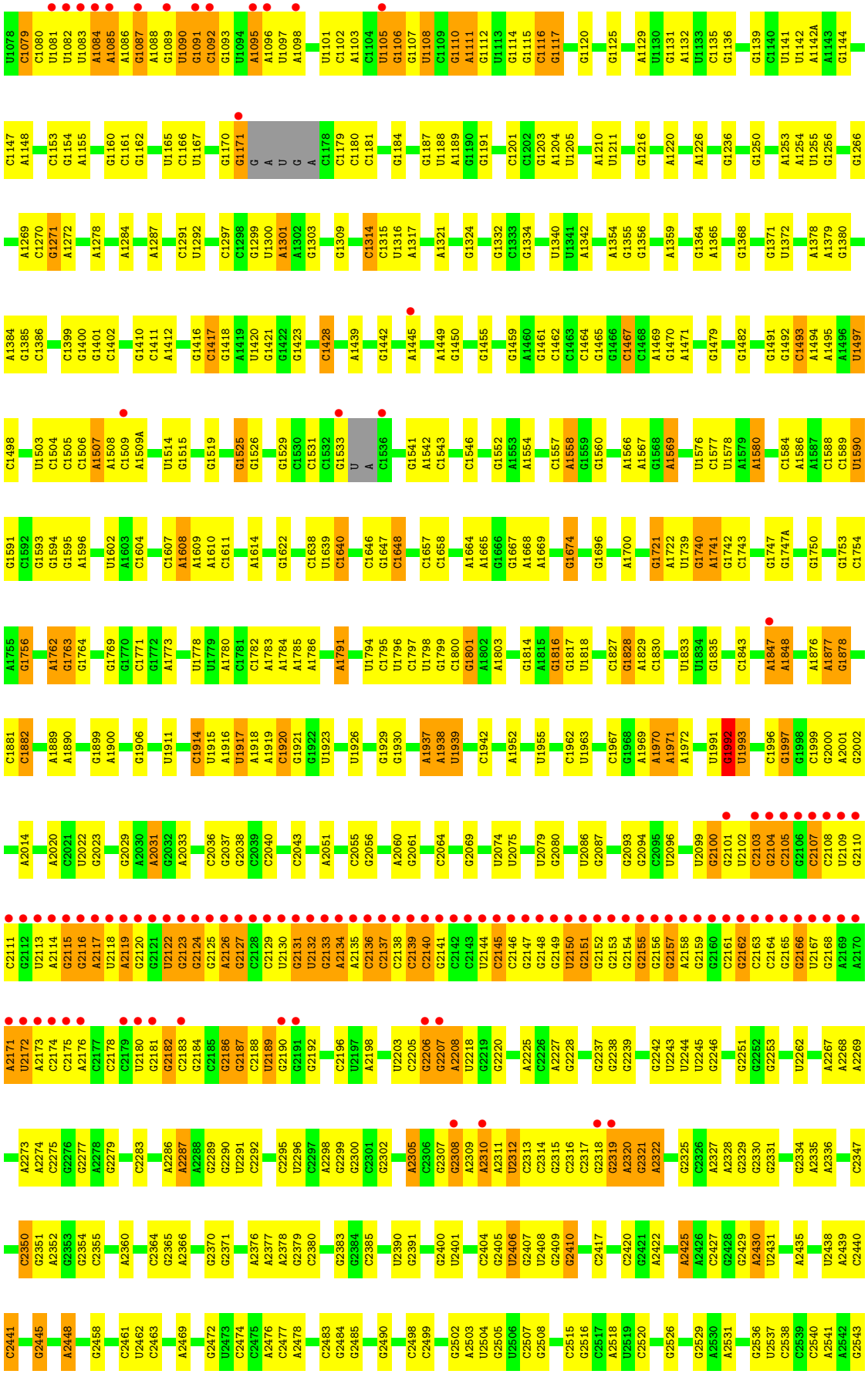


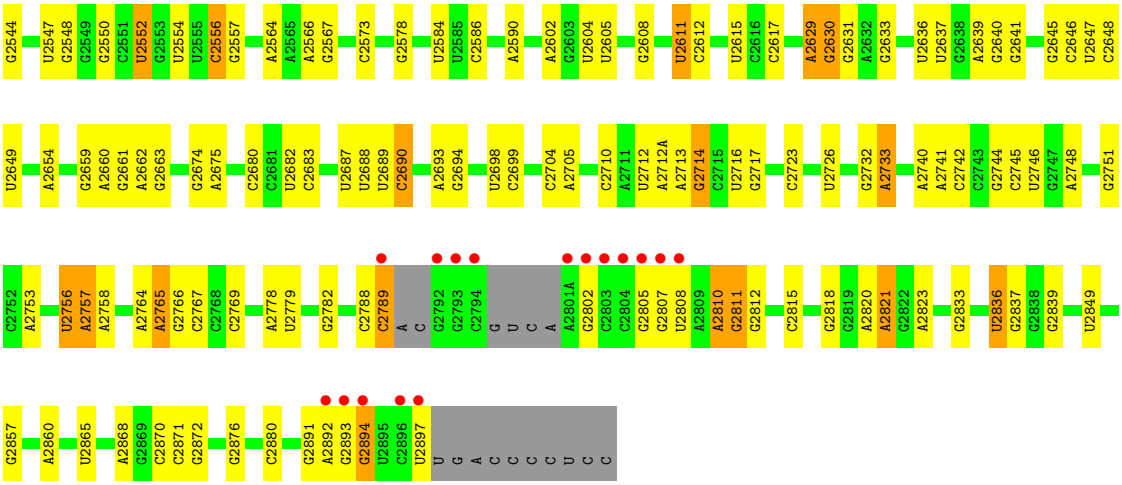


• Molecule 1: 23S Ribosomal RNA

Chain 2A:

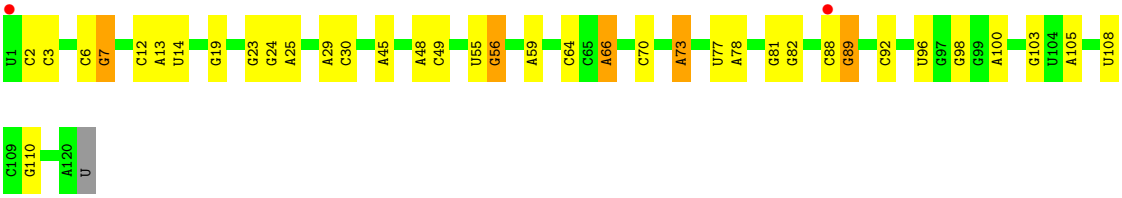



U1078 C1079 C1080 U1081 U1082 U1083 A1084 A1085 A1086 G1087 A1088 G1089 U1090 G1091 C1092 G1093 U1094 A1095 A1096 U1097 A1098 U1101 C1102 A1103 C1104 U1105 G1106 G1107 U1108 C1109 G1110 A1111 G1112 U1113 G1114 G1115 C1116 G1117 G1120 G1125 A1129 U1130 G1131 A1132 U1133 C1135 G1136 G1139 C1140 U1141 U1142 A1142A A1143 G1144
C1147 A1148 C1153 G1154 A1155 G1160 C1161 G1162 U1165 C1166 U1167 G1170 G1171 G A U G A C1178 C1179 C1180 C1181 G1184 G1187 U1188 A1189 G1190 G1191 C1201 G1202 G1203 A1204 U1205 A1210 U1211 G1216 A1220 A1226 G1236 G1250 A1253 A1254 U1255 G1256 G1266
A1269 C1270 G1271 A1272 A1278 A1284 A1287 C1291 U1292 C1297 C1298 G1299 U1300 A1301 A1302 G1303 G1309 C1314 C1315 U1316 A1317 A1321 G1324 G1332 C1333 G1334 U1340 U1341 A1342 A1354 G1355 G1356 A1359 G1364 A1365 G1368 G1371 U1372 A1378 A1379 G1380
A1384 G1385 C1386 C1399 G1400 G1401 C1402 G1410 C1411 A1412 G1416 C1417 G1418 A1419 U1420 G1421 G1422 G1423 C1428 A1439 G1442 A1445 A1449 G1450 G1455 G1459 A1460 G1461 C1462 C1463 C1464 G1465 G1466 C1467 C1468 A1469 G1470 A1471 G1479 G1482 G1491 G1492 C1493 A1494 A1495 A1496 U1497
C1498 U1503 C1504 C1505 C1506 A1507 A1508 C1509 A1509A U1514 G1515 G1519 G1525 G1526 G1529 C1530 C1531 C1532 G1533 U A C1536 G1541 A1542 C1543 C1546 G1552 A1553 A1554 C1557 A1558 G1559 G1560 A1566 A1567 G1568 A1569 U1576 C1577 U1578 A1579 A1580 C1584 A1586 A1587 C1588 C1589 U1590
G1591 C1592 G1593 G1594 G1595 A1596 U1602 A1603 C1604 C1607 A1608 A1609 A1610 C1611 A1614 G1622 C1638 U1639 C1640 C1646 G1647 C1648 C1657 C1658 A1664 A1665 G1666 G1667 A1668 A1669 G1674 G1696 A1700 G1721 A1722 U1739 G1740 A1741 G1742 C1743 G1747 G1747A G1750 G1753 C1754
A1755 G1756 A1762 G1763 G1764 G1769 G1770 C1771 G1772 A1773 U1778 U1779 A1780 C1781 C1782 A1783 A1784 A1785 A1786 A1791 U1794 C1795 U1796 C1797 U1798 G1799 C1800 G1801 A1802 A1803 G1814 A1815 G1816 G1817 U1818 C1827 G1828 A1829 C1830 U1833 U1834 G1835 C1843 A1847 A1848 A1876 A1877 G1878
C1881 C1882 A1889 A1890 G1899 A1900 G1906 U1911 C1914 U1915 A1916 U1917 A1918 A1919 C1920 G1921 G1922 U1923 U1926 G1929 G1930 A1937 A1938 U1939 C1942 A1952 U1955 C1962 U1963 C1967 G1968 A1969 A1970 A1971 A1972 U1991 G1992 U1993 C1996 G1997 G1998 C1999 G2000 A2001 G2002
A2014 A2020 C2021 U2022 G2023 G2029 A2030 A2031 G2032 A2033 C2036 G2037 G2038 C2039 C2040 C2043 A2051 C2055 G2056 A2060 G2061 C2064 G2069 U2074 U2075 U2079 G2080 U2086 G2087 G2093 G2094 C2095 U2096 U2099 G2100 G2101 U2102 C2103 G2104 C2105 G2106 C2107 C2108 U2109 G2110
C2111 G2112 U2113 A2114 G2115 G2116 A2117 U2118 A2119 G2120 G2121 U2122 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 G2164 G2165 G2166 U2167 G2168 A2169 A2170
A2171 U2172 A2173 C2174 C2175 A2176 C2177 C2178 C2179 U2180 G2181 G2182 C2183 G2184 C2185 G2186 G2187 C2188 U2189 G2190 G2191 G2192 C2196 U2197 A2198 U2203 C2205 G2206 G2207 A2208 U2218 G2219 G2220 A2225 C2226 A2227 G2228 G2237 G2238 G2239 G2242 U2243 U2244 U2245 G2246 G2251 G2252 G2253 U2262 A2267 A2268 A2269
A2273 A2274 C2275 G2276 G2277 A2278 G2279 C2283 A2286 A2287 A2288 G2289 G2290 U2291 C2292 C2295 U2296 C2297 A2298 G2299 G2300 C2301 G2302 A2305 C2306 G2307 G2308 A2309 A2310 A2311 U2312 C2313 C2314 G2315 C2316 C2317 G2318 G2319 A2320 G2321 A2322 G2325 C2326 A2327 A2328 G2329 G2330 G2331 G2334 A2335 A2336 C2347
C2350 G2351 A2352 G2353 G2354 C2355 A2360 C2364 G2365 A2366 G2370 G2371 A2376 A2377 A2378 G2379 C2380 G2383 G2384 C2385 U2390 G2391 G2400 U2401 C2404 G2405 U2406 G2407 U2408 G2409 G2410 C2417 C2420 G2421 A2422 A2425 A2426 C2427 G2428 G2429 A2430 U2431 A2435 U2438 A2439 C2440
C2441 G2445 A2448 G2458 C2461 U2462 C2463 A2469 G2472 U2473 C2474 C2475 A2476 C2477 A2478 C2483 G2484 G2485 G2490 C2498 C2499 G2502 A2503 U2504 G2505 U2506 C2507 G2508 C2515 G2516 C2517 A2518 U2519 C2520 G2526 G2529 A2530 A2531 G2536 U2537 C2538 C2539 C2540 A2541 A2542 G2543



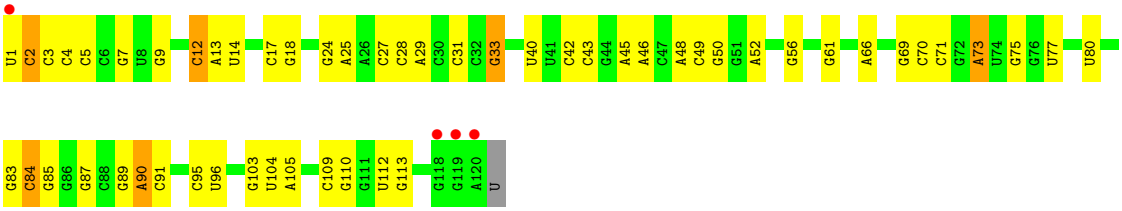
• Molecule 2: 5S Ribosomal RNA

Chain 1B:



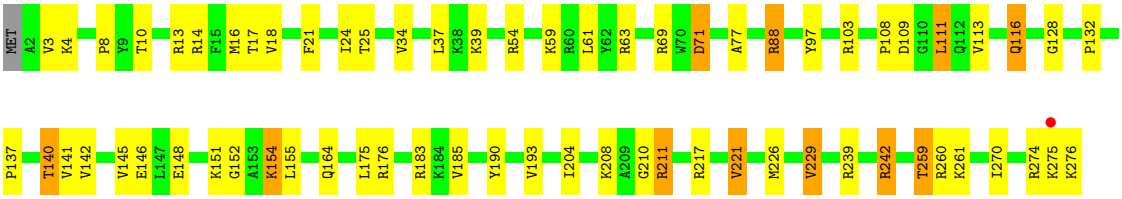
• Molecule 2: 5S Ribosomal RNA

Chain 2B:



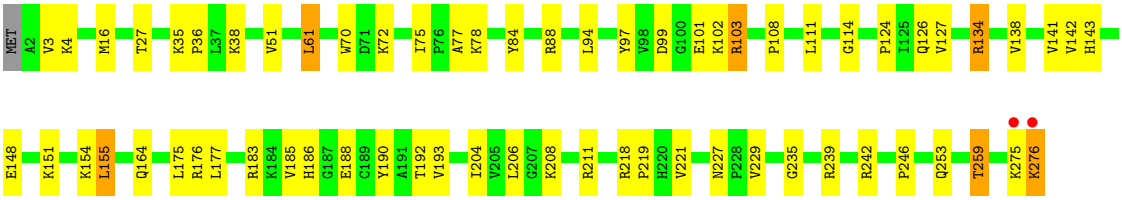
• Molecule 3: 50S ribosomal protein L2

Chain 1D:



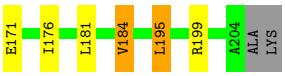
• Molecule 3: 50S ribosomal protein L2

Chain 2D:



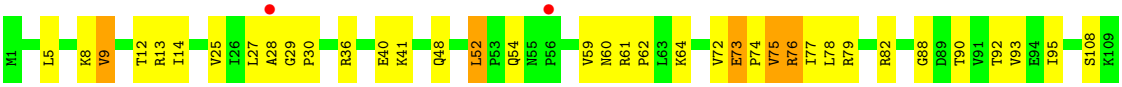
• Molecule 4: 50S ribosomal protein L3

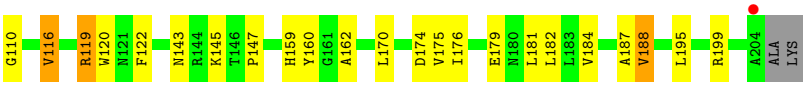
Chain 1E:



• Molecule 4: 50S ribosomal protein L3

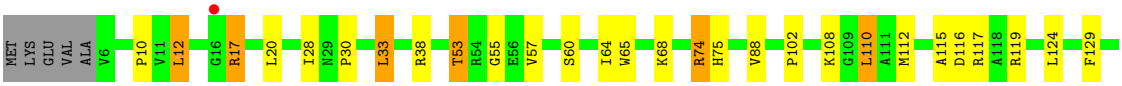
Chain 2E:

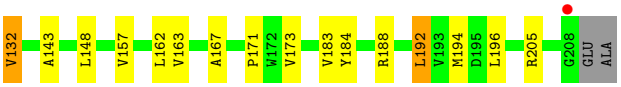




• Molecule 5: 50S ribosomal protein L4

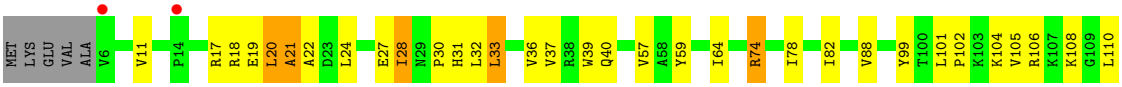
Chain 1F:

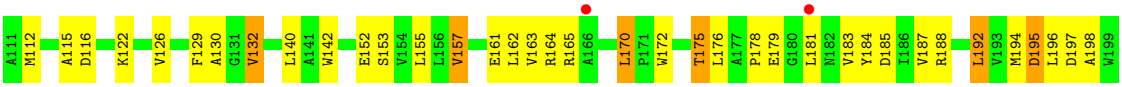


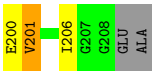


• Molecule 5: 50S ribosomal protein L4

Chain 2F:

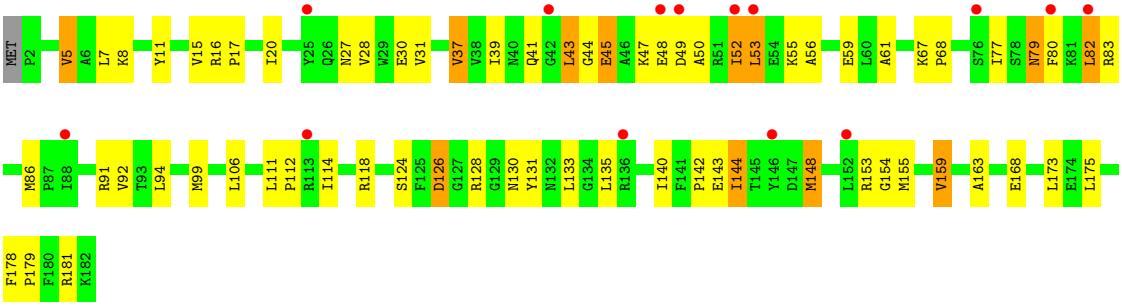






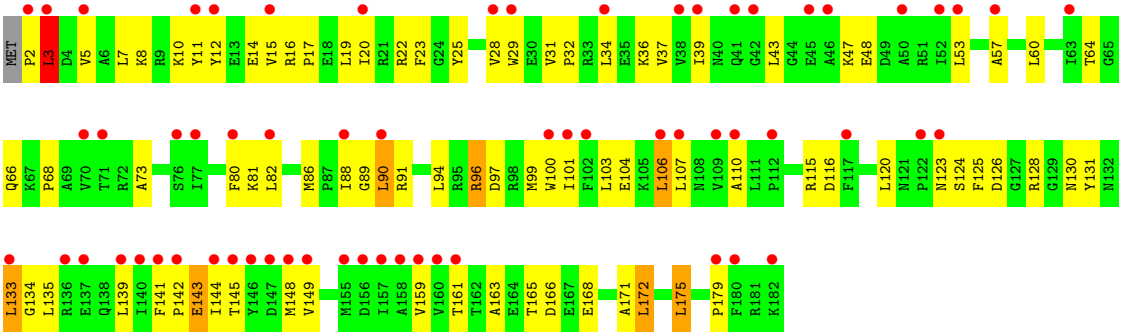
• Molecule 6: 50S ribosomal protein L5

Chain 1G:



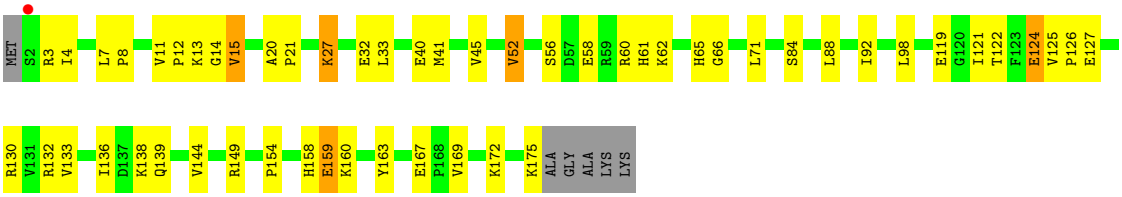
• Molecule 6: 50S ribosomal protein L5

Chain 2G:



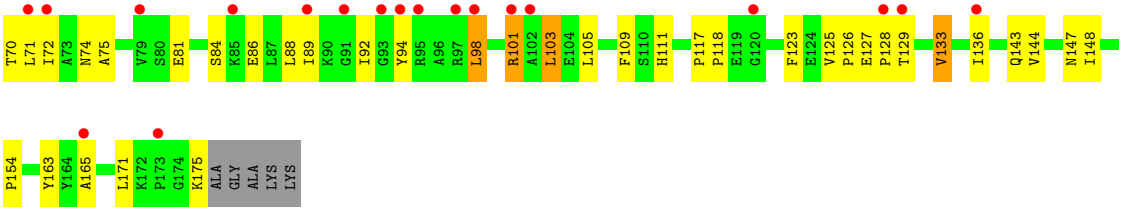
• Molecule 7: 50S ribosomal protein L6

Chain 1H:



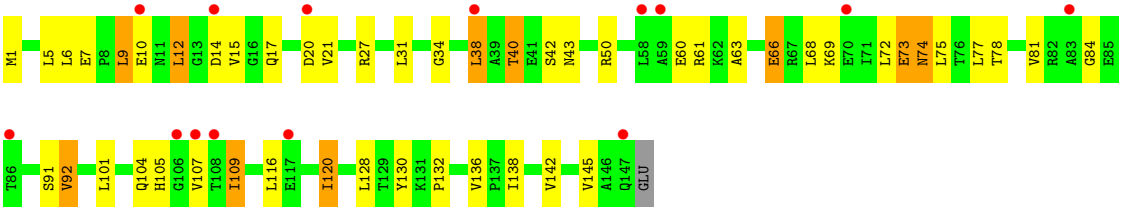
• Molecule 7: 50S ribosomal protein L6

Chain 2H:



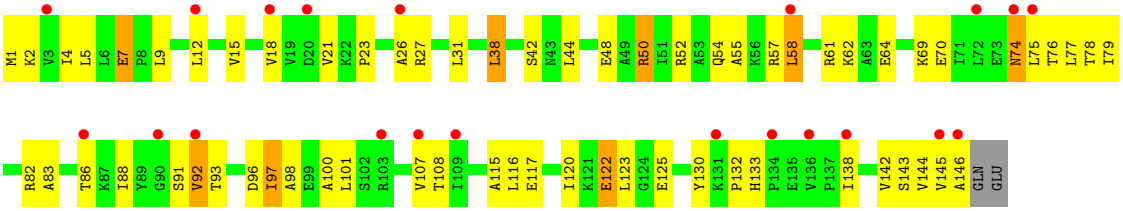
• Molecule 8: 50S ribosomal protein L9

Chain 1I:



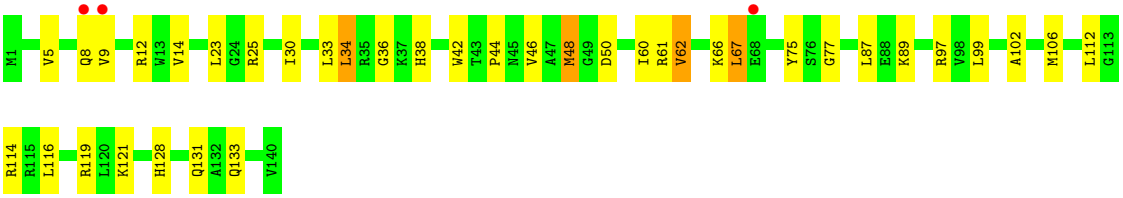
• Molecule 8: 50S ribosomal protein L9

Chain 2I:



• Molecule 9: 50S ribosomal protein L13

Chain 1N:

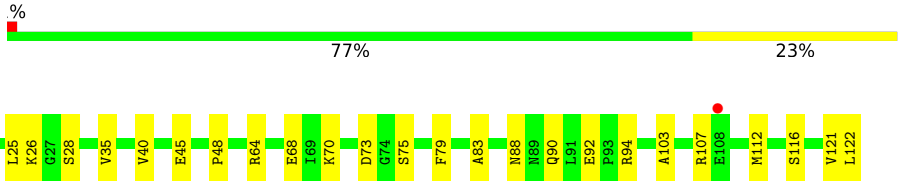


• Molecule 9: 50S ribosomal protein L13

Chain 2N:

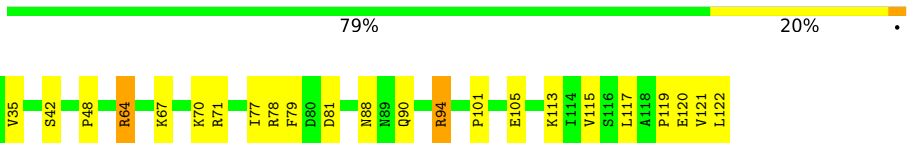
• Molecule 10: 50S ribosomal protein L14

Chain 1O:



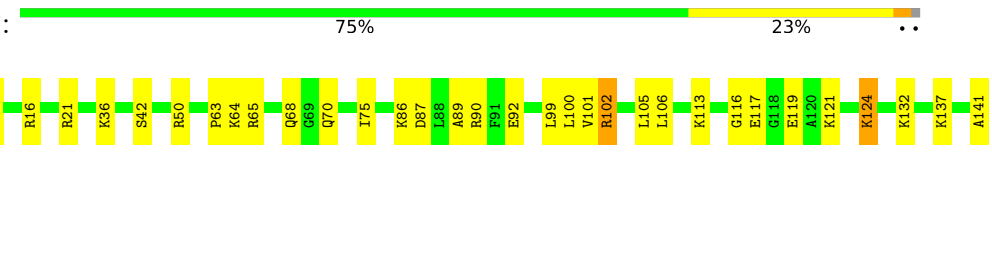
• Molecule 10: 50S ribosomal protein L14

Chain 2O:



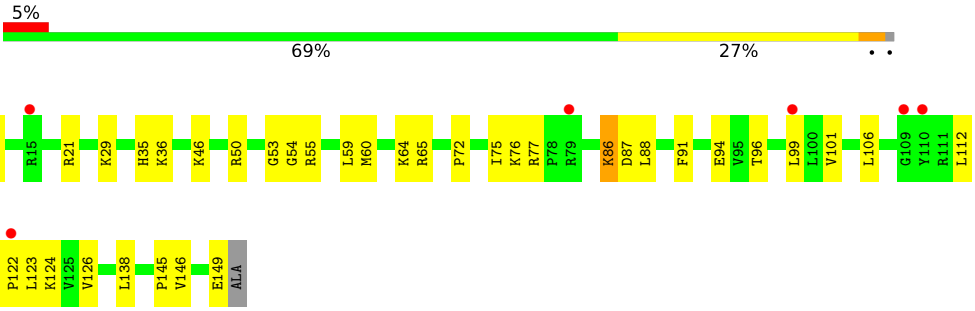
• Molecule 11: 50S ribosomal protein L15

Chain 1P:



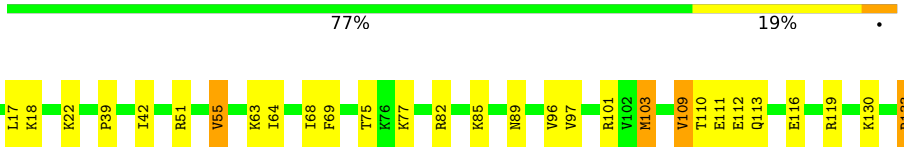
• Molecule 11: 50S ribosomal protein L15

Chain 2P:



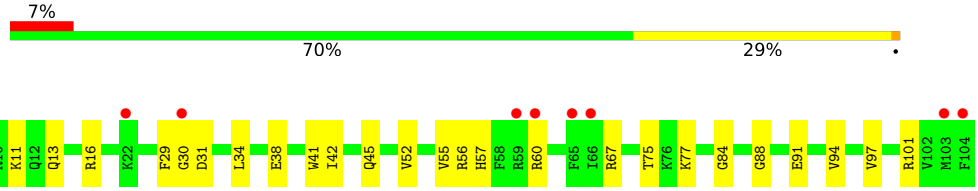
• Molecule 12: 50S ribosomal protein L16

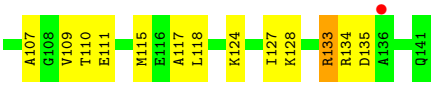
Chain 1Q:



• Molecule 12: 50S ribosomal protein L16

Chain 2Q:



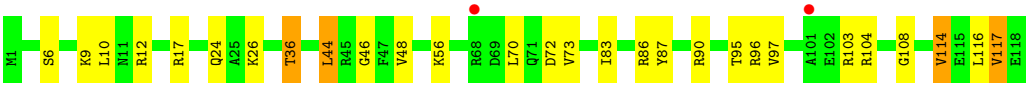


• Molecule 13: 50S ribosomal protein L17

Chain 1R:

• Molecule 13: 50S ribosomal protein L17

Chain 2R:

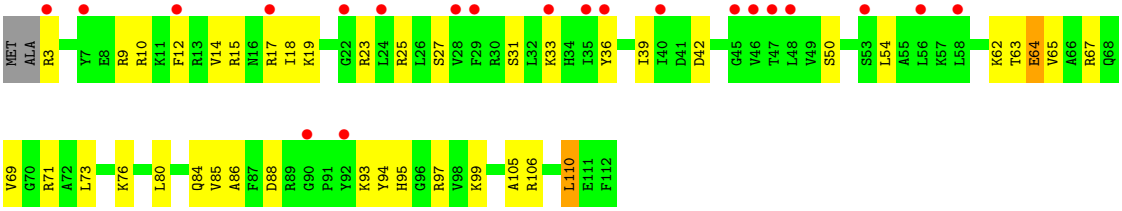


• Molecule 14: 50S ribosomal protein L18

Chain 1S:

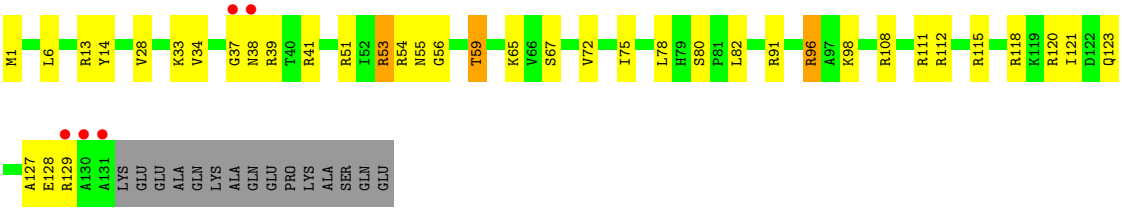
• Molecule 14: 50S ribosomal protein L18

Chain 2S:



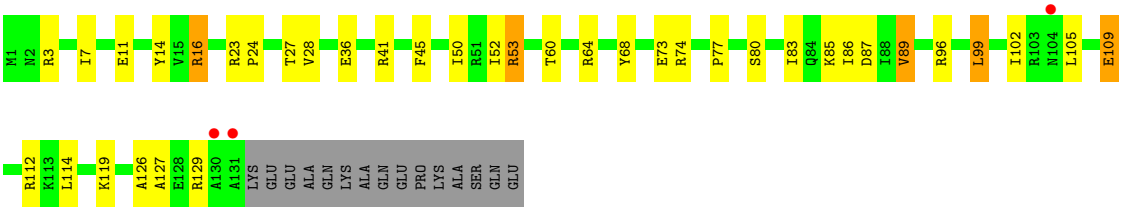
• Molecule 15: 50S ribosomal protein L19

Chain 1T:



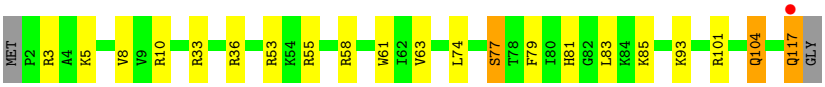
• Molecule 15: 50S ribosomal protein L19

Chain 2T:



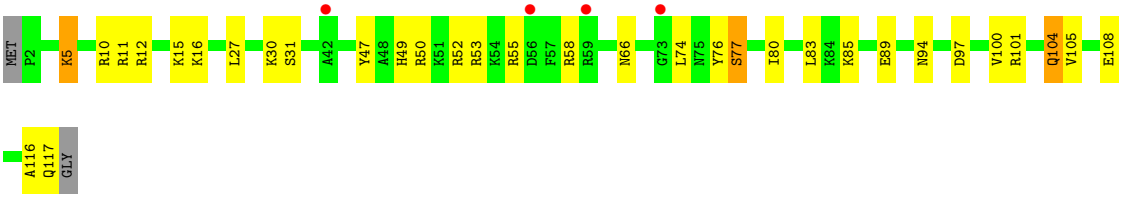
• Molecule 16: 50S ribosomal protein L20

Chain 1U:



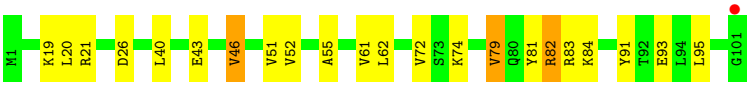
• Molecule 16: 50S ribosomal protein L20

Chain 2U:



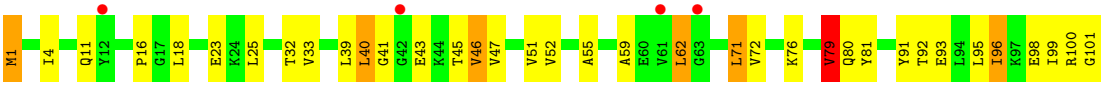
• Molecule 17: 50S ribosomal protein L21

Chain 1V:



• Molecule 17: 50S ribosomal protein L21

Chain 2V:

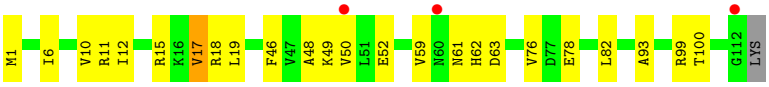


• Molecule 18: 50S ribosomal protein L22

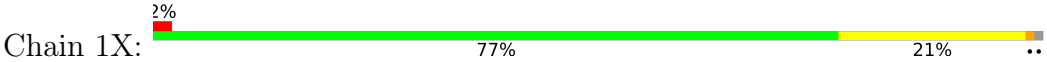
Chain 1W:

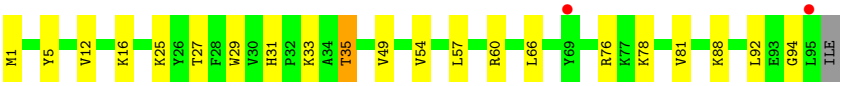
• Molecule 18: 50S ribosomal protein L22

Chain 2W:

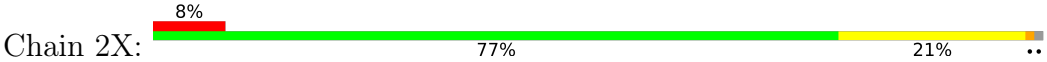


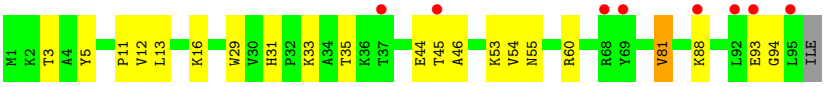
• Molecule 19: 50S ribosomal protein L23



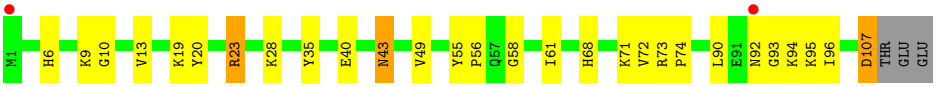


• Molecule 19: 50S ribosomal protein L23

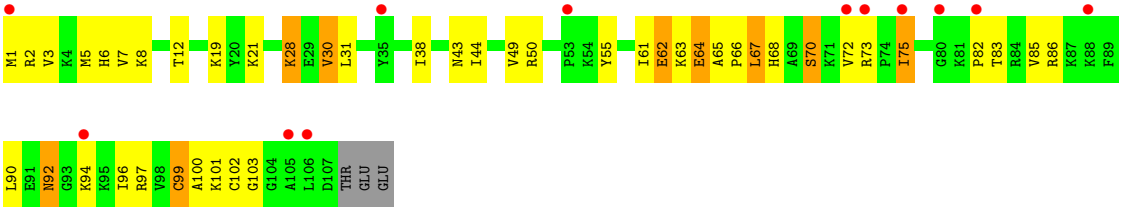




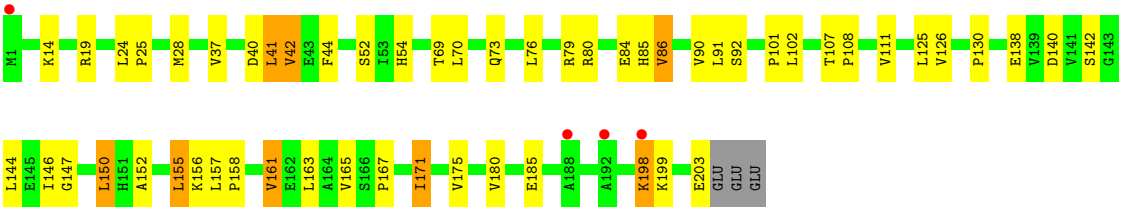
• Molecule 20: 50S ribosomal protein L24



• Molecule 20: 50S ribosomal protein L24

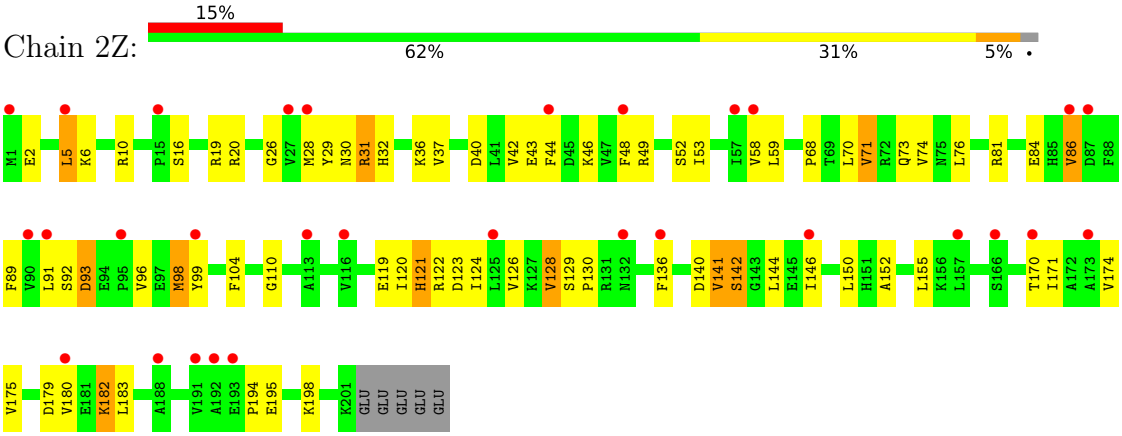


• Molecule 21: 50S ribosomal protein L25



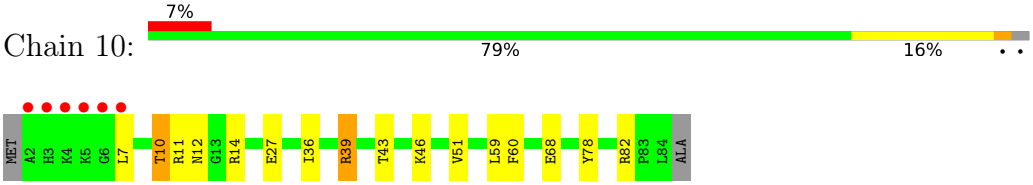
• Molecule 21: 50S ribosomal protein L25

Chain 2Z:



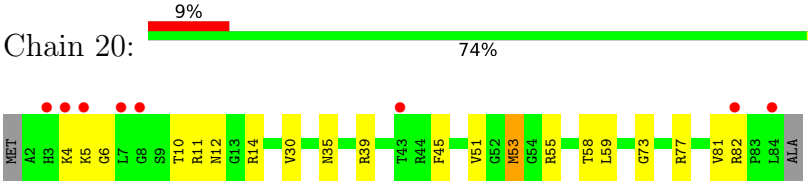
• Molecule 22: 50S ribosomal protein L27

Chain 10:



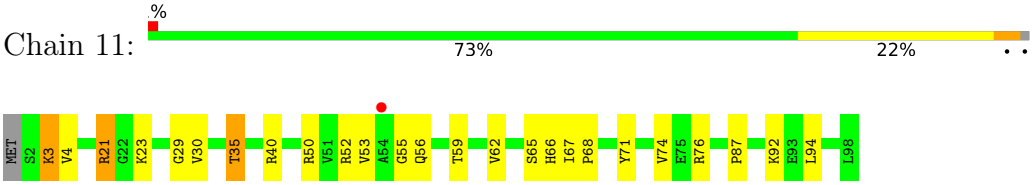
• Molecule 22: 50S ribosomal protein L27

Chain 20:



• Molecule 23: 50S ribosomal protein L28

Chain 11:

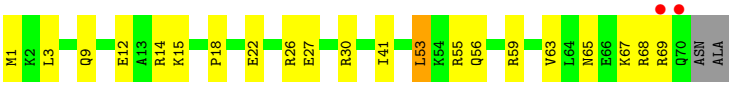


• Molecule 23: 50S ribosomal protein L28

Chain 21:

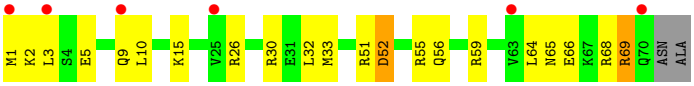
• Molecule 24: 50S ribosomal protein L29

Chain 12:



• Molecule 24: 50S ribosomal protein L29

Chain 22:

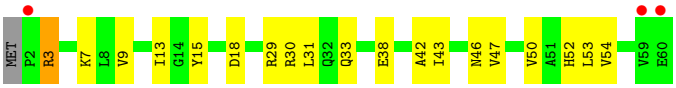


• Molecule 25: 50S ribosomal protein L30

Chain 13:

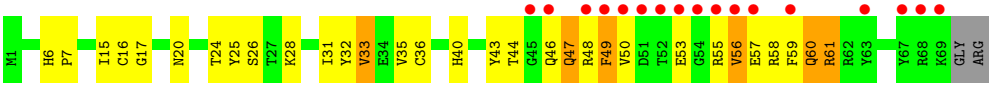
• Molecule 25: 50S ribosomal protein L30

Chain 23:



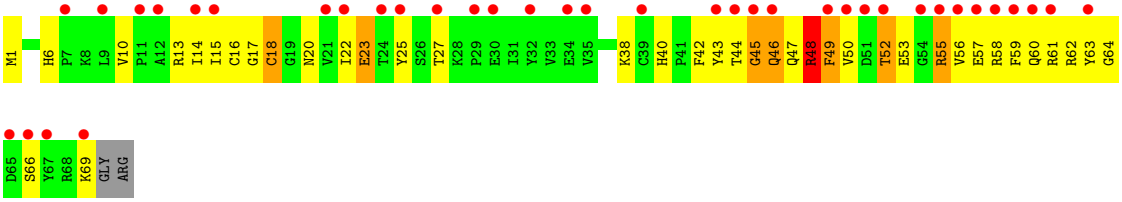
• Molecule 26: 50S ribosomal protein L31

Chain 14:



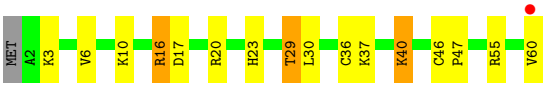
• Molecule 26: 50S ribosomal protein L31

Chain 24:



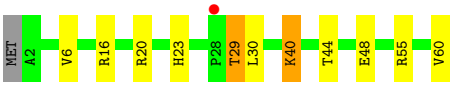
• Molecule 27: 50S ribosomal protein L32

Chain 15:



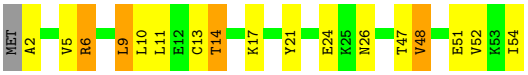
• Molecule 27: 50S ribosomal protein L32

Chain 25:



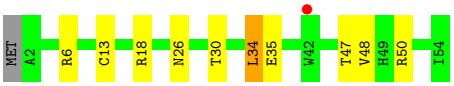
• Molecule 28: 50S ribosomal protein L33

Chain 16:



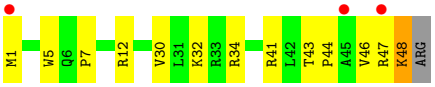
• Molecule 28: 50S ribosomal protein L33

Chain 26:



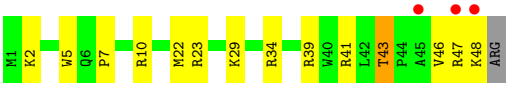
• Molecule 29: 50S ribosomal protein L34

Chain 17:



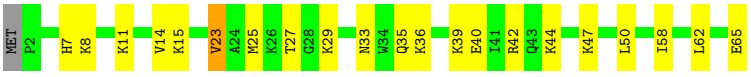
• Molecule 29: 50S ribosomal protein L34

Chain 27:



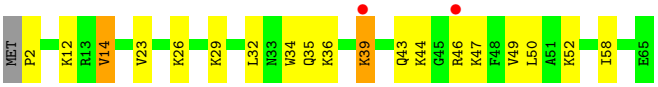
• Molecule 30: 50S ribosomal protein L35

Chain 18:



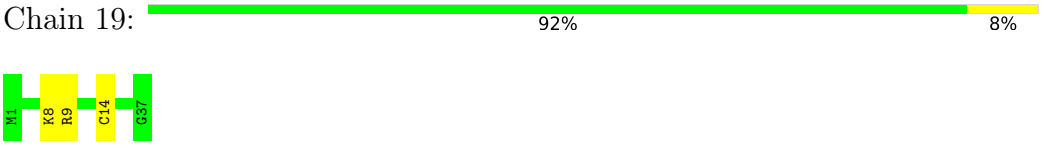
• Molecule 30: 50S ribosomal protein L35

Chain 28:



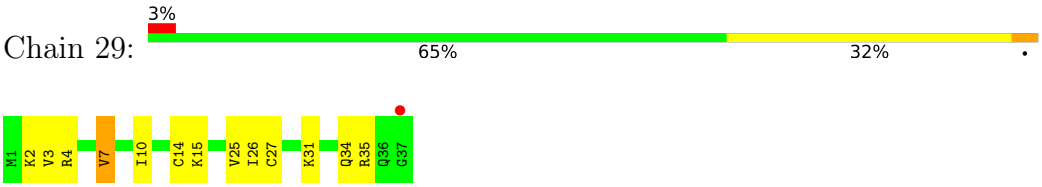
• Molecule 31: 50S ribosomal protein L36

Chain 19:



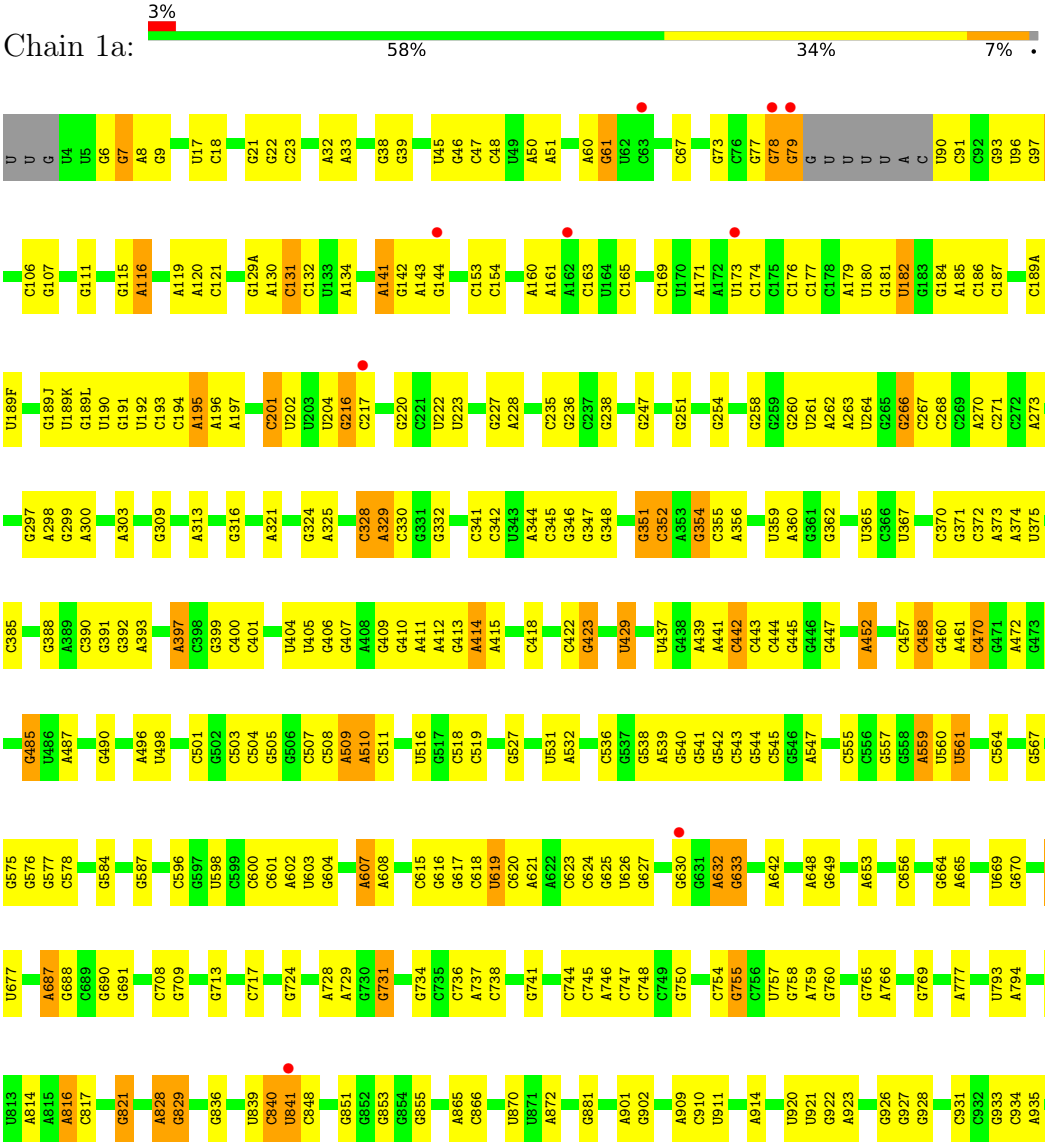
• Molecule 31: 50S ribosomal protein L36

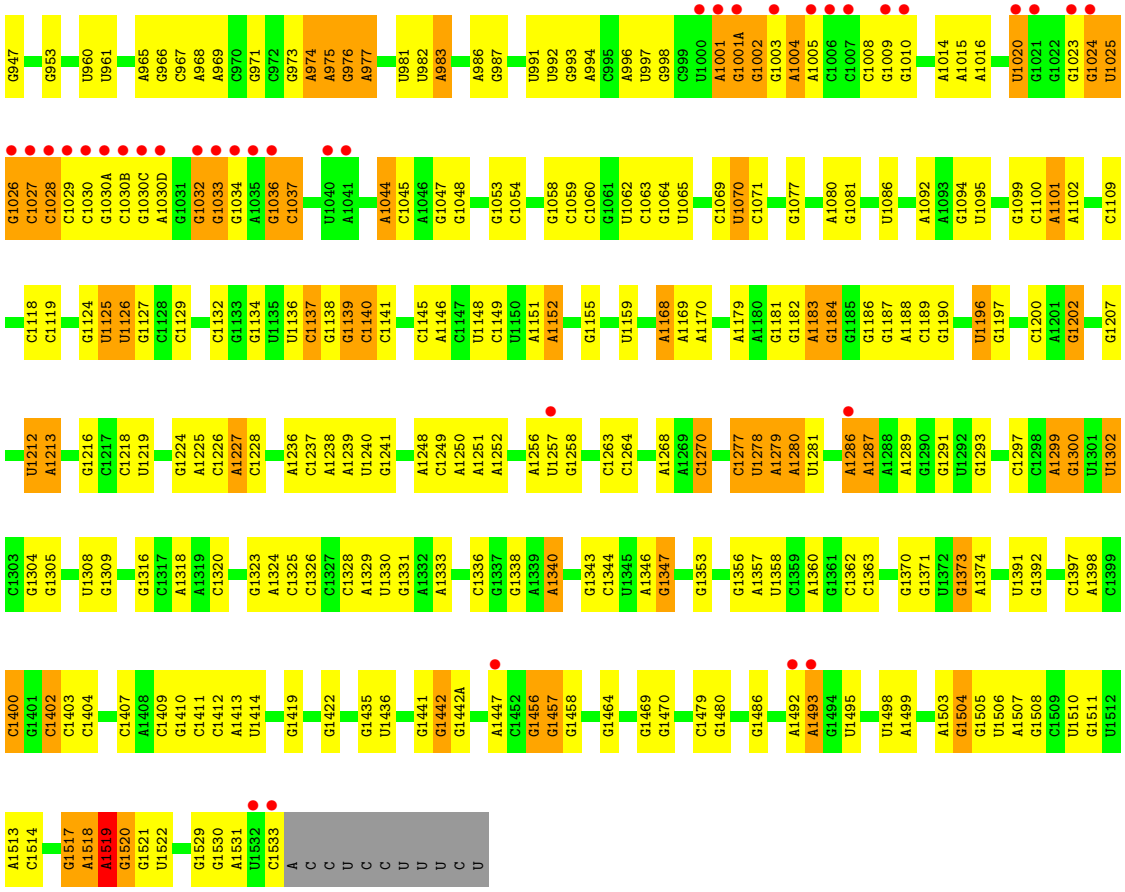
Chain 29:



• Molecule 32: 16S Ribosomal RNA

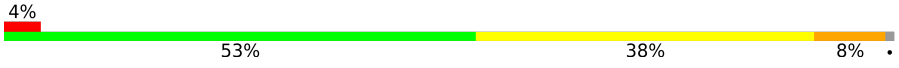
Chain 1a:

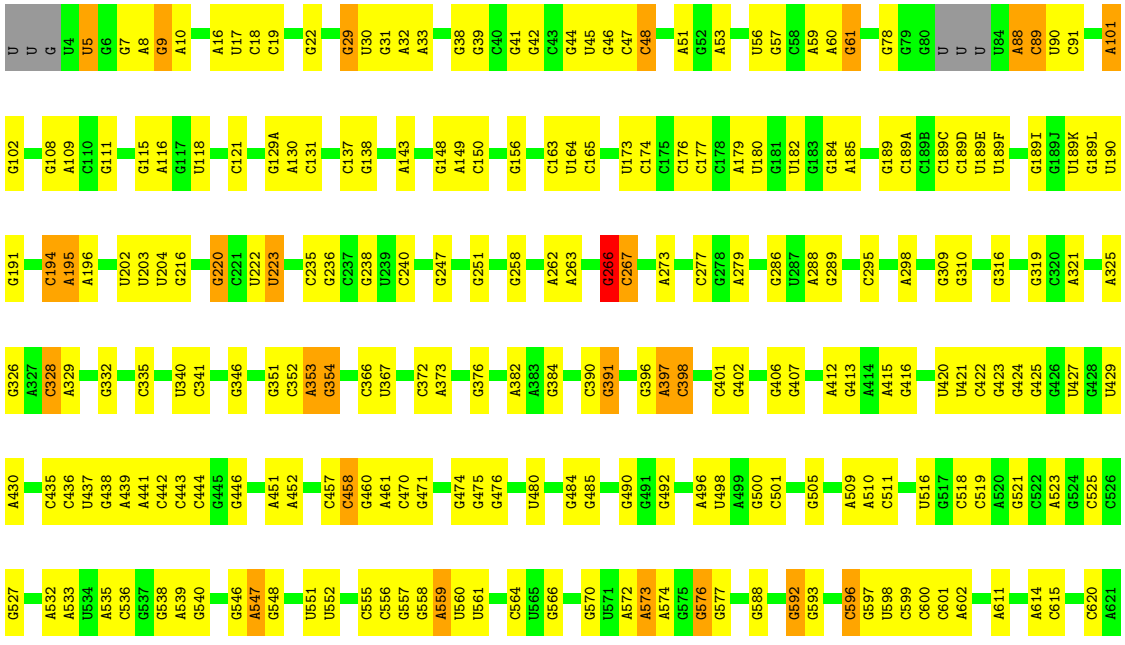


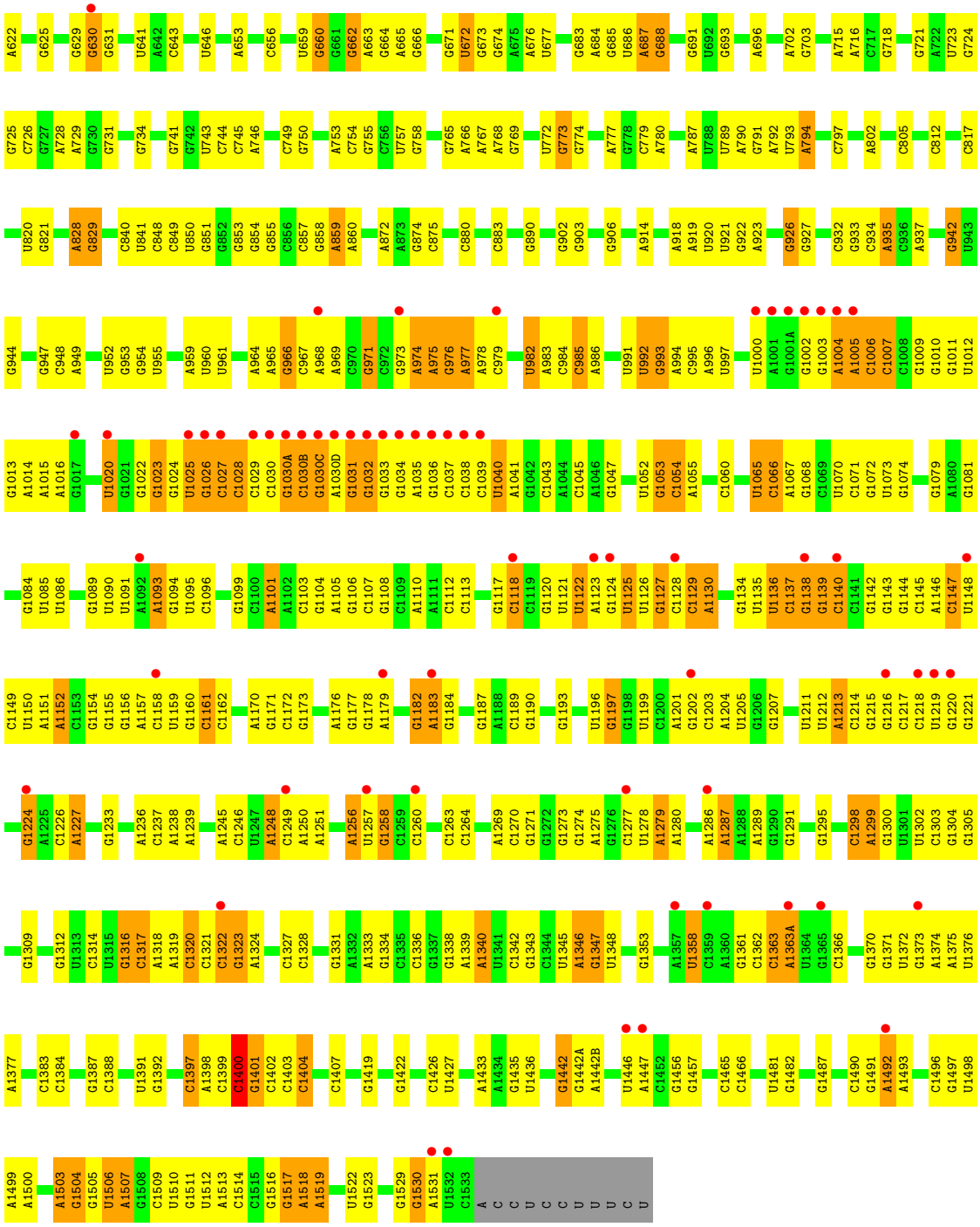


• Molecule 32: 16S Ribosomal RNA

Chain 2a:

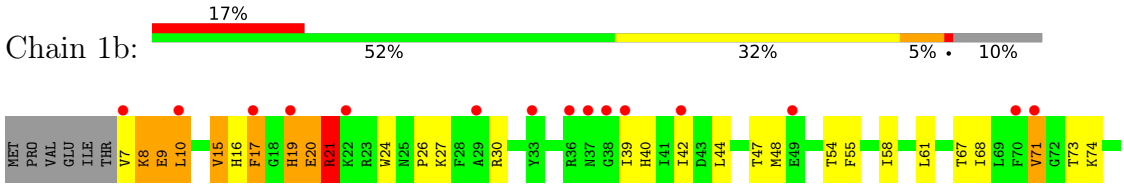


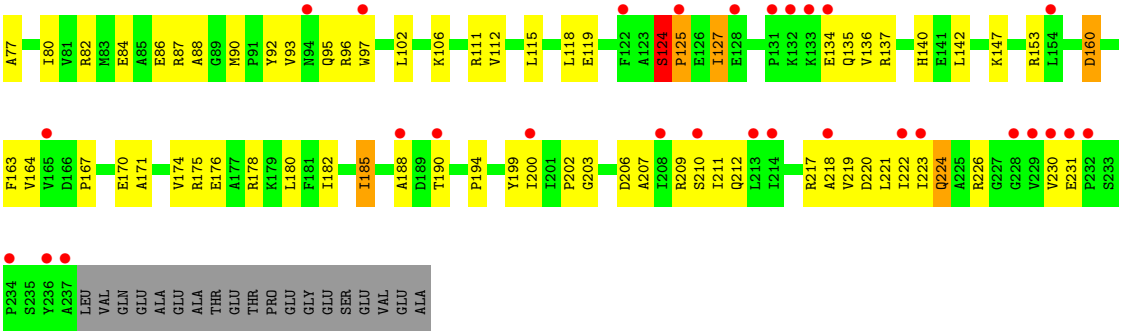




• Molecule 33: 30S ribosomal protein S2

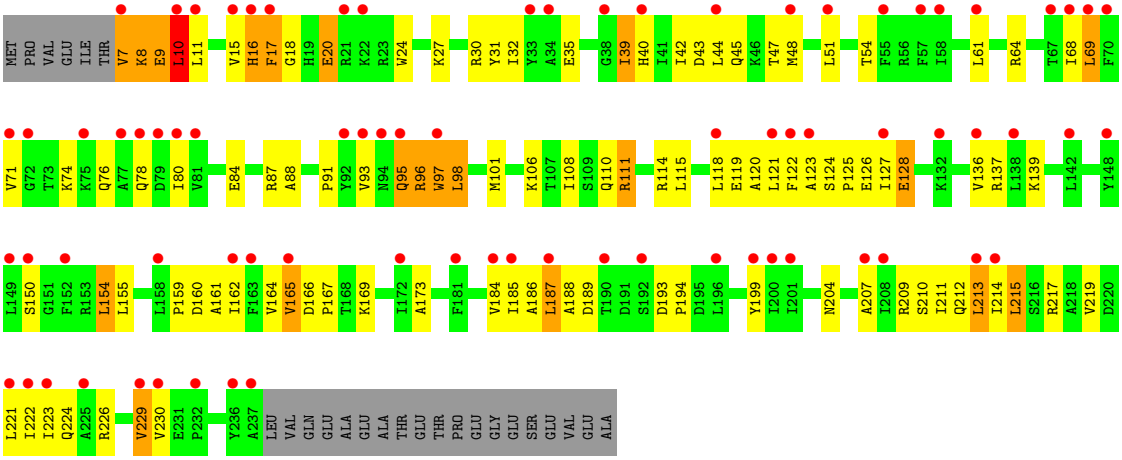
Chain 1b:





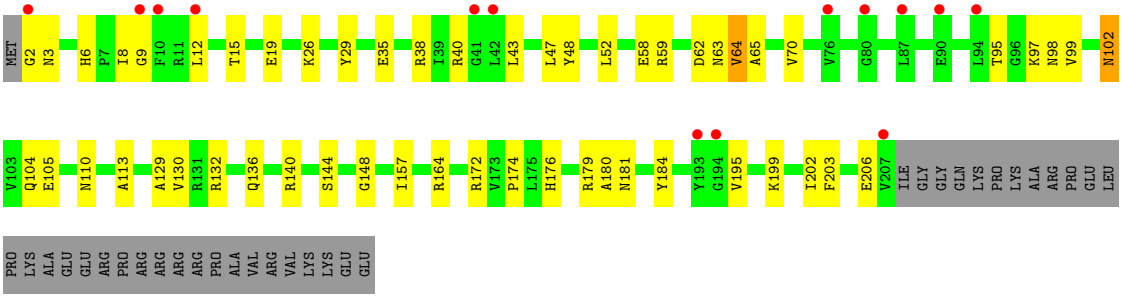
• Molecule 33: 30S ribosomal protein S2

Chain 2b:



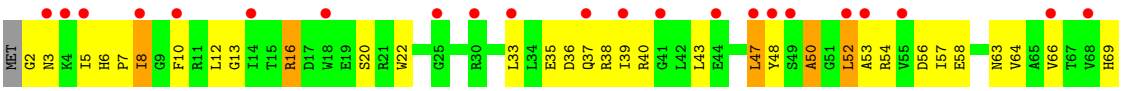
• Molecule 34: 30S ribosomal protein S3

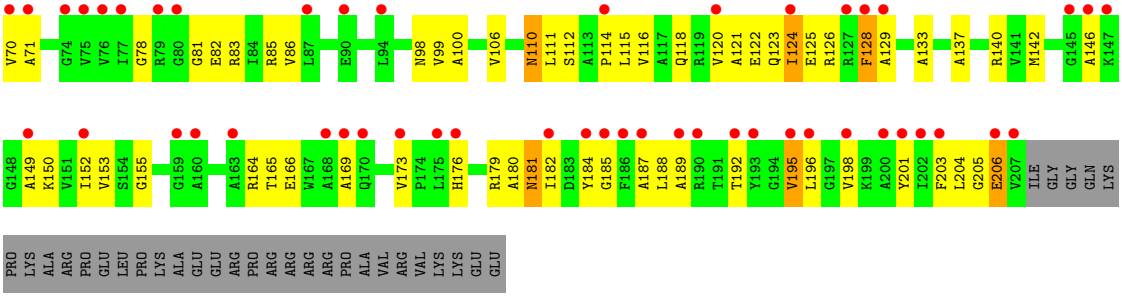
Chain 1c:



• Molecule 34: 30S ribosomal protein S3

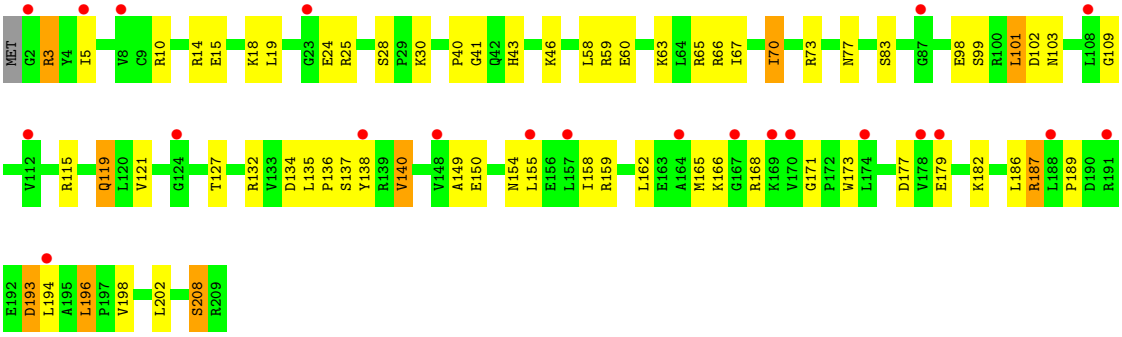
Chain 2c:





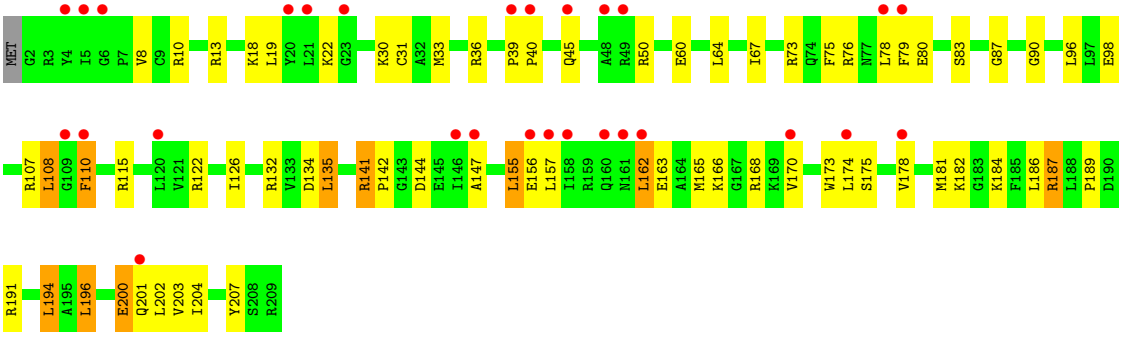
• Molecule 35: 30S ribosomal protein S4

Chain 1d:



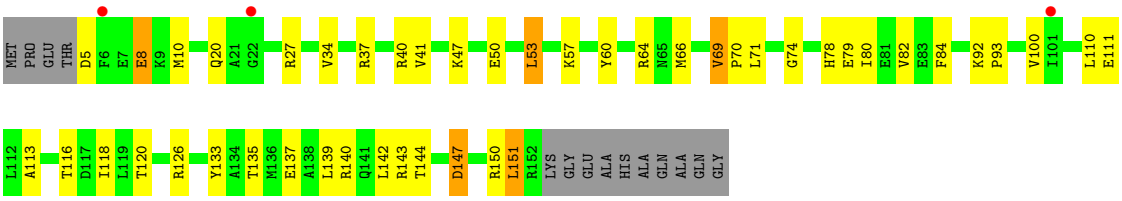
• Molecule 35: 30S ribosomal protein S4

Chain 2d:



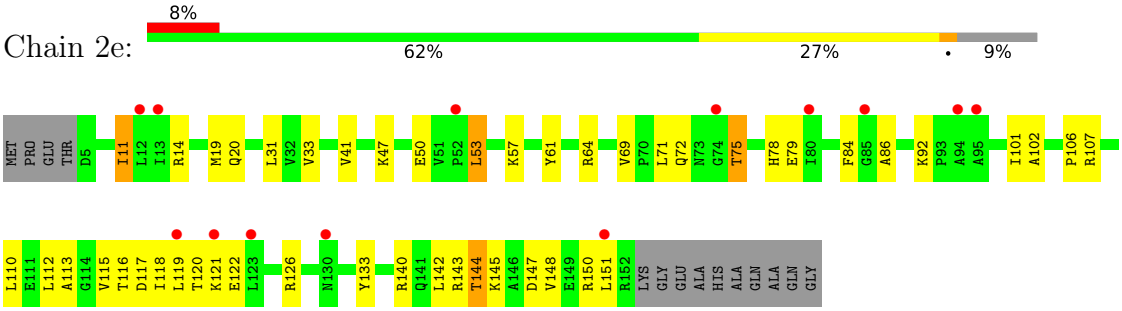
• Molecule 36: 30S ribosomal protein S5

Chain 1e:



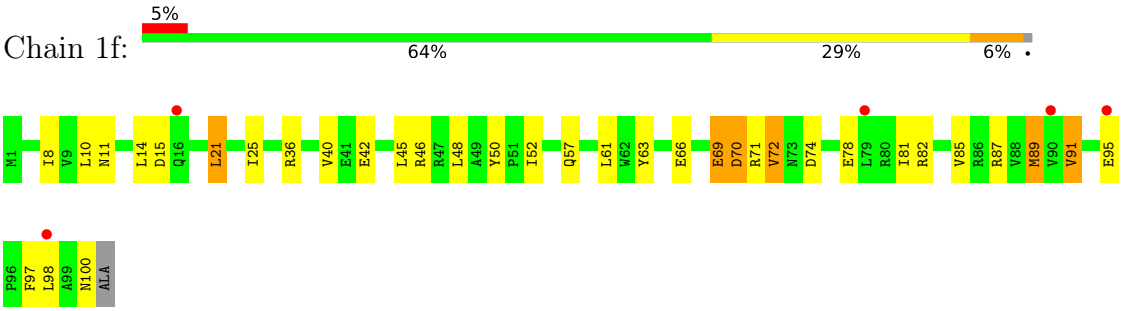
• Molecule 36: 30S ribosomal protein S5

Chain 2e:



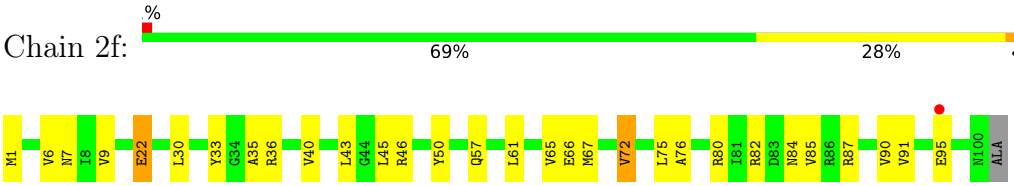
• Molecule 37: 30S ribosomal protein S6

Chain 1f:



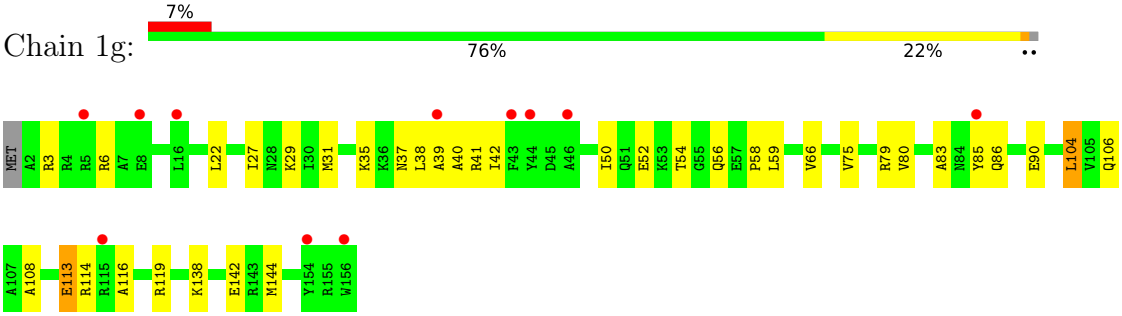
• Molecule 37: 30S ribosomal protein S6

Chain 2f:



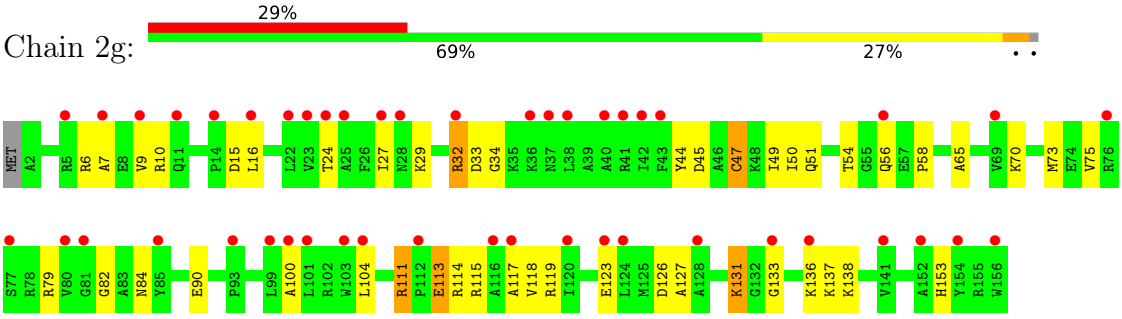
• Molecule 38: 30S ribosomal protein S7

Chain 1g:



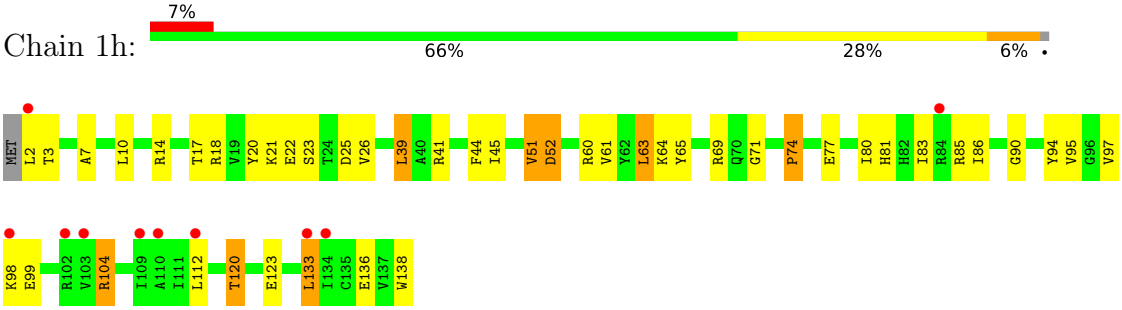
• Molecule 38: 30S ribosomal protein S7

Chain 2g:



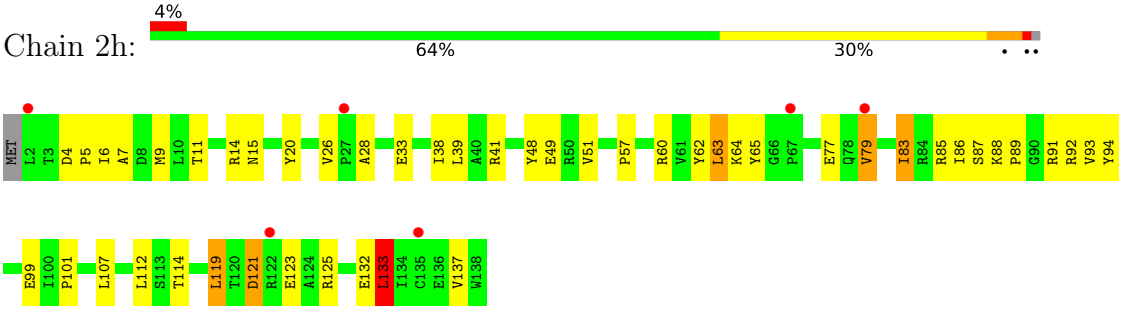
• Molecule 39: 30S ribosomal protein S8

Chain 1h:



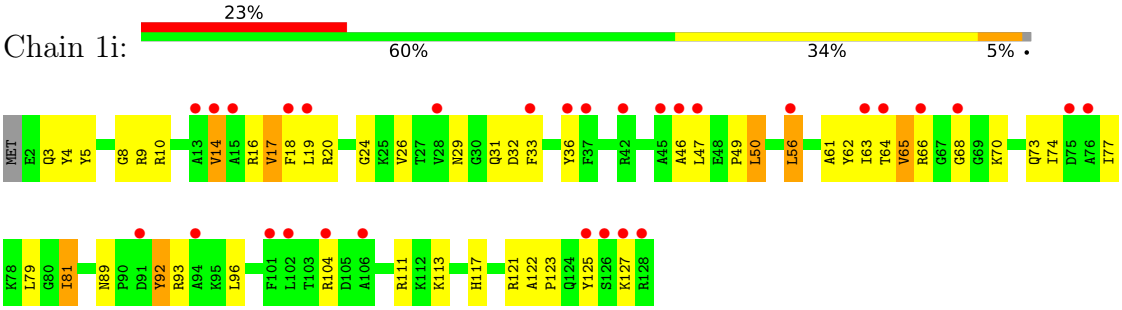
• Molecule 39: 30S ribosomal protein S8

Chain 2h:



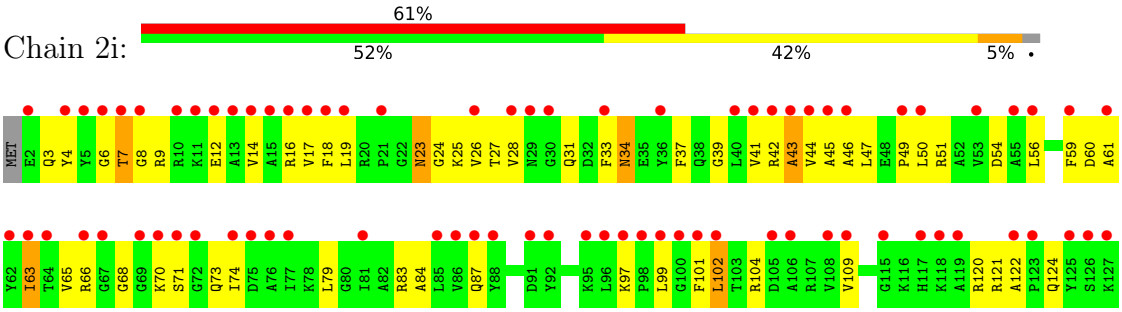
• Molecule 40: 30S ribosomal protein S9

Chain 1i:



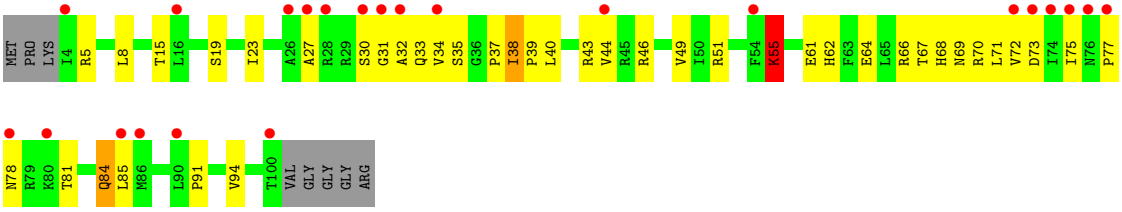
• Molecule 40: 30S ribosomal protein S9

Chain 2i:

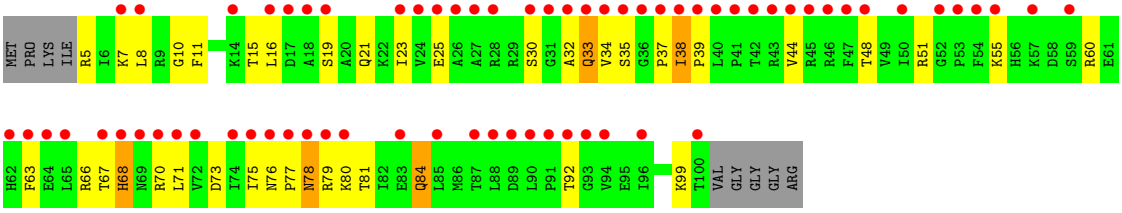


• Molecule 41: 30S ribosomal protein S10

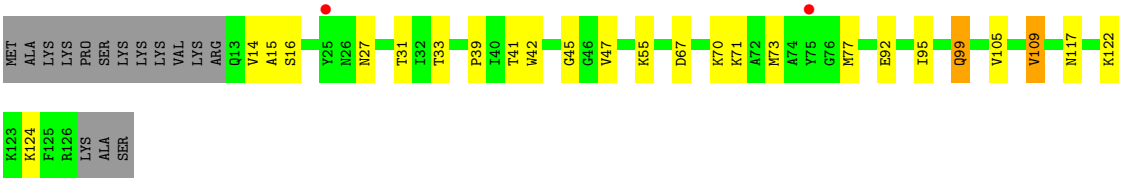
Chain 1j:



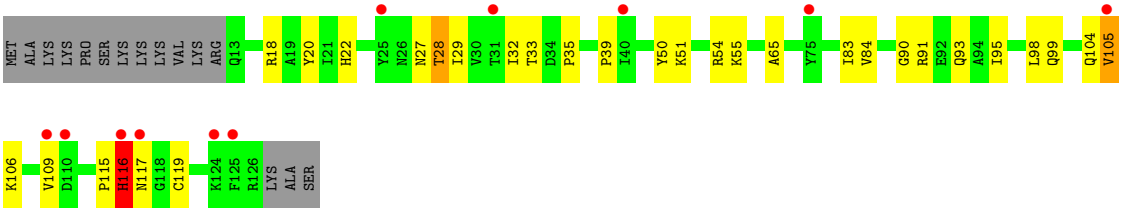
• Molecule 41: 30S ribosomal protein S10



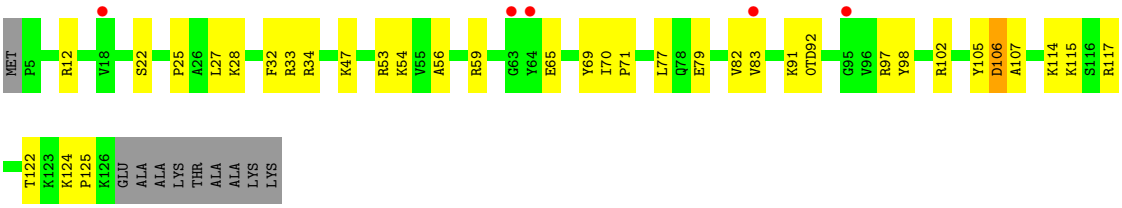
• Molecule 42: 30S ribosomal protein S11



• Molecule 42: 30S ribosomal protein S11



• Molecule 43: 30S ribosomal protein S12

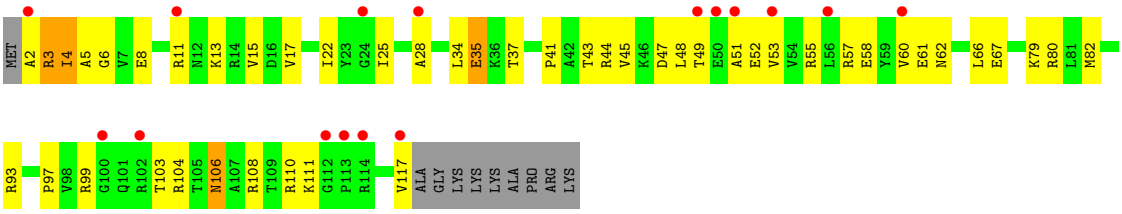


• Molecule 43: 30S ribosomal protein S12

Chain 2l:

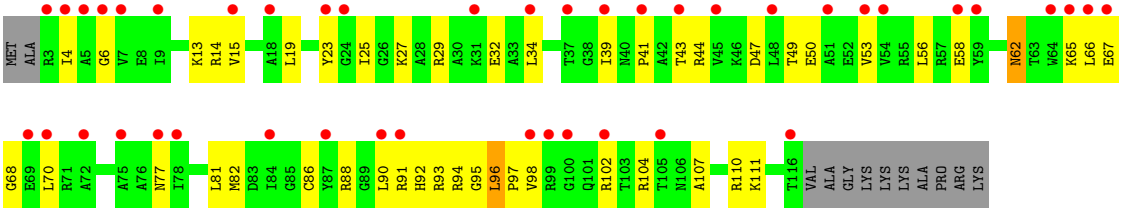
• Molecule 44: 30S ribosomal protein S13

Chain 1m:



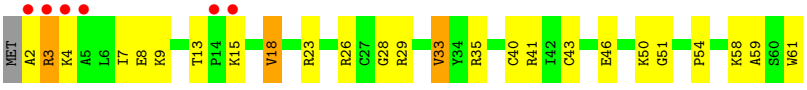
• Molecule 44: 30S ribosomal protein S13

Chain 2m:



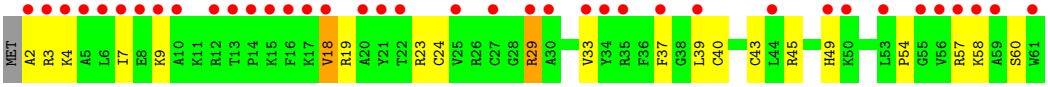
• Molecule 45: 30S ribosomal protein S14 type Z

Chain 1n:



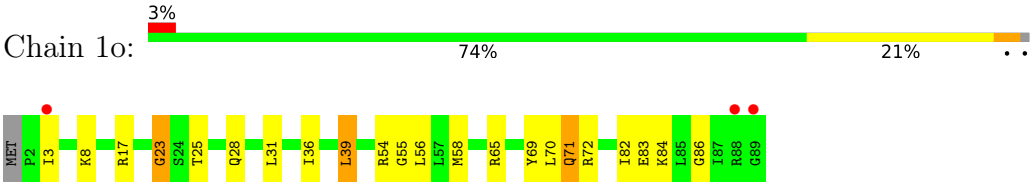
• Molecule 45: 30S ribosomal protein S14 type Z

Chain 2n:



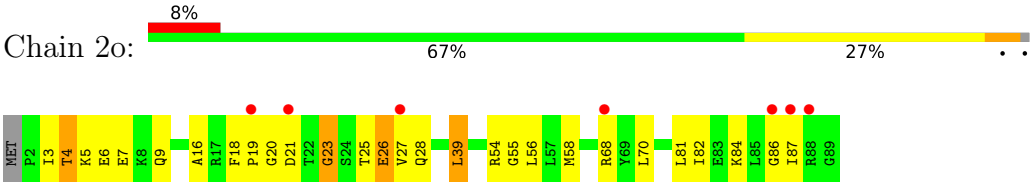
• Molecule 46: 30S ribosomal protein S15

Chain 1o:



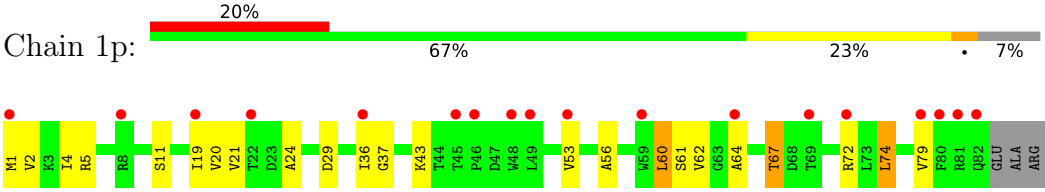
• Molecule 46: 30S ribosomal protein S15

Chain 2o:



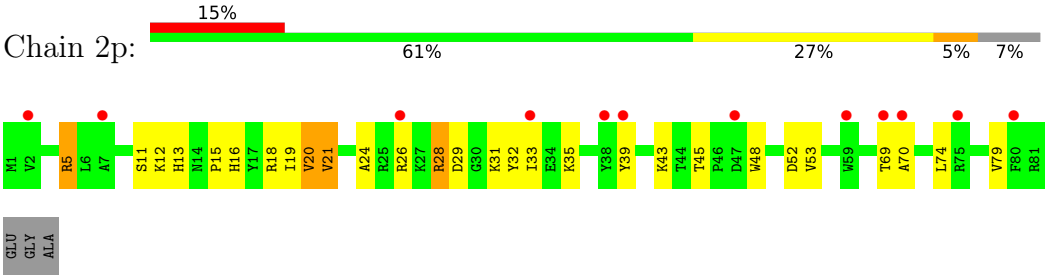
• Molecule 47: 30S ribosomal protein S16

Chain 1p:



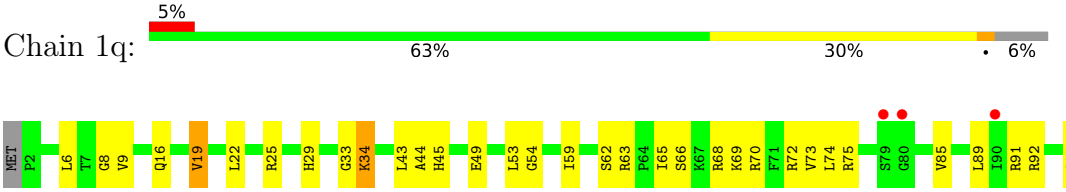
• Molecule 47: 30S ribosomal protein S16

Chain 2p:



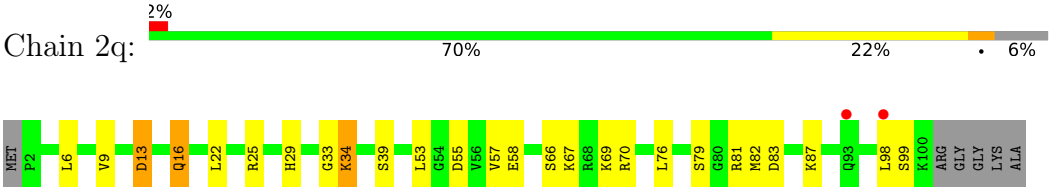
• Molecule 48: 30S ribosomal protein S17

Chain 1q:



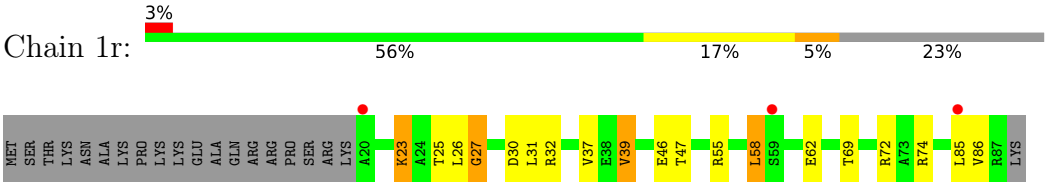
• Molecule 48: 30S ribosomal protein S17

Chain 2q:



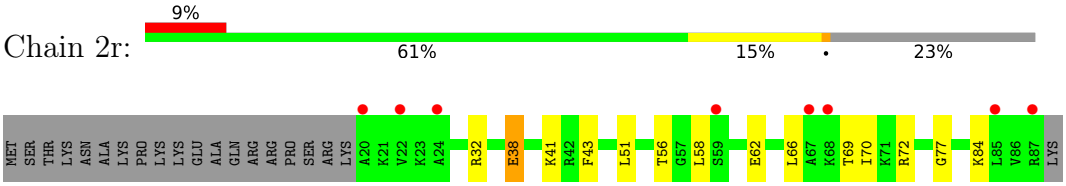
• Molecule 49: 30S ribosomal protein S18

Chain 1r:



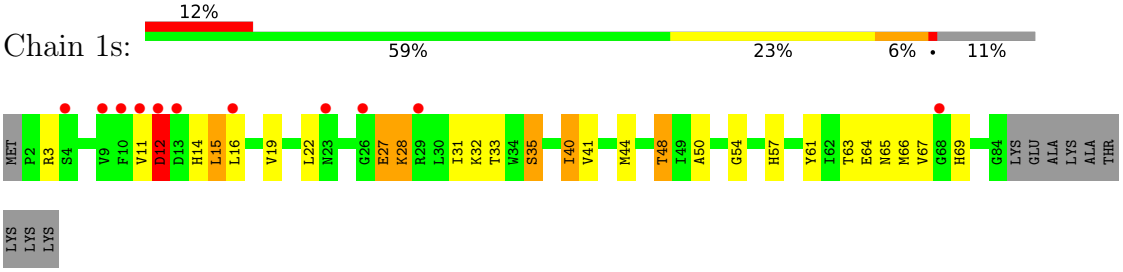
• Molecule 49: 30S ribosomal protein S18

Chain 2r:



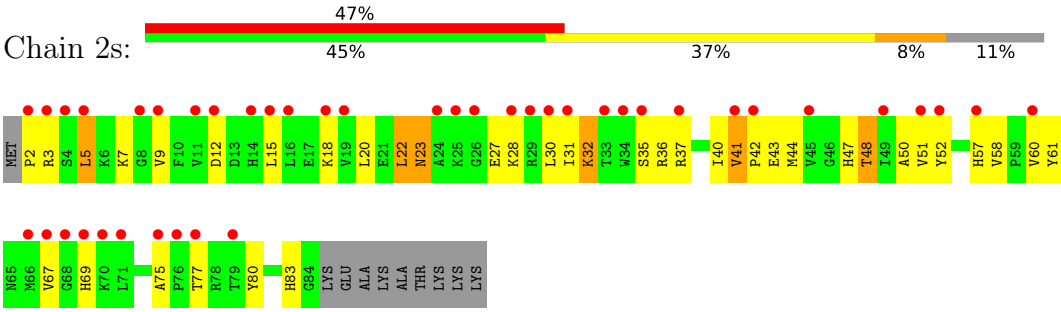
• Molecule 50: 30S ribosomal protein S19

Chain 1s:



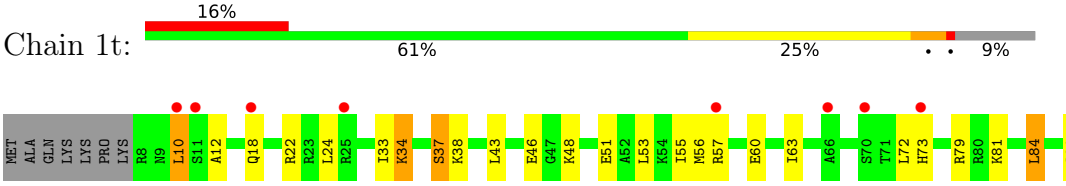
• Molecule 50: 30S ribosomal protein S19

Chain 2s:



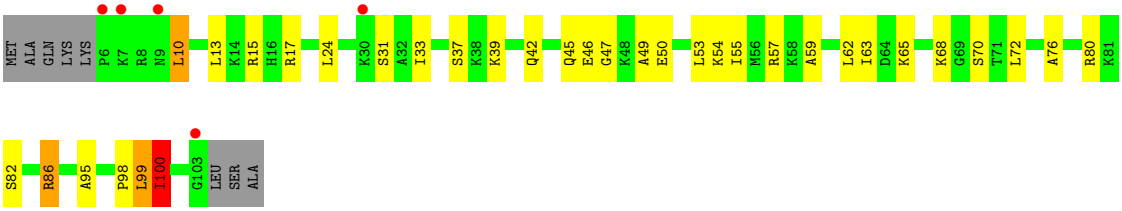
• Molecule 51: 30S ribosomal protein S20

Chain 1t:



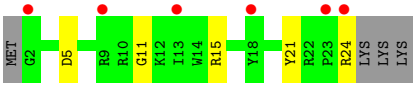
• Molecule 51: 30S ribosomal protein S20

Chain 2t:



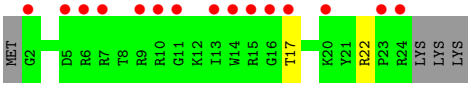
• Molecule 52: 30S ribosomal protein Thx

Chain 1u:



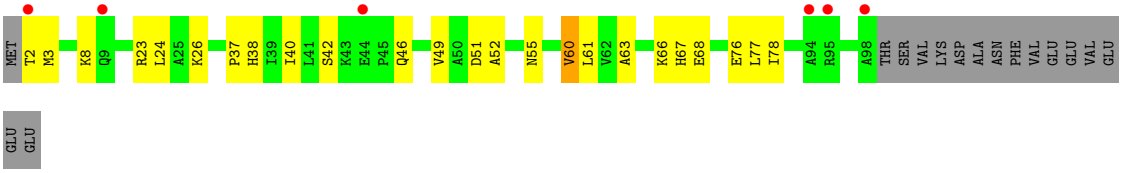
• Molecule 52: 30S ribosomal protein Thx

Chain 2u:



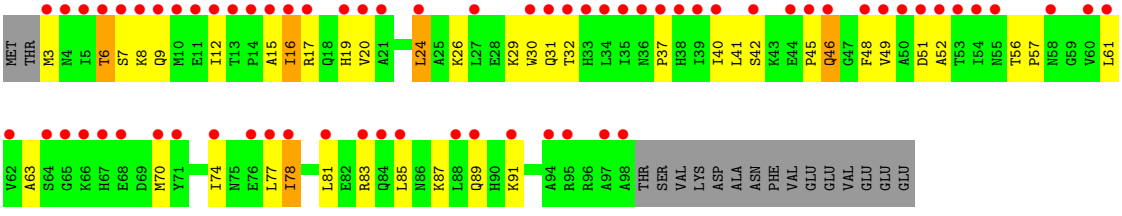
• Molecule 53: Ribosome-associated inhibitor A

Chain 1y:



• Molecule 53: Ribosome-associated inhibitor A

Chain 2y:

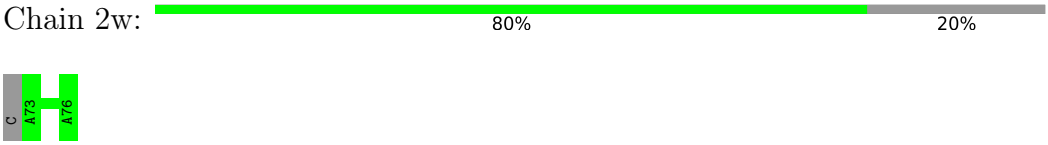


• Molecule 54: A-site Deacylated tRNA Analog

Chain 1w:

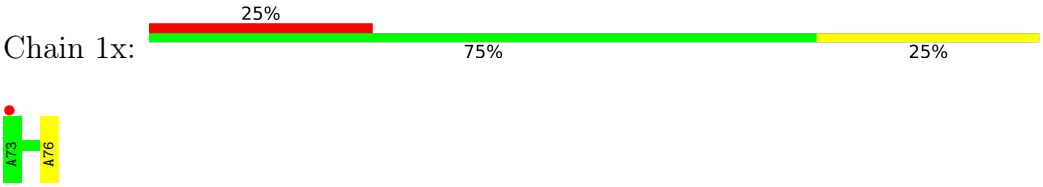
• Molecule 54: A-site Deacylated tRNA Analog

Chain 2w:



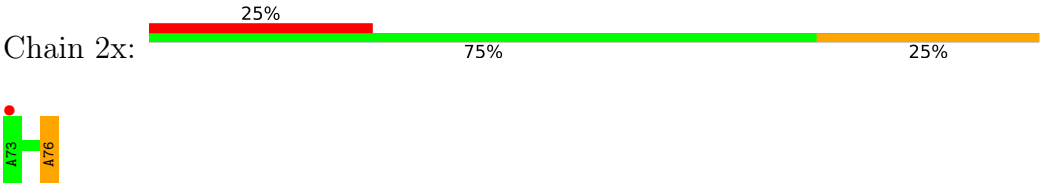
• Molecule 55: P-site Peptidyl-tRNA Analog RNA

Chain 1x:



• Molecule 55: P-site Peptidyl-tRNA Analog RNA

Chain 2x:



• Molecule 56: P-site Peptidyl-tRNA Analog Peptide

Chain 1v:

• Molecule 56: P-site Peptidyl-tRNA Analog Peptide

Chain 2v:

There are no outlier residues recorded for this chain.

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	209.81Å 449.56Å 621.47Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	211.38 – 2.40 211.38 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.7 (211.38-2.40) 99.7 (211.38-2.40)	Depositor EDS
R_{merge}	0.25	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.12 (at 2.40Å)	Xtriage
Refinement program	PHENIX 1.8.2	Depositor
R, R_{free}	0.225 , 0.269 0.228 , 0.272	Depositor DCC
R_{free} test set	112792 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	44.8	Xtriage
Anisotropy	0.136	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 62.5	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	0.91	EDS
Total number of atoms	297868	wwPDB-VP
Average B, all atoms (Å^2)	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.59% 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: 0TD, 5MC, G7M, MPD, 2MG, 2MA, 4OC, OMG, MA6, OMC, SF4, UR3, ZN, CLM, MG, PSU, 5MU, 8AN, OMU, M2G

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	1A	0.28	1/69031 (0.0%)	0.48	4/107754 (0.0%)
1	2A	0.22	0/68903	0.42	3/107552 (0.0%)
2	1B	0.23	0/2876	0.43	0/4486
2	2B	0.19	0/2878	0.36	0/4490
3	1D	0.27	0/2181	0.53	0/2940
3	2D	0.22	0/2186	0.47	0/2944
4	1E	0.26	0/1592	0.48	0/2149
4	2E	0.21	0/1592	0.43	0/2149
5	1F	0.25	0/1619	0.47	0/2193
5	2F	0.21	0/1615	0.47	2/2188 (0.1%)
6	1G	0.21	0/1451	0.45	0/1961
6	2G	0.20	0/1449	0.44	0/1957
7	1H	0.21	0/1356	0.41	0/1834
7	2H	0.20	0/1350	0.42	0/1826
8	1I	0.19	0/1109	0.47	1/1512 (0.1%)
8	2I	0.19	0/1091	0.41	0/1490
9	1N	0.24	0/1148	0.47	0/1547
9	2N	0.19	0/1144	0.38	0/1543
10	1O	0.24	0/943	0.46	0/1269
10	2O	0.21	0/943	0.40	0/1269
11	1P	0.26	0/1152	0.50	0/1533
11	2P	0.22	0/1152	0.47	0/1533
12	1Q	0.26	0/1143	0.48	0/1527
12	2Q	0.21	0/1143	0.43	0/1527
13	1R	0.27	0/982	0.50	0/1312
13	2R	0.21	0/982	0.47	0/1312
14	1S	0.22	0/887	0.49	0/1180
14	2S	0.20	0/880	0.43	0/1172
15	1T	0.25	0/1105	0.49	0/1477
15	2T	0.21	0/1097	0.44	0/1468
16	1U	0.29	0/977	0.50	0/1301

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\| > 5$	RMSZ	$\#\|Z\| > 5$
16	2U	0.19	0/977	0.39	0/1301
17	1V	0.29	0/786	0.49	0/1053
17	2V	0.19	0/782	0.40	0/1049
18	1W	0.29	0/897	0.47	0/1205
18	2W	0.20	0/897	0.41	0/1205
19	1X	0.27	0/764	0.49	0/1025
19	2X	0.20	0/764	0.42	0/1025
20	1Y	0.23	0/823	0.50	0/1099
20	2Y	0.19	0/823	0.44	0/1100
21	1Z	0.21	0/1620	0.44	0/2200
21	2Z	0.19	0/1590	0.43	0/2162
22	10	0.27	0/662	0.49	0/881
22	20	0.21	0/659	0.49	0/877
23	11	0.25	0/761	0.43	0/1013
23	21	0.22	0/766	0.44	0/1018
24	12	0.22	0/590	0.46	0/781
24	22	0.22	0/594	0.47	0/785
25	13	0.25	0/474	0.49	0/635
25	23	0.17	0/469	0.39	0/630
26	14	0.23	0/559	0.59	0/754
26	24	0.27	0/549	0.67	0/741
27	15	0.27	0/473	0.52	0/639
27	25	0.21	0/469	0.43	0/635
28	16	0.24	0/460	0.46	0/613
28	26	0.20	0/456	0.40	0/608
29	17	0.30	0/426	0.54	0/561
29	27	0.24	0/426	0.46	0/561
30	18	0.26	0/525	0.51	0/691
30	28	0.20	0/525	0.38	0/691
31	19	0.28	0/310	0.49	0/407
31	29	0.21	0/310	0.45	0/407
32	1a	0.20	0/35795	0.38	0/55864
32	2a	0.19	0/35890	0.38	2/56012 (0.0%)
33	1b	0.22	0/1876	0.47	0/2533
33	2b	0.23	0/1860	0.52	0/2518
34	1c	0.19	0/1582	0.42	0/2137
34	2c	0.20	0/1566	0.40	0/2119
35	1d	0.20	0/1695	0.46	0/2274
35	2d	0.19	0/1698	0.45	0/2277
36	1e	0.20	0/1149	0.43	0/1548
36	2e	0.20	0/1149	0.41	0/1548
37	1f	0.19	0/827	0.39	0/1120
37	2f	0.18	0/829	0.39	0/1123

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
38	1g	0.19	0/1254	0.40	0/1683
38	2g	0.20	0/1248	0.38	0/1676
39	1h	0.18	0/1118	0.42	0/1506
39	2h	0.17	0/1108	0.40	0/1494
40	1i	0.19	0/1005	0.43	0/1351
40	2i	0.24	0/985	0.50	0/1329
41	1j	0.19	0/732	0.39	0/993
41	2j	0.22	0/723	0.45	0/984
42	1k	0.19	0/849	0.44	0/1150
42	2k	0.19	0/848	0.48	2/1149 (0.2%)
43	1l	0.20	0/937	0.46	0/1260
43	2l	0.19	0/937	0.41	0/1260
44	1m	0.21	0/924	0.46	0/1242
44	2m	0.22	0/905	0.46	0/1217
45	1n	0.18	0/501	0.40	0/664
45	2n	0.21	0/501	0.41	0/664
46	1o	0.18	0/739	0.36	0/985
46	2o	0.18	0/739	0.37	0/985
47	1p	0.22	0/697	0.50	0/939
47	2p	0.20	0/693	0.43	0/935
48	1q	0.19	0/836	0.41	0/1117
48	2q	0.18	0/836	0.42	0/1117
49	1r	0.19	0/560	0.42	0/746
49	2r	0.19	0/560	0.42	0/746
50	1s	0.17	0/663	0.44	0/895
50	2s	0.24	0/660	0.46	0/893
51	1t	0.19	0/734	0.43	0/969
51	2t	0.20	0/736	0.44	0/976
52	1u	0.19	0/203	0.40	0/266
52	2u	0.21	0/203	0.45	0/266
53	1y	0.18	0/776	0.37	0/1048
53	2y	0.22	0/761	0.43	0/1030
54	1w	0.30	0/69	0.57	0/106
54	2w	0.18	0/69	0.30	0/106
55	1x	0.29	0/44	0.54	0/67
55	2x	0.20	0/44	0.44	0/67
56	1v	0.31	0/20	0.33	0/25
56	2v	0.18	0/20	0.31	0/25
All	All	0.23	1/310296 (0.0%)	0.43	14/463751 (0.0%)

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

sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
21	2Z	0	1
26	24	0	1
All	All	0	2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1A	2552	OMU	O3'-P	5.09	1.61	1.56

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	1A	1042	G	OP1-P-O3'	-9.51	79.46	108.00
1	1A	1042	G	OP2-P-O3'	-6.82	87.55	108.00
1	2A	752	A	C2'-C3'-O3'	6.32	118.98	109.50
1	2A	1992	G	C2'-C3'-O3'	6.16	118.74	109.50
1	1A	2689	U	C4'-C3'-O3'	5.68	117.92	109.40
32	2a	266	G	P-O3'-C3'	5.57	128.55	120.20
42	2k	116	HIS	CA-C-N	5.55	131.69	121.70
42	2k	116	HIS	C-N-CA	5.55	131.69	121.70
8	1I	84	GLY	N-CA-C	-5.17	105.98	111.93
5	2F	21	ALA	CA-C-N	5.14	130.95	121.70
5	2F	21	ALA	C-N-CA	5.14	130.95	121.70
1	1A	512	G	O4'-C1'-N9	5.11	115.86	108.20
32	2a	266	G	C2'-C3'-O3'	5.11	117.16	109.50
1	2A	752	A	P-O3'-C3'	5.06	127.79	120.20

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
26	24	18	CYS	Peptide
21	2Z	136	PHE	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	1A	61869	0	31205	608	0
1	2A	61758	0	31153	738	0
2	1B	2572	0	1305	29	0
2	2B	2573	0	1306	41	0
3	1D	2131	0	2207	47	0
3	2D	2136	0	2218	46	0
4	1E	1559	0	1618	24	0
4	2E	1559	0	1618	37	0
5	1F	1584	0	1625	29	0
5	2F	1580	0	1619	51	0
6	1G	1426	0	1445	49	0
6	2G	1424	0	1441	56	0
7	1H	1330	0	1407	31	0
7	2H	1324	0	1402	37	0
8	1I	1094	0	1127	27	0
8	2I	1076	0	1094	35	0
9	1N	1121	0	1195	23	0
9	2N	1117	0	1184	23	0
10	1O	933	0	996	21	0
10	2O	933	0	996	20	0
11	1P	1135	0	1212	28	0
11	2P	1135	0	1212	34	0
12	1Q	1122	0	1177	28	0
12	2Q	1122	0	1177	29	0
13	1R	968	0	1033	14	0
13	2R	968	0	1033	19	0
14	1S	877	0	938	17	0
14	2S	870	0	923	31	0
15	1T	1091	0	1151	29	0
15	2T	1083	0	1136	28	0
16	1U	959	0	1019	15	0
16	2U	959	0	1019	25	0
17	1V	775	0	841	12	0
17	2V	771	0	830	20	0
18	1W	886	0	940	11	0
18	2W	886	0	940	13	0
19	1X	750	0	814	15	0
19	2X	750	0	814	15	0
20	1Y	810	0	892	23	0
20	2Y	810	0	887	27	0
21	1Z	1587	0	1598	35	0
21	2Z	1557	0	1564	49	0
22	10	653	0	674	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
22	20	650	0	665	13	0
23	11	754	0	823	16	0
23	21	759	0	837	33	0
24	12	588	0	643	14	0
24	22	592	0	654	14	0
25	13	469	0	518	12	0
25	23	464	0	514	16	0
26	14	546	0	522	25	0
26	24	536	0	514	27	0
27	15	459	0	476	9	0
27	25	455	0	465	7	0
28	16	453	0	473	12	0
28	26	449	0	469	5	0
29	17	418	0	467	13	0
29	27	418	0	467	10	0
30	18	517	0	582	14	0
30	28	517	0	582	13	0
31	19	307	0	335	2	0
31	29	307	0	335	9	0
32	1a	32246	0	16293	396	0
32	2a	32331	0	16337	449	0
33	1b	1842	0	1862	59	0
33	2b	1825	0	1828	67	0
34	1c	1558	0	1557	32	0
34	2c	1542	0	1517	63	0
35	1d	1665	0	1687	45	0
35	2d	1668	0	1703	43	0
36	1e	1133	0	1191	28	0
36	2e	1133	0	1191	32	0
37	1f	814	0	808	23	0
37	2f	816	0	808	19	0
38	1g	1235	0	1249	22	0
38	2g	1229	0	1238	27	0
39	1h	1098	0	1143	31	0
39	2h	1088	0	1126	30	0
40	1i	986	0	990	43	0
40	2i	966	0	953	51	0
41	1j	719	0	672	28	0
41	2j	710	0	661	33	0
42	1k	834	0	838	15	0
42	2k	833	0	836	17	0
43	1l	932	0	981	22	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
43	2l	932	0	981	20	0
44	1m	914	0	954	33	0
44	2m	895	0	920	25	0
45	1n	492	0	529	21	0
45	2n	492	0	529	22	0
46	1o	728	0	760	14	0
46	2o	728	0	760	15	0
47	1p	681	0	697	11	0
47	2p	677	0	686	16	0
48	1q	823	0	891	21	0
48	2q	823	0	891	17	0
49	1r	555	0	618	16	0
49	2r	555	0	618	10	0
50	1s	648	0	658	23	0
50	2s	645	0	635	29	0
51	1t	732	0	809	21	0
51	2t	733	0	795	18	0
52	1u	199	0	208	5	0
52	2u	199	0	208	1	0
53	1y	764	0	786	15	0
53	2y	749	0	757	30	0
54	1w	63	0	34	0	0
54	2w	63	0	34	0	0
55	1x	63	0	33	0	0
55	2x	63	0	33	1	0
56	1v	21	0	27	0	0
56	2v	21	0	27	0	0
57	10	8	0	0	0	0
57	11	5	0	0	0	0
57	13	3	0	0	0	0
57	15	7	0	0	0	0
57	17	5	0	0	0	0
57	18	3	0	0	0	0
57	19	3	0	0	0	0
57	1A	1016	0	0	0	0
57	1B	30	0	0	0	0
57	1D	21	0	0	0	0
57	1E	8	0	0	0	0
57	1F	18	0	0	0	0
57	1G	4	0	0	0	0
57	1H	2	0	0	0	0
57	1N	4	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
57	1O	1	0	0	0	0
57	1P	5	0	0	0	0
57	1Q	5	0	0	0	0
57	1R	5	0	0	0	0
57	1T	7	0	0	0	0
57	1U	6	0	0	0	0
57	1V	7	0	0	0	0
57	1W	3	0	0	0	0
57	1X	1	0	0	0	0
57	1Y	2	0	0	0	0
57	1Z	1	0	0	0	0
57	1a	266	0	0	0	0
57	1b	1	0	0	0	0
57	1d	4	0	0	0	0
57	1e	2	0	0	0	0
57	1f	2	0	0	0	0
57	1g	2	0	0	0	0
57	1h	2	0	0	0	0
57	1i	1	0	0	0	0
57	1l	2	0	0	0	0
57	1m	1	0	0	0	0
57	1n	3	0	0	0	0
57	1o	2	0	0	0	0
57	1t	2	0	0	0	0
57	1x	2	0	0	0	0
57	1y	2	0	0	0	0
57	20	2	0	0	0	0
57	21	1	0	0	0	0
57	23	1	0	0	0	0
57	25	3	0	0	0	0
57	27	1	0	0	0	0
57	28	2	0	0	0	0
57	2A	746	0	0	0	0
57	2B	19	0	0	0	0
57	2D	8	0	0	0	0
57	2E	8	0	0	0	0
57	2F	4	0	0	0	0
57	2G	3	0	0	0	0
57	2I	1	0	0	0	0
57	2N	1	0	0	0	0
57	2O	2	0	0	0	0
57	2P	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
57	2Q	3	0	0	0	0
57	2R	2	0	0	0	0
57	2T	4	0	0	0	0
57	2U	1	0	0	0	0
57	2V	3	0	0	0	0
57	2W	3	0	0	0	0
57	2X	1	0	0	0	0
57	2Y	1	0	0	0	0
57	2a	190	0	0	0	0
57	2e	1	0	0	0	0
57	2f	1	0	0	0	0
57	2j	2	0	0	0	0
57	2r	1	0	0	0	0
57	2t	1	0	0	0	0
57	2x	1	0	0	0	0
58	1A	20	0	11	0	0
58	2A	20	0	11	0	0
59	1A	12	0	12	2	0
59	1B	12	0	12	2	0
60	18	8	0	14	1	0
60	1A	8	0	14	1	0
60	1T	8	0	14	0	0
60	1a	8	0	11	5	0
60	2A	8	0	14	0	0
60	2B	8	0	14	1	0
61	14	1	0	0	0	0
61	15	1	0	0	0	0
61	16	1	0	0	0	0
61	19	1	0	0	0	0
61	1Y	1	0	0	0	0
61	1n	1	0	0	0	0
61	24	1	0	0	0	0
61	25	1	0	0	0	0
61	26	1	0	0	0	0
61	29	1	0	0	0	0
61	2Y	1	0	0	0	0
61	2n	1	0	0	0	0
62	1d	8	0	0	0	0
62	2d	8	0	0	0	0
63	10	25	0	0	0	0
63	11	22	0	0	0	0
63	12	13	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
63	13	21	0	0	1	0
63	14	2	0	0	0	0
63	15	26	0	0	1	0
63	16	20	0	0	2	0
63	17	16	0	0	2	0
63	18	30	0	0	3	0
63	19	6	0	0	0	0
63	1A	4023	0	0	127	0
63	1B	93	0	0	6	0
63	1D	112	0	0	5	0
63	1E	81	0	0	2	0
63	1F	61	0	0	0	0
63	1G	20	0	0	0	0
63	1H	12	0	0	1	0
63	1I	6	0	0	0	0
63	1N	51	0	0	1	0
63	1O	24	0	0	3	0
63	1P	71	0	0	5	0
63	1Q	41	0	0	4	0
63	1R	33	0	0	1	0
63	1S	16	0	0	0	0
63	1T	34	0	0	2	0
63	1U	54	0	0	6	0
63	1V	42	0	0	1	0
63	1W	29	0	0	1	0
63	1X	23	0	0	1	0
63	1Y	16	0	0	1	0
63	1Z	12	0	0	1	0
63	1a	378	0	0	13	0
63	1b	1	0	0	0	0
63	1d	3	0	0	0	0
63	1e	3	0	0	1	0
63	1f	2	0	0	0	0
63	1h	1	0	0	0	0
63	1j	1	0	0	0	0
63	1l	6	0	0	1	0
63	1o	2	0	0	1	0
63	1p	3	0	0	0	0
63	1t	1	0	0	0	0
63	1w	5	0	0	0	0
63	1x	3	0	0	0	0
63	1y	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
63	20	11	0	0	0	0
63	21	20	0	0	3	0
63	22	1	0	0	0	0
63	23	3	0	0	1	0
63	25	13	0	0	0	0
63	26	5	0	0	0	0
63	27	9	0	0	1	0
63	28	11	0	0	1	0
63	29	2	0	0	0	0
63	2A	2284	0	0	124	0
63	2B	46	0	0	3	0
63	2D	57	0	0	3	0
63	2E	32	0	0	3	0
63	2F	27	0	0	0	0
63	2G	6	0	0	1	0
63	2H	3	0	0	0	0
63	2I	4	0	0	2	0
63	2N	6	0	0	0	0
63	2O	21	0	0	2	0
63	2P	24	0	0	3	0
63	2Q	17	0	0	2	0
63	2R	16	0	0	3	0
63	2S	5	0	0	2	0
63	2T	13	0	0	0	0
63	2U	16	0	0	3	0
63	2V	5	0	0	1	0
63	2W	17	0	0	0	0
63	2X	8	0	0	1	0
63	2Y	5	0	0	0	0
63	2Z	11	0	0	3	0
63	2a	317	0	0	26	0
63	2d	2	0	0	0	0
63	2e	1	0	0	0	0
63	2f	3	0	0	0	0
63	2j	2	0	0	0	0
63	2l	2	0	0	0	0
63	2n	2	0	0	0	0
63	2o	4	0	0	1	0
63	2p	2	0	0	0	0
63	2r	3	0	0	0	0
63	2t	2	0	0	0	0
63	2w	3	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
63	2x	3	0	0	1	0
63	2y	3	0	0	0	0
All	All	297868	0	194800	4145	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 9.

All (4145) 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)
1:1A:1082:U:H3	1:1A:1086:A:N6	1.35	1.24
1:2A:2139:C:H42	1:2A:2152:G:H1	0.96	0.96
1:1A:1082:U:O4	1:1A:1086:A:N1	1.99	0.94
1:1A:2137:C:N4	1:1A:2154:G:H1	1.67	0.93
1:2A:2319:G:H22	14:2S:3:ARG:HD3	1.34	0.92
1:1A:1082:U:H3	1:1A:1086:A:H61	0.96	0.92
34:2c:181:ASN:HD21	34:2c:205:GLY:H	1.16	0.92
1:1A:1054:A:H61	1:1A:1105:U:H3	1.19	0.91
1:1A:279:C:H42	1:1A:361:G:H1	1.19	0.90
36:1e:37:ARG:HH12	36:1e:111:GLU:HG2	1.37	0.90
1:2A:2139:C:N4	1:2A:2152:G:H1	1.70	0.89
32:2a:664:G:H22	32:2a:741:G:H1	1.22	0.88
32:1a:664:G:H22	32:1a:741:G:H1	1.19	0.88
1:1A:2319:G:H22	14:1S:3:ARG:HD3	1.38	0.87
1:1A:2137:C:N3	1:1A:2154:G:N2	2.22	0.87
10:2O:48:PRO:HB3	32:2a:1422:G:H5"	1.53	0.87
1:1A:517:C:OP1	27:15:16:ARG:NH2	2.08	0.87
1:2A:1087:G:H1	1:2A:1102:C:H42	1.22	0.87
1:1A:1082:U:N3	1:1A:1086:A:N6	2.13	0.86
1:1A:1665:A:OP2	63:1A:4102:HOH:O	1.92	0.86
1:1A:1023:U:OP2	63:1A:4101:HOH:O	1.92	0.86
1:1A:1041:C:H42	1:1A:1114:G:H1	1.21	0.86
1:2A:2427:C:OP1	63:2A:3803:HOH:O	1.93	0.84
47:1p:53:VAL:HG23	47:1p:79:VAL:HG12	1.60	0.84
20:1Y:92:ASN:HB2	20:1Y:94:LYS:H	1.42	0.84
32:2a:501:C:OP1	43:2l:117:ARG:NH2	2.11	0.84
55:2x:76:8AN:O2P	63:2x:201:HOH:O	1.95	0.83
1:2A:491:G:N2	63:2A:3828:HOH:O	2.11	0.83
22:20:10:THR:HG22	22:20:12:ASN:H	1.43	0.83
1:1A:2821:A:OP2	63:1A:4104:HOH:O	1.96	0.82
32:2a:1003:G:H2'	32:2a:1004:A:H4'	1.60	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:2s:41:VAL:HG12	50:2s:44:MET:HG3	1.62	0.82
32:1a:78:G:H1	32:1a:91:C:H42	1.22	0.82
1:2A:2122:U:H3	1:2A:2176:A:H61	1.27	0.81
1:1A:1085:A:O2'	1:1A:1104:C:O2'	1.99	0.81
15:1T:54:ARG:HA	15:1T:59:THR:HB	1.61	0.81
1:2A:1184:G:OP1	25:23:30:ARG:NH1	2.14	0.81
1:2A:2296:U:OP2	14:2S:9:ARG:NH2	2.14	0.81
1:2A:691:C:OP1	63:2A:3804:HOH:O	1.97	0.81
1:1A:1970:A:OP1	63:1A:4105:HOH:O	1.97	0.81
19:1X:76:ARG:NH1	63:1X:201:HOH:O	2.14	0.80
32:1a:78:G:H1	32:1a:91:C:N4	1.79	0.80
1:2A:1359:A:N6	1:2A:1372:U:O4	2.14	0.80
38:2g:111:ARG:NH1	38:2g:113:GLU:OE2	2.14	0.80
50:2s:50:ALA:HB1	50:2s:57:HIS:HB3	1.63	0.80
25:13:8:LEU:HD13	25:13:31:LEU:HD23	1.62	0.80
32:1a:1441:G:H5"	32:1a:1442:G:H5'	1.63	0.80
1:1A:1634:A:OP2	63:1A:4106:HOH:O	1.99	0.80
40:1i:17:VAL:HG21	40:1i:81:ILE:HG22	1.62	0.80
1:1A:2822:G:OP2	63:1A:4104:HOH:O	2.00	0.80
23:11:50:ARG:HG2	23:11:59:THR:HG22	1.64	0.80
8:1I:92:VAL:HG13	8:1I:120:ILE:HB	1.62	0.80
1:2A:1920:OMC:HM22	1:2A:1921:G:H5'	1.64	0.80
8:2I:92:VAL:HG23	8:2I:120:ILE:HB	1.64	0.80
17:2V:18:LEU:HB3	17:2V:96:ILE:HD11	1.64	0.79
1:2A:1602:U:O4	63:2A:3808:HOH:O	2.01	0.79
31:29:2:LYS:NZ	31:29:31:LYS:O	2.15	0.79
44:1m:11:ARG:HA	44:1m:45:VAL:HB	1.64	0.79
1:2A:962:G:OP1	63:2A:3807:HOH:O	2.01	0.78
1:2A:993:G:OP1	16:2U:50:ARG:NH2	2.15	0.78
1:1A:1057:A:N6	1:1A:1087:G:OP1	2.17	0.78
1:2A:194:G:OP2	63:2A:3805:HOH:O	2.00	0.78
1:2A:1647:G:OP1	63:2A:3806:HOH:O	2.00	0.78
32:2a:875:C:H1'	39:2h:15:ASN:HD21	1.48	0.78
18:1W:94:ASP:OD1	63:1W:301:HOH:O	2.01	0.77
1:2A:1607:C:N4	1:2A:1622:G:OP2	2.17	0.77
5:2F:20:LEU:HD23	5:2F:21:ALA:H	1.48	0.77
26:14:56:VAL:O	26:14:60:GLN:NE2	2.17	0.77
32:1a:1518:MA6:H93	32:1a:1519:MA6:H92	1.65	0.77
17:1V:40:LEU:HB2	17:1V:46:VAL:HG13	1.64	0.77
1:2A:2430:A:OP2	63:2A:3809:HOH:O	2.02	0.77
1:2A:1798:U:H5'	3:2D:259:THR:HG22	1.66	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2141:G:O6	1:2A:2150:U:O2	2.03	0.77
11:2P:2:LYS:HE2	11:2P:4:SER:H	1.50	0.77
15:2T:41:ARG:NH2	32:2a:346:G:OP1	2.18	0.77
1:1A:1771:C:OP1	63:1A:4107:HOH:O	2.03	0.77
44:2m:19:LEU:HD21	44:2m:56:LEU:HD21	1.67	0.77
1:2A:1090:U:H2'	1:2A:1091:G:H8	1.50	0.77
32:2a:1129:C:N4	32:2a:1143:G:H1	1.82	0.77
1:1A:249:C:O2'	11:1P:64:LYS:NZ	2.18	0.77
12:1Q:69:PHE:O	63:1Q:301:HOH:O	2.03	0.76
1:2A:1314:C:OP1	63:2A:3810:HOH:O	2.04	0.76
32:2a:1182:G:H4'	32:2a:1183:A:H3'	1.65	0.76
32:1a:1182:G:H4'	32:1a:1183:A:H5'	1.65	0.76
32:1a:1025:U:O2	32:1a:1036:G:O6	2.02	0.76
33:1b:67:THR:HA	33:1b:90:MET:HE2	1.66	0.76
1:2A:1041:C:H42	1:2A:1114:G:H1	1.32	0.76
32:1a:1033:G:H2'	32:1a:1034:G:H8	1.51	0.76
34:1c:179:ARG:NH1	34:1c:206:GLU:OE1	2.19	0.76
32:2a:812:C:N3	63:2a:3217:HOH:O	2.19	0.76
1:2A:2079:U:OP1	23:21:21:ARG:NH2	2.18	0.76
1:2A:2807:G:H22	1:2A:2892:A:H62	1.34	0.76
5:2F:30:PRO:HB3	11:2P:1:MET:HE1	1.66	0.76
32:2a:593:G:H1	32:2a:646:U:H3	1.31	0.76
32:2a:1189:C:OP1	41:2j:51:ARG:NH2	2.18	0.76
32:2a:1346:A:OP1	40:2i:120:ARG:NH1	2.18	0.76
1:2A:1057:A:N6	1:2A:1087:G:OP1	2.18	0.76
29:17:34:ARG:NH2	63:17:201:HOH:O	2.19	0.76
1:2A:375:C:OP1	63:2A:3811:HOH:O	2.04	0.76
1:1A:1070:A:O2'	1:1A:1098:A:OP1	2.04	0.76
1:1A:1798:U:H5'	3:1D:259:THR:HG22	1.67	0.76
1:1A:2137:C:N4	1:1A:2154:G:N1	2.32	0.76
11:1P:141:ALA:HA	25:23:38:GLU:HG2	1.66	0.76
23:21:50:ARG:HG2	23:21:59:THR:HG22	1.66	0.76
1:2A:1648:C:OP1	63:2A:3806:HOH:O	2.04	0.75
1:2A:1332:G:OP1	63:2A:3810:HOH:O	2.03	0.75
1:2A:994:C:OP1	16:2U:53:ARG:NH2	2.19	0.75
32:2a:548:G:OP1	63:2a:3203:HOH:O	2.05	0.75
37:2f:43:LEU:HB3	37:2f:46:ARG:HH22	1.51	0.75
26:24:48:ARG:HB3	26:24:52:THR:HA	1.67	0.75
1:1A:1671:U:O4	63:1A:4110:HOH:O	2.04	0.75
3:1D:88:ARG:NH1	63:1D:403:HOH:O	2.19	0.75
1:2A:2499:C:OP1	63:2A:3812:HOH:O	2.05	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:353:A:OP1	63:2a:3201:HOH:O	2.04	0.74
33:2b:111:ARG:HH11	33:2b:111:ARG:HA	1.51	0.74
1:2A:1271:G:OP2	63:2A:3806:HOH:O	2.05	0.74
4:2E:119:ARG:HD3	4:2E:160:TYR:HB2	1.69	0.74
4:1E:119:ARG:HD3	4:1E:160:TYR:HB2	1.70	0.74
33:1b:82:ARG:NH1	33:1b:86:GLU:OE2	2.20	0.74
33:1b:15:VAL:HG22	33:1b:209:ARG:HB3	1.68	0.74
1:1A:760:G:OP1	63:1A:4109:HOH:O	2.04	0.74
1:1A:2292:C:OP1	14:1S:17:ARG:NH2	2.18	0.74
10:1O:35:VAL:HG11	10:1O:103:ALA:HB3	1.70	0.74
41:1j:84:GLN:HE21	41:1j:85:LEU:HG	1.51	0.74
26:24:47:GLN:O	26:24:49:PHE:N	2.19	0.74
32:2a:1147:C:O2	40:2i:16:ARG:NH1	2.21	0.74
36:2e:140:ARG:O	36:2e:143:ARG:NH2	2.20	0.74
1:1A:2577:A:H5'	27:15:3:LYS:HE3	1.69	0.74
32:1a:812:C:N3	63:1a:1913:HOH:O	2.20	0.74
48:2q:66:SER:O	48:2q:70:ARG:NH1	2.21	0.74
1:2A:2107:C:H42	1:2A:2182:G:H1	1.33	0.74
38:2g:70:LYS:O	38:2g:138:LYS:NZ	2.16	0.74
32:1a:1024:G:H21	32:1a:1025:U:H5"	1.52	0.74
1:2A:1053:C:H2'	1:2A:1054:A:H8	1.52	0.74
34:2c:181:ASN:ND2	34:2c:205:GLY:O	2.20	0.74
21:2Z:152:ALA:HA	21:2Z:155:LEU:HD13	1.69	0.74
1:1A:348:G:N7	63:1A:4177:HOH:O	2.20	0.74
1:1A:2308:G:O2'	1:1A:2310:A:N7	2.21	0.74
1:2A:826:U:OP1	63:2A:3803:HOH:O	2.05	0.74
1:2A:2139:C:N3	1:2A:2152:G:N2	2.33	0.73
5:2F:21:ALA:HB3	5:2F:22:ALA:HA	1.70	0.73
32:2a:573:A:OP2	63:2a:3202:HOH:O	2.04	0.73
33:2b:98:LEU:HB2	33:2b:101:MET:HE3	1.68	0.73
1:1A:654:A:OP2	63:1A:4116:HOH:O	2.06	0.73
1:1A:2616:C:O2	63:1A:4111:HOH:O	2.04	0.73
32:1a:38:G:H22	32:1a:397:A:H5'	1.53	0.73
32:1a:1069:C:OP2	63:1a:1905:HOH:O	2.06	0.73
32:2a:101:A:H5'	51:2t:10:LEU:HD21	1.68	0.73
32:2a:535:A:OP1	63:2a:3204:HOH:O	2.06	0.73
26:14:57:GLU:HB2	26:14:58:ARG:HD2	1.68	0.73
6:2G:106:LEU:HA	6:2G:110:ALA:HB3	1.69	0.73
1:1A:1648:C:OP1	63:1A:4112:HOH:O	2.05	0.73
32:1a:1291:G:OP1	38:1g:37:ASN:ND2	2.21	0.73
1:2A:81:G:N7	63:2A:3892:HOH:O	2.21	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:585:G:OP2	63:2A:3813:HOH:O	2.07	0.73
8:2I:48:GLU:HG3	8:2I:52:ARG:HH11	1.52	0.73
1:1A:1865:G:OP1	63:1A:4113:HOH:O	2.05	0.73
1:1A:1757:U:OP1	63:1A:4114:HOH:O	2.05	0.73
32:1a:111:G:OP2	63:1a:1904:HOH:O	2.06	0.73
32:1a:501:C:OP1	43:1l:117:ARG:NH2	2.22	0.73
40:2i:97:LYS:HA	40:2i:102:LEU:HD11	1.69	0.73
36:1e:79:GLU:HG2	36:1e:92:LYS:HG3	1.71	0.73
1:1A:1031:G:OP1	63:1A:4115:HOH:O	2.06	0.72
26:24:16:CYS:SG	26:24:17:GLY:N	2.62	0.72
32:2a:1271:G:O2'	63:2a:3205:HOH:O	2.06	0.72
15:1T:39:ARG:HH21	32:1a:345:C:H5"	1.53	0.72
15:1T:55:ASN:H	15:1T:59:THR:HG22	1.54	0.72
1:2A:881:G:H1	1:2A:895:U:H3	1.36	0.72
32:1a:1402:4OC:HM22	32:1a:1403:C:H5'	1.70	0.72
19:2X:31:HIS:HD2	19:2X:33:LYS:H	1.35	0.72
32:2a:977:A:N6	32:2a:1224:G:OP1	2.22	0.72
32:1a:974:A:OP2	45:1n:29:ARG:NH2	2.23	0.72
1:2A:412:A:OP1	63:2A:3817:HOH:O	2.08	0.72
1:2A:607:U:OP1	5:2F:102:PRO:HA	1.90	0.72
1:1A:278:A:O2'	1:1A:279:C:OP1	2.07	0.72
12:2Q:11:LYS:NZ	12:2Q:88:GLY:O	2.19	0.72
1:1A:1173:G:N2	1:1A:1176:G:OP2	2.23	0.72
32:1a:1003:G:H2'	32:1a:1004:A:H4'	1.70	0.72
50:1s:50:ALA:HB1	50:1s:57:HIS:HB3	1.71	0.72
1:2A:1084:A:H3'	1:2A:1085:A:H4'	1.70	0.72
5:1F:53:THR:HG22	5:1F:55:GLY:H	1.54	0.72
1:2A:2640:G:O3'	9:2N:74:ARG:NH2	2.22	0.72
12:2Q:135:ASP:OD1	21:2Z:49:ARG:NH1	2.18	0.72
32:2a:557:G:OP1	63:2a:3206:HOH:O	2.07	0.72
32:2a:954:G:H21	32:2a:1227:A:H62	1.36	0.72
1:1A:2069:G:O3'	63:1A:4118:HOH:O	2.08	0.72
1:2A:991:C:OP2	63:2A:3814:HOH:O	2.07	0.71
1:2A:2125:G:H22	1:2A:2172:U:H3'	1.54	0.71
1:2A:2206:G:H8	1:2A:2207:G:N7	1.88	0.71
6:2G:57:ALA:HB2	6:2G:90:LEU:HD13	1.70	0.71
32:1a:538:G:H5"	43:1l:114:LYS:HB2	1.71	0.71
1:2A:1763:G:OP1	63:2A:3815:HOH:O	2.07	0.71
1:1A:741:G:OP2	63:1A:4117:HOH:O	2.08	0.71
32:1a:201:C:H42	32:1a:216:G:H1	1.37	0.71
46:1o:17:ARG:NH2	63:1o:201:HOH:O	2.23	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:29:25:VAL:HB	31:29:34:GLN:HB2	1.70	0.71
46:1o:54:ARG:HG2	46:1o:58:MET:HE2	1.71	0.71
50:1s:41:VAL:HG22	50:1s:44:MET:HE3	1.73	0.71
32:1a:1325:C:OP1	52:1u:15:ARG:NH2	2.23	0.71
1:2A:2000:G:OP2	63:2A:3816:HOH:O	2.08	0.71
12:2Q:111:GLU:OE2	12:2Q:133:ARG:NH2	2.23	0.71
24:22:66:GLU:HG2	24:22:69:ARG:HH22	1.56	0.71
42:2k:18:ARG:NH2	42:2k:35:PRO:O	2.23	0.71
6:1G:41:GLN:HB3	6:1G:43:LEU:HD13	1.73	0.71
39:1h:86:ILE:HG13	39:1h:133:LEU:HD22	1.71	0.71
1:2A:2805:G:H2'	1:2A:2807:G:C8	2.25	0.71
1:2A:775:G:O3'	63:2A:3821:HOH:O	2.08	0.71
23:21:54:ALA:HB1	23:21:83:GLU:HG3	1.72	0.71
1:2A:1833:U:OP1	63:2A:3818:HOH:O	2.08	0.71
1:1A:2334:G:H5'	14:1S:9:ARG:HG2	1.73	0.70
44:1m:58:GLU:O	44:1m:62:ASN:ND2	2.23	0.70
1:2A:2407:G:OP1	63:2A:3819:HOH:O	2.08	0.70
32:2a:559:A:OP1	36:2e:126:ARG:NH2	2.24	0.70
32:2a:942:G:N2	40:2i:124:GLN:OE1	2.24	0.70
1:1A:2114:A:H1'	1:1A:2168:G:H5'	1.72	0.70
7:1H:124:GLU:HG3	7:1H:132:ARG:HB3	1.71	0.70
32:1a:77:G:H2'	32:1a:78:G:H5'	1.71	0.70
1:2A:2100:G:H1	1:2A:2189:U:H3	1.38	0.70
1:2A:2630:G:H2'	1:2A:2631:G:C8	2.26	0.70
32:2a:1500:A:OP1	63:2a:3207:HOH:O	2.08	0.70
1:2A:940:G:O2'	63:2A:3822:HOH:O	2.09	0.70
41:2j:81:THR:HA	41:2j:84:GLN:HB3	1.72	0.70
1:1A:135:G:N7	63:1A:4203:HOH:O	2.23	0.70
1:1A:1332:G:OP1	63:1A:4119:HOH:O	2.09	0.70
3:1D:108:PRO:HD2	3:1D:111:LEU:HG	1.73	0.70
1:2A:1658:C:OP1	63:2E:401:HOH:O	2.10	0.70
34:2c:54:ARG:HB2	34:2c:69:HIS:HB2	1.73	0.70
1:2A:1762:A:N1	63:2A:3927:HOH:O	2.24	0.70
1:2A:2137:C:C2	1:2A:2154:G:N1	2.59	0.70
1:2A:2753:A:N3	31:29:15:LYS:NZ	2.39	0.70
26:14:53:GLU:HB2	26:14:56:VAL:HG12	1.73	0.70
1:2A:2206:G:H3'	1:2A:2207:G:H8	1.56	0.70
1:2A:1065:U:H3	1:2A:1073:A:H61	1.40	0.70
1:2A:2839:G:H5'	13:2R:46:GLY:HA2	1.74	0.70
32:2a:266:G:O2'	32:2a:267:C:OP2	2.08	0.70
1:2A:400:G:N7	63:2A:3929:HOH:O	2.25	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:1D:148:GLU:HB2	3:1D:151:LYS:HD2	1.74	0.69
1:2A:1604:C:OP1	63:2A:3823:HOH:O	2.09	0.69
1:2A:2788:C:OP1	4:2E:61:ARG:NH2	2.24	0.69
4:2E:54:GLN:HB2	4:2E:76:ARG:HG3	1.74	0.69
4:2E:110:GLY:O	63:2R:301:HOH:O	2.09	0.69
1:1A:1298:C:N4	63:1A:4122:HOH:O	2.24	0.69
49:1r:32:ARG:HA	49:1r:69:THR:HG21	1.75	0.69
1:2A:789:A:N1	63:2A:3938:HOH:O	2.26	0.69
1:1A:271(R):G:OP1	23:11:76:ARG:NH2	2.26	0.69
1:1A:1971:A:OP1	63:1A:4105:HOH:O	2.10	0.69
1:1A:2851:A:OP2	63:1A:4123:HOH:O	2.10	0.69
1:2A:1816:G:O6	3:2D:35:LYS:NZ	2.25	0.69
32:2a:44:G:OP2	47:2p:12:LYS:NZ	2.19	0.69
32:2a:975:A:H4'	32:2a:976:G:H5"	1.74	0.69
34:2c:57:ILE:HG12	34:2c:66:VAL:HG13	1.74	0.69
6:1G:114:ILE:HG12	6:1G:140:ILE:HG12	1.73	0.69
36:1e:8:GLU:HB2	36:1e:34:VAL:HG12	1.75	0.69
41:1j:49:VAL:HG23	45:1n:41:ARG:HB2	1.73	0.69
1:2A:511:U:OP2	63:2A:3826:HOH:O	2.10	0.69
21:2Z:81:ARG:NH2	63:2Z:301:HOH:O	2.24	0.69
41:2j:38:ILE:HD13	41:2j:71:LEU:HD22	1.73	0.69
1:1A:330:A:H2	1:1A:1210:A:HO2'	1.40	0.69
41:1j:64:GLU:HB2	45:1n:59:ALA:HB2	1.74	0.69
41:1j:81:THR:O	41:1j:84:GLN:NE2	2.25	0.69
32:2a:959:A:HO2'	32:2a:984:C:HO2'	1.32	0.69
32:2a:1172:C:H2'	32:2a:1173:G:H8	1.56	0.69
1:2A:1284:A:N7	63:2A:3931:HOH:O	2.25	0.69
1:2A:1356:G:O6	63:2A:3820:HOH:O	2.08	0.69
32:2a:1399:C:H4'	32:2a:1400:5MC:H5'	1.73	0.69
32:1a:1340:A:OP2	63:1a:1906:HOH:O	2.09	0.69
50:1s:32:LYS:HA	50:1s:50:ALA:HB3	1.75	0.69
12:2Q:34:LEU:HB2	12:2Q:118:LEU:HD22	1.75	0.69
32:2a:937:A:OP2	63:2a:3209:HOH:O	2.10	0.69
34:2c:180:ALA:HA	34:2c:206:GLU:HA	1.75	0.69
1:1A:1060:U:H4'	1:1A:1061:U:H5'	1.75	0.69
1:1A:1754:C:OP1	15:1T:96:ARG:NH1	2.25	0.69
37:2f:1:MET:HE3	37:2f:66:GLU:HG2	1.75	0.69
1:1A:1698:A:OP2	63:1A:4120:HOH:O	2.10	0.69
1:2A:1938:A:OP2	63:2A:3824:HOH:O	2.10	0.69
1:1A:1047:G:H2'	1:1A:1110:G:H22	1.57	0.68
1:1A:1642:G:O6	63:1A:4122:HOH:O	2.10	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:12:22:GLU:OE2	24:12:68:ARG:NH2	2.26	0.68
32:2a:1289:A:N1	32:2a:1371:G:O2'	2.25	0.68
1:1A:2690:C:OP1	13:1R:17:ARG:NH2	2.26	0.68
1:1A:749:C:OP2	63:1A:4128:HOH:O	2.12	0.68
3:1D:242:ARG:HG3	3:1D:242:ARG:HH11	1.57	0.68
25:13:3:ARG:NH1	25:13:60:GLU:OE2	2.26	0.68
51:1t:46:GLU:HG3	51:1t:48:LYS:HD2	1.74	0.68
1:2A:1519:G:OP2	63:2A:3827:HOH:O	2.10	0.68
21:1Z:158:PRO:HG2	21:1Z:161:VAL:HG11	1.75	0.68
6:2G:145:THR:HG22	6:2G:148:MET:HE3	1.75	0.68
34:2c:43:LEU:HD22	34:2c:47:LEU:HD12	1.75	0.68
36:2e:71:LEU:HD21	36:2e:115:VAL:HG22	1.75	0.68
50:2s:36:ARG:HH12	50:2s:75:ALA:HB3	1.58	0.68
1:1A:1054:A:N6	1:1A:1105:U:H3	1.89	0.68
32:2a:115:G:OP1	63:2a:3208:HOH:O	2.10	0.68
32:1a:1202:G:H1'	45:1n:29:ARG:HD2	1.76	0.68
37:1f:11:ASN:HB3	37:1f:14:LEU:HG	1.74	0.68
1:2A:1721:G:H8	1:2A:1741:A:H62	1.41	0.68
5:2F:132:VAL:HG21	5:2F:163:VAL:HG22	1.76	0.68
22:20:11:ARG:O	22:20:14:ARG:NH2	2.27	0.68
32:2a:1197:G:OP2	63:2a:3211:HOH:O	2.12	0.68
3:1D:69:ARG:NH2	3:1D:128:GLY:O	2.27	0.68
1:2A:731:C:OP1	63:2A:3830:HOH:O	2.11	0.68
1:2A:1024:G:OP2	63:2A:3831:HOH:O	2.11	0.68
12:2Q:31:ASP:OD1	12:2Q:134:ARG:NH1	2.22	0.68
32:2a:1005:A:OP2	32:2a:1024:G:N2	2.26	0.68
41:2j:10:GLY:H	41:2j:16:LEU:HD11	1.59	0.68
40:2i:23:ASN:N	40:2i:23:ASN:OD1	2.26	0.68
1:1A:1542:A:O2'	63:1A:4125:HOH:O	2.11	0.68
1:1A:2539:C:OP2	63:1A:4130:HOH:O	2.12	0.68
1:1A:217:G:OP2	63:1A:4126:HOH:O	2.11	0.68
1:1A:1045:A:H5'	1:1A:1046:A:H5'	1.73	0.68
13:1R:24:GLN:NE2	63:1R:301:HOH:O	2.26	0.68
36:1e:147:ASP:OD1	36:1e:147:ASP:N	2.27	0.68
1:2A:2364:C:OP1	22:20:55:ARG:NH1	2.27	0.68
8:1I:68:LEU:HD21	8:1I:109:ILE:HD11	1.76	0.67
51:1t:92:LEU:O	51:1t:96:GLY:N	2.27	0.67
16:2U:49:HIS:HA	16:2U:52:ARG:HB3	1.74	0.67
1:2A:530:G:O6	63:2A:3833:HOH:O	2.12	0.67
1:2A:641:C:O2'	1:2A:2350:C:OP1	2.08	0.67
36:2e:50:GLU:HB2	36:2e:53:LEU:HD12	1.77	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:599:G:N7	63:2A:3944:HOH:O	2.26	0.67
1:2A:848:G:OP1	63:2A:3829:HOH:O	2.11	0.67
1:2A:1189:A:OP2	63:2A:3832:HOH:O	2.12	0.67
1:1A:1890:A:OP2	63:1A:4124:HOH:O	2.11	0.67
1:1A:2783:G:N7	63:1A:4254:HOH:O	2.27	0.67
19:1X:5:TYR:CE1	24:12:30:ARG:HG3	2.29	0.67
1:2A:2126:A:H4'	1:2A:2127:G:O5'	1.92	0.67
47:2p:21:VAL:HG22	47:2p:33:ILE:HB	1.77	0.67
1:1A:469:G:OP1	63:1A:4131:HOH:O	2.12	0.67
32:1a:1086:U:H3	32:1a:1099:G:H22	1.42	0.67
1:2A:382:G:OP2	63:2A:3834:HOH:O	2.13	0.67
1:1A:529:A:OP2	9:1N:114:ARG:NH2	2.26	0.67
13:1R:97:VAL:HG22	13:1R:114:VAL:HG13	1.76	0.67
20:1Y:23:ARG:NH1	63:1Y:303:HOH:O	2.28	0.67
32:1a:1015:A:H2'	32:1a:1016:A:C8	2.29	0.67
36:1e:137:GLU:OE1	36:1e:140:ARG:NH1	2.27	0.67
41:1j:40:LEU:HB2	41:1j:69:ASN:HB2	1.77	0.67
7:2H:9:ILE:HD11	7:2H:69:ARG:HG2	1.76	0.67
1:1A:323:G:C8	5:1F:171:PRO:HG3	2.30	0.67
6:1G:77:ILE:HG22	6:1G:80:PHE:H	1.60	0.67
1:2A:2137:C:N3	1:2A:2154:G:O6	2.27	0.67
32:2a:1226:C:OP2	44:2m:91:ARG:NH1	2.28	0.67
1:1A:2427:C:OP1	63:1A:4127:HOH:O	2.12	0.67
25:13:7:LYS:HE3	25:13:32:GLN:HE21	1.60	0.67
32:1a:352:C:OP2	63:1a:1907:HOH:O	2.13	0.67
1:2A:2469:A:H4'	12:2Q:56:ARG:HG2	1.77	0.67
5:2F:188:ARG:HA	11:2P:3:LEU:HD11	1.77	0.67
26:24:59:PHE:HA	26:24:61:ARG:N	2.10	0.67
1:1A:1762:A:N1	63:1A:4238:HOH:O	2.26	0.67
1:1A:2608:G:N7	63:1A:4243:HOH:O	2.27	0.67
1:2A:1090:U:H2'	1:2A:1091:G:C8	2.30	0.67
1:2A:2140:C:H2'	1:2A:2141:G:H8	1.59	0.67
24:22:1:MET:N	24:22:52:ASP:OD1	2.28	0.67
35:2d:13:ARG:HH22	35:2d:36:ARG:CZ	2.08	0.67
1:1A:2275:C:OP1	63:1A:4133:HOH:O	2.13	0.67
24:12:14:ARG:O	24:12:67:LYS:NZ	2.27	0.66
1:2A:2660:A:N7	7:2H:175:LYS:NZ	2.38	0.66
1:1A:2447:G:OP2	63:1A:4137:HOH:O	2.13	0.66
1:1A:2843:G:O6	63:1A:4121:HOH:O	2.10	0.66
12:1Q:111:GLU:OE2	12:1Q:133:ARG:NH2	2.27	0.66
1:1A:120:U:OP2	63:1A:4129:HOH:O	2.12	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:1k:99:GLN:HG3	42:1k:105:VAL:HG21	1.77	0.66
1:2A:956:G:OP1	63:2A:3836:HOH:O	2.13	0.66
1:1A:1890:A:N7	63:1A:4269:HOH:O	2.28	0.66
29:27:5:TRP:NE1	29:27:7:PRO:HG3	2.11	0.66
33:2b:71:VAL:HG12	33:2b:93:VAL:HB	1.78	0.66
1:1A:1756:G:OP2	63:1A:4140:HOH:O	2.14	0.66
6:1G:5:VAL:HG22	6:1G:8:LYS:H	1.59	0.66
14:1S:3:ARG:NH1	14:1S:4:LEU:O	2.29	0.66
33:1b:80:ILE:HD11	33:1b:212:GLN:HB2	1.77	0.66
6:2G:7:LEU:HD23	6:2G:100:TRP:HE3	1.60	0.66
6:2G:123:ASN:O	6:2G:125:PHE:N	2.27	0.66
1:1A:79:G:OP1	63:1A:4136:HOH:O	2.13	0.66
1:1A:1101:U:H2'	1:1A:1102:C:H6	1.59	0.66
3:2D:239:ARG:NH1	63:2D:404:HOH:O	2.27	0.66
51:2t:49:ALA:HB3	51:2t:99:LEU:HD12	1.76	0.66
1:1A:588:U:H2'	1:1A:589:C:C6	2.30	0.66
1:1A:2145:C:O2'	1:1A:2147:G:N2	2.29	0.66
35:1d:109:GLY:HA3	35:1d:165:MET:HG3	1.77	0.66
44:1m:15:VAL:HG11	44:1m:48:LEU:HD21	1.77	0.66
33:2b:123:ALA:H	33:2b:127:ILE:HD11	1.60	0.66
1:1A:409:C:OP1	63:1A:4135:HOH:O	2.13	0.66
10:1O:48:PRO:HB3	32:1a:1422:G:H5"	1.78	0.66
39:1h:95:VAL:HB	39:1h:99:GLU:HG3	1.78	0.66
1:2A:813:U:OP1	63:2A:3844:HOH:O	2.14	0.66
1:2A:1155:A:H5"	16:2U:55:ARG:HD3	1.78	0.66
32:2a:1249:C:O2'	40:2i:68:GLY:O	2.11	0.66
1:1A:1024:G:OP2	63:1A:4101:HOH:O	2.14	0.66
1:1A:1309:G:H4'	29:17:7:PRO:HB2	1.78	0.66
2:1B:103:G:H21	21:1Z:73:GLN:HE22	1.42	0.66
32:1a:1270:C:OP2	52:1u:24:ARG:NH2	2.29	0.66
3:2D:134:ARG:NH1	3:2D:188:GLU:OE2	2.29	0.66
36:2e:102:ALA:O	36:2e:107:ARG:NH1	2.28	0.66
4:1E:77:ILE:HD13	4:1E:195:LEU:HD13	1.77	0.66
6:2G:15:VAL:HA	6:2G:175:LEU:HD23	1.78	0.66
35:2d:175:SER:HB3	35:2d:184:LYS:HB3	1.78	0.66
1:1A:759:G:N7	63:1A:4276:HOH:O	2.29	0.65
44:1m:37:THR:O	44:1m:55:ARG:NH1	2.26	0.65
1:1A:219:G:OP2	63:1A:4139:HOH:O	2.14	0.65
33:1b:178:ARG:NH2	39:1h:74:PRO:HB3	2.12	0.65
1:2A:450:G:OP2	63:2A:3841:HOH:O	2.13	0.65
32:2a:854:G:O6	63:2a:3210:HOH:O	2.10	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:209:C:OP1	63:2A:3846:HOH:O	2.14	0.65
1:2A:971:C:OP2	63:2A:3848:HOH:O	2.14	0.65
1:2A:1771:C:OP1	63:2A:3843:HOH:O	2.14	0.65
14:2S:105:ALA:HB1	14:2S:110:LEU:HD23	1.78	0.65
50:2s:20:LEU:HA	50:2s:23:ASN:HB2	1.77	0.65
1:1A:1315:C:OP2	63:1A:4119:HOH:O	2.15	0.65
1:1A:1702:G:N7	63:1A:4285:HOH:O	2.29	0.65
33:1b:178:ARG:HH21	39:1h:74:PRO:HB3	1.61	0.65
1:2A:1315:C:OP2	63:2A:3810:HOH:O	2.14	0.65
14:2S:50:SER:O	14:2S:76:LYS:NZ	2.23	0.65
1:1A:1470:G:N2	1:1A:1520:G:OP2	2.26	0.65
48:1q:66:SER:O	48:1q:70:ARG:NH1	2.29	0.65
1:2A:749:C:OP2	63:2A:3837:HOH:O	2.13	0.65
2:2B:77:U:OP1	21:2Z:19:ARG:NH2	2.30	0.65
32:2a:1123:A:H4'	41:2j:37:PRO:HD2	1.79	0.65
1:1A:2126:A:H4'	1:1A:2127:G:O5'	1.95	0.65
6:1G:83:ARG:H	6:1G:86:MET:HE3	1.60	0.65
40:1i:46:ALA:HB2	40:1i:74:ILE:HG23	1.77	0.65
1:2A:1993:U:OP2	63:2A:3838:HOH:O	2.13	0.65
1:2A:2137:C:O2	1:2A:2154:G:N1	2.29	0.65
1:2A:2218:U:O4'	23:21:52:ARG:NH2	2.29	0.65
8:2I:4:ILE:HG12	8:2I:18:VAL:HG22	1.79	0.65
16:2U:5:LYS:NZ	63:2U:301:HOH:O	2.27	0.65
32:2a:1457:G:OP1	51:2t:39:LYS:NZ	2.28	0.65
1:1A:2534:A:N7	63:1A:4255:HOH:O	2.27	0.65
36:1e:143:ARG:NH1	39:1h:77:GLU:OE2	2.30	0.65
1:2A:2815:C:H5'	27:25:29:THR:HG21	1.77	0.65
41:2j:51:ARG:O	45:2n:45:ARG:NH1	2.29	0.65
48:2q:13:ASP:OD1	48:2q:13:ASP:N	2.30	0.65
1:1A:1664:A:OP1	63:1A:4102:HOH:O	2.15	0.65
38:2g:50:ILE:HD11	38:2g:58:PRO:HA	1.79	0.65
52:2u:17:THR:O	52:2u:22:ARG:NH1	2.28	0.65
1:1A:2115:G:N3	1:1A:2117:A:N6	2.44	0.65
21:1Z:19:ARG:NH1	21:1Z:84:GLU:O	2.30	0.65
44:1m:80:ARG:HH22	50:1s:69:HIS:HE1	1.42	0.65
1:2A:2290:G:O2'	63:2A:3840:HOH:O	2.13	0.65
1:1A:392:C:OP1	63:1A:4135:HOH:O	2.13	0.65
1:1A:1187:G:H5"	17:1V:81:TYR:CE1	2.31	0.65
32:1a:1356:G:H2'	32:1a:1357:A:C8	2.31	0.65
1:2A:1669:A:OP2	63:2A:3849:HOH:O	2.15	0.65
21:2Z:19:ARG:NH1	21:2Z:84:GLU:O	2.30	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:22:10:LEU:HD21	24:22:59:ARG:HG2	1.78	0.65
39:2h:89:PRO:HA	39:2h:92:ARG:HE	1.62	0.65
51:2t:57:ARG:HH22	51:2t:100:ILE:HD12	1.60	0.65
1:1A:1016:G:N7	63:1A:4284:HOH:O	2.29	0.64
32:1a:330:C:OP2	63:1a:1908:HOH:O	2.13	0.64
1:2A:668:G:H5'	1:2A:669:G:OP2	1.97	0.64
1:2A:805:G:OP1	63:2A:3845:HOH:O	2.14	0.64
32:2a:1277:C:O2'	32:2a:1279:A:N7	2.30	0.64
34:2c:8:ILE:HG23	34:2c:16:ARG:HD3	1.77	0.64
32:1a:189(A):C:H42	32:1a:189(J):G:H1	1.45	0.64
1:2A:2765:A:OP2	63:2A:3850:HOH:O	2.15	0.64
1:1A:2404:C:OP2	63:1A:4138:HOH:O	2.14	0.64
15:1T:39:ARG:HH12	15:1T:41:ARG:HD3	1.63	0.64
40:1i:17:VAL:HG23	40:1i:63:ILE:HG12	1.79	0.64
1:2A:61:G:OP1	24:22:51:ARG:NH2	2.31	0.64
1:2A:2550:G:OP1	63:2A:3849:HOH:O	2.15	0.64
32:2a:1309:G:O2'	44:2m:77:ASN:ND2	2.30	0.64
44:2m:94:ARG:HB3	44:2m:96:LEU:HD12	1.78	0.64
1:1A:432:A:N6	63:1A:4198:HOH:O	2.22	0.64
1:2A:2483:C:N3	12:2Q:124:LYS:NZ	2.46	0.64
2:2B:25:A:OP1	63:2B:301:HOH:O	2.15	0.64
32:2a:1366:C:O2'	41:2j:60:ARG:NH2	2.28	0.64
1:1A:675:A:OP2	63:1A:4142:HOH:O	2.15	0.64
1:1A:2252:G:OP2	63:1A:4143:HOH:O	2.15	0.64
1:2A:1843:C:H5'	3:2D:253:GLN:NE2	2.12	0.64
1:2A:2490:G:O6	63:2A:3852:HOH:O	2.15	0.64
1:1A:2839:G:H5'	13:1R:46:GLY:HA2	1.80	0.64
40:1i:18:PHE:HB2	40:1i:62:TYR:HB3	1.78	0.64
24:22:65:ASN:OD1	24:22:69:ARG:NH1	2.30	0.64
32:2a:656:C:O2'	46:2o:28:GLN:NE2	2.30	0.64
33:2b:84:GLU:HG3	33:2b:215:LEU:HB3	1.79	0.64
44:2m:82:MET:O	44:2m:93:ARG:NH1	2.31	0.64
22:10:11:ARG:O	22:10:14:ARG:NH2	2.23	0.64
34:1c:35:GLU:HA	34:1c:38:ARG:HB2	1.78	0.64
3:2D:72:LYS:NZ	3:2D:99:ASP:OD2	2.31	0.64
1:1A:2079:U:OP1	23:11:21:ARG:NH2	2.30	0.64
43:1l:53:ARG:HB3	43:1l:69:TYR:HE1	1.63	0.64
1:2A:2405:G:O2'	1:2A:2406:U:OP1	2.15	0.64
1:2A:2448:A:OP1	63:2A:3812:HOH:O	2.15	0.64
40:2i:9:ARG:HB2	40:2i:104:ARG:HE	1.63	0.64
8:1I:77:LEU:HB3	8:1I:142:VAL:HG22	1.79	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:1Q:97:VAL:HG11	12:1Q:103:MET:HE3	1.79	0.64
32:1a:975:A:H4'	32:1a:976:G:H5"	1.79	0.64
51:1t:33:ILE:O	51:1t:37:SER:OG	2.15	0.64
1:2A:489:G:N7	18:2W:49:LYS:NZ	2.45	0.64
1:2A:2105:C:H42	1:2A:2184:G:H1	1.46	0.64
32:2a:1505:G:OP1	63:2a:3207:HOH:O	2.15	0.64
40:2i:8:GLY:HA3	40:2i:79:LEU:HB3	1.80	0.64
9:1N:46:VAL:HG23	9:1N:48:MET:HG2	1.78	0.64
20:1Y:92:ASN:N	20:1Y:93:GLY:HA2	2.12	0.64
32:1a:324:G:N7	63:1a:1928:HOH:O	2.29	0.64
32:1a:1003:G:C2'	32:1a:1004:A:H4'	2.28	0.64
32:1a:1305:G:N2	32:1a:1331:G:H1'	2.12	0.64
11:2P:91:PHE:O	11:2P:121:LYS:NZ	2.31	0.64
12:2Q:29:PHE:O	21:2Z:122:ARG:NH2	2.31	0.64
32:2a:574:A:OP2	63:2a:3202:HOH:O	2.15	0.64
33:2b:16:HIS:CG	33:2b:210:SER:HB3	2.32	0.64
1:1A:1796:U:H2'	1:1A:1797:C:C6	2.34	0.63
12:1Q:85:LYS:HG2	22:10:7:LEU:HB3	1.79	0.63
32:2a:538:G:H5"	43:2l:114:LYS:HB2	1.79	0.63
32:2a:1202:G:H1'	45:2n:29:ARG:HD2	1.79	0.63
34:2c:5:ILE:HD11	45:2n:58:LYS:HE3	1.80	0.63
1:1A:607:U:OP1	5:1F:102:PRO:HA	1.98	0.63
1:1A:1900:A:OP2	63:1A:4141:HOH:O	2.15	0.63
33:1b:88:ALA:O	33:1b:226:ARG:NH2	2.31	0.63
1:2A:526:A:OP1	63:2A:3847:HOH:O	2.14	0.63
32:2a:1013:G:N2	32:2a:1016:A:OP2	2.31	0.63
33:2b:9:GLU:O	33:2b:11:LEU:N	2.31	0.63
35:2d:13:ARG:HG2	35:2d:39:PRO:HA	1.80	0.63
21:2Z:144:LEU:HD11	21:2Z:150:LEU:HG	1.80	0.63
1:1A:1570:A:OP1	63:1A:4145:HOH:O	2.16	0.63
1:2A:362:U:O2'	1:2A:363:G:H5'	1.97	0.63
1:2A:1055:G:H3'	1:2A:1056:G:H8	1.63	0.63
43:2l:28:LYS:HA	43:2l:28:LYS:HE3	1.80	0.63
46:2o:54:ARG:HG2	46:2o:58:MET:HE2	1.81	0.63
33:1b:185:ILE:HG22	33:1b:199:TYR:HD2	1.62	0.63
34:1c:129:ALA:HB3	34:1c:132:ARG:HG2	1.80	0.63
51:1t:57:ARG:HH12	51:1t:100:ILE:HD12	1.64	0.63
34:1c:29:TYR:OH	45:1n:54:PRO:O	2.16	0.63
20:2Y:5:MET:HE2	20:2Y:30:VAL:HG13	1.80	0.63
32:2a:1129:C:H2'	32:2a:1139:G:N7	2.14	0.63
34:2c:164:ARG:NH1	34:2c:166:GLU:OE1	2.32	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:2e:102:ALA:HB1	36:2e:106:PRO:HG2	1.81	0.63
32:1a:262:A:H2'	32:1a:263:A:C8	2.33	0.63
32:1a:677:U:H3	32:1a:713:G:H22	1.46	0.63
37:1f:95:GLU:O	49:1r:32:ARG:NH1	2.31	0.63
1:2A:2821:A:OP2	63:2R:301:HOH:O	2.14	0.63
1:2A:2630:G:H2'	1:2A:2631:G:H8	1.63	0.63
18:2W:78:GLU:OE2	18:2W:99:ARG:NH1	2.27	0.63
32:2a:991:U:H2'	32:2a:1212:U:C4	2.34	0.63
22:10:27:GLU:HG3	22:10:68:GLU:HA	1.81	0.63
32:1a:60:A:H4'	32:1a:61:G:H5'	1.80	0.63
32:2a:53:A:OP2	63:2a:3212:HOH:O	2.16	0.63
44:2m:13:LYS:HA	44:2m:44:ARG:HH11	1.64	0.63
1:1A:1013:C:OP2	63:1A:4144:HOH:O	2.15	0.62
2:1B:81:G:N7	59:1B:231:ARG:NH1	2.46	0.62
32:1a:976:G:OP2	32:1a:1358:U:O2'	2.16	0.62
32:1a:1028:C:H2'	32:1a:1029:C:H4'	1.80	0.62
1:2A:889:C:O2'	1:2A:890:A:O5'	2.17	0.62
6:2G:179:PRO:HB2	26:24:42:PHE:HE2	1.64	0.62
18:2W:12:ILE:HD13	18:2W:17:VAL:HG13	1.81	0.62
1:1A:2115:G:H2'	1:1A:2117:A:N6	2.13	0.62
36:1e:140:ARG:O	36:1e:143:ARG:NH2	2.31	0.62
34:2c:180:ALA:HB1	34:2c:203:PHE:HE1	1.64	0.62
33:1b:87:ARG:NH2	33:1b:220:ASP:OD1	2.26	0.62
1:2A:1014:U:H2'	1:2A:1015:G:H8	1.63	0.62
1:2A:1062:G:H2'	1:2A:1063:G:H8	1.63	0.62
1:2A:2267:A:H5"	1:2A:2268:A:H5'	1.82	0.62
11:2P:54:GLY:O	63:2P:301:HOH:O	2.16	0.62
32:2a:184:G:H2'	32:2a:185:A:C8	2.35	0.62
40:2i:4:TYR:HD1	40:2i:87:GLN:HE22	1.46	0.62
36:1e:79:GLU:HG3	36:1e:93:PRO:HD2	1.80	0.62
1:2A:2541:A:N7	63:2A:3976:HOH:O	2.31	0.62
2:2B:48:A:H4'	14:2S:95:HIS:HD2	1.64	0.62
44:2m:58:GLU:O	44:2m:62:ASN:ND2	2.32	0.62
48:2q:53:LEU:HD23	48:2q:82:MET:HE1	1.81	0.62
1:1A:886:C:H3'	1:1A:887:A:H5"	1.81	0.62
32:1a:1060:C:C5	34:1c:2:GLY:HA3	2.35	0.62
9:2N:12:ARG:NH1	9:2N:50:ASP:OD2	2.33	0.62
2:1B:6:C:H2'	2:1B:7:G:H5"	1.80	0.62
37:1f:25:ILE:HG21	37:1f:82:ARG:HD3	1.82	0.62
35:2d:60:GLU:HG3	35:2d:202:LEU:HD12	1.80	0.62
1:1A:670:A:OP1	63:1A:4147:HOH:O	2.16	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1604:C:N4	63:1A:4316:HOH:O	2.32	0.62
10:1O:64:ARG:HG2	10:1O:83:ALA:HB3	1.82	0.62
49:2r:32:ARG:HA	49:2r:69:THR:HG21	1.80	0.62
21:1Z:198:LYS:H	21:1Z:198:LYS:HD2	1.63	0.62
37:1f:36:ARG:NH2	37:1f:66:GLU:OE1	2.33	0.62
39:1h:10:LEU:HD22	39:1h:83:ILE:HD11	1.82	0.62
32:2a:17:U:H2'	32:2a:18:C:C6	2.34	0.62
35:1d:15:GLU:OE2	35:1d:66:ARG:NH1	2.33	0.62
53:1y:3:MET:HG2	53:1y:37:PRO:HG2	1.81	0.62
1:2A:11:G:H2'	1:2A:12:U:H5'	1.81	0.62
8:2I:78:THR:HA	8:2I:143:SER:HB2	1.81	0.62
25:23:7:LYS:HE3	25:23:9:VAL:HG12	1.81	0.62
1:1A:2133:G:H3'	1:1A:2157:G:H21	1.65	0.62
34:1c:64:VAL:HG22	34:1c:99:VAL:HA	1.82	0.62
1:2A:857:C:OP2	22:20:77:ARG:NH2	2.33	0.62
33:2b:74:LYS:O	33:2b:78:GLN:N	2.33	0.62
32:1a:78:G:N2	32:1a:91:C:N3	2.47	0.61
1:2A:2122:U:H3	1:2A:2176:A:N6	1.96	0.61
2:2B:5:C:OP1	2:2B:61:G:O2'	2.18	0.61
32:2a:1060:C:C5	34:2c:2:GLY:HA2	2.35	0.61
32:2a:1286:A:H2'	32:2a:1287:A:H4'	1.80	0.61
37:1f:46:ARG:HH22	49:1r:37:VAL:HG11	1.65	0.61
33:2b:223:ILE:HA	33:2b:226:ARG:HB2	1.80	0.61
1:2A:588:U:H2'	1:2A:589:C:C6	2.35	0.61
1:2A:993:G:N2	17:2V:23:GLU:OE2	2.33	0.61
34:2c:180:ALA:HB1	34:2c:203:PHE:CE1	2.35	0.61
34:2c:181:ASN:HD21	34:2c:205:GLY:N	1.94	0.61
35:2d:122:ARG:NH1	35:2d:134:ASP:O	2.34	0.61
1:1A:189:G:N7	63:1A:4299:HOH:O	2.31	0.61
1:1A:483:A:O2'	20:1Y:49:VAL:O	2.17	0.61
1:1A:1919:A:O2'	32:1a:1517:G:N3	2.25	0.61
1:2A:82:G:N1	1:2A:103:A:OP2	2.30	0.61
32:2a:1108:G:H5'	34:2c:176:HIS:HD2	1.64	0.61
1:1A:1670:C:OP2	63:1A:4110:HOH:O	2.16	0.61
1:1A:2646:C:OP2	1:1A:2732:G:O2'	2.17	0.61
1:2A:1324:G:O6	63:2A:3842:HOH:O	2.14	0.61
1:2A:1796:U:H2'	1:2A:1797:C:C6	2.36	0.61
32:2a:926:G:O6	53:2y:87:LYS:NZ	2.31	0.61
1:1A:1382:G:N7	63:1A:4289:HOH:O	2.30	0.61
26:14:59:PHE:CE1	50:1s:64:GLU:HG3	2.36	0.61
29:17:34:ARG:NH1	29:17:41:ARG:O	2.33	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1843:C:H5'	3:2D:253:GLN:HE22	1.65	0.61
4:2E:9:VAL:HB	15:2T:3:ARG:HG2	1.82	0.61
32:2a:1103:C:OP1	33:2b:96:ARG:NH2	2.32	0.61
40:2i:37:PHE:CZ	40:2i:74:ILE:HG12	2.35	0.61
1:1A:1468:C:OP1	63:1A:4148:HOH:O	2.16	0.61
3:1D:164:GLN:OE1	3:1D:176:ARG:NH2	2.34	0.61
32:1a:300:A:O2'	32:1a:564:C:N3	2.31	0.61
35:1d:65:ARG:HG3	35:1d:70:ILE:HG22	1.81	0.61
1:2A:98:G:H5'	24:22:3:LEU:HD23	1.82	0.61
1:2A:1011:G:OP2	16:2U:66:ASN:ND2	2.33	0.61
1:2A:1332:G:OP2	63:2A:3855:HOH:O	2.16	0.61
7:1H:3:ARG:HH21	7:1H:65:HIS:HB3	1.66	0.61
7:1H:159:GLU:HG2	7:1H:169:VAL:HG11	1.83	0.61
1:1A:1418:G:OP2	63:1A:4146:HOH:O	2.16	0.61
4:1E:105:THR:OG1	4:1E:199:ARG:NH2	2.32	0.61
10:1O:68:GLU:OE1	63:1O:301:HOH:O	2.16	0.61
26:14:16:CYS:SG	26:14:17:GLY:N	2.74	0.61
2:2B:14:U:OP2	2:2B:70:C:O2'	2.18	0.61
32:2a:1295:G:O3'	44:2m:14:ARG:NH1	2.34	0.61
32:2a:1518:MA6:H93	32:2a:1519:MA6:H102	1.81	0.61
35:2d:165:MET:SD	35:2d:168:ARG:NH1	2.73	0.61
1:1A:1359:A:H61	1:1A:1372:U:H3	1.46	0.61
33:1b:21:ARG:H	33:1b:21:ARG:HD2	1.66	0.61
45:2n:24:CYS:HB3	45:2n:29:ARG:H	1.64	0.61
1:1A:2162:G:H4'	1:1A:2172:U:H2'	1.82	0.60
1:1A:2319:G:N2	14:1S:3:ARG:HD3	2.14	0.60
33:1b:82:ARG:NH1	33:1b:92:TYR:OH	2.34	0.60
2:2B:66:A:H61	2:2B:109:C:H5'	1.66	0.60
19:2X:88:LYS:HE3	19:2X:93:GLU:HG3	1.81	0.60
32:2a:992:U:H4'	32:2a:993:G:O5'	1.99	0.60
33:1b:77:ALA:HA	33:1b:80:ILE:HG22	1.81	0.60
44:1m:79:LYS:HA	44:1m:82:MET:HE2	1.81	0.60
1:2A:2115:G:H2'	1:2A:2117:A:N6	2.15	0.60
1:2A:2836:U:H2'	1:2A:2837:G:C8	2.35	0.60
15:2T:50:ILE:HG22	15:2T:102:ILE:HD11	1.82	0.60
21:2Z:53:ILE:HG22	21:2Z:71:VAL:HG13	1.82	0.60
41:2j:44:VAL:HG13	41:2j:66:ARG:HG2	1.83	0.60
1:1A:2793:G:N2	1:1A:2803:C:O2	2.31	0.60
8:1I:9:LEU:HB3	8:1I:12:LEU:HB3	1.84	0.60
21:1Z:102:LEU:HD11	21:1Z:155:LEU:HD11	1.83	0.60
32:1a:184:G:H2'	32:1a:185:A:H8	1.65	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:249:C:O2'	11:2P:64:LYS:NZ	2.33	0.60
1:2A:682:G:N7	63:2A:3977:HOH:O	2.31	0.60
1:2A:1009:A:OP2	63:2A:3854:HOH:O	2.16	0.60
1:2A:1791:A:H5'	3:2D:206:LEU:HD12	1.83	0.60
1:2A:2870:C:H2'	1:2A:2871:C:O4'	2.02	0.60
32:2a:1079:G:O3'	36:2e:14:ARG:NH2	2.35	0.60
37:2f:9:VAL:HB	37:2f:87:ARG:HB2	1.81	0.60
53:2y:40:ILE:HB	53:2y:51:ASP:HB2	1.83	0.60
3:2D:148:GLU:HB2	3:2D:151:LYS:HD2	1.83	0.60
8:2I:115:ALA:O	63:2I:302:HOH:O	2.17	0.60
14:2S:27:SER:HA	14:2S:88:ASP:HB3	1.81	0.60
35:2d:196:LEU:H	35:2d:196:LEU:HD12	1.66	0.60
51:2t:50:GLU:HB2	51:2t:99:LEU:HD13	1.83	0.60
32:1a:8:A:N7	35:1d:208:SER:OG	2.34	0.60
1:2A:492:A:OP2	63:2A:3856:HOH:O	2.17	0.60
3:2D:108:PRO:HD2	3:2D:111:LEU:HD22	1.83	0.60
24:22:2:LYS:N	24:22:5:GLU:OE1	2.29	0.60
32:2a:1005:A:H1'	32:2a:1025:U:C2	2.36	0.60
32:2a:1435:G:H2'	32:2a:1436:U:C6	2.37	0.60
8:1I:1:MET:N	8:1I:21:VAL:O	2.29	0.60
8:1I:109:ILE:HG13	8:1I:130:TYR:CZ	2.37	0.60
32:1a:1129:C:O2'	32:1a:1139:G:N7	2.24	0.60
34:1c:58:GLU:HB2	34:1c:65:ALA:HB3	1.84	0.60
47:1p:19:ILE:HG23	47:1p:36:ILE:HG13	1.82	0.60
50:2s:41:VAL:HG13	50:2s:43:GLU:H	1.66	0.60
1:1A:1031:G:H5"	31:19:8:LYS:HE3	1.84	0.60
30:18:11:LYS:O	63:18:201:HOH:O	2.16	0.60
32:1a:289:G:OP2	63:1a:1909:HOH:O	2.17	0.60
1:2A:2319:G:N2	14:2S:3:ARG:HD3	2.12	0.60
1:1A:889:C:O2'	1:1A:890:A:O5'	2.19	0.60
2:1B:82:G:N3	63:1B:307:HOH:O	2.31	0.60
10:1O:73:ASP:HB2	15:1T:82:LEU:HD13	1.84	0.60
16:2U:85:LYS:HB3	16:2U:116:ALA:HB1	1.83	0.60
1:1A:67:U:O4	63:1A:4153:HOH:O	2.17	0.60
1:1A:2023:G:H5'	1:1A:2617:C:H4'	1.83	0.60
4:1E:54:GLN:O	63:1E:403:HOH:O	2.16	0.60
16:1U:33:ARG:NH2	63:1U:301:HOH:O	2.33	0.60
32:1a:946:A:H2'	32:1a:947:G:C8	2.37	0.60
44:1m:5:ALA:HB2	44:1m:61:GLU:HG2	1.84	0.60
1:2A:1639:U:H2'	1:2A:1640:C:H5"	1.83	0.60
1:2A:2228:G:O6	63:2A:3839:HOH:O	2.13	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:2O:24:VAL:HG13	10:2O:33:ALA:HB2	1.82	0.60
21:2Z:99:TYR:HB3	21:2Z:123:ASP:HB2	1.82	0.60
32:1a:45:U:H2'	32:1a:46:G:C8	2.37	0.60
49:1r:58:LEU:HD23	49:1r:62:GLU:HB3	1.83	0.60
1:2A:1470:G:N7	63:2A:3988:HOH:O	2.32	0.60
8:2I:7:GLU:OE1	63:2I:301:HOH:O	2.16	0.60
12:2Q:101:ARG:NH1	63:2Q:302:HOH:O	2.29	0.60
32:2a:335:C:O2'	32:2a:1433:A:N3	2.32	0.60
32:2a:944:G:N1	32:2a:1338:G:OP2	2.35	0.60
1:1A:1721:G:H5'	1:1A:1722:A:OP2	2.01	0.59
3:1D:275:LYS:HD2	3:1D:276:LYS:N	2.17	0.59
6:1G:144:ILE:HA	6:1G:148:MET:HE2	1.84	0.59
32:1a:401:C:OP2	35:1d:73:ARG:NH1	2.35	0.59
1:2A:2152:G:H2'	1:2A:2153:G:C8	2.37	0.59
1:2A:2291:U:OP1	1:2A:2380:C:O2'	2.17	0.59
1:2A:2659:G:N2	1:2A:2662:A:OP2	2.31	0.59
30:28:29:LYS:O	63:28:3901:HOH:O	2.15	0.59
3:1D:34:VAL:HG12	3:1D:63:ARG:HG3	1.83	0.59
5:2F:28:ILE:HG22	5:2F:112:MET:HB3	1.84	0.59
35:2d:98:GLU:OE2	35:2d:107:ARG:NH2	2.34	0.59
1:1A:302:C:OP2	20:1Y:73:ARG:NH2	2.30	0.59
1:1A:2830:G:N7	63:1A:4294:HOH:O	2.31	0.59
1:2A:2134:A:N6	1:2A:2156:G:O2'	2.35	0.59
8:2I:77:LEU:HD22	8:2I:101:LEU:HG	1.82	0.59
32:2a:1399:C:H4'	32:2a:1400:5MC:C5'	2.33	0.59
1:2A:2807:G:N2	1:2A:2892:A:H62	1.99	0.59
3:2D:36:PRO:HA	3:2D:61:LEU:HD12	1.84	0.59
20:2Y:82:PRO:O	20:2Y:101:LYS:NZ	2.26	0.59
29:27:34:ARG:NH1	29:27:41:ARG:O	2.35	0.59
6:1G:47:LYS:HG3	6:1G:48:GLU:H	1.67	0.59
11:1P:63:PRO:HD3	30:18:27:THR:HG22	1.84	0.59
32:1a:1414:U:H3	32:1a:1486:G:H1	1.50	0.59
39:1h:44:PHE:HB3	39:1h:80:ILE:HD11	1.85	0.59
1:2A:1064:C:H42	1:2A:1074:G:H1	1.50	0.59
1:2A:2504:U:OP1	63:2A:3858:HOH:O	2.17	0.59
6:2G:126:ASP:HB2	6:2G:130:ASN:HB2	1.84	0.59
8:2I:77:LEU:HD21	8:2I:100:ALA:HB3	1.84	0.59
41:2j:32:ALA:HB1	41:2j:33:GLN:HE21	1.67	0.59
44:2m:82:MET:HE3	44:2m:93:ARG:HG2	1.84	0.59
1:1A:1011:G:OP1	16:1U:77:SER:OG	2.20	0.59
1:1A:1267:U:OP1	63:1A:4154:HOH:O	2.17	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:11:65:SER:HG	23:11:66:HIS:HD1	1.51	0.59
32:1a:96:U:H2'	32:1a:97:G:H8	1.68	0.59
43:1l:117:ARG:NH1	63:1l:302:HOH:O	2.34	0.59
1:2A:2064:C:OP2	63:2A:3857:HOH:O	2.17	0.59
1:2A:2690:C:OP1	13:2R:17:ARG:NH2	2.36	0.59
5:2F:187:VAL:HG12	11:2P:3:LEU:HG	1.84	0.59
7:2H:3:ARG:HH11	7:2H:4:ILE:H	1.49	0.59
32:2a:184:G:H2'	32:2a:185:A:H8	1.66	0.59
32:2a:519:C:OP2	43:2l:50:SER:OG	2.20	0.59
32:2a:921:U:O2	36:2e:19:MET:HB2	2.02	0.59
32:2a:1391:U:H2'	32:2a:1392:G:C8	2.38	0.59
1:1A:1266:G:O5'	18:1W:15:ARG:NH2	2.35	0.59
1:1A:1356:G:OP2	63:1A:4149:HOH:O	2.16	0.59
17:2V:16:PRO:HD3	17:2V:99:ILE:HD11	1.83	0.59
21:2Z:119:GLU:OE1	21:2Z:122:ARG:NH1	2.36	0.59
32:2a:1338:G:H2'	32:2a:1339:A:C8	2.37	0.59
1:1A:278:A:H2'	1:1A:279:C:C6	2.38	0.59
1:1A:1803:A:O2'	3:1D:259:THR:HG21	2.01	0.59
1:2A:2134:A:O2'	1:2A:2159:G:H1'	2.02	0.59
32:2a:1052:U:O2'	32:2a:1055:A:OP2	2.15	0.59
33:2b:213:LEU:HD23	33:2b:214:ILE:HG12	1.84	0.59
40:2i:4:TYR:HB2	40:2i:19:LEU:HB2	1.83	0.59
1:1A:1260:G:OP1	63:1A:4150:HOH:O	2.17	0.59
1:2A:2136:C:H2'	1:2A:2155:G:H22	1.67	0.59
5:2F:122:LYS:NZ	5:2F:152:GLU:OE2	2.31	0.59
32:2a:1105:A:H2'	32:2a:1106:G:H8	1.67	0.59
1:1A:279:C:N4	1:1A:361:G:H1	1.97	0.59
8:1I:72:LEU:C	8:1I:74:ASN:H	2.11	0.59
1:2A:1970:A:N1	63:2A:3984:HOH:O	2.31	0.59
1:1A:1070:A:N7	1:1A:1097:U:O2'	2.36	0.58
35:1d:15:GLU:OE2	35:1d:59:ARG:NH1	2.35	0.58
36:1e:74:GLY:HA3	36:1e:116:THR:HG22	1.85	0.58
1:2A:1069:A:H2'	1:2A:1073:A:N7	2.18	0.58
13:2R:56:LYS:NZ	13:2R:90:ARG:O	2.36	0.58
1:1A:1025:G:C4	1:1A:1135:C:H1'	2.39	0.58
6:1G:16:ARG:HE	6:1G:31:VAL:HG21	1.67	0.58
1:2A:23:G:OP1	1:2A:504:U:N3	2.33	0.58
1:2A:1970:A:OP1	63:2A:3853:HOH:O	2.15	0.58
7:2H:17:VAL:HA	7:2H:25:LYS:O	2.03	0.58
32:2a:1273:G:H3'	32:2a:1274:G:H8	1.68	0.58
32:2a:1305:G:N2	32:2a:1331:G:H1'	2.17	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:2i:121:ARG:NH1	40:2i:122:ALA:O	2.36	0.58
1:1A:2814:C:OP2	63:1A:4152:HOH:O	2.17	0.58
3:1D:239:ARG:NH1	63:1D:408:HOH:O	2.32	0.58
19:1X:54:VAL:HG22	19:1X:81:VAL:HG12	1.84	0.58
26:14:59:PHE:HE1	50:1s:64:GLU:HG3	1.67	0.58
1:2A:1076:C:H1'	1:2A:1077:A:H5'	1.85	0.58
1:2A:2837:G:N7	63:2A:3995:HOH:O	2.32	0.58
43:2l:32:PHE:HB3	43:2l:84:LEU:HD11	1.85	0.58
43:2l:82:VAL:O	43:2l:106:ASP:HB2	2.03	0.58
1:1A:1126:A:OP2	63:1A:4103:HOH:O	2.17	0.58
1:1A:1178:C:H2'	1:1A:1179:C:C6	2.39	0.58
1:1A:2123:G:H1	1:1A:2175:C:H42	1.50	0.58
12:1Q:5:ARG:NH2	63:1Q:302:HOH:O	2.36	0.58
32:1a:100:C:H2'	32:1a:101:A:C8	2.39	0.58
34:1c:12:LEU:HD11	45:1n:51:GLY:HA2	1.85	0.58
41:1j:84:GLN:NE2	41:1j:85:LEU:HG	2.17	0.58
1:2A:811:U:H2'	11:2P:21:ARG:HA	1.85	0.58
1:2A:1187:G:N2	1:2A:1188:U:O4	2.36	0.58
5:2F:32:LEU:HD22	5:2F:112:MET:HE2	1.85	0.58
8:2I:74:ASN:N	8:2I:74:ASN:OD1	2.37	0.58
15:2T:16:ARG:NH1	15:2T:83:ILE:O	2.33	0.58
32:2a:1187:G:N2	45:2n:60:SER:OG	2.32	0.58
1:1A:2130:U:O2'	1:1A:2133:G:O2'	2.21	0.58
1:1A:2763:G:OP2	63:1A:4151:HOH:O	2.17	0.58
3:1D:16:MET:HG2	3:1D:211:ARG:HH21	1.68	0.58
7:2H:46:GLU:HB2	7:2H:49:VAL:HG12	1.85	0.58
32:2a:611:A:H61	32:2a:629:G:H1	1.50	0.58
42:2k:27:ASN:OD1	42:2k:28:THR:N	2.37	0.58
1:1A:1405:U:H2'	1:1A:1406:U:C6	2.39	0.58
44:1m:52:GLU:HG2	44:1m:55:ARG:HH21	1.68	0.58
34:2c:20:SER:HB2	34:2c:40:ARG:HH21	1.69	0.58
1:1A:882:G:H1	1:1A:894:C:H42	1.52	0.58
1:1A:1340:U:OP1	19:1X:16:LYS:NZ	2.31	0.58
1:1A:1815:A:OP2	3:1D:54:ARG:NH2	2.31	0.58
1:1A:2683:C:O2	10:1O:70:LYS:NZ	2.29	0.58
32:1a:201:C:H2'	32:1a:202:U:H2'	1.86	0.58
32:1a:626:U:H2'	32:1a:627:G:C8	2.38	0.58
41:1j:35:SER:HB3	41:1j:73:ASP:HB2	1.85	0.58
1:2A:2036:C:OP2	63:2A:3859:HOH:O	2.17	0.58
21:2Z:48:PHE:HE1	21:2Z:71:VAL:HG11	1.68	0.58
21:2Z:96:VAL:N	21:2Z:128:VAL:O	2.28	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1149:C:H4'	40:2i:66:ARG:HH12	1.69	0.58
33:2b:7:VAL:O	33:2b:217:ARG:NH1	2.36	0.58
36:2e:92:LYS:HB3	36:2e:119:LEU:HB2	1.86	0.58
1:1A:1065:U:O2	1:1A:1073:A:N6	2.37	0.58
1:1A:1371:G:N7	63:1A:4315:HOH:O	2.32	0.58
7:1H:84:SER:OG	7:1H:132:ARG:NH1	2.37	0.58
1:2A:323:G:O2'	1:2A:1205:U:N3	2.34	0.58
32:2a:1027:C:H5"	32:2a:1028:C:C5	2.39	0.58
34:2c:36:ASP:HA	34:2c:39:ILE:HD12	1.86	0.58
41:2j:68:HIS:CD2	41:2j:68:HIS:H	2.20	0.58
5:1F:192:LEU:HD13	5:1F:194:MET:HE2	1.86	0.58
31:19:9:ARG:HG2	31:19:14:CYS:HB2	1.84	0.58
1:2A:2865:U:OP2	15:2T:119:LYS:NZ	2.36	0.58
6:2G:125:PHE:HB3	6:2G:166:ASP:CG	2.29	0.58
32:2a:266:G:H3'	48:2q:67:LYS:HB2	1.84	0.58
32:2a:683:G:O6	63:2a:3214:HOH:O	2.17	0.58
32:2a:1348:U:H4'	40:2i:120:ARG:HD2	1.86	0.58
40:2i:7:THR:O	40:2i:83:ARG:NH2	2.34	0.58
1:1A:60:G:OP1	63:1A:4155:HOH:O	2.17	0.58
1:1A:1101:U:H2'	1:1A:1102:C:C6	2.38	0.58
41:1j:33:GLN:O	41:1j:75:ILE:N	2.37	0.58
1:2A:2295:C:OP1	14:2S:10:ARG:NH1	2.36	0.58
19:2X:31:HIS:CD2	19:2X:33:LYS:H	2.19	0.58
32:2a:286:G:N7	63:2a:3234:HOH:O	2.32	0.58
1:1A:2749:A:OP1	7:1H:3:ARG:NH1	2.37	0.57
5:1F:143:ALA:HB1	5:1F:148:LEU:HB2	1.86	0.57
7:1H:40:GLU:OE2	7:1H:60:ARG:NH1	2.37	0.57
1:2A:1378:A:OP1	29:27:10:ARG:NH2	2.37	0.57
32:2a:1003:G:H3'	32:2a:1003:G:N3	2.19	0.57
32:1a:1347:G:N7	40:1i:10:ARG:NH2	2.49	0.57
21:2Z:32:HIS:NE2	63:2Z:302:HOH:O	2.31	0.57
40:2i:17:VAL:HA	40:2i:63:ILE:HG12	1.85	0.57
46:2o:4:THR:HG23	46:2o:7:GLU:HG2	1.86	0.57
9:1N:36:GLY:HA2	9:1N:38:HIS:CE1	2.39	0.57
32:1a:745:C:H2'	32:1a:746:A:C8	2.40	0.57
50:1s:33:THR:OG1	50:1s:35:SER:OG	2.22	0.57
32:2a:1016:A:HO2'	32:2a:1217:C:HO2'	1.46	0.57
33:2b:139:LYS:O	33:2b:139:LYS:NZ	2.37	0.57
34:2c:57:ILE:HG23	34:2c:66:VAL:HG22	1.87	0.57
38:2g:54:THR:O	38:2g:56:GLN:NE2	2.37	0.57
1:1A:456:C:H4'	63:1A:5331:HOH:O	2.05	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1791:A:H5"	1:1A:1791:A:H8	1.69	0.57
32:1a:1237:C:HO2'	32:1a:1300:G:H1	1.51	0.57
1:2A:275:G:H2'	1:2A:276:A:H8	1.68	0.57
9:2N:74:ARG:HG3	9:2N:83:LYS:HB3	1.85	0.57
18:2W:18:ARG:NH1	18:2W:76:VAL:O	2.37	0.57
28:16:6:ARG:NH1	28:16:26:ASN:HB2	2.20	0.57
39:1h:41:ARG:NH2	39:1h:123:GLU:OE2	2.37	0.57
1:2A:770:G:OP2	63:2A:3863:HOH:O	2.18	0.57
32:2a:1239:A:H62	32:2a:1299:A:H62	1.53	0.57
1:1A:1041:C:N3	1:1A:1114:G:N2	2.37	0.57
27:15:47:PRO:O	27:15:60:VAL:HG21	2.04	0.57
29:17:47:ARG:HB3	29:17:47:ARG:HH11	1.69	0.57
40:1i:18:PHE:HD2	40:1i:62:TYR:HD2	1.52	0.57
1:2A:1287:A:H8	13:2R:104:ARG:HD3	1.70	0.57
1:2A:2328:A:H2'	1:2A:2329:G:C8	2.39	0.57
32:2a:768:A:OP2	63:2a:3213:HOH:O	2.16	0.57
35:2d:78:LEU:HD22	35:2d:96:LEU:HB3	1.86	0.57
35:2d:142:PRO:HB3	35:2d:187:ARG:HA	1.85	0.57
36:2e:110:LEU:HD13	36:2e:118:ILE:HD13	1.85	0.57
46:2o:39:LEU:HD13	46:2o:56:LEU:HB2	1.85	0.57
25:13:7:LYS:HE3	25:13:32:GLN:NE2	2.19	0.57
38:1g:27:ILE:HD12	38:1g:40:ALA:HA	1.86	0.57
5:2F:185:ASP:HA	5:2F:188:ARG:HD3	1.86	0.57
1:1A:1098:A:H2'	1:1A:1099:G:O4'	2.04	0.57
1:1A:1179:C:H2'	1:1A:1180:C:H6	1.70	0.57
1:1A:2140:C:N3	1:1A:2151:G:O6	2.37	0.57
32:1a:437:U:H5'	35:1d:155:LEU:HD11	1.86	0.57
33:1b:54:THR:HG23	33:1b:199:TYR:HB3	1.87	0.57
1:2A:422:A:H2'	1:2A:423:A:C8	2.40	0.57
1:2A:1053:C:H2'	1:2A:1054:A:C8	2.36	0.57
1:2A:2417:C:OP1	11:2P:65:ARG:NH2	2.37	0.57
8:2I:9:LEU:HD13	8:2I:12:LEU:HD12	1.87	0.57
32:2a:1129:C:OP1	40:2i:16:ARG:NH1	2.37	0.57
1:1A:2748:A:H5'	7:1H:4:ILE:HD13	1.86	0.57
32:1a:567:G:N3	63:1a:1935:HOH:O	2.32	0.57
32:1a:1218:C:H2'	32:1a:1219:U:C6	2.40	0.57
35:1d:101:LEU:HB2	35:1d:138:TYR:HB3	1.87	0.57
51:1t:18:GLN:O	51:1t:22:ARG:HG3	2.04	0.57
1:2A:2788:C:N3	1:2A:2789:C:N4	2.52	0.57
5:2F:172:TRP:H	5:2F:172:TRP:CD1	2.22	0.57
19:2X:53:LYS:NZ	19:2X:55:ASN:OD1	2.37	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1010:G:H2'	32:2a:1011:G:C8	2.40	0.57
1:1A:2143:C:H2'	1:1A:2144:U:H4'	1.86	0.57
1:1A:2432:A:OP1	63:1A:4158:HOH:O	2.18	0.57
20:1Y:28:LYS:HG3	20:1Y:40:GLU:HG2	1.87	0.57
39:1h:39:LEU:HB3	39:1h:45:ILE:HG12	1.87	0.57
43:1l:77:LEU:HD21	43:1l:107:ALA:HA	1.86	0.57
43:1l:82:VAL:O	43:1l:106:ASP:HB2	2.04	0.57
1:2A:2206:G:H5"	1:2A:2207:G:C8	2.39	0.57
11:2P:126:VAL:HA	11:2P:146:VAL:HB	1.87	0.57
50:2s:27:GLU:OE1	50:2s:47:HIS:NE2	2.28	0.57
1:1A:1379:A:H4'	1:1A:1380:G:OP2	2.05	0.56
19:1X:60:ARG:NH2	29:17:47:ARG:HH21	2.03	0.56
39:1h:86:ILE:HG21	39:1h:133:LEU:HD13	1.87	0.56
41:1j:61:GLU:OE2	45:1n:58:LYS:NZ	2.37	0.56
1:2A:1278:A:OP1	13:2R:36:THR:HG23	2.05	0.56
1:2A:1754:C:P	15:2T:96:ARG:HH12	2.28	0.56
32:2a:1030:C:N4	32:2a:1032:G:O6	2.37	0.56
36:2e:143:ARG:NH1	39:2h:77:GLU:OE2	2.33	0.56
3:2D:78:LYS:HE2	3:2D:114:GLY:HA2	1.87	0.56
32:2a:1135:U:H2'	32:2a:1137:C:N3	2.19	0.56
53:2y:87:LYS:O	53:2y:91:LYS:HB2	2.04	0.56
1:1A:809:G:OP1	63:1A:4160:HOH:O	2.18	0.56
1:1A:1086:A:H3'	1:1A:1086:A:N3	2.20	0.56
1:1A:2286:A:H4'	1:1A:2287:A:O4'	2.05	0.56
1:1A:2611:U:H5'	1:1A:2611:U:H6	1.70	0.56
4:1E:116:VAL:HG13	4:1E:122:PHE:HB2	1.87	0.56
6:1G:126:ASP:HB2	6:1G:130:ASN:H	1.69	0.56
32:1a:1010:G:H22	32:1a:1020:U:H1'	1.70	0.56
39:1h:14:ARG:O	39:1h:18:ARG:HG2	2.05	0.56
45:1n:23:ARG:NH1	45:1n:28:GLY:O	2.38	0.56
50:1s:63:THR:OG1	50:1s:65:ASN:OD1	2.22	0.56
1:2A:1079:C:N4	1:2A:1080:C:O2	2.38	0.56
1:2A:1541:G:O6	63:2A:3835:HOH:O	2.13	0.56
1:2A:2683:C:OP1	15:2T:53:ARG:NH2	2.37	0.56
6:2G:32:PRO:HB2	6:2G:172:LEU:HD13	1.87	0.56
32:2a:601:C:H2'	32:2a:602:A:C8	2.40	0.56
32:2a:1005:A:O2'	32:2a:1036:G:N2	2.38	0.56
32:2a:1016:A:O2'	32:2a:1217:C:O2'	2.22	0.56
33:2b:54:THR:HG23	33:2b:199:TYR:HB3	1.87	0.56
43:2l:83:VAL:HG21	43:2l:100:ILE:HD13	1.88	0.56
45:2n:37:PHE:HB3	45:2n:39:LEU:HD12	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:2q:29:HIS:N	48:2q:33:GLY:O	2.38	0.56
32:1a:96:U:H2'	32:1a:97:G:C8	2.40	0.56
1:2A:249:C:O2	30:28:12:LYS:NZ	2.29	0.56
1:2A:775:G:OP1	63:2A:3861:HOH:O	2.18	0.56
1:2A:2520:C:O2	63:2A:3862:HOH:O	2.18	0.56
6:2G:43:LEU:HD12	6:2G:89:GLY:HA2	1.87	0.56
32:2a:1513:A:H2'	32:2a:1514:C:C6	2.41	0.56
46:2o:55:GLY:HA2	46:2o:58:MET:HE3	1.87	0.56
50:2s:15:LEU:HA	50:2s:18:LYS:HE3	1.88	0.56
1:2A:586:A:N1	1:2A:809:G:O2'	2.36	0.56
1:2A:1525:G:H2'	1:2A:1526:G:C8	2.40	0.56
23:21:52:ARG:NH1	23:21:55:GLY:O	2.38	0.56
32:2a:1273:G:H3'	32:2a:1274:G:C8	2.41	0.56
1:1A:371:A:N3	63:1A:4164:HOH:O	2.33	0.56
1:1A:2789:C:O2	1:1A:2894:G:N1	2.36	0.56
6:1G:143:GLU:OE2	26:14:26:SER:OG	2.17	0.56
11:1P:89:ALA:O	11:1P:121:LYS:NZ	2.30	0.56
53:1y:26:LYS:HD3	53:1y:78:ILE:HG21	1.87	0.56
7:2H:143:GLN:NE2	7:2H:147:ASN:OD1	2.38	0.56
32:2a:164:U:H2'	32:2a:165:C:C6	2.41	0.56
32:2a:696:A:N1	32:2a:797:C:O2'	2.33	0.56
15:1T:112:ARG:HG3	15:1T:115:ARG:HH21	1.70	0.56
30:18:33:ASN:HA	30:18:36:LYS:HD2	1.86	0.56
32:1a:1053:G:N7	32:1a:1200:C:H5"	2.21	0.56
1:2A:131:G:OP1	63:2A:3860:HOH:O	2.17	0.56
1:2A:1971:A:N1	63:2A:4003:HOH:O	2.33	0.56
1:2A:2107:C:N4	1:2A:2182:G:H1	2.01	0.56
7:2H:144:VAL:O	7:2H:148:ILE:HG12	2.05	0.56
10:2O:5:GLN:O	63:2O:301:HOH:O	2.18	0.56
32:2a:588:G:H5"	39:2h:5:PRO:HG3	1.87	0.56
32:2a:1004:A:H5"	32:2a:1025:U:C5	2.40	0.56
32:2a:1190:G:H5'	34:2c:176:HIS:CE1	2.41	0.56
32:1a:176:C:H2'	32:1a:177:C:H6	1.71	0.56
32:1a:560:U:O2'	32:1a:561:U:OP2	2.20	0.56
1:2A:2186:G:H5'	1:2A:2187:G:OP2	2.06	0.56
2:2B:12:C:H2'	22:20:73:GLY:HA3	1.88	0.56
2:2B:84:C:OP1	25:23:15:TYR:OH	2.18	0.56
36:2e:57:LYS:HG2	36:2e:61:TYR:HE2	1.71	0.56
2:1B:66:A:H61	2:1B:108:U:H2'	1.71	0.56
6:1G:179:PRO:HG3	26:14:43:TYR:OH	2.06	0.56
10:1O:122:LEU:HD13	15:1T:72:VAL:HG11	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:8:A:H2'	1:2A:9:U:C6	2.41	0.56
1:2A:275:G:H2'	1:2A:276:A:C8	2.40	0.56
1:2A:2405:G:H5'	11:2P:75:ILE:HD13	1.88	0.56
1:2A:2892:A:H2'	1:2A:2893:G:H5'	1.87	0.56
20:2Y:55:TYR:CZ	20:2Y:61:ILE:HG21	2.41	0.56
28:26:6:ARG:NH1	28:26:26:ASN:HB2	2.21	0.56
32:2a:662:G:H2'	32:2a:663:A:C8	2.41	0.56
35:2d:201:GLN:NE2	36:2e:116:THR:O	2.39	0.56
1:1A:2183:C:H2'	1:1A:2184:G:H8	1.71	0.56
11:1P:70:GLN:NE2	63:1P:303:HOH:O	2.38	0.56
32:1a:309:G:O2'	32:1a:607:A:N1	2.37	0.56
32:1a:328:C:H4'	32:1a:329:A:H5"	1.87	0.56
32:1a:1263:C:H2'	32:1a:1264:C:C6	2.41	0.56
1:2A:172:C:H2'	1:2A:173:G:H8	1.71	0.56
4:2E:77:ILE:HD13	4:2E:195:LEU:HD13	1.87	0.56
6:2G:37:VAL:HG21	6:2G:103:LEU:HD21	1.88	0.56
1:1A:1786:A:H1'	1:1A:1938:A:N6	2.22	0.55
1:1A:2228:G:OP1	3:1D:261:LYS:NZ	2.38	0.55
6:1G:118:ARG:O	6:1G:181:ARG:HB3	2.06	0.55
14:1S:59:LYS:NZ	14:1S:68:GLN:HE22	2.04	0.55
34:1c:6:HIS:CD2	34:1c:9:GLY:H	2.24	0.55
32:2a:1002:G:N2	32:2a:1039:C:N3	2.54	0.55
50:2s:22:LEU:HD12	50:2s:31:ILE:HD11	1.88	0.55
32:1a:1240:U:OP2	38:1g:116:ALA:N	2.39	0.55
32:1a:1400:5MC:C2	53:1y:63:ALA:HA	2.41	0.55
1:2A:918:A:N3	2:2B:80:U:O2'	2.36	0.55
1:2A:1794:U:H2'	1:2A:1795:C:C6	2.41	0.55
32:2a:547:A:OP1	63:2a:3216:HOH:O	2.18	0.55
40:2i:46:ALA:HB2	40:2i:74:ILE:HG22	1.87	0.55
1:2A:2206:G:H3'	1:2A:2207:G:C8	2.39	0.55
32:2a:56:U:H2'	32:2a:57:G:C8	2.41	0.55
32:2a:979:C:H42	45:2n:18:VAL:HB	1.72	0.55
32:2a:1005:A:H5"	32:2a:1006:C:C5	2.40	0.55
35:2d:98:GLU:CD	35:2d:107:ARG:HH21	2.14	0.55
39:2h:4:ASP:OD1	39:2h:7:ALA:N	2.30	0.55
40:2i:42:ARG:NH2	40:2i:71:SER:OG	2.37	0.55
40:2i:43:ALA:O	40:2i:45:ALA:N	2.39	0.55
43:2l:103:GLY:N	43:2l:107:ALA:O	2.37	0.55
1:1A:173:G:H2'	1:1A:174:C:C6	2.41	0.55
1:1A:1143:A:OP1	9:1N:25:ARG:NH2	2.40	0.55
1:1A:2155:G:H3'	1:1A:2156:G:H8	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2269:A:N6	63:1A:4219:HOH:O	2.25	0.55
7:1H:7:LEU:HD12	7:1H:8:PRO:HD2	1.89	0.55
34:1c:15:THR:HG21	34:1c:181:ASN:HA	1.89	0.55
1:2A:192:C:O2'	1:2A:802:A:N3	2.39	0.55
1:2A:1747:G:H2'	1:2A:1747(A):G:H8	1.72	0.55
4:2E:5:LEU:HD21	4:2E:79:ARG:HB2	1.89	0.55
7:2H:41:MET:HE3	7:2H:64:LEU:HB2	1.88	0.55
7:2H:98:LEU:HD13	7:2H:125:VAL:HG12	1.87	0.55
20:2Y:43:ASN:HB3	20:2Y:65:ALA:HB3	1.89	0.55
32:2a:16:A:OP2	63:2a:3215:HOH:O	2.18	0.55
1:1A:888:C:H4'	1:1A:889:C:OP1	2.05	0.55
1:1A:2116:G:P	1:1A:2166:G:H21	2.28	0.55
16:1U:85:LYS:HD3	16:1U:117:GLN:HB3	1.87	0.55
32:1a:222:U:H2'	32:1a:223:U:C6	2.41	0.55
8:2I:83:ALA:HA	8:2I:88:ILE:HA	1.88	0.55
41:2j:30:SER:OG	41:2j:84:GLN:NE2	2.40	0.55
43:2l:77:LEU:HD21	43:2l:107:ALA:HA	1.88	0.55
1:1A:1441:G:O6	63:1A:4157:HOH:O	2.17	0.55
1:1A:2137:C:C2	1:1A:2154:G:N2	2.75	0.55
51:1t:10:LEU:HB3	51:1t:12:ALA:H	1.71	0.55
1:2A:1611:C:OP1	63:2A:3867:HOH:O	2.18	0.55
2:2B:90:A:N7	2:2B:91:C:H1'	2.22	0.55
32:2a:390:C:O3'	47:2p:28:ARG:NH2	2.37	0.55
33:2b:122:PHE:HA	33:2b:127:ILE:HG12	1.89	0.55
1:1A:796:C:H2'	1:1A:797:C:C6	2.42	0.55
63:1A:4104:HOH:O	13:1R:3:HIS:NE2	2.33	0.55
32:1a:656:C:O2'	46:1o:28:GLN:NE2	2.33	0.55
33:1b:95:GLN:HG3	33:1b:147:LYS:O	2.07	0.55
51:1t:53:LEU:HD12	51:1t:100:ILE:HG13	1.88	0.55
1:2A:800:A:H8	1:2A:800:A:OP1	1.89	0.55
2:2B:49:C:H2'	2:2B:50:G:C8	2.42	0.55
5:2F:164:ARG:HD2	5:2F:175:THR:HG23	1.88	0.55
32:2a:922:G:H4'	36:2e:20:GLN:HA	1.88	0.55
32:2a:1086:U:H3	32:2a:1099:G:H22	1.53	0.55
37:2f:50:TYR:CE2	49:2r:77:GLY:HA2	2.41	0.55
1:1A:1173:G:O2'	1:1A:1174:A:O5'	2.25	0.55
1:1A:2206:G:OP2	1:1A:2206:G:H4'	2.07	0.55
5:1F:64:ILE:HD11	5:1F:75:HIS:HB2	1.87	0.55
7:1H:149:ARG:NH1	7:1H:167:GLU:OE2	2.40	0.55
28:16:11:LEU:HB2	28:16:21:TYR:HB2	1.89	0.55
32:1a:1278:U:H5'	32:1a:1279:A:O4'	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:1b:219:VAL:HA	33:1b:222:ILE:HD12	1.88	0.55
8:2I:5:LEU:HG	8:2I:9:LEU:HD12	1.88	0.55
32:2a:425:G:O3'	35:2d:45:GLN:NE2	2.30	0.55
32:2a:920:U:H2'	32:2a:921:U:C6	2.42	0.55
32:2a:1014:A:C2	32:2a:1219:U:H1'	2.42	0.55
42:2k:20:TYR:CZ	42:2k:83:ILE:HD12	2.42	0.55
1:1A:2887:U:H2'	1:1A:2888:C:C6	2.42	0.55
2:1B:25:A:OP2	63:1B:301:HOH:O	2.18	0.55
32:1a:299:G:H2'	32:1a:300:A:C8	2.42	0.55
32:1a:673:G:H2'	32:1a:674:G:C8	2.42	0.55
1:2A:1721:G:N1	1:2A:1739:U:OP2	2.40	0.55
1:2A:1803:A:O2'	3:2D:259:THR:HG21	2.06	0.55
1:2A:2400:G:H4'	28:26:18:ARG:HG2	1.88	0.55
4:2E:143:ASN:HD22	4:2E:147:PRO:HD3	1.72	0.55
8:2I:27:ARG:HG2	23:21:71:TYR:CZ	2.42	0.55
1:1A:1669:A:OP2	63:1A:4110:HOH:O	2.18	0.55
18:1W:68:ARG:HH12	18:1W:112:GLY:H	1.55	0.55
32:1a:1492:A:H4'	32:1a:1493:A:C2	2.42	0.55
46:1o:69:TYR:HD1	46:1o:72:ARG:HH22	1.53	0.55
3:2D:16:MET:HG3	3:2D:206:LEU:O	2.07	0.55
32:2a:769:G:H4'	32:2a:1513:A:H4'	1.88	0.55
32:2a:1248:A:N3	40:2i:70:LYS:NZ	2.37	0.55
32:2a:1376:U:H2'	32:2a:1377:A:H8	1.72	0.55
33:2b:74:LYS:HB3	33:2b:76:GLN:HE21	1.72	0.55
41:2j:8:LEU:HB2	41:2j:70:ARG:HB2	1.88	0.55
47:2p:18:ARG:NH1	47:2p:32:TYR:OH	2.40	0.55
1:1A:1509(A):A:H2'	1:1A:1509(B):A:O4'	2.07	0.54
12:1Q:85:LYS:HB2	22:10:7:LEU:HD12	1.89	0.54
41:1j:44:VAL:HG22	41:1j:66:ARG:HG2	1.89	0.54
1:2A:1062:G:C5	1:2A:1070:A:H1'	2.42	0.54
1:2A:1525:G:H2'	1:2A:1526:G:H8	1.72	0.54
21:2Z:92:SER:O	21:2Z:130:PRO:HG2	2.07	0.54
30:28:23:VAL:HG22	30:28:47:LYS:HB3	1.89	0.54
32:2a:1221:G:OP1	32:2a:1320:C:N4	2.40	0.54
20:1Y:92:ASN:HB2	20:1Y:94:LYS:N	2.19	0.54
32:1a:1289:A:N1	32:1a:1371:G:O2'	2.36	0.54
32:1a:1435:G:H2'	32:1a:1436:U:C6	2.43	0.54
1:2A:1062:G:N7	1:2A:1070:A:H1'	2.22	0.54
63:2A:3887:HOH:O	22:20:4:LYS:NZ	2.36	0.54
32:2a:875:C:H1'	39:2h:15:ASN:ND2	2.21	0.54
33:2b:78:GLN:NE2	33:2b:95:GLN:HA	2.23	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:2f:30:LEU:HD23	37:2f:75:LEU:HD11	1.89	0.54
38:2g:133:GLY:O	38:2g:137:LYS:N	2.31	0.54
40:2i:19:LEU:HD23	40:2i:61:ALA:HB2	1.89	0.54
1:1A:1570:A:H2'	1:1A:1571:A:C8	2.41	0.54
1:1A:1688:U:O2	1:1A:1700:A:H5'	2.07	0.54
8:1I:63:ALA:HA	8:1I:66:GLU:HB2	1.89	0.54
32:1a:270:A:H2'	32:1a:271:C:C6	2.42	0.54
32:1a:946:A:O2'	32:1a:1333:A:N3	2.35	0.54
42:1k:122:LYS:HB3	42:1k:124:LYS:HE3	1.90	0.54
1:2A:1504:C:H2'	1:2A:1505:C:H6	1.72	0.54
10:2O:77:ILE:HD12	15:2T:74:ARG:HD3	1.89	0.54
31:29:14:CYS:HA	31:29:27:CYS:HB2	1.88	0.54
32:2a:390:C:H2'	32:2a:391:G:C8	2.42	0.54
1:1A:2082:A:N1	63:1A:4326:HOH:O	2.33	0.54
1:1A:2784:C:H1'	4:1E:37:ARG:HH12	1.72	0.54
1:2A:205:G:O6	23:21:39:LYS:NZ	2.30	0.54
1:2A:1147:C:H2'	1:2A:1148:A:H8	1.72	0.54
1:2A:2639:A:H2'	1:2A:2640:G:O4'	2.07	0.54
32:2a:353:A:H5'	32:2a:353:A:H8	1.72	0.54
32:2a:971:G:N2	32:2a:1363(A):A:OP2	2.40	0.54
32:2a:1316:G:N2	32:2a:1318:A:H3'	2.22	0.54
33:2b:91:PRO:HG3	33:2b:155:LEU:HD13	1.90	0.54
39:2h:49:GLU:OE2	39:2h:62:TYR:OH	2.19	0.54
1:1A:153:C:OP2	23:11:92:LYS:NZ	2.39	0.54
1:1A:336:C:HO2'	20:1Y:35:TYR:HH	1.56	0.54
10:1O:28:SER:HB3	63:1O:321:HOH:O	2.06	0.54
37:1f:91:VAL:HG21	49:1r:72:ARG:HH12	1.71	0.54
41:1j:35:SER:HB3	41:1j:73:ASP:CB	2.37	0.54
47:1p:5:ARG:HH21	47:1p:24:ALA:HA	1.72	0.54
9:2N:4:TYR:CD2	16:2U:100:VAL:HG11	2.43	0.54
21:2Z:40:ASP:HB3	21:2Z:43:GLU:HB2	1.90	0.54
32:2a:1010:G:H2'	32:2a:1011:G:H8	1.72	0.54
45:2n:7:ILE:HA	45:2n:23:ARG:HD2	1.89	0.54
1:1A:2167:U:H2'	1:1A:2168:G:C8	2.42	0.54
28:16:9:LEU:HD13	28:16:51:GLU:HG3	1.89	0.54
32:1a:669:U:H2'	32:1a:670:G:C8	2.43	0.54
38:1g:113:GLU:HG2	38:1g:119:ARG:HG2	1.88	0.54
1:2A:889:C:O2'	1:2A:890:A:O4'	2.25	0.54
1:2A:2637:U:OP1	4:2E:82:ARG:NH1	2.39	0.54
19:2X:44:GLU:OE2	63:2X:201:HOH:O	2.18	0.54
32:2a:1143:G:H2'	32:2a:1144:G:H8	1.72	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:999:U:OP2	63:2A:3865:HOH:O	2.18	0.54
1:2A:2782:G:OP2	63:2A:3868:HOH:O	2.18	0.54
25:23:29:ARG:HD2	25:23:30:ARG:HH12	1.72	0.54
32:2a:1128:C:H1'	32:2a:1147:C:H42	1.71	0.54
38:2g:44:TYR:HA	38:2g:47:CYS:HB2	1.90	0.54
38:2g:113:GLU:HG2	38:2g:119:ARG:HG2	1.89	0.54
1:1A:2183:C:H2'	1:1A:2184:G:C8	2.42	0.54
13:1R:67:LEU:HG	13:1R:76:VAL:HG21	1.90	0.54
33:1b:9:GLU:HG3	33:1b:217:ARG:HH22	1.71	0.54
35:1d:14:ARG:HG3	35:1d:59:ARG:NH1	2.23	0.54
39:1h:81:HIS:N	39:1h:138:TRP:O	2.41	0.54
46:1o:39:LEU:HD13	46:1o:56:LEU:HB2	1.90	0.54
53:1y:52:ALA:HB2	53:1y:77:LEU:HD21	1.90	0.54
53:1y:55:ASN:HA	53:1y:60:VAL:HA	1.89	0.54
1:2A:1115:G:H2'	1:2A:1116:C:C6	2.42	0.54
1:2A:1364:G:OP2	23:21:3:LYS:HG3	2.08	0.54
32:2a:664:G:N2	32:2a:741:G:H1	2.00	0.54
32:2a:1054:C:H41	53:2y:46:GLN:NE2	2.05	0.54
32:2a:1073:U:H2'	32:2a:1074:G:H8	1.73	0.54
1:1A:1877:A:H5'	1:1A:1878:G:OP2	2.08	0.54
33:1b:24:TRP:CZ3	33:1b:26:PRO:HA	2.43	0.54
3:2D:275:LYS:NZ	63:2D:407:HOH:O	2.30	0.54
5:2F:178:PRO:HB3	5:2F:198:ALA:HA	1.90	0.54
17:2V:33:VAL:HG23	17:2V:59:ALA:HB3	1.89	0.54
23:21:6:GLU:OE1	23:21:91:LYS:NZ	2.26	0.54
32:2a:757:U:H2'	32:2a:758:G:O4'	2.07	0.54
33:2b:20:GLU:C	33:2b:39:ILE:HG12	2.33	0.54
43:2l:69:TYR:HD2	43:2l:99:HIS:CE1	2.26	0.54
1:1A:1143:A:OP2	63:1A:4161:HOH:O	2.18	0.54
1:1A:2020:A:OP2	63:1A:4163:HOH:O	2.18	0.54
1:1A:2086:U:H2'	1:1A:2087:G:C8	2.43	0.54
23:11:3:LYS:HG2	23:11:4:VAL:HG23	1.89	0.54
32:1a:6:G:H4'	32:1a:298:A:H4'	1.90	0.54
32:1a:263:A:OP1	51:1t:79:ARG:NH1	2.41	0.54
32:1a:410:G:OP1	35:1d:30:LYS:NZ	2.41	0.54
1:2A:2150:U:H2'	1:2A:2151:G:C8	2.43	0.54
6:2G:60:LEU:HD23	6:2G:68:PRO:HG3	1.90	0.54
7:2H:33:LEU:HD12	7:2H:75:ALA:HA	1.89	0.54
32:2a:149:A:H2'	32:2a:150:C:C6	2.43	0.54
1:1A:1385:G:O2'	1:1A:1396:U:O2	2.24	0.53
1:1A:1508:A:H4'	1:1A:1509(A):A:C5	2.44	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1639:U:O2'	1:1A:1640:C:H5'	2.08	0.53
10:1O:64:ARG:HB2	10:1O:79:PHE:CD2	2.43	0.53
21:1Z:150:LEU:O	21:1Z:171:ILE:HG13	2.07	0.53
32:1a:266:G:H5"	32:1a:268:C:H41	1.72	0.53
33:1b:217:ARG:O	33:1b:221:LEU:HD12	2.08	0.53
40:1i:50:LEU:HD13	40:1i:56:LEU:HG	1.90	0.53
1:2A:83:G:H1	1:2A:102:G:HO2'	1.54	0.53
1:2A:1116:C:H2'	1:2A:1117:G:C8	2.43	0.53
1:2A:1580:A:H8	1:2A:1580:A:OP2	1.91	0.53
1:2A:2648:C:H2'	1:2A:2649:U:C6	2.44	0.53
2:2B:66:A:N6	2:2B:109:C:H5'	2.23	0.53
4:2E:179:GLU:HB2	4:2E:181:LEU:HG	1.89	0.53
6:2G:16:ARG:CZ	6:2G:31:VAL:HG21	2.37	0.53
26:24:59:PHE:HA	26:24:60:GLN:C	2.33	0.53
32:2a:5:U:H5	35:2d:87:GLY:H	1.54	0.53
32:2a:625:G:H4'	47:2p:16:HIS:CD2	2.43	0.53
32:2a:1376:U:O4	38:2g:10:ARG:NH1	2.42	0.53
34:2c:13:GLY:HA3	45:2n:57:ARG:HH21	1.72	0.53
50:2s:27:GLU:HB3	50:2s:47:HIS:CD2	2.42	0.53
1:1A:644:A:H4'	1:1A:645:C:C5	2.44	0.53
1:1A:811:U:H2'	11:1P:21:ARG:HA	1.90	0.53
32:1a:769:G:H4'	32:1a:1513:A:H4'	1.89	0.53
32:1a:1510:U:H2'	32:1a:1511:G:C8	2.43	0.53
1:2A:904:C:H2'	1:2A:905:U:C6	2.43	0.53
32:2a:1129:C:N3	32:2a:1143:G:N2	2.52	0.53
48:2q:22:LEU:HD11	48:2q:39:SER:HB3	1.90	0.53
1:1A:911:A:H2'	12:1Q:9:TYR:OH	2.09	0.53
25:13:29:ARG:HG3	25:13:30:ARG:HG3	1.90	0.53
32:1a:474:G:H2'	32:1a:475:G:C8	2.43	0.53
33:1b:185:ILE:HG22	33:1b:199:TYR:CD2	2.42	0.53
1:2A:1055:G:H3'	1:2A:1056:G:C8	2.42	0.53
1:2A:1101:U:H2'	1:2A:1102:C:C6	2.44	0.53
6:2G:64:THR:HB	6:2G:94:LEU:HD21	1.90	0.53
32:2a:1323:G:HO2'	32:2a:1362:C:HO2'	1.55	0.53
33:2b:101:MET:HA	33:2b:108:ILE:HG13	1.90	0.53
21:1Z:157:LEU:HD11	21:1Z:163:LEU:HB2	1.91	0.53
32:1a:1183:A:H3'	32:1a:1184:G:H5"	1.91	0.53
41:1j:39:PRO:HA	41:1j:70:ARG:HD3	1.89	0.53
1:2A:300:A:OP1	20:2Y:86:ARG:NH2	2.41	0.53
1:2A:1011:G:OP1	16:2U:77:SER:OG	2.26	0.53
2:2B:104:U:HO2'	21:2Z:29:TYR:HH	1.56	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:452:A:H4'	47:1p:72:ARG:NH1	2.24	0.53
33:1b:42:ILE:HD12	33:1b:203:GLY:HA2	1.90	0.53
1:2A:2536:G:O6	63:2A:3871:HOH:O	2.19	0.53
13:2R:95:THR:HG22	13:2R:116:LEU:HD23	1.90	0.53
14:2S:94:TYR:CE2	14:2S:99:LYS:HE3	2.44	0.53
15:2T:24:PRO:HD3	15:2T:52:ILE:HD12	1.91	0.53
15:2T:85:LYS:NZ	15:2T:87:ASP:OD2	2.42	0.53
26:24:40:HIS:O	26:24:44:THR:HG22	2.08	0.53
34:2c:128:PHE:HD1	34:2c:129:ALA:H	1.55	0.53
46:2o:82:ILE:O	46:2o:86:GLY:N	2.41	0.53
1:1A:784:A:H5'	1:1A:785:G:OP1	2.09	0.53
21:1Z:199:LYS:NZ	63:1Z:403:HOH:O	2.42	0.53
34:1c:102:ASN:HD22	34:1c:102:ASN:N	2.05	0.53
1:2A:1188:U:H4'	17:2V:79:VAL:HG22	1.90	0.53
1:2A:2140:C:H2'	1:2A:2141:G:C8	2.42	0.53
1:2A:2410:G:N7	63:2A:4016:HOH:O	2.34	0.53
4:2E:72:VAL:HG12	4:2E:73:GLU:O	2.09	0.53
6:2G:97:ASP:HA	6:2G:100:TRP:HD1	1.73	0.53
9:2N:46:VAL:HG23	9:2N:48:MET:HG2	1.90	0.53
23:21:91:LYS:HE2	23:21:95:LEU:HD21	1.90	0.53
1:1A:1155:A:OP1	16:1U:55:ARG:HD3	2.09	0.53
1:1A:1626:G:O6	63:1A:4156:HOH:O	2.17	0.53
1:1A:2589:A:OP2	63:1A:4165:HOH:O	2.19	0.53
2:1B:81:G:O6	59:1B:231:ARG:NH1	2.41	0.53
3:1D:109:ASP:O	63:1D:402:HOH:O	2.19	0.53
16:1U:104:GLN:CD	16:1U:104:GLN:H	2.16	0.53
32:1a:444:C:H2'	32:1a:445:G:H8	1.73	0.53
32:1a:539:A:N7	43:1l:115:LYS:NZ	2.53	0.53
32:1a:1062:U:H2'	32:1a:1063:C:C6	2.44	0.53
32:1a:1442:G:H2'	32:1a:1442:G:N3	2.24	0.53
33:1b:178:ARG:HH12	39:1h:71:GLY:H	1.56	0.53
52:1u:11:GLY:O	52:1u:15:ARG:HG3	2.09	0.53
1:2A:271(D):G:H2'	1:2A:271(E):U:C6	2.43	0.53
3:2D:164:GLN:CD	3:2D:176:ARG:HH22	2.17	0.53
32:2a:108:G:C6	51:2t:15:ARG:HG2	2.43	0.53
32:2a:1442:G:H2'	32:2a:1442:G:N3	2.24	0.53
38:2g:115:ARG:HG3	38:2g:117:ALA:HB3	1.90	0.53
40:2i:70:LYS:O	40:2i:74:ILE:HG13	2.09	0.53
53:2y:12:ILE:HG22	53:2y:17:ARG:HG3	1.90	0.53
1:1A:11:G:H2'	1:1A:12:U:H5'	1.91	0.53
1:1A:2079:U:O3'	23:11:35:THR:OG1	2.23	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2243:U:H2'	1:1A:2244:U:C6	2.43	0.53
1:1A:2379:G:O2'	14:1S:17:ARG:NH1	2.33	0.53
5:1F:53:THR:CG2	5:1F:55:GLY:H	2.21	0.53
32:1a:1126:U:O2	32:1a:1280:A:H2'	2.09	0.53
1:2A:190:A:OP2	23:21:39:LYS:HE3	2.08	0.53
1:2A:2390:U:P	30:28:35:GLN:HE22	2.31	0.53
20:2Y:28:LYS:NZ	20:2Y:64:GLU:OE1	2.37	0.53
21:2Z:6:LYS:NZ	21:2Z:43:GLU:OE1	2.29	0.53
32:2a:976:G:H5'	32:2a:1358:U:O2'	2.09	0.53
32:2a:1218:C:H2'	32:2a:1219:U:C6	2.43	0.53
32:2a:1402:4OC:HM22	32:2a:1403:C:H5'	1.91	0.53
1:1A:530:G:N1	1:1A:2023:G:OP1	2.32	0.53
1:1A:2279:G:O6	22:10:14:ARG:HG3	2.08	0.53
6:1G:79:ASN:OD1	6:1G:79:ASN:N	2.39	0.53
32:1a:803:G:OP1	63:1a:1910:HOH:O	2.18	0.53
1:2A:1410:G:H2'	1:2A:1411:C:C6	2.44	0.53
1:2A:2315:G:H2'	1:2A:2316:C:C6	2.44	0.53
2:2B:49:C:H2'	2:2B:50:G:H8	1.74	0.53
5:2F:33:LEU:HD22	5:2F:112:MET:HE3	1.91	0.53
34:2c:8:ILE:HD12	34:2c:16:ARG:HD2	1.91	0.53
1:1A:759:G:OP2	63:1A:4167:HOH:O	2.19	0.53
8:1I:116:LEU:HD13	8:1I:128:LEU:HD21	1.91	0.53
44:1m:3:ARG:HD2	44:1m:4:ILE:HG22	1.91	0.53
1:2A:1494:A:H2'	1:2A:1495:A:C8	2.44	0.53
1:2A:2693:A:H2'	1:2A:2694:G:H8	1.74	0.53
14:2S:67:ARG:HG2	14:2S:71:ARG:NH1	2.24	0.53
32:2a:1071:C:H2'	32:2a:1072:G:H8	1.73	0.53
32:2a:1090:U:H2'	32:2a:1091:U:C6	2.44	0.53
1:1A:826:U:OP1	63:1A:4127:HOH:O	2.19	0.52
7:1H:3:ARG:HH22	7:1H:66:GLY:N	2.07	0.52
23:11:56:GLN:HE21	23:11:87:PRO:HD3	1.75	0.52
32:1a:17:U:H2'	32:1a:18:C:C6	2.44	0.52
32:1a:409:G:OP1	35:1d:24:GLU:HB2	2.08	0.52
35:1d:59:ARG:HH12	35:1d:66:ARG:HH12	1.57	0.52
1:2A:71:A:N7	19:2X:31:HIS:HE1	2.07	0.52
1:2A:1971:A:OP2	3:2D:242:ARG:NH2	2.41	0.52
1:2A:2203:U:H2'	1:2A:2205:C:C6	2.44	0.52
12:2Q:38:GLU:HG3	12:2Q:127:ILE:HG22	1.91	0.52
21:2Z:110:GLY:HA3	21:2Z:174:VAL:HG11	1.91	0.52
23:21:75:GLU:HA	23:21:78:LYS:HZ2	1.73	0.52
32:2a:1397:C:H4'	32:2a:1398:A:OP2	2.08	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:2j:63:PHE:HE1	45:2n:58:LYS:HG2	1.74	0.52
47:2p:26:ARG:HH21	47:2p:31:LYS:HB3	1.74	0.52
1:1A:2336:A:H61	22:10:43:THR:CG2	2.23	0.52
1:1A:2591:C:H2'	1:1A:2592:G:C8	2.44	0.52
27:15:36:CYS:O	63:15:201:HOH:O	2.19	0.52
32:1a:755:G:OP2	46:1o:65:ARG:HD2	2.08	0.52
32:1a:920:U:H2'	32:1a:921:U:C6	2.45	0.52
32:1a:1513:A:H2'	32:1a:1514:C:C6	2.45	0.52
46:1o:55:GLY:HA2	46:1o:58:MET:HE3	1.91	0.52
1:2A:2552:OMU:H6	1:2A:2552:OMU:O5'	2.10	0.52
14:2S:62:LYS:HD3	14:2S:97:ARG:CZ	2.40	0.52
20:2Y:6:HIS:CD2	20:2Y:7:VAL:HG23	2.43	0.52
26:24:53:GLU:H	26:24:53:GLU:CD	2.17	0.52
32:2a:38:G:H22	32:2a:397:A:H5"	1.73	0.52
32:2a:978:A:OP1	32:2a:1361:G:N1	2.35	0.52
1:1A:2537:U:H2'	1:1A:2538:C:C6	2.45	0.52
10:1O:116:SER:HA	60:1a:1867:MPD:HM2	1.91	0.52
32:1a:186:C:H2'	32:1a:187:C:C6	2.45	0.52
32:1a:626:U:H2'	32:1a:627:G:H8	1.73	0.52
33:1b:185:ILE:HB	33:1b:199:TYR:HB2	1.91	0.52
1:2A:271(Q):G:H2'	1:2A:271(R):G:H8	1.74	0.52
1:2A:1514:U:H2'	1:2A:1515:G:H8	1.74	0.52
1:2A:2171:A:H4'	1:2A:2172:U:OP1	2.09	0.52
1:2A:2680:C:H1'	4:2E:187:ALA:HB1	1.91	0.52
6:2G:106:LEU:HD23	6:2G:107:LEU:HD23	1.91	0.52
8:2I:123:LEU:HD12	8:2I:144:VAL:HG12	1.91	0.52
9:2N:71:ILE:HG21	9:2N:84:LYS:HD3	1.91	0.52
32:2a:118:U:H3'	32:2a:288:A:H61	1.74	0.52
24:12:9:GLN:HE22	24:12:56:GLN:HB3	1.74	0.52
40:1i:32:ASP:OD1	40:1i:33:PHE:N	2.42	0.52
47:1p:4:ILE:HA	47:1p:20:VAL:O	2.08	0.52
1:2A:1102:C:H2'	1:2A:1103:A:H8	1.74	0.52
6:2G:22:ARG:HH21	6:2G:171:ALA:HB2	1.74	0.52
36:2e:122:GLU:O	36:2e:126:ARG:NH1	2.42	0.52
38:2g:32:ARG:O	38:2g:34:GLY:N	2.43	0.52
1:1A:2181:G:H2'	1:1A:2182:G:C8	2.45	0.52
32:1a:559:A:OP1	36:1e:126:ARG:NH2	2.36	0.52
32:1a:1492:A:H4'	32:1a:1493:A:C6	2.45	0.52
40:1i:9:ARG:HG2	40:1i:14:VAL:HG12	1.92	0.52
1:2A:1769:G:O6	63:2A:3851:HOH:O	2.15	0.52
5:2F:37:VAL:HG13	5:2F:184:TYR:HD1	1.75	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:2I:26:ALA:O	8:2I:31:LEU:HB2	2.09	0.52
17:2V:43:GLU:OE1	17:2V:43:GLU:N	2.42	0.52
50:2s:22:LEU:HD13	50:2s:28:LYS:H	1.73	0.52
1:1A:1637:A:N7	63:1A:4331:HOH:O	2.34	0.52
12:1Q:55:VAL:HG12	12:1Q:64:ILE:HD12	1.91	0.52
25:13:39:ASP:OD2	25:13:44:ARG:NH2	2.34	0.52
1:2A:252:G:OP1	11:2P:50:ARG:NH1	2.36	0.52
12:2Q:67:ARG:O	12:2Q:101:ARG:NH2	2.36	0.52
15:2T:60:THR:HG22	15:2T:77:PRO:HA	1.90	0.52
27:25:40:LYS:NZ	27:25:44:THR:O	2.42	0.52
32:2a:1465:C:H2'	32:2a:1466:C:O4'	2.09	0.52
38:2g:126:ASP:HB3	38:2g:131:LYS:HB2	1.90	0.52
1:1A:639:U:H2'	1:1A:640:C:C6	2.45	0.52
1:1A:2820:A:OP2	13:1R:2:ARG:NH2	2.43	0.52
19:1X:57:LEU:HD11	19:1X:78:LYS:HE3	1.91	0.52
38:1g:80:VAL:HB	38:1g:85:TYR:CD2	2.44	0.52
1:2A:62:C:OP1	63:2A:3873:HOH:O	2.19	0.52
1:2A:997:G:OP2	16:2U:58:ARG:NH1	2.43	0.52
1:2A:1250:G:H5"	63:2A:4814:HOH:O	2.09	0.52
1:2A:1309:G:H4'	29:27:7:PRO:HB2	1.92	0.52
3:2D:186:HIS:CE1	3:2D:188:GLU:HG2	2.45	0.52
4:2E:116:VAL:HG13	4:2E:122:PHE:HB2	1.92	0.52
6:2G:19:LEU:HD11	6:2G:172:LEU:HB2	1.91	0.52
38:2g:90:GLU:OE1	38:2g:90:GLU:N	2.42	0.52
42:2k:99:GLN:HG2	42:2k:105:VAL:HG21	1.90	0.52
1:1A:878:A:H2'	1:1A:879:G:H5'	1.91	0.52
6:1G:5:VAL:HG13	6:1G:8:LYS:HE2	1.92	0.52
7:1H:40:GLU:CD	7:1H:60:ARG:HH12	2.16	0.52
10:1O:121:VAL:HG23	60:1a:1867:MPD:H13	1.91	0.52
21:1Z:144:LEU:HD21	21:1Z:150:LEU:HD13	1.92	0.52
26:14:15:ILE:HB	26:14:32:TYR:CD1	2.45	0.52
32:1a:414:A:H2'	32:1a:415:A:H8	1.75	0.52
32:1a:911:U:OP2	43:1l:97:ARG:NH2	2.35	0.52
32:1a:1140:C:H2'	32:1a:1141:C:H6	1.75	0.52
32:1a:1410:G:H2'	32:1a:1411:C:C6	2.44	0.52
1:2A:667:U:O2	30:28:2:PRO:HD2	2.10	0.52
1:2A:850:C:H5"	25:23:18:ASP:HB2	1.90	0.52
1:2A:2313:C:H2'	1:2A:2314:C:C6	2.45	0.52
2:2B:17:C:H2'	2:2B:18:G:O4'	2.10	0.52
7:2H:20:ALA:HB3	7:2H:23:ARG:HB2	1.90	0.52
32:2a:1112:C:O2	34:2c:179:ARG:N	2.39	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2791:C:H5'	1:1A:2893:G:N2	2.25	0.52
13:1R:2:ARG:HG2	13:1R:5:LYS:HB2	1.92	0.52
34:1c:47:LEU:HB2	34:1c:52:LEU:HD22	1.92	0.52
48:1q:8:GLY:HA3	48:1q:22:LEU:O	2.10	0.52
1:2A:911:A:H2'	12:2Q:9:TYR:OH	2.09	0.52
1:2A:938:G:OP2	30:28:52:LYS:NZ	2.32	0.52
1:2A:2376:A:N3	14:2S:106:ARG:NH2	2.52	0.52
6:2G:64:THR:HG22	6:2G:94:LEU:HD11	1.92	0.52
7:2H:70:THR:O	7:2H:74:ASN:ND2	2.43	0.52
26:24:18:CYS:HB2	26:24:20:ASN:HB2	1.91	0.52
1:1A:2139:C:H42	1:1A:2152:G:H1	1.58	0.52
1:1A:2366:A:H2'	1:1A:2367:G:O4'	2.10	0.52
1:1A:2619:C:H4'	4:1E:151:TYR:O	2.10	0.52
5:1F:184:TYR:CE2	5:1F:188:ARG:HD2	2.45	0.52
9:1N:75:TYR:CE2	9:1N:77:GLY:HA2	2.45	0.52
32:1a:587:G:N7	63:1a:1941:HOH:O	2.34	0.52
32:1a:1521:G:H2'	32:1a:1522:U:C6	2.45	0.52
1:2A:1171:G:N2	1:2A:1179:C:N3	2.57	0.52
4:2E:119:ARG:HD2	63:2E:408:HOH:O	2.10	0.52
12:2Q:77:LYS:NZ	12:2Q:84:GLY:O	2.43	0.52
14:2S:23:ARG:HD2	14:2S:86:ALA:HB2	1.91	0.52
32:2a:90:U:H2'	32:2a:91:C:H6	1.75	0.52
32:2a:376:G:H5"	47:2p:5:ARG:HD3	1.91	0.52
1:1A:2785:C:O2'	63:1A:4166:HOH:O	2.19	0.51
16:1U:101:ARG:NH2	63:1U:304:HOH:O	2.41	0.51
17:1V:52:VAL:CG2	17:1V:55:ALA:HB3	2.41	0.51
21:1Z:144:LEU:HD11	21:1Z:150:LEU:HD22	1.92	0.51
32:1a:429:U:H2'	35:1d:25:ARG:NH1	2.25	0.51
32:1a:674:G:N2	32:1a:717:C:O2	2.43	0.51
33:1b:163:PHE:HA	33:1b:185:ILE:HG12	1.92	0.51
26:24:44:THR:O	26:24:46:GLN:N	2.43	0.51
32:2a:56:U:H2'	32:2a:57:G:H8	1.75	0.51
32:2a:148:G:H2'	32:2a:149:A:H8	1.75	0.51
32:2a:1375:A:H4'	38:2g:29:LYS:HE3	1.92	0.51
32:2a:1493:A:N3	63:2a:3239:HOH:O	2.34	0.51
37:2f:35:ALA:HA	37:2f:67:MET:HB3	1.92	0.51
40:2i:99:LEU:HB3	40:2i:101:PHE:CE2	2.45	0.51
51:2t:33:ILE:O	51:2t:37:SER:OG	2.21	0.51
32:1a:77:G:C2'	32:1a:78:G:H5'	2.40	0.51
32:1a:1101:A:H4'	32:1a:1102:A:O5'	2.10	0.51
32:1a:1412:C:H2'	32:1a:1413:A:C8	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:1h:21:LYS:O	39:1h:65:TYR:OH	2.18	0.51
1:2A:2031:A:C6	1:2A:2498:C:H1'	2.45	0.51
1:2A:2849:U:O4	15:2T:23:ARG:NH2	2.31	0.51
4:2E:36:ARG:NH2	4:2E:88:GLY:O	2.44	0.51
8:2I:57:ARG:HH11	8:2I:61:ARG:HH21	1.58	0.51
32:2a:90:U:H2'	32:2a:91:C:C6	2.45	0.51
32:2a:1035:A:O2'	32:2a:1036:G:H8	1.93	0.51
34:2c:187:ALA:O	34:2c:198:VAL:HG12	2.09	0.51
1:1A:1593:G:H2'	1:1A:1594:G:C8	2.46	0.51
23:11:35:THR:OG1	23:11:35:THR:O	2.28	0.51
32:1a:737:A:H2'	32:1a:738:C:C6	2.45	0.51
34:1c:6:HIS:HD2	34:1c:9:GLY:H	1.57	0.51
39:1h:17:THR:HG22	39:1h:63:LEU:HG	1.91	0.51
40:1i:121:ARG:NH1	40:1i:122:ALA:O	2.42	0.51
48:1q:19:VAL:HG23	48:1q:44:ALA:HB3	1.91	0.51
1:2A:1037:G:H2'	1:2A:1038:C:O4'	2.10	0.51
1:2A:1665:A:H4'	10:2O:67:LYS:HB2	1.91	0.51
2:2B:75:G:H5'	21:2Z:36:LYS:HD3	1.92	0.51
4:2E:199:ARG:NH2	63:2E:404:HOH:O	2.42	0.51
7:2H:33:LEU:HD21	7:2H:136:ILE:HG13	1.93	0.51
8:2I:57:ARG:O	8:2I:61:ARG:HG2	2.10	0.51
32:2a:1224:G:N1	32:2a:1322:C:O4'	2.43	0.51
32:2a:1510:U:H2'	32:2a:1511:G:C8	2.46	0.51
43:2l:47:LYS:HG2	43:2l:48:PRO:HA	1.92	0.51
1:1A:404:C:OP1	63:1A:4168:HOH:O	2.19	0.51
63:1A:6484:HOH:O	3:1D:229:VAL:HG22	2.09	0.51
18:1W:79:GLY:HA3	18:1W:100:THR:HG22	1.93	0.51
32:1a:973:G:H3'	32:1a:974:A:H5"	1.92	0.51
32:1a:1249:C:O2'	40:1i:73:GLN:NE2	2.43	0.51
32:1a:1400:5MC:N3	53:1y:63:ALA:HA	2.26	0.51
1:2A:1074:G:C2	1:2A:1075:C:H1'	2.46	0.51
1:2A:1139:G:OP2	9:2N:70:LYS:NZ	2.43	0.51
4:2E:75:VAL:HG13	4:2E:77:ILE:H	1.75	0.51
18:2W:18:ARG:HG3	18:2W:76:VAL:HB	1.93	0.51
33:2b:88:ALA:HB1	33:2b:222:ILE:HD11	1.92	0.51
46:2o:5:LYS:O	46:2o:9:GLN:HG2	2.10	0.51
1:1A:330:A:H2	1:1A:1210:A:O2'	1.92	0.51
1:1A:1750:G:O2'	1:1A:2860:A:N1	2.35	0.51
3:1D:71:ASP:HB3	3:1D:103:ARG:HH12	1.76	0.51
7:1H:12:PRO:O	7:1H:15:VAL:HG13	2.10	0.51
29:17:12:ARG:NH2	29:17:44:PRO:HB3	2.25	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:7:G:H5'	32:1a:298:A:O4'	2.11	0.51
32:1a:404:U:H2'	32:1a:405:U:C6	2.46	0.51
32:1a:544:G:OP1	35:1d:59:ARG:NH2	2.43	0.51
44:1m:82:MET:HB3	44:1m:93:ARG:HD3	1.92	0.51
45:1n:33:VAL:HA	45:1n:40:CYS:HA	1.91	0.51
1:2A:272:G:N7	1:2A:421:U:H2'	2.26	0.51
6:2G:15:VAL:HG22	6:2G:175:LEU:HB3	1.93	0.51
7:2H:37:VAL:HG13	7:2H:68:THR:HG21	1.92	0.51
14:2S:31:SER:O	14:2S:97:ARG:NH2	2.43	0.51
39:2h:121:ASP:OD1	39:2h:121:ASP:N	2.39	0.51
40:2i:9:ARG:O	40:2i:104:ARG:HG3	2.10	0.51
41:2j:21:GLN:O	41:2j:25:GLU:HG2	2.11	0.51
1:1A:2870:C:H2'	1:1A:2871:C:O4'	2.10	0.51
4:1E:9:VAL:HG13	4:1E:25:VAL:O	2.10	0.51
9:1N:128:HIS:O	9:1N:131:GLN:NE2	2.43	0.51
25:13:25:ALA:O	63:13:201:HOH:O	2.19	0.51
36:1e:78:HIS:HE1	36:1e:80:ILE:HD13	1.75	0.51
37:1f:69:GLU:H	37:1f:69:GLU:CD	2.17	0.51
39:1h:2:LEU:HD12	39:1h:3:THR:H	1.76	0.51
1:2A:720:C:H2'	1:2A:721:C:H6	1.74	0.51
1:2A:1161:C:H2'	1:2A:1162:G:C8	2.45	0.51
1:2A:1818:U:O2'	3:2D:154:LYS:O	2.21	0.51
2:2B:75:G:O3'	21:2Z:10:ARG:NH2	2.43	0.51
2:2B:85:G:OP1	63:2B:302:HOH:O	2.18	0.51
3:2D:275:LYS:HA	3:2D:276:LYS:C	2.36	0.51
13:2R:87:TYR:OH	13:2R:117:VAL:O	2.27	0.51
44:2m:81:LEU:HD13	44:2m:88:ARG:HG2	1.91	0.51
1:1A:1087:G:H2'	1:1A:1089:G:O4'	2.10	0.51
1:1A:1721:G:H8	1:1A:1741:A:H62	1.57	0.51
1:1A:2815:C:H5'	27:15:29:THR:HG21	1.93	0.51
33:1b:74:LYS:NZ	33:1b:206:ASP:OD1	2.32	0.51
44:1m:34:LEU:HD13	44:1m:41:PRO:HA	1.92	0.51
15:2T:127:ALA:C	15:2T:129:ARG:H	2.18	0.51
53:2y:48:PHE:HD2	53:2y:70:MET:HB2	1.75	0.51
1:1A:1918:A:O2'	1:1A:1920:OMC:N4	2.42	0.51
1:1A:2674:G:H5"	10:1O:26:LYS:HE2	1.93	0.51
32:1a:1492:A:H4'	32:1a:1493:A:N1	2.25	0.51
1:2A:121:G:H4'	1:2A:149:A:H5'	1.93	0.51
1:2A:1107:G:H2'	1:2A:1108:U:H5"	1.91	0.51
7:2H:55:PRO:HG2	7:2H:61:HIS:CE1	2.46	0.51
7:2H:89:ILE:HG22	7:2H:94:TYR:HB3	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:2S:15:ARG:O	14:2S:19:LYS:HG2	2.11	0.51
15:2T:28:VAL:HG13	15:2T:86:ILE:HG23	1.93	0.51
20:2Y:86:ARG:NH1	20:2Y:100:ALA:O	2.43	0.51
25:23:52:HIS:CD2	25:23:53:LEU:HG	2.46	0.51
32:2a:1189:C:H5"	34:2c:5:ILE:HD12	1.93	0.51
33:2b:127:ILE:O	33:2b:128:GLU:HB2	2.10	0.51
42:2k:51:LYS:HA	42:2k:55:LYS:HG3	1.91	0.51
46:2o:25:THR:HG21	46:2o:70:LEU:HB2	1.93	0.51
49:2r:58:LEU:HD23	49:2r:62:GLU:HB3	1.91	0.51
3:1D:21:PHE:HB3	3:1D:24:ILE:HD12	1.93	0.51
8:1I:116:LEU:HD21	8:1I:120:ILE:HD11	1.93	0.51
11:1P:99:LEU:HD23	11:1P:102:ARG:HH21	1.76	0.51
21:1Z:70:LEU:HG	21:1Z:91:LEU:HD11	1.93	0.51
26:14:44:THR:OG1	26:14:47:GLN:NE2	2.38	0.51
1:2A:2808:U:H5"	1:2A:2891:G:O6	2.11	0.51
60:2B:220:MPD:O4	60:2B:220:MPD:O2	2.29	0.51
10:2O:88:ASN:HD21	10:2O:90:GLN:HB2	1.75	0.51
11:2P:94:GLU:HG3	11:2P:124:LYS:HD2	1.93	0.51
23:21:3:LYS:HB2	23:21:61:ARG:HH22	1.75	0.51
32:2a:194:C:H2'	32:2a:195:A:H5"	1.93	0.51
32:2a:539:A:H2'	32:2a:540:G:C8	2.46	0.51
32:2a:1002:G:C2	32:2a:1003:G:N7	2.79	0.51
32:2a:1342:C:H2'	32:2a:1343:G:H8	1.75	0.51
44:2m:65:LYS:C	44:2m:66:LEU:HG	2.35	0.51
1:1A:271(M):G:OP1	8:1I:50:ARG:NH1	2.44	0.51
1:1A:1048:A:N1	1:1A:1112:G:O2'	2.38	0.51
2:1B:96:U:OP1	21:1Z:14:LYS:NZ	2.43	0.51
3:1D:10:THR:OG1	3:1D:13:ARG:HG2	2.12	0.51
8:1I:75:LEU:HD13	8:1I:105:HIS:CE1	2.46	0.51
32:1a:176:C:H2'	32:1a:177:C:C6	2.46	0.51
32:1a:347:G:H8	60:1a:1867:MPD:H53	1.75	0.51
32:1a:608:A:OP2	63:1a:1911:HOH:O	2.19	0.51
32:1a:1008:C:H2'	32:1a:1009:G:O4'	2.11	0.51
45:1n:29:ARG:HD3	45:1n:40:CYS:SG	2.51	0.51
1:2A:2115:G:H21	1:2A:2171:A:H61	1.59	0.51
1:2A:2445:G:OP1	5:2F:74:ARG:NH2	2.38	0.51
1:2A:2823:A:OP1	4:2E:159:HIS:NE2	2.44	0.51
32:2a:1203:C:H2'	32:2a:1204:A:O4'	2.10	0.51
33:2b:7:VAL:HG12	33:2b:8:LYS:HG3	1.92	0.51
37:2f:95:GLU:O	49:2r:32:ARG:NH1	2.44	0.51
1:1A:493:G:OP2	63:1A:4171:HOH:O	2.19	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1429:G:H2'	1:1A:1430:C:C6	2.46	0.50
32:1a:1124:G:N7	32:1a:1145:C:O2'	2.35	0.50
1:2A:2857:G:N2	1:2A:2860:A:OP2	2.39	0.50
14:2S:36:TYR:HE1	14:2S:54:LEU:HB2	1.76	0.50
21:2Z:93:ASP:OD1	21:2Z:93:ASP:N	2.30	0.50
32:2a:222:U:H2'	32:2a:223:U:C6	2.46	0.50
33:2b:30:ARG:NH2	33:2b:194:PRO:HB2	2.25	0.50
34:2c:8:ILE:HG12	34:2c:184:TYR:HB3	1.92	0.50
38:2g:65:ALA:HB1	38:2g:127:ALA:HB3	1.92	0.50
53:2y:30:TRP:CD1	53:2y:89:GLN:HG3	2.46	0.50
1:1A:564:C:H5'	63:1A:4411:HOH:O	2.11	0.50
1:1A:910:A:N1	1:1A:2277:G:H1'	2.26	0.50
1:1A:2101:G:H2'	1:1A:2102:U:C6	2.46	0.50
1:1A:2506:U:C2	1:1A:2585:U:O4	2.64	0.50
21:1Z:54:HIS:HB3	21:1Z:101:PRO:HD3	1.93	0.50
32:1a:540:G:H2'	32:1a:541:G:O4'	2.11	0.50
32:1a:976:G:H5'	32:1a:1358:U:O2'	2.11	0.50
41:1j:62:HIS:HB3	45:1n:59:ALA:HB3	1.93	0.50
43:1l:28:LYS:HA	43:1l:28:LYS:HE2	1.91	0.50
1:2A:120:U:OP2	63:2A:3872:HOH:O	2.19	0.50
1:2A:300:A:H2'	1:2A:334:C:H1'	1.93	0.50
1:2A:657:U:H2'	1:2A:658:C:C6	2.46	0.50
1:2A:956:G:H5"	12:2Q:77:LYS:HD2	1.93	0.50
1:2A:1827:C:O2'	1:2A:1970:A:N3	2.37	0.50
3:2D:127:VAL:HA	3:2D:193:VAL:HG23	1.92	0.50
5:2F:108:LYS:O	5:2F:112:MET:HG3	2.11	0.50
24:22:9:GLN:HE22	24:22:56:GLN:HG2	1.75	0.50
32:2a:196:A:OP1	51:2t:68:LYS:NZ	2.44	0.50
32:2a:676:A:H1'	42:2k:115:PRO:HB3	1.93	0.50
32:2a:979:C:O2	45:2n:19:ARG:NE	2.45	0.50
32:2a:1372:U:H5"	40:2i:71:SER:HB3	1.92	0.50
42:2k:33:THR:HA	42:2k:39:PRO:HA	1.94	0.50
1:1A:636:G:OP1	11:1P:132:LYS:HE2	2.12	0.50
1:1A:644:A:H4'	1:1A:645:C:H5	1.77	0.50
1:1A:2099:U:H3	1:1A:2190:G:H1	1.57	0.50
1:1A:2355:C:H1'	22:10:39:ARG:HH21	1.75	0.50
1:1A:2693:A:H2'	1:1A:2694:G:H8	1.77	0.50
15:1T:33:LYS:HG2	15:1T:82:LEU:HD23	1.94	0.50
15:1T:111:ARG:NH2	32:1a:1464:G:OP2	2.44	0.50
24:12:65:ASN:O	24:12:69:ARG:HG3	2.11	0.50
32:1a:153:C:H2'	32:1a:154:C:C6	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1003:G:C2	32:1a:1004:A:H1'	2.46	0.50
37:1f:91:VAL:HG21	49:1r:72:ARG:NH1	2.26	0.50
1:2A:328:U:H4'	20:2Y:68:HIS:CD2	2.46	0.50
1:2A:2243:U:H2'	1:2A:2244:U:C6	2.46	0.50
1:2A:2646:C:H2'	1:2A:2647:U:O4'	2.11	0.50
1:2A:2748:A:H5'	7:2H:4:ILE:HD13	1.93	0.50
3:2D:124:PRO:HB2	3:2D:126:GLN:HG2	1.92	0.50
32:2a:1004:A:N7	32:2a:1037:C:H2'	2.26	0.50
32:2a:1047:G:OP1	45:2n:4:LYS:NZ	2.37	0.50
36:2e:102:ALA:HB2	36:2e:120:THR:HG21	1.93	0.50
39:2h:91:ARG:HD3	48:2q:33:GLY:HA3	1.93	0.50
42:2k:104:GLN:O	42:2k:106:LYS:N	2.44	0.50
53:2y:29:LYS:HG2	53:2y:30:TRP:CE3	2.46	0.50
1:1A:2496:C:OP2	12:1Q:82:ARG:HD3	2.12	0.50
32:1a:181:G:H4'	32:1a:182:U:H5'	1.93	0.50
32:1a:370:C:H2'	32:1a:371:G:C8	2.46	0.50
40:1i:16:ARG:HB2	40:1i:64:THR:HG22	1.93	0.50
1:2A:1044:G:O2'	1:2A:1048:A:H1'	2.11	0.50
32:2a:490:G:P	35:2d:132:ARG:HH22	2.35	0.50
32:2a:1314:C:N4	50:2s:2:PRO:O	2.37	0.50
1:1A:1173:G:H21	1:1A:1177:A:H2	1.59	0.50
1:1A:2346:A:N1	63:1A:4342:HOH:O	2.35	0.50
26:14:46:GLN:O	26:14:48:ARG:N	2.45	0.50
28:16:10:LEU:HD21	28:16:54:ILE:HG13	1.93	0.50
32:1a:97:G:H2'	32:1a:98:G:O4'	2.10	0.50
32:1a:347:G:C8	60:1a:1867:MPD:H53	2.46	0.50
32:1a:828:A:H2'	32:1a:829:G:O4'	2.11	0.50
1:2A:7:G:H2'	1:2A:8:A:C8	2.47	0.50
1:2A:1051:G:O2'	1:2A:1052:C:H6	1.94	0.50
1:2A:1073:A:H2'	1:2A:1074:G:C8	2.47	0.50
1:2A:1657:C:H2'	1:2A:1658:C:C6	2.47	0.50
1:2A:2138:C:H2'	1:2A:2139:C:O4'	2.11	0.50
4:2E:59:VAL:HG21	4:2E:74:PRO:HB3	1.94	0.50
4:2E:92:THR:O	4:2E:95:ILE:HG23	2.12	0.50
23:21:80:LEU:HD11	23:21:97:LEU:HD11	1.94	0.50
28:26:35:GLU:OE2	28:26:50:ARG:NH1	2.44	0.50
32:2a:1291:G:O3'	40:2i:39:GLY:HA3	2.11	0.50
39:2h:20:TYR:HA	39:2h:65:TYR:CZ	2.46	0.50
44:2m:107:ALA:O	44:2m:111:LYS:N	2.28	0.50
48:2q:83:ASP:O	48:2q:87:LYS:HG3	2.12	0.50
1:1A:192:C:H2'	1:1A:193:U:H5'	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:529:A:N1	63:1A:4340:HOH:O	2.34	0.50
1:1A:2354:G:H21	22:10:36:ILE:HD11	1.77	0.50
7:1H:27:LYS:HB3	7:1H:32:GLU:HG2	1.94	0.50
8:1I:132:PRO:HD2	8:1I:136:VAL:O	2.12	0.50
32:1a:1457:G:H2'	32:1a:1458:G:H8	1.77	0.50
36:1e:50:GLU:HB2	36:1e:53:LEU:HD12	1.93	0.50
39:1h:51:VAL:HG21	39:1h:60:ARG:HD2	1.94	0.50
5:2F:178:PRO:HG2	5:2F:179:GLU:OE2	2.11	0.50
17:2V:1:MET:HG3	17:2V:41:GLY:O	2.12	0.50
25:23:15:TYR:CE2	25:23:53:LEU:HD21	2.46	0.50
32:2a:555:C:H2'	32:2a:556:C:C6	2.47	0.50
32:2a:986:A:N3	50:2s:52:TYR:OH	2.30	0.50
32:2a:1143:G:H2'	32:2a:1144:G:C8	2.47	0.50
33:2b:48:MET:HA	33:2b:51:LEU:HD12	1.93	0.50
34:2c:120:VAL:HG21	34:2c:137:ALA:HB2	1.93	0.50
1:1A:247:G:H4'	1:1A:386:G:C5	2.46	0.50
1:1A:604:G:OP2	11:1P:90:ARG:NH1	2.44	0.50
6:1G:27:ASN:HB3	6:1G:30:GLU:HG3	1.92	0.50
21:1Z:28:MET:HG3	21:1Z:37:VAL:HG11	1.94	0.50
32:1a:141:A:H1'	32:1a:182:U:O2	2.11	0.50
32:1a:542:G:P	35:1d:10:ARG:HH22	2.34	0.50
32:1a:1216:G:OP1	45:1n:2:ALA:HA	2.12	0.50
38:1g:83:ALA:HB3	38:1g:85:TYR:CE2	2.46	0.50
46:1o:82:ILE:O	46:1o:86:GLY:N	2.44	0.50
15:2T:109:GLU:HG3	15:2T:112:ARG:HH12	1.77	0.50
21:2Z:10:ARG:NH1	21:2Z:26:GLY:O	2.44	0.50
32:2a:41:G:H2'	32:2a:42:G:C8	2.47	0.50
38:2g:113:GLU:HG3	38:2g:118:VAL:HG12	1.93	0.50
40:2i:9:ARG:HG2	40:2i:14:VAL:HG12	1.92	0.50
50:2s:12:ASP:OD2	50:2s:35:SER:HB3	2.11	0.50
53:2y:30:TRP:HD1	53:2y:89:GLN:HG3	1.76	0.50
1:1A:864:G:H2'	1:1A:865:C:C6	2.47	0.50
1:1A:1175:U:H4'	1:1A:1176:G:OP2	2.10	0.50
1:1A:1238:G:OP2	63:1A:4173:HOH:O	2.20	0.50
1:1A:1250:G:H5"	63:1U:331:HOH:O	2.11	0.50
22:10:43:THR:OG1	22:10:46:LYS:HD3	2.11	0.50
32:1a:607:A:H2'	32:1a:608:A:C8	2.46	0.50
46:1o:25:THR:HG21	46:1o:70:LEU:HB2	1.93	0.50
1:2A:455:C:N3	1:2A:472:A:H2'	2.27	0.50
1:2A:687:C:H5"	29:27:2:LYS:HE2	1.93	0.50
1:2A:2298:A:H62	1:2A:2318:G:H8	1.60	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:2F:11:VAL:HB	5:2F:18:ARG:HG2	1.94	0.50
12:2Q:111:GLU:O	12:2Q:115:MET:HG2	2.11	0.50
21:2Z:179:ASP:HB3	21:2Z:182:LYS:HE2	1.93	0.50
32:2a:492:G:OP2	63:2a:3218:HOH:O	2.20	0.50
37:2f:33:TYR:HB2	37:2f:75:LEU:HD12	1.93	0.50
40:2i:4:TYR:O	40:2i:19:LEU:N	2.38	0.50
1:1A:185:U:H4'	1:1A:218:A:H4'	1.94	0.50
1:1A:1352:U:OP1	63:1A:4169:HOH:O	2.19	0.50
1:1A:2189:U:C2'	1:1A:2190:G:H5'	2.42	0.50
1:1A:2445:G:OP1	5:1F:74:ARG:NH2	2.40	0.50
6:1G:50:ALA:C	6:1G:52:ILE:H	2.19	0.50
32:1a:297:G:H4'	32:1a:557:G:H4'	1.93	0.50
32:1a:316:G:OP2	32:1a:351:G:O2'	2.29	0.50
32:1a:1358:U:OP1	45:1n:35:ARG:HG2	2.12	0.50
1:2A:588:U:H2'	1:2A:589:C:H6	1.77	0.50
1:2A:1166:C:H2'	1:2A:1167:U:C6	2.47	0.50
1:2A:1418:G:OP2	63:2A:3877:HOH:O	2.20	0.50
32:2a:189(K):U:H2'	32:2a:189(L):G:C8	2.47	0.50
33:2b:84:GLU:HB3	33:2b:219:VAL:HG21	1.94	0.50
35:2d:173:TRP:CE2	35:2d:189:PRO:HG3	2.47	0.50
1:1A:660:G:O3'	5:1F:38:ARG:NH2	2.45	0.49
1:1A:2646:C:H2'	1:1A:2647:U:O4'	2.12	0.49
2:1B:103:G:H21	21:1Z:73:GLN:NE2	2.10	0.49
6:1G:16:ARG:O	6:1G:20:ILE:HG13	2.12	0.49
19:1X:31:HIS:CD2	19:1X:33:LYS:H	2.30	0.49
1:2A:342:G:O6	63:2A:3864:HOH:O	2.18	0.49
1:2A:900:A:H2'	1:2A:901:A:H8	1.77	0.49
1:2A:1050:A:H2	1:2A:2751:G:C4	2.30	0.49
1:2A:1889:A:H2'	1:2A:1890:A:C8	2.47	0.49
1:2A:2115:G:H3'	1:2A:2116:G:C5'	2.41	0.49
1:2A:2687:U:H2'	1:2A:2688:U:O4'	2.12	0.49
32:2a:148:G:H2'	32:2a:149:A:C8	2.46	0.49
32:2a:1346:A:C8	32:2a:1348:U:C2	3.00	0.49
40:2i:25:LYS:H	40:2i:60:ASP:HB3	1.77	0.49
1:1A:2242:G:OP1	63:1A:4159:HOH:O	2.18	0.49
32:1a:457:C:H2'	32:1a:458:C:C6	2.47	0.49
32:1a:1026:G:H2'	32:1a:1026:G:N3	2.27	0.49
1:2A:1876:A:H2'	1:2A:1877:A:C8	2.47	0.49
1:2A:2321:G:O2'	1:2A:2322:A:OP1	2.28	0.49
2:2B:87:G:N2	2:2B:90:A:OP2	2.35	0.49
32:2a:415:A:H2'	32:2a:416:G:O4'	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1237:C:H2'	32:2a:1336:C:H5	1.76	0.49
39:2h:7:ALA:O	39:2h:11:THR:OG1	2.17	0.49
1:1A:30:G:OP1	63:1A:4175:HOH:O	2.20	0.49
1:1A:2662:A:H8	1:1A:2662:A:O5'	1.96	0.49
4:1E:176:ILE:HB	4:1E:181:LEU:HB2	1.94	0.49
20:1Y:6:HIS:H	20:1Y:6:HIS:CD2	2.30	0.49
26:14:35:VAL:HG22	26:14:36:CYS:H	1.77	0.49
26:14:60:GLN:HE21	26:14:60:GLN:H	1.60	0.49
32:1a:1109:C:OP2	34:1c:176:HIS:ND1	2.45	0.49
34:1c:95:THR:O	34:1c:97:LYS:HE3	2.12	0.49
14:2S:14:VAL:O	14:2S:18:ILE:HG12	2.12	0.49
21:2Z:42:VAL:HG13	21:2Z:43:GLU:HG3	1.95	0.49
33:2b:165:VAL:HG13	33:2b:166:ASP:H	1.77	0.49
34:2c:164:ARG:HG2	34:2c:165:THR:H	1.76	0.49
39:2h:91:ARG:HG2	48:2q:34:LYS:H	1.77	0.49
1:1A:1778:U:H2'	1:1A:1784:A:N6	2.27	0.49
1:1A:2273:A:H2'	1:1A:2274:A:C8	2.47	0.49
1:1A:2563:U:H4'	10:1O:28:SER:HA	1.93	0.49
11:1P:50:ARG:HD3	30:18:7:HIS:CD2	2.48	0.49
32:1a:153:C:H2'	32:1a:154:C:H6	1.78	0.49
32:1a:674:G:H2'	32:1a:675:A:C8	2.47	0.49
32:1a:965:A:OP2	53:1y:8:LYS:NZ	2.45	0.49
32:1a:1148:U:H2'	32:1a:1149:C:O4'	2.13	0.49
1:2A:740:U:H2'	1:2A:741:G:C8	2.48	0.49
1:2A:2245:U:H5"	1:2A:2246:G:H5'	1.94	0.49
12:2Q:41:TRP:HB3	12:2Q:94:VAL:HB	1.94	0.49
20:2Y:44:ILE:HA	20:2Y:63:LYS:O	2.13	0.49
32:2a:611:A:H2	32:2a:630:G:H22	1.59	0.49
32:2a:1025:U:O2'	32:2a:1026:G:N7	2.45	0.49
32:2a:1323:G:H2'	32:2a:1324:A:C8	2.48	0.49
34:2c:6:HIS:HD2	34:2c:7:PRO:HD2	1.76	0.49
1:1A:2100:G:H1	1:1A:2189:U:H3	1.59	0.49
1:1A:2809:A:H62	1:1A:2891:G:H2'	1.78	0.49
11:1P:42:SER:O	63:1P:301:HOH:O	2.18	0.49
11:1P:86:LYS:HG3	11:1P:87:ASP:N	2.26	0.49
24:12:59:ARG:NH2	63:12:104:HOH:O	2.40	0.49
32:1a:142:G:O2'	32:1a:196:A:N1	2.43	0.49
32:1a:490:G:OP2	35:1d:132:ARG:NH2	2.38	0.49
32:1a:1118:C:H1'	32:1a:1179:A:C4	2.47	0.49
42:1k:15:ALA:HA	42:1k:77:MET:HA	1.94	0.49
1:2A:2286:A:H4'	1:2A:2287:A:O4'	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
63:2A:4573:HOH:O	5:2F:74:ARG:HG3	2.11	0.49
5:2F:110:LEU:HD11	5:2F:181:LEU:HG	1.94	0.49
8:2I:1:MET:HE2	8:2I:38:LEU:HD21	1.95	0.49
33:2b:164:VAL:HB	33:2b:186:ALA:HB2	1.95	0.49
1:1A:1359:A:N1	1:1A:1372:U:O4	2.46	0.49
1:1A:2417:C:OP1	11:1P:65:ARG:NH2	2.45	0.49
11:1P:36:LYS:NZ	63:1P:308:HOH:O	2.46	0.49
15:1T:108:ARG:HA	15:1T:111:ARG:NH1	2.27	0.49
27:15:40:LYS:HD3	27:15:46:CYS:HA	1.95	0.49
32:1a:536:C:OP2	63:1a:1912:HOH:O	2.20	0.49
32:1a:994:A:H61	32:1a:1047:G:H4'	1.76	0.49
43:1l:97:ARG:HB2	43:1l:98:TYR:CE2	2.47	0.49
1:2A:11:G:C2'	1:2A:12:U:H5'	2.42	0.49
1:2A:218:A:C2	1:2A:235:U:H4'	2.47	0.49
1:2A:1799:G:N2	3:2D:155:LEU:HD12	2.27	0.49
1:2A:2319:G:N1	14:2S:3:ARG:HA	2.27	0.49
5:2F:64:ILE:HG21	5:2F:78:ILE:HG23	1.95	0.49
20:2Y:85:VAL:HG13	20:2Y:97:ARG:HB3	1.95	0.49
32:2a:474:G:H2'	32:2a:475:G:C8	2.47	0.49
34:2c:58:GLU:HB3	41:2j:92:THR:HG21	1.94	0.49
34:2c:98:ASN:O	34:2c:100:ALA:N	2.45	0.49
37:2f:91:VAL:HG11	49:2r:72:ARG:NH1	2.28	0.49
46:2o:6:GLU:OE2	46:2o:6:GLU:N	2.45	0.49
1:1A:652(V):C:H2'	1:1A:653:A:O4'	2.13	0.49
1:1A:774:A:N3	1:1A:774:A:H2'	2.27	0.49
20:1Y:56:PRO:C	20:1Y:58:GLY:H	2.21	0.49
27:15:20:ARG:HG2	27:15:23:HIS:CE1	2.47	0.49
32:1a:1304:G:C6	32:1a:1305:G:N1	2.80	0.49
1:2A:637:A:H2'	11:2P:117:GLU:OE1	2.13	0.49
1:2A:2548:G:O6	63:2A:3879:HOH:O	2.20	0.49
26:24:40:HIS:HB3	26:24:43:TYR:HB2	1.94	0.49
50:2s:41:VAL:HG22	50:2s:42:PRO:HD2	1.94	0.49
1:1A:286:C:H2'	1:1A:287:C:C6	2.48	0.49
3:1D:16:MET:HG2	3:1D:211:ARG:NH2	2.28	0.49
3:1D:183:ARG:HG3	3:1D:270:ILE:HG12	1.93	0.49
9:1N:89:LYS:NZ	63:1N:303:HOH:O	2.40	0.49
10:1O:107:ARG:NH2	32:1a:346:G:OP2	2.45	0.49
12:1Q:55:VAL:HG23	21:1Z:180:VAL:HG12	1.95	0.49
20:1Y:13:VAL:HG12	20:1Y:74:PRO:HA	1.95	0.49
28:16:13:CYS:SG	28:16:47:THR:HG21	2.53	0.49
32:1a:578:C:O2'	32:1a:728:A:N3	2.41	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1025:U:C2	32:1a:1036:G:O6	2.66	0.49
33:1b:19:HIS:CG	33:1b:20:GLU:N	2.80	0.49
33:1b:178:ARG:HG3	39:1h:71:GLY:O	2.12	0.49
44:1m:51:ALA:O	44:1m:55:ARG:HG3	2.12	0.49
1:2A:1116:C:H2'	1:2A:1117:G:H8	1.78	0.49
1:2A:1952:A:OP1	10:2O:42:SER:OG	2.30	0.49
7:2H:35:VAL:HG13	7:2H:71:LEU:HD23	1.95	0.49
12:2Q:45:GLN:N	12:2Q:45:GLN:OE1	2.45	0.49
22:20:5:LYS:HG3	22:20:6:GLY:H	1.76	0.49
32:2a:1125:U:O2'	32:2a:1126:U:O5'	2.27	0.49
32:2a:1142:G:H2'	32:2a:1143:G:O4'	2.13	0.49
32:2a:1522:U:H2'	32:2a:1523:G:H8	1.78	0.49
1:1A:579:G:H2'	1:1A:580:C:C6	2.48	0.49
32:1a:186:C:H2'	32:1a:187:C:H6	1.77	0.49
32:1a:757:U:H2'	32:1a:758:G:O4'	2.13	0.49
33:1b:55:PHE:HD1	33:1b:58:ILE:HD12	1.77	0.49
38:1g:104:LEU:O	38:1g:108:ALA:N	2.38	0.49
1:2A:247:G:H4'	1:2A:386:G:C5	2.48	0.49
1:2A:568:U:H5'	1:2A:945:A:N6	2.27	0.49
1:2A:774:A:H2'	1:2A:774:A:N3	2.25	0.49
1:2A:876:C:H2'	1:2A:877:U:O4'	2.13	0.49
1:2A:1014:U:H2'	1:2A:1015:G:C8	2.45	0.49
1:2A:1647:G:H3'	1:2A:1647:G:OP2	2.13	0.49
1:2A:1801:G:OP2	3:2D:154:LYS:NZ	2.45	0.49
1:2A:1916:A:H2'	1:2A:1917:PSU:O4'	2.13	0.49
1:2A:2114:A:O2'	1:2A:2167:U:H4'	2.13	0.49
1:2A:2167:U:H2'	1:2A:2168:G:C4	2.47	0.49
32:2a:458:C:H2'	32:2a:460:G:O4'	2.12	0.49
32:2a:674:G:OP1	37:2f:87:ARG:NH2	2.40	0.49
32:2a:923:A:O2'	32:2a:1399:C:OP2	2.27	0.49
1:1A:661:C:H4'	11:1P:13:ASN:OD1	2.13	0.49
1:1A:1066:U:H2'	1:1A:1067:A:C2	2.48	0.49
1:1A:1239:G:H2'	1:1A:1240:U:O4'	2.12	0.49
3:1D:71:ASP:CB	3:1D:103:ARG:HH12	2.26	0.49
26:14:55:ARG:H	26:14:56:VAL:HA	1.78	0.49
32:1a:411:A:OP1	35:1d:30:LYS:NZ	2.45	0.49
32:1a:457:C:H2'	32:1a:458:C:H6	1.77	0.49
38:1g:75:VAL:HG21	38:1g:144:MET:HE3	1.95	0.49
1:2A:252:G:P	11:2P:50:ARG:HH12	2.36	0.49
1:2A:271(Q):G:H2'	1:2A:271(R):G:C8	2.47	0.49
1:2A:729:G:C5	3:2D:208:LYS:HB2	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1287:A:C8	13:2R:104:ARG:HD3	2.47	0.49
2:2B:95:C:H2'	2:2B:96:U:C6	2.47	0.49
32:2a:975:A:N1	41:2j:48:THR:HB	2.27	0.49
1:1A:1900:A:N1	1:1A:1970:A:C6	2.81	0.48
1:1A:2006:C:O5'	1:1A:2006:C:H6	1.96	0.48
1:1A:2328:A:H2'	1:1A:2329:G:C8	2.48	0.48
29:17:30:VAL:O	29:17:34:ARG:HG3	2.12	0.48
32:1a:194:C:H2'	32:1a:195:A:H5"	1.95	0.48
32:1a:648:A:H2'	32:1a:649:G:H8	1.78	0.48
33:1b:221:LEU:HA	33:1b:224:GLN:HG2	1.95	0.48
1:2A:639:U:H2'	1:2A:640:C:C6	2.48	0.48
1:2A:2406:U:C2	11:2P:72:PRO:HG2	2.48	0.48
1:2A:2704:C:H2'	1:2A:2705:A:O4'	2.13	0.48
3:2D:242:ARG:HG2	3:2D:246:PRO:HG3	1.94	0.48
12:2Q:52:VAL:HA	12:2Q:55:VAL:HG22	1.96	0.48
32:2a:1014:A:H2	32:2a:1219:U:H1'	1.77	0.48
40:2i:6:GLY:N	40:2i:84:ALA:HB2	2.27	0.48
1:1A:270:A:OP2	1:1A:271(X):G:N1	2.42	0.48
1:1A:1165:U:H2'	1:1A:1166:C:C6	2.48	0.48
3:1D:175:LEU:HD12	3:1D:185:VAL:HG21	1.95	0.48
5:1F:28:ILE:HD11	5:1F:115:ALA:HB3	1.95	0.48
33:1b:71:VAL:HB	33:1b:164:VAL:HG22	1.95	0.48
34:1c:136:GLN:O	34:1c:140:ARG:HG3	2.13	0.48
51:1t:34:LYS:O	51:1t:38:LYS:HG2	2.13	0.48
1:2A:539:G:H2'	1:2A:540:C:C6	2.48	0.48
1:2A:1266:G:O5'	18:2W:15:ARG:NH2	2.39	0.48
1:2A:1877:A:H5'	1:2A:1878:G:OP2	2.13	0.48
1:2A:2102:U:O2	1:2A:2187:G:O6	2.30	0.48
1:2A:2123:G:H2'	1:2A:2124:G:H8	1.77	0.48
1:2A:2133:G:O2'	1:2A:2158:A:N1	2.46	0.48
2:2B:52:A:H62	14:2S:33:LYS:NZ	2.11	0.48
6:2G:47:LYS:HG3	6:2G:48:GLU:H	1.77	0.48
13:2R:83:ILE:O	13:2R:86:ARG:HG2	2.13	0.48
24:22:51:ARG:O	24:22:55:ARG:HG3	2.13	0.48
32:2a:1146:A:H3'	32:2a:1147:C:H5"	1.93	0.48
40:2i:65:VAL:HG21	40:2i:73:GLN:HB3	1.95	0.48
43:2l:71:PRO:O	43:2l:102:ARG:NH1	2.46	0.48
50:2s:51:VAL:H	50:2s:58:VAL:H	1.60	0.48
1:1A:2683:C:OP1	15:1T:53:ARG:NH2	2.46	0.48
8:1I:14:ASP:O	8:1I:17:GLN:HB3	2.13	0.48
1:2A:577:G:O2'	1:2A:1254:A:OP1	2.27	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1567:A:OP2	3:2D:84:TYR:OH	2.27	0.48
1:2A:2810:A:N6	1:2A:2891:G:O2'	2.46	0.48
32:2a:978:A:O2'	32:2a:1322:C:N3	2.44	0.48
1:1A:879:G:H2'	1:1A:880:G:O4'	2.13	0.48
6:1G:53:LEU:O	6:1G:56:ALA:N	2.40	0.48
7:1H:154:PRO:HB3	7:1H:163:TYR:CZ	2.48	0.48
9:1N:62:VAL:HG12	9:1N:67:LEU:HD22	1.95	0.48
10:1O:88:ASN:ND2	10:1O:90:GLN:OE1	2.46	0.48
17:1V:82:ARG:NH2	63:1V:305:HOH:O	2.46	0.48
28:16:6:ARG:NE	28:16:24:GLU:OE2	2.27	0.48
32:1a:303:A:HO2'	32:1a:555:C:HO2'	1.61	0.48
32:1a:1168:A:H2'	32:1a:1169:A:C8	2.47	0.48
32:1a:1226:C:H2'	44:1m:103:THR:HB	1.95	0.48
40:1i:16:ARG:HH11	40:1i:64:THR:HG21	1.77	0.48
40:1i:26:VAL:HG22	40:1i:61:ALA:HB3	1.94	0.48
1:2A:320:A:H4'	1:2A:322:A:C8	2.49	0.48
1:2A:833:U:O2'	63:2A:3870:HOH:O	2.19	0.48
1:2A:2000:G:OP1	63:2A:3874:HOH:O	2.20	0.48
1:2A:2641:G:P	9:2N:74:ARG:HH22	2.35	0.48
4:2E:174:ASP:OD1	4:2E:175:VAL:N	2.47	0.48
6:2G:80:PHE:O	6:2G:82:LEU:N	2.46	0.48
21:2Z:16:SER:HA	63:2Z:304:HOH:O	2.12	0.48
32:2a:903:G:OP1	63:2a:3220:HOH:O	2.20	0.48
32:2a:996:A:H2'	32:2a:997:U:C6	2.49	0.48
40:2i:33:PHE:HE1	40:2i:47:LEU:HD21	1.78	0.48
1:1A:1039:G:H1	1:1A:1116:C:H42	1.61	0.48
5:1F:12:LEU:HD13	5:1F:124:LEU:HD11	1.96	0.48
26:14:16:CYS:HA	26:14:33:VAL:HG23	1.95	0.48
32:1a:1124:G:N2	32:1a:1125:U:O4	2.39	0.48
35:1d:173:TRP:HB3	35:1d:187:ARG:HE	1.77	0.48
1:2A:1342:A:OP2	63:2A:3808:HOH:O	2.20	0.48
1:2A:2307:G:H4'	1:2A:2308:G:O5'	2.14	0.48
1:2A:2537:U:H2'	1:2A:2538:C:C6	2.48	0.48
1:2A:2789:C:N3	1:2A:2894:G:N1	2.61	0.48
21:2Z:121:HIS:HB2	21:2Z:171:ILE:HG22	1.96	0.48
22:20:53:MET:HA	22:20:58:THR:O	2.14	0.48
32:2a:952:U:H4'	32:2a:964:A:N1	2.28	0.48
32:2a:1005:A:OP1	32:2a:1006:C:N4	2.46	0.48
32:2a:1148:U:H2'	32:2a:1149:C:O4'	2.14	0.48
38:2g:133:GLY:HA2	38:2g:136:LYS:HB2	1.95	0.48
1:1A:62:C:OP1	63:1A:4172:HOH:O	2.19	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:918:A:H5"	2:1B:98:G:O2'	2.14	0.48
1:1A:1781:C:H41	29:17:1:MET:HE1	1.78	0.48
1:1A:2147:G:H2'	1:1A:2148:G:C4'	2.42	0.48
5:1F:116:ASP:OD1	5:1F:119:ARG:NH2	2.47	0.48
5:1F:116:ASP:OD2	5:1F:117:ARG:NH1	2.45	0.48
6:1G:55:LYS:O	6:1G:59:GLU:HG3	2.13	0.48
24:12:55:ARG:NH1	63:12:101:HOH:O	2.32	0.48
32:1a:254:G:H21	48:1q:16:GLN:NE2	2.12	0.48
32:1a:441:A:H8	32:1a:441:A:OP2	1.97	0.48
32:1a:840:C:H4'	32:1a:841:U:OP2	2.14	0.48
32:1a:881:G:P	43:1l:12:ARG:HH22	2.36	0.48
32:1a:1014:A:H4'	50:1s:14:HIS:NE2	2.28	0.48
33:1b:134:GLU:HG3	33:1b:137:ARG:HH21	1.77	0.48
40:1i:3:GLN:NE2	40:1i:20:ARG:HH21	2.12	0.48
1:2A:172:C:H2'	1:2A:173:G:C8	2.48	0.48
1:2A:271(E):U:H2'	1:2A:271(F):C:C6	2.48	0.48
1:2A:994:C:O2'	1:2A:996:A:OP1	2.20	0.48
1:2A:2531:A:H61	1:2A:2662:A:H61	1.62	0.48
7:2H:98:LEU:HD12	7:2H:103:LEU:HB2	1.96	0.48
15:2T:102:ILE:HG22	15:2T:105:LEU:HD12	1.96	0.48
23:21:16:ASN:O	63:21:201:HOH:O	2.20	0.48
32:2a:715:A:H2'	32:2a:716:A:C8	2.48	0.48
33:2b:187:LEU:HD23	33:2b:188:ALA:H	1.79	0.48
1:1A:586:A:N1	1:1A:809:G:O2'	2.42	0.48
1:1A:1040:C:H2'	1:1A:1041:C:O4'	2.14	0.48
1:1A:1399:C:OP1	19:1X:25:LYS:NZ	2.46	0.48
3:1D:8:PRO:HB3	3:1D:14:ARG:HG3	1.95	0.48
4:1E:143:ASN:HD22	4:1E:147:PRO:HD3	1.79	0.48
5:1F:132:VAL:HG22	5:1F:163:VAL:HG22	1.96	0.48
9:1N:42:TRP:CH2	9:1N:44:PRO:HB3	2.49	0.48
13:1R:53:HIS:ND1	13:1R:94:TYR:OH	2.36	0.48
20:1Y:9:LYS:HA	20:1Y:10:GLY:HA2	1.59	0.48
32:1a:607:A:H2'	32:1a:608:A:H8	1.79	0.48
33:1b:84:GLU:HB3	33:1b:219:VAL:HG21	1.95	0.48
33:1b:160:ASP:OD1	33:1b:160:ASP:N	2.46	0.48
35:1d:43:HIS:HB3	35:1d:46:LYS:HD2	1.96	0.48
38:1g:31:MET:HG3	38:1g:39:ALA:HB2	1.96	0.48
1:2A:1030:G:OP2	12:2Q:128:LYS:NZ	2.47	0.48
1:2A:1226:A:OP1	16:2U:16:LYS:NZ	2.39	0.48
1:2A:1464:C:H2'	1:2A:1465:G:C8	2.48	0.48
1:2A:2438:U:O2'	1:2A:2440:C:OP1	2.31	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2B:27:C:H5”	14:2S:54:LEU:HD11	1.96	0.48
10:2O:88:ASN:HB3	10:2O:94:ARG:HD3	1.96	0.48
10:2O:119:PRO:HG3	63:2O:314:HOH:O	2.14	0.48
17:2V:40:LEU:HD12	17:2V:46:VAL:HG11	1.95	0.48
26:24:20:ASN:HD21	26:24:38:LYS:HG3	1.77	0.48
32:2a:129(A):G:C6	32:2a:189(E):U:H4’	2.49	0.48
32:2a:546:G:OP1	35:2d:73:ARG:HG2	2.14	0.48
32:2a:1362:C:H2’	32:2a:1363:C:H5”	1.96	0.48
41:2j:63:PHE:HZ	45:2n:49:HIS:CE1	2.32	0.48
41:2j:78:ASN:O	41:2j:80:LYS:N	2.47	0.48
47:2p:5:ARG:HH21	47:2p:24:ALA:HA	1.78	0.48
49:2r:38:GLU:HA	49:2r:41:LYS:HE3	1.95	0.48
1:1A:528:A:OP2	9:1N:114:ARG:NH1	2.45	0.48
1:1A:1980:G:N7	63:1A:4344:HOH:O	2.35	0.48
1:1A:2331:G:O2’	1:1A:2336:A:N1	2.41	0.48
3:1D:148:GLU:OE1	3:1D:151:LYS:NZ	2.39	0.48
8:1I:104:GLN:HB2	8:1I:105:HIS:HD2	1.79	0.48
17:1V:52:VAL:HG23	17:1V:55:ALA:HB3	1.94	0.48
22:10:46:LYS:HB2	22:10:78:TYR:CD1	2.48	0.48
32:1a:1469:G:H2’	32:1a:1470:G:C8	2.48	0.48
34:1c:8:ILE:HG13	34:1c:184:TYR:HB3	1.95	0.48
37:1f:8:ILE:HD12	37:1f:63:TYR:HE2	1.79	0.48
1:2A:143:G:H4’	19:2X:35:THR:HG21	1.95	0.48
1:2A:1371:G:O6	63:2A:3866:HOH:O	2.18	0.48
1:2A:2086:U:H2’	1:2A:2087:G:C8	2.49	0.48
7:2H:127:GLU:C	7:2H:129:THR:H	2.22	0.48
14:2S:65:VAL:O	14:2S:69:VAL:HG23	2.13	0.48
17:2V:91:TYR:HE1	17:2V:93:GLU:HG3	1.78	0.48
17:2V:99:ILE:O	17:2V:101:GLY:N	2.47	0.48
20:2Y:102:CYS:SG	20:2Y:103:GLY:N	2.86	0.48
32:2a:179:A:H2’	32:2a:180:U:H6	1.79	0.48
32:2a:1371:G:OP1	40:2i:12:GLU:HB2	2.14	0.48
33:2b:80:ILE:HD13	33:2b:211:ILE:HG22	1.96	0.48
34:2c:35:GLU:HA	34:2c:38:ARG:HD2	1.96	0.48
34:2c:71:ALA:HA	34:2c:106:VAL:HB	1.96	0.48
36:2e:57:LYS:HG2	36:2e:61:TYR:CE2	2.48	0.48
47:2p:53:VAL:HG13	47:2p:79:VAL:HG22	1.95	0.48
48:2q:57:VAL:HG12	48:2q:76:LEU:HA	1.94	0.48
1:1A:2096:U:H2’	1:1A:2097:C:C6	2.49	0.48
1:1A:2319:G:H1	14:1S:3:ARG:HA	1.78	0.48
17:1V:74:LYS:HB2	17:1V:83:ARG:HB2	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:262:A:H2'	32:1a:263:A:H8	1.76	0.48
32:1a:441:A:H3'	32:1a:442:C:C6	2.48	0.48
32:1a:1151:A:N3	41:1j:39:PRO:HG3	2.29	0.48
32:1a:1189:C:OP1	41:1j:51:ARG:NH2	2.44	0.48
32:1a:1237:C:H3'	32:1a:1336:C:H41	1.79	0.48
1:2A:185:U:H4'	1:2A:218:A:H4'	1.96	0.48
1:2A:652(C):G:N1	1:2A:652(V):C:O2	2.36	0.48
1:2A:2103:C:O2	1:2A:2187:G:N1	2.47	0.48
1:2A:2131:G:H5'	1:2A:2133:G:O4'	2.14	0.48
8:2I:50:ARG:O	8:2I:54:GLN:HG2	2.14	0.48
23:21:75:GLU:HA	23:21:78:LYS:NZ	2.29	0.48
32:2a:137:C:H2'	32:2a:138:G:C8	2.49	0.48
32:2a:614:A:H2'	32:2a:615:C:C6	2.49	0.48
41:2j:11:PHE:HE1	41:2j:67:THR:HG22	1.78	0.48
1:1A:251:A:C5	1:1A:252:G:H1'	2.49	0.48
7:1H:13:LYS:HA	7:1H:14:GLY:HA2	1.57	0.48
13:1R:24:GLN:HE21	13:1R:44:LEU:HG	1.77	0.48
18:1W:79:GLY:CA	18:1W:100:THR:HG22	2.44	0.48
32:1a:624:C:H2'	32:1a:625:G:C8	2.49	0.48
32:1a:1228:C:P	44:1m:108:ARG:HH22	2.37	0.48
1:2A:521:G:H2'	1:2A:522:G:H8	1.79	0.48
1:2A:1786:A:H1'	1:2A:1938:A:N6	2.29	0.48
1:2A:2134:A:C5	1:2A:2157:G:H5'	2.49	0.48
32:2a:190:U:C2	32:2a:191:G:C8	3.02	0.48
1:1A:388:G:O2'	1:1A:389:G:N7	2.45	0.47
2:1B:29:A:H2'	2:1B:30:C:O4'	2.14	0.47
4:1E:3:GLY:HA3	4:1E:81:ILE:HD12	1.96	0.47
26:14:57:GLU:HB2	26:14:58:ARG:HA	1.94	0.47
30:18:23:VAL:HG11	30:18:47:LYS:HD3	1.96	0.47
32:1a:189(B):C:H2'	32:1a:189(C):C:H6	1.79	0.47
32:1a:982:U:H4'	32:1a:983:A:O5'	2.14	0.47
33:1b:47:THR:HA	33:1b:202:PRO:HG2	1.95	0.47
41:1j:27:ALA:HA	41:1j:30:SER:OG	2.14	0.47
47:1p:19:ILE:HG22	47:1p:37:GLY:O	2.13	0.47
1:2A:495:G:N3	18:2W:61:ASN:ND2	2.55	0.47
1:2A:1439:A:OP1	63:2A:3878:HOH:O	2.20	0.47
1:2A:2037:G:H2'	1:2A:2038:G:C8	2.49	0.47
2:2B:40:U:O2'	2:2B:43:C:OP2	2.25	0.47
4:2E:119:ARG:HG2	4:2E:120:TRP:CD1	2.49	0.47
20:2Y:83:THR:HG21	20:2Y:99:CYS:HB2	1.96	0.47
26:24:57:GLU:HA	26:24:58:ARG:HA	1.52	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:600:C:H2'	32:2a:601:C:C6	2.49	0.47
32:2a:1151:A:O2'	32:2a:1152:A:H8	1.97	0.47
40:2i:24:GLY:HA2	40:2i:59:PHE:O	2.14	0.47
53:2y:16:ILE:HA	53:2y:19:HIS:HB3	1.96	0.47
1:1A:1210:A:H5"	1:1A:1212:G:O4'	2.13	0.47
1:1A:2155:G:H3'	1:1A:2156:G:C8	2.48	0.47
2:1B:88:C:H2'	2:1B:89:G:O4'	2.15	0.47
16:1U:33:ARG:NH1	63:1U:308:HOH:O	2.46	0.47
19:1X:60:ARG:HH21	29:17:47:ARG:HH21	1.60	0.47
24:12:65:ASN:OD1	24:12:69:ARG:NH1	2.47	0.47
32:1a:460:G:H1'	32:1a:472:A:H61	1.79	0.47
32:1a:624:C:H2'	32:1a:625:G:H8	1.79	0.47
32:1a:1048:G:OP1	45:1n:3:ARG:HB3	2.14	0.47
33:1b:115:LEU:O	33:1b:119:GLU:HG2	2.14	0.47
40:1i:8:GLY:HA2	40:1i:79:LEU:HD23	1.96	0.47
1:2A:521:G:H2'	1:2A:522:G:C8	2.49	0.47
1:2A:886:C:H2'	1:2A:887:A:O4'	2.14	0.47
1:2A:1071:G:H1'	1:2A:1089:G:N7	2.29	0.47
1:2A:2074:U:H2'	1:2A:2075:U:C6	2.49	0.47
1:2A:2144:U:OP1	1:2A:2145:C:N4	2.47	0.47
1:2A:2327:A:H2'	1:2A:2328:A:C8	2.48	0.47
1:2A:2564:A:C2	1:2A:2647:U:H4'	2.48	0.47
1:2A:2659:G:O2'	1:2A:2661:G:N7	2.42	0.47
4:2E:52:LEU:O	4:2E:76:ARG:N	2.39	0.47
4:2E:176:ILE:HB	4:2E:181:LEU:HB2	1.95	0.47
7:2H:18:GLU:HG2	7:2H:19:VAL:N	2.29	0.47
23:21:6:GLU:HG3	23:21:61:ARG:O	2.15	0.47
32:2a:539:A:C6	32:2a:540:G:C6	3.02	0.47
40:2i:26:VAL:HA	40:2i:61:ALA:O	2.14	0.47
46:2o:18:PHE:O	46:2o:20:GLY:N	2.47	0.47
1:1A:969:U:H2'	1:1A:970:C:C6	2.49	0.47
1:1A:1268:A:H2'	1:1A:1269:A:O4'	2.14	0.47
1:1A:2377:A:H2'	1:1A:2378:A:C8	2.49	0.47
1:1A:2808:U:H5"	1:1A:2891:G:O6	2.14	0.47
4:1E:7:VAL:HG11	15:1T:1:MET:HE1	1.95	0.47
5:1F:33:LEU:HD21	5:1F:112:MET:HB2	1.95	0.47
9:1N:23:LEU:HA	9:1N:60:ILE:HD11	1.96	0.47
26:14:24:THR:OG1	26:14:25:TYR:N	2.42	0.47
32:1a:507:C:OP2	32:1a:508:C:O2'	2.27	0.47
32:1a:933:G:O6	38:1g:3:ARG:NH2	2.46	0.47
32:1a:1241:G:OP1	38:1g:35:LYS:NZ	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:1f:98:LEU:HD23	49:1r:30:ASP:HA	1.95	0.47
46:1o:36:ILE:HG23	46:1o:56:LEU:HD11	1.96	0.47
1:2A:2227:A:O2'	63:2A:3880:HOH:O	2.20	0.47
1:2A:2379:G:O2'	14:2S:17:ARG:NH1	2.36	0.47
1:2A:2745:C:H2'	1:2A:2746:U:O4'	2.14	0.47
12:2Q:6:ARG:HB2	21:2Z:195:GLU:O	2.14	0.47
13:2R:56:LYS:NZ	13:2R:87:TYR:O	2.46	0.47
13:2R:97:VAL:HG22	13:2R:114:VAL:HG13	1.96	0.47
19:2X:12:VAL:HG22	19:2X:29:TRP:CE2	2.50	0.47
23:21:53:VAL:HG22	23:21:74:VAL:HG13	1.95	0.47
32:2a:718:G:C8	42:2k:116:HIS:HB3	2.48	0.47
32:2a:792:A:O2'	32:2a:794:A:N7	2.41	0.47
32:2a:954:G:O6	44:2m:104:ARG:NH1	2.47	0.47
32:2a:965:A:N7	53:2y:8:LYS:NZ	2.55	0.47
32:2a:1503:A:OP1	32:2a:1531:A:O2'	2.21	0.47
33:2b:84:GLU:OE1	33:2b:87:ARG:NH2	2.47	0.47
34:2c:81:GLY:O	34:2c:85:ARG:HB2	2.13	0.47
1:1A:55:G:O2'	1:1A:127:A:N1	2.43	0.47
1:1A:1301:A:C8	1:1A:1303:G:C8	3.02	0.47
1:1A:1430:C:H2'	1:1A:1431:U:C6	2.50	0.47
1:1A:1923:U:H2'	1:1A:1924:C:C6	2.50	0.47
1:1A:2267:A:OP1	63:1A:4176:HOH:O	2.20	0.47
1:1A:2291:U:H2'	1:1A:2292:C:C6	2.50	0.47
5:1F:116:ASP:OD2	11:1P:1:MET:HB3	2.14	0.47
6:1G:43:LEU:HD11	6:1G:153:ARG:HD2	1.96	0.47
12:1Q:63:LYS:HD2	21:1Z:175:VAL:HG21	1.96	0.47
15:1T:37:GLY:HA2	15:1T:38:ASN:HA	1.49	0.47
27:15:16:ARG:HG3	27:15:17:ASP:N	2.29	0.47
28:16:2:ALA:N	63:16:602:HOH:O	2.47	0.47
32:1a:227:G:H2'	32:1a:228:A:O4'	2.13	0.47
32:1a:620:C:H2'	32:1a:621:A:O4'	2.14	0.47
32:1a:1308:U:H2'	32:1a:1309:G:H8	1.80	0.47
40:1i:4:TYR:HB2	40:1i:19:LEU:HB2	1.96	0.47
1:2A:2115:G:H4'	1:2A:2166:G:O2'	2.15	0.47
4:2E:119:ARG:HG2	4:2E:120:TRP:NE1	2.28	0.47
27:25:20:ARG:HG2	27:25:23:HIS:CE1	2.49	0.47
32:2a:309:G:H2'	32:2a:310:G:H8	1.79	0.47
32:2a:576:G:O6	32:2a:880:C:O2'	2.24	0.47
32:2a:666:G:H5'	32:2a:726:C:H1'	1.97	0.47
32:2a:1263:C:H2'	32:2a:1264:C:C6	2.50	0.47
32:2a:1320:C:H2'	32:2a:1321:C:O4'	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1347:G:N2	32:2a:1373:G:H2'	2.30	0.47
33:2b:80:ILE:HD11	33:2b:212:GLN:HA	1.96	0.47
33:2b:211:ILE:O	33:2b:215:LEU:HB2	2.15	0.47
34:2c:123:GLN:O	34:2c:128:PHE:HB2	2.13	0.47
40:2i:34:ASN:N	40:2i:34:ASN:OD1	2.48	0.47
44:2m:91:ARG:NE	44:2m:97:PRO:O	2.31	0.47
47:2p:43:LYS:HG2	47:2p:48:TRP:CD2	2.49	0.47
6:1G:16:ARG:HH21	6:1G:31:VAL:HG21	1.79	0.47
10:1O:64:ARG:HB2	10:1O:79:PHE:CG	2.50	0.47
21:1Z:146:ILE:HA	21:1Z:147:GLY:HA2	1.61	0.47
32:1a:731:G:H5'	32:1a:766:A:H4'	1.95	0.47
32:1a:1202:G:O2'	45:1n:29:ARG:HG3	2.14	0.47
45:1n:26:ARG:HD3	45:1n:43:CYS:HB3	1.97	0.47
47:1p:74:LEU:HD23	47:1p:79:VAL:HG11	1.96	0.47
1:2A:2316:C:O2'	6:2G:128:ARG:NH1	2.48	0.47
1:2A:2355:C:O2	22:20:39:ARG:NH2	2.46	0.47
1:2A:2645:G:N2	1:2A:2767:C:OP2	2.47	0.47
1:2A:2698:U:H2'	1:2A:2699:C:C6	2.49	0.47
4:2E:48:GLN:NE2	4:2E:78:LEU:HD13	2.30	0.47
5:2F:129:PHE:CD2	5:2F:163:VAL:HG21	2.49	0.47
6:2G:179:PRO:HG3	26:24:43:TYR:CZ	2.49	0.47
8:2I:86:THR:O	8:2I:122:GLU:HG2	2.14	0.47
16:2U:11:ARG:O	16:2U:15:LYS:HG3	2.14	0.47
19:2X:60:ARG:HH21	29:27:47:ARG:NH2	2.13	0.47
21:2Z:58:VAL:HA	21:2Z:68:PRO:HA	1.97	0.47
21:2Z:104:PHE:HB3	21:2Z:141:VAL:HG21	1.96	0.47
27:25:16:ARG:HG2	27:25:16:ARG:HH11	1.78	0.47
33:2b:10:LEU:HD23	33:2b:10:LEU:H	1.79	0.47
34:2c:150:LYS:HG3	34:2c:169:ALA:HB2	1.95	0.47
1:1A:264:C:O2'	1:1A:265:A:H2'	2.15	0.47
1:1A:493:G:H2'	1:1A:494:G:O4'	2.14	0.47
1:1A:1568:G:H4'	3:1D:59:LYS:HG2	1.96	0.47
1:1A:1693:U:H1'	3:1D:14:ARG:NH1	2.30	0.47
1:1A:2336:A:H61	22:10:43:THR:HG22	1.79	0.47
1:1A:2889:C:H2'	1:1A:2891:G:O4'	2.15	0.47
2:1B:7:G:H5"	2:1B:7:G:H8	1.80	0.47
6:1G:143:GLU:HA	26:14:28:LYS:HD2	1.97	0.47
20:1Y:20:TYR:HB3	20:1Y:23:ARG:HD3	1.96	0.47
21:1Z:152:ALA:HB1	21:1Z:163:LEU:HD21	1.96	0.47
26:14:58:ARG:HG2	50:1s:67:VAL:H	1.79	0.47
32:1a:38:G:N2	32:1a:397:A:H5'	2.27	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:235:C:H2'	32:1a:236:G:H8	1.78	0.47
1:2A:922:U:H2'	1:2A:923:C:C6	2.49	0.47
1:2A:1153:C:H2'	1:2A:1154:G:O4'	2.15	0.47
1:2A:1796:U:H2'	1:2A:1797:C:H6	1.79	0.47
1:2A:2188:C:H2'	1:2A:2189:U:O4'	2.14	0.47
7:2H:101:ARG:NH2	7:2H:117:PRO:O	2.47	0.47
20:2Y:73:ARG:HG2	20:2Y:73:ARG:HH11	1.78	0.47
32:2a:457:C:H2'	32:2a:458:C:H6	1.79	0.47
32:2a:765:G:H5"	32:2a:766:A:OP1	2.14	0.47
32:2a:1038:C:H2'	32:2a:1039:C:C6	2.50	0.47
32:2a:1263:C:H2'	32:2a:1264:C:H6	1.79	0.47
39:2h:63:LEU:HD23	39:2h:65:TYR:OH	2.13	0.47
46:2o:26:GLU:HG3	46:2o:81:LEU:HD13	1.95	0.47
1:1A:324:A:H2'	1:1A:325:G:O4'	2.15	0.47
1:1A:424:G:O6	60:1A:4019:MPD:H51	2.14	0.47
1:1A:1936:A:OP1	1:1A:1937:A:H5'	2.15	0.47
1:1A:2492:U:H2'	1:1A:2493:U:C6	2.50	0.47
59:1A:4018:ARG:HA	59:1A:4018:ARG:HD2	1.71	0.47
3:1D:25:THR:HG21	3:1D:113:VAL:HG21	1.97	0.47
6:1G:16:ARG:HB2	6:1G:17:PRO:HD3	1.96	0.47
21:1Z:125:LEU:HB3	21:1Z:165:VAL:HG13	1.95	0.47
32:1a:1286:A:H2'	32:1a:1287:A:H4'	1.97	0.47
32:1a:1308:U:H2'	32:1a:1309:G:C8	2.49	0.47
34:1c:113:ALA:HB2	34:1c:202:ILE:HG13	1.97	0.47
36:1e:71:LEU:HD11	36:1e:113:ALA:O	2.14	0.47
37:1f:50:TYR:OH	49:1r:74:ARG:O	2.31	0.47
39:1h:51:VAL:HG12	39:1h:52:ASP:H	1.80	0.47
46:1o:82:ILE:HG13	46:1o:83:GLU:N	2.29	0.47
50:1s:12:ASP:OD2	50:1s:35:SER:HB3	2.14	0.47
53:1y:40:ILE:HB	53:1y:51:ASP:HB2	1.95	0.47
1:2A:213:A:H5'	1:2A:214:G:OP2	2.15	0.47
1:2A:359:A:H2'	1:2A:360:G:O4'	2.15	0.47
1:2A:729:G:C6	3:2D:208:LYS:HB2	2.49	0.47
1:2A:859:G:O2'	1:2A:916:G:O6	2.23	0.47
1:2A:1497:U:H5"	1:2A:1498:C:H5	1.79	0.47
1:2A:1504:C:H2'	1:2A:1505:C:C6	2.49	0.47
1:2A:2543:G:H2'	1:2A:2544:G:C8	2.49	0.47
6:2G:11:TYR:HA	6:2G:15:VAL:HB	1.96	0.47
6:2G:161:THR:HG22	6:2G:163:ALA:H	1.78	0.47
11:2P:35:HIS:O	63:2P:302:HOH:O	2.20	0.47
32:2a:1340:A:OP1	53:2y:57:PRO:HB3	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:2d:18:LYS:HD2	35:2d:33:MET:HE3	1.97	0.47
1:1A:110:G:O6	63:1A:4162:HOH:O	2.18	0.47
1:1A:1113:U:H2'	1:1A:1114:G:C8	2.50	0.47
1:1A:2165:G:H2'	1:1A:2166:G:C8	2.49	0.47
42:1k:109:VAL:HG12	49:1r:86:VAL:HG22	1.95	0.47
1:2A:320:A:H4'	1:2A:322:A:N7	2.28	0.47
1:2A:1106:G:OP2	1:2A:1106:G:H8	1.97	0.47
1:2A:1593:G:H2'	1:2A:1594:G:C8	2.50	0.47
1:2A:1614:A:C2	18:2W:93:ALA:HB2	2.50	0.47
8:2I:130:TYR:CE2	8:2I:132:PRO:HB3	2.49	0.47
21:2Z:26:GLY:HA3	21:2Z:86:VAL:HG23	1.97	0.47
32:2a:143:A:H2	32:2a:220:G:H1	1.61	0.47
32:2a:1027:C:H5"	32:2a:1028:C:C6	2.50	0.47
32:2a:1490:C:H2'	32:2a:1491:G:C8	2.50	0.47
41:2j:21:GLN:HG3	41:2j:25:GLU:HG2	1.96	0.47
50:2s:32:LYS:HE2	50:2s:57:HIS:NE2	2.29	0.47
50:2s:58:VAL:O	50:2s:60:VAL:HG23	2.15	0.47
1:1A:2137:C:H2'	1:1A:2138:C:O4'	2.14	0.47
6:1G:43:LEU:O	6:1G:45:GLU:N	2.48	0.47
8:1I:77:LEU:HD22	8:1I:101:LEU:HG	1.96	0.47
15:1T:51:ARG:NH1	63:1T:303:HOH:O	2.48	0.47
32:1a:1102:A:O3'	33:1b:96:ARG:NH2	2.48	0.47
1:2A:1996:C:H4'	1:2A:1997:G:OP1	2.14	0.47
1:2A:2320:A:N3	1:2A:2320:A:H2'	2.30	0.47
1:2A:2556:C:H2'	1:2A:2557:G:O4'	2.14	0.47
5:2F:21:ALA:CB	5:2F:22:ALA:HA	2.43	0.47
10:2O:64:ARG:HB2	10:2O:79:PHE:CD2	2.50	0.47
10:2O:64:ARG:HB2	10:2O:79:PHE:CG	2.49	0.47
14:2S:23:ARG:NH1	14:2S:84:GLN:HG2	2.30	0.47
32:2a:9:G:H2'	32:2a:10:A:C8	2.49	0.47
32:2a:437:U:H5'	35:2d:155:LEU:HD11	1.95	0.47
32:2a:932:C:H2'	32:2a:933:G:C8	2.50	0.47
32:2a:1030(A):G:H2'	32:2a:1030(B):C:H5"	1.97	0.47
33:2b:97:TRP:NE1	33:2b:173:ALA:HB2	2.30	0.47
34:2c:114:PRO:O	34:2c:118:GLN:HB2	2.15	0.47
1:1A:226:G:H21	1:1A:228:A:H62	1.63	0.47
3:1D:146:GLU:HG2	3:1D:152:GLY:C	2.40	0.47
32:1a:865:A:H2'	32:1a:866:C:C6	2.49	0.47
32:1a:909:A:H2'	32:1a:910:C:O4'	2.15	0.47
32:1a:933:G:OP2	38:1g:3:ARG:HB2	2.14	0.47
32:1a:977:A:O2'	32:1a:981:U:N3	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1297:C:O2'	38:1g:114:ARG:NH1	2.42	0.47
35:1d:154:ASN:HA	35:1d:159:ARG:HE	1.79	0.47
41:1j:8:LEU:HB2	41:1j:70:ARG:HB2	1.97	0.47
43:1l:34:ARG:HD3	43:1l:105:TYR:CE2	2.50	0.47
1:2A:579:G:H2'	1:2A:580:C:C6	2.49	0.47
1:2A:1639:U:C2'	1:2A:1640:C:H5"	2.45	0.47
5:2F:17:ARG:HH12	5:2F:19:GLU:HG2	1.79	0.47
5:2F:155:LEU:HD11	5:2F:176:LEU:HD12	1.96	0.47
32:2a:1342:C:H2'	32:2a:1343:G:C8	2.50	0.47
32:2a:1387:G:H2'	32:2a:1388:C:C6	2.50	0.47
33:2b:27:LYS:HE3	33:2b:193:ASP:HB2	1.97	0.47
34:2c:63:ASN:HB2	34:2c:98:ASN:HB2	1.96	0.47
49:2r:66:LEU:O	49:2r:70:ILE:HG13	2.15	0.47
1:1A:173:G:H2'	1:1A:174:C:H6	1.77	0.46
1:1A:886:C:C3'	1:1A:887:A:H5"	2.44	0.46
1:1A:919:G:N2	1:1A:2269:A:OP2	2.47	0.46
1:1A:1176:G:H4'	1:1A:1177:A:OP1	2.15	0.46
63:1B:303:HOH:O	12:1Q:18:LYS:HB2	2.14	0.46
25:13:15:TYR:CE2	25:13:53:LEU:HD21	2.50	0.46
32:1a:79:G:N1	32:1a:90:U:N3	2.63	0.46
32:1a:382:A:H2'	32:1a:383:A:C8	2.50	0.46
32:1a:390:C:H2'	32:1a:391:G:C8	2.51	0.46
35:1d:173:TRP:C	35:1d:186:LEU:HB2	2.40	0.46
50:1s:11:VAL:HG11	50:1s:16:LEU:HB2	1.96	0.46
1:2A:974:G:N2	63:2A:3895:HOH:O	2.27	0.46
1:2A:1316:U:H2'	1:2A:1317:A:C8	2.50	0.46
1:2A:2262:U:H4'	1:2A:2328:A:C2	2.50	0.46
3:2D:101:GLU:OE2	3:2D:103:ARG:HD3	2.16	0.46
11:2P:96:THR:HG22	11:2P:126:VAL:HB	1.97	0.46
32:2a:31:G:O2'	32:2a:48:C:N4	2.48	0.46
32:2a:1012:U:H2'	32:2a:1013:G:C8	2.50	0.46
40:2i:43:ALA:C	40:2i:45:ALA:H	2.22	0.46
41:2j:5:ARG:N	41:2j:99:LYS:O	2.48	0.46
50:2s:3:ARG:HH11	50:2s:7:LYS:HB3	1.80	0.46
1:1A:118:A:C8	1:1A:119:A:C8	3.03	0.46
1:1A:222:A:H3'	1:1A:421:U:H5'	1.97	0.46
1:1A:1818:U:O4	3:1D:154:LYS:HE3	2.16	0.46
2:1B:24:G:N7	2:1B:56:G:H2'	2.30	0.46
6:1G:37:VAL:HG22	6:1G:94:LEU:HB2	1.95	0.46
6:1G:77:ILE:HG21	6:1G:80:PHE:CD2	2.50	0.46
32:1a:996:A:H2'	32:1a:997:U:C6	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1077:G:N2	32:1a:1080:A:OP2	2.43	0.46
32:1a:1248:A:N3	40:1i:70:LYS:HE3	2.30	0.46
35:1d:155:LEU:HB3	35:1d:158:ILE:HG12	1.97	0.46
38:1g:29:LYS:HD3	38:1g:29:LYS:HA	1.68	0.46
40:1i:3:GLN:HE21	40:1i:20:ARG:HH21	1.62	0.46
40:1i:24:GLY:O	40:1i:26:VAL:HG23	2.15	0.46
46:1o:8:LYS:HE3	46:1o:31:LEU:HD22	1.96	0.46
53:1y:2:THR:OG1	53:1y:3:MET:N	2.47	0.46
1:2A:251:A:C5	1:2A:252:G:H1'	2.50	0.46
1:2A:330:A:HO2'	1:2A:331:A:H8	1.56	0.46
1:2A:1105:U:H2'	1:2A:1106:G:C8	2.50	0.46
5:2F:155:LEU:HB3	5:2F:192:LEU:HD23	1.97	0.46
11:2P:138:LEU:HD23	11:2P:145:PRO:HB3	1.96	0.46
14:2S:105:ALA:O	14:2S:110:LEU:HB2	2.14	0.46
30:28:39:LYS:O	30:28:43:GLN:HG3	2.14	0.46
32:2a:1006:C:H2'	32:2a:1007:C:C6	2.51	0.46
32:2a:1030(C):G:H2'	32:2a:1030(D):A:C8	2.51	0.46
35:2d:18:LYS:NZ	35:2d:31:CYS:SG	2.73	0.46
44:2m:97:PRO:N	44:2m:110:ARG:HG2	2.29	0.46
50:2s:36:ARG:NH1	50:2s:75:ALA:HB3	2.26	0.46
1:1A:1140:C:O3'	9:1N:25:ARG:NH1	2.48	0.46
1:1A:1800:C:OP1	3:1D:260:ARG:NH2	2.48	0.46
1:1A:1826:G:H4'	3:1D:242:ARG:CZ	2.46	0.46
4:1E:1:MET:HB3	4:1E:83:ASP:O	2.16	0.46
5:1F:184:TYR:O	5:1F:188:ARG:HG3	2.16	0.46
7:1H:3:ARG:NH1	7:1H:4:ILE:H	2.12	0.46
24:12:12:GLU:HA	24:12:15:LYS:HE2	1.97	0.46
32:1a:73:G:H1	32:1a:96:U:H3	1.63	0.46
32:1a:131:C:H2'	32:1a:132:C:C6	2.50	0.46
32:1a:134:A:H1'	32:1a:325:A:C5	2.51	0.46
38:1g:80:VAL:HB	38:1g:85:TYR:CE2	2.50	0.46
48:1q:74:LEU:HD23	48:1q:75:ARG:HG2	1.97	0.46
1:2A:271(M):G:O2'	1:2A:271(N):U:O5'	2.26	0.46
1:2A:1503:U:H2'	1:2A:1504:C:C6	2.50	0.46
1:2A:1753:G:N1	1:2A:1756:G:OP2	2.47	0.46
1:2A:2849:U:H4'	1:2A:2868:A:C2	2.51	0.46
19:2X:46:ALA:HB1	24:22:33:MET:HE1	1.96	0.46
23:21:83:GLU:HA	23:21:84:GLY:HA2	1.65	0.46
32:2a:525:C:OP1	43:2l:91:LYS:HB2	2.15	0.46
32:2a:1047:G:H5"	45:2n:4:LYS:HE3	1.97	0.46
32:2a:1161:C:H2'	32:2a:1162:C:C6	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1401:G:O6	53:2y:83:ARG:NH2	2.48	0.46
47:2p:70:ALA:O	47:2p:74:LEU:HD13	2.15	0.46
1:1A:218:A:C2	1:1A:235:U:H4'	2.50	0.46
1:1A:2327:A:H2'	1:1A:2328:A:C8	2.51	0.46
3:1D:3:VAL:HG22	3:1D:17:THR:HB	1.97	0.46
3:1D:77:ALA:HB2	3:1D:97:TYR:CD1	2.50	0.46
5:1F:74:ARG:H	5:1F:74:ARG:HG3	1.37	0.46
8:1I:81:VAL:HG22	8:1I:145:VAL:O	2.14	0.46
19:1X:12:VAL:HG21	19:1X:27:THR:HG22	1.98	0.46
21:1Z:150:LEU:HD12	21:1Z:150:LEU:HA	1.85	0.46
25:13:3:ARG:HH11	25:13:60:GLU:CD	2.23	0.46
33:1b:61:LEU:HD23	33:1b:68:ILE:HD11	1.97	0.46
36:1e:69:VAL:HG21	36:1e:113:ALA:HB1	1.97	0.46
40:1i:64:THR:HG23	40:1i:66:ARG:NH2	2.29	0.46
1:2A:208:C:H2'	1:2A:209:C:C6	2.51	0.46
1:2A:858:U:O2	1:2A:2268:A:H2'	2.15	0.46
1:2A:1593:G:H2'	1:2A:1594:G:H8	1.80	0.46
3:2D:175:LEU:HD12	3:2D:185:VAL:HG21	1.97	0.46
5:2F:179:GLU:CD	5:2F:179:GLU:H	2.24	0.46
11:2P:121:LYS:O	11:2P:123:LEU:N	2.48	0.46
19:2X:5:TYR:HE1	24:22:30:ARG:HH11	1.63	0.46
32:2a:1491:G:O2'	32:2a:1492:A:OP1	2.29	0.46
33:2b:120:ALA:C	33:2b:122:PHE:H	2.23	0.46
1:1A:1386:C:H2'	1:1A:1387:C:C6	2.51	0.46
6:1G:16:ARG:NE	6:1G:31:VAL:HG21	2.30	0.46
6:1G:112:PRO:HG3	26:14:43:TYR:CE2	2.50	0.46
32:1a:346:G:H5"	60:1a:1867:MPD:H4	1.96	0.46
1:2A:1778:U:H2'	1:2A:1784:A:N6	2.31	0.46
1:2A:2051:A:H5'	1:2A:2578:G:O4'	2.16	0.46
8:2I:5:LEU:HD21	8:2I:12:LEU:HB3	1.98	0.46
14:2S:97:ARG:NH2	63:2S:201:HOH:O	2.24	0.46
16:2U:89:GLU:O	17:2V:11:GLN:NE2	2.49	0.46
32:2a:724:G:C2	32:2a:725:G:C8	3.04	0.46
32:2a:1123:A:C2	41:2j:39:PRO:HD2	2.51	0.46
35:2d:76:ARG:HD2	35:2d:207:TYR:CZ	2.51	0.46
37:2f:22:GLU:OE1	37:2f:84:ASN:HB2	2.16	0.46
44:2m:23:TYR:HE2	44:2m:70:LEU:HD22	1.80	0.46
1:1A:1518:U:H2'	1:1A:1519:G:O4'	2.16	0.46
1:1A:1588:C:H2'	1:1A:1589:C:C6	2.50	0.46
1:1A:2126:A:N1	1:1A:2162:G:O2'	2.46	0.46
1:1A:2443:C:OP1	5:1F:68:LYS:HD3	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:1N:62:VAL:HG13	9:1N:66:LYS:HB2	1.97	0.46
28:16:17:LYS:HA	28:16:17:LYS:HD3	1.80	0.46
32:1a:474:G:H2'	32:1a:475:G:H8	1.81	0.46
32:1a:503:C:H2'	32:1a:504:C:H6	1.80	0.46
33:1b:167:PRO:HG2	33:1b:188:ALA:HB2	1.98	0.46
34:1c:63:ASN:HA	34:1c:98:ASN:HB2	1.98	0.46
37:1f:70:ASP:OD1	37:1f:70:ASP:N	2.27	0.46
40:1i:64:THR:HG23	40:1i:66:ARG:HH21	1.80	0.46
44:1m:52:GLU:HG2	44:1m:55:ARG:NH2	2.30	0.46
1:2A:153:C:OP2	23:21:92:LYS:NZ	2.45	0.46
1:2A:1552:G:N7	63:2A:4040:HOH:O	2.36	0.46
1:2A:2155:G:H2'	1:2A:2156:G:O4'	2.15	0.46
2:2B:33:G:H5'	6:2G:2:PRO:CG	2.46	0.46
17:2V:25:LEU:N	17:2V:92:THR:OG1	2.46	0.46
32:2a:8:A:H5'	36:2e:101:ILE:HG22	1.97	0.46
32:2a:17:U:O2'	32:2a:1079:G:N3	2.42	0.46
32:2a:559:A:H5'	32:2a:559:A:N3	2.31	0.46
32:2a:1124:G:H4'	32:2a:1125:U:OP1	2.15	0.46
38:2g:114:ARG:HB2	38:2g:115:ARG:NH2	2.30	0.46
1:1A:77:C:OP1	24:12:59:ARG:HD3	2.15	0.46
1:1A:548:A:O2'	1:1A:549:G:OP1	2.25	0.46
1:1A:1453:U:O2'	1:1A:1455:G:N7	2.48	0.46
15:1T:112:ARG:HG3	15:1T:115:ARG:NH2	2.29	0.46
30:18:42:ARG:HD2	63:18:206:HOH:O	2.14	0.46
32:1a:189(C):C:H2'	32:1a:189(D):C:O4'	2.16	0.46
32:1a:238:G:OP1	48:1q:25:ARG:NH2	2.48	0.46
32:1a:266:G:H2'	32:1a:266:G:N3	2.30	0.46
32:1a:266:G:C5'	32:1a:268:C:H41	2.29	0.46
32:1a:273:A:H1'	48:1q:16:GLN:NE2	2.31	0.46
32:1a:1003:G:C2	32:1a:1004:A:N3	2.84	0.46
32:1a:1182:G:C4'	32:1a:1183:A:H5'	2.43	0.46
35:1d:119:GLN:HG3	35:1d:119:GLN:O	2.16	0.46
40:1i:125:TYR:CE1	40:1i:127:LYS:HA	2.50	0.46
44:1m:2:ALA:HB1	44:1m:6:GLY:HA2	1.97	0.46
1:2A:271(W):G:O6	63:2A:3883:HOH:O	2.20	0.46
1:2A:363(F):A:O4'	1:2A:364:C:H5	1.99	0.46
1:2A:706:A:H2'	1:2A:707:G:O4'	2.16	0.46
1:2A:839:U:H2'	1:2A:840:C:C6	2.51	0.46
1:2A:1668:A:O2'	1:2A:1674:G:N7	2.41	0.46
1:2A:2113:U:H3	1:2A:2168:G:H4'	1.80	0.46
1:2A:2360:A:OP2	63:2A:3881:HOH:O	2.20	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2683:C:O2	10:2O:70:LYS:NZ	2.49	0.46
1:2A:2693:A:H2'	1:2A:2694:G:C8	2.51	0.46
11:2P:121:LYS:HG2	11:2P:122:PRO:HD2	1.97	0.46
25:23:13:ILE:O	63:23:201:HOH:O	2.21	0.46
32:2a:558:G:OP1	63:2a:3221:HOH:O	2.21	0.46
32:2a:1073:U:H2'	32:2a:1074:G:C8	2.49	0.46
44:2m:27:LYS:HD2	44:2m:27:LYS:HA	1.65	0.46
47:2p:13:HIS:C	47:2p:15:PRO:HD3	2.40	0.46
53:2y:48:PHE:CD2	53:2y:70:MET:HB2	2.48	0.46
1:1A:265:A:N1	1:1A:427:U:O2'	2.47	0.46
1:1A:1063:G:H2'	1:1A:1063:G:N3	2.31	0.46
24:12:18:PRO:O	24:12:22:GLU:HG3	2.15	0.46
32:1a:1026:G:H5"	32:1a:1027:C:H5	1.80	0.46
1:2A:818:G:O6	63:2A:3876:HOH:O	2.20	0.46
1:2A:946:G:OP1	63:2A:3885:HOH:O	2.21	0.46
1:2A:1899:G:H2'	1:2A:1899:G:N3	2.31	0.46
1:2A:2001:A:H2'	1:2A:2002:G:C8	2.51	0.46
1:2A:2029:G:H2'	1:2A:2031:A:OP1	2.14	0.46
1:2A:2140:C:N3	1:2A:2151:G:O6	2.49	0.46
1:2A:2141:G:O6	1:2A:2150:U:C2	2.68	0.46
3:2D:102:LYS:C	3:2D:103:ARG:HG2	2.40	0.46
5:2F:129:PHE:HA	5:2F:142:TRP:NE1	2.30	0.46
16:2U:105:VAL:O	16:2U:108:GLU:HB3	2.16	0.46
32:2a:130:A:H1'	32:2a:263:A:O2'	2.15	0.46
32:2a:474:G:H2'	32:2a:475:G:H8	1.81	0.46
32:2a:573:A:N3	32:2a:883:C:O2'	2.47	0.46
32:2a:1138:G:H2'	32:2a:1140:C:H5"	1.97	0.46
32:2a:1327:C:H2'	32:2a:1328:C:H6	1.80	0.46
39:2h:60:ARG:HG2	39:2h:62:TYR:CZ	2.51	0.46
1:1A:1092:C:C2'	1:1A:1093:G:H5'	2.46	0.46
1:1A:1583:A:H5'	1:1A:1584:C:OP1	2.16	0.46
1:1A:2114:A:H2'	1:1A:2115:G:O4'	2.16	0.46
1:1A:2168:G:C2	1:1A:2171:A:C8	3.04	0.46
25:13:3:ARG:HD3	25:13:60:GLU:CD	2.41	0.46
33:1b:97:TRP:HH2	33:1b:176:GLU:CD	2.24	0.46
35:1d:63:LYS:HD2	35:1d:198:VAL:HG22	1.97	0.46
41:1j:31:GLY:HA2	41:1j:32:ALA:HA	1.51	0.46
48:1q:62:SER:HB3	48:1q:72:ARG:HH11	1.80	0.46
1:2A:185:U:H2'	1:2A:186:G:H8	1.81	0.46
1:2A:954:G:H5"	12:2Q:13:GLN:HB3	1.98	0.46
1:2A:1411:C:H2'	1:2A:1412:A:C8	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1449:A:N3	1:2A:1529:G:H1'	2.31	0.46
1:2A:2103:C:H2'	1:2A:2104:G:H8	1.81	0.46
1:2A:2584:U:O4	63:2A:3869:HOH:O	2.18	0.46
2:2B:95:C:H2'	2:2B:96:U:H6	1.79	0.46
5:2F:112:MET:O	5:2F:116:ASP:N	2.47	0.46
32:2a:790:A:H4'	53:2y:31:GLN:OE1	2.16	0.46
32:2a:1038:C:H2'	32:2a:1039:C:H6	1.81	0.46
32:2a:1400:5MC:C2	53:2y:63:ALA:HA	2.51	0.46
34:2c:142:MET:HG2	34:2c:149:ALA:HB3	1.97	0.46
36:2e:145:LYS:HA	39:2h:107:LEU:HD21	1.97	0.46
1:1A:171:G:H2'	1:1A:172:C:C6	2.51	0.46
1:1A:1988:C:OP2	63:1A:4180:HOH:O	2.21	0.46
1:1A:2166:G:N2	1:1A:2172:U:O4	2.49	0.46
1:1A:2187:G:H5'	1:1A:2188:C:OP2	2.17	0.46
1:1A:2687:U:H2'	1:1A:2688:U:O4'	2.14	0.46
1:1A:2698:U:H2'	1:1A:2699:C:C6	2.51	0.46
32:1a:90:U:H2'	32:1a:91:C:C6	2.51	0.46
33:1b:124:SER:HA	33:1b:125:PRO:HA	1.72	0.46
36:1e:110:LEU:HD13	36:1e:118:ILE:HG21	1.98	0.46
39:1h:20:TYR:HA	39:1h:65:TYR:CZ	2.51	0.46
1:2A:195:A:N7	63:2A:4047:HOH:O	2.36	0.46
1:2A:207:A:OP2	63:2A:3886:HOH:O	2.21	0.46
1:2A:372:G:H8	23:21:65:SER:O	1.99	0.46
1:2A:893:C:H2'	1:2A:894:C:H6	1.81	0.46
1:2A:2131:G:C6	1:2A:2158:A:N7	2.84	0.46
21:2Z:30:ASN:HA	21:2Z:89:PHE:HE1	1.81	0.46
23:21:59:THR:HG23	63:21:209:HOH:O	2.15	0.46
26:24:13:ARG:HH12	26:24:23:GLU:HB3	1.80	0.46
27:25:48:GLU:O	27:25:60:VAL:HG11	2.16	0.46
35:2d:162:LEU:HD22	35:2d:181:MET:HE3	1.98	0.46
39:2h:41:ARG:NH2	39:2h:123:GLU:OE1	2.49	0.46
46:2o:16:ALA:HB1	46:2o:21:ASP:HB3	1.98	0.46
49:2r:43:PHE:HA	49:2r:51:LEU:HD12	1.97	0.46
1:1A:965:C:OP2	63:1A:4181:HOH:O	2.21	0.45
1:1A:1510:G:H2'	1:1A:1511:C:C6	2.51	0.45
1:1A:2135:A:H4'	1:1A:2160:G:H5'	1.97	0.45
1:1A:2612:C:H3'	63:1A:6592:HOH:O	2.15	0.45
10:1O:17:ARG:HB2	10:1O:45:GLU:HG2	1.97	0.45
12:1Q:17:LEU:HD21	12:1Q:96:VAL:HG13	1.98	0.45
30:18:62:LEU:HB3	30:18:65:GLU:HG2	1.98	0.45
34:1c:110:ASN:HD22	34:1c:140:ARG:HB3	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:1h:104:ARG:HD3	39:1h:104:ARG:HA	1.63	0.45
53:1y:3:MET:HE3	53:1y:3:MET:HB3	1.79	0.45
1:2A:1297:C:OP1	1:2A:2710:C:H4'	2.16	0.45
1:2A:1506:C:C2'	1:2A:1507:A:H5'	2.46	0.45
27:25:16:ARG:HD2	27:25:20:ARG:NH1	2.31	0.45
39:2h:119:LEU:HB3	39:2h:123:GLU:HB2	1.98	0.45
1:1A:207:A:H2'	1:1A:208:C:O4'	2.14	0.45
1:1A:271(E):U:H2'	1:1A:271(F):C:C6	2.51	0.45
7:1H:41:MET:HE3	7:1H:41:MET:HB3	1.80	0.45
7:1H:98:LEU:HD13	7:1H:125:VAL:HG23	1.97	0.45
15:1T:13:ARG:NH2	15:1T:14:TYR:OH	2.49	0.45
20:1Y:107:ASP:OD1	20:1Y:107:ASP:N	2.49	0.45
22:10:10:THR:CG2	22:10:12:ASN:H	2.28	0.45
26:14:40:HIS:HB3	26:14:43:TYR:HD2	1.81	0.45
32:1a:922:G:H4'	36:1e:20:GLN:HA	1.98	0.45
32:1a:1002:G:H3'	32:1a:1003:G:C8	2.51	0.45
33:1b:102:LEU:HB3	33:1b:180:LEU:HD12	1.98	0.45
36:1e:69:VAL:O	36:1e:71:LEU:N	2.50	0.45
1:2A:241:A:H5"	63:2A:5758:HOH:O	2.17	0.45
1:2A:608:A:H2'	1:2A:609:A:C8	2.51	0.45
1:2A:796:C:H2'	1:2A:797:C:C6	2.51	0.45
1:2A:2400:G:H2'	1:2A:2401:U:H6	1.79	0.45
1:2A:2540:C:H2'	1:2A:2541:A:O4'	2.17	0.45
22:20:51:VAL:HG22	22:20:81:VAL:HG23	1.97	0.45
32:2a:111:G:OP2	63:2a:3219:HOH:O	2.20	0.45
32:2a:279:A:N6	48:2q:98:LEU:O	2.49	0.45
32:2a:620:C:C2	35:2d:135:LEU:HG	2.52	0.45
32:2a:1226:C:H4'	50:2s:80:TYR:OH	2.16	0.45
32:2a:1387:G:H2'	32:2a:1388:C:H6	1.81	0.45
33:2b:204:ASN:OD1	33:2b:210:SER:OG	2.31	0.45
37:2f:82:ARG:HB2	37:2f:85:VAL:HG23	1.99	0.45
40:2i:28:VAL:N	40:2i:31:GLN:O	2.45	0.45
42:2k:84:VAL:HG21	42:2k:95:ILE:HD11	1.99	0.45
51:2t:54:LYS:HA	51:2t:57:ARG:CZ	2.46	0.45
1:1A:1141:U:OP1	9:1N:25:ARG:NH1	2.49	0.45
1:1A:2171:A:H1'	1:1A:2172:U:C6	2.50	0.45
1:1A:2173:A:OP2	1:1A:2174:C:N4	2.48	0.45
1:1A:2331:G:O2'	22:10:43:THR:HG22	2.16	0.45
1:1A:2441:C:OP2	1:1A:2586:C:O2'	2.29	0.45
4:1E:73:GLU:H	4:1E:73:GLU:CD	2.24	0.45
6:1G:131:TYR:HB3	6:1G:159:VAL:CG1	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:1H:33:LEU:HD21	7:1H:136:ILE:HG13	1.99	0.45
32:1a:600:C:OP1	39:1h:97:VAL:HG12	2.16	0.45
32:1a:1227:A:OP2	44:1m:111:LYS:NZ	2.49	0.45
34:1c:164:ARG:HE	34:1c:164:ARG:HB3	1.56	0.45
35:1d:101:LEU:HD23	35:1d:140:VAL:HG22	1.99	0.45
44:1m:45:VAL:C	44:1m:47:ASP:H	2.24	0.45
50:1s:22:LEU:HD22	50:1s:28:LYS:HA	1.99	0.45
53:1y:23:ARG:NH1	53:1y:26:LYS:HD2	2.31	0.45
1:2A:1203:G:C6	1:2A:1204:A:N6	2.85	0.45
1:2A:1783:A:H5'	1:2A:2608:G:H4'	1.99	0.45
1:2A:2472:G:N1	1:2A:2477:C:OP1	2.44	0.45
1:2A:2633:G:H5"	1:2A:2812:G:H5'	1.98	0.45
17:2V:39:LEU:HD12	17:2V:47:VAL:HG22	1.99	0.45
17:2V:76:LYS:HB2	17:2V:81:TYR:HB3	1.98	0.45
32:2a:402:G:N7	63:2a:3242:HOH:O	2.36	0.45
32:2a:596:C:H2'	32:2a:597:G:H8	1.81	0.45
32:2a:687:A:N3	32:2a:688:G:H1'	2.30	0.45
32:2a:1089:G:C6	32:2a:1090:U:C4	3.04	0.45
32:2a:1376:U:H2'	32:2a:1377:A:C8	2.51	0.45
34:2c:20:SER:HB2	34:2c:40:ARG:NH2	2.31	0.45
36:2e:72:GLN:O	36:2e:75:THR:HG22	2.16	0.45
41:2j:10:GLY:N	41:2j:16:LEU:HD11	2.26	0.45
1:1A:2038:G:H2'	1:1A:2039:C:O4'	2.17	0.45
1:1A:2574:G:H2'	1:1A:2575:C:C6	2.52	0.45
6:1G:131:TYR:HB3	6:1G:159:VAL:HG13	1.98	0.45
15:1T:120:ARG:HA	15:1T:123:GLN:HB2	1.99	0.45
18:1W:18:ARG:HG3	18:1W:76:VAL:HB	1.98	0.45
29:17:5:TRP:NE1	29:17:7:PRO:HG3	2.32	0.45
32:1a:509:A:N3	32:1a:543:C:O2'	2.43	0.45
32:1a:545:C:OP2	35:1d:65:ARG:NH2	2.50	0.45
32:1a:953:G:N7	44:1m:104:ARG:NH2	2.65	0.45
32:1a:1457:G:H2'	32:1a:1458:G:C8	2.52	0.45
33:1b:16:HIS:HB3	33:1b:210:SER:HB2	1.98	0.45
40:1i:125:TYR:OH	40:1i:127:LYS:HG3	2.17	0.45
43:1l:59:ARG:NH1	43:1l:65:GLU:OE1	2.50	0.45
43:1l:71:PRO:O	43:1l:102:ARG:NH1	2.49	0.45
44:1m:60:VAL:HG12	44:1m:66:LEU:HD11	1.99	0.45
1:2A:1068:G:N1	1:2A:1095:A:C8	2.85	0.45
1:2A:1340:U:OP1	19:2X:16:LYS:NZ	2.43	0.45
1:2A:1379:A:H4'	1:2A:1380:G:OP2	2.17	0.45
1:2A:2238:G:H2'	1:2A:2238:G:N3	2.32	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2740:A:H2'	1:2A:2741:A:C8	2.52	0.45
23:21:3:LYS:HB3	23:21:4:VAL:H	1.61	0.45
32:2a:443:C:H2'	32:2a:444:C:C6	2.51	0.45
32:2a:1023:G:H3'	32:2a:1024:G:H8	1.80	0.45
34:2c:47:LEU:HB3	34:2c:52:LEU:HG	1.98	0.45
34:2c:110:ASN:HD21	34:2c:140:ARG:HB3	1.81	0.45
35:2d:110:PHE:N	35:2d:110:PHE:CD1	2.84	0.45
35:2d:110:PHE:N	35:2d:110:PHE:HD1	2.15	0.45
37:2f:6:VAL:HG13	37:2f:90:VAL:HG22	1.97	0.45
42:2k:91:ARG:HE	42:2k:91:ARG:HB3	1.56	0.45
1:1A:1177:A:O2'	1:1A:1178:C:O4'	2.29	0.45
1:1A:2137:C:N3	1:1A:2154:G:C2	2.84	0.45
1:1A:2147:G:H2'	1:1A:2148:G:O4'	2.16	0.45
1:1A:2347:C:H2'	1:1A:2348:U:C6	2.52	0.45
3:1D:137:PRO:O	3:1D:140:THR:HG23	2.16	0.45
18:1W:37:ARG:HD3	18:1W:38:TYR:CE2	2.52	0.45
32:1a:341:C:H2'	32:1a:342:C:H6	1.82	0.45
32:1a:584:G:H5'	48:1q:91:ARG:NH2	2.32	0.45
32:1a:601:C:H2'	32:1a:602:A:H8	1.81	0.45
33:1b:207:ALA:O	33:1b:211:ILE:HG13	2.17	0.45
40:1i:19:LEU:HD23	40:1i:19:LEU:HA	1.83	0.45
53:1y:55:ASN:OD1	53:1y:60:VAL:HG12	2.16	0.45
1:2A:220:G:O2'	1:2A:233:A:N3	2.39	0.45
1:2A:851:U:O2'	25:23:42:ALA:O	2.30	0.45
1:2A:1747:G:H2'	1:2A:1747(A):G:C8	2.51	0.45
1:2A:1833:U:O2'	1:2A:1969:A:N1	2.37	0.45
2:2B:90:A:C5	2:2B:91:C:H1'	2.51	0.45
5:2F:36:VAL:O	5:2F:40:GLN:HG3	2.17	0.45
26:24:14:ILE:HB	26:24:22:ILE:HB	1.99	0.45
26:24:45:GLY:O	26:24:47:GLN:N	2.48	0.45
32:2a:1035:A:O2'	32:2a:1036:G:C8	2.70	0.45
32:2a:1118:C:H1'	32:2a:1179:A:C4	2.52	0.45
32:2a:1121:U:H2'	32:2a:1122:U:O4'	2.17	0.45
33:2b:91:PRO:HB3	33:2b:154:LEU:O	2.16	0.45
36:2e:75:THR:OG1	36:2e:117:ASP:O	2.32	0.45
1:1A:394:A:C6	1:1A:395:U:C4	3.05	0.45
1:1A:987:G:O2'	1:1A:1000:A:N3	2.45	0.45
1:1A:1028:A:N3	1:1A:2486:G:O2'	2.46	0.45
1:1A:2188:C:H2'	1:1A:2189:U:O4'	2.17	0.45
1:1A:2461:C:H2'	1:1A:2462:U:C6	2.51	0.45
4:1E:52:LEU:O	4:1E:76:ARG:N	2.45	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:14:59:PHE:C	26:14:61:ARG:H	2.25	0.45
32:1a:184:G:H2'	32:1a:185:A:C8	2.49	0.45
33:1b:119:GLU:OE2	33:1b:153:ARG:NH1	2.41	0.45
37:1f:100:ASN:HB2	49:1r:27:GLY:O	2.17	0.45
39:1h:112:LEU:HD22	39:1h:133:LEU:HA	1.98	0.45
1:2A:583:G:OP2	16:2U:10:ARG:HD2	2.17	0.45
1:2A:747:U:O2	1:2A:2014:A:H1'	2.15	0.45
1:2A:2352:A:N6	1:2A:2365:G:O2'	2.50	0.45
7:2H:117:PRO:HG3	7:2H:123:PHE:CE2	2.51	0.45
20:2Y:38:ILE:HD13	20:2Y:66:PRO:HA	1.98	0.45
21:2Z:146:ILE:H	21:2Z:146:ILE:HD12	1.81	0.45
32:2a:1150:U:H1'	32:2a:1280:A:N6	2.30	0.45
32:2a:1157:A:H4'	32:2a:1158:C:O5'	2.16	0.45
39:2h:101:PRO:HG3	39:2h:133:LEU:HD11	1.99	0.45
44:2m:29:ARG:HA	44:2m:32:GLU:HB3	1.98	0.45
1:1A:518:G:H2'	1:1A:519:U:C6	2.52	0.45
1:1A:1045:A:H8	1:1A:1111:A:C6	2.35	0.45
1:1A:2359:C:H2'	1:1A:2360:A:O4'	2.17	0.45
2:1B:48:A:H2'	2:1B:49:C:C6	2.51	0.45
5:1F:167:ALA:HB1	5:1F:173:VAL:HG11	1.99	0.45
6:1G:124:SER:HB2	6:1G:131:TYR:CE1	2.52	0.45
19:1X:29:TRP:CZ3	19:1X:78:LYS:HG3	2.52	0.45
23:11:67:ILE:N	23:11:68:PRO:HD2	2.32	0.45
32:1a:542:G:H5'	35:1d:41:GLY:HA3	1.98	0.45
39:1h:7:ALA:HB2	39:1h:85:ARG:HG3	1.97	0.45
47:1p:56:ALA:O	47:1p:60:LEU:HD22	2.16	0.45
1:2A:9:U:O4	1:2A:2629:A:H2	2.00	0.45
1:2A:523:C:H4'	1:2A:540:C:O2	2.16	0.45
1:2A:1028:A:N6	1:2A:1125:G:H2'	2.31	0.45
1:2A:1216:G:P	16:2U:12:ARG:HH21	2.39	0.45
2:2B:3:C:H2'	2:2B:4:C:C6	2.52	0.45
4:2E:59:VAL:O	4:2E:64:LYS:HE3	2.17	0.45
16:2U:97:ASP:HB3	63:2U:302:HOH:O	2.16	0.45
17:2V:52:VAL:CG2	17:2V:55:ALA:HB3	2.47	0.45
21:2Z:180:VAL:HG13	21:2Z:183:LEU:HD12	1.98	0.45
23:21:91:LYS:NZ	63:21:202:HOH:O	2.36	0.45
32:2a:600:C:H2'	32:2a:601:C:H6	1.81	0.45
32:2a:849:C:H2'	32:2a:850:U:O4'	2.15	0.45
32:2a:890:G:O2'	32:2a:906:G:O6	2.20	0.45
32:2a:1053:G:O2'	32:2a:1199:U:H5	1.99	0.45
32:2a:1084:G:C5	32:2a:1085:U:C4	3.05	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1505:G:H4'	32:2a:1506:U:H5"	1.99	0.45
40:2i:26:VAL:HG13	40:2i:61:ALA:HB3	1.97	0.45
41:2j:33:GLN:H	41:2j:75:ILE:H	1.65	0.45
44:2m:50:GLU:HA	44:2m:53:VAL:HB	1.97	0.45
53:2y:3:MET:HB2	53:2y:37:PRO:HG2	1.98	0.45
1:1A:616:G:H5'	5:1F:205:ARG:HD3	1.99	0.45
1:1A:1047:G:H2'	1:1A:1110:G:N2	2.29	0.45
1:1A:1050:A:H2'	1:1A:1051:G:O4'	2.16	0.45
1:1A:1762:A:H2'	63:1A:7370:HOH:O	2.17	0.45
1:1A:2074:U:H2'	1:1A:2075:U:C6	2.52	0.45
1:1A:2239:G:OP2	63:1A:4179:HOH:O	2.20	0.45
1:1A:2690:C:OP2	1:1A:2690:C:H6	1.99	0.45
2:1B:14:U:OP2	2:1B:70:C:O2'	2.30	0.45
2:1B:77:U:OP1	21:1Z:19:ARG:NH2	2.49	0.45
8:1I:31:LEU:HD21	8:1I:38:LEU:HD13	1.99	0.45
32:1a:130:A:C8	48:1q:63:ARG:HD3	2.51	0.45
32:1a:616:G:O2'	32:1a:617:G:H5'	2.17	0.45
32:1a:619:U:N3	35:1d:134:ASP:OD1	2.38	0.45
32:1a:1469:G:H2'	32:1a:1470:G:H8	1.82	0.45
34:1c:35:GLU:CD	34:1c:59:ARG:HH22	2.25	0.45
36:1e:151:LEU:HD12	36:1e:151:LEU:HA	1.77	0.45
50:1s:15:LEU:O	50:1s:19:VAL:HG23	2.17	0.45
1:2A:483:A:H5"	20:2Y:50:ARG:HD3	1.99	0.45
1:2A:760:G:H2'	1:2A:761:A:O4'	2.15	0.45
1:2A:2205:C:H1'	1:2A:2220:G:N2	2.32	0.45
4:2E:9:VAL:HG22	4:2E:25:VAL:HB	1.99	0.45
5:2F:176:LEU:HD23	5:2F:176:LEU:HA	1.80	0.45
6:2G:66:GLN:HG3	26:24:1:MET:HE3	1.98	0.45
8:2I:1:MET:N	8:2I:21:VAL:O	2.46	0.45
11:2P:6:LEU:HA	11:2P:6:LEU:HD23	1.63	0.45
20:2Y:6:HIS:CD2	20:2Y:6:HIS:H	2.34	0.45
32:2a:396:G:O2'	32:2a:398:C:OP1	2.30	0.45
37:2f:36:ARG:NH2	37:2f:66:GLU:OE1	2.49	0.45
1:1A:297:C:OP1	20:1Y:95:LYS:NZ	2.42	0.45
6:1G:61:ALA:O	26:14:7:PRO:HG2	2.17	0.45
30:18:40:GLU:OE2	30:18:44:LYS:NZ	2.50	0.45
32:1a:399:G:H2'	32:1a:400:C:C6	2.52	0.45
32:1a:814:A:N7	32:1a:816:A:C4	2.85	0.45
34:1c:62:ASP:O	34:1c:97:LYS:HB2	2.17	0.45
38:1g:54:THR:CB	38:1g:56:GLN:HE22	2.29	0.45
1:2A:323:G:H1'	1:2A:1205:U:O2	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1010:A:H1'	1:2A:1153:C:H1'	1.98	0.45
3:2D:70:TRP:HB3	3:2D:190:TYR:CE2	2.52	0.45
5:2F:184:TYR:CE2	5:2F:188:ARG:HD2	2.51	0.45
13:2R:12:ARG:O	13:2R:17:ARG:NH1	2.50	0.45
20:2Y:67:LEU:HD23	20:2Y:67:LEU:HA	1.78	0.45
21:2Z:40:ASP:O	21:2Z:44:PHE:N	2.46	0.45
32:2a:1177:G:H2'	32:2a:1178:G:O4'	2.17	0.45
33:2b:35:GLU:HG3	33:2b:39:ILE:O	2.17	0.45
38:2g:79:ARG:HA	38:2g:84:ASN:HA	1.99	0.45
48:2q:55:ASP:OD1	48:2q:79:SER:OG	2.33	0.45
53:2y:74:ILE:O	53:2y:78:ILE:HG12	2.16	0.45
1:1A:746:A:H2'	1:1A:2612:C:H5"	1.98	0.45
1:1A:922:U:H2'	1:1A:923:C:C6	2.52	0.45
1:1A:1070:A:H2'	1:1A:1097:U:O5'	2.18	0.45
1:1A:1174:A:H1'	1:1A:1175:U:H5'	1.98	0.45
1:1A:1358:G:O2'	1:1A:1359:A:H5"	2.17	0.45
1:1A:1791:A:H5'	1:1A:1792:G:OP2	2.17	0.45
12:1Q:51:ARG:O	12:1Q:55:VAL:HG13	2.17	0.45
18:1W:10:VAL:HG12	18:1W:12:ILE:HG22	1.99	0.45
37:1f:97:PHE:O	49:1r:31:LEU:N	2.44	0.45
49:1r:26:LEU:HD13	49:1r:39:VAL:HG22	1.99	0.45
53:1y:49:VAL:HG22	53:1y:66:LYS:HG2	1.99	0.45
1:2A:171:G:H2'	1:2A:172:C:C6	2.52	0.45
1:2A:709:U:H2'	1:2A:710:G:C8	2.51	0.45
1:2A:1047:G:H21	1:2A:1111:A:H62	1.64	0.45
1:2A:1334:G:OP2	63:2A:3884:HOH:O	2.21	0.45
1:2A:2267:A:OP1	63:2A:3890:HOH:O	2.21	0.45
6:2G:8:LYS:HG2	6:2G:12:TYR:HE2	1.82	0.45
6:2G:23:PHE:HB2	6:2G:25:TYR:CE2	2.52	0.45
25:23:29:ARG:HB2	25:23:30:ARG:CZ	2.47	0.45
26:24:64:GLY:C	26:24:66:SER:H	2.25	0.45
32:2a:407:G:H5"	35:2d:115:ARG:HB3	1.98	0.45
32:2a:592:G:H2'	32:2a:593:G:H8	1.82	0.45
32:2a:772:U:H2'	32:2a:773:G:O4'	2.17	0.45
32:2a:848:C:O5'	32:2a:848:C:H6	2.00	0.45
32:2a:1156:G:H8	32:2a:1156:G:O5'	1.99	0.45
32:2a:1251:A:H4'	40:2i:12:GLU:OE1	2.17	0.45
34:2c:150:LYS:HE3	34:2c:201:TYR:CD2	2.52	0.45
35:2d:108:LEU:HD11	35:2d:174:LEU:HB3	1.98	0.45
41:2j:11:PHE:CE1	41:2j:67:THR:HG22	2.52	0.45
1:1A:2181:G:H2'	1:1A:2182:G:H8	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2316:C:O2'	6:1G:128:ARG:NH2	2.50	0.44
1:1A:2533:A:OP1	1:1A:2665:A:O2'	2.25	0.44
1:1A:2693:A:H2'	1:1A:2694:G:C8	2.53	0.44
15:1T:65:LYS:HE3	15:1T:67:SER:HB2	1.99	0.44
21:1Z:140:ASP:OD1	21:1Z:142:SER:OG	2.33	0.44
30:18:23:VAL:CG1	30:18:47:LYS:HD3	2.47	0.44
32:1a:79:G:C2	32:1a:90:U:O2	2.70	0.44
32:1a:623:C:H2'	32:1a:624:C:O4'	2.17	0.44
32:1a:1054:C:O2	32:1a:1196:U:O2'	2.34	0.44
1:2A:479:A:H4'	1:2A:480:A:OP1	2.17	0.44
1:2A:530:G:H4'	1:2A:531:C:OP1	2.16	0.44
1:2A:720:C:H2'	1:2A:721:C:C6	2.51	0.44
1:2A:940:G:OP1	63:2A:3888:HOH:O	2.21	0.44
1:2A:2105:C:N4	1:2A:2184:G:H1	2.11	0.44
1:2A:2139:C:C2'	1:2A:2140:C:H5'	2.48	0.44
3:2D:276:LYS:H	3:2D:276:LYS:HG3	1.42	0.44
7:2H:22:GLY:O	7:2H:37:VAL:N	2.42	0.44
13:2R:44:LEU:HD22	13:2R:48:VAL:HG23	1.98	0.44
15:2T:27:THR:HB	15:2T:89:VAL:HG22	1.99	0.44
16:2U:80:ILE:HD13	16:2U:83:LEU:HD12	1.97	0.44
19:2X:54:VAL:HG22	19:2X:81:VAL:HG12	1.98	0.44
32:2a:743:U:H2'	32:2a:744:C:C6	2.52	0.44
32:2a:857:C:H2'	32:2a:858:G:O4'	2.17	0.44
37:2f:76:ALA:O	37:2f:80:ARG:HG3	2.18	0.44
44:2m:86:CYS:O	44:2m:90:LEU:HG	2.16	0.44
47:2p:20:VAL:HG23	47:2p:35:LYS:HA	1.99	0.44
50:2s:61:TYR:CE2	50:2s:63:THR:HG22	2.52	0.44
1:1A:1578:U:C2'	1:1A:1579:A:H5'	2.48	0.44
1:1A:2138:C:H2'	1:1A:2139:C:C6	2.52	0.44
1:1A:2405:G:O2'	1:1A:2406:U:OP1	2.25	0.44
32:1a:1151:A:O2'	32:1a:1152:A:H8	2.00	0.44
32:1a:1316:G:N2	32:1a:1318:A:H3'	2.32	0.44
32:1a:1504:G:OP1	32:1a:1507:A:H4'	2.17	0.44
33:1b:136:VAL:O	33:1b:140:HIS:HB2	2.17	0.44
33:1b:174:VAL:O	33:1b:178:ARG:HB2	2.17	0.44
33:1b:218:ALA:O	33:1b:222:ILE:HG13	2.18	0.44
53:1y:67:HIS:CD2	53:1y:68:GLU:H	2.35	0.44
1:2A:300:A:H1'	1:2A:319:C:H1'	1.98	0.44
1:2A:1999:C:H4'	1:2A:2723:C:O2	2.16	0.44
1:2A:2162:G:H4'	1:2A:2172:U:O2'	2.17	0.44
1:2A:2298:A:N6	1:2A:2318:G:H8	2.15	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:2F:104:LYS:O	5:2F:108:LYS:HG3	2.18	0.44
6:2G:142:PRO:HG2	6:2G:143:GLU:OE1	2.17	0.44
8:2I:123:LEU:HD21	8:2I:146:ALA:HB2	1.99	0.44
10:2O:113:LYS:O	10:2O:117:LEU:HG	2.16	0.44
16:2U:27:LEU:HA	16:2U:30:LYS:HB2	1.97	0.44
17:2V:52:VAL:HG23	17:2V:55:ALA:HB3	2.00	0.44
22:20:5:LYS:HG3	22:20:6:GLY:N	2.32	0.44
25:23:30:ARG:HH21	25:23:33:GLN:NE2	2.15	0.44
32:2a:789:U:H2'	32:2a:791:G:OP2	2.18	0.44
32:2a:1135:U:H4'	32:2a:1136:U:C5	2.51	0.44
33:2b:31:TYR:O	33:2b:42:ILE:HG23	2.18	0.44
38:2g:50:ILE:HG13	38:2g:51:GLN:N	2.31	0.44
53:2y:52:ALA:HB2	53:2y:77:LEU:HD21	1.98	0.44
1:1A:143:G:H4'	19:1X:35:THR:HG21	1.98	0.44
1:1A:478:A:C6	1:1A:480:A:C6	3.05	0.44
1:1A:645:C:H5'	1:1A:646:A:OP2	2.17	0.44
1:1A:1082:U:C4	1:1A:1086:A:N1	2.82	0.44
1:1A:1783:A:H5'	1:1A:2608:G:H4'	2.00	0.44
2:1B:103:G:N2	21:1Z:73:GLN:HE22	2.13	0.44
7:1H:3:ARG:NH2	7:1H:65:HIS:HB3	2.31	0.44
8:1I:69:LYS:HE2	8:1I:73:GLU:OE1	2.17	0.44
20:1Y:68:HIS:HB3	20:1Y:71:LYS:HG3	1.99	0.44
32:1a:648:A:H2'	32:1a:649:G:C8	2.52	0.44
32:1a:1001:A:H2'	32:1a:1001(A):G:H8	1.83	0.44
32:1a:1032:G:H2'	32:1a:1033:G:O4'	2.18	0.44
32:1a:1058:G:OP1	34:1c:199:LYS:HE3	2.17	0.44
39:1h:83:ILE:HA	39:1h:136:GLU:O	2.18	0.44
1:2A:271(R):G:OP1	23:21:76:ARG:NH1	2.51	0.44
1:2A:1131:G:O6	1:2A:2040:C:H1'	2.17	0.44
1:2A:1469:A:H2'	1:2A:1470:G:O4'	2.17	0.44
1:2A:1588:C:H2'	1:2A:1589:C:H6	1.82	0.44
1:2A:1847:A:H3'	1:2A:1848:A:H5'	1.99	0.44
6:2G:96:ARG:O	6:2G:99:MET:HB3	2.17	0.44
8:2I:123:LEU:HD11	8:2I:145:VAL:C	2.42	0.44
15:2T:45:PHE:CE1	15:2T:74:ARG:HG3	2.52	0.44
32:2a:176:C:H2'	32:2a:177:C:H6	1.81	0.44
32:2a:1312:G:H5'	50:2s:5:LEU:HD21	1.99	0.44
32:2a:1509:C:H2'	32:2a:1510:U:O4'	2.18	0.44
34:2c:120:VAL:HG13	34:2c:133:ALA:HB1	1.99	0.44
34:2c:123:GLN:HA	34:2c:126:ARG:HD2	2.00	0.44
34:2c:124:ILE:HG13	34:2c:189:ALA:HB1	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:2h:64:LYS:HE3	39:2h:79:VAL:HG21	2.00	0.44
1:1A:226:G:N2	1:1A:228:A:H62	2.15	0.44
1:1A:757:U:H2'	1:1A:758:C:O4'	2.18	0.44
1:1A:1686:C:H2'	1:1A:1687:G:O4'	2.17	0.44
1:1A:1759:A:H1'	1:1A:2711:A:C2	2.52	0.44
63:1A:5961:HOH:O	4:1E:129:HIS:HE1	1.99	0.44
15:1T:56:GLY:O	15:1T:59:THR:HG23	2.16	0.44
23:11:52:ARG:NH2	23:11:55:GLY:O	2.50	0.44
32:1a:370:C:H2'	32:1a:371:G:H8	1.83	0.44
32:1a:928:G:O2'	32:1a:1533:C:OP1	2.36	0.44
32:1a:1251:A:H2'	32:1a:1252:A:C8	2.53	0.44
32:1a:1308:U:OP2	44:1m:99:ARG:HG3	2.16	0.44
1:2A:394:A:O2'	1:2A:395:U:H5'	2.16	0.44
1:2A:568:U:H5'	1:2A:945:A:H62	1.83	0.44
1:2A:724:U:H2'	1:2A:725:G:O4'	2.17	0.44
1:2A:1161:C:H2'	1:2A:1162:G:H8	1.81	0.44
6:2G:120:LEU:HB3	6:2G:131:TYR:OH	2.17	0.44
6:2G:144:ILE:HA	6:2G:148:MET:SD	2.57	0.44
7:2H:15:VAL:HB	7:2H:27:LYS:O	2.17	0.44
9:2N:108:PRO:O	9:2N:113:GLY:HA3	2.17	0.44
11:2P:2:LYS:HE3	11:2P:2:LYS:HB2	1.87	0.44
15:2T:126:ALA:HA	15:2T:129:ARG:NH1	2.32	0.44
32:2a:918:A:H2'	32:2a:919:A:O4'	2.18	0.44
32:2a:1127:G:H2'	32:2a:1128:C:H6	1.82	0.44
32:2a:1269:A:H2	32:2a:1312:G:N3	2.15	0.44
1:1A:569:U:C4	1:1A:570:G:C6	3.06	0.44
1:1A:620:G:N3	1:1A:620:G:H5'	2.33	0.44
1:1A:1045:A:OP1	1:1A:1045:A:H4'	2.18	0.44
1:1A:1067:A:H3'	1:1A:1067:A:N3	2.33	0.44
1:1A:1174:A:H4'	1:1A:1175:U:OP1	2.17	0.44
1:1A:1864:U:OP1	1:1A:2410:G:O2'	2.27	0.44
1:1A:2469:A:H5'	1:1A:2470:G:OP2	2.18	0.44
10:1O:3:GLN:NE2	63:1O:309:HOH:O	2.50	0.44
16:1U:36:ARG:NH2	63:1U:314:HOH:O	2.51	0.44
32:1a:189(F):U:O2	48:1q:63:ARG:NH2	2.50	0.44
32:1a:750:G:N3	46:1o:23:GLY:HA3	2.33	0.44
32:1a:765:G:C6	32:1a:812:C:C2	3.05	0.44
32:1a:1456:G:N2	51:1t:43:LEU:HD11	2.33	0.44
35:1d:177:ASP:HB3	35:1d:182:LYS:HG3	2.00	0.44
1:2A:1754:C:OP1	15:2T:96:ARG:NH1	2.51	0.44
1:2A:2115:G:N1	1:2A:2119:A:OP2	2.45	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2253:G:O6	63:2A:3887:HOH:O	2.21	0.44
1:2A:2404:C:O3'	11:2P:77:ARG:NH2	2.50	0.44
1:2A:2543:G:H21	1:2A:2646:C:H5"	1.83	0.44
1:2A:2629:A:H1'	1:2A:2630:G:H5"	2.00	0.44
11:2P:106:LEU:HD13	11:2P:112:LEU:HD13	2.00	0.44
31:29:3:VAL:HA	31:29:35:ARG:O	2.17	0.44
32:2a:570:G:H1'	32:2a:820:U:C4	2.53	0.44
32:2a:1117:G:H4'	40:2i:104:ARG:NH1	2.33	0.44
32:2a:1274:G:H2'	32:2a:1275:A:H8	1.82	0.44
34:2c:179:ARG:NH1	34:2c:206:GLU:OE1	2.48	0.44
53:2y:20:VAL:O	53:2y:24:LEU:HB2	2.17	0.44
1:1A:220:G:O2'	1:1A:233:A:N3	2.43	0.44
1:1A:354:G:H2'	1:1A:355:G:C8	2.53	0.44
1:1A:589:C:OP1	11:1P:16:ARG:NH1	2.49	0.44
1:1A:998:C:OP1	63:1A:4170:HOH:O	2.19	0.44
1:1A:1919:A:N1	32:1a:1495:U:O2'	2.41	0.44
1:1A:2869:G:H2'	1:1A:2870:C:C6	2.52	0.44
6:1G:163:ALA:HB1	6:1G:168:GLU:HB2	1.99	0.44
7:1H:20:ALA:HB1	7:1H:21:PRO:HD2	1.99	0.44
7:1H:121:ILE:HG13	7:1H:144:VAL:HG21	1.98	0.44
21:1Z:69:THR:HG22	21:1Z:90:VAL:HA	1.99	0.44
32:1a:160:A:H2'	32:1a:161:A:O4'	2.18	0.44
32:1a:1329:A:P	44:1m:28:ALA:HB3	2.58	0.44
36:1e:27:ARG:NH1	63:1e:302:HOH:O	2.50	0.44
51:1t:93:GLU:C	51:1t:95:ALA:H	2.26	0.44
53:1y:23:ARG:HH11	53:1y:26:LYS:HD2	1.82	0.44
1:2A:212:G:H2'	1:2A:213:A:O4'	2.17	0.44
1:2A:494:G:H4'	18:2W:6:ILE:HB	2.00	0.44
1:2A:989:G:O2'	63:2A:3895:HOH:O	2.21	0.44
1:2A:1084:A:H3'	1:2A:1085:A:C4'	2.46	0.44
1:2A:2134:A:N7	1:2A:2157:G:H5'	2.33	0.44
1:2A:2312:U:OP1	6:2G:73:ALA:HA	2.16	0.44
5:2F:112:MET:HA	5:2F:115:ALA:HB3	2.00	0.44
6:2G:34:LEU:HD21	6:2G:172:LEU:HD21	2.00	0.44
11:2P:46:LYS:HE3	11:2P:46:LYS:HB3	1.84	0.44
15:2T:99:LEU:O	15:2T:102:ILE:HG12	2.17	0.44
21:2Z:140:ASP:OD1	21:2Z:142:SER:OG	2.35	0.44
32:2a:677:U:H1'	42:2k:119:CYS:SG	2.58	0.44
32:2a:691:G:H1'	32:2a:696:A:N6	2.32	0.44
36:2e:84:PHE:CZ	36:2e:133:TYR:HD2	2.36	0.44
38:2g:100:ALA:O	38:2g:104:LEU:HD13	2.16	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:375:C:H2'	1:1A:376:C:C6	2.53	0.44
1:1A:885:C:H2'	1:1A:886:C:O4'	2.18	0.44
1:1A:1026:U:OP1	63:1A:4101:HOH:O	2.21	0.44
1:1A:1794:U:H2'	1:1A:1795:C:C6	2.53	0.44
1:1A:2287:A:O2'	1:1A:2288:A:H3'	2.18	0.44
1:1A:2572:A:N7	4:1E:145:LYS:HB2	2.33	0.44
4:1E:7:VAL:HG12	4:1E:27:LEU:HB3	1.98	0.44
6:1G:37:VAL:HG13	6:1G:99:MET:HG3	2.00	0.44
9:1N:12:ARG:NH1	9:1N:50:ASP:OD2	2.50	0.44
11:1P:116:GLY:O	11:1P:137:LYS:NZ	2.49	0.44
15:1T:127:ALA:C	15:1T:129:ARG:H	2.26	0.44
35:1d:127:THR:HG23	35:1d:149:ALA:HA	2.00	0.44
36:1e:84:PHE:CE2	36:1e:133:TYR:HD2	2.36	0.44
1:2A:412:A:OP2	1:2A:412:A:H8	2.00	0.44
1:2A:1467:C:C5	1:2A:1546:C:H2'	2.53	0.44
1:2A:1919:A:O3'	32:2a:1517:G:H1'	2.18	0.44
5:2F:184:TYR:O	5:2F:188:ARG:HG3	2.18	0.44
6:2G:3:LEU:HD11	6:2G:97:ASP:HB3	2.00	0.44
7:2H:117:PRO:HA	7:2H:118:PRO:HD3	1.89	0.44
29:27:43:THR:HB	63:27:206:HOH:O	2.18	0.44
32:2a:996:A:N1	32:2a:1045:C:O2'	2.45	0.44
32:2a:1030(B):C:H41	32:2a:1030(C):G:H21	1.65	0.44
32:2a:1065:U:H4'	32:2a:1066:C:O5'	2.18	0.44
32:2a:1317:C:H5	45:2n:18:VAL:HG21	1.82	0.44
34:2c:114:PRO:HA	34:2c:185:GLY:HA3	2.00	0.44
41:2j:66:ARG:HE	41:2j:68:HIS:HE1	1.65	0.44
53:2y:42:SER:HB2	53:2y:49:VAL:HB	1.99	0.44
1:1A:1226:A:OP1	17:1V:84:LYS:NZ	2.40	0.44
1:1A:2189:U:H2'	1:1A:2190:G:H5'	1.99	0.44
1:1A:2722:G:H2'	1:1A:2723:C:C6	2.53	0.44
8:1I:27:ARG:HD2	23:11:71:TYR:CE2	2.53	0.44
17:1V:21:ARG:NH1	17:1V:93:GLU:OE1	2.50	0.44
21:1Z:198:LYS:H	21:1Z:198:LYS:CD	2.29	0.44
32:1a:116:A:H61	32:1a:313:A:H1'	1.83	0.44
32:1a:191:G:H1'	51:1t:103:GLY:HA3	2.00	0.44
32:1a:192:U:H2'	32:1a:193:C:H6	1.82	0.44
32:1a:344:A:H4'	32:1a:345:C:OP2	2.17	0.44
32:1a:603:U:H2'	32:1a:604:G:C8	2.53	0.44
32:1a:618:C:H3'	32:1a:619:U:H5"	2.00	0.44
32:1a:717:C:H4'	42:1k:117:ASN:HD22	1.81	0.44
32:1a:1010:G:N2	32:1a:1020:U:O2'	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1028:C:H2'	32:1a:1029:C:C4'	2.44	0.44
32:1a:1499:A:H1'	32:1a:1520:G:H5'	1.98	0.44
33:1b:30:ARG:NH2	33:1b:194:PRO:HB2	2.33	0.44
33:1b:73:THR:OG1	33:1b:170:GLU:OE2	2.30	0.44
33:1b:217:ARG:HA	33:1b:217:ARG:HD3	1.84	0.44
35:1d:187:ARG:NH2	35:1d:193:ASP:OD2	2.50	0.44
39:1h:90:GLY:O	48:1q:34:LYS:HD2	2.18	0.44
42:1k:27:ASN:HA	42:1k:55:LYS:O	2.18	0.44
43:1l:47:LYS:HE3	43:1l:47:LYS:HB2	1.75	0.44
47:1p:2:VAL:HG13	47:1p:64:ALA:HA	2.00	0.44
1:2A:538:G:H2'	1:2A:539:G:H8	1.83	0.44
1:2A:784:A:O4'	3:2D:227:ASN:ND2	2.51	0.44
1:2A:1576:U:H2'	1:2A:1577:C:C6	2.53	0.44
1:2A:1576:U:H2'	1:2A:1577:C:H6	1.83	0.44
1:2A:2291:U:H2'	1:2A:2292:C:C6	2.53	0.44
1:2A:2391:G:O6	1:2A:2425:A:H8	2.00	0.44
1:2A:2400:G:H2'	1:2A:2401:U:C6	2.53	0.44
25:23:46:ASN:O	25:23:50:VAL:HG22	2.18	0.44
32:2a:1039:C:H2'	32:2a:1040:U:O4'	2.18	0.44
36:2e:144:THR:H	36:2e:147:ASP:HB2	1.83	0.44
40:2i:50:LEU:HB3	40:2i:56:LEU:HA	1.98	0.44
50:2s:22:LEU:HA	50:2s:22:LEU:HD23	1.69	0.44
1:1A:2031:A:C6	1:1A:2498:C:H1'	2.53	0.44
2:1B:48:A:H4'	14:1S:95:HIS:HD2	1.83	0.44
8:1I:69:LYS:HG3	8:1I:138:ILE:HG23	2.00	0.44
8:1I:72:LEU:C	8:1I:74:ASN:N	2.76	0.44
20:1Y:28:LYS:HG3	20:1Y:40:GLU:CG	2.47	0.44
22:10:46:LYS:HB2	22:10:78:TYR:CE1	2.52	0.44
32:1a:1002:G:N1	32:1a:1003:G:C2	2.85	0.44
32:1a:1118:C:H2'	32:1a:1119:C:C6	2.52	0.44
32:1a:1318:A:H5"	50:1s:3:ARG:HH12	1.83	0.44
32:1a:1343:G:H2'	32:1a:1344:C:C6	2.53	0.44
34:1c:180:ALA:HB1	34:1c:203:PHE:CE1	2.53	0.44
40:1i:49:PRO:HD2	40:1i:81:ILE:HD11	2.00	0.44
44:1m:4:ILE:HA	44:1m:5:ALA:HA	1.62	0.44
1:2A:1423:G:OP1	1:2A:1492:G:O2'	2.35	0.44
1:2A:1588:C:H2'	1:2A:1589:C:C6	2.53	0.44
1:2A:2131:G:OP1	1:2A:2132:U:H5'	2.18	0.44
7:2H:109:PHE:C	7:2H:111:HIS:H	2.25	0.44
21:2Z:48:PHE:CE1	21:2Z:71:VAL:HG11	2.52	0.44
32:2a:1176:A:H2'	32:2a:1177:G:C8	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1245:A:H2'	32:2a:1246:C:O4'	2.17	0.44
34:2c:155:GLY:HA3	34:2c:196:LEU:HG	2.00	0.44
37:2f:46:ARG:CZ	37:2f:46:ARG:HB2	2.48	0.44
39:2h:87:SER:HA	39:2h:93:VAL:HG23	1.99	0.44
43:2l:24:VAL:HG12	43:2l:98:TYR:HE1	1.83	0.44
44:2m:95:GLY:O	44:2m:110:ARG:HG3	2.18	0.44
53:2y:85:LEU:O	53:2y:89:GLN:HG2	2.18	0.44
1:1A:1062:G:OP2	1:1A:1070:A:H4'	2.18	0.43
1:1A:2206:G:H2'	1:1A:2207:G:C2	2.53	0.43
1:1A:2543:G:H2'	1:1A:2544:G:C8	2.53	0.43
2:1B:23:G:O6	63:1B:302:HOH:O	2.20	0.43
3:1D:4:LYS:HB3	3:1D:18:VAL:HG22	2.00	0.43
3:1D:77:ALA:O	3:1D:116:GLN:HG3	2.17	0.43
11:1P:1:MET:HE3	11:1P:5:ASP:HB2	2.00	0.43
25:13:5:LYS:HG3	25:13:36:VAL:HG22	2.00	0.43
28:16:17:LYS:HD2	63:16:619:HOH:O	2.17	0.43
32:1a:341:C:H2'	32:1a:342:C:C6	2.53	0.43
32:1a:598:U:H4'	39:1h:94:TYR:CD2	2.53	0.43
32:1a:1402:4OC:O5'	32:1a:1402:4OC:H6	2.18	0.43
34:1c:130:VAL:HG21	34:1c:157:ILE:HG23	1.98	0.43
36:1e:135:THR:O	36:1e:139:LEU:HG	2.18	0.43
1:2A:11:G:N7	63:2A:4034:HOH:O	2.35	0.43
1:2A:776:G:P	63:2A:3821:HOH:O	2.75	0.43
1:2A:995:C:O2	9:2N:3:THR:OG1	2.34	0.43
1:2A:1401:G:H2'	1:2A:1402:C:O4'	2.18	0.43
1:2A:1991:U:H2'	1:2A:1992:G:H5"	1.99	0.43
1:2A:2105:C:N3	1:2A:2184:G:N2	2.64	0.43
1:2A:2309:A:H2'	1:2A:2310:A:C8	2.53	0.43
1:2A:2390:U:O2'	1:2A:2391:G:H5'	2.18	0.43
23:21:49:VAL:O	23:21:59:THR:HA	2.17	0.43
32:2a:7:G:H5'	32:2a:298:A:O4'	2.18	0.43
32:2a:29:G:O2'	32:2a:295:C:H4'	2.18	0.43
32:2a:1030(A):G:N1	32:2a:1031:G:O6	2.51	0.43
33:2b:162:ILE:HD11	33:2b:184:VAL:HG13	2.00	0.43
35:2d:13:ARG:HH22	35:2d:36:ARG:NH2	2.16	0.43
38:2g:51:GLN:HB2	38:2g:58:PRO:HG3	2.00	0.43
50:2s:32:LYS:HG3	50:2s:57:HIS:CE1	2.53	0.43
1:1A:27:G:N2	1:1A:512:G:H1'	2.33	0.43
1:1A:636:G:N7	11:1P:113:LYS:HE3	2.33	0.43
1:1A:747:U:O2	1:1A:2014:A:H1'	2.18	0.43
1:1A:1179:C:H2'	1:1A:1180:C:C6	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:1A:4018:ARG:HB3	59:1A:4018:ARG:HH21	1.82	0.43
15:1T:39:ARG:HH12	15:1T:41:ARG:CD	2.29	0.43
32:1a:503:C:H2'	32:1a:504:C:C6	2.53	0.43
32:1a:1044:A:C5	32:1a:1045:C:H1'	2.53	0.43
32:1a:1181:G:O2'	32:1a:1182:G:N7	2.48	0.43
36:1e:142:LEU:O	36:1e:143:ARG:NE	2.48	0.43
1:2A:831:G:N2	11:2P:53:GLY:O	2.49	0.43
1:2A:1803:A:H4'	3:2D:259:THR:HG23	2.00	0.43
1:2A:2674:G:H2'	1:2A:2675:A:C8	2.53	0.43
7:2H:154:PRO:HB3	7:2H:163:TYR:CZ	2.53	0.43
14:2S:25:ARG:HD3	14:2S:42:ASP:OD1	2.17	0.43
20:2Y:12:THR:O	20:2Y:75:ILE:HB	2.17	0.43
32:2a:420:U:H2'	32:2a:422:C:C5	2.53	0.43
32:2a:684:A:C6	32:2a:685:G:C6	3.06	0.43
40:2i:16:ARG:NH2	40:2i:18:PHE:HZ	2.17	0.43
40:2i:26:VAL:HB	40:2i:33:PHE:HB2	1.99	0.43
40:2i:46:ALA:O	40:2i:49:PRO:HD2	2.18	0.43
46:2o:68:ARG:NH1	63:2o:101:HOH:O	2.50	0.43
48:2q:81:ARG:NH1	48:2q:83:ASP:OD2	2.51	0.43
53:2y:61:LEU:HB3	53:2y:81:LEU:HD22	2.00	0.43
1:1A:185:U:H2'	1:1A:186:G:C8	2.53	0.43
1:1A:2093:G:C6	1:1A:2225:A:C8	3.06	0.43
1:1A:2103:C:H1'	1:1A:2187:G:N2	2.33	0.43
1:1A:2396:G:H4'	23:11:29:GLY:O	2.18	0.43
1:1A:2777:G:O6	63:1A:4174:HOH:O	2.20	0.43
32:1a:303:A:O2'	32:1a:555:C:O2'	2.36	0.43
35:1d:171:GLY:C	35:1d:173:TRP:H	2.26	0.43
36:1e:151:LEU:HD21	39:1h:77:GLU:HG2	2.00	0.43
38:1g:138:LYS:HE3	38:1g:142:GLU:CD	2.43	0.43
40:1i:3:GLN:HE21	40:1i:20:ARG:HE	1.64	0.43
41:1j:5:ARG:NE	41:1j:73:ASP:OD1	2.39	0.43
1:2A:995:C:N4	9:2N:2:LYS:HD2	2.32	0.43
1:2A:2408:U:H2'	1:2A:2409:G:C8	2.53	0.43
5:2F:161:GLU:O	5:2F:165:ARG:HG3	2.18	0.43
7:2H:54:ARG:HB2	7:2H:61:HIS:HB3	1.99	0.43
14:2S:36:TYR:CE1	14:2S:54:LEU:HB2	2.52	0.43
18:2W:46:PHE:O	18:2W:50:VAL:HG23	2.18	0.43
21:2Z:19:ARG:NH1	21:2Z:84:GLU:HB2	2.33	0.43
32:2a:435:C:H2'	32:2a:436:C:H6	1.83	0.43
32:2a:1035:A:HO2'	32:2a:1036:G:H8	1.66	0.43
32:2a:1074:G:OP1	36:2e:64:ARG:NH1	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1202:G:N2	45:2n:43:CYS:SG	2.91	0.43
32:2a:1239:A:O2'	38:2g:114:ARG:O	2.22	0.43
33:2b:97:TRP:CH2	33:2b:101:MET:HB2	2.53	0.43
38:2g:113:GLU:HG2	38:2g:119:ARG:CG	2.49	0.43
40:2i:6:GLY:O	40:2i:17:VAL:HG22	2.18	0.43
51:2t:65:LYS:HA	51:2t:68:LYS:HG3	2.00	0.43
1:1A:1066:U:C2	1:1A:1067:A:N1	2.86	0.43
1:1A:2319:G:N1	14:1S:3:ARG:HA	2.33	0.43
2:1B:92:C:OP2	63:1B:303:HOH:O	2.20	0.43
3:1D:132:PRO:HD3	3:1D:190:TYR:CZ	2.53	0.43
6:1G:11:TYR:O	6:1G:16:ARG:HG2	2.18	0.43
6:1G:142:PRO:HB2	26:14:31:ILE:HG21	1.99	0.43
10:1O:25:LEU:HG	10:1O:40:VAL:HG23	1.99	0.43
32:1a:384:G:H2'	32:1a:385:C:H6	1.83	0.43
32:1a:986:A:H2'	32:1a:987:G:O4'	2.18	0.43
32:1a:1152:A:OP1	41:1j:68:HIS:ND1	2.52	0.43
38:1g:90:GLU:OE1	38:1g:90:GLU:N	2.34	0.43
43:1l:56:ALA:HB2	43:1l:70:ILE:HD11	2.01	0.43
45:1n:4:LYS:HA	45:1n:7:ILE:HG12	1.99	0.43
48:1q:69:LYS:O	48:1q:70:ARG:HD3	2.18	0.43
1:2A:7:G:H2'	1:2A:8:A:H8	1.82	0.43
1:2A:952:G:P	12:2Q:16:ARG:HH12	2.41	0.43
1:2A:1355:G:P	3:2D:38:LYS:HE2	2.58	0.43
1:2A:1638:C:H2'	1:2A:1639:U:O4'	2.18	0.43
1:2A:1827:C:C2'	1:2A:1828:G:H5'	2.49	0.43
1:2A:1914:C:OP1	63:2A:3891:HOH:O	2.21	0.43
1:2A:2130:U:H2'	1:2A:2158:A:N6	2.32	0.43
1:2A:2189:U:H2'	1:2A:2190:G:C8	2.53	0.43
1:2A:2515:C:H2'	1:2A:2516:G:H8	1.83	0.43
6:2G:16:ARG:HA	6:2G:16:ARG:HD2	1.81	0.43
10:2O:119:PRO:HB2	15:2T:68:TYR:CE2	2.53	0.43
12:2Q:91:GLU:O	63:2Q:301:HOH:O	2.21	0.43
30:28:29:LYS:HD2	30:28:44:LYS:HB3	2.00	0.43
32:2a:1030(A):G:H21	32:2a:1030(C):G:H3'	1.83	0.43
32:2a:1279:A:H5"	41:2j:7:LYS:HE2	2.01	0.43
1:1A:1252:G:C2	1:1A:1253:A:C2	3.06	0.43
1:1A:1297:C:OP1	1:1A:2710:C:H4'	2.19	0.43
1:1A:1429:G:H2'	1:1A:1430:C:H6	1.82	0.43
1:1A:2109:U:H2'	1:1A:2110:G:C8	2.53	0.43
1:1A:2206:G:H5"	1:1A:2207:G:C6	2.53	0.43
63:1A:4982:HOH:O	20:1Y:19:LYS:HD3	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:1T:39:ARG:NH1	15:1T:41:ARG:HB3	2.34	0.43
18:1W:88:ARG:HG3	18:1W:92:ARG:HH21	1.84	0.43
21:1Z:40:ASP:OD2	21:1Z:42:VAL:HG22	2.19	0.43
28:16:14:THR:HB	28:16:48:VAL:O	2.18	0.43
32:1a:509:A:O2'	32:1a:510:A:OP1	2.34	0.43
32:1a:1183:A:H3'	32:1a:1184:G:C5'	2.48	0.43
32:1a:1325:C:H2'	32:1a:1326:C:H6	1.83	0.43
41:1j:19:SER:O	41:1j:23:ILE:HG12	2.18	0.43
41:1j:35:SER:N	41:1j:73:ASP:O	2.48	0.43
1:2A:13:A:N1	1:2A:525:U:H2'	2.34	0.43
1:2A:234:C:H2'	1:2A:235:U:C6	2.52	0.43
1:2A:1005:C:H2'	1:2A:1006:C:H6	1.83	0.43
1:2A:1316:U:H2'	1:2A:1317:A:H8	1.84	0.43
1:2A:1999:C:H5"	1:2A:2723:C:O2'	2.17	0.43
1:2A:2302:G:H21	6:2G:126:ASP:CG	2.27	0.43
1:2A:2377:A:N3	63:2A:4046:HOH:O	2.36	0.43
2:2B:50:G:OP1	14:2S:63:THR:OG1	2.27	0.43
3:2D:143:HIS:CD2	3:2D:192:THR:HB	2.54	0.43
3:2D:218:ARG:HB3	3:2D:219:PRO:HD2	2.01	0.43
5:2F:31:HIS:HB2	11:2P:9:ASN:OD1	2.19	0.43
9:2N:30:ILE:HG23	9:2N:52:VAL:HG11	2.00	0.43
9:2N:39:ARG:NH2	9:2N:41:ASP:OD2	2.46	0.43
10:2O:120:GLU:HG2	10:2O:122:LEU:HG	2.01	0.43
20:2Y:92:ASN:HD22	20:2Y:94:LYS:HG2	1.84	0.43
32:2a:108:G:O6	51:2t:15:ARG:HG2	2.19	0.43
32:2a:659:U:H5"	46:2o:9:GLN:HE22	1.84	0.43
32:2a:685:G:O2'	32:2a:686:U:H5'	2.18	0.43
32:2a:926:G:C6	53:2y:87:LYS:HG3	2.53	0.43
32:2a:1070:U:H2'	32:2a:1071:C:C6	2.54	0.43
32:2a:1327:C:H2'	32:2a:1328:C:C6	2.53	0.43
35:2d:64:LEU:HD23	35:2d:75:PHE:HZ	1.82	0.43
35:2d:126:ILE:HG23	35:2d:147:ALA:O	2.19	0.43
48:2q:66:SER:HB3	48:2q:69:LYS:HD3	2.00	0.43
1:1A:359:A:H2'	1:1A:360:G:O4'	2.18	0.43
1:1A:821:A:H2'	1:1A:946:G:H5"	1.99	0.43
1:1A:1540:U:O4	63:1A:4132:HOH:O	2.12	0.43
1:1A:2065:C:H2'	1:1A:2066:C:C6	2.53	0.43
1:1A:2086:U:H2'	1:1A:2087:G:H8	1.83	0.43
1:1A:2103:C:H1'	1:1A:2187:G:H22	1.83	0.43
1:1A:2111:C:OP2	1:1A:2145:C:N4	2.51	0.43
1:1A:2627:G:N2	1:1A:2777:G:OP2	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1B:73:A:C4	2:1B:105:A:C2	3.07	0.43
11:1P:68:GLN:HG3	63:1P:330:HOH:O	2.19	0.43
20:1Y:90:LEU:HD21	20:1Y:96:ILE:HG12	2.01	0.43
32:1a:539:A:H2'	32:1a:540:G:C8	2.53	0.43
32:1a:708:C:H2'	32:1a:709:G:H8	1.83	0.43
32:1a:744:C:O2'	32:1a:851:G:N2	2.51	0.43
32:1a:811:C:O2'	32:1a:901:A:N1	2.49	0.43
33:1b:178:ARG:NH1	39:1h:71:GLY:H	2.17	0.43
40:1i:89:ASN:O	40:1i:92:TYR:HB2	2.19	0.43
43:1l:27:LEU:HD13	43:1l:33:ARG:HB2	1.99	0.43
44:1m:11:ARG:C	44:1m:13:LYS:H	2.25	0.43
1:2A:140:G:N2	1:2A:1596:A:H4'	2.34	0.43
1:2A:361:G:O2'	1:2A:362:U:H5'	2.19	0.43
1:2A:1399:C:H2'	1:2A:1400:G:H8	1.83	0.43
8:2I:2:LYS:HD3	8:2I:18:VAL:HG12	2.00	0.43
23:21:64:ALA:HA	23:21:67:ILE:HG13	2.00	0.43
32:2a:59:A:H1'	32:2a:354:G:N2	2.34	0.43
32:2a:523:A:H61	43:2l:92:0TD:CG	2.31	0.43
32:2a:560:U:H5'	32:2a:566:G:N2	2.33	0.43
32:2a:1104:G:H4'	33:2b:111:ARG:NH2	2.34	0.43
32:2a:1304:G:C6	32:2a:1305:G:N1	2.86	0.43
33:2b:98:LEU:HD23	33:2b:98:LEU:HA	1.76	0.43
34:2c:189:ALA:HB3	34:2c:196:LEU:HB2	2.00	0.43
35:2d:90:GLY:HA3	35:2d:200:GLU:HG3	2.00	0.43
42:2k:51:LYS:HA	42:2k:55:LYS:HZ3	1.83	0.43
9:1N:102:ALA:O	9:1N:106:MET:HG3	2.19	0.43
32:1a:352:C:O2'	32:1a:354:G:OP1	2.29	0.43
33:1b:10:LEU:HG	33:1b:48:MET:HE1	2.01	0.43
35:1d:196:LEU:O	35:1d:198:VAL:N	2.46	0.43
41:1j:38:ILE:HG13	41:1j:71:LEU:HB3	2.01	0.43
46:1o:71:GLN:HE21	46:1o:71:GLN:HB3	1.59	0.43
47:1p:4:ILE:HG22	47:1p:19:ILE:HD11	2.00	0.43
47:1p:5:ARG:HA	47:1p:67:THR:OG1	2.19	0.43
1:2A:1091:G:H2'	1:2A:1091:G:N3	2.34	0.43
1:2A:1721:G:H2'	1:2A:1740:G:O6	2.18	0.43
1:2A:2317:C:H2'	1:2A:2318:G:H5'	2.01	0.43
1:2A:2526:G:H5'	1:2A:2742:C:O2'	2.18	0.43
1:2A:2590:A:O3'	3:2D:239:ARG:NH2	2.51	0.43
5:2F:157:VAL:HB	5:2F:194:MET:HG2	2.00	0.43
9:2N:73:THR:C	9:2N:74:ARG:HG2	2.43	0.43
12:2Q:55:VAL:HG23	21:2Z:183:LEU:HD11	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:2R:10:LEU:HD23	13:2R:10:LEU:HA	1.87	0.43
28:26:13:CYS:SG	28:26:47:THR:HG21	2.59	0.43
32:2a:744:C:H2'	32:2a:745:C:H6	1.83	0.43
32:2a:922:G:C6	32:2a:923:A:C6	3.07	0.43
32:2a:1161:C:H2'	32:2a:1162:C:H6	1.83	0.43
32:2a:1481:U:H2'	32:2a:1482:G:C8	2.53	0.43
35:2d:141:ARG:N	35:2d:144:ASP:OD2	2.49	0.43
41:2j:67:THR:O	41:2j:67:THR:OG1	2.34	0.43
1:1A:286:C:H2'	1:1A:287:C:H6	1.82	0.43
1:1A:400:G:N7	63:1A:4380:HOH:O	2.37	0.43
1:1A:2112:G:H8	1:1A:2112:G:OP2	2.02	0.43
1:1A:2123:G:H1	1:1A:2175:C:N4	2.15	0.43
1:1A:2345:G:N3	1:1A:2381:C:H2'	2.34	0.43
1:1A:2365:G:H4'	22:10:60:PHE:CZ	2.54	0.43
5:1F:129:PHE:CD2	5:1F:163:VAL:HG21	2.53	0.43
7:1H:56:SER:OG	7:1H:61:HIS:ND1	2.40	0.43
14:1S:67:ARG:HG2	14:1S:71:ARG:NH1	2.33	0.43
32:1a:22:G:H2'	32:1a:23:C:C6	2.54	0.43
32:1a:193:C:H2'	32:1a:194:C:C6	2.54	0.43
40:1i:31:GLN:NE2	40:1i:36:TYR:HD1	2.17	0.43
40:1i:31:GLN:HE21	40:1i:36:TYR:HD1	1.66	0.43
48:1q:45:HIS:HB2	48:1q:65:ILE:HD13	2.01	0.43
1:2A:8:A:H2'	1:2A:9:U:H6	1.84	0.43
1:2A:581:C:H5"	63:2U:304:HOH:O	2.19	0.43
1:2A:630:G:N2	1:2A:633:A:OP2	2.44	0.43
1:2A:1047:G:C4	1:2A:1110:G:N1	2.86	0.43
1:2A:1153:C:H5'	16:2U:76:TYR:CE2	2.53	0.43
1:2A:1354:A:H2'	1:2A:1355:G:O4'	2.18	0.43
1:2A:1506:C:H2'	1:2A:1507:A:H5'	2.01	0.43
1:2A:1817:G:OP1	3:2D:88:ARG:NH2	2.44	0.43
2:2B:28:C:H2'	2:2B:29:A:O4'	2.19	0.43
10:2O:71:ARG:HE	10:2O:105:GLU:CD	2.26	0.43
12:2Q:42:ILE:HD13	12:2Q:97:VAL:HB	2.00	0.43
16:2U:97:ASP:OD1	16:2U:101:ARG:HD2	2.19	0.43
21:2Z:20:ARG:HE	21:2Z:20:ARG:HB2	1.62	0.43
26:24:1:MET:HE2	26:24:6:HIS:CE1	2.53	0.43
32:2a:328:C:H4'	32:2a:329:A:H5'	2.01	0.43
32:2a:457:C:C2'	32:2a:458:C:H5'	2.49	0.43
32:2a:693:G:H1'	38:2g:82:GLY:H	1.83	0.43
32:2a:718:G:H5'	42:2k:117:ASN:OD1	2.19	0.43
32:2a:1129:C:N4	32:2a:1143:G:N1	2.57	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1516:G:N1	32:2a:1519:MA6:OP2	2.51	0.43
33:2b:166:ASP:HB3	33:2b:169:LYS:HB3	2.00	0.43
1:1A:876:C:H2'	1:1A:877:U:O4'	2.19	0.43
1:1A:1582:C:H2'	1:1A:1583:A:O4'	2.19	0.43
1:1A:2653:U:H5"	1:1A:2654:A:OP2	2.19	0.43
3:1D:132:PRO:HG3	3:1D:190:TYR:CE2	2.54	0.43
16:1U:81:HIS:CE1	16:1U:85:LYS:HD2	2.54	0.43
24:12:63:VAL:O	24:12:67:LYS:HG2	2.19	0.43
32:1a:160:A:H1'	32:1a:344:A:N7	2.34	0.43
32:1a:384:G:H2'	32:1a:385:C:C6	2.54	0.43
32:1a:632:A:H3'	32:1a:633:G:H8	1.84	0.43
32:1a:1028:C:H3'	32:1a:1028:C:H6	1.83	0.43
38:1g:50:ILE:HD11	38:1g:58:PRO:HA	2.01	0.43
39:1h:120:THR:H	39:1h:123:GLU:HB2	1.83	0.43
43:1l:54:LYS:HD2	43:1l:54:LYS:N	2.34	0.43
44:1m:22:ILE:HD12	44:1m:25:ILE:HD13	1.99	0.43
51:1t:43:LEU:HD12	51:1t:55:ILE:HG13	2.00	0.43
51:1t:43:LEU:HD23	51:1t:43:LEU:HA	1.93	0.43
1:2A:1005:C:H2'	1:2A:1006:C:C6	2.54	0.43
1:2A:1020:A:N1	1:2A:1141:U:O2'	2.46	0.43
1:2A:2103:C:H2'	1:2A:2104:G:C8	2.54	0.43
1:2A:2302:G:N2	6:2G:126:ASP:OD1	2.48	0.43
2:2B:70:C:H2'	2:2B:71:C:H6	1.83	0.43
3:2D:77:ALA:HB2	3:2D:97:TYR:CD1	2.54	0.43
6:2G:7:LEU:HD13	6:2G:104:GLU:HA	2.00	0.43
6:2G:116:ASP:OD1	44:2m:68:GLY:HA3	2.18	0.43
6:2G:135:LEU:HD22	6:2G:141:PHE:HE2	1.84	0.43
31:29:7:VAL:HG12	31:29:34:GLN:HB3	2.00	0.43
32:2a:973:G:H3'	32:2a:974:A:H5"	2.00	0.43
32:2a:1002:G:N2	32:2a:1039:C:C2	2.87	0.43
32:2a:1122:U:H2'	32:2a:1123:A:C8	2.54	0.43
34:2c:7:PRO:HA	34:2c:10:PHE:HB3	2.00	0.43
34:2c:22:TRP:CZ2	45:2n:54:PRO:HG2	2.54	0.43
34:2c:53:ALA:HB2	34:2c:115:LEU:HD11	2.01	0.43
34:2c:63:ASN:HB3	34:2c:98:ASN:OD1	2.19	0.43
35:2d:13:ARG:HH22	35:2d:36:ARG:NE	2.17	0.43
53:2y:6:THR:HG22	53:2y:40:ILE:HG23	2.01	0.43
1:1A:263:C:H2'	1:1A:264:C:O4'	2.19	0.43
1:1A:864:G:OP2	12:1Q:22:LYS:HE3	2.19	0.43
1:1A:1104:C:H2'	1:1A:1105:U:C5	2.53	0.43
1:1A:1405:U:H2'	1:1A:1406:U:H6	1.82	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1815:A:P	3:1D:54:ARG:HH22	2.40	0.43
1:1A:2712:U:H2'	1:1A:2714:G:H5"	2.01	0.43
5:1F:64:ILE:HD12	5:1F:65:TRP:CZ3	2.54	0.43
7:1H:11:VAL:HG13	7:1H:15:VAL:HG22	2.01	0.43
14:1S:59:LYS:HZ1	14:1S:68:GLN:HE22	1.67	0.43
21:1Z:44:PHE:CZ	21:1Z:86:VAL:HG11	2.54	0.43
29:17:32:LYS:NZ	63:17:202:HOH:O	2.41	0.43
32:1a:374:A:C6	32:1a:375:U:C4	3.07	0.43
32:1a:411:A:OP2	35:1d:25:ARG:NH2	2.47	0.43
32:1a:747:C:H3'	32:1a:748:C:C6	2.54	0.43
32:1a:1226:C:H4'	32:1a:1227:A:OP1	2.18	0.43
35:1d:102:ASP:HB3	35:1d:136:PRO:HB3	2.01	0.43
1:2A:636:G:H5'	1:2A:639:U:OP1	2.19	0.43
1:2A:2330:G:H2'	1:2A:2331:G:O4'	2.19	0.43
1:2A:2751:G:H4'	7:2H:4:ILE:HD11	2.00	0.43
2:2B:31:C:H4'	6:2G:29:TRP:CZ2	2.54	0.43
9:2N:14:VAL:HG11	9:2N:138:LEU:HD12	2.01	0.43
10:2O:70:LYS:HE2	10:2O:70:LYS:HB3	1.61	0.43
13:2R:9:LYS:O	13:2R:17:ARG:HD3	2.19	0.43
20:2Y:68:HIS:CE1	20:2Y:70:SER:HB3	2.54	0.43
23:21:62:VAL:HG22	23:21:63:ALA:O	2.19	0.43
32:2a:7:G:O2'	36:2e:120:THR:O	2.37	0.43
32:2a:1154:G:H2'	32:2a:1155:G:C8	2.54	0.43
36:2e:33:VAL:HG13	36:2e:112:LEU:HD22	2.00	0.43
38:2g:73:MET:HG2	38:2g:90:GLU:HA	2.01	0.43
41:2j:32:ALA:O	41:2j:76:ASN:N	2.50	0.43
1:1A:1164:G:H2'	1:1A:1165:U:C6	2.53	0.42
1:1A:2747:G:O6	1:1A:2755:C:H5"	2.19	0.42
2:1B:66:A:N6	2:1B:108:U:H2'	2.34	0.42
5:1F:10:PRO:HB3	5:1F:17:ARG:HH21	1.83	0.42
6:1G:135:LEU:O	6:1G:154:GLY:HA3	2.18	0.42
12:1Q:110:THR:HG23	12:1Q:113:GLN:OE1	2.18	0.42
13:1R:59:ASP:OD1	13:1R:59:ASP:N	2.51	0.42
21:1Z:25:PRO:O	21:1Z:85:HIS:HA	2.19	0.42
32:1a:355:C:O2'	32:1a:388:G:N3	2.41	0.42
32:1a:765:G:H5"	32:1a:766:A:OP1	2.18	0.42
32:1a:1032:G:N2	32:1a:1033:G:N3	2.67	0.42
32:1a:1179:A:OP2	40:1i:93:ARG:NH2	2.50	0.42
32:1a:1277:C:O2'	32:1a:1279:A:H1'	2.19	0.42
32:1a:1279:A:H5"	32:1a:1280:A:OP1	2.19	0.42
37:1f:21:LEU:O	37:1f:25:ILE:HG12	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:1f:100:ASN:HD21	49:1r:23:LYS:HD3	1.83	0.42
52:1u:5:ASP:O	52:1u:11:GLY:HA3	2.19	0.42
1:2A:311:A:C6	1:2A:328:U:C4	3.06	0.42
1:2A:1031:G:O2'	31:29:7:VAL:O	2.32	0.42
1:2A:1667:G:O2'	1:2A:1991:U:O4	2.27	0.42
2:2B:112:U:O2'	2:2B:113:G:H5'	2.19	0.42
6:2G:5:VAL:HG11	6:2G:101:ILE:HG12	2.01	0.42
7:2H:24:VAL:HG21	7:2H:72:ILE:HD11	2.00	0.42
7:2H:27:LYS:NZ	7:2H:32:GLU:OE1	2.52	0.42
32:2a:935:A:O2'	32:2a:1383:C:N3	2.49	0.42
32:2a:1239:A:C4	32:2a:1298:C:N4	2.87	0.42
34:2c:112:SER:O	34:2c:116:VAL:HG23	2.19	0.42
1:1A:1364:G:N7	23:11:3:LYS:HE2	2.33	0.42
1:1A:2140:C:H2'	1:1A:2141:G:C8	2.53	0.42
1:1A:2850:A:C2	1:1A:2851:A:C4	3.07	0.42
3:1D:221:VAL:HG22	3:1D:226:MET:HE3	2.01	0.42
4:1E:170:LEU:HD23	4:1E:184:VAL:CG1	2.48	0.42
11:1P:2:LYS:NZ	63:1P:311:HOH:O	2.52	0.42
21:1Z:152:ALA:HB3	21:1Z:167:PRO:HA	2.00	0.42
28:16:47:THR:HG22	28:16:48:VAL:O	2.18	0.42
34:1c:35:GLU:OE2	34:1c:95:THR:HA	2.19	0.42
37:1f:61:LEU:HD23	37:1f:63:TYR:OH	2.20	0.42
37:1f:69:GLU:O	37:1f:72:VAL:HG13	2.19	0.42
42:1k:41:THR:OG1	42:1k:42:TRP:N	2.52	0.42
43:1l:117:ARG:HD2	43:1l:122:THR:HG22	2.00	0.42
1:2A:350:U:H2'	1:2A:351:G:O4'	2.19	0.42
1:2A:652(V):C:H2'	1:2A:653:A:O4'	2.19	0.42
1:2A:2206:G:C8	1:2A:2207:G:N7	2.78	0.42
63:2B:311:HOH:O	21:2Z:31:ARG:N	2.52	0.42
6:2G:10:LYS:HG3	6:2G:14:GLU:OE1	2.19	0.42
7:2H:84:SER:HA	7:2H:133:VAL:O	2.20	0.42
33:2b:43:ASP:O	33:2b:47:THR:HG23	2.19	0.42
34:2c:181:ASN:N	34:2c:181:ASN:HD22	2.15	0.42
35:2d:10:ARG:HB2	35:2d:40:PRO:HG3	2.02	0.42
35:2d:173:TRP:O	35:2d:186:LEU:HB2	2.20	0.42
36:2e:78:HIS:CE1	36:2e:142:LEU:HD23	2.54	0.42
37:2f:67:MET:HE1	37:2f:75:LEU:HD22	2.01	0.42
51:2t:13:LEU:O	51:2t:17:ARG:HG3	2.19	0.42
1:1A:102:G:O6	20:1Y:94:LYS:HE2	2.19	0.42
1:1A:446:G:OP1	16:1U:3:ARG:NH1	2.51	0.42
1:1A:515:A:H1'	1:1A:581:C:H1'	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1486:A:H2'	1:1A:1487:G:C8	2.54	0.42
1:1A:1528:A:OP2	63:1A:4185:HOH:O	2.21	0.42
1:1A:2114:A:H3'	1:1A:2115:G:H8	1.85	0.42
2:1B:55:U:H2'	2:1B:56:G:O4'	2.19	0.42
8:1I:43:ASN:HD22	8:1I:43:ASN:HA	1.60	0.42
11:1P:124:LYS:HE2	11:1P:146:VAL:HG21	2.02	0.42
15:1T:91:ARG:HB2	15:1T:121:ILE:HG13	2.00	0.42
17:1V:21:ARG:HD3	17:1V:91:TYR:CE1	2.54	0.42
34:1c:97:LYS:HE2	34:1c:97:LYS:HB3	1.85	0.42
34:1c:148:GLY:HA3	34:1c:172:ARG:O	2.19	0.42
36:1e:57:LYS:HE3	36:1e:57:LYS:HB2	1.85	0.42
40:1i:117:HIS:CE1	40:1i:123:PRO:HB3	2.54	0.42
42:1k:92:GLU:HA	42:1k:95:ILE:HD12	2.01	0.42
42:1k:109:VAL:HA	49:1r:85:LEU:O	2.19	0.42
49:1r:47:THR:O	49:1r:47:THR:OG1	2.37	0.42
1:2A:443:A:H1'	1:2A:1201:C:O4'	2.18	0.42
1:2A:896:A:C4	21:2Z:146:ILE:HG21	2.54	0.42
1:2A:1073:A:H2'	1:2A:1074:G:H8	1.85	0.42
1:2A:2080:G:H5'	23:21:35:THR:HG23	2.01	0.42
2:2B:13:A:N1	2:2B:69:G:O2'	2.47	0.42
2:2B:73:A:C4	2:2B:105:A:C2	3.07	0.42
4:2E:108:SER:O	4:2E:162:ALA:HA	2.19	0.42
8:2I:96:ASP:O	8:2I:98:ALA:N	2.44	0.42
9:2N:29:LYS:HD3	9:2N:140:VAL:HB	2.01	0.42
32:2a:685:G:C2	32:2a:686:U:C4	3.08	0.42
32:2a:1090:U:H2'	32:2a:1091:U:H6	1.83	0.42
32:2a:1346:A:H61	32:2a:1374:A:H3'	1.84	0.42
36:2e:148:VAL:HG21	39:2h:107:LEU:HD22	2.00	0.42
50:2s:30:LEU:HD12	50:2s:48:THR:O	2.19	0.42
1:1A:2017:U:O2	27:15:10:LYS:HB2	2.20	0.42
1:1A:2030:A:H4'	1:1A:2031:A:C8	2.54	0.42
5:1F:110:LEU:HD23	5:1F:110:LEU:HA	1.90	0.42
32:1a:33:A:N3	43:1l:32:PHE:HE2	2.18	0.42
32:1a:1149:C:P	40:1i:9:ARG:HH21	2.42	0.42
44:1m:4:ILE:HG13	44:1m:57:ARG:HA	2.00	0.42
1:2A:2116:G:O2'	1:2A:2117:A:O5'	2.36	0.42
1:2A:2207:G:H2'	1:2A:2208:A:C2	2.55	0.42
1:2A:2364:C:H2'	1:2A:2365:G:O4'	2.19	0.42
9:2N:75:TYR:CE2	9:2N:77:GLY:HA2	2.54	0.42
11:2P:86:LYS:HG3	11:2P:87:ASP:N	2.34	0.42
32:2a:659:U:C2'	32:2a:660:G:H5'	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:954:G:H21	32:2a:1227:A:N6	2.10	0.42
32:2a:1426:C:H2'	32:2a:1427:U:C6	2.54	0.42
32:2a:1496:C:OP2	53:2y:26:LYS:NZ	2.24	0.42
37:2f:67:MET:HE3	37:2f:72:VAL:HB	2.02	0.42
45:2n:4:LYS:HA	45:2n:7:ILE:HG12	2.01	0.42
53:2y:15:ALA:O	53:2y:19:HIS:N	2.50	0.42
1:1A:729:G:N7	3:1D:210:GLY:N	2.67	0.42
1:1A:1062:G:C4	1:1A:1088:A:C8	3.08	0.42
1:1A:1100:C:H2'	1:1A:1101:U:O4'	2.19	0.42
1:1A:1450(A):C:C2'	1:1A:1451:C:H5'	2.50	0.42
1:1A:1769:G:O2'	1:1A:1958:C:OP1	2.25	0.42
12:1Q:109:VAL:HG22	12:1Q:113:GLN:OE1	2.18	0.42
19:1X:12:VAL:CG2	19:1X:27:THR:HG22	2.50	0.42
30:18:62:LEU:HB3	30:18:65:GLU:CG	2.49	0.42
32:1a:119:A:H5'	32:1a:120:A:C4	2.54	0.42
32:1a:1305:G:H22	32:1a:1331:G:H1'	1.84	0.42
34:1c:3:ASN:OD1	34:1c:3:ASN:N	2.52	0.42
34:1c:172:ARG:HB3	34:1c:174:PRO:HD3	2.01	0.42
40:1i:77:ILE:O	40:1i:81:ILE:HG23	2.20	0.42
42:1k:33:THR:HG22	42:1k:39:PRO:HA	2.01	0.42
1:2A:57:C:H2'	1:2A:58:G:O4'	2.19	0.42
1:2A:634:C:H2'	1:2A:635:C:C6	2.54	0.42
1:2A:945:A:H5"	63:2A:4100:HOH:O	2.19	0.42
1:2A:981:A:OP1	63:2A:3893:HOH:O	2.21	0.42
1:2A:1110:G:H8	1:2A:1110:G:OP2	2.02	0.42
1:2A:1153:C:H5'	16:2U:76:TYR:HE2	1.84	0.42
1:2A:1557:C:H5"	1:2A:1558:A:OP2	2.19	0.42
1:2A:2277:G:OP2	22:20:10:THR:HG21	2.19	0.42
2:2B:43:C:OP1	26:24:6:HIS:NE2	2.52	0.42
5:2F:140:LEU:HD11	5:2F:170:LEU:HD11	2.01	0.42
5:2F:192:LEU:HD13	5:2F:194:MET:HE2	2.01	0.42
5:2F:196:LEU:O	5:2F:200:GLU:N	2.51	0.42
15:2T:77:PRO:HB2	15:2T:80:SER:HB2	2.02	0.42
20:2Y:1:MET:HE2	20:2Y:1:MET:HB3	1.98	0.42
21:2Z:152:ALA:O	21:2Z:155:LEU:HB2	2.19	0.42
32:2a:189:G:H2'	32:2a:189(A):C:C6	2.55	0.42
32:2a:949:A:C4	32:2a:1233:G:N2	2.88	0.42
33:2b:115:LEU:O	33:2b:119:GLU:N	2.52	0.42
33:2b:221:LEU:HD12	33:2b:224:GLN:HB3	2.01	0.42
33:2b:229:VAL:HG12	33:2b:230:VAL:H	1.85	0.42
51:2t:42:GLN:O	51:2t:45:GLN:HB3	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:557:U:H2'	1:1A:558:G:C8	2.54	0.42
1:1A:729:G:C5	3:1D:208:LYS:HB2	2.55	0.42
1:1A:1503:U:H2'	1:1A:1504:C:H6	1.84	0.42
1:1A:2055:C:O2	63:1A:4188:HOH:O	2.21	0.42
1:1A:2142:C:H2'	1:1A:2143:C:C6	2.55	0.42
1:1A:2824:C:N4	63:1A:4262:HOH:O	2.28	0.42
4:1E:152:LYS:HG3	9:1N:77:GLY:O	2.19	0.42
6:1G:153:ARG:HB2	6:1G:153:ARG:NH2	2.34	0.42
14:1S:14:VAL:O	14:1S:18:ILE:HG12	2.20	0.42
14:1S:65:VAL:O	14:1S:69:VAL:HG12	2.19	0.42
14:1S:99:LYS:HE2	14:1S:103:GLU:OE2	2.19	0.42
32:1a:575:G:O2'	32:1a:821:G:H5'	2.19	0.42
32:1a:669:U:H2'	32:1a:670:G:H8	1.84	0.42
32:1a:1137:C:H5'	32:1a:1138:G:C5	2.54	0.42
32:1a:1149:C:OP2	40:1i:9:ARG:NH2	2.50	0.42
32:1a:1212:U:H5"	32:1a:1213:A:O5'	2.19	0.42
32:1a:1324:A:O4'	32:1a:1362:C:H4'	2.20	0.42
36:1e:100:VAL:HG13	36:1e:118:ILE:HG22	2.01	0.42
44:1m:97:PRO:HA	44:1m:110:ARG:HG3	2.01	0.42
48:1q:54:GLY:HA2	48:1q:85:VAL:HG21	2.01	0.42
1:2A:30:G:H2'	1:2A:31:C:C6	2.55	0.42
1:2A:185:U:H2'	1:2A:186:G:C8	2.55	0.42
1:2A:828:U:H4'	1:2A:831:G:N1	2.35	0.42
1:2A:863:A:C2	1:2A:864:G:C4	3.08	0.42
1:2A:1814:G:C4'	3:2D:51:VAL:HG21	2.49	0.42
8:2I:69:LYS:HD2	8:2I:138:ILE:HG12	2.01	0.42
14:2S:64:GLU:H	14:2S:64:GLU:CD	2.28	0.42
24:22:55:ARG:O	24:22:59:ARG:HB2	2.19	0.42
32:2a:262:A:C6	32:2a:263:A:C6	3.07	0.42
32:2a:443:C:H2'	32:2a:444:C:H6	1.85	0.42
32:2a:551:U:H2'	32:2a:552:U:C6	2.53	0.42
32:2a:750:G:N3	46:2o:23:GLY:HA3	2.34	0.42
32:2a:859:A:H2'	32:2a:860:A:O4'	2.20	0.42
42:2k:65:ALA:HB1	42:2k:98:LEU:HD21	2.01	0.42
1:1A:244:A:C2	1:1A:255:A:C4	3.07	0.42
13:1R:72:ASP:HB3	13:1R:75:LEU:HB3	2.01	0.42
32:1a:260:G:H2'	32:1a:261:U:C6	2.55	0.42
32:1a:461:A:O2'	32:1a:470:C:H5'	2.20	0.42
32:1a:1100:C:OP2	33:1b:96:ARG:HD3	2.20	0.42
32:1a:1302:U:C5	44:1m:17:VAL:HG21	2.54	0.42
32:1a:1323:G:H2'	32:1a:1324:A:C8	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:1b:118:LEU:HB3	33:1b:142:LEU:HD12	2.02	0.42
35:1d:99:SER:O	35:1d:140:VAL:HG23	2.19	0.42
40:1i:111:ARG:HG3	45:1n:61:TRP:HE1	1.84	0.42
43:1l:25:PRO:O	43:1l:28:LYS:HE3	2.19	0.42
1:2A:888:C:H2'	1:2A:889:C:C2	2.54	0.42
1:2A:1668:A:H4'	1:2A:1669:A:O5'	2.20	0.42
3:2D:77:ALA:HA	3:2D:97:TYR:HA	2.00	0.42
3:2D:155:LEU:HG	3:2D:177:LEU:HD22	2.01	0.42
4:2E:12:THR:HB	4:2E:13:ARG:H	1.62	0.42
9:2N:83:LYS:HB2	9:2N:83:LYS:HE3	1.81	0.42
11:2P:88:LEU:HD11	11:2P:114:ILE:HD12	2.01	0.42
13:2R:26:LYS:HE2	13:2R:70:LEU:O	2.19	0.42
18:2W:1:MET:HE3	18:2W:62:HIS:HB3	2.02	0.42
20:2Y:8:LYS:HG2	20:2Y:97:ARG:HH12	1.84	0.42
20:2Y:19:LYS:HB3	20:2Y:19:LYS:HE2	1.80	0.42
32:2a:189:G:C2	32:2a:189(L):G:C2	3.08	0.42
32:2a:673:G:H5'	37:2f:87:ARG:CZ	2.50	0.42
32:2a:1060:C:H4'	41:2j:51:ARG:HB3	2.00	0.42
33:2b:32:ILE:HG21	33:2b:40:HIS:CD2	2.55	0.42
33:2b:69:LEU:HD12	33:2b:159:PRO:CG	2.49	0.42
39:2h:28:ALA:HB3	39:2h:57:PRO:HB2	2.02	0.42
43:2l:46:LYS:HD2	43:2l:94:PRO:HG3	2.02	0.42
1:1A:657:U:H2'	1:1A:658:C:C6	2.55	0.42
1:1A:1889:A:H2'	1:1A:1890:A:C8	2.55	0.42
6:1G:28:VAL:O	6:1G:31:VAL:HG22	2.20	0.42
9:1N:12:ARG:HB3	9:1N:50:ASP:OD1	2.20	0.42
9:1N:30:ILE:HG22	9:1N:34:LEU:HD22	2.00	0.42
12:1Q:89:ASN:ND2	63:1Q:304:HOH:O	2.52	0.42
32:1a:673:G:H5"	37:1f:87:ARG:CZ	2.50	0.42
33:1b:16:HIS:CG	33:1b:17:PHE:N	2.87	0.42
34:1c:19:GLU:HB3	34:1c:40:ARG:NH2	2.33	0.42
38:1g:22:LEU:HD21	38:1g:66:VAL:HG11	2.01	0.42
50:1s:11:VAL:CG1	50:1s:16:LEU:HB2	2.50	0.42
51:1t:57:ARG:HH22	51:1t:100:ILE:HD12	1.85	0.42
1:2A:746:A:HO2'	1:2A:2611:U:HO2'	1.68	0.42
4:2E:8:LYS:HD2	4:2E:188:VAL:HG12	2.02	0.42
6:2G:11:TYR:OH	6:2G:16:ARG:HD3	2.20	0.42
8:2I:55:ALA:HA	8:2I:58:LEU:HD23	2.02	0.42
11:2P:59:LEU:HD13	30:28:58:ILE:HG12	2.02	0.42
19:2X:3:THR:HG21	24:22:26:ARG:HG3	2.02	0.42
21:2Z:58:VAL:HG22	21:2Z:68:PRO:HB3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:20:45:PHE:O	22:20:59:LEU:HD11	2.19	0.42
23:21:5:CYS:HB3	23:21:10:LYS:H	1.84	0.42
31:29:2:LYS:HB2	31:29:34:GLN:HG2	2.02	0.42
32:2a:427:U:OP1	35:2d:13:ARG:NH1	2.53	0.42
32:2a:779:C:H2'	32:2a:780:A:O4'	2.20	0.42
32:2a:984:C:H2'	32:2a:985:C:H6	1.84	0.42
32:2a:1009:G:H1	32:2a:1020:U:H3	1.68	0.42
32:2a:1216:G:OP1	45:2n:2:ALA:HA	2.20	0.42
33:2b:7:VAL:O	33:2b:217:ARG:HD3	2.20	0.42
33:2b:24:TRP:HB3	33:2b:40:HIS:CE1	2.55	0.42
33:2b:167:PRO:HD3	33:2b:187:LEU:O	2.20	0.42
34:2c:78:GLY:HA3	34:2c:83:ARG:H	1.84	0.42
34:2c:82:GLU:O	34:2c:86:VAL:N	2.52	0.42
38:2g:114:ARG:HB2	38:2g:115:ARG:HH21	1.83	0.42
42:2k:22:HIS:HB3	42:2k:29:ILE:HB	2.02	0.42
53:2y:12:ILE:HG23	53:2y:16:ILE:HG12	2.01	0.42
1:1A:58:G:O2'	1:1A:73:A:N1	2.46	0.42
1:1A:184:C:H2'	1:1A:185:U:C6	2.55	0.42
1:1A:2615:U:H2'	1:1A:2616:C:C6	2.55	0.42
4:1E:101:ARG:CZ	4:1E:171:GLU:HB2	2.50	0.42
8:1I:38:LEU:HB3	8:1I:40:THR:HG22	2.02	0.42
16:1U:79:PHE:CZ	16:1U:83:LEU:HD11	2.55	0.42
17:1V:20:LEU:HD12	17:1V:20:LEU:HA	1.85	0.42
18:1W:25:ARG:NH2	18:1W:74:ALA:O	2.44	0.42
20:1Y:19:LYS:HB3	20:1Y:19:LYS:HE2	1.88	0.42
23:11:53:VAL:HG22	23:11:74:VAL:HG13	2.01	0.42
28:16:6:ARG:HH12	28:16:26:ASN:HB2	1.84	0.42
32:1a:392:G:H2'	32:1a:393:A:H8	1.85	0.42
32:1a:447:G:H2'	32:1a:485:G:N2	2.35	0.42
32:1a:1028:C:H3'	32:1a:1028:C:C6	2.55	0.42
32:1a:1058:G:C5	32:1a:1059:C:C4	3.08	0.42
33:1b:180:LEU:O	33:1b:182:ILE:HG13	2.20	0.42
35:1d:10:ARG:HB2	35:1d:40:PRO:HG3	2.01	0.42
40:1i:29:ASN:OD1	40:1i:65:VAL:N	2.47	0.42
40:1i:111:ARG:HG3	45:1n:61:TRP:NE1	2.35	0.42
48:1q:43:LEU:HD12	48:1q:68:ARG:HB2	2.01	0.42
50:1s:40:ILE:HA	50:1s:44:MET:SD	2.60	0.42
1:2A:1590:U:H2'	1:2A:1591:G:C8	2.55	0.42
1:2A:2636:U:H2'	1:2A:2637:U:H6	1.84	0.42
25:23:43:ILE:O	25:23:47:VAL:HG23	2.19	0.42
26:24:46:GLN:C	26:24:48:ARG:H	2.27	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:9:G:OP2	36:2e:121:LYS:NZ	2.45	0.42
32:2a:88:A:H4'	32:2a:89:C:H5"	2.01	0.42
32:2a:325:A:H2'	32:2a:326:G:O4'	2.19	0.42
32:2a:1122:U:H2'	32:2a:1123:A:H8	1.85	0.42
32:2a:1205:U:H4'	34:2c:195:VAL:HG23	2.02	0.42
32:2a:1220:G:H2'	32:2a:1221:G:O4'	2.20	0.42
38:2g:45:ASP:O	38:2g:49:ILE:HG13	2.20	0.42
39:2h:48:TYR:HA	39:2h:60:ARG:O	2.19	0.42
45:2n:29:ARG:HD3	45:2n:40:CYS:SG	2.60	0.42
1:1A:637:A:H2'	11:1P:117:GLU:OE1	2.20	0.42
1:1A:740:U:H2'	1:1A:741:G:C8	2.55	0.42
1:1A:1899:G:N3	1:1A:1899:G:H2'	2.34	0.42
4:1E:29:GLY:HA3	63:1E:418:HOH:O	2.19	0.42
6:1G:83:ARG:H	6:1G:86:MET:CE	2.28	0.42
7:1H:98:LEU:HD12	7:1H:98:LEU:HA	1.88	0.42
16:1U:10:ARG:NH2	63:1U:313:HOH:O	2.51	0.42
32:1a:1003:G:N2	32:1a:1004:A:N3	2.68	0.42
35:1d:173:TRP:CD1	35:1d:189:PRO:HB3	2.55	0.42
42:1k:77:MET:HE2	42:1k:77:MET:HB2	1.83	0.42
1:2A:302:C:H2'	1:2A:303:U:C6	2.55	0.42
1:2A:864:G:N2	1:2A:913:U:C2	2.88	0.42
1:2A:1087:G:N7	1:2A:1089:G:C8	2.87	0.42
1:2A:1417:C:H2'	1:2A:1418:G:O4'	2.20	0.42
1:2A:2180:U:H2'	1:2A:2181:G:C8	2.54	0.42
2:2B:1:U:H2'	2:2B:2:C:C6	2.55	0.42
11:2P:59:LEU:HD23	11:2P:60:MET:HE2	2.02	0.42
12:2Q:7:MET:HE2	21:2Z:194:PRO:HB2	2.02	0.42
17:2V:4:ILE:HD12	17:2V:39:LEU:HD22	2.02	0.42
32:2a:982:U:OP2	45:2n:23:ARG:NH2	2.44	0.42
32:2a:1074:G:O2'	32:2a:1101:A:N1	2.47	0.42
32:2a:1091:U:H2'	32:2a:1093:A:OP2	2.20	0.42
32:2a:1170:A:C5	32:2a:1171:G:H1'	2.55	0.42
33:2b:161:ALA:HB1	33:2b:185:ILE:HD13	2.01	0.42
39:2h:9:MET:HG3	39:2h:26:VAL:HG11	2.00	0.42
44:2m:81:LEU:HD22	44:2m:88:ARG:HB3	2.02	0.42
1:1A:1503:U:H2'	1:1A:1504:C:C6	2.55	0.41
1:1A:2319:G:H4'	1:1A:2320:A:OP1	2.20	0.41
1:1A:2607:G:H2'	1:1A:2608:G:O4'	2.20	0.41
4:1E:72:VAL:HG12	4:1E:73:GLU:O	2.20	0.41
10:1O:4:PRO:O	10:1O:5:GLN:HB2	2.20	0.41
11:1P:2:LYS:HE2	11:1P:4:SER:H	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:12:53:LEU:HD23	24:12:53:LEU:HA	1.71	0.41
32:1a:67:C:O2'	32:1a:171:A:H1'	2.19	0.41
32:1a:359:U:H2'	32:1a:360:A:C8	2.55	0.41
32:1a:922:G:C6	32:1a:923:A:C6	3.08	0.41
32:1a:1070:U:H2'	32:1a:1071:C:C6	2.55	0.41
32:1a:1169:A:H2'	32:1a:1170:A:C8	2.54	0.41
32:1a:1328:C:OP1	52:1u:21:TYR:OH	2.35	0.41
35:1d:98:GLU:O	35:1d:103:ASN:ND2	2.53	0.41
37:1f:82:ARG:HB2	37:1f:85:VAL:HG23	2.02	0.41
40:1i:5:TYR:HB2	40:1i:18:PHE:CD1	2.55	0.41
51:1t:63:ILE:HG21	51:1t:81:LYS:HG3	2.02	0.41
1:2A:244:A:C2	1:2A:255:A:C4	3.08	0.41
1:2A:262:A:H2'	1:2A:263:C:O4'	2.20	0.41
1:2A:885:C:H2'	1:2A:886:C:O4'	2.20	0.41
1:2A:2139:C:N4	1:2A:2152:G:N1	2.42	0.41
8:2I:23:PRO:O	8:2I:27:ARG:HB2	2.20	0.41
10:2O:64:ARG:HD2	10:2O:81:ASP:OD1	2.20	0.41
15:2T:114:LEU:HA	15:2T:114:LEU:HD23	1.70	0.41
21:2Z:10:ARG:NH1	21:2Z:26:GLY:H	2.18	0.41
24:22:64:LEU:O	24:22:68:ARG:HG2	2.20	0.41
25:23:3:ARG:HG2	25:23:38:GLU:HA	2.02	0.41
26:24:48:ARG:O	26:24:49:PHE:HB2	2.20	0.41
30:28:14:VAL:HG11	30:28:58:ILE:HG21	2.02	0.41
32:2a:19:C:H5"	36:2e:86:ALA:HB3	2.00	0.41
32:2a:235:C:H2'	32:2a:236:G:H8	1.84	0.41
32:2a:451:A:N6	32:2a:480:U:H2'	2.35	0.41
32:2a:643:C:O2'	39:2h:132:GLU:OE2	2.37	0.41
32:2a:853:G:C4	32:2a:854:G:C8	3.09	0.41
32:2a:1026:G:N3	32:2a:1026:G:H2'	2.34	0.41
32:2a:1120:G:H2'	32:2a:1121:U:H6	1.84	0.41
33:2b:61:LEU:HD11	33:2b:160:ASP:HB3	2.02	0.41
33:2b:69:LEU:HD12	33:2b:159:PRO:HG2	2.02	0.41
47:2p:18:ARG:HG2	47:2p:35:LYS:HE3	2.01	0.41
1:1A:797:C:H2'	1:1A:798:G:O4'	2.20	0.41
1:1A:829:A:N7	1:1A:2248:C:H5'	2.35	0.41
1:1A:1045:A:H1'	1:1A:1047:G:N3	2.35	0.41
1:1A:1328:G:O2'	1:1A:1329:U:H2'	2.20	0.41
1:1A:1796:U:H2'	1:1A:1797:C:H6	1.83	0.41
1:1A:2022:U:O2'	1:1A:2617:C:H5'	2.21	0.41
2:1B:19:G:H1	2:1B:64:C:H42	1.67	0.41
2:1B:24:G:H4'	2:1B:25:A:C8	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:1G:68:PRO:HB3	6:1G:92:VAL:HB	2.02	0.41
7:1H:52:VAL:HG12	7:1H:65:HIS:CD2	2.55	0.41
12:1Q:101:ARG:NH1	63:1Q:306:HOH:O	2.53	0.41
13:1R:83:ILE:O	13:1R:86:ARG:HG2	2.20	0.41
21:1Z:92:SER:O	21:1Z:130:PRO:HG2	2.21	0.41
32:1a:179:A:H2'	32:1a:180:U:C6	2.55	0.41
32:1a:404:U:H2'	32:1a:405:U:H6	1.85	0.41
32:1a:1347:G:H22	32:1a:1374:A:P	2.43	0.41
33:1b:40:HIS:CB	33:1b:190:THR:HG21	2.50	0.41
37:1f:48:LEU:HD13	37:1f:52:ILE:HG13	2.02	0.41
41:1j:37:PRO:HA	41:1j:71:LEU:O	2.20	0.41
1:2A:321:G:C2	1:2A:341:G:H4'	2.55	0.41
1:2A:468:G:N7	29:27:39:ARG:NH2	2.64	0.41
1:2A:517:C:OP1	27:25:16:ARG:NH2	2.53	0.41
1:2A:656:G:H2'	1:2A:657:U:O4'	2.20	0.41
1:2A:852:G:H2'	1:2A:853:G:C8	2.55	0.41
1:2A:2370:G:C6	1:2A:2371:G:C6	3.08	0.41
1:2A:2636:U:H2'	1:2A:2637:U:C6	2.55	0.41
1:2A:2876:G:OP1	63:2A:3896:HOH:O	2.21	0.41
3:2D:235:GLY:O	63:2D:401:HOH:O	2.21	0.41
4:2E:29:GLY:HA3	4:2E:30:PRO:HA	1.82	0.41
6:2G:179:PRO:HG3	26:24:43:TYR:OH	2.19	0.41
7:2H:13:LYS:HA	7:2H:14:GLY:HA2	1.71	0.41
14:2S:93:LYS:NZ	63:2S:203:HOH:O	2.53	0.41
29:27:29:LYS:HD3	29:27:29:LYS:HA	1.94	0.41
32:2a:1530:G:H2'	32:2a:1531:A:C8	2.55	0.41
33:2b:114:ARG:HH21	33:2b:118:LEU:HD21	1.85	0.41
33:2b:219:VAL:O	33:2b:222:ILE:HG12	2.20	0.41
34:2c:121:ALA:HB1	34:2c:188:LEU:O	2.20	0.41
34:2c:122:GLU:HA	34:2c:125:GLU:OE1	2.20	0.41
40:2i:47:LEU:O	40:2i:51:ARG:HG3	2.20	0.41
50:2s:50:ALA:HA	50:2s:58:VAL:O	2.19	0.41
51:2t:53:LEU:HD23	51:2t:53:LEU:HA	1.83	0.41
51:2t:55:ILE:HD12	51:2t:55:ILE:HA	1.97	0.41
1:1A:582:G:H2'	1:1A:583:G:C8	2.56	0.41
1:1A:1857:G:C6	1:1A:1858:G:C6	3.08	0.41
1:1A:2298:A:H2'	1:1A:2299:G:O4'	2.19	0.41
1:1A:2406:U:H6	1:1A:2406:U:H2'	1.66	0.41
32:1a:760:G:N2	48:1q:97:SER:HB2	2.34	0.41
32:1a:1010:G:N2	32:1a:1020:U:H1'	2.34	0.41
32:1a:1024:G:N2	32:1a:1025:U:H5"	2.28	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:1k:45:GLY:HA3	42:1k:55:LYS:HB2	2.03	0.41
42:1k:67:ASP:OD1	42:1k:71:LYS:NZ	2.51	0.41
50:1s:12:ASP:O	50:1s:14:HIS:N	2.51	0.41
1:2A:848:G:H2'	1:2A:849:A:C8	2.55	0.41
13:2R:103:ARG:NH1	13:2R:108:GLY:O	2.49	0.41
16:2U:47:TYR:HA	16:2U:50:ARG:NH2	2.35	0.41
17:2V:71:LEU:HD22	17:2V:71:LEU:HA	1.85	0.41
17:2V:80:GLN:HB2	63:2V:303:HOH:O	2.20	0.41
32:2a:671:G:H2'	32:2a:672:U:O4'	2.20	0.41
32:2a:1071:C:H2'	32:2a:1072:G:C8	2.54	0.41
32:2a:1512:U:H2'	32:2a:1513:A:C8	2.55	0.41
33:2b:16:HIS:O	33:2b:18:GLY:N	2.52	0.41
34:2c:48:TYR:O	34:2c:50:ALA:N	2.48	0.41
39:2h:86:ILE:O	39:2h:88:LYS:HG3	2.20	0.41
40:2i:46:ALA:HB2	40:2i:74:ILE:CG2	2.50	0.41
43:2l:91:LYS:HG2	43:2l:92:0TD:H8	2.01	0.41
44:2m:34:LEU:HD13	44:2m:41:PRO:HB3	2.02	0.41
1:1A:912:C:OP1	12:1Q:9:TYR:OH	2.31	0.41
1:1A:1803:A:H4'	3:1D:259:THR:HG23	2.02	0.41
2:1B:59:A:N6	63:1B:305:HOH:O	2.30	0.41
6:1G:11:TYR:HA	6:1G:15:VAL:HB	2.03	0.41
30:18:8:LYS:NZ	63:18:209:HOH:O	2.45	0.41
32:1a:1347:G:N2	32:1a:1373:G:H2'	2.35	0.41
36:1e:40:ARG:HE	36:1e:66:MET:HE2	1.85	0.41
1:2A:407:G:H5"	63:2A:3962:HOH:O	2.19	0.41
1:2A:578:A:OP1	1:2A:1255:U:O2'	2.24	0.41
1:2A:900:A:H2'	1:2A:901:A:C8	2.55	0.41
1:2A:1371:G:O2'	1:2A:1372:U:H5	2.03	0.41
1:2A:1428:C:C5	1:2A:1569:A:H5"	2.55	0.41
1:2A:1461:G:H2'	1:2A:1462:C:O4'	2.20	0.41
5:2F:32:LEU:HB3	5:2F:112:MET:HE1	2.02	0.41
7:2H:92:ILE:C	7:2H:94:TYR:H	2.28	0.41
9:2N:69:GLN:O	9:2N:71:ILE:HD12	2.20	0.41
10:2O:115:VAL:HG13	10:2O:121:VAL:HG21	2.02	0.41
11:2P:86:LYS:HZ3	11:2P:86:LYS:HG2	1.59	0.41
18:2W:48:ALA:O	18:2W:52:GLU:HG2	2.20	0.41
26:24:64:GLY:C	26:24:66:SER:N	2.78	0.41
30:28:46:ARG:HE	30:28:46:ARG:HB3	1.61	0.41
32:2a:137:C:H2'	32:2a:138:G:H8	1.83	0.41
32:2a:273:A:H1'	48:2q:16:GLN:NE2	2.34	0.41
32:2a:1305:G:H22	32:2a:1331:G:H1'	1.83	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:2d:191:ARG:HH11	35:2d:194:LEU:HD12	1.86	0.41
36:2e:11:ILE:H	36:2e:11:ILE:HG13	1.66	0.41
44:2m:107:ALA:HB3	44:2m:111:LYS:HD2	2.03	0.41
49:2r:56:THR:HB	49:2r:58:LEU:HD13	2.03	0.41
1:1A:1001:A:H2'	1:1A:1002:G:O4'	2.20	0.41
1:1A:1158:C:H4'	25:13:32:GLN:HB2	2.03	0.41
1:1A:2169:A:H8	1:1A:2169:A:OP1	2.03	0.41
1:1A:2390:U:P	30:18:35:GLN:HE22	2.44	0.41
1:1A:2637:U:OP2	63:1A:4187:HOH:O	2.21	0.41
13:1R:28:LEU:HD23	13:1R:48:VAL:HG21	2.02	0.41
22:10:43:THR:O	22:10:43:THR:HG23	2.21	0.41
32:1a:418:C:H1'	32:1a:540:G:O2'	2.20	0.41
32:1a:1391:U:H2'	32:1a:1392:G:C8	2.56	0.41
32:1a:1402:4OC:H2'	32:1a:1403:C:O4'	2.20	0.41
42:1k:70:LYS:HA	42:1k:73:MET:HE2	2.02	0.41
48:1q:29:HIS:N	48:1q:33:GLY:O	2.53	0.41
50:1s:48:THR:HA	50:1s:61:TYR:HA	2.02	0.41
51:1t:51:GLU:O	51:1t:55:ILE:HG12	2.20	0.41
1:2A:574:C:H42	4:2E:145:LYS:HZ1	1.68	0.41
1:2A:824:A:H2'	1:2A:825:C:O4'	2.20	0.41
1:2A:900:A:H2'	1:2A:901:A:O4'	2.21	0.41
1:2A:1075:C:C2	1:2A:1076:C:H3'	2.56	0.41
1:2A:1269:A:H2'	1:2A:1270:C:C6	2.55	0.41
1:2A:1479:G:H5"	1:2A:1560:G:H4'	2.02	0.41
1:2A:2114:A:H2'	1:2A:2115:G:O4'	2.21	0.41
1:2A:2187:G:N7	1:2A:2188:C:C4	2.88	0.41
1:2A:2273:A:H2'	1:2A:2274:A:C8	2.56	0.41
1:2A:2305:A:H5"	6:2G:134:GLY:HA3	2.02	0.41
1:2A:2461:C:H2'	1:2A:2462:U:C6	2.55	0.41
2:2B:24:G:H4'	2:2B:25:A:C8	2.55	0.41
2:2B:83:G:H4'	25:23:52:HIS:HB3	2.02	0.41
7:2H:86:GLU:HB2	7:2H:165:ALA:HB3	2.03	0.41
23:21:85:LEU:HD12	23:21:85:LEU:HA	1.86	0.41
30:28:32:LEU:O	30:28:36:LYS:HE3	2.20	0.41
32:2a:1105:A:H2'	32:2a:1106:G:C8	2.52	0.41
32:2a:1145:C:H4'	32:2a:1146:A:H8	1.85	0.41
35:2d:173:TRP:NE1	35:2d:189:PRO:HG3	2.36	0.41
39:2h:6:ILE:HB	39:2h:85:ARG:NH1	2.35	0.41
47:2p:28:ARG:NH1	47:2p:29:ASP:OD2	2.52	0.41
3:1D:145:VAL:HG12	3:1D:146:GLU:O	2.21	0.41
5:1F:28:ILE:O	5:1F:30:PRO:HD3	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:1G:173:LEU:O	6:1G:178:PHE:HD1	2.04	0.41
7:1H:138:LYS:HE3	63:1H:306:HOH:O	2.20	0.41
9:1N:60:ILE:O	9:1N:61:ARG:HD3	2.19	0.41
11:1P:63:PRO:HG2	30:18:25:MET:HB2	2.01	0.41
16:1U:58:ARG:HA	16:1U:61:TRP:CE3	2.55	0.41
32:1a:1004:A:N7	32:1a:1036:G:N2	2.68	0.41
32:1a:1291:G:P	38:1g:37:ASN:HD22	2.44	0.41
35:1d:3:ARG:H	35:1d:3:ARG:HG3	1.42	0.41
35:1d:168:ARG:HD3	35:1d:168:ARG:HA	1.90	0.41
38:1g:38:LEU:O	38:1g:42:ILE:HG13	2.20	0.41
44:1m:15:VAL:HG13	44:1m:43:THR:O	2.21	0.41
48:1q:85:VAL:O	48:1q:89:LEU:HG	2.20	0.41
51:1t:60:GLU:HG3	51:1t:81:LYS:HE3	2.01	0.41
1:2A:248:G:C2	1:2A:2431:U:H4'	2.56	0.41
1:2A:310:A:H1'	1:2A:311:A:H2'	2.02	0.41
1:2A:441:U:H2'	1:2A:442:G:C8	2.55	0.41
1:2A:470:A:OP1	5:2F:59:TYR:HE1	2.04	0.41
1:2A:1065:U:H4'	1:2A:1066:U:H5'	2.03	0.41
1:2A:1092:C:H2'	1:2A:1092:C:O2	2.20	0.41
1:2A:1107:G:C3'	1:2A:1108:U:H5"	2.51	0.41
1:2A:1939:5MU:OP1	1:2A:2604:U:O2'	2.36	0.41
1:2A:2299:G:H2'	1:2A:2300:G:C8	2.55	0.41
1:2A:2712:U:OP1	1:2A:2714:G:H4'	2.21	0.41
4:2E:61:ARG:N	4:2E:62:PRO:HD2	2.36	0.41
5:2F:178:PRO:HB2	5:2F:201:VAL:HG21	2.02	0.41
6:2G:5:VAL:HG12	26:24:25:TYR:CE2	2.56	0.41
6:2G:165:THR:OG1	6:2G:168:GLU:HG2	2.20	0.41
8:2I:93:THR:OG1	8:2I:96:ASP:OD1	2.37	0.41
10:2O:101:PRO:HB3	10:2O:120:GLU:HB3	2.02	0.41
12:2Q:30:GLY:HA2	12:2Q:107:ALA:HB2	2.01	0.41
20:2Y:44:ILE:HG22	20:2Y:62:GLU:HG2	2.03	0.41
32:2a:45:U:H2'	32:2a:46:G:C8	2.56	0.41
32:2a:1504:G:OP1	32:2a:1507:A:H4'	2.20	0.41
33:2b:106:LYS:O	33:2b:110:GLN:HB2	2.21	0.41
43:2l:24:VAL:HG12	43:2l:98:TYR:CE1	2.56	0.41
49:2r:41:LYS:HE3	49:2r:41:LYS:HB3	1.75	0.41
1:1A:839:U:H1'	1:1A:1191:G:H1'	2.02	0.41
1:1A:1754:C:H5	15:1T:96:ARG:NH2	2.19	0.41
1:1A:2493:U:H2'	1:1A:2494:G:O4'	2.20	0.41
3:1D:274:ARG:NH1	63:1D:423:HOH:O	2.50	0.41
8:1I:6:LEU:HD12	8:1I:34:GLY:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:1N:42:TRP:CE3	16:1U:63:VAL:HG11	2.56	0.41
10:1O:75:SER:HB2	15:1T:75:ILE:O	2.20	0.41
14:1S:20:ARG:NH2	22:10:51:VAL:O	2.53	0.41
30:18:15:LYS:HB2	60:18:104:MPD:H11	2.02	0.41
32:1a:235:C:H2'	32:1a:236:G:C8	2.55	0.41
32:1a:422:C:O4'	32:1a:423:G:C2	2.73	0.41
32:1a:687:A:H4'	42:1k:47:VAL:HG22	2.03	0.41
33:1b:171:ALA:O	33:1b:175:ARG:N	2.49	0.41
35:1d:60:GLU:HG3	35:1d:202:LEU:HD12	2.02	0.41
37:1f:45:LEU:HD21	37:1f:57:GLN:HE22	1.85	0.41
41:1j:30:SER:OG	41:1j:81:THR:HG22	2.20	0.41
43:1l:124:LYS:HA	43:1l:125:PRO:HD3	1.88	0.41
50:1s:33:THR:HG22	50:1s:50:ALA:O	2.20	0.41
51:1t:56:MET:HG3	51:1t:84:LEU:HD13	2.02	0.41
1:2A:79:G:O2'	1:2A:346:A:N3	2.45	0.41
1:2A:721:C:H2'	1:2A:722:A:C8	2.55	0.41
1:2A:1007:C:OP1	9:2N:37:LYS:NZ	2.42	0.41
1:2A:1493:C:N4	1:2A:2206:G:O2'	2.52	0.41
1:2A:2104:G:N3	1:2A:2104:G:H2'	2.34	0.41
1:2A:2130:U:H2'	1:2A:2158:A:N1	2.36	0.41
1:2A:2462:U:H2'	1:2A:2463:C:C6	2.56	0.41
1:2A:2477:C:N4	31:29:10:ILE:HG23	2.35	0.41
1:2A:2507:C:H2'	1:2A:2508:G:O4'	2.20	0.41
1:2A:2611:U:H6	1:2A:2611:U:H5'	1.84	0.41
1:2A:2732:G:H3'	1:2A:2733:A:O4'	2.20	0.41
2:2B:89:G:H8	2:2B:89:G:OP2	2.03	0.41
20:2Y:21:LYS:HB2	20:2Y:21:LYS:HE3	1.67	0.41
21:2Z:5:LEU:O	21:2Z:59:LEU:HA	2.21	0.41
32:2a:46:G:H2'	32:2a:366:C:C5	2.56	0.41
32:2a:500:G:H2'	32:2a:501:C:C6	2.56	0.41
32:2a:1122:U:C4	32:2a:1123:A:N7	2.87	0.41
32:2a:1172:C:H2'	32:2a:1173:G:C8	2.46	0.41
34:2c:111:LEU:HD21	34:2c:146:ALA:HB2	2.02	0.41
51:2t:59:ALA:O	51:2t:63:ILE:HG13	2.20	0.41
1:1A:271(M):G:H21	8:1I:50:ARG:HD3	1.86	0.41
1:1A:271(M):G:O2'	1:1A:271(N):U:H5"	2.21	0.41
1:1A:468:G:H5"	5:1F:60:SER:HB2	2.02	0.41
1:1A:548:A:N6	17:1V:19:LYS:H	2.19	0.41
1:1A:994:C:OP1	16:1U:53:ARG:NH2	2.53	0.41
1:1A:2849:U:H4'	1:1A:2868:A:C2	2.56	0.41
6:1G:82:LEU:HD23	6:1G:82:LEU:HA	1.97	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:1N:112:LEU:O	9:1N:116:LEU:HG	2.19	0.41
14:1S:110:LEU:HD12	14:1S:110:LEU:HA	1.82	0.41
18:1W:1:MET:HE2	18:1W:62:HIS:HB3	2.03	0.41
32:1a:1280:A:O2'	32:1a:1281:U:H5'	2.20	0.41
39:1h:23:SER:HA	39:1h:61:VAL:O	2.21	0.41
50:1s:22:LEU:O	50:1s:27:GLU:N	2.54	0.41
1:2A:286:C:H2'	1:2A:287:C:H6	1.85	0.41
1:2A:890:A:C2'	1:2A:892:G:H5'	2.50	0.41
1:2A:1165:U:H2'	1:2A:1166:C:C6	2.56	0.41
1:2A:1784:A:H4'	1:2A:1785:A:C5'	2.50	0.41
1:2A:2022:U:O2'	1:2A:2617:C:H5'	2.21	0.41
5:2F:195:ASP:O	5:2F:198:ALA:N	2.53	0.41
8:2I:57:ARG:NH1	8:2I:61:ARG:HH21	2.18	0.41
11:2P:55:ARG:HA	63:2P:301:HOH:O	2.21	0.41
19:2X:11:PRO:HG2	19:2X:13:LEU:HD21	2.03	0.41
21:2Z:10:ARG:HD3	21:2Z:37:VAL:O	2.21	0.41
32:2a:828:A:H2'	32:2a:829:G:O4'	2.21	0.41
32:2a:984:C:H2'	32:2a:985:C:C6	2.56	0.41
32:2a:991:U:H4'	32:2a:992:U:O5'	2.20	0.41
32:2a:1095:U:H2'	32:2a:1096:C:C6	2.55	0.41
32:2a:1121:U:C2'	32:2a:1122:U:H5'	2.51	0.41
32:2a:1151:A:N3	41:2j:39:PRO:HG3	2.36	0.41
32:2a:1157:A:H5'	32:2a:1158:C:C6	2.56	0.41
32:2a:1333:A:H2'	32:2a:1334:G:O4'	2.21	0.41
33:2b:185:ILE:HG13	33:2b:199:TYR:HB2	2.03	0.41
35:2d:76:ARG:NH2	35:2d:80:GLU:OE1	2.51	0.41
1:1A:196:A:O2'	1:1A:805:G:O6	2.36	0.41
1:1A:330:A:H2	1:1A:1210:A:C2'	2.33	0.41
1:1A:1055:G:H2'	1:1A:1056:G:O4'	2.21	0.41
1:1A:1359:A:N6	1:1A:1372:U:H3	2.15	0.41
1:1A:1721:G:H3'	1:1A:1722:A:H5"	2.02	0.41
1:1A:1780:A:OP1	63:1A:4189:HOH:O	2.22	0.41
1:1A:1894:C:H6	1:1A:1894:C:O5'	2.04	0.41
1:1A:2025:C:H2'	1:1A:2026:C:C6	2.55	0.41
1:1A:2050:C:H5"	63:1A:6976:HOH:O	2.21	0.41
1:1A:2145:C:H5"	1:1A:2146:C:C5	2.56	0.41
1:1A:2246:G:H2'	1:1A:2247:A:C8	2.55	0.41
1:1A:2251:OMG:HM23	1:1A:2251:OMG:H1'	1.86	0.41
1:1A:2322:A:H2'	1:1A:2323:G:O4'	2.21	0.41
1:1A:2515:C:H2'	1:1A:2516:G:H8	1.86	0.41
3:1D:54:ARG:HD3	63:1D:413:HOH:O	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:1H:154:PRO:HB3	7:1H:163:TYR:CE1	2.56	0.41
12:1Q:7:MET:HE3	12:1Q:7:MET:HB2	1.55	0.41
12:1Q:68:ILE:HD13	12:1Q:103:MET:HE2	2.02	0.41
12:1Q:109:VAL:HG22	12:1Q:113:GLN:CD	2.45	0.41
15:1T:51:ARG:HG3	15:1T:98:LYS:HE3	2.03	0.41
19:1X:92:LEU:HA	19:1X:92:LEU:HD23	1.72	0.41
21:1Z:24:LEU:HA	21:1Z:25:PRO:HD3	1.93	0.41
32:1a:189(K):U:H2'	32:1a:189(L):G:C8	2.56	0.41
32:1a:362:G:N1	32:1a:365:U:OP2	2.51	0.41
32:1a:728:A:H2'	32:1a:729:A:C8	2.56	0.41
32:1a:986:A:H1'	50:1s:54:GLY:O	2.21	0.41
32:1a:1183:A:O2'	32:1a:1184:G:OP1	2.33	0.41
32:1a:1330:U:H2'	32:1a:1331:G:H5'	2.03	0.41
32:1a:1356:G:H2'	32:1a:1357:A:H8	1.80	0.41
32:1a:1479:C:H2'	32:1a:1480:G:C8	2.56	0.41
40:1i:79:LEU:HD22	40:1i:104:ARG:HB2	2.03	0.41
41:1j:55:LYS:H	41:1j:55:LYS:HG3	1.48	0.41
44:1m:13:LYS:C	44:1m:44:ARG:HD3	2.45	0.41
44:1m:49:THR:O	44:1m:53:VAL:HG23	2.21	0.41
48:1q:59:ILE:HG22	48:1q:73:VAL:HA	2.02	0.41
51:1t:72:LEU:HB3	51:1t:73:HIS:H	1.65	0.41
1:2A:614(A):U:H4'	1:2A:614(B):G:H5"	2.02	0.41
1:2A:927:G:H2'	1:2A:928:G:O4'	2.20	0.41
1:2A:1056:G:H21	1:2A:1103:A:H62	1.68	0.41
1:2A:1160:G:C6	1:2A:1161:C:C4	3.08	0.41
1:2A:1411:C:H2'	1:2A:1412:A:H8	1.86	0.41
1:2A:1646:C:OP2	63:2A:3899:HOH:O	2.22	0.41
1:2A:1742:G:H2'	1:2A:1743:C:C6	2.56	0.41
1:2A:1937:A:N7	1:2A:1939:5MU:O2'	2.42	0.41
1:2A:2103:C:N4	1:2A:2104:G:O6	2.54	0.41
1:2A:2130:U:H2'	1:2A:2158:A:H61	1.85	0.41
1:2A:2149:G:C2	1:2A:2150:U:H1'	2.56	0.41
1:2A:2187:G:H5'	1:2A:2188:C:OP2	2.21	0.41
1:2A:2484:G:C2	1:2A:2485:G:C8	3.08	0.41
1:2A:2716:U:H2'	1:2A:2717:G:H8	1.86	0.41
3:2D:242:ARG:N	3:2D:242:ARG:HD3	2.35	0.41
4:2E:28:ALA:HB3	4:2E:93:VAL:HG12	2.03	0.41
6:2G:14:GLU:C	6:2G:17:PRO:HD2	2.46	0.41
6:2G:20:ILE:HD12	63:2G:305:HOH:O	2.21	0.41
7:2H:32:GLU:O	7:2H:33:LEU:HD23	2.21	0.41
8:2I:93:THR:O	8:2I:97:ILE:HG13	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:2T:64:ARG:HB2	15:2T:73:GLU:HG2	2.03	0.41
21:2Z:70:LEU:HD11	21:2Z:98:MET:HE3	2.03	0.41
23:21:32:LYS:HE3	23:21:32:LYS:HB3	1.94	0.41
26:24:55:ARG:C	26:24:57:GLU:H	2.28	0.41
32:2a:598:U:H2'	32:2a:599:C:C6	2.56	0.41
32:2a:953:G:C2	32:2a:954:G:H1'	2.55	0.41
32:2a:1004:A:H62	32:2a:1037:C:H3'	1.86	0.41
32:2a:1028:C:H2'	32:2a:1033:G:H22	1.85	0.41
32:2a:1130:A:H5'	40:2i:18:PHE:CE2	2.55	0.41
32:2a:1256:A:H5'	32:2a:1258:G:O4'	2.21	0.41
33:2b:97:TRP:CZ3	33:2b:101:MET:HB2	2.55	0.41
35:2d:79:PHE:HZ	35:2d:204:ILE:HA	1.86	0.41
39:2h:14:ARG:HH11	39:2h:83:ILE:HG23	1.86	0.41
40:2i:8:GLY:HA2	40:2i:79:LEU:HD23	2.02	0.41
41:2j:77:PRO:O	41:2j:81:THR:OG1	2.31	0.41
50:2s:37:ARG:HE	50:2s:37:ARG:HB2	1.73	0.41
50:2s:40:ILE:HA	50:2s:44:MET:SD	2.61	0.41
1:1A:7:G:H2'	1:1A:8:A:O4'	2.21	0.41
1:1A:181:A:H1'	1:1A:435:C:H5'	2.02	0.41
1:1A:1354:A:H2'	1:1A:1355:G:O4'	2.21	0.41
1:1A:2145:C:H6	1:1A:2145:C:OP1	2.03	0.41
6:1G:67:LYS:H	26:14:6:HIS:CE1	2.39	0.41
6:1G:155:MET:HE2	6:1G:155:MET:HB3	1.86	0.41
7:1H:158:HIS:O	7:1H:160:LYS:N	2.53	0.41
8:1I:6:LEU:O	8:1I:7:GLU:HG3	2.21	0.41
9:1N:62:VAL:CG1	9:1N:66:LYS:HB2	2.50	0.41
12:1Q:42:ILE:HD13	12:1Q:97:VAL:HB	2.02	0.41
19:1X:1:MET:HE1	24:12:26:ARG:NH2	2.36	0.41
20:1Y:20:TYR:CE2	20:1Y:43:ASN:HA	2.55	0.41
20:1Y:55:TYR:CE1	20:1Y:61:ILE:HG21	2.55	0.41
32:1a:1004:A:C6	32:1a:1037:C:C2	3.09	0.41
32:1a:1250:A:H4'	40:1i:68:GLY:N	2.36	0.41
32:1a:1309:G:OP2	44:1m:99:ARG:NH2	2.36	0.41
32:1a:1316:G:O2'	45:1n:18:VAL:HG11	2.21	0.41
33:1b:21:ARG:HA	33:1b:39:ILE:HG12	2.03	0.41
33:1b:27:LYS:HB2	33:1b:194:PRO:HD2	2.02	0.41
1:2A:1180:C:H2'	1:2A:1181:C:C6	2.56	0.41
1:2A:1291:C:H2'	1:2A:1292:U:C6	2.55	0.41
1:2A:1299:G:H5'	1:2A:1301:A:O4'	2.20	0.41
1:2A:1881:C:H2'	1:2A:1882:C:C6	2.56	0.41
1:2A:2242:G:H2'	1:2A:2243:U:O4'	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2441:C:OP2	1:2A:2586:C:O2'	2.36	0.41
1:2A:2458:G:C2	1:2A:2490:G:C2	3.09	0.41
1:2A:2564:A:OP1	1:2A:2648:C:H4'	2.22	0.41
1:2A:2717:G:O2'	15:2T:96:ARG:HD3	2.21	0.41
5:2F:39:TRP:NE1	5:2F:99:TYR:O	2.54	0.41
5:2F:101:LEU:HD11	5:2F:105:VAL:HG11	2.02	0.41
9:2N:20:GLY:HA2	9:2N:61:ARG:NE	2.36	0.41
18:2W:10:VAL:HG12	18:2W:12:ILE:HG22	2.01	0.41
32:2a:238:G:OP1	48:2q:25:ARG:NH2	2.54	0.41
32:2a:401:C:H1'	32:2a:622:A:H1'	2.02	0.41
48:2q:9:VAL:HA	48:2q:55:ASP:O	2.20	0.41
1:1A:125:G:O2'	29:17:48:LYS:HE2	2.21	0.40
1:1A:1062:G:N3	1:1A:1088:A:N7	2.70	0.40
1:1A:1668:A:H4'	1:1A:1669:A:O5'	2.20	0.40
1:1A:2106:G:C4	1:1A:2107:C:H1'	2.55	0.40
1:1A:2190:G:H2'	1:1A:2191:G:O4'	2.21	0.40
1:1A:2207:G:H2'	1:1A:2208:A:C2	2.55	0.40
2:1B:78:A:C2	2:1B:100:A:C4	3.09	0.40
11:1P:100:LEU:HD22	11:1P:105:LEU:HD12	2.03	0.40
23:11:23:LYS:HE3	23:11:23:LYS:HB2	1.89	0.40
32:1a:106:C:H2'	32:1a:107:G:H8	1.86	0.40
32:1a:1456:G:H22	51:1t:43:LEU:HD11	1.86	0.40
49:1r:55:ARG:CZ	49:1r:55:ARG:HB3	2.49	0.40
50:1s:12:ASP:C	50:1s:14:HIS:H	2.30	0.40
1:2A:290:G:H2'	1:2A:291:C:O4'	2.21	0.40
1:2A:519:U:H2'	1:2A:520:G:H8	1.85	0.40
1:2A:554:U:C4	1:2A:555:U:C4	3.08	0.40
1:2A:2756:U:H1'	1:2A:2757:A:H5"	2.02	0.40
2:2B:45:A:H2'	2:2B:46:A:O4'	2.21	0.40
8:2I:62:LYS:HG2	8:2I:133:HIS:NE2	2.36	0.40
9:2N:1:MET:HE1	16:2U:94:ASN:ND2	2.35	0.40
32:2a:767:A:H2'	32:2a:768:A:O4'	2.21	0.40
32:2a:947:G:H2'	32:2a:948:C:O4'	2.21	0.40
39:2h:51:VAL:HG11	39:2h:60:ARG:HH11	1.86	0.40
51:2t:82:SER:O	51:2t:86:ARG:HB2	2.21	0.40
1:1A:657:U:H2'	1:1A:658:C:H6	1.87	0.40
1:1A:1070:A:C4	1:1A:1097:U:H4'	2.56	0.40
1:1A:2051:A:H5'	1:1A:2578:G:O4'	2.21	0.40
1:1A:2784:C:H1'	4:1E:37:ARG:NH1	2.35	0.40
2:1B:92:C:OP1	21:1Z:79:ARG:NH1	2.49	0.40
11:1P:101:VAL:HA	11:1P:106:LEU:O	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:1T:55:ASN:H	15:1T:59:THR:CG2	2.29	0.40
17:1V:43:GLU:OE1	17:1V:43:GLU:N	2.51	0.40
21:1Z:108:PRO:HB2	21:1Z:111:VAL:HG23	2.02	0.40
29:17:47:ARG:HB3	29:17:47:ARG:NH1	2.35	0.40
32:1a:278:G:OP2	48:1q:92:ARG:NH2	2.54	0.40
32:1a:615:C:C2	32:1a:616:G:C8	3.10	0.40
32:1a:690:G:C6	32:1a:691:G:C6	3.09	0.40
32:1a:1236:A:H4'	32:1a:1304:G:H4'	2.03	0.40
32:1a:1479:C:H2'	32:1a:1480:G:H8	1.87	0.40
32:1a:1518:MA6:H8	32:1a:1518:MA6:O5'	2.21	0.40
36:1e:60:TYR:O	36:1e:64:ARG:HG3	2.22	0.40
1:2A:225:A:O2'	1:2A:257:A:H4'	2.21	0.40
1:2A:523:C:O2	1:2A:554:U:O2'	2.38	0.40
1:2A:2115:G:H2'	1:2A:2117:A:H62	1.84	0.40
1:2A:2377:A:H2'	1:2A:2378:A:C8	2.56	0.40
5:2F:11:VAL:O	5:2F:17:ARG:HA	2.20	0.40
12:2Q:57:HIS:HD2	12:2Q:117:ALA:HB2	1.85	0.40
15:2T:7:ILE:O	15:2T:11:GLU:HG3	2.21	0.40
32:2a:1067:A:O5'	32:2a:1067:A:H8	2.04	0.40
32:2a:1104:G:H4'	33:2b:111:ARG:HH21	1.86	0.40
32:2a:1217:C:OP1	45:2n:9:LYS:HE2	2.21	0.40
50:2s:51:VAL:HB	50:2s:75:ALA:HB2	2.03	0.40
53:2y:32:THR:HG21	53:2y:85:LEU:HD11	2.04	0.40
1:1A:414:C:H2'	1:1A:415:A:C8	2.56	0.40
1:1A:448:U:O4	1:1A:583:G:H1'	2.21	0.40
1:1A:861:A:H2'	1:1A:862:G:O4'	2.21	0.40
1:1A:1098:A:H8	1:1A:1098:A:OP2	2.03	0.40
1:1A:1272:A:H3'	1:1A:1273:U:H5"	2.03	0.40
1:1A:1578:U:H2'	1:1A:1579:A:H5'	2.02	0.40
1:1A:1641:A:H2'	1:1A:1642:G:O4'	2.22	0.40
1:1A:2507:C:H2'	1:1A:2508:G:O4'	2.21	0.40
1:1A:2892:A:C5	1:1A:2893:G:C6	3.10	0.40
12:1Q:116:GLU:OE2	12:1Q:119:ARG:NH2	2.41	0.40
32:1a:21:G:H2'	32:1a:22:G:C8	2.56	0.40
32:1a:407:G:H5"	35:1d:115:ARG:HB3	2.03	0.40
32:1a:1033:G:H2'	32:1a:1034:G:C8	2.42	0.40
32:1a:1064:G:H1'	32:1a:1190:G:N2	2.35	0.40
32:1a:1187:G:OP1	40:1i:113:LYS:HE3	2.22	0.40
32:1a:1239:A:H62	32:1a:1299:A:N6	2.19	0.40
35:1d:173:TRP:H	35:1d:173:TRP:CD1	2.39	0.40
37:1f:89:MET:HE2	37:1f:89:MET:HB2	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:1n:46:GLU:O	45:1n:50:LYS:HG3	2.21	0.40
1:2A:370:G:H8	1:2A:370:G:OP2	2.04	0.40
1:2A:493:G:H2'	1:2A:494:G:O4'	2.21	0.40
1:2A:839:U:H1'	1:2A:1191:G:H1'	2.03	0.40
1:2A:1079:C:C4	1:2A:1080:C:H1'	2.56	0.40
1:2A:1131:G:C2	1:2A:1132:A:C4	3.10	0.40
1:2A:2237:G:OP1	63:2A:3894:HOH:O	2.21	0.40
5:2F:102:PRO:O	5:2F:106:ARG:HG3	2.22	0.40
6:2G:131:TYR:HE2	6:2G:133:LEU:HD22	1.86	0.40
16:2U:104:GLN:CD	16:2U:104:GLN:H	2.30	0.40
32:2a:60:A:N3	32:2a:61:G:H1'	2.37	0.40
32:2a:109:A:C6	32:2a:326:G:C6	3.09	0.40
32:2a:1107:C:C4	32:2a:1108:G:C8	3.09	0.40
33:2b:126:GLU:H	33:2b:126:GLU:CD	2.28	0.40
43:2l:54:LYS:N	43:2l:54:LYS:HD2	2.36	0.40
51:2t:76:ALA:O	51:2t:80:ARG:HG3	2.21	0.40
1:1A:35:G:H2'	1:1A:36:G:O4'	2.22	0.40
1:1A:83:G:O6	63:1A:4194:HOH:O	2.22	0.40
1:1A:848:G:H2'	1:1A:849:A:C8	2.57	0.40
1:1A:907:U:HO2'	12:1Q:101:ARG:HH22	1.67	0.40
1:1A:1541:G:H3'	1:1A:1542:A:H2'	2.02	0.40
1:1A:2139:C:N4	1:1A:2152:G:H1	2.19	0.40
1:1A:2155:G:H2'	1:1A:2156:G:O4'	2.20	0.40
1:1A:2159:G:H2'	1:1A:2160:G:C8	2.56	0.40
1:1A:2630:G:H2'	1:1A:2631:G:C8	2.56	0.40
1:1A:2721:A:H2'	1:1A:2722:G:O4'	2.21	0.40
12:1Q:17:LEU:HA	12:1Q:17:LEU:HD23	1.72	0.40
12:1Q:17:LEU:HD13	12:1Q:39:PRO:HB2	2.03	0.40
15:1T:59:THR:HG21	63:1T:323:HOH:O	2.22	0.40
32:1a:664:G:N2	32:1a:741:G:H1	2.02	0.40
32:1a:736:C:H2'	32:1a:737:A:C8	2.56	0.40
32:1a:1343:G:O2'	40:1i:121:ARG:HD2	2.22	0.40
35:1d:121:VAL:O	35:1d:134:ASP:HA	2.21	0.40
1:2A:493:G:OP2	63:2A:3900:HOH:O	2.22	0.40
1:2A:528:A:O2'	1:2A:529:A:H5'	2.20	0.40
1:2A:699:A:H2'	1:2A:700:G:O4'	2.20	0.40
1:2A:818:G:H5'	1:2A:839:U:OP1	2.21	0.40
1:2A:1847:A:C3'	1:2A:1848:A:H5'	2.50	0.40
1:2A:2648:C:H2'	1:2A:2649:U:H6	1.85	0.40
2:2B:103:G:H21	21:2Z:73:GLN:HE22	1.70	0.40
6:2G:39:ILE:O	6:2G:91:ARG:HA	2.20	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:2I:96:ASP:C	8:2I:98:ALA:H	2.27	0.40
9:2N:96:GLU:O	9:2N:100:GLU:HB2	2.21	0.40
12:2Q:1:MET:HE2	12:2Q:1:MET:HB3	1.91	0.40
13:2R:72:ASP:HA	63:2R:310:HOH:O	2.20	0.40
14:2S:39:ILE:HG13	14:2S:73:LEU:HD11	2.03	0.40
23:21:67:ILE:N	23:21:68:PRO:HD2	2.36	0.40
32:2a:9:G:H2'	32:2a:10:A:H8	1.86	0.40
32:2a:340:U:H2'	32:2a:341:C:C6	2.57	0.40
32:2a:1403:C:H2'	32:2a:1404:5MC:HM53	2.03	0.40
34:2c:35:GLU:O	34:2c:39:ILE:HG13	2.21	0.40
35:2d:18:LYS:HB3	35:2d:18:LYS:HE2	1.95	0.40
36:2e:71:LEU:HD11	36:2e:113:ALA:O	2.19	0.40
41:2j:19:SER:O	41:2j:23:ILE:HG12	2.21	0.40
42:2k:50:TYR:HE1	42:2k:54:ARG:HH21	1.68	0.40
43:2l:66:VAL:HG11	43:2l:98:TYR:HE2	1.87	0.40
47:2p:19:ILE:HD11	47:2p:39:TYR:HB2	2.02	0.40
1:1A:380:U:OP1	63:1A:4191:HOH:O	2.22	0.40
1:1A:735:A:N7	1:1A:761:A:H2	2.20	0.40
1:1A:1268:A:C2	1:1A:2013:A:C4	3.09	0.40
1:1A:1682:G:C2	1:1A:1757:U:H1'	2.56	0.40
1:1A:1802:A:H2'	1:1A:1803:A:C8	2.57	0.40
1:1A:2140:C:H2'	1:1A:2141:G:H8	1.87	0.40
1:1A:2659:G:O2'	7:1H:175:LYS:NZ	2.53	0.40
1:1A:2690:C:N4	1:1A:2713:A:H1'	2.37	0.40
1:1A:2893:G:H4'	1:1A:2894:G:O5'	2.22	0.40
5:1F:196:LEU:HD23	5:1F:196:LEU:HA	1.79	0.40
6:1G:39:ILE:HB	6:1G:92:VAL:CG1	2.51	0.40
6:1G:106:LEU:O	6:1G:111:LEU:HG	2.20	0.40
7:1H:84:SER:HA	7:1H:133:VAL:O	2.22	0.40
21:1Z:24:LEU:HB2	21:1Z:41:LEU:HG	2.03	0.40
32:1a:1125:U:H4'	41:1j:5:ARG:NH2	2.37	0.40
36:1e:40:ARG:HE	36:1e:40:ARG:HB3	1.80	0.40
41:1j:15:THR:O	41:1j:19:SER:OG	2.30	0.40
44:1m:35:GLU:H	44:1m:35:GLU:HG3	1.49	0.40
1:2A:483:A:O2'	20:2Y:49:VAL:O	2.31	0.40
1:2A:831:G:O5'	1:2A:831:G:H8	2.04	0.40
1:2A:1607:C:H4'	1:2A:1608:A:O5'	2.22	0.40
1:2A:1881:C:H2'	1:2A:1882:C:H6	1.87	0.40
1:2A:2094:G:C2	1:2A:2196:C:C2	3.09	0.40
1:2A:2286:A:C5	28:26:34:LEU:HD11	2.57	0.40
1:2A:2350:C:H2'	1:2A:2351:G:O4'	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2420:C:OP1	30:28:34:TRP:HB3	2.22	0.40
1:2A:2811:G:OP1	4:2E:60:ASN:HB2	2.22	0.40
4:2E:14:ILE:HB	15:2T:14:TYR:CZ	2.56	0.40
13:2R:24:GLN:OE1	13:2R:36:THR:HG21	2.22	0.40
17:2V:62:LEU:HD21	17:2V:95:LEU:HB2	2.03	0.40
29:27:22:MET:HE3	29:27:22:MET:HB3	1.77	0.40
32:2a:597:G:N2	39:2h:94:TYR:OH	2.50	0.40
32:2a:965:A:O2'	53:2y:40:ILE:HG21	2.21	0.40
32:2a:1138:G:N3	32:2a:1138:G:H3'	2.37	0.40
32:2a:1142:G:H3'	32:2a:1143:G:H8	1.86	0.40
32:2a:1212:U:H4'	32:2a:1213:A:C8	2.57	0.40
33:2b:32:ILE:HA	33:2b:42:ILE:HA	2.03	0.40
35:2d:163:GLU:O	35:2d:166:LYS:HB2	2.22	0.40
35:2d:182:LYS:H	35:2d:182:LYS:HG2	1.73	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	1D	273/276 (99%)	261 (96%)	12 (4%)	0	100 100
3	2D	273/276 (99%)	255 (93%)	18 (7%)	0	100 100
4	1E	202/206 (98%)	192 (95%)	9 (4%)	1 (0%)	24 37
4	2E	202/206 (98%)	193 (96%)	8 (4%)	1 (0%)	24 37
5	1F	201/210 (96%)	195 (97%)	6 (3%)	0	100 100
5	2F	201/210 (96%)	187 (93%)	13 (6%)	1 (0%)	24 37
6	1G	179/182 (98%)	155 (87%)	22 (12%)	2 (1%)	11 18
6	2G	179/182 (98%)	157 (88%)	18 (10%)	4 (2%)	5 6
7	1H	172/180 (96%)	164 (95%)	5 (3%)	3 (2%)	7 10

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
7	2H	171/180 (95%)	150 (88%)	17 (10%)	4 (2%)	5 6
8	1I	145/148 (98%)	126 (87%)	18 (12%)	1 (1%)	18 28
8	2I	144/148 (97%)	128 (89%)	14 (10%)	2 (1%)	9 13
9	1N	138/140 (99%)	134 (97%)	4 (3%)	0	100 100
9	2N	138/140 (99%)	132 (96%)	6 (4%)	0	100 100
10	1O	120/122 (98%)	114 (95%)	6 (5%)	0	100 100
10	2O	120/122 (98%)	112 (93%)	8 (7%)	0	100 100
11	1P	147/150 (98%)	139 (95%)	8 (5%)	0	100 100
11	2P	147/150 (98%)	138 (94%)	6 (4%)	3 (2%)	6 7
12	1Q	139/141 (99%)	132 (95%)	7 (5%)	0	100 100
12	2Q	139/141 (99%)	131 (94%)	8 (6%)	0	100 100
13	1R	116/118 (98%)	114 (98%)	2 (2%)	0	100 100
13	2R	116/118 (98%)	113 (97%)	3 (3%)	0	100 100
14	1S	108/112 (96%)	98 (91%)	9 (8%)	1 (1%)	14 22
14	2S	108/112 (96%)	99 (92%)	9 (8%)	0	100 100
15	1T	129/146 (88%)	125 (97%)	4 (3%)	0	100 100
15	2T	129/146 (88%)	123 (95%)	6 (5%)	0	100 100
16	1U	114/118 (97%)	114 (100%)	0	0	100 100
16	2U	114/118 (97%)	111 (97%)	3 (3%)	0	100 100
17	1V	99/101 (98%)	94 (95%)	4 (4%)	1 (1%)	12 20
17	2V	99/101 (98%)	88 (89%)	9 (9%)	2 (2%)	6 7
18	1W	110/113 (97%)	109 (99%)	1 (1%)	0	100 100
18	2W	110/113 (97%)	110 (100%)	0	0	100 100
19	1X	93/96 (97%)	89 (96%)	3 (3%)	1 (1%)	11 18
19	2X	93/96 (97%)	89 (96%)	3 (3%)	1 (1%)	11 18
20	1Y	105/110 (96%)	96 (91%)	9 (9%)	0	100 100
20	2Y	105/110 (96%)	98 (93%)	7 (7%)	0	100 100
21	1Z	201/206 (98%)	186 (92%)	14 (7%)	1 (0%)	24 37
21	2Z	199/206 (97%)	179 (90%)	19 (10%)	1 (0%)	24 37
22	10	81/85 (95%)	78 (96%)	3 (4%)	0	100 100
22	20	81/85 (95%)	76 (94%)	5 (6%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
23	11	95/98 (97%)	92 (97%)	2 (2%)	1 (1%)	11 18
23	21	95/98 (97%)	93 (98%)	1 (1%)	1 (1%)	11 18
24	12	68/72 (94%)	68 (100%)	0	0	100 100
24	22	68/72 (94%)	67 (98%)	0	1 (2%)	8 12
25	13	57/60 (95%)	55 (96%)	2 (4%)	0	100 100
25	23	57/60 (95%)	54 (95%)	3 (5%)	0	100 100
26	14	67/71 (94%)	51 (76%)	13 (19%)	3 (4%)	2 1
26	24	67/71 (94%)	49 (73%)	12 (18%)	6 (9%)	0 0
27	15	57/60 (95%)	56 (98%)	1 (2%)	0	100 100
27	25	57/60 (95%)	54 (95%)	3 (5%)	0	100 100
28	16	51/54 (94%)	49 (96%)	2 (4%)	0	100 100
28	26	51/54 (94%)	49 (96%)	2 (4%)	0	100 100
29	17	46/49 (94%)	46 (100%)	0	0	100 100
29	27	46/49 (94%)	46 (100%)	0	0	100 100
30	18	62/65 (95%)	61 (98%)	1 (2%)	0	100 100
30	28	62/65 (95%)	62 (100%)	0	0	100 100
31	19	35/37 (95%)	35 (100%)	0	0	100 100
31	29	35/37 (95%)	32 (91%)	3 (9%)	0	100 100
33	1b	229/256 (90%)	183 (80%)	39 (17%)	7 (3%)	3 3
33	2b	229/256 (90%)	185 (81%)	34 (15%)	10 (4%)	2 1
34	1c	204/239 (85%)	180 (88%)	24 (12%)	0	100 100
34	2c	204/239 (85%)	175 (86%)	25 (12%)	4 (2%)	6 7
35	1d	206/209 (99%)	189 (92%)	17 (8%)	0	100 100
35	2d	206/209 (99%)	185 (90%)	19 (9%)	2 (1%)	12 20
36	1e	146/162 (90%)	143 (98%)	2 (1%)	1 (1%)	18 28
36	2e	146/162 (90%)	135 (92%)	11 (8%)	0	100 100
37	1f	98/101 (97%)	94 (96%)	4 (4%)	0	100 100
37	2f	98/101 (97%)	94 (96%)	4 (4%)	0	100 100
38	1g	153/156 (98%)	144 (94%)	9 (6%)	0	100 100
38	2g	153/156 (98%)	136 (89%)	13 (8%)	4 (3%)	4 4
39	1h	135/138 (98%)	127 (94%)	7 (5%)	1 (1%)	18 28

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
39	2h	135/138 (98%)	122 (90%)	11 (8%)	2 (2%)	8 12
40	1i	125/128 (98%)	114 (91%)	11 (9%)	0	100 100
40	2i	124/128 (97%)	110 (89%)	11 (9%)	3 (2%)	4 5
41	1j	95/105 (90%)	82 (86%)	9 (10%)	4 (4%)	2 2
41	2j	94/105 (90%)	79 (84%)	11 (12%)	4 (4%)	2 1
42	1k	112/129 (87%)	100 (89%)	12 (11%)	0	100 100
42	2k	112/129 (87%)	101 (90%)	9 (8%)	2 (2%)	6 9
43	1l	119/132 (90%)	110 (92%)	8 (7%)	1 (1%)	16 25
43	2l	119/132 (90%)	108 (91%)	10 (8%)	1 (1%)	16 25
44	1m	114/126 (90%)	104 (91%)	8 (7%)	2 (2%)	6 9
44	2m	112/126 (89%)	94 (84%)	17 (15%)	1 (1%)	14 22
45	1n	58/61 (95%)	57 (98%)	1 (2%)	0	100 100
45	2n	58/61 (95%)	55 (95%)	3 (5%)	0	100 100
46	1o	86/89 (97%)	80 (93%)	5 (6%)	1 (1%)	10 16
46	2o	86/89 (97%)	79 (92%)	5 (6%)	2 (2%)	5 6
47	1p	80/88 (91%)	71 (89%)	9 (11%)	0	100 100
47	2p	80/88 (91%)	70 (88%)	9 (11%)	1 (1%)	9 14
48	1q	97/105 (92%)	88 (91%)	8 (8%)	1 (1%)	12 20
48	2q	97/105 (92%)	89 (92%)	7 (7%)	1 (1%)	12 20
49	1r	66/88 (75%)	62 (94%)	3 (4%)	1 (2%)	8 12
49	2r	66/88 (75%)	60 (91%)	6 (9%)	0	100 100
50	1s	81/93 (87%)	73 (90%)	6 (7%)	2 (2%)	4 5
50	2s	81/93 (87%)	66 (82%)	15 (18%)	0	100 100
51	1t	94/106 (89%)	83 (88%)	10 (11%)	1 (1%)	11 18
51	2t	96/106 (91%)	86 (90%)	6 (6%)	4 (4%)	2 2
52	1u	21/27 (78%)	20 (95%)	1 (5%)	0	100 100
52	2u	21/27 (78%)	19 (90%)	2 (10%)	0	100 100
53	1y	95/113 (84%)	90 (95%)	5 (5%)	0	100 100
53	2y	94/113 (83%)	82 (87%)	11 (12%)	1 (1%)	11 18
56	1v	1/3 (33%)	1 (100%)	0	0	100 100
56	2v	1/3 (33%)	1 (100%)	0	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	11643/12360 (94%)	10729 (92%)	808 (7%)	106 (1%)	14 22

All (106) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	1G	49	ASP
14	1S	59	LYS
26	14	61	ARG
33	1b	21	ARG
33	1b	124	SER
33	1b	127	ILE
41	1j	55	LYS
43	1l	91	LYS
48	1q	34	LYS
5	2F	130	ALA
6	2G	124	SER
7	2H	126	PRO
26	24	48	ARG
26	24	62	ARG
33	2b	9	GLU
33	2b	10	LEU
33	2b	17	PHE
40	2i	43	ALA
42	2k	105	VAL
43	2l	91	LYS
48	2q	34	LYS
7	1H	92	ILE
7	1H	159	GLU
19	1X	94	GLY
26	14	47	GLN
33	1b	17	PHE
44	1m	67	GLU
50	1s	27	GLU
8	2I	97	ILE
11	2P	36	LYS
17	2V	100	ARG
21	2Z	52	SER
26	24	45	GLY
26	24	46	GLN
26	24	49	PHE
33	2b	128	GLU
34	2c	12	LEU

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Mol	Chain	Res	Type
38	2g	7	ALA
38	2g	32	ARG
38	2g	33	ASP
40	2i	54	ASP
41	2j	79	ARG
47	2p	52	ASP
51	2t	95	ALA
4	1E	52	LEU
7	1H	126	PRO
41	1j	78	ASN
50	1s	12	ASP
6	2G	3	LEU
6	2G	96	ARG
17	2V	79	VAL
23	21	3	LYS
33	2b	64	ARG
33	2b	95	GLN
39	2h	83	ILE
39	2h	133	LEU
41	2j	55	LYS
51	2t	47	GLY
53	2y	45	PRO
6	1G	44	GLY
8	1I	73	GLU
21	1Z	52	SER
33	1b	8	LYS
41	1j	77	PRO
4	2E	52	LEU
6	2G	81	LYS
7	2H	65	HIS
8	2I	117	GLU
11	2P	29	LYS
11	2P	76	LYS
26	24	55	ARG
33	2b	20	GLU
35	2d	22	LYS
41	2j	78	ASN
44	2m	6	GLY
17	1V	79	VAL
23	11	3	LYS
26	14	49	PHE
44	1m	106	ASN

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Mol	Chain	Res	Type
49	1r	27	GLY
7	2H	17	VAL
19	2X	94	GLY
33	2b	125	PRO
34	2c	99	VAL
35	2d	196	LEU
38	2g	131	LYS
40	2i	44	VAL
41	2j	35	SER
24	22	69	ARG
33	2b	207	ALA
34	2c	50	ALA
42	2k	90	GLY
33	1b	231	GLU
36	1e	70	PRO
51	1t	100	ILE
46	2o	19	PRO
39	1h	74	PRO
46	1o	23	GLY
51	2t	100	ILE
7	2H	128	PRO
46	2o	23	GLY
51	2t	98	PRO
41	1j	91	PRO
33	2b	124	SER
34	2c	64	VAL
33	1b	125	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	1D	214/218 (98%)	194 (91%)	20 (9%)	8 14
3	2D	215/218 (99%)	196 (91%)	19 (9%)	9 15
4	1E	164/166 (99%)	156 (95%)	8 (5%)	22 39

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
4	2E	164/166 (99%)	150 (92%)	14 (8%)	10 16
5	1F	160/166 (96%)	145 (91%)	15 (9%)	8 13
5	2F	159/166 (96%)	137 (86%)	22 (14%)	3 4
6	1G	144/156 (92%)	128 (89%)	16 (11%)	6 9
6	2G	142/156 (91%)	126 (89%)	16 (11%)	5 8
7	1H	144/148 (97%)	129 (90%)	15 (10%)	7 10
7	2H	143/148 (97%)	128 (90%)	15 (10%)	6 10
8	1I	111/124 (90%)	92 (83%)	19 (17%)	2 2
8	2I	108/124 (87%)	86 (80%)	22 (20%)	1 1
9	1N	119/119 (100%)	104 (87%)	15 (13%)	4 6
9	2N	118/119 (99%)	110 (93%)	8 (7%)	14 25
10	1O	100/100 (100%)	97 (97%)	3 (3%)	36 58
10	2O	100/100 (100%)	96 (96%)	4 (4%)	28 47
11	1P	115/116 (99%)	109 (95%)	6 (5%)	21 36
11	2P	115/116 (99%)	107 (93%)	8 (7%)	14 24
12	1Q	111/111 (100%)	100 (90%)	11 (10%)	7 11
12	2Q	111/111 (100%)	104 (94%)	7 (6%)	16 29
13	1R	101/101 (100%)	92 (91%)	9 (9%)	9 15
13	2R	101/101 (100%)	94 (93%)	7 (7%)	14 24
14	1S	87/88 (99%)	78 (90%)	9 (10%)	7 11
14	2S	85/88 (97%)	80 (94%)	5 (6%)	18 31
15	1T	115/127 (91%)	105 (91%)	10 (9%)	9 16
15	2T	113/127 (89%)	107 (95%)	6 (5%)	20 36
16	1U	93/94 (99%)	86 (92%)	7 (8%)	12 21
16	2U	93/94 (99%)	87 (94%)	6 (6%)	15 27
17	1V	81/82 (99%)	72 (89%)	9 (11%)	6 9
17	2V	80/82 (98%)	68 (85%)	12 (15%)	3 3
18	1W	90/92 (98%)	85 (94%)	5 (6%)	19 33
18	2W	90/92 (98%)	83 (92%)	7 (8%)	11 20
19	1X	77/78 (99%)	73 (95%)	4 (5%)	21 36
19	2X	77/78 (99%)	75 (97%)	2 (3%)	40 63

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
20	1Y	86/91 (94%)	82 (95%)	4 (5%)	23 41
20	2Y	86/91 (94%)	71 (83%)	15 (17%)	2 2
21	1Z	169/179 (94%)	153 (90%)	16 (10%)	8 13
21	2Z	165/179 (92%)	141 (86%)	24 (14%)	3 4
22	10	65/67 (97%)	61 (94%)	4 (6%)	16 29
22	20	64/67 (96%)	60 (94%)	4 (6%)	16 29
23	11	79/83 (95%)	73 (92%)	6 (8%)	12 21
23	21	81/83 (98%)	73 (90%)	8 (10%)	7 11
24	12	65/67 (97%)	60 (92%)	5 (8%)	12 20
24	22	66/67 (98%)	63 (96%)	3 (4%)	24 42
25	13	51/52 (98%)	45 (88%)	6 (12%)	5 7
25	23	50/52 (96%)	47 (94%)	3 (6%)	17 31
26	14	58/63 (92%)	52 (90%)	6 (10%)	7 11
26	24	54/63 (86%)	44 (82%)	10 (18%)	1 2
27	15	51/52 (98%)	44 (86%)	7 (14%)	3 5
27	25	50/52 (96%)	45 (90%)	5 (10%)	7 11
28	16	51/52 (98%)	45 (88%)	6 (12%)	5 7
28	26	50/52 (96%)	47 (94%)	3 (6%)	17 31
29	17	41/42 (98%)	38 (93%)	3 (7%)	13 22
29	27	41/42 (98%)	37 (90%)	4 (10%)	7 12
30	18	54/55 (98%)	48 (89%)	6 (11%)	6 9
30	28	54/55 (98%)	49 (91%)	5 (9%)	8 14
31	19	34/34 (100%)	34 (100%)	0	100 100
31	29	34/34 (100%)	31 (91%)	3 (9%)	9 15
33	1b	191/220 (87%)	168 (88%)	23 (12%)	5 7
33	2b	187/220 (85%)	160 (86%)	27 (14%)	3 4
34	1c	144/188 (77%)	134 (93%)	10 (7%)	14 24
34	2c	140/188 (74%)	119 (85%)	21 (15%)	3 3
35	1d	171/181 (94%)	147 (86%)	24 (14%)	3 4
35	2d	172/181 (95%)	152 (88%)	20 (12%)	5 8
36	1e	114/123 (93%)	101 (89%)	13 (11%)	5 8

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
36	2e	114/123 (93%)	103 (90%)	11 (10%)	8 12
37	1f	85/90 (94%)	71 (84%)	14 (16%)	2 3
37	2f	85/90 (94%)	77 (91%)	8 (9%)	8 13
38	1g	120/127 (94%)	111 (92%)	9 (8%)	12 21
38	2g	119/127 (94%)	107 (90%)	12 (10%)	7 11
39	1h	116/119 (98%)	103 (89%)	13 (11%)	6 9
39	2h	114/119 (96%)	101 (89%)	13 (11%)	5 8
40	1i	91/99 (92%)	82 (90%)	9 (10%)	7 11
40	2i	88/99 (89%)	79 (90%)	9 (10%)	7 11
41	1j	68/92 (74%)	59 (87%)	9 (13%)	4 5
41	2j	68/92 (74%)	61 (90%)	7 (10%)	7 11
42	1k	83/99 (84%)	78 (94%)	5 (6%)	17 31
42	2k	83/99 (84%)	78 (94%)	5 (6%)	17 31
43	1l	96/108 (89%)	92 (96%)	4 (4%)	26 45
43	2l	96/108 (89%)	86 (90%)	10 (10%)	7 10
44	1m	90/101 (89%)	84 (93%)	6 (7%)	15 26
44	2m	87/101 (86%)	74 (85%)	13 (15%)	3 3
45	1n	49/50 (98%)	42 (86%)	7 (14%)	3 4
45	2n	49/50 (98%)	45 (92%)	4 (8%)	10 18
46	1o	78/80 (98%)	74 (95%)	4 (5%)	21 37
46	2o	78/80 (98%)	71 (91%)	7 (9%)	9 15
47	1p	69/74 (93%)	59 (86%)	10 (14%)	3 4
47	2p	68/74 (92%)	61 (90%)	7 (10%)	7 11
48	1q	94/97 (97%)	89 (95%)	5 (5%)	20 36
48	2q	94/97 (97%)	89 (95%)	5 (5%)	20 36
49	1r	59/77 (77%)	54 (92%)	5 (8%)	10 16
49	2r	59/77 (77%)	57 (97%)	2 (3%)	32 54
50	1s	68/80 (85%)	60 (88%)	8 (12%)	5 7
50	2s	67/80 (84%)	54 (81%)	13 (19%)	1 2
51	1t	71/82 (87%)	64 (90%)	7 (10%)	7 11
51	2t	70/82 (85%)	60 (86%)	10 (14%)	3 4

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
52	1u	18/22 (82%)	18 (100%)	0	100 100
52	2u	18/22 (82%)	18 (100%)	0	100 100
53	1y	82/98 (84%)	75 (92%)	7 (8%)	10 16
53	2y	79/98 (81%)	70 (89%)	9 (11%)	5 8
56	1v	2/2 (100%)	1 (50%)	1 (50%)	0 0
56	2v	2/2 (100%)	2 (100%)	0	100 100
All	All	9535/10264 (93%)	8612 (90%)	923 (10%)	8 12

All (923) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	1D	37	LEU
3	1D	39	LYS
3	1D	61	LEU
3	1D	71	ASP
3	1D	88	ARG
3	1D	111	LEU
3	1D	116	GLN
3	1D	140	THR
3	1D	141	VAL
3	1D	142	VAL
3	1D	154	LYS
3	1D	155	LEU
3	1D	193	VAL
3	1D	204	ILE
3	1D	211	ARG
3	1D	217	ARG
3	1D	221	VAL
3	1D	229	VAL
3	1D	242	ARG
3	1D	259	THR
4	1E	9	VAL
4	1E	38	THR
4	1E	41	LYS
4	1E	49	LEU
4	1E	75	VAL
4	1E	116	VAL
4	1E	184	VAL
4	1E	195	LEU
5	1F	12	LEU

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Mol	Chain	Res	Type
5	1F	17	ARG
5	1F	20	LEU
5	1F	33	LEU
5	1F	53	THR
5	1F	57	VAL
5	1F	74	ARG
5	1F	88	VAL
5	1F	108	LYS
5	1F	110	LEU
5	1F	132	VAL
5	1F	157	VAL
5	1F	162	LEU
5	1F	183	VAL
5	1F	192	LEU
6	1G	5	VAL
6	1G	7	LEU
6	1G	37	VAL
6	1G	43	LEU
6	1G	45	GLU
6	1G	52	ILE
6	1G	53	LEU
6	1G	79	ASN
6	1G	82	LEU
6	1G	91	ARG
6	1G	126	ASP
6	1G	133	LEU
6	1G	144	ILE
6	1G	148	MET
6	1G	159	VAL
6	1G	175	LEU
7	1H	15	VAL
7	1H	27	LYS
7	1H	45	VAL
7	1H	52	VAL
7	1H	58	GLU
7	1H	62	LYS
7	1H	71	LEU
7	1H	88	LEU
7	1H	119	GLU
7	1H	122	THR
7	1H	124	GLU
7	1H	127	GLU

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Mol	Chain	Res	Type
7	1H	130	ARG
7	1H	139	GLN
7	1H	172	LYS
8	1I	5	LEU
8	1I	9	LEU
8	1I	10	GLU
8	1I	12	LEU
8	1I	15	VAL
8	1I	20	ASP
8	1I	38	LEU
8	1I	40	THR
8	1I	42	SER
8	1I	60	GLU
8	1I	61	ARG
8	1I	66	GLU
8	1I	74	ASN
8	1I	78	THR
8	1I	91	SER
8	1I	92	VAL
8	1I	107	VAL
8	1I	109	ILE
8	1I	120	ILE
9	1N	5	VAL
9	1N	8	GLN
9	1N	9	VAL
9	1N	14	VAL
9	1N	33	LEU
9	1N	34	LEU
9	1N	48	MET
9	1N	62	VAL
9	1N	67	LEU
9	1N	87	LEU
9	1N	97	ARG
9	1N	99	LEU
9	1N	119	ARG
9	1N	121	LYS
9	1N	133	GLN
10	1O	92	GLU
10	1O	94	ARG
10	1O	112	MET
11	1P	1	MET
11	1P	75	ILE

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Mol	Chain	Res	Type
11	1P	92	GLU
11	1P	102	ARG
11	1P	119	GLU
11	1P	124	LYS
12	1Q	5	ARG
12	1Q	6	ARG
12	1Q	7	MET
12	1Q	55	VAL
12	1Q	75	THR
12	1Q	77	LYS
12	1Q	103	MET
12	1Q	109	VAL
12	1Q	112	GLU
12	1Q	130	LYS
12	1Q	133	ARG
13	1R	36	THR
13	1R	44	LEU
13	1R	54	LEU
13	1R	67	LEU
13	1R	88	ARG
13	1R	96	ARG
13	1R	102	GLU
13	1R	104	ARG
13	1R	114	VAL
14	1S	17	ARG
14	1S	27	SER
14	1S	46	VAL
14	1S	50	SER
14	1S	52	SER
14	1S	59	LYS
14	1S	69	VAL
14	1S	80	LEU
14	1S	110	LEU
15	1T	6	LEU
15	1T	28	VAL
15	1T	34	VAL
15	1T	53	ARG
15	1T	59	THR
15	1T	78	LEU
15	1T	80	SER
15	1T	96	ARG
15	1T	118	ARG

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Mol	Chain	Res	Type
15	1T	128	GLU
16	1U	5	LYS
16	1U	8	VAL
16	1U	74	LEU
16	1U	77	SER
16	1U	93	LYS
16	1U	104	GLN
16	1U	117	GLN
17	1V	26	ASP
17	1V	46	VAL
17	1V	51	VAL
17	1V	61	VAL
17	1V	62	LEU
17	1V	72	VAL
17	1V	79	VAL
17	1V	82	ARG
17	1V	95	LEU
18	1W	11	ARG
18	1W	17	VAL
18	1W	19	LEU
18	1W	37	ARG
18	1W	100	THR
19	1X	35	THR
19	1X	49	VAL
19	1X	66	LEU
19	1X	88	LYS
20	1Y	23	ARG
20	1Y	43	ASN
20	1Y	72	VAL
20	1Y	107	ASP
21	1Z	41	LEU
21	1Z	42	VAL
21	1Z	76	LEU
21	1Z	80	ARG
21	1Z	86	VAL
21	1Z	107	THR
21	1Z	126	VAL
21	1Z	138	GLU
21	1Z	150	LEU
21	1Z	155	LEU
21	1Z	156	LYS
21	1Z	161	VAL

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Mol	Chain	Res	Type
21	1Z	171	ILE
21	1Z	185	GLU
21	1Z	198	LYS
21	1Z	203	GLU
22	10	10	THR
22	10	39	ARG
22	10	59	LEU
22	10	82	ARG
23	11	21	ARG
23	11	30	VAL
23	11	35	THR
23	11	40	ARG
23	11	62	VAL
23	11	94	LEU
24	12	1	MET
24	12	3	LEU
24	12	27	GLU
24	12	41	ILE
24	12	53	LEU
25	13	8	LEU
25	13	23	LEU
25	13	32	GLN
25	13	54	VAL
25	13	56	VAL
25	13	58	VAL
26	14	20	ASN
26	14	33	VAL
26	14	49	PHE
26	14	50	VAL
26	14	56	VAL
26	14	60	GLN
27	15	6	VAL
27	15	16	ARG
27	15	29	THR
27	15	30	LEU
27	15	37	LYS
27	15	40	LYS
27	15	55	ARG
28	16	5	VAL
28	16	6	ARG
28	16	9	LEU
28	16	14	THR

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Mol	Chain	Res	Type
28	16	48	VAL
28	16	52	VAL
29	17	43	THR
29	17	46	VAL
29	17	48	LYS
30	18	14	VAL
30	18	23	VAL
30	18	29	LYS
30	18	39	LYS
30	18	50	LEU
30	18	58	ILE
33	1b	7	VAL
33	1b	8	LYS
33	1b	9	GLU
33	1b	10	LEU
33	1b	15	VAL
33	1b	19	HIS
33	1b	20	GLU
33	1b	21	ARG
33	1b	44	LEU
33	1b	71	VAL
33	1b	93	VAL
33	1b	106	LYS
33	1b	111	ARG
33	1b	112	VAL
33	1b	124	SER
33	1b	127	ILE
33	1b	135	GLN
33	1b	160	ASP
33	1b	185	ILE
33	1b	200	ILE
33	1b	223	ILE
33	1b	224	GLN
33	1b	230	VAL
34	1c	26	LYS
34	1c	43	LEU
34	1c	48	TYR
34	1c	64	VAL
34	1c	70	VAL
34	1c	102	ASN
34	1c	104	GLN
34	1c	105	GLU

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Mol	Chain	Res	Type
34	1c	144	SER
34	1c	195	VAL
35	1d	3	ARG
35	1d	5	ILE
35	1d	18	LYS
35	1d	19	LEU
35	1d	28	SER
35	1d	58	LEU
35	1d	67	ILE
35	1d	70	ILE
35	1d	77	ASN
35	1d	83	SER
35	1d	101	LEU
35	1d	119	GLN
35	1d	135	LEU
35	1d	137	SER
35	1d	140	VAL
35	1d	150	GLU
35	1d	162	LEU
35	1d	166	LYS
35	1d	179	GLU
35	1d	187	ARG
35	1d	193	ASP
35	1d	194	LEU
35	1d	196	LEU
35	1d	208	SER
36	1e	5	ASP
36	1e	8	GLU
36	1e	10	MET
36	1e	41	VAL
36	1e	47	LYS
36	1e	53	LEU
36	1e	69	VAL
36	1e	82	VAL
36	1e	120	THR
36	1e	144	THR
36	1e	147	ASP
36	1e	150	ARG
36	1e	151	LEU
37	1f	10	LEU
37	1f	15	ASP
37	1f	21	LEU

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Mol	Chain	Res	Type
37	1f	40	VAL
37	1f	42	GLU
37	1f	69	GLU
37	1f	70	ASP
37	1f	71	ARG
37	1f	72	VAL
37	1f	74	ASP
37	1f	78	GLU
37	1f	81	ILE
37	1f	89	MET
37	1f	91	VAL
38	1g	6	ARG
38	1g	41	ARG
38	1g	52	GLU
38	1g	59	LEU
38	1g	79	ARG
38	1g	86	GLN
38	1g	104	LEU
38	1g	106	GLN
38	1g	113	GLU
39	1h	22	GLU
39	1h	25	ASP
39	1h	26	VAL
39	1h	39	LEU
39	1h	51	VAL
39	1h	52	ASP
39	1h	63	LEU
39	1h	64	LYS
39	1h	69	ARG
39	1h	98	LYS
39	1h	104	ARG
39	1h	120	THR
39	1h	133	LEU
40	1i	14	VAL
40	1i	17	VAL
40	1i	47	LEU
40	1i	50	LEU
40	1i	56	LEU
40	1i	65	VAL
40	1i	81	ILE
40	1i	92	TYR
40	1i	96	LEU

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Mol	Chain	Res	Type
41	1j	34	VAL
41	1j	38	ILE
41	1j	43	ARG
41	1j	46	ARG
41	1j	55	LYS
41	1j	67	THR
41	1j	72	VAL
41	1j	84	GLN
41	1j	94	VAL
42	1k	14	VAL
42	1k	16	SER
42	1k	31	THR
42	1k	99	GLN
42	1k	109	VAL
43	1l	22	SER
43	1l	79	GLU
43	1l	83	VAL
43	1l	106	ASP
44	1m	3	ARG
44	1m	4	ILE
44	1m	8	GLU
44	1m	35	GLU
44	1m	106	ASN
44	1m	117	VAL
45	1n	3	ARG
45	1n	8	GLU
45	1n	9	LYS
45	1n	13	THR
45	1n	15	LYS
45	1n	18	VAL
45	1n	33	VAL
46	1o	3	ILE
46	1o	39	LEU
46	1o	71	GLN
46	1o	84	LYS
47	1p	1	MET
47	1p	11	SER
47	1p	21	VAL
47	1p	29	ASP
47	1p	43	LYS
47	1p	60	LEU
47	1p	61	SER

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Mol	Chain	Res	Type
47	1p	62	VAL
47	1p	67	THR
47	1p	74	LEU
48	1q	6	LEU
48	1q	9	VAL
48	1q	19	VAL
48	1q	49	GLU
48	1q	53	LEU
49	1r	23	LYS
49	1r	25	THR
49	1r	39	VAL
49	1r	46	GLU
49	1r	58	LEU
50	1s	12	ASP
50	1s	15	LEU
50	1s	28	LYS
50	1s	31	ILE
50	1s	35	SER
50	1s	40	ILE
50	1s	48	THR
50	1s	66	MET
51	1t	10	LEU
51	1t	24	LEU
51	1t	34	LYS
51	1t	37	SER
51	1t	84	LEU
51	1t	90	GLN
51	1t	100	ILE
53	1y	24	LEU
53	1y	38	HIS
53	1y	42	SER
53	1y	46	GLN
53	1y	60	VAL
53	1y	61	LEU
53	1y	76	GLU
56	1v	1	MET
3	2D	3	VAL
3	2D	4	LYS
3	2D	27	THR
3	2D	61	LEU
3	2D	75	ILE
3	2D	94	LEU

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Mol	Chain	Res	Type
3	2D	103	ARG
3	2D	134	ARG
3	2D	138	VAL
3	2D	141	VAL
3	2D	142	VAL
3	2D	155	LEU
3	2D	183	ARG
3	2D	204	ILE
3	2D	211	ARG
3	2D	221	VAL
3	2D	229	VAL
3	2D	259	THR
3	2D	276	LYS
4	2E	9	VAL
4	2E	27	LEU
4	2E	40	GLU
4	2E	41	LYS
4	2E	73	GLU
4	2E	75	VAL
4	2E	76	ARG
4	2E	90	THR
4	2E	116	VAL
4	2E	119	ARG
4	2E	170	LEU
4	2E	182	LEU
4	2E	184	VAL
4	2E	188	VAL
5	2F	20	LEU
5	2F	24	LEU
5	2F	27	GLU
5	2F	28	ILE
5	2F	33	LEU
5	2F	57	VAL
5	2F	74	ARG
5	2F	82	ILE
5	2F	88	VAL
5	2F	126	VAL
5	2F	132	VAL
5	2F	153	SER
5	2F	157	VAL
5	2F	162	LEU
5	2F	170	LEU

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Mol	Chain	Res	Type
5	2F	175	THR
5	2F	183	VAL
5	2F	192	LEU
5	2F	195	ASP
5	2F	197	ASP
5	2F	201	VAL
5	2F	206	ILE
6	2G	3	LEU
6	2G	28	VAL
6	2G	36	LYS
6	2G	53	LEU
6	2G	86	MET
6	2G	88	ILE
6	2G	90	LEU
6	2G	106	LEU
6	2G	115	ARG
6	2G	133	LEU
6	2G	139	LEU
6	2G	143	GLU
6	2G	149	VAL
6	2G	159	VAL
6	2G	172	LEU
6	2G	175	LEU
7	2H	26	VAL
7	2H	45	VAL
7	2H	47	GLU
7	2H	49	VAL
7	2H	50	VAL
7	2H	52	VAL
7	2H	68	THR
7	2H	81	GLU
7	2H	88	LEU
7	2H	98	LEU
7	2H	101	ARG
7	2H	103	LEU
7	2H	105	LEU
7	2H	133	VAL
7	2H	171	LEU
8	2I	7	GLU
8	2I	15	VAL
8	2I	38	LEU
8	2I	42	SER

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Mol	Chain	Res	Type
8	2I	44	LEU
8	2I	50	ARG
8	2I	58	LEU
8	2I	64	GLU
8	2I	70	GLU
8	2I	74	ASN
8	2I	75	LEU
8	2I	76	THR
8	2I	79	ILE
8	2I	82	ARG
8	2I	91	SER
8	2I	92	VAL
8	2I	107	VAL
8	2I	108	THR
8	2I	116	LEU
8	2I	122	GLU
8	2I	125	GLU
8	2I	142	VAL
9	2N	14	VAL
9	2N	28	THR
9	2N	33	LEU
9	2N	48	MET
9	2N	60	ILE
9	2N	67	LEU
9	2N	74	ARG
9	2N	83	LYS
10	2O	35	VAL
10	2O	64	ARG
10	2O	78	ARG
10	2O	94	ARG
11	2P	2	LYS
11	2P	3	LEU
11	2P	86	LYS
11	2P	99	LEU
11	2P	101	VAL
11	2P	117	GLU
11	2P	119	GLU
11	2P	149	GLU
12	2Q	1	MET
12	2Q	5	ARG
12	2Q	60	ARG
12	2Q	75	THR

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Mol	Chain	Res	Type
12	2Q	109	VAL
12	2Q	110	THR
12	2Q	133	ARG
13	2R	6	SER
13	2R	36	THR
13	2R	44	LEU
13	2R	73	VAL
13	2R	96	ARG
13	2R	114	VAL
13	2R	117	VAL
14	2S	12	PHE
14	2S	64	GLU
14	2S	80	LEU
14	2S	85	VAL
14	2S	110	LEU
15	2T	16	ARG
15	2T	36	GLU
15	2T	53	ARG
15	2T	89	VAL
15	2T	99	LEU
15	2T	109	GLU
16	2U	5	LYS
16	2U	31	SER
16	2U	74	LEU
16	2U	77	SER
16	2U	104	GLN
16	2U	117	GLN
17	2V	1	MET
17	2V	32	THR
17	2V	40	LEU
17	2V	45	THR
17	2V	46	VAL
17	2V	51	VAL
17	2V	62	LEU
17	2V	71	LEU
17	2V	72	VAL
17	2V	79	VAL
17	2V	96	ILE
17	2V	98	GLU
18	2W	11	ARG
18	2W	17	VAL
18	2W	19	LEU

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Mol	Chain	Res	Type
18	2W	59	VAL
18	2W	63	ASP
18	2W	82	LEU
18	2W	100	THR
19	2X	45	THR
19	2X	81	VAL
20	2Y	2	ARG
20	2Y	3	VAL
20	2Y	28	LYS
20	2Y	30	VAL
20	2Y	31	LEU
20	2Y	62	GLU
20	2Y	64	GLU
20	2Y	67	LEU
20	2Y	70	SER
20	2Y	72	VAL
20	2Y	75	ILE
20	2Y	90	LEU
20	2Y	92	ASN
20	2Y	96	ILE
20	2Y	99	CYS
21	2Z	2	GLU
21	2Z	5	LEU
21	2Z	28	MET
21	2Z	31	ARG
21	2Z	46	LYS
21	2Z	71	VAL
21	2Z	74	VAL
21	2Z	76	LEU
21	2Z	86	VAL
21	2Z	91	LEU
21	2Z	93	ASP
21	2Z	98	MET
21	2Z	120	ILE
21	2Z	121	HIS
21	2Z	124	ILE
21	2Z	126	VAL
21	2Z	128	VAL
21	2Z	129	SER
21	2Z	141	VAL
21	2Z	142	SER
21	2Z	170	THR

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Mol	Chain	Res	Type
21	2Z	175	VAL
21	2Z	182	LYS
21	2Z	198	LYS
22	20	30	VAL
22	20	35	ASN
22	20	53	MET
22	20	82	ARG
23	21	4	VAL
23	21	21	ARG
23	21	35	THR
23	21	40	ARG
23	21	46	LEU
23	21	51	VAL
23	21	85	LEU
23	21	95	LEU
24	22	15	LYS
24	22	32	LEU
24	22	52	ASP
25	23	3	ARG
25	23	31	LEU
25	23	54	VAL
26	24	10	VAL
26	24	15	ILE
26	24	23	GLU
26	24	27	THR
26	24	48	ARG
26	24	50	VAL
26	24	52	THR
26	24	56	VAL
26	24	63	TYR
26	24	69	LYS
27	25	6	VAL
27	25	29	THR
27	25	30	LEU
27	25	40	LYS
27	25	55	ARG
28	26	30	THR
28	26	34	LEU
28	26	48	VAL
29	27	23	ARG
29	27	43	THR
29	27	46	VAL

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Mol	Chain	Res	Type
29	27	48	LYS
30	28	14	VAL
30	28	26	LYS
30	28	39	LYS
30	28	49	VAL
30	28	50	LEU
31	29	4	ARG
31	29	7	VAL
31	29	26	ILE
33	2b	7	VAL
33	2b	8	LYS
33	2b	10	LEU
33	2b	15	VAL
33	2b	16	HIS
33	2b	17	PHE
33	2b	39	ILE
33	2b	44	LEU
33	2b	45	GLN
33	2b	68	ILE
33	2b	69	LEU
33	2b	96	ARG
33	2b	97	TRP
33	2b	98	LEU
33	2b	111	ARG
33	2b	121	LEU
33	2b	136	VAL
33	2b	137	ARG
33	2b	150	SER
33	2b	154	LEU
33	2b	165	VAL
33	2b	187	LEU
33	2b	189	ASP
33	2b	209	ARG
33	2b	213	LEU
33	2b	215	LEU
33	2b	229	VAL
34	2c	3	ASN
34	2c	8	ILE
34	2c	16	ARG
34	2c	33	LEU
34	2c	37	GLN
34	2c	47	LEU

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Mol	Chain	Res	Type
34	2c	52	LEU
34	2c	56	ASP
34	2c	70	VAL
34	2c	110	ASN
34	2c	124	ILE
34	2c	128	PHE
34	2c	152	ILE
34	2c	153	VAL
34	2c	173	VAL
34	2c	181	ASN
34	2c	182	ILE
34	2c	192	THR
34	2c	195	VAL
34	2c	204	LEU
34	2c	206	GLU
35	2d	8	VAL
35	2d	19	LEU
35	2d	30	LYS
35	2d	50	ARG
35	2d	67	ILE
35	2d	83	SER
35	2d	108	LEU
35	2d	110	PHE
35	2d	135	LEU
35	2d	141	ARG
35	2d	155	LEU
35	2d	156	GLU
35	2d	157	LEU
35	2d	162	LEU
35	2d	170	VAL
35	2d	178	VAL
35	2d	187	ARG
35	2d	194	LEU
35	2d	200	GLU
35	2d	203	VAL
36	2e	11	ILE
36	2e	31	LEU
36	2e	41	VAL
36	2e	47	LYS
36	2e	53	LEU
36	2e	69	VAL
36	2e	75	THR

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Mol	Chain	Res	Type
36	2e	79	GLU
36	2e	144	THR
36	2e	150	ARG
36	2e	151	LEU
37	2f	7	ASN
37	2f	22	GLU
37	2f	40	VAL
37	2f	45	LEU
37	2f	57	GLN
37	2f	61	LEU
37	2f	65	VAL
37	2f	72	VAL
38	2g	6	ARG
38	2g	9	VAL
38	2g	15	ASP
38	2g	16	LEU
38	2g	24	THR
38	2g	27	ILE
38	2g	47	CYS
38	2g	75	VAL
38	2g	111	ARG
38	2g	113	GLU
38	2g	123	GLU
38	2g	153	HIS
39	2h	33	GLU
39	2h	38	ILE
39	2h	39	LEU
39	2h	63	LEU
39	2h	79	VAL
39	2h	99	GLU
39	2h	112	LEU
39	2h	114	THR
39	2h	119	LEU
39	2h	121	ASP
39	2h	125	ARG
39	2h	133	LEU
39	2h	137	VAL
40	2i	3	GLN
40	2i	7	THR
40	2i	23	ASN
40	2i	27	THR
40	2i	34	ASN

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Mol	Chain	Res	Type
40	2i	41	VAL
40	2i	63	ILE
40	2i	102	LEU
40	2i	109	VAL
41	2j	15	THR
41	2j	33	GLN
41	2j	34	VAL
41	2j	38	ILE
41	2j	68	HIS
41	2j	73	ASP
41	2j	84	GLN
42	2k	28	THR
42	2k	32	ILE
42	2k	93	GLN
42	2k	109	VAL
42	2k	116	HIS
43	2l	6	THR
43	2l	10	LEU
43	2l	18	VAL
43	2l	28	LYS
43	2l	33	ARG
43	2l	39	VAL
43	2l	58	VAL
43	2l	67	THR
43	2l	83	VAL
43	2l	123	LYS
44	2m	4	ILE
44	2m	15	VAL
44	2m	25	ILE
44	2m	39	ILE
44	2m	43	THR
44	2m	47	ASP
44	2m	49	THR
44	2m	62	ASN
44	2m	67	GLU
44	2m	92	HIS
44	2m	96	LEU
44	2m	98	VAL
44	2m	102	ARG
45	2n	3	ARG
45	2n	18	VAL
45	2n	29	ARG

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Mol	Chain	Res	Type
45	2n	33	VAL
46	2o	3	ILE
46	2o	4	THR
46	2o	26	GLU
46	2o	27	VAL
46	2o	39	LEU
46	2o	84	LYS
46	2o	87	ILE
47	2p	5	ARG
47	2p	11	SER
47	2p	20	VAL
47	2p	21	VAL
47	2p	28	ARG
47	2p	45	THR
47	2p	69	THR
48	2q	6	LEU
48	2q	13	ASP
48	2q	16	GLN
48	2q	58	GLU
48	2q	99	SER
49	2r	38	GLU
49	2r	84	LYS
50	2s	5	LEU
50	2s	9	VAL
50	2s	22	LEU
50	2s	23	ASN
50	2s	32	LYS
50	2s	41	VAL
50	2s	48	THR
50	2s	63	THR
50	2s	64	GLU
50	2s	67	VAL
50	2s	69	HIS
50	2s	77	THR
50	2s	83	HIS
51	2t	10	LEU
51	2t	24	LEU
51	2t	31	SER
51	2t	46	GLU
51	2t	62	LEU
51	2t	70	SER
51	2t	72	LEU

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Mol	Chain	Res	Type
51	2t	86	ARG
51	2t	99	LEU
51	2t	100	ILE
53	2y	6	THR
53	2y	7	SER
53	2y	9	GLN
53	2y	16	ILE
53	2y	24	LEU
53	2y	41	LEU
53	2y	46	GLN
53	2y	56	THR
53	2y	78	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (142) such sidechains are listed below:

Mol	Chain	Res	Type
3	1D	87	ASN
3	1D	253	GLN
5	1F	69	HIS
6	1G	26	GLN
6	1G	132	ASN
8	1I	43	ASN
9	1N	69	GLN
9	1N	133	GLN
10	1O	3	GLN
12	1Q	89	ASN
13	1R	50	HIS
13	1R	71	GLN
14	1S	68	GLN
15	1T	123	GLN
16	1U	72	HIS
16	1U	81	HIS
16	1U	94	ASN
19	1X	31	HIS
19	1X	82	GLN
20	1Y	43	ASN
21	1Z	73	GLN
22	10	35	ASN
23	11	19	GLN
23	11	56	GLN
24	12	9	GLN
25	13	32	GLN

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Mol	Chain	Res	Type
26	14	20	ASN
26	14	60	GLN
30	18	35	GLN
33	1b	76	GLN
33	1b	110	GLN
33	1b	135	GLN
33	1b	212	GLN
34	1c	6	HIS
34	1c	37	GLN
34	1c	69	HIS
34	1c	102	ASN
34	1c	104	GLN
35	1d	45	GLN
35	1d	77	ASN
35	1d	129	ASN
35	1d	160	GLN
36	1e	56	GLN
36	1e	141	GLN
37	1f	32	ASN
37	1f	84	ASN
38	1g	28	ASN
38	1g	37	ASN
38	1g	56	GLN
38	1g	64	GLN
38	1g	148	ASN
40	1i	3	GLN
40	1i	31	GLN
40	1i	73	GLN
41	1j	56	HIS
42	1k	93	GLN
42	1k	117	ASN
43	1l	99	HIS
44	1m	106	ASN
46	1o	28	GLN
46	1o	71	GLN
47	1p	16	HIS
47	1p	76	GLN
48	1q	16	GLN
48	1q	26	GLN
50	1s	56	GLN
50	1s	57	HIS
50	1s	69	HIS

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Mol	Chain	Res	Type
50	1s	83	HIS
51	1t	45	GLN
51	1t	75	ASN
3	2D	143	HIS
3	2D	253	GLN
4	2E	48	GLN
4	2E	143	ASN
5	2F	69	HIS
5	2F	133	ASN
7	2H	74	ASN
8	2I	43	ASN
8	2I	104	GLN
10	2O	88	ASN
10	2O	90	GLN
12	2Q	89	ASN
13	2R	13	HIS
13	2R	31	HIS
13	2R	71	GLN
16	2U	94	ASN
17	2V	64	HIS
19	2X	31	HIS
19	2X	82	GLN
20	2Y	92	ASN
21	2Z	73	GLN
24	22	9	GLN
24	22	38	GLN
25	23	32	GLN
26	24	20	ASN
26	24	46	GLN
26	24	60	GLN
27	25	23	HIS
28	26	20	ASN
30	28	35	GLN
33	2b	40	HIS
33	2b	76	GLN
33	2b	78	GLN
33	2b	212	GLN
34	2c	102	ASN
34	2c	110	ASN
34	2c	162	GLN
34	2c	176	HIS
34	2c	181	ASN

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Mol	Chain	Res	Type
35	2d	77	ASN
35	2d	116	GLN
35	2d	199	ASN
35	2d	201	GLN
36	2e	56	GLN
36	2e	130	ASN
37	2f	64	GLN
37	2f	100	ASN
38	2g	56	GLN
38	2g	64	GLN
39	2h	15	ASN
39	2h	81	HIS
40	2i	3	GLN
40	2i	58	HIS
41	2j	33	GLN
41	2j	62	HIS
41	2j	68	HIS
41	2j	69	ASN
41	2j	84	GLN
42	2k	22	HIS
43	2l	99	HIS
44	2m	62	ASN
44	2m	77	ASN
45	2n	49	HIS
45	2n	52	GLN
46	2o	9	GLN
46	2o	28	GLN
46	2o	71	GLN
48	2q	26	GLN
50	2s	14	HIS
50	2s	23	ASN
53	2y	46	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1A	2865/2915 (98%)	413 (14%)	30 (1%)
1	2A	2858/2915 (98%)	476 (16%)	29 (1%)
2	1B	119/121 (98%)	11 (9%)	0
2	2B	119/121 (98%)	11 (9%)	0
32	1a	1497/1521 (98%)	248 (16%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
32	2a	1501/1521 (98%)	289 (19%)	0
54	1w	2/5 (40%)	0	0
54	2w	2/5 (40%)	0	0
55	1x	1/4 (25%)	0	0
55	2x	1/4 (25%)	0	0
All	All	8965/9132 (98%)	1448 (16%)	59 (0%)

All (1448) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1A	23	G
1	1A	34	C
1	1A	45	C
1	1A	71	A
1	1A	74	A
1	1A	75	G
1	1A	81	G
1	1A	100	G
1	1A	118	A
1	1A	119	A
1	1A	120	U
1	1A	154(A)	C
1	1A	181	A
1	1A	196	A
1	1A	197	A
1	1A	199	A
1	1A	205	G
1	1A	215	G
1	1A	216	A
1	1A	221	A
1	1A	222	A
1	1A	229	A
1	1A	248	G
1	1A	266	G
1	1A	271(I)	G
1	1A	271(K)	U
1	1A	271(L)	U
1	1A	271(M)	G
1	1A	271(N)	U
1	1A	271(O)	C
1	1A	272(A)	U
1	1A	272(B)	G

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Mol	Chain	Res	Type
1	1A	272(H)	C
1	1A	272(J)	C
1	1A	275	G
1	1A	279	C
1	1A	280	C
1	1A	291	C
1	1A	311	A
1	1A	330	A
1	1A	352	G
1	1A	363	G
1	1A	386	G
1	1A	396	G
1	1A	405	U
1	1A	406	G
1	1A	411	G
1	1A	412	A
1	1A	421	U
1	1A	422	A
1	1A	428	A
1	1A	454	A
1	1A	456	C
1	1A	457	A
1	1A	481	G
1	1A	504	U
1	1A	505	A
1	1A	509	C
1	1A	528	A
1	1A	530	G
1	1A	531	C
1	1A	532	A
1	1A	533	G
1	1A	545	G
1	1A	549	G
1	1A	563	G
1	1A	573	G
1	1A	575	A
1	1A	603	A
1	1A	604	G
1	1A	607	U
1	1A	615	G
1	1A	616	G
1	1A	627	A

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Mol	Chain	Res	Type
1	1A	637	A
1	1A	645	C
1	1A	646	A
1	1A	652(A)	A
1	1A	652(E)	G
1	1A	652(U)	G
1	1A	668	G
1	1A	669	G
1	1A	686	G
1	1A	730	C
1	1A	746	A
1	1A	747	U
1	1A	775	G
1	1A	776	G
1	1A	782	A
1	1A	784	A
1	1A	785	G
1	1A	790	C
1	1A	792	G
1	1A	805	G
1	1A	812	C
1	1A	827	U
1	1A	828	U
1	1A	859	G
1	1A	866	A
1	1A	884	C
1	1A	888	C
1	1A	889	C
1	1A	890	A
1	1A	896	A
1	1A	897	C
1	1A	900	A
1	1A	910	A
1	1A	931	G
1	1A	932	G
1	1A	945	A
1	1A	946	G
1	1A	953	A
1	1A	959	A
1	1A	961	C
1	1A	974	G
1	1A	975	C

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Mol	Chain	Res	Type
1	1A	983	A
1	1A	996	A
1	1A	1012	U
1	1A	1013	C
1	1A	1026	U
1	1A	1033	U
1	1A	1039	G
1	1A	1043	C
1	1A	1046	A
1	1A	1047	G
1	1A	1048	A
1	1A	1054	A
1	1A	1056	G
1	1A	1061	U
1	1A	1062	G
1	1A	1063	G
1	1A	1065	U
1	1A	1067	A
1	1A	1070	A
1	1A	1071	G
1	1A	1072	C
1	1A	1073	A
1	1A	1074	G
1	1A	1075	C
1	1A	1077	A
1	1A	1079	C
1	1A	1088	A
1	1A	1089	G
1	1A	1090	U
1	1A	1091	G
1	1A	1093	G
1	1A	1096	A
1	1A	1097	U
1	1A	1098	A
1	1A	1100	C
1	1A	1109	C
1	1A	1110	G
1	1A	1111	A
1	1A	1112	G
1	1A	1128	A
1	1A	1130	U
1	1A	1135	C

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Mol	Chain	Res	Type
1	1A	1136	G
1	1A	1139	G
1	1A	1150	C
1	1A	1171	G
1	1A	1173	G
1	1A	1174	A
1	1A	1175	U
1	1A	1176	G
1	1A	1177	A
1	1A	1178	C
1	1A	1210	A
1	1A	1211	U
1	1A	1218	C
1	1A	1220	A
1	1A	1221(A)	C
1	1A	1241	A
1	1A	1253	A
1	1A	1256	G
1	1A	1271	G
1	1A	1272	A
1	1A	1273	U
1	1A	1300	U
1	1A	1301	A
1	1A	1303	G
1	1A	1352	U
1	1A	1359	A
1	1A	1360	A
1	1A	1365	A
1	1A	1370	C
1	1A	1380	G
1	1A	1384	A
1	1A	1385	G
1	1A	1416	G
1	1A	1417	C
1	1A	1420	U
1	1A	1421	G
1	1A	1428	C
1	1A	1445	A
1	1A	1450	G
1	1A	1451	C
1	1A	1455	G
1	1A	1459	G

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Mol	Chain	Res	Type
1	1A	1460	A
1	1A	1467	C
1	1A	1471	A
1	1A	1482	G
1	1A	1493	C
1	1A	1508	A
1	1A	1509	C
1	1A	1509(A)	A
1	1A	1525	G
1	1A	1530	C
1	1A	1531	C
1	1A	1542	A
1	1A	1543	C
1	1A	1547	C
1	1A	1558	A
1	1A	1566	A
1	1A	1569	A
1	1A	1578	U
1	1A	1579	A
1	1A	1580	A
1	1A	1581	G
1	1A	1584	C
1	1A	1586	A
1	1A	1608	A
1	1A	1609	A
1	1A	1610	A
1	1A	1644	C
1	1A	1648	C
1	1A	1654	A
1	1A	1664	A
1	1A	1674	G
1	1A	1696	G
1	1A	1700	A
1	1A	1701	A
1	1A	1703	G
1	1A	1722	A
1	1A	1739	U
1	1A	1747	G
1	1A	1756	G
1	1A	1757	U
1	1A	1758	G
1	1A	1762	A

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Mol	Chain	Res	Type
1	1A	1763	G
1	1A	1764	G
1	1A	1773	A
1	1A	1780	A
1	1A	1782	C
1	1A	1791	A
1	1A	1800	C
1	1A	1801	G
1	1A	1816	G
1	1A	1828	G
1	1A	1839	G
1	1A	1847	A
1	1A	1877	A
1	1A	1878	G
1	1A	1900	A
1	1A	1906	G
1	1A	1913	A
1	1A	1929	G
1	1A	1930	G
1	1A	1937	A
1	1A	1938	A
1	1A	1941	C
1	1A	1955	U
1	1A	1960	A
1	1A	1963	U
1	1A	1967	C
1	1A	1970	A
1	1A	1971	A
1	1A	1972	A
1	1A	1993	U
1	1A	1997	G
1	1A	2020	A
1	1A	2023	G
1	1A	2031	A
1	1A	2032	G
1	1A	2033	A
1	1A	2043	C
1	1A	2055	C
1	1A	2056	G
1	1A	2060	A
1	1A	2061	G
1	1A	2069	G

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Mol	Chain	Res	Type
1	1A	2102	U
1	1A	2103	C
1	1A	2104	G
1	1A	2107	C
1	1A	2108	C
1	1A	2110	G
1	1A	2111	C
1	1A	2112	G
1	1A	2116	G
1	1A	2117	A
1	1A	2119	A
1	1A	2123	G
1	1A	2126	A
1	1A	2127	G
1	1A	2131	G
1	1A	2132	U
1	1A	2133	G
1	1A	2134	A
1	1A	2135	A
1	1A	2137	C
1	1A	2142	C
1	1A	2146	C
1	1A	2158	A
1	1A	2159	G
1	1A	2160	G
1	1A	2162	G
1	1A	2164	C
1	1A	2166	G
1	1A	2167	U
1	1A	2172	U
1	1A	2174	C
1	1A	2186	G
1	1A	2187	G
1	1A	2189	U
1	1A	2190	G
1	1A	2192	G
1	1A	2198	A
1	1A	2206	G
1	1A	2207	G
1	1A	2208	A
1	1A	2225	A
1	1A	2238	G

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Mol	Chain	Res	Type
1	1A	2239	G
1	1A	2267	A
1	1A	2269	A
1	1A	2278	A
1	1A	2280	G
1	1A	2283	C
1	1A	2287	A
1	1A	2289	G
1	1A	2305	A
1	1A	2307	G
1	1A	2308	G
1	1A	2318	G
1	1A	2320	A
1	1A	2325	G
1	1A	2334	G
1	1A	2336	A
1	1A	2347	C
1	1A	2350	C
1	1A	2354	G
1	1A	2383	G
1	1A	2385	C
1	1A	2393	A
1	1A	2406	U
1	1A	2422	A
1	1A	2423	U
1	1A	2424	C
1	1A	2425	A
1	1A	2429	G
1	1A	2430	A
1	1A	2435	A
1	1A	2439	A
1	1A	2441	C
1	1A	2448	A
1	1A	2468	G
1	1A	2476	A
1	1A	2478	A
1	1A	2502	G
1	1A	2505	G
1	1A	2518	A
1	1A	2525	G
1	1A	2529	G
1	1A	2554	U

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Mol	Chain	Res	Type
1	1A	2566	A
1	1A	2567	G
1	1A	2573	C
1	1A	2574	G
1	1A	2588	G
1	1A	2602	A
1	1A	2609	U
1	1A	2611	U
1	1A	2612	C
1	1A	2629	A
1	1A	2630	G
1	1A	2654	A
1	1A	2689	U
1	1A	2690	C
1	1A	2702	U
1	1A	2703	C
1	1A	2712(A)	A
1	1A	2713	A
1	1A	2714	G
1	1A	2726	U
1	1A	2733	A
1	1A	2744	G
1	1A	2751	G
1	1A	2757	A
1	1A	2758	A
1	1A	2764	A
1	1A	2765	A
1	1A	2766	G
1	1A	2778	A
1	1A	2790	A
1	1A	2791	C
1	1A	2792	G
1	1A	2794	C
1	1A	2802	G
1	1A	2805	G
1	1A	2808	U
1	1A	2818	G
1	1A	2820	A
1	1A	2821	A
1	1A	2833	G
1	1A	2835	A
1	1A	2872	G

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Mol	Chain	Res	Type
1	1A	2892	A
1	1A	2893	G
1	1A	2894	G
2	1B	2	C
2	1B	3	C
2	1B	7	G
2	1B	12	C
2	1B	13	A
2	1B	45	A
2	1B	56	G
2	1B	66	A
2	1B	73	A
2	1B	89	G
2	1B	110	G
32	1a	7	G
32	1a	9	G
32	1a	32	A
32	1a	39	G
32	1a	47	C
32	1a	48	C
32	1a	50	A
32	1a	51	A
32	1a	61	G
32	1a	78	G
32	1a	79	G
32	1a	93	G
32	1a	98	G
32	1a	101	A
32	1a	115	G
32	1a	116	A
32	1a	121	C
32	1a	129(A)	G
32	1a	131	C
32	1a	141	A
32	1a	143	A
32	1a	144	G
32	1a	163	C
32	1a	165	C
32	1a	169	C
32	1a	173	U
32	1a	174	C
32	1a	182	U

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Mol	Chain	Res	Type
32	1a	190	U
32	1a	195	A
32	1a	197	A
32	1a	201	C
32	1a	204	U
32	1a	216	G
32	1a	217	C
32	1a	220	G
32	1a	247	G
32	1a	251	G
32	1a	258	G
32	1a	264	U
32	1a	266	G
32	1a	267	C
32	1a	289	G
32	1a	321	A
32	1a	328	C
32	1a	329	A
32	1a	332	G
32	1a	348	G
32	1a	351	G
32	1a	352	C
32	1a	354	G
32	1a	356	A
32	1a	367	U
32	1a	372	C
32	1a	373	A
32	1a	397	A
32	1a	406	G
32	1a	412	A
32	1a	413	G
32	1a	414	A
32	1a	423	G
32	1a	429	U
32	1a	439	A
32	1a	442	C
32	1a	443	C
32	1a	452	A
32	1a	458	C
32	1a	470	C
32	1a	475	G
32	1a	477	A

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Mol	Chain	Res	Type
32	1a	485	G
32	1a	487	A
32	1a	496	A
32	1a	498	U
32	1a	505	G
32	1a	509	A
32	1a	510	A
32	1a	511	C
32	1a	518	C
32	1a	519	C
32	1a	531	U
32	1a	532	A
32	1a	547	A
32	1a	559	A
32	1a	561	U
32	1a	572	A
32	1a	573	A
32	1a	576	G
32	1a	577	G
32	1a	596	C
32	1a	607	A
32	1a	619	U
32	1a	630	G
32	1a	632	A
32	1a	633	G
32	1a	642	A
32	1a	653	A
32	1a	665	A
32	1a	673	G
32	1a	687	A
32	1a	688	G
32	1a	724	G
32	1a	731	G
32	1a	734	G
32	1a	754	C
32	1a	755	G
32	1a	759	A
32	1a	777	A
32	1a	793	U
32	1a	794	A
32	1a	816	A
32	1a	817	C

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Mol	Chain	Res	Type
32	1a	821	G
32	1a	828	A
32	1a	829	G
32	1a	836	G
32	1a	839	U
32	1a	840	C
32	1a	841	U
32	1a	848	C
32	1a	853	G
32	1a	855	G
32	1a	870	U
32	1a	872	A
32	1a	902	G
32	1a	914	A
32	1a	926	G
32	1a	927	G
32	1a	931	C
32	1a	934	C
32	1a	935	A
32	1a	942	G
32	1a	960	U
32	1a	961	U
32	1a	968	A
32	1a	969	A
32	1a	971	G
32	1a	974	A
32	1a	975	A
32	1a	976	G
32	1a	977	A
32	1a	983	A
32	1a	991	U
32	1a	992	U
32	1a	993	G
32	1a	998	G
32	1a	1001	A
32	1a	1001(A)	G
32	1a	1002	G
32	1a	1004	A
32	1a	1005	A
32	1a	1020	U
32	1a	1023	G
32	1a	1024	G

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Mol	Chain	Res	Type
32	1a	1025	U
32	1a	1026	G
32	1a	1027	C
32	1a	1028	C
32	1a	1030	C
32	1a	1030(A)	G
32	1a	1030(B)	C
32	1a	1030(C)	G
32	1a	1030(D)	A
32	1a	1032	G
32	1a	1033	G
32	1a	1036	G
32	1a	1037	C
32	1a	1044	A
32	1a	1065	U
32	1a	1070	U
32	1a	1081	G
32	1a	1092	A
32	1a	1094	G
32	1a	1095	U
32	1a	1101	A
32	1a	1125	U
32	1a	1126	U
32	1a	1127	G
32	1a	1132	C
32	1a	1134	G
32	1a	1136	U
32	1a	1137	C
32	1a	1139	G
32	1a	1140	C
32	1a	1146	A
32	1a	1152	A
32	1a	1155	G
32	1a	1159	U
32	1a	1168	A
32	1a	1183	A
32	1a	1184	G
32	1a	1186	G
32	1a	1188	A
32	1a	1196	U
32	1a	1197	G
32	1a	1202	G

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Mol	Chain	Res	Type
32	1a	1212	U
32	1a	1213	A
32	1a	1224	G
32	1a	1225	A
32	1a	1227	A
32	1a	1238	A
32	1a	1256	A
32	1a	1257	U
32	1a	1258	G
32	1a	1268	A
32	1a	1270	C
32	1a	1277	C
32	1a	1278	U
32	1a	1279	A
32	1a	1280	A
32	1a	1286	A
32	1a	1287	A
32	1a	1293	G
32	1a	1299	A
32	1a	1300	G
32	1a	1302	U
32	1a	1320	C
32	1a	1338	G
32	1a	1340	A
32	1a	1346	A
32	1a	1347	G
32	1a	1353	G
32	1a	1360	A
32	1a	1363	C
32	1a	1370	G
32	1a	1373	G
32	1a	1397	C
32	1a	1398	A
32	1a	1409	C
32	1a	1419	G
32	1a	1442	G
32	1a	1442(A)	G
32	1a	1447	A
32	1a	1456	G
32	1a	1457	G
32	1a	1493	A
32	1a	1503	A

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Mol	Chain	Res	Type
32	1a	1504	G
32	1a	1505	G
32	1a	1506	U
32	1a	1508	G
32	1a	1517	G
32	1a	1519	MA6
32	1a	1520	G
32	1a	1529	G
32	1a	1530	G
32	1a	1531	A
1	2A	10	G
1	2A	11	G
1	2A	12	U
1	2A	15	G
1	2A	34	C
1	2A	36	G
1	2A	45	C
1	2A	50	U
1	2A	61	G
1	2A	63	U
1	2A	71	A
1	2A	74	A
1	2A	75	G
1	2A	84	A
1	2A	92	A
1	2A	102	G
1	2A	118	A
1	2A	119	A
1	2A	120	U
1	2A	131	G
1	2A	141	A
1	2A	149	A
1	2A	157	U
1	2A	181	A
1	2A	182	A
1	2A	196	A
1	2A	197	A
1	2A	199	A
1	2A	205	G
1	2A	214	G
1	2A	215	G
1	2A	216	A

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Mol	Chain	Res	Type
1	2A	221	A
1	2A	222	A
1	2A	229	A
1	2A	230	U
1	2A	248	G
1	2A	271(K)	U
1	2A	271(L)	U
1	2A	271(M)	G
1	2A	271(N)	U
1	2A	271(O)	C
1	2A	272(A)	U
1	2A	272(B)	G
1	2A	277	C
1	2A	278	A
1	2A	283	A
1	2A	311	A
1	2A	317	G
1	2A	324	A
1	2A	329	G
1	2A	330	A
1	2A	333	G
1	2A	352	G
1	2A	363	G
1	2A	370	G
1	2A	386	G
1	2A	396	G
1	2A	411	G
1	2A	412	A
1	2A	428	A
1	2A	429	A
1	2A	444	C
1	2A	455	C
1	2A	457	A
1	2A	470	A
1	2A	481	G
1	2A	496	G
1	2A	504	U
1	2A	505	A
1	2A	509	C
1	2A	530	G
1	2A	531	C
1	2A	532	A

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Mol	Chain	Res	Type
1	2A	545	G
1	2A	551	G
1	2A	563	G
1	2A	568	U
1	2A	573	G
1	2A	574	C
1	2A	575	A
1	2A	603	A
1	2A	604	G
1	2A	607	U
1	2A	614(B)	G
1	2A	614(C)	A
1	2A	615	G
1	2A	616	G
1	2A	627	A
1	2A	634	C
1	2A	637	A
1	2A	645	C
1	2A	646	A
1	2A	652(B)	A
1	2A	652(C)	G
1	2A	652(U)	G
1	2A	653	A
1	2A	669	G
1	2A	686	G
1	2A	730	C
1	2A	740	U
1	2A	752	A
1	2A	753	C
1	2A	774	A
1	2A	775	G
1	2A	776	G
1	2A	782	A
1	2A	784	A
1	2A	785	G
1	2A	790	C
1	2A	792	G
1	2A	805	G
1	2A	812	C
1	2A	827	U
1	2A	828	U
1	2A	847	U

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Mol	Chain	Res	Type
1	2A	857	C
1	2A	859	G
1	2A	869	G
1	2A	873	G
1	2A	877	U
1	2A	880	G
1	2A	886	C
1	2A	887	A
1	2A	888	C
1	2A	889	C
1	2A	890	A
1	2A	892	G
1	2A	893	C
1	2A	896	A
1	2A	897	C
1	2A	901	A
1	2A	910	A
1	2A	914	C
1	2A	915	C
1	2A	917	A
1	2A	932	G
1	2A	938	G
1	2A	941	A
1	2A	945	A
1	2A	946	G
1	2A	959	A
1	2A	961	C
1	2A	968	G
1	2A	974	G
1	2A	975	C
1	2A	983	A
1	2A	996	A
1	2A	997	G
1	2A	1006	C
1	2A	1012	U
1	2A	1013	C
1	2A	1017	G
1	2A	1026	U
1	2A	1033	U
1	2A	1034	G
1	2A	1038	C
1	2A	1042	G

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Mol	Chain	Res	Type
1	2A	1044	G
1	2A	1045	A
1	2A	1046	A
1	2A	1047	G
1	2A	1048	A
1	2A	1052	C
1	2A	1054	A
1	2A	1060	U
1	2A	1064	C
1	2A	1065	U
1	2A	1066	U
1	2A	1067	A
1	2A	1068	G
1	2A	1070	A
1	2A	1071	G
1	2A	1073	A
1	2A	1074	G
1	2A	1075	C
1	2A	1076	C
1	2A	1077	A
1	2A	1079	C
1	2A	1081	U
1	2A	1082	U
1	2A	1083	U
1	2A	1084	A
1	2A	1085	A
1	2A	1086	A
1	2A	1087	G
1	2A	1088	A
1	2A	1090	U
1	2A	1091	G
1	2A	1092	C
1	2A	1093	G
1	2A	1095	A
1	2A	1096	A
1	2A	1097	U
1	2A	1098	A
1	2A	1105	U
1	2A	1106	G
1	2A	1108	U
1	2A	1110	G
1	2A	1111	A

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Mol	Chain	Res	Type
1	2A	1112	G
1	2A	1116	C
1	2A	1117	G
1	2A	1120	G
1	2A	1129	A
1	2A	1135	C
1	2A	1136	G
1	2A	1142	U
1	2A	1142(A)	A
1	2A	1144	G
1	2A	1170	G
1	2A	1171	G
1	2A	1211	U
1	2A	1220	A
1	2A	1236	G
1	2A	1253	A
1	2A	1256	G
1	2A	1271	G
1	2A	1272	A
1	2A	1300	U
1	2A	1301	A
1	2A	1303	G
1	2A	1314	C
1	2A	1321	A
1	2A	1365	A
1	2A	1368	G
1	2A	1384	A
1	2A	1385	G
1	2A	1386	C
1	2A	1416	G
1	2A	1417	C
1	2A	1420	U
1	2A	1421	G
1	2A	1428	C
1	2A	1445	A
1	2A	1450	G
1	2A	1455	G
1	2A	1459	G
1	2A	1467	C
1	2A	1471	A
1	2A	1482	G
1	2A	1493	C

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Mol	Chain	Res	Type
1	2A	1497	U
1	2A	1507	A
1	2A	1508	A
1	2A	1509	C
1	2A	1509(A)	A
1	2A	1525	G
1	2A	1531	C
1	2A	1533	G
1	2A	1542	A
1	2A	1543	C
1	2A	1554	A
1	2A	1558	A
1	2A	1566	A
1	2A	1569	A
1	2A	1578	U
1	2A	1580	A
1	2A	1584	C
1	2A	1586	A
1	2A	1590	U
1	2A	1595	G
1	2A	1608	A
1	2A	1609	A
1	2A	1610	A
1	2A	1640	C
1	2A	1648	C
1	2A	1664	A
1	2A	1674	G
1	2A	1696	G
1	2A	1700	A
1	2A	1721	G
1	2A	1722	A
1	2A	1740	G
1	2A	1741	A
1	2A	1750	G
1	2A	1756	G
1	2A	1762	A
1	2A	1763	G
1	2A	1764	G
1	2A	1773	A
1	2A	1780	A
1	2A	1782	C
1	2A	1791	A

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Mol	Chain	Res	Type
1	2A	1800	C
1	2A	1801	G
1	2A	1816	G
1	2A	1828	G
1	2A	1829	A
1	2A	1830	C
1	2A	1835	G
1	2A	1847	A
1	2A	1848	A
1	2A	1877	A
1	2A	1878	G
1	2A	1882	C
1	2A	1900	A
1	2A	1906	G
1	2A	1914	C
1	2A	1918	A
1	2A	1923	U
1	2A	1926	U
1	2A	1929	G
1	2A	1930	G
1	2A	1937	A
1	2A	1938	A
1	2A	1955	U
1	2A	1963	U
1	2A	1967	C
1	2A	1970	A
1	2A	1971	A
1	2A	1972	A
1	2A	1993	U
1	2A	1997	G
1	2A	2020	A
1	2A	2023	G
1	2A	2031	A
1	2A	2033	A
1	2A	2043	C
1	2A	2055	C
1	2A	2056	G
1	2A	2060	A
1	2A	2061	G
1	2A	2069	G
1	2A	2093	G
1	2A	2096	U

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Mol	Chain	Res	Type
1	2A	2099	U
1	2A	2100	G
1	2A	2101	G
1	2A	2103	C
1	2A	2104	G
1	2A	2105	C
1	2A	2107	C
1	2A	2108	C
1	2A	2109	U
1	2A	2110	G
1	2A	2111	C
1	2A	2115	G
1	2A	2116	G
1	2A	2117	A
1	2A	2118	U
1	2A	2119	A
1	2A	2120	G
1	2A	2122	U
1	2A	2123	G
1	2A	2124	G
1	2A	2126	A
1	2A	2127	G
1	2A	2129	C
1	2A	2131	G
1	2A	2132	U
1	2A	2133	G
1	2A	2134	A
1	2A	2135	A
1	2A	2136	C
1	2A	2137	C
1	2A	2139	C
1	2A	2140	C
1	2A	2145	C
1	2A	2146	C
1	2A	2147	G
1	2A	2148	G
1	2A	2150	U
1	2A	2151	G
1	2A	2155	G
1	2A	2157	G
1	2A	2161	C
1	2A	2162	G

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Mol	Chain	Res	Type
1	2A	2163	C
1	2A	2164	C
1	2A	2165	G
1	2A	2166	G
1	2A	2172	U
1	2A	2173	A
1	2A	2174	C
1	2A	2175	C
1	2A	2178	C
1	2A	2182	G
1	2A	2183	C
1	2A	2186	G
1	2A	2187	G
1	2A	2189	U
1	2A	2192	G
1	2A	2198	A
1	2A	2206	G
1	2A	2207	G
1	2A	2208	A
1	2A	2225	A
1	2A	2239	G
1	2A	2269	A
1	2A	2275	C
1	2A	2279	G
1	2A	2283	C
1	2A	2287	A
1	2A	2289	G
1	2A	2305	A
1	2A	2308	G
1	2A	2310	A
1	2A	2311	A
1	2A	2312	U
1	2A	2319	G
1	2A	2320	A
1	2A	2321	G
1	2A	2322	A
1	2A	2325	G
1	2A	2334	G
1	2A	2335	A
1	2A	2336	A
1	2A	2347	C
1	2A	2350	C

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Mol	Chain	Res	Type
1	2A	2354	G
1	2A	2366	A
1	2A	2383	G
1	2A	2385	C
1	2A	2406	U
1	2A	2410	G
1	2A	2422	A
1	2A	2425	A
1	2A	2429	G
1	2A	2430	A
1	2A	2435	A
1	2A	2439	A
1	2A	2441	C
1	2A	2445	G
1	2A	2448	A
1	2A	2474	C
1	2A	2476	A
1	2A	2478	A
1	2A	2502	G
1	2A	2505	G
1	2A	2518	A
1	2A	2529	G
1	2A	2547	U
1	2A	2554	U
1	2A	2556	C
1	2A	2566	A
1	2A	2567	G
1	2A	2573	C
1	2A	2602	A
1	2A	2611	U
1	2A	2612	C
1	2A	2615	U
1	2A	2629	A
1	2A	2630	G
1	2A	2654	A
1	2A	2663	G
1	2A	2682	U
1	2A	2689	U
1	2A	2690	C
1	2A	2712(A)	A
1	2A	2713	A
1	2A	2714	G

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Mol	Chain	Res	Type
1	2A	2726	U
1	2A	2733	A
1	2A	2744	G
1	2A	2757	A
1	2A	2758	A
1	2A	2764	A
1	2A	2765	A
1	2A	2766	G
1	2A	2769	C
1	2A	2778	A
1	2A	2779	U
1	2A	2789	C
1	2A	2802	G
1	2A	2810	A
1	2A	2811	G
1	2A	2818	G
1	2A	2820	A
1	2A	2821	A
1	2A	2833	G
1	2A	2836	U
1	2A	2872	G
1	2A	2880	C
1	2A	2894	G
1	2A	2897	U
2	2B	2	C
2	2B	7	G
2	2B	9	G
2	2B	12	C
2	2B	33	G
2	2B	42	C
2	2B	56	G
2	2B	73	A
2	2B	84	C
2	2B	90	A
2	2B	110	G
32	2a	5	U
32	2a	9	G
32	2a	22	G
32	2a	29	G
32	2a	30	U
32	2a	32	A
32	2a	33	A

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Mol	Chain	Res	Type
32	2a	39	G
32	2a	47	C
32	2a	48	C
32	2a	51	A
32	2a	61	G
32	2a	78	G
32	2a	88	A
32	2a	89	C
32	2a	101	A
32	2a	102	G
32	2a	116	A
32	2a	121	C
32	2a	131	C
32	2a	156	G
32	2a	163	C
32	2a	173	U
32	2a	174	C
32	2a	182	U
32	2a	189(C)	C
32	2a	189(D)	C
32	2a	189(F)	U
32	2a	189(I)	G
32	2a	194	C
32	2a	195	A
32	2a	202	U
32	2a	203	U
32	2a	204	U
32	2a	216	G
32	2a	220	G
32	2a	223	U
32	2a	240	C
32	2a	247	G
32	2a	251	G
32	2a	258	G
32	2a	266	G
32	2a	267	C
32	2a	277	C
32	2a	289	G
32	2a	316	G
32	2a	319	G
32	2a	321	A
32	2a	328	C

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Mol	Chain	Res	Type
32	2a	332	G
32	2a	351	G
32	2a	352	C
32	2a	353	A
32	2a	354	G
32	2a	367	U
32	2a	372	C
32	2a	373	A
32	2a	382	A
32	2a	384	G
32	2a	391	G
32	2a	397	A
32	2a	398	C
32	2a	406	G
32	2a	412	A
32	2a	413	G
32	2a	421	U
32	2a	423	G
32	2a	424	G
32	2a	429	U
32	2a	430	A
32	2a	438	G
32	2a	439	A
32	2a	441	A
32	2a	442	C
32	2a	446	G
32	2a	452	A
32	2a	458	C
32	2a	461	A
32	2a	470	C
32	2a	471	G
32	2a	476	G
32	2a	484	G
32	2a	485	G
32	2a	496	A
32	2a	498	U
32	2a	505	G
32	2a	509	A
32	2a	510	A
32	2a	511	C
32	2a	518	C
32	2a	521	G

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Mol	Chain	Res	Type
32	2a	532	A
32	2a	533	A
32	2a	536	C
32	2a	547	A
32	2a	559	A
32	2a	561	U
32	2a	564	C
32	2a	572	A
32	2a	573	A
32	2a	576	G
32	2a	577	G
32	2a	592	G
32	2a	596	C
32	2a	630	G
32	2a	631	G
32	2a	641	U
32	2a	653	A
32	2a	660	G
32	2a	662	G
32	2a	665	A
32	2a	672	U
32	2a	687	A
32	2a	688	G
32	2a	702	A
32	2a	703	G
32	2a	721	G
32	2a	723	U
32	2a	728	A
32	2a	729	A
32	2a	731	G
32	2a	734	G
32	2a	746	A
32	2a	749	C
32	2a	753	A
32	2a	754	C
32	2a	755	G
32	2a	773	G
32	2a	774	G
32	2a	777	A
32	2a	787	A
32	2a	793	U
32	2a	794	A

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Mol	Chain	Res	Type
32	2a	802	A
32	2a	805	C
32	2a	817	C
32	2a	821	G
32	2a	828	A
32	2a	829	G
32	2a	840	C
32	2a	841	U
32	2a	851	G
32	2a	855	G
32	2a	859	A
32	2a	872	A
32	2a	874	G
32	2a	902	G
32	2a	914	A
32	2a	926	G
32	2a	927	G
32	2a	934	C
32	2a	935	A
32	2a	942	G
32	2a	955	U
32	2a	960	U
32	2a	961	U
32	2a	966	M2G
32	2a	968	A
32	2a	969	A
32	2a	971	G
32	2a	974	A
32	2a	975	A
32	2a	976	G
32	2a	977	A
32	2a	982	U
32	2a	983	A
32	2a	985	C
32	2a	992	U
32	2a	993	G
32	2a	994	A
32	2a	995	C
32	2a	1000	U
32	2a	1004	A
32	2a	1005	A
32	2a	1006	C

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Mol	Chain	Res	Type
32	2a	1007	C
32	2a	1015	A
32	2a	1020	U
32	2a	1022	G
32	2a	1023	G
32	2a	1025	U
32	2a	1026	G
32	2a	1027	C
32	2a	1028	C
32	2a	1029	C
32	2a	1030(A)	G
32	2a	1030(B)	C
32	2a	1030(C)	G
32	2a	1031	G
32	2a	1032	G
32	2a	1034	G
32	2a	1040	U
32	2a	1041	A
32	2a	1043	C
32	2a	1053	G
32	2a	1054	C
32	2a	1065	U
32	2a	1066	C
32	2a	1068	G
32	2a	1081	G
32	2a	1093	A
32	2a	1094	G
32	2a	1101	A
32	2a	1110	A
32	2a	1113	C
32	2a	1118	C
32	2a	1122	U
32	2a	1125	U
32	2a	1127	G
32	2a	1129	C
32	2a	1130	A
32	2a	1134	G
32	2a	1136	U
32	2a	1137	C
32	2a	1138	G
32	2a	1139	G
32	2a	1140	C

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Mol	Chain	Res	Type
32	2a	1147	C
32	2a	1152	A
32	2a	1159	U
32	2a	1160	G
32	2a	1161	C
32	2a	1182	G
32	2a	1183	A
32	2a	1184	G
32	2a	1193	G
32	2a	1196	U
32	2a	1197	G
32	2a	1201	A
32	2a	1211	U
32	2a	1213	A
32	2a	1214	C
32	2a	1215	G
32	2a	1224	G
32	2a	1227	A
32	2a	1236	A
32	2a	1238	A
32	2a	1248	A
32	2a	1250	A
32	2a	1256	A
32	2a	1257	U
32	2a	1258	G
32	2a	1260	C
32	2a	1270	C
32	2a	1278	U
32	2a	1279	A
32	2a	1287	A
32	2a	1298	C
32	2a	1299	A
32	2a	1300	G
32	2a	1302	U
32	2a	1303	C
32	2a	1316	G
32	2a	1317	C
32	2a	1319	A
32	2a	1320	C
32	2a	1322	C
32	2a	1323	G
32	2a	1340	A

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Mol	Chain	Res	Type
32	2a	1345	U
32	2a	1346	A
32	2a	1347	G
32	2a	1353	G
32	2a	1358	U
32	2a	1363	C
32	2a	1363(A)	A
32	2a	1370	G
32	2a	1384	C
32	2a	1397	C
32	2a	1400	5MC
32	2a	1401	G
32	2a	1419	G
32	2a	1442	G
32	2a	1442(A)	G
32	2a	1442(B)	A
32	2a	1446	U
32	2a	1447	A
32	2a	1456	G
32	2a	1487	G
32	2a	1492	A
32	2a	1497	G
32	2a	1499	A
32	2a	1503	A
32	2a	1504	G
32	2a	1506	U
32	2a	1507	A
32	2a	1517	G
32	2a	1529	G
32	2a	1530	G

All (59) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1A	196	A
1	1A	199	A
1	1A	266	G
1	1A	278	A
1	1A	573	G
1	1A	746	A
1	1A	764	A
1	1A	839	U

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Mol	Chain	Res	Type
1	1A	840	C
1	1A	888	C
1	1A	895	U
1	1A	974	G
1	1A	1047	G
1	1A	1089	G
1	1A	1175	U
1	1A	1210	A
1	1A	1301	A
1	1A	1379	A
1	1A	1442	G
1	1A	1608	A
1	1A	1653	G
1	1A	2126	A
1	1A	2238	G
1	1A	2406	U
1	1A	2422	A
1	1A	2439	A
1	1A	2611	U
1	1A	2689	U
1	1A	2756	U
1	1A	2893	G
1	2A	195	A
1	2A	196	A
1	2A	266	G
1	2A	271(M)	G
1	2A	277	C
1	2A	752	A
1	2A	764	A
1	2A	774	A
1	2A	827	U
1	2A	840	C
1	2A	856	C
1	2A	900	A
1	2A	1051	G
1	2A	1053	C
1	2A	1065	U
1	2A	1067	A
1	2A	1073	A
1	2A	1076	C
1	2A	1210	A
1	2A	1420	U

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Mol	Chain	Res	Type
1	2A	1442	G
1	2A	1491	G
1	2A	1992	G
1	2A	2126	A
1	2A	2171	A
1	2A	2172	U
1	2A	2321	G
1	2A	2689	U
1	2A	2756	U

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

50 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	$\#\|Z\| > 2$
1	OMC	2A	1920	1	19,22,23	0.82	0	25,31,34	1.08	2 (8%)
1	2MA	1A	2503	1,57	22,25,26	1.49	5 (22%)	32,37,40	2.33	8 (25%)
1	PSU	1A	1917	1	18,21,22	1.36	2 (11%)	21,30,33	2.02	3 (14%)
32	G7M	1a	527	57,32	23,26,27	1.52	3 (13%)	34,39,42	1.65	5 (14%)
32	5MC	2a	967	32	19,22,23	1.75	3 (15%)	26,32,35	1.09	3 (11%)
32	UR3	1a	1498	32	19,22,23	0.99	1 (5%)	26,32,35	1.77	4 (15%)
32	UR3	2a	1498	32	19,22,23	1.02	2 (10%)	26,32,35	1.64	2 (7%)
32	PSU	1a	516	32	18,21,22	1.36	2 (11%)	21,30,33	1.94	5 (23%)
1	PSU	1A	2605	1	18,21,22	1.47	4 (22%)	21,30,33	1.99	4 (19%)
1	OMC	1A	1920	1	19,22,23	0.83	0	25,31,34	0.98	1 (4%)
1	5MU	2A	1915	1	19,22,23	1.44	4 (21%)	27,32,35	2.12	8 (29%)
1	OMG	1A	2251	1,57,55	23,26,27	1.23	3 (13%)	32,38,41	2.06	6 (18%)
1	PSU	2A	1917	1,57	18,21,22	1.37	2 (11%)	21,30,33	2.01	3 (14%)
32	5MC	2a	1407	32	19,22,23	1.62	2 (10%)	26,32,35	1.12	3 (11%)
1	5MC	2A	1942	1	19,22,23	1.69	3 (15%)	26,32,35	1.15	2 (7%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
32	MA6	1a	1519	32	23,26,27	0.43	0	33,38,41	2.02	9 (27%)
32	5MC	2a	1404	32	19,22,23	1.77	3 (15%)	26,32,35	1.23	4 (15%)
32	M2G	2a	966	57,32	24,27,28	1.33	3 (12%)	33,40,43	1.82	5 (15%)
32	5MC	1a	1400	32	19,22,23	1.70	3 (15%)	26,32,35	1.11	2 (7%)
32	MA6	2a	1519	32	23,26,27	0.45	0	33,38,41	2.14	10 (30%)
32	5MC	2a	1400	32	19,22,23	1.53	2 (10%)	26,32,35	1.27	3 (11%)
1	5MC	2A	1962	1,57	19,22,23	1.69	3 (15%)	26,32,35	1.12	2 (7%)
55	8AN	2x	76	57,55	21,24,25	1.38	3 (14%)	26,35,38	2.29	10 (38%)
1	5MC	1A	1962	1,57	19,22,23	1.64	3 (15%)	26,32,35	1.13	4 (15%)
1	OMU	1A	2552	1,57	19,22,23	1.31	3 (15%)	25,31,34	1.83	6 (24%)
43	0TD	1l	92	43	8,9,10	4.61	2 (25%)	6,11,13	2.73	3 (50%)
1	PSU	2A	1911	1	18,21,22	1.39	2 (11%)	21,30,33	2.02	4 (19%)
1	OMG	2A	2251	1,57,55	23,26,27	1.22	3 (13%)	32,38,41	1.98	7 (21%)
32	PSU	2a	516	57,32	18,21,22	1.33	2 (11%)	21,30,33	2.10	5 (23%)
1	5MC	1A	1942	1	19,22,23	1.42	3 (15%)	26,32,35	1.10	2 (7%)
32	M2G	1a	966	32	24,27,28	1.29	3 (12%)	33,40,43	1.84	5 (15%)
32	4OC	1a	1402	32	20,23,24	0.75	0	25,32,35	1.01	1 (4%)
32	G7M	2a	527	32	23,26,27	1.49	3 (13%)	34,39,42	1.69	5 (14%)
43	0TD	2l	92	43	8,9,10	4.54	1 (12%)	6,11,13	5.96	3 (50%)
32	4OC	2a	1402	32	20,23,24	0.76	0	25,32,35	0.96	0
55	8AN	1x	76	57,55	21,24,25	1.38	3 (14%)	26,35,38	2.40	9 (34%)
1	5MU	2A	1939	1	19,22,23	1.48	5 (26%)	27,32,35	2.16	8 (29%)
1	PSU	2A	2605	1	18,21,22	1.35	2 (11%)	21,30,33	1.92	4 (19%)
32	5MC	1a	967	32	19,22,23	1.65	3 (15%)	26,32,35	1.12	2 (7%)
32	5MC	1a	1407	32	19,22,23	1.72	2 (10%)	26,32,35	1.17	3 (11%)
1	PSU	1A	1911	1	18,21,22	1.38	2 (11%)	21,30,33	2.10	5 (23%)
1	2MA	2A	2503	1,57	22,25,26	1.47	4 (18%)	32,37,40	2.36	9 (28%)
32	MA6	2a	1518	32	23,26,27	0.39	0	33,38,41	2.08	9 (27%)
1	5MU	1A	1915	1	19,22,23	1.44	4 (21%)	27,32,35	2.19	9 (33%)
1	OMU	2A	2552	1,57	19,22,23	1.23	3 (15%)	25,31,34	1.91	6 (24%)
1	5MU	1A	1939	1,57	19,22,23	1.43	5 (26%)	27,32,35	2.19	8 (29%)
32	MA6	1a	1518	32	23,26,27	0.38	0	33,38,41	2.00	10 (30%)
32	5MC	1a	1404	32	19,22,23	1.66	3 (15%)	26,32,35	1.13	2 (7%)
32	2MG	1a	1207	32	23,26,27	1.26	3 (13%)	33,38,41	2.18	6 (18%)
32	2MG	2a	1207	32	23,26,27	1.23	3 (13%)	33,38,41	2.15	8 (24%)

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
1	OMC	2A	1920	1	-	1/9/27/28	0/2/2/2
1	2MA	1A	2503	1,57	-	1/7/25/26	0/3/3/3
1	PSU	1A	1917	1	-	0/7/25/26	0/2/2/2
32	G7M	1a	527	57,32	-	2/7/25/26	0/3/3/3
32	5MC	2a	967	32	-	0/7/25/26	0/2/2/2
32	UR3	1a	1498	32	-	0/7/25/26	0/2/2/2
32	UR3	2a	1498	32	-	0/7/25/26	0/2/2/2
32	PSU	1a	516	32	-	1/7/25/26	0/2/2/2
1	PSU	1A	2605	1	-	0/7/25/26	0/2/2/2
1	OMC	1A	1920	1	-	1/9/27/28	0/2/2/2
1	5MU	2A	1915	1	-	2/7/25/26	0/2/2/2
1	OMG	1A	2251	1,57,55	-	0/9/27/28	0/3/3/3
1	PSU	2A	1917	1,57	-	0/7/25/26	0/2/2/2
32	5MC	2a	1407	32	-	0/7/25/26	0/2/2/2
1	5MC	2A	1942	1	-	0/7/25/26	0/2/2/2
32	MA6	1a	1519	32	-	2/11/29/30	0/3/3/3
32	5MC	2a	1404	32	-	0/7/25/26	0/2/2/2
32	M2G	2a	966	57,32	-	0/11/29/30	0/3/3/3
32	5MC	1a	1400	32	-	0/7/25/26	0/2/2/2
32	MA6	2a	1519	32	-	2/11/29/30	0/3/3/3
32	5MC	2a	1400	32	-	0/7/25/26	0/2/2/2
1	5MC	2A	1962	1,57	-	0/7/25/26	0/2/2/2
55	8AN	2x	76	57,55	-	1/7/25/26	0/3/3/3
1	5MC	1A	1962	1,57	-	0/7/25/26	0/2/2/2
1	OMU	1A	2552	1,57	-	0/9/27/28	0/2/2/2
43	0TD	1l	92	43	-	2/7/12/14	-
1	PSU	2A	1911	1	-	0/7/25/26	0/2/2/2
1	OMG	2A	2251	1,57,55	-	0/9/27/28	0/3/3/3
32	PSU	2a	516	57,32	-	0/7/25/26	0/2/2/2
1	5MC	1A	1942	1	-	0/7/25/26	0/2/2/2
32	M2G	1a	966	32	-	0/11/29/30	0/3/3/3
32	4OC	1a	1402	32	-	2/9/29/30	0/2/2/2
32	G7M	2a	527	32	-	2/7/25/26	0/3/3/3
43	0TD	2l	92	43	-	2/7/12/14	-
32	4OC	2a	1402	32	-	0/9/29/30	0/2/2/2
55	8AN	1x	76	57,55	-	1/7/25/26	0/3/3/3
1	5MU	2A	1939	1	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	PSU	2A	2605	1	-	0/7/25/26	0/2/2/2
32	5MC	1a	967	32	-	0/7/25/26	0/2/2/2
32	5MC	1a	1407	32	-	0/7/25/26	0/2/2/2
1	PSU	1A	1911	1	-	0/7/25/26	0/2/2/2
1	2MA	2A	2503	1,57	-	1/7/25/26	0/3/3/3
32	MA6	2a	1518	32	-	0/11/29/30	0/3/3/3
1	5MU	1A	1915	1	-	2/7/25/26	0/2/2/2
1	OMU	2A	2552	1,57	-	0/9/27/28	0/2/2/2
1	5MU	1A	1939	1,57	-	0/7/25/26	0/2/2/2
32	MA6	1a	1518	32	-	0/11/29/30	0/3/3/3
32	5MC	1a	1404	32	-	0/7/25/26	0/2/2/2
32	2MG	1a	1207	32	-	0/9/27/28	0/3/3/3
32	2MG	2a	1207	32	-	2/9/27/28	0/3/3/3

All (120) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
43	1l	92	0TD	CB-SB	-12.34	1.69	1.82
43	2l	92	0TD	CB-SB	-12.33	1.69	1.82
32	2a	1404	5MC	C5-C4	6.49	1.49	1.44
32	2a	967	5MC	C5-C4	6.44	1.49	1.44
32	1a	1407	5MC	C5-C4	6.29	1.48	1.44
1	2A	1942	5MC	C5-C4	6.25	1.48	1.44
1	2A	1962	5MC	C5-C4	6.15	1.48	1.44
32	1a	1400	5MC	C5-C4	6.08	1.48	1.44
32	1a	1404	5MC	C5-C4	6.04	1.48	1.44
1	1A	1962	5MC	C5-C4	5.96	1.48	1.44
32	1a	967	5MC	C5-C4	5.90	1.48	1.44
32	2a	1407	5MC	C5-C4	5.83	1.48	1.44
32	2a	1400	5MC	C5-C4	5.29	1.48	1.44
32	1a	527	G7M	C5-N7	-4.79	1.33	1.39
1	1A	1942	5MC	C5-C4	4.65	1.47	1.44
32	2a	527	G7M	C5-N7	-4.53	1.34	1.39
1	1A	2503	2MA	C5-C4	4.46	1.47	1.39
1	2A	2503	2MA	C5-C4	4.38	1.46	1.39
55	1x	76	8AN	C5-N7	-4.08	1.31	1.39
1	2A	1911	PSU	C6-C5	3.74	1.39	1.35
55	2x	76	8AN	C5-N7	-3.69	1.32	1.39
32	1a	516	PSU	C6-C5	3.53	1.39	1.35
1	1A	1911	PSU	C6-C5	3.48	1.39	1.35
1	1A	1917	PSU	C6-C5	3.46	1.39	1.35
1	2A	1917	PSU	C6-C5	3.37	1.39	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
32	2a	966	M2G	C5-C4	3.36	1.48	1.38
32	1a	966	M2G	C5-C4	3.27	1.47	1.38
1	1A	2605	PSU	C4-N3	-3.25	1.32	1.38
32	2a	527	G7M	C5-C4	3.24	1.46	1.38
32	1a	527	G7M	C5-C4	3.21	1.46	1.38
32	2a	516	PSU	C6-C5	3.17	1.38	1.35
1	2A	2251	OMG	C5-C4	3.16	1.47	1.38
32	2a	1207	2MG	C5-C4	3.16	1.47	1.38
32	1a	1207	2MG	C5-C4	3.14	1.47	1.38
1	2A	1915	5MU	C6-C5	3.11	1.39	1.34
32	2a	966	M2G	C2-N2	3.09	1.40	1.35
55	2x	76	8AN	C5-C4	-3.07	1.33	1.39
1	2A	1939	5MU	C4-C5	3.06	1.49	1.44
1	1A	2251	OMG	C5-C4	3.05	1.47	1.38
1	2A	2605	PSU	C6-C5	3.03	1.38	1.35
32	1a	1400	5MC	C6-C5	2.99	1.39	1.34
32	2a	1400	5MC	C6-C5	2.97	1.39	1.34
1	1A	2605	PSU	C6-C5	2.96	1.38	1.35
32	2a	1404	5MC	C6-C5	2.96	1.39	1.34
32	1a	1407	5MC	C6-C5	2.96	1.39	1.34
55	1x	76	8AN	C5-C6	-2.94	1.32	1.41
1	1A	1915	5MU	C2-N1	2.92	1.43	1.38
32	2a	967	5MC	C6-C5	2.90	1.39	1.34
1	1A	1939	5MU	C6-C5	2.88	1.39	1.34
1	1A	1939	5MU	C4-C5	2.88	1.49	1.44
1	1A	2503	2MA	C5-N7	-2.86	1.33	1.39
1	2A	1915	5MU	C2-N1	2.85	1.42	1.38
32	2a	1407	5MC	C6-C5	2.85	1.39	1.34
32	1a	967	5MC	C6-C5	2.84	1.39	1.34
32	1a	1404	5MC	C6-C5	2.80	1.39	1.34
1	2A	1962	5MC	C6-C5	2.78	1.39	1.34
1	2A	2503	2MA	C5-C6	2.75	1.48	1.41
1	1A	1915	5MU	C6-C5	2.74	1.39	1.34
1	2A	1939	5MU	C4-N3	-2.74	1.33	1.38
1	1A	2251	OMG	C6-N1	-2.72	1.33	1.38
1	1A	2552	OMU	C2-N1	2.69	1.42	1.38
55	2x	76	8AN	C5-C6	-2.65	1.33	1.41
1	2A	1939	5MU	C6-C5	2.65	1.38	1.34
32	1a	966	M2G	C2-N2	2.64	1.39	1.35
1	2A	2605	PSU	C4-N3	-2.64	1.33	1.38
1	1A	1942	5MC	C6-C5	2.63	1.38	1.34
1	1A	1917	PSU	C4-N3	-2.61	1.34	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1A	2605	PSU	C2-N3	-2.61	1.33	1.37
1	2A	1942	5MC	C6-C5	2.56	1.38	1.34
32	1a	966	M2G	C6-N1	-2.55	1.34	1.38
1	2A	1917	PSU	C4-N3	-2.54	1.34	1.38
1	1A	1911	PSU	C4-N3	-2.51	1.34	1.38
1	1A	1962	5MC	C6-N1	-2.50	1.33	1.38
1	1A	1942	5MC	C6-N1	-2.49	1.33	1.38
1	1A	1939	5MU	C4-N3	-2.49	1.34	1.38
1	1A	1962	5MC	C6-C5	2.48	1.38	1.34
1	2A	1915	5MU	C4-N3	-2.48	1.34	1.38
32	1a	1207	2MG	C6-N1	-2.48	1.34	1.38
1	2A	1911	PSU	C4-N3	-2.45	1.34	1.38
1	1A	1915	5MU	C4-C5	2.45	1.48	1.44
1	2A	2251	OMG	C6-N1	-2.45	1.34	1.38
1	2A	2503	2MA	C8-N7	2.44	1.36	1.31
1	2A	1939	5MU	C6-N1	-2.44	1.33	1.38
1	2A	1915	5MU	C4-C5	2.43	1.48	1.44
1	1A	2552	OMU	C5-C4	2.41	1.48	1.43
1	1A	1915	5MU	C4-N3	-2.41	1.34	1.38
32	2a	527	G7M	C6-N1	-2.40	1.34	1.38
1	2A	2552	OMU	C5-C4	2.40	1.48	1.43
1	2A	2251	OMG	C5-N7	-2.37	1.34	1.39
1	2A	2552	OMU	C4-N3	-2.36	1.34	1.38
32	2a	1207	2MG	C6-N1	-2.36	1.34	1.38
1	1A	2552	OMU	C4-N3	-2.33	1.34	1.38
32	2a	516	PSU	C4-N3	-2.33	1.34	1.38
32	2a	1498	UR3	C2-N1	2.32	1.41	1.38
32	1a	1400	5MC	C6-N1	-2.31	1.34	1.38
1	2A	1962	5MC	C6-N1	-2.29	1.34	1.38
32	1a	516	PSU	C4-N3	-2.29	1.34	1.38
43	1l	92	0TD	CB-CA	2.27	1.55	1.54
32	2a	1404	5MC	C6-N1	-2.26	1.34	1.38
1	2A	1939	5MU	C2-N1	2.26	1.42	1.38
1	2A	1942	5MC	C6-N1	-2.25	1.34	1.38
32	2a	966	M2G	C6-N1	-2.25	1.34	1.38
55	1x	76	8AN	C5-C4	-2.23	1.35	1.39
32	1a	527	G7M	C6-N1	-2.21	1.34	1.38
1	2A	2503	2MA	C5-N7	-2.15	1.35	1.39
1	1A	1939	5MU	C6-N1	-2.15	1.34	1.38
32	1a	1498	UR3	C6-C5	2.13	1.40	1.35
32	1a	967	5MC	C6-N1	-2.11	1.34	1.38
1	1A	2503	2MA	C5-C6	2.11	1.46	1.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1A	2503	2MA	C8-N7	2.11	1.35	1.31
32	1a	1207	2MG	C2-N3	2.10	1.36	1.32
32	1a	1404	5MC	C6-N1	-2.09	1.34	1.38
1	1A	1939	5MU	C2-N3	-2.08	1.34	1.38
1	2A	2552	OMU	C2-N1	2.07	1.41	1.38
1	1A	2605	PSU	C2-N1	-2.07	1.34	1.36
1	1A	2251	OMG	C5-N7	-2.06	1.34	1.39
32	2a	1498	UR3	C6-C5	2.05	1.39	1.35
1	1A	2503	2MA	C4-N9	-2.04	1.33	1.37
32	2a	1207	2MG	C5-N7	-2.04	1.35	1.39
32	2a	967	5MC	C6-N1	-2.00	1.34	1.38

All (247) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
43	2l	92	0TD	CSB-SB-CB	-13.86	77.44	102.36
1	2A	2503	2MA	C5-C4-N3	-8.11	118.64	127.18
1	1A	2503	2MA	C5-C4-N3	-7.81	118.95	127.18
32	1a	1498	UR3	C4-N3-C2	-7.19	118.79	124.58
32	1a	1207	2MG	C2-N3-C4	7.13	120.92	112.00
1	1A	2503	2MA	N3-C4-N9	6.71	135.50	126.99
32	2a	1207	2MG	C2-N3-C4	6.65	120.33	112.00
1	1A	1911	PSU	N1-C2-N3	6.57	122.10	115.17
32	2a	1498	UR3	C4-N3-C2	-6.44	119.40	124.58
1	1A	2251	OMG	C5-C4-N3	-6.41	118.19	128.39
32	2a	516	PSU	N1-C2-N3	6.38	121.89	115.17
1	2A	1917	PSU	N1-C2-N3	6.31	121.82	115.17
1	2A	2251	OMG	C5-C4-N3	-6.24	118.46	128.39
1	1A	1917	PSU	N1-C2-N3	6.23	121.74	115.17
1	2A	1911	PSU	N1-C2-N3	6.22	121.73	115.17
1	2A	2503	2MA	N3-C4-N9	6.08	134.71	126.99
1	1A	2605	PSU	N1-C2-N3	6.07	121.58	115.17
32	2a	966	M2G	C5-C4-N3	-6.07	118.72	128.39
32	1a	966	M2G	C5-C4-N3	-5.97	118.89	128.39
32	1a	1207	2MG	C5-C4-N3	-5.82	119.12	128.39
55	2x	76	8AN	N1-C2-N3	-5.80	119.81	128.58
55	1x	76	8AN	N1-C2-N3	-5.72	119.92	128.58
1	2A	2605	PSU	N1-C2-N3	5.70	121.18	115.17
32	2a	1207	2MG	C5-C4-N3	-5.69	119.33	128.39
1	2A	1939	5MU	N3-C2-N1	5.58	122.16	114.89
55	1x	76	8AN	C5-C4-N3	-5.47	119.19	126.72
1	1A	2251	OMG	C2-N3-C4	5.46	121.71	112.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
32	1a	516	PSU	N1-C2-N3	5.41	120.88	115.17
1	2A	1939	5MU	C4-N3-C2	-5.34	120.34	127.34
55	2x	76	8AN	C5-C4-N3	-5.31	119.41	126.72
1	1A	1939	5MU	C4-N3-C2	-5.24	120.47	127.34
32	1a	527	G7M	N9-C4-N3	5.22	136.39	125.95
1	2A	2552	OMU	N3-C2-N1	5.20	121.66	114.89
32	2a	527	G7M	C5-C4-N3	-5.15	118.42	128.15
32	2a	527	G7M	N9-C4-N3	5.13	136.21	125.95
1	2A	1915	5MU	N3-C2-N1	5.05	121.47	114.89
43	1l	92	0TD	CSB-SB-CB	-5.04	93.30	102.36
1	1A	1939	5MU	N3-C2-N1	5.01	121.41	114.89
32	1a	527	G7M	C5-C4-N3	-5.01	118.69	128.15
1	2A	2251	OMG	C2-N3-C4	4.92	120.77	112.30
32	2a	1519	MA6	N1-C2-N3	-4.89	121.19	128.58
32	1a	1519	MA6	N1-C2-N3	-4.84	121.26	128.58
32	2a	1518	MA6	N1-C2-N3	-4.78	121.35	128.58
1	2A	2552	OMU	C4-N3-C2	-4.74	120.72	126.61
1	1A	1915	5MU	C4-N3-C2	-4.70	121.18	127.34
1	1A	1915	5MU	N3-C2-N1	4.67	120.97	114.89
32	2a	1519	MA6	C5-C4-N3	-4.65	120.31	126.72
1	2A	2251	OMG	N9-C4-N3	4.65	135.26	125.95
1	2A	1915	5MU	C4-N3-C2	-4.65	121.25	127.34
32	2a	527	G7M	C2-N3-C4	4.64	120.30	112.30
32	1a	527	G7M	C2-N3-C4	4.56	120.16	112.30
32	1a	1518	MA6	N1-C2-N3	-4.56	121.68	128.58
32	2a	1518	MA6	C5-C4-N3	-4.54	120.46	126.72
1	1A	2251	OMG	N9-C4-N3	4.54	135.03	125.95
1	1A	1915	5MU	C5-C4-N3	4.52	119.25	115.32
1	1A	1939	5MU	C5-C4-N3	4.51	119.24	115.32
32	2a	966	M2G	C2-N3-C4	4.51	120.85	112.51
1	1A	2552	OMU	N3-C2-N1	4.48	120.72	114.89
32	1a	966	M2G	C2-N3-C4	4.47	120.78	112.51
32	1a	1518	MA6	C5-C4-N3	-4.43	120.62	126.72
32	2a	966	M2G	N9-C4-N3	4.41	134.78	125.95
32	1a	1519	MA6	C5-C4-N3	-4.39	120.67	126.72
1	1A	2552	OMU	C4-N3-C2	-4.30	121.27	126.61
32	2a	516	PSU	C4-N3-C2	-4.25	120.51	126.37
32	2a	1519	MA6	C4-C5-N7	-4.23	105.75	110.58
32	2a	516	PSU	O2-C2-N1	-4.21	118.44	122.79
1	1A	1917	PSU	C4-N3-C2	-4.20	120.59	126.37
32	1a	1519	MA6	C2-N1-C6	4.15	121.97	111.83
1	1A	1911	PSU	C4-N3-C2	-4.11	120.71	126.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	2A	1911	PSU	C4-N3-C2	-4.08	120.75	126.37
32	1a	1207	2MG	N9-C4-N3	4.07	134.09	125.95
1	1A	2605	PSU	C4-N3-C2	-4.07	120.77	126.37
32	1a	516	PSU	C4-N3-C2	-4.04	120.81	126.37
1	1A	1915	5MU	O4-C4-C5	-4.03	120.30	124.92
1	2A	2503	2MA	C4-C5-N7	-4.02	105.98	110.58
32	2a	1519	MA6	C5-N7-C8	4.02	109.77	103.45
1	2A	1917	PSU	O2-C2-N1	-4.02	118.64	122.79
1	1A	2503	2MA	N6-C6-N1	4.01	122.44	117.03
32	1a	966	M2G	N9-C4-N3	4.01	133.97	125.95
32	2a	1518	MA6	C2-N1-C6	4.00	121.61	111.83
1	2A	2605	PSU	C4-N3-C2	-3.97	120.90	126.37
1	2A	1915	5MU	C5-C4-N3	3.95	118.76	115.32
32	2a	1518	MA6	C5-N7-C8	3.95	109.65	103.45
32	1a	1518	MA6	C2-N1-C6	3.95	121.47	111.83
32	2a	1207	2MG	N9-C4-N3	3.91	133.78	125.95
1	1A	1939	5MU	C5-C6-N1	-3.89	119.09	123.31
32	2a	1519	MA6	C2-N1-C6	3.88	121.31	111.83
1	2A	1939	5MU	C5-C4-N3	3.88	118.69	115.32
1	1A	1911	PSU	O2-C2-N1	-3.84	118.82	122.79
1	2A	1917	PSU	C4-N3-C2	-3.84	121.08	126.37
1	1A	1939	5MU	O2-C2-N1	-3.80	117.85	122.80
55	1x	76	8AN	C5-N7-C8	3.79	109.40	103.45
32	2a	1518	MA6	C4-C5-N7	-3.77	106.27	110.58
32	1a	1519	MA6	C4-C5-N7	-3.77	106.27	110.58
1	2A	1915	5MU	O4-C4-C5	-3.71	120.67	124.92
55	1x	76	8AN	N9-C8-N7	-3.71	108.67	113.94
32	1a	1518	MA6	C5-N7-C8	3.69	109.25	103.45
1	2A	1942	5MC	C5-C6-N1	-3.68	119.32	123.31
1	1A	1915	5MU	C1'-N1-C2	3.65	124.16	117.59
32	1a	1519	MA6	C5-N7-C8	3.63	109.16	103.45
32	2a	1404	5MC	C5-C4-N3	-3.61	118.06	121.75
32	1a	967	5MC	C5-C6-N1	-3.60	119.41	123.31
32	1a	966	M2G	C6-C5-N7	3.60	136.84	130.29
32	1a	1207	2MG	C6-C5-N7	3.58	136.81	130.29
32	2a	1519	MA6	C2-N3-C4	3.56	120.53	111.83
32	1a	1404	5MC	C5-C6-N1	-3.56	119.45	123.31
32	2a	1518	MA6	N9-C8-N7	-3.55	108.90	113.94
55	1x	76	8AN	C2-N3-C4	3.54	120.47	111.83
1	2A	1962	5MC	C5-C6-N1	-3.52	119.49	123.31
1	1A	2251	OMG	C6-C5-N7	3.52	136.69	130.29
1	2A	1915	5MU	C1'-N1-C2	3.50	123.87	117.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	2A	1939	5MU	C5-C6-N1	-3.49	119.52	123.31
32	2a	1207	2MG	C6-C5-N7	3.49	136.64	130.29
55	2x	76	8AN	C2-N3-C4	3.48	120.33	111.83
1	2A	2605	PSU	O2-C2-N1	-3.48	119.20	122.79
43	2l	92	0TD	OD2-CG-CB	3.44	120.59	113.15
55	2x	76	8AN	N9-C8-N7	-3.44	109.06	113.94
32	1a	1518	MA6	N9-C8-N7	-3.43	109.07	113.94
32	1a	1400	5MC	C5-C6-N1	-3.41	119.61	123.31
1	1A	1939	5MU	O4-C4-C5	-3.40	121.02	124.92
32	1a	1518	MA6	C4-C5-N7	-3.40	106.70	110.58
43	1l	92	0TD	OD2-CG-CB	3.39	120.48	113.15
32	2a	1518	MA6	C2-N3-C4	3.38	120.08	111.83
32	2a	1519	MA6	N9-C8-N7	-3.37	109.15	113.94
1	1A	1917	PSU	O2-C2-N1	-3.37	119.31	122.79
32	1a	1519	MA6	C2-N3-C4	3.32	119.94	111.83
1	1A	2552	OMU	C2'-C1'-N1	-3.27	108.03	114.24
1	1A	1962	5MC	C5-C6-N1	-3.27	119.76	123.31
1	2A	1911	PSU	O2-C2-N1	-3.27	119.42	122.79
1	1A	1942	5MC	C5-C6-N1	-3.26	119.77	123.31
32	2a	1404	5MC	C5-C6-N1	-3.25	119.78	123.31
32	1a	1518	MA6	C2-N3-C4	3.24	119.74	111.83
1	1A	1915	5MU	C1'-N1-C6	-3.24	115.82	121.15
1	1A	2503	2MA	C4-N9-C8	3.23	109.13	105.74
55	1x	76	8AN	C4-C5-N7	-3.20	106.92	110.58
32	1a	1407	5MC	C5-C6-N1	-3.14	119.90	123.31
32	2a	1498	UR3	C5-C4-N3	3.12	119.15	115.04
32	2a	966	M2G	C6-C5-N7	3.08	135.89	130.29
32	1a	1498	UR3	C5-C4-N3	3.05	119.06	115.04
1	1A	2503	2MA	C4-C5-N7	-3.05	107.10	110.58
1	1A	2552	OMU	O4-C4-C5	-3.04	119.91	125.16
32	1a	1402	4OC	C6-C5-C4	3.03	120.66	117.00
32	2a	1407	5MC	C5-C4-N3	-3.03	118.65	121.75
32	2a	967	5MC	C5-C6-N1	-3.03	120.03	123.31
1	2A	2503	2MA	C5-N7-C8	3.02	108.20	103.45
1	2A	2552	OMU	C5-C4-N3	3.02	119.03	114.80
32	1a	1400	5MC	C5-C4-N3	-3.02	118.66	121.75
32	1a	1518	MA6	N3-C4-N9	3.02	132.30	127.17
32	1a	1519	MA6	N9-C8-N7	-3.01	109.67	113.94
1	2A	2503	2MA	C4-N9-C8	2.99	108.88	105.74
55	2x	76	8AN	C5-N7-C8	2.97	108.12	103.45
1	2A	1939	5MU	O2-C2-N1	-2.97	118.93	122.80
32	1a	516	PSU	O2-C2-N1	-2.96	119.73	122.79

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	2A	2251	OMG	C6-C5-N7	2.95	135.66	130.29
1	2A	2503	2MA	N6-C6-N1	2.94	120.99	117.03
32	2a	1518	MA6	N3-C4-N9	2.90	132.10	127.17
32	2a	1207	2MG	N1-C2-N2	2.89	119.51	116.56
1	2A	2552	OMU	C2'-C1'-N1	-2.88	108.77	114.24
55	1x	76	8AN	C5-C4-N9	2.87	108.94	105.81
1	1A	2251	OMG	C4-C5-N7	-2.85	106.16	110.67
32	2a	1207	2MG	C4-C5-N7	-2.82	106.20	110.67
1	2A	1939	5MU	C5M-C5-C4	2.80	121.77	118.78
32	1a	966	M2G	C4-C5-N7	-2.78	106.26	110.67
55	2x	76	8AN	C5-C4-N9	2.78	108.84	105.81
1	2A	2552	OMU	O4-C4-C5	-2.77	120.39	125.16
55	1x	76	8AN	N3-C4-N9	2.77	131.87	127.17
1	2A	1915	5MU	C1'-N1-C6	-2.76	116.61	121.15
1	1A	2605	PSU	O2-C2-N1	-2.75	119.95	122.79
32	1a	1407	5MC	C5-C4-N3	-2.74	118.94	121.75
32	2a	1400	5MC	C5-C4-N3	-2.73	118.96	121.75
32	1a	1518	MA6	C4-C5-C6	2.71	118.71	115.91
32	1a	967	5MC	C5-C4-N3	-2.71	118.98	121.75
1	1A	1939	5MU	C5M-C5-C4	2.70	121.67	118.78
32	2a	1407	5MC	C5-C6-N1	-2.70	120.38	123.31
55	2x	76	8AN	N3-C4-N9	2.70	131.75	127.17
32	2a	1207	2MG	N2-C2-N3	-2.69	117.08	120.51
32	1a	1207	2MG	C4-C5-N7	-2.68	106.43	110.67
32	1a	1519	MA6	C4-C5-C6	2.68	118.68	115.91
32	2a	1518	MA6	C4-C5-C6	2.66	118.66	115.91
1	1A	2552	OMU	C5-C4-N3	2.66	118.52	114.80
1	2A	1920	OMC	O2-C2-N3	-2.66	118.14	122.33
1	2A	2552	OMU	O2-C2-N1	-2.65	119.34	122.80
32	1a	1404	5MC	C5-C4-N3	-2.64	119.05	121.75
1	2A	1939	5MU	C5M-C5-C6	-2.63	119.29	122.85
55	2x	76	8AN	C4'-O4'-C1'	-2.63	103.67	109.47
32	2a	1400	5MC	C5-C6-N1	-2.62	120.47	123.31
1	1A	2503	2MA	C2-N1-C6	2.60	122.10	118.10
32	2a	966	M2G	C4-C5-N7	-2.58	106.58	110.67
32	1a	516	PSU	C6-C5-C4	-2.58	116.43	118.17
1	2A	1939	5MU	O4-C4-C5	-2.58	121.97	124.92
1	2A	2503	2MA	N9-C8-N7	-2.57	110.30	113.94
55	2x	76	8AN	C6-C5-C4	2.56	120.68	117.18
1	1A	2503	2MA	C5-N7-C8	2.56	107.48	103.45
32	2a	1519	MA6	N3-C4-N9	2.55	131.51	127.17
1	2A	1915	5MU	C5-C6-N1	-2.55	120.54	123.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
32	1a	1407	5MC	O2-C2-N3	-2.53	118.33	122.33
1	2A	1962	5MC	C5-C4-N3	-2.51	119.18	121.75
43	2l	92	0TD	OD1-CG-CB	-2.51	117.18	122.44
55	1x	76	8AN	C4'-O4'-C1'	-2.51	103.93	109.47
1	2A	2251	OMG	C4-C5-N7	-2.51	106.70	110.67
32	2a	967	5MC	C5-C4-N3	-2.50	119.19	121.75
32	1a	1519	MA6	N3-C4-N9	2.50	131.42	127.17
1	2A	2503	2MA	C6-C5-N7	2.48	136.87	132.09
1	2A	2503	2MA	C2-N1-C6	2.43	121.84	118.10
1	1A	1915	5MU	C5-C6-N1	-2.43	120.68	123.31
32	1a	1207	2MG	N1-C2-N2	2.41	119.02	116.56
1	2A	1942	5MC	C5-C4-N3	-2.40	119.30	121.75
32	1a	527	G7M	O6-C6-C5	-2.38	122.69	128.01
32	1a	1498	UR3	C3U-N3-C2	2.37	121.46	117.33
1	1A	2605	PSU	C5-C6-N1	-2.35	118.88	122.14
32	2a	1519	MA6	C4-C5-C6	2.34	118.33	115.91
1	1A	1942	5MC	C5-C4-N3	-2.32	119.38	121.75
1	1A	1920	OMC	O2-C2-N3	-2.31	118.69	122.33
32	2a	1400	5MC	O2-C2-N3	-2.29	118.72	122.33
55	2x	76	8AN	C4-C5-N7	-2.29	107.97	110.58
1	1A	1962	5MC	C5-C4-N3	-2.27	119.43	121.75
1	1A	2503	2MA	N9-C8-N7	-2.25	110.74	113.94
32	2a	527	G7M	O6-C6-C5	-2.24	123.00	128.01
32	2a	516	PSU	C5-C6-N1	-2.22	119.06	122.14
32	2a	1407	5MC	O2-C2-N3	-2.18	118.89	122.33
1	1A	1915	5MU	C5M-C5-C4	2.17	121.10	118.78
32	2a	1519	MA6	C5-C4-N9	2.17	108.17	105.81
1	2A	2605	PSU	C5-C6-N1	-2.17	119.14	122.14
32	2a	516	PSU	O4'-C1'-C2'	2.16	108.14	105.15
1	1A	1911	PSU	C5-C6-N1	-2.16	119.14	122.14
1	1A	1915	5MU	O2-C2-N3	-2.14	117.53	121.49
1	2A	1911	PSU	C6-C5-C4	-2.14	116.73	118.17
32	1a	1498	UR3	C6-N1-C2	-2.14	120.05	121.80
32	1a	516	PSU	O4'-C1'-C2'	2.12	108.08	105.15
1	1A	1939	5MU	C5M-C5-C6	-2.11	119.99	122.85
1	1A	1962	5MC	CM5-C5-C6	-2.11	120.00	122.85
1	2A	1920	OMC	C1'-N1-C2	2.10	123.08	118.44
1	2A	2251	OMG	CM2-O2'-C2'	-2.10	109.08	114.47
1	1A	2552	OMU	O2-C2-N1	-2.10	120.06	122.80
1	2A	2251	OMG	O6-C6-C5	-2.10	121.00	126.53
1	1A	1911	PSU	O4'-C1'-C2'	2.09	108.05	105.15
1	2A	1915	5MU	O2-C2-N3	-2.09	117.64	121.49

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
32	2a	527	G7M	C5-C6-N1	2.09	116.15	111.84
43	1l	92	0TD	OD1-CG-CB	-2.07	118.11	122.44
1	1A	1962	5MC	C1'-N1-C6	-2.06	117.75	121.15
32	1a	1518	MA6	C4-N9-C8	2.06	107.90	105.74
32	2a	1207	2MG	CM2-N2-C2	-2.03	119.28	123.65
32	2a	967	5MC	O2-C2-N3	-2.03	119.13	122.33
1	1A	2251	OMG	C5-C6-N1	2.02	118.39	113.25
32	2a	1404	5MC	O2-C2-N3	-2.01	119.15	122.33
32	2a	1404	5MC	CM5-C5-C6	-2.01	120.13	122.85
32	1a	527	G7M	C5-C6-N1	2.00	115.98	111.84

There are no chirality outliers.

All (27) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	1A	1915	5MU	O4'-C1'-N1-C2
1	1A	1915	5MU	O4'-C1'-N1-C6
43	1l	92	0TD	CG-CB-SB-CSB
1	2A	1915	5MU	O4'-C1'-N1-C2
1	2A	1915	5MU	O4'-C1'-N1-C6
32	2a	1207	2MG	N1-C2-N2-CM2
32	2a	1207	2MG	N3-C2-N2-CM2
43	2l	92	0TD	CA-CB-SB-CSB
43	2l	92	0TD	CG-CB-SB-CSB
55	1x	76	8AN	C4'-C5'-O5'-P
32	1a	1519	MA6	O4'-C4'-C5'-O5'
55	2x	76	8AN	C4'-C5'-O5'-P
32	1a	527	G7M	C3'-C4'-C5'-O5'
32	1a	1402	4OC	O4'-C4'-C5'-O5'
32	1a	1519	MA6	C3'-C4'-C5'-O5'
32	2a	527	G7M	C3'-C4'-C5'-O5'
32	1a	516	PSU	O4'-C1'-C5-C4
32	1a	1402	4OC	C3'-C4'-C5'-O5'
1	1A	2503	2MA	C4'-C5'-O5'-P
32	2a	1519	MA6	O4'-C4'-C5'-O5'
43	1l	92	0TD	CA-CB-SB-CSB
32	2a	1519	MA6	C4'-C5'-O5'-P
1	2A	2503	2MA	O4'-C4'-C5'-O5'
32	1a	527	G7M	O4'-C4'-C5'-O5'
1	1A	1920	OMC	C2'-C1'-N1-C2
1	2A	1920	OMC	C2'-C1'-N1-C2
32	2a	527	G7M	C4'-C5'-O5'-P

There are no ring outliers.

17 monomers are involved in 24 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	2A	1920	OMC	1	0
1	1A	1920	OMC	1	0
1	1A	2251	OMG	1	0
1	2A	1917	PSU	1	0
32	1a	1519	MA6	1	0
32	2a	1404	5MC	1	0
32	1a	1400	5MC	2	0
32	2a	1519	MA6	2	0
32	2a	1400	5MC	3	0
55	2x	76	8AN	1	0
32	1a	1402	4OC	3	0
43	2l	92	0TD	2	0
32	2a	1402	4OC	1	0
1	2A	1939	5MU	2	0
32	2a	1518	MA6	1	0
1	2A	2552	OMU	1	0
32	1a	1518	MA6	2	0

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 2517 ligands modelled in this entry, 2505 are monoatomic - leaving 12 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	$\#\|Z\| > 2$
58	CLM	2A	3747	-	20,20,20	0.85	0	23,27,27	1.25	2 (8%)
58	CLM	1A	4017	-	20,20,20	1.10	2 (10%)	23,27,27	1.96	7 (30%)
59	ARG	1A	4018	57	10,11,11	0.76	1 (10%)	9,13,13	0.90	1 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
60	MPD	2B	220	-	7,7,7	0.31	0	9,10,10	0.19	0
60	MPD	1T	208	-	7,7,7	0.31	0	9,10,10	0.24	0
60	MPD	1A	4019	-	7,7,7	0.31	0	9,10,10	0.16	0
59	ARG	1B	231	-	10,11,11	0.78	1 (10%)	9,13,13	1.01	1 (11%)
62	SF4	2d	501	35	0,12,12	-	-	-		
62	SF4	1d	305	35	0,12,12	-	-	-		
60	MPD	18	104	-	7,7,7	0.29	0	9,10,10	0.22	0
60	MPD	1a	1867	-	7,7,7	0.37	0	9,10,10	0.41	0
60	MPD	2A	3748	-	7,7,7	0.29	0	9,10,10	0.18	0

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
58	CLM	2A	3747	-	-	0/20/22/22	0/1/1/1
58	CLM	1A	4017	-	-	2/20/22/22	0/1/1/1
59	ARG	1A	4018	57	-	2/11/11/11	-
60	MPD	2B	220	-	-	4/5/5/5	-
60	MPD	1T	208	-	-	1/5/5/5	-
60	MPD	1A	4019	-	-	3/5/5/5	-
59	ARG	1B	231	-	-	3/11/11/11	-
62	SF4	2d	501	35	-	-	0/6/5/5
62	SF4	1d	305	35	-	-	0/6/5/5
60	MPD	18	104	-	-	1/5/5/5	-
60	MPD	1a	1867	-	-	4/5/5/5	-
60	MPD	2A	3748	-	-	2/5/5/5	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
58	1A	4017	CLM	C6-C5	-2.97	1.47	1.51
58	1A	4017	CLM	C9-N9	-2.47	1.39	1.45
59	1B	231	ARG	OXT-C	-2.26	1.23	1.30
59	1A	4018	ARG	OXT-C	-2.15	1.23	1.30

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
58	1A	4017	CLM	C8-C9-N9	4.57	123.33	119.34
58	1A	4017	CLM	C10-C9-N9	-4.56	115.35	119.34
58	1A	4017	CLM	C6-C5-C3	3.44	117.89	111.72
58	2A	3747	CLM	C6-C5-C3	3.04	117.17	111.72
58	1A	4017	CLM	O5-C5-C6	-2.72	105.30	111.20
59	1A	4018	ARG	OXT-C-O	-2.53	118.33	124.08
58	2A	3747	CLM	C3-N2-C2	-2.52	118.86	123.25
59	1B	231	ARG	OXT-C-O	-2.50	118.40	124.08
58	1A	4017	CLM	C11-C6-C5	-2.22	117.36	120.71
58	1A	4017	CLM	C11-C6-C7	2.11	120.93	118.30
58	1A	4017	CLM	O9B-N9-C9	2.10	121.70	118.82

There are no chirality outliers.

All (22) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
59	1B	231	ARG	O-C-CA-N
60	1A	4019	MPD	C2-C3-C4-O4
60	1A	4019	MPD	C2-C3-C4-C5
60	2B	220	MPD	C2-C3-C4-C5
59	1B	231	ARG	CA-CB-CG-CD
59	1A	4018	ARG	NE-CD-CG-CB
59	1B	231	ARG	OXT-C-CA-N
59	1A	4018	ARG	CA-CB-CG-CD
58	1A	4017	CLM	C5-C3-C4-O4
60	1a	1867	MPD	CM-C2-C3-C4
60	2A	3748	MPD	C1-C2-C3-C4
60	2B	220	MPD	C1-C2-C3-C4
60	1a	1867	MPD	C2-C3-C4-C5
58	1A	4017	CLM	N2-C3-C4-O4
60	1T	208	MPD	C2-C3-C4-O4
60	18	104	MPD	C2-C3-C4-O4
60	1a	1867	MPD	C2-C3-C4-O4
60	2B	220	MPD	C2-C3-C4-O4
60	1A	4019	MPD	CM-C2-C3-C4
60	1a	1867	MPD	C1-C2-C3-C4
60	2A	3748	MPD	CM-C2-C3-C4
60	2B	220	MPD	CM-C2-C3-C4

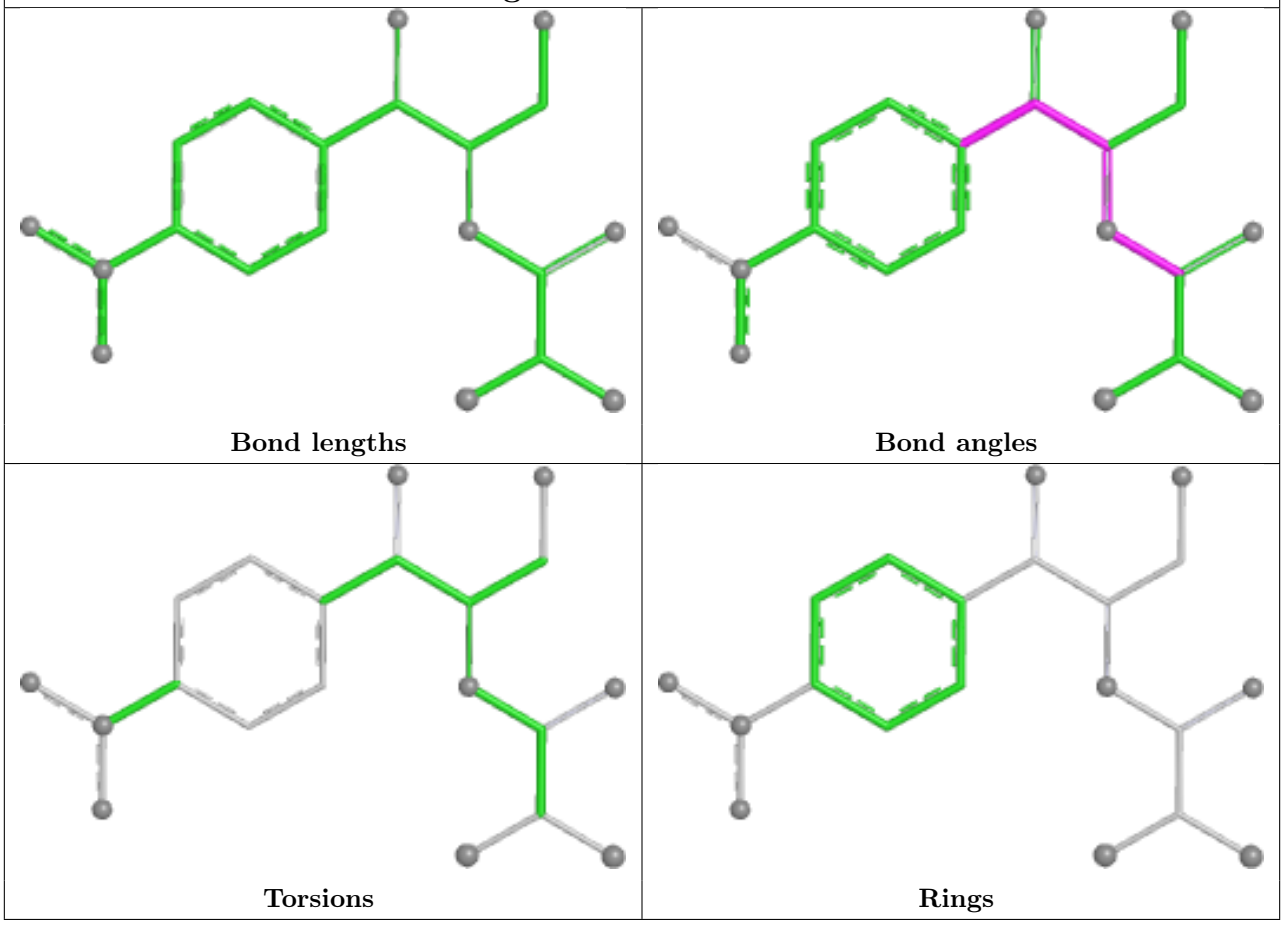
There are no ring outliers.

6 monomers are involved in 12 short contacts:

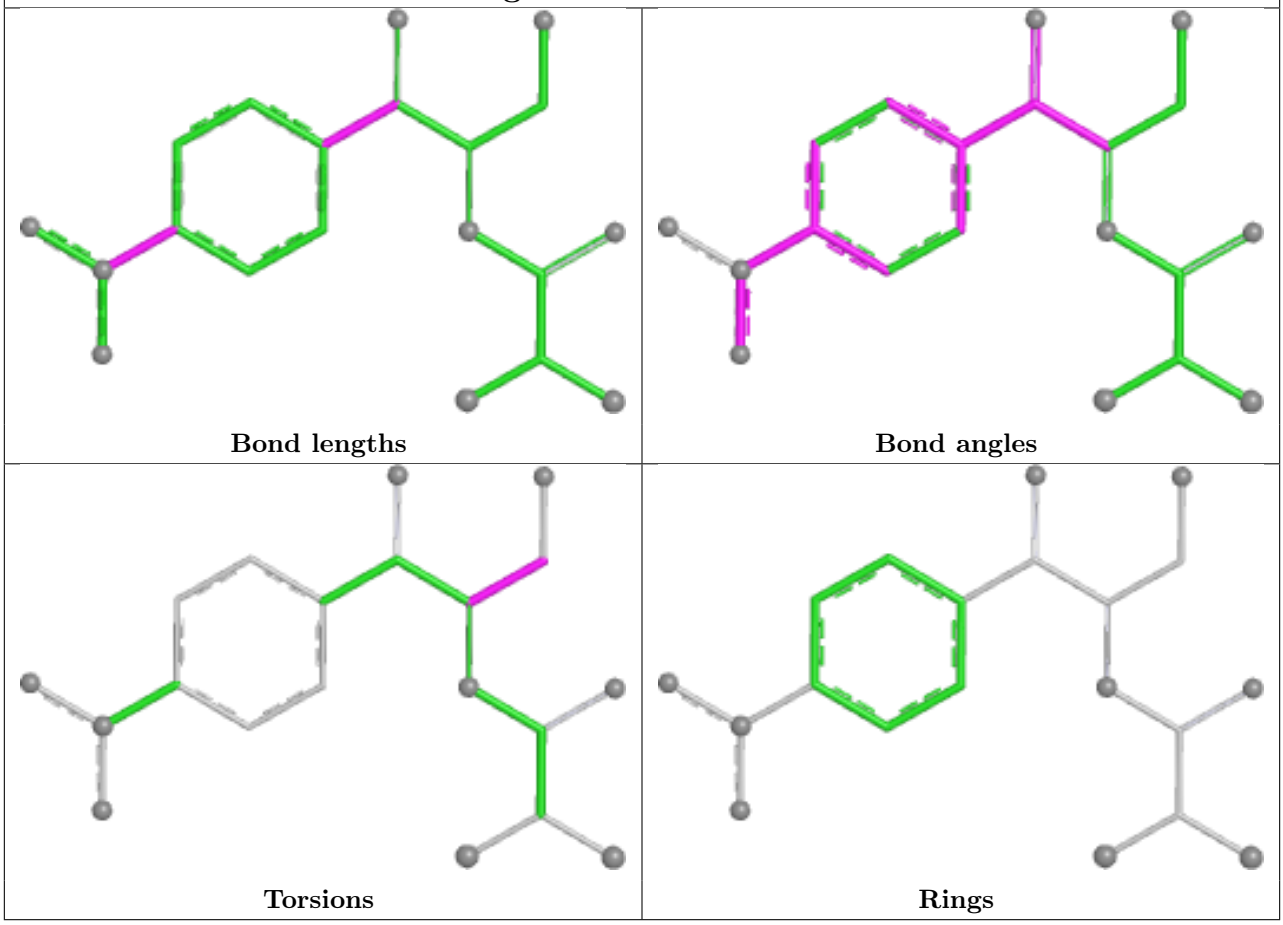
Mol	Chain	Res	Type	Clashes	Symm-Clashes
59	1A	4018	ARG	2	0
60	2B	220	MPD	1	0
60	1A	4019	MPD	1	0
59	1B	231	ARG	2	0
60	18	104	MPD	1	0
60	1a	1867	MPD	5	0

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 CLM 2A 3747



Ligand CLM 1A 4017



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	1A	2861/2915 (98%)	-0.49	139 (4%) 35 31	19, 36, 84, 95	0
1	2A	2856/2915 (97%)	0.04	148 (5%) 33 29	32, 53, 85, 95	0
2	1B	120/121 (99%)	-0.25	2 (1%) 69 65	30, 48, 62, 74	0
2	2B	120/121 (99%)	0.76	4 (3%) 49 45	58, 70, 78, 82	0
3	1D	275/276 (99%)	-0.11	1 (0%) 88 86	21, 36, 49, 61	0
3	2D	275/276 (99%)	0.27	2 (0%) 84 81	29, 48, 60, 71	0
4	1E	204/206 (99%)	-0.05	0 100 100	18, 40, 57, 66	0
4	2E	204/206 (99%)	0.42	3 (1%) 72 68	32, 53, 66, 75	0
5	1F	203/210 (96%)	0.05	2 (0%) 79 76	19, 41, 64, 77	0
5	2F	203/210 (96%)	0.70	4 (1%) 65 60	31, 62, 71, 78	0
6	1G	181/182 (99%)	0.88	14 (7%) 19 16	45, 59, 70, 79	0
6	2G	181/182 (99%)	1.76	63 (34%) 1 1	63, 73, 80, 84	0
7	1H	174/180 (96%)	0.39	1 (0%) 85 83	37, 52, 62, 66	0
7	2H	173/180 (96%)	1.41	35 (20%) 3 2	58, 71, 77, 80	0
8	1I	147/148 (99%)	1.04	14 (9%) 14 11	41, 66, 73, 78	0
8	2I	146/148 (98%)	1.30	21 (14%) 6 4	54, 68, 77, 84	0
9	1N	140/140 (100%)	0.04	3 (2%) 63 59	25, 38, 57, 72	0
9	2N	140/140 (100%)	0.75	6 (4%) 40 36	44, 60, 69, 71	0
10	1O	122/122 (100%)	-0.06	1 (0%) 82 80	28, 41, 56, 64	0
10	2O	122/122 (100%)	0.46	0 100 100	42, 51, 62, 68	0
11	1P	149/150 (99%)	0.09	0 100 100	19, 45, 65, 74	0
11	2P	149/150 (99%)	0.70	8 (5%) 31 28	37, 61, 72, 78	0
12	1Q	141/141 (100%)	0.02	0 100 100	25, 39, 50, 60	0
12	2Q	141/141 (100%)	0.97	10 (7%) 22 18	43, 60, 68, 72	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
13	1R	118/118 (100%)	-0.17	0 100 100	25, 34, 48, 54	0
13	2R	118/118 (100%)	0.33	2 (1%) 69 65	37, 49, 58, 65	0
14	1S	110/112 (98%)	0.47	4 (3%) 46 42	37, 48, 59, 63	0
14	2S	110/112 (98%)	1.48	21 (19%) 3 2	59, 66, 71, 71	0
15	1T	131/146 (89%)	0.22	5 (3%) 44 40	33, 45, 64, 80	0
15	2T	131/146 (89%)	0.53	3 (2%) 61 57	42, 55, 68, 77	0
16	1U	116/118 (98%)	-0.28	1 (0%) 81 78	21, 30, 45, 59	0
16	2U	116/118 (98%)	0.68	4 (3%) 48 44	40, 56, 67, 72	0
17	1V	101/101 (100%)	0.03	1 (0%) 79 76	22, 40, 55, 63	0
17	2V	101/101 (100%)	0.87	4 (3%) 42 38	40, 64, 71, 77	0
18	1W	112/113 (99%)	-0.18	1 (0%) 81 78	24, 31, 50, 72	0
18	2W	112/113 (99%)	0.48	3 (2%) 56 52	35, 49, 63, 81	0
19	1X	95/96 (98%)	0.03	2 (2%) 63 59	27, 38, 57, 64	0
19	2X	95/96 (98%)	0.91	8 (8%) 17 14	45, 56, 68, 75	0
20	1Y	107/110 (97%)	0.31	2 (1%) 66 62	34, 47, 59, 71	0
20	2Y	107/110 (97%)	1.20	12 (11%) 10 7	55, 65, 73, 78	0
21	1Z	203/206 (98%)	0.65	4 (1%) 65 60	39, 55, 67, 75	0
21	2Z	201/206 (97%)	1.40	30 (14%) 5 4	61, 69, 76, 80	0
22	10	83/85 (97%)	0.18	6 (7%) 21 18	27, 36, 55, 69	0
22	20	83/85 (97%)	1.15	8 (9%) 13 10	45, 58, 68, 70	0
23	11	97/98 (98%)	0.19	1 (1%) 79 76	27, 43, 63, 68	0
23	21	97/98 (98%)	0.53	1 (1%) 79 76	38, 52, 68, 73	0
24	12	70/72 (97%)	0.29	2 (2%) 53 50	37, 48, 58, 68	0
24	22	70/72 (97%)	1.06	6 (8%) 16 13	55, 64, 69, 71	0
25	13	59/60 (98%)	0.00	0 100 100	24, 35, 57, 63	0
25	23	59/60 (98%)	0.67	3 (5%) 33 30	53, 58, 70, 76	0
26	14	69/71 (97%)	1.34	17 (24%) 2 1	54, 70, 80, 85	0
26	24	69/71 (97%)	2.22	38 (55%) 0 0	72, 78, 82, 84	0
27	15	59/60 (98%)	-0.26	1 (1%) 69 65	22, 32, 45, 54	0
27	25	59/60 (98%)	0.20	1 (1%) 69 65	33, 48, 60, 66	0
28	16	53/54 (98%)	-0.00	0 100 100	33, 42, 52, 57	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
28	26	53/54 (98%)	0.58	1 (1%) 66 62	47, 56, 63, 67	0
29	17	48/49 (97%)	-0.19	3 (6%) 26 22	21, 28, 52, 61	0
29	27	48/49 (97%)	0.07	3 (6%) 26 22	34, 39, 60, 66	0
30	18	64/65 (98%)	-0.21	0 100 100	27, 34, 40, 54	0
30	28	64/65 (98%)	0.57	2 (3%) 51 47	40, 51, 58, 63	0
31	19	37/37 (100%)	-0.00	0 100 100	30, 39, 51, 58	0
31	29	37/37 (100%)	1.03	1 (2%) 56 52	51, 60, 71, 71	0
32	1a	1488/1521 (97%)	0.32	45 (3%) 52 48	35, 64, 82, 95	0
32	2a	1492/1521 (98%)	0.62	64 (4%) 40 36	44, 69, 84, 95	0
33	1b	231/256 (90%)	1.40	44 (19%) 3 2	60, 70, 77, 82	0
33	2b	231/256 (90%)	1.69	77 (33%) 1 1	66, 75, 80, 84	0
34	1c	206/239 (86%)	1.01	14 (6%) 23 20	56, 67, 75, 80	0
34	2c	206/239 (86%)	1.72	71 (34%) 1 1	65, 75, 79, 81	0
35	1d	208/209 (99%)	1.15	22 (10%) 11 8	54, 65, 73, 79	0
35	2d	208/209 (99%)	1.32	28 (13%) 7 5	56, 66, 73, 75	0
36	1e	148/162 (91%)	0.79	3 (2%) 65 60	43, 61, 68, 74	0
36	2e	148/162 (91%)	1.07	13 (8%) 15 12	58, 66, 73, 81	0
37	1f	100/101 (99%)	0.72	5 (5%) 34 30	50, 59, 68, 70	0
37	2f	100/101 (99%)	0.73	1 (1%) 79 76	56, 64, 72, 77	0
38	1g	155/156 (99%)	0.93	11 (7%) 22 18	53, 65, 71, 77	0
38	2g	155/156 (99%)	1.61	46 (29%) 1 1	66, 73, 78, 80	0
39	1h	137/138 (99%)	0.86	10 (7%) 21 17	52, 62, 67, 72	0
39	2h	137/138 (99%)	1.09	6 (4%) 39 34	61, 68, 73, 75	0
40	1i	127/128 (99%)	1.53	30 (23%) 2 1	56, 69, 75, 77	0
40	2i	126/128 (98%)	2.31	78 (61%) 0 0	68, 76, 80, 83	0
41	1j	97/105 (92%)	1.48	23 (23%) 2 1	57, 71, 76, 78	0
41	2j	96/105 (91%)	2.51	68 (70%) 0 0	68, 76, 81, 84	0
42	1k	114/129 (88%)	0.69	2 (1%) 67 63	42, 59, 68, 71	0
42	2k	114/129 (88%)	1.11	11 (9%) 13 10	56, 67, 73, 76	0
43	1l	121/132 (91%)	0.72	5 (4%) 41 37	48, 57, 65, 70	0
43	2l	121/132 (91%)	0.91	9 (7%) 20 17	53, 61, 68, 71	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
44	1m	116/126 (92%)	1.23	16 (13%) 6 5	56, 67, 73, 77	0
44	2m	114/126 (90%)	1.87	43 (37%) 1 0	69, 74, 79, 80	0
45	1n	60/61 (98%)	1.23	6 (10%) 12 9	58, 64, 72, 74	0
45	2n	60/61 (98%)	2.48	38 (63%) 0 0	66, 74, 79, 84	0
46	1o	88/89 (98%)	0.89	3 (3%) 48 44	43, 60, 70, 73	0
46	2o	88/89 (98%)	1.02	7 (7%) 18 15	58, 67, 72, 76	0
47	1p	82/88 (93%)	1.51	18 (21%) 2 2	55, 66, 73, 82	0
47	2p	82/88 (93%)	1.30	13 (15%) 5 4	57, 64, 69, 74	0
48	1q	99/105 (94%)	0.99	5 (5%) 33 30	49, 62, 71, 73	0
48	2q	99/105 (94%)	0.82	2 (2%) 65 60	54, 65, 71, 74	0
49	1r	68/88 (77%)	0.75	3 (4%) 39 34	52, 59, 71, 73	0
49	2r	68/88 (77%)	1.17	8 (11%) 9 6	61, 67, 74, 77	0
50	1s	83/93 (89%)	1.29	11 (13%) 7 5	59, 69, 74, 77	0
50	2s	83/93 (89%)	2.10	44 (53%) 0 0	63, 75, 80, 81	0
51	1t	96/106 (90%)	1.34	17 (17%) 4 3	59, 65, 73, 76	0
51	2t	98/106 (92%)	1.00	5 (5%) 33 30	54, 64, 72, 74	0
52	1u	23/27 (85%)	1.56	6 (26%) 1 1	61, 66, 69, 71	0
52	2u	23/27 (85%)	2.65	15 (65%) 0 0	71, 74, 76, 79	0
53	1y	97/113 (85%)	0.90	6 (6%) 26 23	49, 60, 70, 77	0
53	2y	96/113 (84%)	2.59	69 (71%) 0 0	69, 78, 84, 85	0
54	1w	4/5 (80%)	-0.17	0 100 100	28, 31, 44, 61	0
54	2w	4/5 (80%)	0.21	0 100 100	39, 46, 55, 70	0
55	1x	3/4 (75%)	0.38	1 (33%) 1 1	29, 29, 34, 51	0
55	2x	3/4 (75%)	0.53	1 (33%) 1 1	43, 43, 45, 60	0
56	1v	3/3 (100%)	-0.06	0 100 100	23, 23, 29, 38	0
56	2v	3/3 (100%)	0.94	0 100 100	46, 46, 51, 57	0
All	All	20798/21492 (96%)	0.49	1705 (8%) 17 14	18, 59, 79, 95	0

All (1705) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
45	2n	2	ALA	9.3
1	1A	1087	G	7.0

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Mol	Chain	Res	Type	RSRZ
41	2j	37	PRO	6.7
1	1A	2804	C	6.6
45	1n	2	ALA	6.5
53	2y	98	ALA	6.3
53	1y	98	ALA	6.3
41	2j	34	VAL	6.1
1	1A	1090	U	6.0
26	24	56	VAL	5.8
1	2A	2174	C	5.8
53	2y	40	ILE	5.7
1	1A	1072	C	5.5
51	2t	6	PRO	5.4
6	2G	146	TYR	5.3
1	1A	1076	C	5.3
7	1H	2	SER	5.3
1	2A	2125	G	5.2
1	2A	2793	G	5.1
32	2a	1030(A)	G	5.1
21	1Z	192	ALA	5.1
53	2y	52	ALA	4.9
1	2A	2803	C	4.9
1	2A	2124	G	4.9
45	2n	33	VAL	4.9
22	10	7	LEU	4.9
53	2y	45	PRO	4.8
50	1s	9	VAL	4.8
1	1A	2803	C	4.7
1	2A	2147	G	4.7
1	2A	2145	C	4.7
35	1d	179	GLU	4.7
26	14	56	VAL	4.6
1	2A	1536	C	4.6
53	2y	62	VAL	4.6
23	21	2	SER	4.6
1	1A	1078	U	4.5
1	2A	2133	G	4.5
1	2A	2162	G	4.5
32	1a	1036	G	4.5
1	1A	1075	C	4.5
1	1A	1095	A	4.5
40	2i	106	ALA	4.5
1	2A	2169	A	4.5

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Mol	Chain	Res	Type	RSRZ
52	2u	14	TRP	4.4
1	1A	1071	G	4.4
40	2i	14	VAL	4.4
53	2y	51	ASP	4.4
1	2A	2804	C	4.4
1	1A	2805	G	4.4
41	2j	24	VAL	4.4
1	2A	2136	C	4.3
1	1A	1089	G	4.3
1	1A	1093	G	4.3
1	1A	2793	G	4.3
51	1t	103	GLY	4.3
22	20	7	LEU	4.3
32	2a	1030(B)	C	4.3
40	2i	102	LEU	4.2
1	2A	1067	A	4.2
1	2A	2173	A	4.2
1	2A	2805	G	4.2
32	2a	1036	G	4.2
41	2j	46	ARG	4.2
51	2t	103	GLY	4.2
41	2j	75	ILE	4.2
50	2s	41	VAL	4.2
1	2A	2153	G	4.2
26	24	51	ASP	4.1
38	2g	7	ALA	4.1
26	14	63	TYR	4.1
1	1A	2794	C	4.1
22	20	3	HIS	4.1
41	2j	32	ALA	4.1
44	1m	2	ALA	4.1
1	1A	1091	G	4.1
26	24	50	VAL	4.1
1	1A	1070	A	4.1
53	2y	38	HIS	4.1
29	27	45	ALA	4.1
1	1A	1066	U	4.1
33	2b	38	GLY	4.1
40	1i	126	SER	4.1
44	2m	4	ILE	4.1
1	2A	2126	A	4.1
26	14	59	PHE	4.1

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Mol	Chain	Res	Type	RSRZ
1	2A	1076	C	4.0
41	2j	35	SER	4.0
1	1A	1068	G	4.0
45	2n	14	PRO	4.0
1	2A	2135	A	4.0
1	1A	2167	U	4.0
52	2u	16	GLY	4.0
44	2m	116	THR	4.0
1	2A	2127	G	4.0
38	2g	5	ARG	4.0
1	1A	888	C	4.0
53	2y	12	ILE	4.0
38	2g	16	LEU	4.0
6	2G	159	VAL	4.0
53	2y	60	VAL	4.0
26	14	49	PHE	4.0
1	1A	1077	A	4.0
40	1i	106	ALA	3.9
1	1A	1067	A	3.9
1	1A	1094	U	3.9
1	2A	2111	C	3.9
12	2Q	104	PHE	3.9
52	2u	2	GLY	3.9
41	2j	38	ILE	3.9
53	2y	81	LEU	3.9
1	2A	2172	U	3.9
45	2n	18	VAL	3.9
40	2i	43	ALA	3.9
44	2m	6	GLY	3.9
40	2i	2	GLU	3.9
1	1A	1074	G	3.9
18	2W	60	ASN	3.9
53	2y	5	ILE	3.9
47	1p	46	PRO	3.9
6	2G	160	VAL	3.9
1	2A	2139	C	3.8
45	2n	5	ALA	3.8
40	2i	75	ASP	3.8
51	1t	18	GLN	3.8
26	24	43	TYR	3.8
1	2A	2129	C	3.8
39	1h	2	LEU	3.8

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Mol	Chain	Res	Type	RSRZ
40	1i	28	VAL	3.8
41	2j	54	PHE	3.8
52	2u	6	ARG	3.8
1	2A	1091	G	3.8
50	2s	33	THR	3.8
40	2i	11	LYS	3.8
45	2n	59	ALA	3.8
32	2a	1286	A	3.8
41	2j	90	LEU	3.8
1	1A	1064	C	3.8
1	2A	2149	G	3.8
21	2Z	192	ALA	3.7
7	2H	21	PRO	3.7
32	1a	1030	C	3.7
32	2a	1030	C	3.7
1	2A	2154	G	3.7
8	2I	3	VAL	3.7
14	2S	3	ARG	3.7
40	1i	66	ARG	3.7
45	2n	13	THR	3.7
26	24	46	GLN	3.7
1	2A	2119	A	3.7
26	24	67	TYR	3.7
1	1A	1092	C	3.7
1	2A	2152	G	3.7
45	2n	30	ALA	3.7
47	1p	19	ILE	3.7
50	1s	13	ASP	3.7
1	1A	1088	A	3.7
6	2G	71	THR	3.7
1	1A	1063	G	3.7
1	2A	2894	G	3.7
50	2s	71	LEU	3.7
1	1A	1081	U	3.7
1	2A	2144	U	3.7
1	1A	1103	A	3.6
6	2G	112	PRO	3.6
52	2u	23	PRO	3.6
1	2A	2146	C	3.6
48	2q	98	LEU	3.6
34	2c	77	ILE	3.6
40	2i	21	PRO	3.6

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Mol	Chain	Res	Type	RSRZ
1	1A	1176	G	3.6
5	1F	208	GLY	3.6
22	20	8	GLY	3.6
40	2i	56	LEU	3.6
53	2y	27	LEU	3.6
1	2A	2137	C	3.6
1	1A	2123	G	3.6
1	2A	2893	G	3.6
52	2u	24	ARG	3.6
53	2y	10	MET	3.6
53	2y	46	GLN	3.6
34	2c	152	ILE	3.6
1	2A	2138	C	3.5
35	1d	170	VAL	3.5
1	2A	2123	G	3.5
1	2A	2148	G	3.5
6	2G	28	VAL	3.5
50	2s	9	VAL	3.5
53	2y	49	VAL	3.5
6	1G	146	TYR	3.5
26	24	63	TYR	3.5
26	24	9	LEU	3.5
18	2W	112	GLY	3.5
45	1n	5	ALA	3.5
25	23	2	PRO	3.5
50	2s	2	PRO	3.5
33	1b	200	ILE	3.5
34	2c	5	ILE	3.5
1	1A	1062	G	3.5
1	2A	2165	G	3.5
33	1b	17	PHE	3.5
43	2l	123	LYS	3.5
8	1I	147	GLN	3.5
32	2a	1257	U	3.5
19	2X	92	LEU	3.5
40	2i	67	GLY	3.5
1	2A	2171	A	3.5
1	2A	2168	G	3.5
33	2b	165	VAL	3.5
53	2y	6	THR	3.5
41	2j	71	LEU	3.5
6	2G	76	SER	3.5

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Mol	Chain	Res	Type	RSRZ
40	2i	76	ALA	3.5
14	2S	33	LYS	3.5
40	2i	18	PHE	3.5
1	2A	1046	A	3.4
12	2Q	59	ARG	3.4
40	1i	128	ARG	3.4
52	2u	15	ARG	3.4
1	1A	2792	G	3.4
1	2A	2157	G	3.4
32	1a	1030(A)	G	3.4
33	1b	213	LEU	3.4
12	2Q	65	PHE	3.4
1	1A	2158	A	3.4
1	2A	2159	G	3.4
32	1a	630	G	3.4
6	2G	139	LEU	3.4
41	2j	26	ALA	3.4
7	2H	136	ILE	3.4
41	1j	4	ILE	3.4
1	2A	1064	C	3.4
50	2s	12	ASP	3.4
8	2I	74	ASN	3.4
14	2S	46	VAL	3.4
33	1b	234	PRO	3.4
22	10	2	ALA	3.4
53	2y	78	ILE	3.4
1	2A	2132	U	3.4
1	2A	2161	C	3.4
1	2A	2134	A	3.4
21	2Z	125	LEU	3.4
33	2b	149	LEU	3.4
51	1t	99	LEU	3.4
15	1T	131	ALA	3.4
33	2b	207	ALA	3.4
33	2b	208	ILE	3.4
53	2y	35	ILE	3.4
32	1a	1024	G	3.3
1	1A	2144	U	3.3
33	2b	236	TYR	3.3
40	2i	5	TYR	3.3
40	2i	36	TYR	3.3
1	1A	2143	C	3.3

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Mol	Chain	Res	Type	RSRZ
21	2Z	191	VAL	3.3
33	1b	230	VAL	3.3
45	2n	56	VAL	3.3
40	2i	117	HIS	3.3
15	2T	131	ALA	3.3
26	24	49	PHE	3.3
1	2A	2118	U	3.3
1	2A	2131	G	3.3
22	10	4	LYS	3.3
32	1a	1026	G	3.3
32	2a	1003	G	3.3
40	2i	105	ASP	3.3
34	2c	3	ASN	3.3
1	2A	1075	C	3.3
1	2A	2140	C	3.3
33	1b	10	LEU	3.3
41	2j	70	ARG	3.3
34	2c	145	GLY	3.3
46	1o	89	GLY	3.3
50	2s	68	GLY	3.3
53	2y	42	SER	3.3
1	2A	2109	U	3.3
1	1A	1080	C	3.3
1	2A	2108	C	3.3
34	1c	207	VAL	3.3
44	2m	54	VAL	3.3
33	2b	237	ALA	3.3
34	2c	53	ALA	3.3
53	2y	50	ALA	3.3
1	1A	1069	A	3.3
51	1t	11	SER	3.3
47	2p	38	TYR	3.3
1	2A	2150	U	3.3
33	2b	118	LEU	3.3
36	2e	12	LEU	3.3
1	1A	2112	G	3.3
1	1A	2147	G	3.3
1	2A	2104	G	3.3
1	1A	2145	C	3.3
33	1b	214	ILE	3.3
40	1i	15	ALA	3.3
44	2m	5	ALA	3.3

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Mol	Chain	Res	Type	RSRZ
40	2i	126	SER	3.2
1	1A	1086	A	3.2
40	2i	101	PHE	3.2
6	2G	147	ASP	3.2
26	14	55	ARG	3.2
38	2g	154	TYR	3.2
44	2m	90	LEU	3.2
50	2s	15	LEU	3.2
53	2y	61	LEU	3.2
26	24	57	GLU	3.2
7	2H	43	VAL	3.2
43	2l	18	VAL	3.2
53	2y	8	LYS	3.2
14	2S	35	ILE	3.2
33	2b	201	ILE	3.2
1	2A	2802	G	3.2
32	1a	1030(B)	C	3.2
40	2i	13	ALA	3.2
14	2S	53	SER	3.2
1	1A	1073	A	3.2
1	1A	2126	A	3.2
1	2A	1085	A	3.2
45	2n	3	ARG	3.2
44	1m	113	PRO	3.2
41	2j	55	LYS	3.2
53	2y	3	MET	3.2
42	2k	109	VAL	3.2
7	2H	93	GLY	3.2
15	1T	37	GLY	3.2
22	10	6	GLY	3.2
45	2n	7	ILE	3.2
1	1A	1102	C	3.2
1	2A	2142	C	3.2
1	2A	2896	C	3.2
32	2a	1027	C	3.2
47	1p	59	TRP	3.2
1	1A	2116	G	3.2
1	2A	2155	G	3.2
32	2a	1031	G	3.2
53	2y	9	GLN	3.2
35	1d	157	LEU	3.2
40	1i	56	LEU	3.2

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Mol	Chain	Res	Type	RSRZ
41	2j	39	PRO	3.2
53	2y	37	PRO	3.2
53	2y	33	HIS	3.2
33	1b	229	VAL	3.2
44	2m	7	VAL	3.2
22	20	43	THR	3.2
40	2i	122	ALA	3.2
40	2i	66	ARG	3.2
50	2s	35	SER	3.2
1	1A	2115	G	3.2
1	1A	2124	G	3.2
1	2A	2160	G	3.2
50	2s	69	HIS	3.2
21	1Z	1	MET	3.2
33	1b	236	TYR	3.2
38	2g	85	TYR	3.2
5	1F	16	GLY	3.2
26	24	21	VAL	3.2
34	1c	80	GLY	3.2
34	2c	185	GLY	3.2
44	2m	100	GLY	3.2
45	2n	25	VAL	3.2
41	2j	33	GLN	3.1
1	2A	645	C	3.1
1	2A	2175	C	3.1
44	2m	69	GLU	3.1
7	2H	41	MET	3.1
1	1A	1096	A	3.1
1	1A	2169	A	3.1
35	2d	6	GLY	3.1
40	2i	6	GLY	3.1
7	2H	89	ILE	3.1
40	2i	63	ILE	3.1
40	2i	64	THR	3.1
53	2y	39	ILE	3.1
4	2E	204	ALA	3.1
21	1Z	188	ALA	3.1
40	2i	42	ARG	3.1
22	10	5	LYS	3.1
45	2n	16	PHE	3.1
1	2A	2116	G	3.1
7	2H	45	VAL	3.1

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Mol	Chain	Res	Type	RSRZ
14	2S	45	GLY	3.1
17	2V	42	GLY	3.1
20	2Y	80	GLY	3.1
14	2S	7	TYR	3.1
19	1X	69	TYR	3.1
32	2a	1001(A)	G	3.1
32	2a	1124	G	3.1
1	1A	2171	A	3.1
19	2X	68	ARG	3.1
32	1a	1001	A	3.1
32	1a	1286	A	3.1
41	2j	100	THR	3.1
1	2A	2167	U	3.1
32	1a	1257	U	3.1
42	2k	124	LYS	3.1
45	2n	4	LYS	3.1
26	24	59	PHE	3.1
34	2c	33	LEU	3.1
53	2y	24	LEU	3.1
53	2y	88	LEU	3.1
50	2s	34	TRP	3.1
33	1b	94	ASN	3.1
33	2b	21	ARG	3.1
39	2h	122	ARG	3.1
40	2i	100	GLY	3.1
41	1j	74	ILE	3.1
41	2j	42	THR	3.1
41	2j	87	THR	3.1
26	14	57	GLU	3.1
6	2G	80	PHE	3.1
35	2d	21	LEU	3.1
39	1h	133	LEU	3.1
44	1m	56	LEU	3.1
45	2n	6	LEU	3.1
48	1q	99	SER	3.1
39	1h	134	ILE	3.1
40	2i	41	VAL	3.1
40	2i	108	VAL	3.1
32	1a	1029	C	3.1
34	2c	187	ALA	3.0
32	1a	1005	A	3.0
32	1a	1492	A	3.0

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Mol	Chain	Res	Type	RSRZ
53	2y	76	GLU	3.0
1	1A	2132	U	3.0
1	2A	1082	U	3.0
1	2A	2130	U	3.0
1	1A	1058	G	3.0
1	1A	2125	G	3.0
40	2i	123	PRO	3.0
33	2b	57	PHE	3.0
53	2y	77	LEU	3.0
41	2j	28	ARG	3.0
52	2u	11	GLY	3.0
34	2c	55	VAL	3.0
9	2N	73	THR	3.0
1	1A	34	C	3.0
1	2A	2107	C	3.0
20	2Y	1	MET	3.0
1	2A	2170	A	3.0
33	1b	131	PRO	3.0
34	1c	94	LEU	3.0
35	1d	188	LEU	3.0
40	2i	91	ASP	3.0
1	1A	2168	G	3.0
1	2A	1071	G	3.0
32	1a	1001(A)	G	3.0
32	2a	1033	G	3.0
38	2g	76	ARG	3.0
46	2o	86	GLY	3.0
6	2G	41	GLN	3.0
16	1U	117	GLN	3.0
34	2c	124	ILE	3.0
40	2i	53	VAL	3.0
40	2i	109	VAL	3.0
41	2j	74	ILE	3.0
33	1b	231	GLU	3.0
41	1j	32	ALA	3.0
18	1W	111	HIS	3.0
1	1A	1079	C	3.0
40	2i	125	TYR	3.0
45	2n	21	TYR	3.0
41	2j	77	PRO	3.0
44	2m	66	LEU	3.0
1	2A	229	A	3.0

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Mol	Chain	Res	Type	RSRZ
1	2A	1083	U	3.0
1	2A	1084	A	3.0
1	2A	2113	U	3.0
40	2i	59	PHE	3.0
1	2A	2110	G	3.0
1	2A	2120	G	3.0
33	2b	223	ILE	3.0
42	2k	25	TYR	3.0
1	2A	2164	C	3.0
6	1G	152	LEU	3.0
38	2g	38	LEU	3.0
41	2j	40	LEU	3.0
53	2y	64	SER	3.0
34	1c	194	GLY	3.0
40	2i	30	GLY	3.0
44	2m	24	GLY	3.0
6	2G	77	ILE	2.9
41	2j	72	VAL	2.9
53	1y	2	THR	2.9
38	2g	128	ALA	2.9
51	1t	66	ALA	2.9
41	2j	91	PRO	2.9
6	2G	53	LEU	2.9
33	2b	44	LEU	2.9
45	2n	39	LEU	2.9
50	2s	5	LEU	2.9
1	1A	889	C	2.9
1	1A	2146	C	2.9
1	1A	2174	C	2.9
6	2G	102	PHE	2.9
41	2j	47	PHE	2.9
53	2y	48	PHE	2.9
1	2A	2180	U	2.9
1	1A	2117	A	2.9
1	2A	2117	A	2.9
49	2r	59	SER	2.9
50	2s	4	SER	2.9
51	1t	70	SER	2.9
26	24	54	GLY	2.9
8	2I	92	VAL	2.9
9	1N	9	VAL	2.9
33	2b	15	VAL	2.9

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Mol	Chain	Res	Type	RSRZ
53	2y	11	GLU	2.9
50	2s	63	THR	2.9
1	1A	1099	G	2.9
1	1A	2159	G	2.9
1	1A	2893	G	2.9
1	2A	2121	G	2.9
44	2m	65	LYS	2.9
33	2b	199	TYR	2.9
40	1i	125	TYR	2.9
1	1A	1082	U	2.9
1	1A	1101	U	2.9
32	1a	1027	C	2.9
32	2a	979	C	2.9
6	2G	42	GLY	2.9
40	2i	115	GLY	2.9
53	2y	4	ASN	2.9
1	2A	2176	A	2.9
6	2G	88	ILE	2.9
32	2a	1035	A	2.9
35	1d	8	VAL	2.9
52	2u	9	ARG	2.9
29	27	48	LYS	2.9
50	2s	28	LYS	2.9
33	2b	121	LEU	2.9
40	2i	96	LEU	2.9
1	2A	2112	G	2.9
35	1d	23	GLY	2.9
35	1d	167	GLY	2.9
38	2g	77	SER	2.9
1	1A	1065	U	2.9
1	1A	2113	U	2.9
1	2A	2897	U	2.9
1	2A	2179	C	2.9
14	2S	28	VAL	2.9
40	1i	14	VAL	2.9
40	1i	42	ARG	2.9
44	2m	98	VAL	2.9
8	2I	86	THR	2.9
6	2G	110	ALA	2.9
8	2I	134	PRO	2.9
15	1T	130	ALA	2.9
40	1i	91	ASP	2.9

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Mol	Chain	Res	Type	RSRZ
1	2A	1062	G	2.9
1	2A	2106	G	2.9
53	2y	70	MET	2.9
26	24	30	GLU	2.9
33	1b	128	GLU	2.9
6	2G	63	ILE	2.8
1	2A	1081	U	2.8
1	2A	2122	U	2.8
45	2n	9	LYS	2.8
34	2c	70	VAL	2.8
35	1d	178	VAL	2.8
1	1A	2107	C	2.8
1	1A	2119	A	2.8
1	2A	2114	A	2.8
41	2j	92	THR	2.8
50	2s	76	PRO	2.8
34	2c	87	LEU	2.8
35	2d	162	LEU	2.8
44	2m	64	TRP	2.8
22	20	4	LYS	2.8
26	24	45	GLY	2.8
44	2m	3	ARG	2.8
1	2A	2156	G	2.8
41	2j	50	ILE	2.8
1	2A	1066	U	2.8
26	24	7	PRO	2.8
53	2y	53	THR	2.8
1	1A	2142	C	2.8
1	2A	2128	C	2.8
6	2G	50	ALA	2.8
1	1A	2173	A	2.8
1	2A	652(B)	A	2.8
1	2A	1073	A	2.8
1	2A	2158	A	2.8
1	2A	2892	A	2.8
52	1u	24	ARG	2.8
33	1b	19	HIS	2.8
34	2c	159	GLY	2.8
44	2m	87	TYR	2.8
20	1Y	92	ASN	2.8
40	2i	81	ILE	2.8
26	24	35	VAL	2.8

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Mol	Chain	Res	Type	RSRZ
33	2b	184	VAL	2.8
35	1d	112	VAL	2.8
1	1A	2155	G	2.8
1	2A	2166	G	2.8
32	1a	1023	G	2.8
32	2a	1034	G	2.8
1	1A	1061	U	2.8
1	1A	2109	U	2.8
6	1G	82	LEU	2.8
15	2T	130	ALA	2.8
33	2b	61	LEU	2.8
33	2b	187	LEU	2.8
34	2c	149	ALA	2.8
34	2c	163	ALA	2.8
35	1d	155	LEU	2.8
39	2h	2	LEU	2.8
41	2j	85	LEU	2.8
44	2m	51	ALA	2.8
32	2a	1029	C	2.8
55	1x	73	A	2.8
41	2j	64	GLU	2.8
44	2m	58	GLU	2.8
38	2g	32	ARG	2.8
41	2j	43	ARG	2.8
34	1c	10	PHE	2.8
41	2j	63	PHE	2.8
41	2j	93	GLY	2.8
26	24	14	ILE	2.8
35	1d	138	TYR	2.8
44	2m	78	ILE	2.8
45	2n	34	TYR	2.8
53	2y	16	ILE	2.8
38	2g	23	VAL	2.8
34	2c	192	THR	2.8
53	1y	94	ALA	2.8
53	2y	32	THR	2.8
1	1A	2118	U	2.8
1	1A	2894	G	2.8
45	2n	27	CYS	2.8
40	1i	104	ARG	2.8
1	2A	6	A	2.8
8	1I	14	ASP	2.8

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Mol	Chain	Res	Type	RSRZ
40	2i	4	TYR	2.7
52	1u	23	PRO	2.7
26	14	50	VAL	2.7
35	2d	174	LEU	2.7
40	2i	99	LEU	2.7
41	2j	67	THR	2.7
41	2j	88	LEU	2.7
1	1A	2130	U	2.7
1	1A	2172	U	2.7
20	2Y	94	LYS	2.7
32	1a	1000	U	2.7
45	2n	57	ARG	2.7
50	2s	3	ARG	2.7
1	2A	2792	G	2.7
1	2A	34	C	2.7
55	2x	73	A	2.7
33	1b	228	GLY	2.7
34	1c	41	GLY	2.7
40	2i	74	ILE	2.7
7	2H	63	SER	2.7
33	1b	165	VAL	2.7
40	2i	62	TYR	2.7
41	2j	44	VAL	2.7
40	1i	47	LEU	2.7
41	2j	14	LYS	2.7
50	2s	66	MET	2.7
53	2y	13	THR	2.7
45	2n	29	ARG	2.7
1	1A	1175	U	2.7
24	22	70	GLN	2.7
34	2c	37	GLN	2.7
52	2u	5	ASP	2.7
32	1a	1033	G	2.7
1	2A	1509	C	2.7
6	2G	180	PHE	2.7
6	1G	88	ILE	2.7
41	1j	78	ASN	2.7
19	2X	69	TYR	2.7
33	1b	133	LYS	2.7
41	2j	30	SER	2.7
38	1g	156	TRP	2.7
8	2I	26	ALA	2.7

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Mol	Chain	Res	Type	RSRZ
26	14	48	ARG	2.7
34	2c	129	ALA	2.7
38	2g	24	THR	2.7
52	2u	7	ARG	2.7
1	1A	1083	U	2.7
2	2B	1	U	2.7
53	2y	19	HIS	2.7
8	2I	90	GLY	2.7
1	1A	2114	A	2.7
1	1A	2166	G	2.7
1	2A	2115	G	2.7
32	2a	1030(C)	G	2.7
1	2A	2163	C	2.7
32	2a	1030(D)	A	2.7
41	2j	69	ASN	2.7
41	2j	80	LYS	2.7
12	2Q	5	ARG	2.7
33	2b	10	LEU	2.7
38	2g	80	VAL	2.7
40	2i	17	VAL	2.7
41	2j	8	LEU	2.7
51	1t	10	LEU	2.7
53	1y	95	ARG	2.7
6	2G	12	TYR	2.7
33	2b	97	TRP	2.7
34	1c	90	GLU	2.7
38	2g	116	ALA	2.7
41	2j	27	ALA	2.7
42	2k	31	THR	2.7
45	2n	10	ALA	2.7
53	2y	97	ALA	2.7
41	1j	73	ASP	2.6
34	2c	41	GLY	2.6
45	2n	55	GLY	2.6
20	2Y	75	ILE	2.6
22	20	5	LYS	2.6
41	1j	75	ILE	2.6
47	2p	33	ILE	2.6
50	2s	49	ILE	2.6
1	2A	1070	A	2.6
15	1T	38	ASN	2.6
41	2j	78	ASN	2.6

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Mol	Chain	Res	Type	RSRZ
49	2r	87	ARG	2.6
33	2b	136	VAL	2.6
44	2m	48	LEU	2.6
1	1A	2141	G	2.6
1	2A	1087	G	2.6
32	2a	630	G	2.6
32	2a	1277	C	2.6
53	2y	44	GLU	2.6
6	2G	161	THR	2.6
33	1b	188	ALA	2.6
33	2b	95	GLN	2.6
34	2c	71	ALA	2.6
38	2g	25	ALA	2.6
38	2g	40	ALA	2.6
40	2i	46	ALA	2.6
42	1k	25	TYR	2.6
6	2G	100	TRP	2.6
33	1b	97	TRP	2.6
34	1c	2	GLY	2.6
40	1i	127	LYS	2.6
40	2i	95	LYS	2.6
6	2G	142	PRO	2.6
9	2N	85	ILE	2.6
33	2b	172	ILE	2.6
40	2i	33	PHE	2.6
45	1n	14	PRO	2.6
46	2o	68	ARG	2.6
22	20	84	LEU	2.6
35	2d	161	ASN	2.6
38	2g	104	LEU	2.6
51	2t	9	ASN	2.6
1	1A	887	A	2.6
32	2a	1123	A	2.6
1	1A	1104	C	2.6
32	2a	1128	C	2.6
33	1b	237	ALA	2.6
40	1i	46	ALA	2.6
41	2j	48	THR	2.6
53	2y	94	ALA	2.6
1	1A	1059	G	2.6
1	1A	2153	G	2.6
2	2B	118	G	2.6

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Mol	Chain	Res	Type	RSRZ
17	2V	12	TYR	2.6
32	2a	1202	G	2.6
6	2G	136	ARG	2.6
7	2H	173	PRO	2.6
7	2H	72	ILE	2.6
11	2P	15	ARG	2.6
35	2d	146	ILE	2.6
36	1e	101	ILE	2.6
6	1G	80	PHE	2.6
40	1i	37	PHE	2.6
6	1G	53	LEU	2.6
7	2H	71	LEU	2.6
40	1i	19	LEU	2.6
41	1j	90	LEU	2.6
44	2m	67	GLU	2.6
33	2b	230	VAL	2.6
38	2g	9	VAL	2.6
40	2i	26	VAL	2.6
8	2I	146	ALA	2.6
38	2g	152	ALA	2.6
41	2j	62	HIS	2.6
1	1A	1100	C	2.6
1	1A	2139	C	2.6
44	2m	23	TYR	2.6
3	1D	275	LYS	2.6
3	2D	275	LYS	2.6
9	2N	104	LYS	2.6
1	2A	2191	G	2.6
6	2G	2	PRO	2.6
29	27	47	ARG	2.6
31	29	37	GLY	2.6
41	2j	17	ASP	2.6
43	1l	95	GLY	2.6
40	1i	63	ILE	2.6
51	1t	100	ILE	2.6
21	2Z	136	PHE	2.6
33	2b	17	PHE	2.6
7	2H	7	LEU	2.6
8	2I	72	LEU	2.6
35	1d	174	LEU	2.6
40	2i	12	GLU	2.6
53	2y	85	LEU	2.6

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Mol	Chain	Res	Type	RSRZ
9	2N	140	VAL	2.6
34	2c	76	VAL	2.6
6	2G	57	ALA	2.6
26	24	66	SER	2.6
26	24	44	THR	2.6
49	2r	20	ALA	2.6
1	1A	2176	A	2.6
1	2A	2801(A)	A	2.6
32	2a	1363(A)	A	2.6
14	2S	92	TYR	2.6
1	2A	2143	C	2.5
13	2R	68	ARG	2.5
26	24	61	ARG	2.5
29	17	47	ARG	2.5
38	2g	41	ARG	2.5
14	2S	22	GLY	2.5
33	2b	232	PRO	2.5
35	1d	87	GLY	2.5
40	1i	75	ASP	2.5
50	2s	42	PRO	2.5
34	2c	14	ILE	2.5
33	1b	122	PHE	2.5
34	2c	128	PHE	2.5
8	1I	38	LEU	2.5
24	22	3	LEU	2.5
37	1f	90	VAL	2.5
53	1y	9	GLN	2.5
45	2n	49	HIS	2.5
26	14	69	LYS	2.5
33	2b	22	LYS	2.5
33	2b	192	SER	2.5
50	2s	37	ARG	2.5
53	2y	95	ARG	2.5
1	1A	2170	A	2.5
1	2A	1445	A	2.5
6	1G	25	TYR	2.5
44	2m	59	TYR	2.5
1	1A	1509	C	2.5
6	2G	29	TRP	2.5
32	1a	63	C	2.5
36	1e	22	GLY	2.5
40	1i	68	GLY	2.5

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Mol	Chain	Res	Type	RSRZ
6	2G	157	ILE	2.5
34	2c	90	GLU	2.5
1	1A	2149	G	2.5
7	2H	98	LEU	2.5
33	2b	163	PHE	2.5
32	1a	1021	G	2.5
33	2b	213	LEU	2.5
47	1p	49	LEU	2.5
33	2b	81	VAL	2.5
33	2b	93	VAL	2.5
41	1j	34	VAL	2.5
43	1l	18	VAL	2.5
49	2r	68	LYS	2.5
50	2s	14	HIS	2.5
50	2s	67	VAL	2.5
38	2g	100	ALA	2.5
40	1i	94	ALA	2.5
41	2j	18	ALA	2.5
47	2p	7	ALA	2.5
49	2r	24	ALA	2.5
50	2s	75	ALA	2.5
40	2i	71	SER	2.5
15	1T	129	ARG	2.5
50	2s	29	ARG	2.5
1	1A	1085	A	2.5
6	1G	49	ASP	2.5
8	2I	20	ASP	2.5
26	14	53	GLU	2.5
26	24	22	ILE	2.5
33	2b	80	ILE	2.5
38	2g	42	ILE	2.5
38	2g	120	ILE	2.5
1	1A	2138	C	2.5
32	1a	1028	C	2.5
32	2a	1039	C	2.5
14	2S	58	LEU	2.5
33	2b	138	LEU	2.5
35	2d	157	LEU	2.5
33	2b	132	LYS	2.5
6	2G	70	VAL	2.5
7	2H	44	VAL	2.5
21	2Z	116	VAL	2.5

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Mol	Chain	Res	Type	RSRZ
1	1A	1055	G	2.5
41	1j	28	ARG	2.5
6	2G	145	THR	2.5
33	2b	190	THR	2.5
21	2Z	1	MET	2.5
26	24	32	TYR	2.5
33	1b	39	ILE	2.5
33	2b	214	ILE	2.5
34	2c	182	ILE	2.5
34	2c	202	ILE	2.5
1	1A	1057	A	2.5
8	2I	131	LYS	2.5
40	2i	127	LYS	2.5
43	2l	23	LYS	2.5
50	2s	18	LYS	2.5
50	2s	25	LYS	2.5
51	2t	30	LYS	2.5
21	2Z	44	PHE	2.5
1	1A	2161	C	2.5
1	2A	886	C	2.5
1	2A	2105	C	2.5
34	2c	176	HIS	2.5
6	2G	38	VAL	2.5
11	2P	79	ARG	2.5
33	1b	37	ASN	2.5
34	2c	75	VAL	2.5
47	1p	79	VAL	2.5
1	1A	1097	U	2.5
5	2F	166	ALA	2.5
7	2H	20	ALA	2.5
35	1d	164	ALA	2.5
35	2d	48	ALA	2.5
40	2i	45	ALA	2.5
41	1j	26	ALA	2.5
47	2p	70	ALA	2.5
1	2A	2141	G	2.5
1	2A	2207	G	2.5
20	1Y	1	MET	2.5
38	2g	14	PRO	2.4
38	2g	123	GLU	2.4
50	2s	8	GLY	2.4
6	2G	182	LYS	2.4

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Mol	Chain	Res	Type	RSRZ
33	2b	185	ILE	2.4
42	1k	75	TYR	2.4
42	2k	75	TYR	2.4
46	2o	87	ILE	2.4
50	2s	31	ILE	2.4
53	2y	54	ILE	2.4
5	2F	181	LEU	2.4
6	2G	90	LEU	2.4
34	1c	42	LEU	2.4
41	1j	85	LEU	2.4
1	1A	2801(A)	A	2.4
9	1N	8	GLN	2.4
26	24	60	GLN	2.4
33	2b	40	HIS	2.4
14	2S	17	ARG	2.4
24	12	69	ARG	2.4
45	2n	12	ARG	2.4
1	1A	2175	C	2.4
18	2W	50	VAL	2.4
21	2Z	90	VAL	2.4
34	2c	195	VAL	2.4
40	2i	29	ASN	2.4
53	2y	20	VAL	2.4
53	2y	55	ASN	2.4
1	1A	2150	U	2.4
4	2E	28	ALA	2.4
29	17	45	ALA	2.4
34	2c	200	ALA	2.4
41	1j	27	ALA	2.4
51	1t	97	ALA	2.4
26	24	24	THR	2.4
26	24	52	THR	2.4
47	1p	22	THR	2.4
5	2F	14	PRO	2.4
34	2c	114	PRO	2.4
53	2y	14	PRO	2.4
41	2j	25	GLU	2.4
1	1A	2165	G	2.4
1	2A	1089	G	2.4
1	2A	2807	G	2.4
12	2Q	30	GLY	2.4
21	1Z	198	LYS	2.4

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Mol	Chain	Res	Type	RSRZ
32	1a	1030(C)	G	2.4
32	2a	1032	G	2.4
32	2a	1216	G	2.4
51	1t	96	GLY	2.4
53	2y	65	GLY	2.4
33	2b	58	ILE	2.4
33	2b	79	ASP	2.4
20	2Y	35	TYR	2.4
20	2Y	106	LEU	2.4
33	2b	11	LEU	2.4
33	2b	69	LEU	2.4
33	2b	148	TYR	2.4
35	2d	120	LEU	2.4
40	2i	19	LEU	2.4
7	2H	97	ARG	2.4
38	1g	115	ARG	2.4
39	1h	84	ARG	2.4
6	2G	109	VAL	2.4
6	2G	149	VAL	2.4
7	2H	35	VAL	2.4
21	2Z	58	VAL	2.4
50	2s	19	VAL	2.4
53	2y	58	ASN	2.4
1	2A	1052	C	2.4
8	1I	59	ALA	2.4
32	1a	1007	C	2.4
32	2a	1037	C	2.4
34	2c	169	ALA	2.4
34	2c	189	ALA	2.4
44	2m	18	ALA	2.4
8	1I	70	GLU	2.4
10	1O	108	GLU	2.4
26	24	11	PRO	2.4
34	2c	49	SER	2.4
38	2g	36	LYS	2.4
40	2i	118	LYS	2.4
17	1V	101	GLY	2.4
26	14	54	GLY	2.4
35	2d	23	GLY	2.4
41	2j	52	GLY	2.4
8	2I	109	ILE	2.4
14	1S	40	ILE	2.4

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Mol	Chain	Res	Type	RSRZ
21	2Z	87	ASP	2.4
26	14	51	ASP	2.4
33	1b	208	ILE	2.4
36	2e	13	ILE	2.4
1	1A	275	G	2.4
1	1A	2148	G	2.4
1	1A	2154	G	2.4
1	2A	614(B)	G	2.4
6	2G	3	LEU	2.4
33	2b	51	LEU	2.4
35	2d	201	GLN	2.4
40	1i	102	LEU	2.4
40	2i	50	LEU	2.4
41	2j	16	LEU	2.4
50	2s	16	LEU	2.4
8	2I	103	ARG	2.4
38	1g	85	TYR	2.4
40	2i	88	TYR	2.4
40	1i	18	PHE	2.4
47	2p	80	PHE	2.4
6	2G	15	VAL	2.4
8	2I	107	VAL	2.4
8	2I	145	VAL	2.4
24	22	1	MET	2.4
46	2o	27	VAL	2.4
41	1j	76	ASN	2.4
41	2j	76	ASN	2.4
33	2b	225	ALA	2.4
9	1N	68	GLU	2.4
40	1i	64	THR	2.4
41	1j	77	PRO	2.4
41	2j	7	LYS	2.4
47	2p	69	THR	2.4
1	1A	1060	U	2.4
52	1u	2	GLY	2.4
6	2G	52	ILE	2.4
26	24	58	ARG	2.4
38	2g	124	LEU	2.4
41	2j	89	ASP	2.4
45	1n	3	ARG	2.4
46	2o	88	ARG	2.4
26	24	39	CYS	2.4

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Mol	Chain	Res	Type	RSRZ
1	1A	2162	G	2.4
1	2A	1051	G	2.4
11	2P	110	TYR	2.4
11	2P	1	MET	2.4
47	1p	80	PHE	2.4
8	1I	107	VAL	2.4
12	2Q	22	LYS	2.4
1	1A	1084	A	2.4
1	1A	1098	A	2.4
1	2A	1095	A	2.4
23	11	54	ALA	2.4
25	23	60	GLU	2.4
32	2a	1447	A	2.4
33	2b	34	ALA	2.4
40	1i	13	ALA	2.4
41	1j	80	LYS	2.4
43	2l	115	LYS	2.4
45	2n	50	LYS	2.4
21	2Z	170	THR	2.3
33	2b	67	THR	2.3
44	2m	105	THR	2.3
45	2n	22	THR	2.3
46	2o	19	PRO	2.3
50	2s	79	THR	2.3
52	2u	17	THR	2.3
32	2a	1038	C	2.3
32	2a	1322	C	2.3
40	2i	69	GLY	2.3
40	2i	72	GLY	2.3
50	1s	68	GLY	2.3
51	1t	101	GLY	2.3
7	2H	60	ARG	2.3
33	2b	158	LEU	2.3
33	2b	162	ILE	2.3
52	1u	9	ARG	2.3
8	2I	75	LEU	2.3
33	2b	16	HIS	2.3
34	2c	175	LEU	2.3
47	1p	82	GLN	2.3
47	2p	82	GLN	2.3
50	2s	30	LEU	2.3
53	2y	84	GLN	2.3

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Mol	Chain	Res	Type	RSRZ
53	2y	89	GLN	2.3
14	2S	36	TYR	2.3
33	2b	33	TYR	2.3
3	2D	276	LYS	2.3
7	2H	85	LYS	2.3
35	1d	169	LYS	2.3
41	1j	44	VAL	2.3
44	1m	117	VAL	2.3
44	2m	45	VAL	2.3
45	2n	17	LYS	2.3
32	1a	1003	G	2.3
34	2c	146	ALA	2.3
34	2c	160	ALA	2.3
40	2i	119	ALA	2.3
7	2H	39	PRO	2.3
20	2Y	82	PRO	2.3
47	1p	69	THR	2.3
34	2c	18	TRP	2.3
20	2Y	73	ARG	2.3
26	24	55	ARG	2.3
35	1d	2	GLY	2.3
40	2i	10	ARG	2.3
44	1m	100	GLY	2.3
44	2m	102	ARG	2.3
51	1t	25	ARG	2.3
1	1A	2122	U	2.3
1	2A	1065	U	2.3
21	2Z	146	ILE	2.3
24	12	70	GLN	2.3
33	2b	200	ILE	2.3
35	2d	160	GLN	2.3
14	2S	24	LEU	2.3
36	2e	80	ILE	2.3
12	2Q	103	MET	2.3
6	2G	141	PHE	2.3
38	2g	43	PHE	2.3
48	1q	100	LYS	2.3
21	2Z	86	VAL	2.3
21	2Z	99	TYR	2.3
34	2c	198	VAL	2.3
38	2g	141	VAL	2.3
50	1s	11	VAL	2.3

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Mol	Chain	Res	Type	RSRZ
6	2G	45	GLU	2.3
16	2U	42	ALA	2.3
33	2b	123	ALA	2.3
35	2d	147	ALA	2.3
40	2i	49	PRO	2.3
49	1r	20	ALA	2.3
49	2r	67	ALA	2.3
1	1A	171	G	2.3
1	1A	2133	G	2.3
1	1A	2807	G	2.3
1	2A	171	G	2.3
7	2H	129	THR	2.3
7	2H	101	ARG	2.3
12	2Q	60	ARG	2.3
32	2a	973	G	2.3
44	2m	37	THR	2.3
35	2d	49	ARG	2.3
38	1g	5	ARG	2.3
8	1I	106	GLY	2.3
16	2U	73	GLY	2.3
41	2j	59	SER	2.3
50	1s	26	GLY	2.3
11	2P	99	LEU	2.3
19	2X	95	LEU	2.3
21	2Z	91	LEU	2.3
34	2c	8	ILE	2.3
34	2c	4	LYS	2.3
53	2y	66	LYS	2.3
33	1b	49	GLU	2.3
33	1b	134	GLU	2.3
34	2c	48	TYR	2.3
35	2d	20	TYR	2.3
40	2i	92	TYR	2.3
41	1j	72	VAL	2.3
53	2y	68	GLU	2.3
6	2G	122	PRO	2.3
15	2T	104	ASN	2.3
21	2Z	15	PRO	2.3
36	2e	94	ALA	2.3
39	2h	27	PRO	2.3
39	2h	67	PRO	2.3
7	2H	3	ARG	2.3

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Mol	Chain	Res	Type	RSRZ
7	2H	42	ARG	2.3
44	1m	11	ARG	2.3
46	1o	88	ARG	2.3
53	2y	17	ARG	2.3
47	1p	45	THR	2.3
44	1m	112	GLY	2.3
1	2A	1171	G	2.3
1	2A	2206	G	2.3
1	2A	2319	G	2.3
33	2b	150	SER	2.3
1	1A	2790	A	2.3
32	2a	1183	A	2.3
33	1b	222	ILE	2.3
33	2b	142	LEU	2.3
35	2d	5	ILE	2.3
26	24	65	ASP	2.3
42	2k	110	ASP	2.3
2	1B	1	U	2.3
1	1A	2108	C	2.3
1	1A	2129	C	2.3
1	1A	2137	C	2.3
2	1B	88	C	2.3
14	2S	29	PHE	2.3
32	2a	1249	C	2.3
34	2c	44	GLU	2.3
34	2c	186	PHE	2.3
37	1f	95	GLU	2.3
34	2c	66	VAL	2.3
40	2i	44	VAL	2.3
38	2g	112	PRO	2.3
7	2H	94	TYR	2.3
44	1m	114	ARG	2.3
33	1b	218	ALA	2.2
44	2m	77	ASN	2.2
47	2p	39	TYR	2.3
52	1u	18	TYR	2.3
53	2y	15	ALA	2.2
8	1I	86	THR	2.2
6	2G	155	MET	2.2
30	28	39	LYS	2.2
34	2c	47	LEU	2.2
40	2i	70	LYS	2.2

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Mol	Chain	Res	Type	RSRZ
41	1j	86	MET	2.2
41	2j	57	LYS	2.2
53	2y	7	SER	2.2
1	2A	1096	A	2.2
8	1I	20	ASP	2.2
32	1a	1035	A	2.2
32	2a	1004	A	2.2
32	2a	1531	A	2.2
38	2g	156	TRP	2.2
1	2A	2101	G	2.2
1	2A	2151	G	2.2
32	1a	1009	G	2.2
32	1a	1032	G	2.2
32	2a	1002	G	2.2
1	2A	2808	U	2.2
32	1a	173	U	2.2
32	1a	1040	U	2.2
32	1a	1532	U	2.2
6	1G	48	GLU	2.2
35	2d	110	PHE	2.2
6	1G	136	ARG	2.2
20	2Y	72	VAL	2.2
27	15	60	VAL	2.2
33	2b	71	VAL	2.2
35	2d	170	VAL	2.2
40	2i	28	VAL	2.2
12	2Q	136	ALA	2.2
33	2b	94	ASN	2.2
40	2i	15	ALA	2.2
51	1t	95	ALA	2.2
53	2y	36	ASN	2.2
34	1c	193	TYR	2.2
40	1i	36	TYR	2.2
53	2y	71	TYR	2.2
41	2j	68	HIS	2.2
51	1t	73	HIS	2.2
33	2b	72	GLY	2.2
38	2g	81	GLY	2.2
39	1h	98	LYS	2.2
50	2s	26	GLY	2.2
6	2G	34	LEU	2.2
6	2G	133	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
36	2e	151	LEU	2.2
40	2i	40	LEU	2.2
44	2m	34	LEU	2.2
49	1r	85	LEU	2.2
49	2r	85	LEU	2.2
53	2y	34	LEU	2.2
26	24	15	ILE	2.2
33	1b	210	SER	2.2
38	2g	27	ILE	2.2
41	2j	19	SER	2.2
41	2j	23	ILE	2.2
41	2j	96	ILE	2.2
44	2m	9	ILE	2.2
47	1p	48	TRP	2.2
1	1A	1046	A	2.2
8	1I	10	GLU	2.2
32	1a	1447	A	2.2
35	2d	156	GLU	2.2
44	1m	50	GLU	2.2
1	1A	271(K)	U	2.2
1	1A	1026	U	2.2
1	1A	1105	U	2.2
1	1A	1173	G	2.2
1	1A	2157	G	2.2
33	1b	36	ARG	2.2
40	2i	16	ARG	2.2
41	2j	45	ARG	2.2
44	2m	91	ARG	2.2
6	2G	5	VAL	2.2
14	1S	46	VAL	2.2
21	2Z	27	VAL	2.2
24	22	25	VAL	2.2
38	2g	93	PRO	2.2
44	2m	41	PRO	2.2
44	2m	53	VAL	2.2
1	2A	2789	C	2.2
1	2A	2794	C	2.2
7	2H	165	ALA	2.2
8	1I	83	ALA	2.2
44	1m	28	ALA	2.2
33	1b	132	LYS	2.2
34	2c	201	TYR	2.2

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Mol	Chain	Res	Type	RSRZ
50	2s	57	HIS	2.2
41	1j	100	THR	2.2
6	1G	42	GLY	2.2
7	2H	120	GLY	2.2
8	2I	12	LEU	2.2
11	2P	109	GLY	2.2
14	2S	56	LEU	2.2
34	2c	74	GLY	2.2
35	1d	194	LEU	2.2
36	2e	74	GLY	2.2
36	2e	119	LEU	2.2
39	1h	112	LEU	2.2
41	2j	31	GLY	2.2
48	1q	80	GLY	2.2
51	1t	102	GLY	2.2
6	2G	140	ILE	2.2
6	2G	144	ILE	2.2
33	1b	42	ILE	2.2
33	1b	223	ILE	2.2
35	2d	158	ILE	2.2
52	1u	13	ILE	2.2
46	2o	21	ASP	2.2
45	2n	8	GLU	2.2
34	2c	127	ARG	2.2
47	1p	8	ARG	2.2
32	1a	1020	U	2.2
32	1a	1041	A	2.2
4	2E	56	PRO	2.2
35	2d	79	PHE	2.2
41	1j	54	PHE	2.2
17	2V	61	VAL	2.2
21	2Z	180	VAL	2.2
33	1b	7	VAL	2.2
33	2b	7	VAL	2.2
47	1p	53	VAL	2.2
50	2s	45	VAL	2.2
1	1A	2110	G	2.2
1	2A	1047	G	2.2
1	2A	2190	G	2.2
2	2B	119	G	2.2
32	1a	1010	G	2.2
32	2a	1017	G	2.2

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Mol	Chain	Res	Type	RSRZ
33	1b	29	ALA	2.2
38	2g	117	ALA	2.2
39	1h	110	ALA	2.2
42	2k	116	HIS	2.2
44	2m	72	ALA	2.2
45	2n	15	LYS	2.2
50	1s	23	ASN	2.2
29	17	1	MET	2.2
33	2b	78	GLN	2.2
53	2y	67	HIS	2.2
1	2A	1092	C	2.2
33	1b	190	THR	2.2
40	2i	7	THR	2.2
6	2G	106	LEU	2.2
26	14	45	GLY	2.2
33	1b	38	GLY	2.2
33	2b	196	LEU	2.2
34	2c	80	GLY	2.2
38	1g	16	LEU	2.2
41	1j	31	GLY	2.2
50	2s	52	TYR	2.2
6	1G	52	ILE	2.2
6	2G	101	ILE	2.2
21	2Z	57	ILE	2.2
53	2y	74	ILE	2.2
34	2c	190	ARG	2.2
39	1h	102	ARG	2.2
53	2y	83	ARG	2.2
20	2Y	53	PRO	2.2
26	24	29	PRO	2.2
33	1b	125	PRO	2.2
1	2A	1847	A	2.1
26	24	69	LYS	2.2
38	1g	43	PHE	2.2
32	2a	1005	A	2.1
38	2g	136	LYS	2.2
45	2n	58	LYS	2.2
34	2c	207	VAL	2.1
38	2g	69	VAL	2.1
50	2s	60	VAL	2.1
7	2H	102	ALA	2.1
21	2Z	113	ALA	2.1

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Mol	Chain	Res	Type	RSRZ
21	2Z	132	ASN	2.1
21	2Z	188	ALA	2.1
35	2d	45	GLN	2.1
36	2e	130	ASN	2.1
38	2g	28	ASN	2.1
38	2g	37	ASN	2.1
38	2g	56	GLN	2.1
40	2i	55	ALA	2.1
42	2k	117	ASN	2.1
1	1A	2206	G	2.1
1	1A	2802	G	2.1
1	2A	1068	G	2.1
1	2A	2181	G	2.1
8	2I	58	LEU	2.1
19	1X	95	LEU	2.1
26	14	52	THR	2.1
32	2a	1373	G	2.1
34	1c	87	LEU	2.1
35	2d	78	LEU	2.1
35	2d	109	GLY	2.1
37	1f	98	LEU	2.1
40	2i	8	GLY	2.1
41	1j	16	LEU	2.1
41	2j	36	GLY	2.1
43	1l	63	GLY	2.1
45	2n	44	LEU	2.1
50	1s	16	LEU	2.1
6	2G	20	ILE	2.1
14	2S	40	ILE	2.1
35	1d	5	ILE	2.1
38	1g	154	TYR	2.1
39	1h	109	ILE	2.1
46	1o	3	ILE	2.1
1	1A	2111	C	2.1
26	24	34	GLU	2.1
30	28	46	ARG	2.1
38	1g	8	GLU	2.1
41	2j	79	ARG	2.1
47	2p	47	ASP	2.1
49	1r	59	SER	2.1
6	2G	179	PRO	2.1
35	2d	39	PRO	2.1

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Mol	Chain	Res	Type	RSRZ
36	2e	52	PRO	2.1
41	2j	53	PRO	2.1
45	1n	4	LYS	2.1
51	1t	98	PRO	2.1
21	2Z	48	PHE	2.1
33	2b	70	PHE	2.1
8	2I	18	VAL	2.1
24	22	63	VAL	2.1
34	2c	173	VAL	2.1
39	1h	103	VAL	2.1
45	2n	61	TRP	2.1
47	2p	59	TRP	2.1
1	2A	1105	U	2.1
32	2a	1025	U	2.1
32	2a	1219	U	2.1
1	2A	2310	A	2.1
2	2B	120	A	2.1
13	2R	101	ALA	2.1
20	2Y	105	ALA	2.1
32	1a	1493	A	2.1
32	2a	1092	A	2.1
37	1f	16	GLN	2.1
40	2i	87	GLN	2.1
33	2b	77	ALA	2.1
44	1m	51	ALA	2.1
50	2s	24	ALA	2.1
7	2H	66	GLY	2.1
7	2H	91	GLY	2.1
14	2S	47	THR	2.1
19	2X	45	THR	2.1
33	2b	221	LEU	2.1
34	1c	12	LEU	2.1
35	1d	108	LEU	2.1
35	1d	124	GLY	2.1
36	2e	85	GLY	2.1
38	2g	101	LEU	2.1
40	2i	85	LEU	2.1
45	2n	53	LEU	2.1
12	2Q	66	ILE	2.1
33	2b	68	ILE	2.1
33	2b	127	ILE	2.1
44	2m	39	ILE	2.1

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Mol	Chain	Res	Type	RSRZ
52	2u	13	ILE	2.1
14	1S	107	GLU	2.1
16	2U	59	ARG	2.1
19	2X	93	GLU	2.1
26	14	68	ARG	2.1
33	1b	33	TYR	2.1
34	2c	79	ARG	2.1
41	2j	83	GLU	2.1
47	1p	81	ARG	2.1
50	1s	29	ARG	2.1
1	1A	1056	G	2.1
1	1A	2127	G	2.1
32	1a	144	G	2.1
32	2a	1026	G	2.1
32	2a	1220	G	2.1
16	2U	56	ASP	2.1
32	1a	217	C	2.1
32	1a	1006	C	2.1
32	1a	1533	C	2.1
32	2a	1118	C	2.1
32	2a	1158	C	2.1
32	2a	1359	C	2.1
34	2c	147	LYS	2.1
44	2m	31	LYS	2.1
21	2Z	28	MET	2.1
22	10	3	HIS	2.1
33	2b	55	PHE	2.1
33	2b	122	PHE	2.1
33	2b	181	PHE	2.1
34	2c	10	PHE	2.1
40	1i	33	PHE	2.1
42	2k	125	PHE	2.1
50	1s	10	PHE	2.1
38	2g	11	GLN	2.1
43	1l	83	VAL	2.1
47	2p	2	VAL	2.1
53	2y	31	GLN	2.1
6	2G	158	ALA	2.1
32	2a	1446	U	2.1
36	2e	95	ALA	2.1
38	1g	46	ALA	2.1
1	1A	2892	A	2.1

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Mol	Chain	Res	Type	RSRZ
6	2G	107	LEU	2.1
14	2S	48	LEU	2.1
32	2a	968	A	2.1
32	2a	1179	A	2.1
14	2S	90	GLY	2.1
34	2c	196	LEU	2.1
43	2l	10	LEU	2.1
26	24	27	THR	2.1
44	2m	43	THR	2.1
50	2s	77	THR	2.1
14	1S	3	ARG	2.1
22	20	82	ARG	2.1
51	1t	57	ARG	2.1
6	2G	39	ILE	2.1
8	2I	138	ILE	2.1
34	2c	39	ILE	2.1
6	1G	76	SER	2.1
6	2G	156	ASP	2.1
43	2l	17	LYS	2.1
50	2s	70	LYS	2.1
51	2t	7	LYS	2.1
39	2h	135	CYS	2.1
41	1j	30	SER	2.1
48	1q	79	SER	2.1
50	1s	4	SER	2.1
50	1s	12	ASP	2.1
1	2A	1056	G	2.1
21	2Z	95	PRO	2.1
27	25	28	PRO	2.1
35	2d	40	PRO	2.1
47	1p	1	MET	2.1
8	2I	136	VAL	2.1
14	2S	12	PHE	2.1
26	14	46	GLN	2.1
5	2F	6	VAL	2.1
33	1b	71	VAL	2.1
34	1c	76	VAL	2.1
34	2c	203	PHE	2.1
36	1e	6	PHE	2.1
44	1m	53	VAL	2.1
44	1m	60	VAL	2.1
45	2n	37	PHE	2.1

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Mol	Chain	Res	Type	RSRZ
50	2s	11	VAL	2.1
21	2Z	173	ALA	2.1
40	1i	76	ALA	2.1
40	2i	61	ALA	2.1
53	2y	21	ALA	2.1
6	1G	113	ARG	2.1
8	1I	58	LEU	2.1
11	2P	3	LEU	2.1
21	2Z	157	LEU	2.1
32	2a	1020	U	2.1
34	2c	94	LEU	2.1
38	2g	22	LEU	2.1
38	2g	99	LEU	2.1
17	2V	63	GLY	2.1
34	1c	9	GLY	2.1
38	2g	133	GLY	2.1
52	2u	10	ARG	2.1
6	2G	137	GLU	2.1
8	1I	117	GLU	2.1
21	2Z	193	GLU	2.1
34	2c	206	GLU	2.1
37	2f	95	GLU	2.1
50	2s	64	GLU	2.1
53	1y	44	GLU	2.1
32	2a	1001	A	2.1
33	1b	22	LYS	2.1
33	2b	75	LYS	2.1
36	2e	121	LYS	2.1
52	2u	20	LYS	2.1
6	2G	11	TYR	2.1
33	2b	92	TYR	2.1
34	2c	193	TYR	2.1
35	2d	4	TYR	2.1
33	1b	232	PRO	2.1
40	2i	98	PRO	2.1
41	2j	41	PRO	2.1
1	1A	1116	C	2.1
1	1A	2136	C	2.1
1	2A	2103	C	2.1
1	2A	2318	G	2.0
24	22	9	GLN	2.0
32	1a	79	G	2.0

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Mol	Chain	Res	Type	RSRZ
32	2a	1140	C	2.1
32	2a	1218	C	2.1
32	2a	1224	G	2.0
32	2a	1260	C	2.1
32	2a	1365	G	2.0
34	2c	170	GLN	2.0
6	2G	117	PHE	2.0
7	2H	79	VAL	2.0
33	2b	229	VAL	2.0
34	2c	68	VAL	2.0
35	1d	148	VAL	2.0
35	2d	178	VAL	2.0
40	2i	86	VAL	2.0
42	2k	105	VAL	2.0
44	2m	15	VAL	2.0
49	2r	22	VAL	2.0
6	2G	46	ALA	2.0
7	2H	95	ARG	2.0
26	24	12	ALA	2.0
34	2c	168	ALA	2.0
38	1g	39	ALA	2.0
43	2l	89	ARG	2.0
44	2m	99	ARG	2.0
45	2n	20	ALA	2.0
47	1p	64	ALA	2.0
47	1p	72	ARG	2.0
47	2p	26	ARG	2.0
47	2p	75	ARG	2.0
6	2G	82	LEU	2.0
7	2H	67	LEU	2.0
33	1b	154	LEU	2.0
36	2e	123	LEU	2.0
37	1f	79	LEU	2.0
41	2j	65	LEU	2.0
44	2m	70	LEU	2.0
19	2X	37	THR	2.0
28	26	42	TRP	2.0
19	2X	88	LYS	2.0
32	1a	841	U	2.0
32	2a	1000	U	2.0
32	2a	1148	U	2.0
32	2a	1532	U	2.0

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Mol	Chain	Res	Type	RSRZ
44	1m	49	THR	2.0
53	2y	30	TRP	2.0
33	2b	222	ILE	2.0
40	2i	77	ILE	2.0
40	2i	97	LYS	2.0
44	2m	84	ILE	2.0
45	1n	15	LYS	2.0
1	1A	1045	A	2.0
1	1A	2135	A	2.0
1	1A	2629	A	2.0
7	2H	128	PRO	2.0
26	14	67	TYR	2.0
43	2l	112	ASP	2.0
6	2G	148	MET	2.0
21	2Z	166	SER	2.0
48	2q	93	GLN	2.0
1	2A	2183	C	2.0
9	2N	9	VAL	2.0
25	23	59	VAL	2.0
33	1b	70	PHE	2.0
33	2b	152	PHE	2.0
34	2c	30	ARG	2.0
34	2c	120	VAL	2.0
35	1d	191	ARG	2.0
39	2h	79	VAL	2.0
40	1i	101	PHE	2.0
41	2j	94	VAL	2.0
44	1m	102	ARG	2.0
45	2n	35	ARG	2.0
50	2s	51	VAL	2.0
1	2A	11	G	2.0
1	2A	1533	G	2.0
1	2A	2308	G	2.0
32	1a	78	G	2.0
32	1a	1034	G	2.0
32	2a	1138	G	2.0
21	2Z	5	LEU	2.0
34	2c	52	LEU	2.0
40	1i	45	ALA	2.0
44	2m	75	ALA	2.0
6	2G	123	ASN	2.0
20	2Y	88	LYS	2.0

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Mol	Chain	Res	Type	RSRZ
43	2l	16	GLU	2.0
34	2c	25	GLY	2.0
44	1m	24	GLY	2.0
53	2y	91	LYS	2.0
7	2H	68	THR	2.0
8	1I	108	THR	2.0
9	2N	63	THR	2.0
42	2k	40	ILE	2.0
47	1p	36	ILE	2.0
48	1q	90	ILE	2.0
1	2A	12	U	2.0
38	2g	103	TRP	2.0
1	2A	1098	A	2.0
11	2P	122	PRO	2.0
32	1a	162	A	2.0
32	1a	1030(D)	A	2.0
32	2a	1357	A	2.0
32	2a	1492	A	2.0
33	2b	48	MET	2.0
26	24	25	TYR	2.0
34	2c	184	TYR	2.0
38	1g	44	TYR	2.0
43	1l	64	TYR	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
1	5MU	2A	1915	21/22	0.82	0.12	71,79,86,100	0
32	2MG	2a	1207	24/25	0.82	0.15	70,77,81,86	0
1	5MU	1A	1915	21/22	0.86	0.13	63,71,76,84	0
32	M2G	2a	966	25/26	0.88	0.16	64,70,83,97	0
1	PSU	2A	1911	20/21	0.89	0.11	66,71,78,83	0
1	PSU	2A	1917	20/21	0.89	0.10	65,74,85,87	0
32	5MC	2a	1400	21/22	0.90	0.18	62,74,78,82	0
43	0TD	1l	92	10/11	0.91	0.12	50,56,60,61	0
43	0TD	2l	92	10/11	0.91	0.13	58,63,69,74	0
32	5MC	1a	967	21/22	0.92	0.13	57,63,72,79	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
1	PSU	1A	1917	20/21	0.92	0.10	55,59,65,69	0
32	5MC	2a	967	21/22	0.92	0.14	65,69,75,77	0
32	PSU	2a	516	20/21	0.93	0.10	65,70,72,79	0
1	OMC	2A	1920	21/22	0.93	0.11	58,64,68,72	0
32	2MG	1a	1207	24/25	0.94	0.10	61,67,72,73	0
32	PSU	1a	516	20/21	0.94	0.09	56,61,65,68	0
32	M2G	1a	966	25/26	0.94	0.11	48,57,63,70	0
32	5MC	2a	1404	21/22	0.94	0.10	51,61,65,69	0
1	PSU	1A	1911	20/21	0.94	0.09	54,60,63,67	0
32	MA6	1a	1519	24/25	0.95	0.10	39,45,50,52	0
32	5MC	1a	1400	21/22	0.95	0.10	49,53,58,60	0
32	4OC	1a	1402	22/23	0.95	0.10	44,50,59,63	0
32	4OC	2a	1402	22/23	0.95	0.10	52,60,68,70	0
32	G7M	2a	527	24/25	0.95	0.09	55,60,64,67	0
32	5MC	2a	1407	21/22	0.95	0.10	52,62,64,65	0
32	UR3	2a	1498	21/22	0.95	0.10	55,61,67,72	0
32	MA6	2a	1518	24/25	0.95	0.11	54,62,66,67	0
32	5MC	1a	1407	21/22	0.95	0.11	42,51,57,59	0
32	5MC	1a	1404	21/22	0.96	0.09	45,48,52,54	0
32	G7M	1a	527	24/25	0.96	0.10	41,53,58,60	0
32	UR3	1a	1498	21/22	0.96	0.09	46,51,54,62	0
32	MA6	1a	1518	24/25	0.96	0.10	38,47,50,52	0
1	5MC	1A	1942	21/22	0.96	0.08	31,40,45,49	0
32	MA6	2a	1519	24/25	0.96	0.12	52,59,63,67	0
1	5MC	2A	1942	21/22	0.96	0.09	47,50,52,62	0
55	8AN	2x	76	22/23	0.96	0.09	39,45,50,54	0
1	OMG	1A	2251	24/25	0.97	0.08	20,26,31,38	0
1	5MC	2A	1962	21/22	0.97	0.08	39,45,49,56	0
1	OMG	2A	2251	24/25	0.97	0.08	33,40,44,48	0
1	2MA	2A	2503	23/24	0.97	0.07	28,33,38,40	0
1	OMC	1A	1920	21/22	0.97	0.09	42,53,58,60	0
1	5MU	2A	1939	21/22	0.97	0.07	32,38,42,45	0
1	2MA	1A	2503	23/24	0.98	0.06	19,23,25,27	0
1	OMU	1A	2552	21/22	0.98	0.07	22,28,34,35	0
1	PSU	1A	2605	20/21	0.98	0.07	22,27,31,33	0
1	5MC	1A	1962	21/22	0.98	0.07	26,34,38,40	0
1	5MU	1A	1939	21/22	0.98	0.07	23,29,33,36	0
1	OMU	2A	2552	21/22	0.98	0.07	33,38,42,43	0
55	8AN	1x	76	22/23	0.98	0.06	21,30,34,34	0
1	PSU	2A	2605	20/21	0.98	0.07	31,36,43,43	0

6.3 Carbohydrates (i)

There are no oligosaccharides in this entry.

6.4 Ligands (i)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3686	1/1	0.48	0.18	76,76,76,76	0
57	MG	1A	3747	1/1	0.55	0.18	66,66,66,66	0
57	MG	1B	230	1/1	0.63	0.18	74,74,74,74	0
57	MG	2G	203	1/1	0.63	0.28	76,76,76,76	0
57	MG	21	101	1/1	0.63	0.21	69,69,69,69	0
57	MG	2O	202	1/1	0.64	0.23	80,80,80,80	0
57	MG	2A	3340	1/1	0.64	0.19	68,68,68,68	0
57	MG	1A	3414	1/1	0.66	0.20	72,72,72,72	0
57	MG	2A	3545	1/1	0.66	0.23	73,73,73,73	0
57	MG	2A	3419	1/1	0.70	0.20	54,54,54,54	0
57	MG	1A	3808	1/1	0.70	0.14	79,79,79,79	0
57	MG	2a	3134	1/1	0.70	0.26	82,82,82,82	0
57	MG	2A	3546	1/1	0.71	0.20	79,79,79,79	0
57	MG	1A	3588	1/1	0.72	0.17	51,51,51,51	0
57	MG	1A	3644	1/1	0.72	0.25	73,73,73,73	0
57	MG	1A	3867	1/1	0.72	0.19	67,67,67,67	0
57	MG	2A	3457	1/1	0.72	0.12	78,78,78,78	0
57	MG	2Q	202	1/1	0.72	0.32	56,56,56,56	0
57	MG	2A	3506	1/1	0.72	0.20	69,69,69,69	0
57	MG	1B	229	1/1	0.72	0.16	66,66,66,66	0
57	MG	1a	1774	1/1	0.73	0.27	69,69,69,69	0
57	MG	2A	3456	1/1	0.73	0.24	68,68,68,68	0
57	MG	1A	3651	1/1	0.73	0.16	65,65,65,65	0
57	MG	1A	3438	1/1	0.74	0.25	67,67,67,67	0
57	MG	1A	3519	1/1	0.75	0.14	52,52,52,52	0
57	MG	2A	3588	1/1	0.75	0.17	46,46,46,46	0
57	MG	1A	3638	1/1	0.75	0.29	37,37,37,37	0
57	MG	2A	3254	1/1	0.75	0.29	76,76,76,76	0
57	MG	1A	3978	1/1	0.76	0.16	35,35,35,35	0
57	MG	1t	3102	1/1	0.76	0.21	64,64,64,64	0
57	MG	2A	3234	1/1	0.76	0.16	65,65,65,65	0
57	MG	2A	3246	1/1	0.76	0.21	70,70,70,70	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3592	1/1	0.76	0.17	58,58,58,58	0
57	MG	1A	3988	1/1	0.76	0.19	55,55,55,55	0
57	MG	1A	4011	1/1	0.76	0.15	33,33,33,33	0
57	MG	2A	3418	1/1	0.76	0.18	58,58,58,58	0
57	MG	1B	218	1/1	0.76	0.18	64,64,64,64	0
57	MG	1A	3602	1/1	0.76	0.13	44,44,44,44	0
57	MG	1A	3924	1/1	0.76	0.15	48,48,48,48	0
57	MG	1A	3420	1/1	0.77	0.21	72,72,72,72	0
57	MG	1A	3571	1/1	0.77	0.14	65,65,65,65	0
57	MG	1A	3855	1/1	0.77	0.13	56,56,56,56	0
57	MG	1A	3861	1/1	0.77	0.17	49,49,49,49	0
57	MG	1A	3578	1/1	0.77	0.14	45,45,45,45	0
57	MG	1A	3323	1/1	0.77	0.45	79,79,79,79	0
57	MG	2a	3022	1/1	0.77	0.36	73,73,73,73	0
57	MG	2a	3050	1/1	0.77	0.41	86,86,86,86	0
57	MG	1a	1745	1/1	0.77	0.18	70,70,70,70	0
59	ARG	1A	4018	12/12	0.77	0.20	41,65,74,75	0
57	MG	2B	211	1/1	0.78	0.21	67,67,67,67	0
57	MG	1a	1700	1/1	0.78	0.22	74,74,74,74	0
57	MG	1A	3624	1/1	0.78	0.15	38,38,38,38	0
57	MG	2A	3330	1/1	0.78	0.14	57,57,57,57	0
57	MG	1A	3709	1/1	0.78	0.17	54,54,54,54	0
57	MG	1d	304	1/1	0.78	0.19	71,71,71,71	0
57	MG	1A	3712	1/1	0.78	0.15	69,69,69,69	0
57	MG	2a	3065	1/1	0.78	0.39	74,74,74,74	0
57	MG	1T	202	1/1	0.78	0.21	67,67,67,67	0
57	MG	2A	3713	1/1	0.78	0.14	61,61,61,61	0
57	MG	2A	3436	1/1	0.79	0.14	70,70,70,70	0
57	MG	2B	207	1/1	0.79	0.22	70,70,70,70	0
57	MG	2A	3200	1/1	0.79	0.29	73,73,73,73	0
57	MG	2G	201	1/1	0.79	0.14	74,74,74,74	0
57	MG	1A	3264	1/1	0.79	0.23	69,69,69,69	0
57	MG	2A	3463	1/1	0.79	0.20	63,63,63,63	0
57	MG	2A	3472	1/1	0.79	0.17	57,57,57,57	0
57	MG	1A	3937	1/1	0.79	0.13	65,65,65,65	0
57	MG	1a	1769	1/1	0.79	0.16	69,69,69,69	0
57	MG	1A	3944	1/1	0.79	0.14	80,80,80,80	0
57	MG	1a	1797	1/1	0.79	0.25	77,77,77,77	0
57	MG	1A	3462	1/1	0.79	0.22	63,63,63,63	0
57	MG	1A	3147	1/1	0.79	0.13	80,80,80,80	0
57	MG	2A	3387	1/1	0.80	0.17	51,51,51,51	0
57	MG	1a	1846	1/1	0.80	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
57	MG	1a	1601	1/1	0.80	0.16	68,68,68,68	0
57	MG	1A	3095	1/1	0.80	0.17	63,63,63,63	0
57	MG	2A	3128	1/1	0.80	0.21	67,67,67,67	0
57	MG	2A	3134	1/1	0.80	0.32	70,70,70,70	0
57	MG	1a	1724	1/1	0.80	0.19	69,69,69,69	0
57	MG	1A	3346	1/1	0.80	0.19	50,50,50,50	0
57	MG	1A	3432	1/1	0.80	0.13	29,29,29,29	0
57	MG	1a	1772	1/1	0.80	0.16	69,69,69,69	0
57	MG	2a	3027	1/1	0.80	0.28	67,67,67,67	0
57	MG	1A	3916	1/1	0.80	0.11	57,57,57,57	0
57	MG	1A	3918	1/1	0.80	0.12	23,23,23,23	0
57	MG	2a	3086	1/1	0.80	0.20	64,64,64,64	0
57	MG	2A	3383	1/1	0.80	0.18	66,66,66,66	0
57	MG	2A	3636	1/1	0.80	0.15	70,70,70,70	0
57	MG	1a	1671	1/1	0.81	0.18	62,62,62,62	0
57	MG	2A	3709	1/1	0.81	0.18	57,57,57,57	0
57	MG	2A	3445	1/1	0.81	0.14	51,51,51,51	0
57	MG	1a	1686	1/1	0.81	0.20	67,67,67,67	0
57	MG	1a	1789	1/1	0.81	0.19	70,70,70,70	0
57	MG	1A	3790	1/1	0.81	0.14	53,53,53,53	0
57	MG	1a	1813	1/1	0.81	0.23	73,73,73,73	0
57	MG	1a	1841	1/1	0.81	0.12	61,61,61,61	0
57	MG	2A	3525	1/1	0.81	0.13	62,62,62,62	0
57	MG	1a	1709	1/1	0.81	0.31	65,65,65,65	0
57	MG	1A	3536	1/1	0.81	0.17	56,56,56,56	0
57	MG	2a	3026	1/1	0.81	0.29	75,75,75,75	0
57	MG	2A	3581	1/1	0.81	0.15	70,70,70,70	0
57	MG	2a	3048	1/1	0.81	0.36	69,69,69,69	0
57	MG	1A	3522	1/1	0.81	0.15	53,53,53,53	0
57	MG	2A	3053	1/1	0.81	0.20	60,60,60,60	0
57	MG	2A	3594	1/1	0.81	0.15	73,73,73,73	0
57	MG	2a	3129	1/1	0.81	0.15	67,67,67,67	0
57	MG	2a	3132	1/1	0.81	0.17	59,59,59,59	0
57	MG	1a	1622	1/1	0.81	0.18	61,61,61,61	0
57	MG	2A	3658	1/1	0.81	0.18	75,75,75,75	0
57	MG	1a	1697	1/1	0.82	0.26	62,62,62,62	0
57	MG	1a	1823	1/1	0.82	0.17	61,61,61,61	0
57	MG	1a	1828	1/1	0.82	0.28	75,75,75,75	0
57	MG	2A	3732	1/1	0.82	0.16	68,68,68,68	0
57	MG	2A	3740	1/1	0.82	0.17	71,71,71,71	0
57	MG	2A	3430	1/1	0.82	0.18	67,67,67,67	0
57	MG	1a	1699	1/1	0.82	0.42	78,78,78,78	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2B	213	1/1	0.82	0.26	70,70,70,70	0
57	MG	1A	3464	1/1	0.82	0.15	37,37,37,37	0
57	MG	1E	304	1/1	0.82	0.12	29,29,29,29	0
57	MG	1n	102	1/1	0.82	0.11	55,55,55,55	0
57	MG	1A	3502	1/1	0.82	0.15	62,62,62,62	0
57	MG	1W	203	1/1	0.82	0.12	67,67,67,67	0
57	MG	2A	3081	1/1	0.82	0.19	61,61,61,61	0
57	MG	2a	3025	1/1	0.82	0.22	69,69,69,69	0
57	MG	1a	1754	1/1	0.82	0.15	60,60,60,60	0
57	MG	1A	3269	1/1	0.82	0.18	56,56,56,56	0
57	MG	1A	3332	1/1	0.82	0.12	26,26,26,26	0
57	MG	2A	3577	1/1	0.82	0.17	73,73,73,73	0
57	MG	2a	3060	1/1	0.82	0.30	81,81,81,81	0
57	MG	1a	1638	1/1	0.82	0.34	70,70,70,70	0
57	MG	1a	1775	1/1	0.82	0.13	67,67,67,67	0
57	MG	1a	1787	1/1	0.82	0.17	61,61,61,61	0
57	MG	1A	3836	1/1	0.82	0.09	44,44,44,44	0
57	MG	1a	1792	1/1	0.82	0.22	65,65,65,65	0
57	MG	1A	3535	1/1	0.82	0.16	58,58,58,58	0
57	MG	1A	3559	1/1	0.83	0.15	59,59,59,59	0
57	MG	1A	3852	1/1	0.83	0.11	58,58,58,58	0
57	MG	1A	3952	1/1	0.83	0.18	58,58,58,58	0
57	MG	2A	3173	1/1	0.83	0.29	74,74,74,74	0
57	MG	1A	3708	1/1	0.83	0.36	63,63,63,63	0
57	MG	2A	3541	1/1	0.83	0.18	58,58,58,58	0
57	MG	1A	3619	1/1	0.83	0.20	58,58,58,58	0
57	MG	2P	202	1/1	0.83	0.17	73,73,73,73	0
57	MG	1a	1650	1/1	0.83	0.22	72,72,72,72	0
57	MG	2A	3547	1/1	0.83	0.20	60,60,60,60	0
57	MG	2a	3010	1/1	0.83	0.43	73,73,73,73	0
57	MG	2A	3548	1/1	0.83	0.13	61,61,61,61	0
57	MG	1A	3185	1/1	0.83	0.18	62,62,62,62	0
57	MG	1A	4014	1/1	0.83	0.15	61,61,61,61	0
57	MG	1a	1688	1/1	0.83	0.25	59,59,59,59	0
57	MG	1B	211	1/1	0.83	0.17	68,68,68,68	0
57	MG	1A	3881	1/1	0.83	0.11	66,66,66,66	0
57	MG	1B	225	1/1	0.83	0.20	55,55,55,55	0
57	MG	2a	3063	1/1	0.83	0.27	71,71,71,71	0
57	MG	2A	3643	1/1	0.83	0.16	68,68,68,68	0
57	MG	1A	3625	1/1	0.83	0.16	54,54,54,54	0
57	MG	2a	3112	1/1	0.83	0.24	74,74,74,74	0
57	MG	1A	3513	1/1	0.83	0.10	20,20,20,20	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1a	1730	1/1	0.83	0.18	63,63,63,63	0
57	MG	1A	3085	1/1	0.83	0.16	66,66,66,66	0
57	MG	1N	204	1/1	0.83	0.09	52,52,52,52	0
57	MG	2A	3715	1/1	0.84	0.15	59,59,59,59	0
57	MG	2A	3722	1/1	0.84	0.14	66,66,66,66	0
57	MG	2A	3728	1/1	0.84	0.18	55,55,55,55	0
57	MG	1A	3897	1/1	0.84	0.14	55,55,55,55	0
57	MG	2A	3449	1/1	0.84	0.17	58,58,58,58	0
57	MG	1a	1776	1/1	0.84	0.15	59,59,59,59	0
57	MG	1A	3528	1/1	0.84	0.21	63,63,63,63	0
57	MG	19	102	1/1	0.84	0.15	65,65,65,65	0
57	MG	2B	215	1/1	0.84	0.16	66,66,66,66	0
57	MG	1A	3664	1/1	0.84	0.09	21,21,21,21	0
57	MG	2A	3476	1/1	0.84	0.20	62,62,62,62	0
57	MG	1A	3256	1/1	0.84	0.17	67,67,67,67	0
57	MG	2A	3520	1/1	0.84	0.16	60,60,60,60	0
57	MG	1a	1628	1/1	0.84	0.25	64,64,64,64	0
57	MG	1A	3437	1/1	0.84	0.10	59,59,59,59	0
57	MG	2a	3002	1/1	0.84	0.17	73,73,73,73	0
57	MG	1A	3431	1/1	0.84	0.16	61,61,61,61	0
57	MG	2A	3264	1/1	0.84	0.15	62,62,62,62	0
57	MG	2A	3271	1/1	0.84	0.40	54,54,54,54	0
57	MG	2A	3318	1/1	0.84	0.16	66,66,66,66	0
57	MG	2A	3560	1/1	0.84	0.12	37,37,37,37	0
57	MG	1a	1832	1/1	0.84	0.20	56,56,56,56	0
57	MG	1a	1839	1/1	0.84	0.14	72,72,72,72	0
57	MG	2a	3051	1/1	0.84	0.34	72,72,72,72	0
57	MG	2A	3373	1/1	0.84	0.20	69,69,69,69	0
57	MG	2a	3061	1/1	0.84	0.20	61,61,61,61	0
57	MG	1a	1756	1/1	0.84	0.15	48,48,48,48	0
57	MG	1a	1757	1/1	0.84	0.12	53,53,53,53	0
57	MG	2a	3073	1/1	0.84	0.30	71,71,71,71	0
57	MG	2a	3077	1/1	0.84	0.16	74,74,74,74	0
57	MG	2A	3403	1/1	0.84	0.12	62,62,62,62	0
57	MG	1a	1866	1/1	0.84	0.18	70,70,70,70	0
57	MG	1A	3737	1/1	0.84	0.12	46,46,46,46	0
57	MG	2A	3423	1/1	0.84	0.12	61,61,61,61	0
57	MG	1A	3746	1/1	0.84	0.17	65,65,65,65	0
57	MG	2j	201	1/1	0.84	0.34	66,66,66,66	0
57	MG	1A	3617	1/1	0.84	0.24	55,55,55,55	0
57	MG	2A	3132	1/1	0.85	0.19	65,65,65,65	0
57	MG	1a	1806	1/1	0.85	0.14	70,70,70,70	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3147	1/1	0.85	0.20	59,59,59,59	0
57	MG	2A	3451	1/1	0.85	0.29	46,46,46,46	0
57	MG	2A	3151	1/1	0.85	0.17	67,67,67,67	0
57	MG	1A	3893	1/1	0.85	0.13	56,56,56,56	0
57	MG	2A	3462	1/1	0.85	0.12	70,70,70,70	0
57	MG	1a	1751	1/1	0.85	0.26	82,82,82,82	0
57	MG	2A	3227	1/1	0.85	0.18	65,65,65,65	0
57	MG	1A	3393	1/1	0.85	0.11	32,32,32,32	0
57	MG	2A	3477	1/1	0.85	0.13	65,65,65,65	0
57	MG	1a	1829	1/1	0.85	0.21	71,71,71,71	0
57	MG	1A	3690	1/1	0.85	0.10	55,55,55,55	0
57	MG	1a	1834	1/1	0.85	0.22	69,69,69,69	0
57	MG	1A	3691	1/1	0.85	0.13	65,65,65,65	0
57	MG	2A	3302	1/1	0.85	0.14	58,58,58,58	0
57	MG	2T	203	1/1	0.85	0.15	74,74,74,74	0
57	MG	2A	3317	1/1	0.85	0.18	64,64,64,64	0
57	MG	1A	3703	1/1	0.85	0.18	64,64,64,64	0
57	MG	1A	3472	1/1	0.85	0.10	60,60,60,60	0
57	MG	2a	3011	1/1	0.85	0.34	75,75,75,75	0
57	MG	2A	3553	1/1	0.85	0.18	76,76,76,76	0
57	MG	2A	3558	1/1	0.85	0.13	61,61,61,61	0
57	MG	1A	3557	1/1	0.85	0.10	46,46,46,46	0
57	MG	2A	3568	1/1	0.85	0.13	57,57,57,57	0
57	MG	2A	3345	1/1	0.85	0.23	69,69,69,69	0
57	MG	1A	3643	1/1	0.85	0.17	64,64,64,64	0
57	MG	2A	3584	1/1	0.85	0.15	43,43,43,43	0
57	MG	1A	3481	1/1	0.85	0.11	30,30,30,30	0
57	MG	1A	3330	1/1	0.85	0.17	62,62,62,62	0
57	MG	17	104	1/1	0.85	0.23	56,56,56,56	0
57	MG	2A	3600	1/1	0.85	0.15	55,55,55,55	0
57	MG	2A	3618	1/1	0.85	0.13	48,48,48,48	0
57	MG	2A	3626	1/1	0.85	0.12	45,45,45,45	0
57	MG	2A	3629	1/1	0.85	0.16	40,40,40,40	0
57	MG	2A	3634	1/1	0.85	0.16	36,36,36,36	0
57	MG	1A	3993	1/1	0.85	0.14	65,65,65,65	0
57	MG	2A	3089	1/1	0.85	0.19	63,63,63,63	0
57	MG	2A	3100	1/1	0.85	0.17	60,60,60,60	0
57	MG	2a	3179	1/1	0.85	0.11	67,67,67,67	0
57	MG	2a	3181	1/1	0.85	0.21	77,77,77,77	0
57	MG	2a	3189	1/1	0.85	0.28	66,66,66,66	0
57	MG	2A	3662	1/1	0.85	0.10	53,53,53,53	0
57	MG	1A	3886	1/1	0.85	0.23	60,60,60,60	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3730	1/1	0.86	0.13	59,59,59,59	0
57	MG	2A	3494	1/1	0.86	0.10	68,68,68,68	0
57	MG	1A	3486	1/1	0.86	0.09	23,23,23,23	0
57	MG	2A	3742	1/1	0.86	0.17	71,71,71,71	0
57	MG	2A	3743	1/1	0.86	0.23	62,62,62,62	0
57	MG	2B	201	1/1	0.86	0.22	71,71,71,71	0
57	MG	2A	3517	1/1	0.86	0.13	67,67,67,67	0
57	MG	1A	3935	1/1	0.86	0.09	57,57,57,57	0
57	MG	1A	3795	1/1	0.86	0.14	69,69,69,69	0
57	MG	2A	3527	1/1	0.86	0.18	65,65,65,65	0
57	MG	1a	1842	1/1	0.86	0.19	74,74,74,74	0
57	MG	1A	3942	1/1	0.86	0.12	43,43,43,43	0
57	MG	1A	3796	1/1	0.86	0.16	61,61,61,61	0
57	MG	1A	3692	1/1	0.86	0.12	65,65,65,65	0
57	MG	1a	1768	1/1	0.86	0.12	67,67,67,67	0
57	MG	1A	3425	1/1	0.86	0.17	41,41,41,41	0
57	MG	2A	3348	1/1	0.86	0.15	64,64,64,64	0
57	MG	2A	3024	1/1	0.86	0.13	62,62,62,62	0
57	MG	1A	3706	1/1	0.86	0.26	44,44,44,44	0
57	MG	2A	3572	1/1	0.86	0.28	61,61,61,61	0
57	MG	1A	3507	1/1	0.86	0.17	61,61,61,61	0
57	MG	2A	3391	1/1	0.86	0.16	69,69,69,69	0
57	MG	1A	3653	1/1	0.86	0.17	58,58,58,58	0
57	MG	2A	3404	1/1	0.86	0.17	76,76,76,76	0
57	MG	2A	3092	1/1	0.86	0.23	64,64,64,64	0
57	MG	1A	3656	1/1	0.86	0.19	56,56,56,56	0
57	MG	2A	3422	1/1	0.86	0.21	56,56,56,56	0
57	MG	2A	3616	1/1	0.86	0.10	64,64,64,64	0
57	MG	1A	3721	1/1	0.86	0.10	36,36,36,36	0
57	MG	2a	3062	1/1	0.86	0.26	75,75,75,75	0
57	MG	2A	3131	1/1	0.86	0.17	66,66,66,66	0
57	MG	1A	3381	1/1	0.86	0.13	51,51,51,51	0
57	MG	1a	1694	1/1	0.86	0.31	68,68,68,68	0
57	MG	1A	3681	1/1	0.86	0.19	68,68,68,68	0
57	MG	1B	227	1/1	0.86	0.11	59,59,59,59	0
57	MG	2A	3650	1/1	0.86	0.14	65,65,65,65	0
57	MG	2a	3120	1/1	0.86	0.16	69,69,69,69	0
57	MG	2a	3121	1/1	0.86	0.22	82,82,82,82	0
57	MG	1A	3344	1/1	0.86	0.08	28,28,28,28	0
57	MG	1A	3768	1/1	0.86	0.17	52,52,52,52	0
57	MG	2A	3460	1/1	0.86	0.23	77,77,77,77	0
57	MG	2a	3147	1/1	0.86	0.20	77,77,77,77	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2a	3167	1/1	0.86	0.11	64,64,64,64	0
57	MG	2A	3223	1/1	0.86	0.27	70,70,70,70	0
57	MG	1a	1717	1/1	0.86	0.39	73,73,73,73	0
57	MG	2a	3182	1/1	0.86	0.17	73,73,73,73	0
57	MG	2a	3185	1/1	0.86	0.21	69,69,69,69	0
57	MG	1a	1721	1/1	0.86	0.23	65,65,65,65	0
57	MG	2A	3244	1/1	0.86	0.15	46,46,46,46	0
57	MG	1A	3788	1/1	0.86	0.22	57,57,57,57	0
60	MPD	1T	208	8/8	0.86	0.18	59,64,68,69	0
57	MG	1A	3183	1/1	0.87	0.12	56,56,56,56	0
57	MG	2A	3739	1/1	0.87	0.18	68,68,68,68	0
57	MG	2A	3096	1/1	0.87	0.22	76,76,76,76	0
57	MG	1A	3885	1/1	0.87	0.14	43,43,43,43	0
57	MG	1A	3418	1/1	0.87	0.13	27,27,27,27	0
57	MG	1A	3723	1/1	0.87	0.13	59,59,59,59	0
57	MG	1A	3537	1/1	0.87	0.13	60,60,60,60	0
57	MG	1A	3554	1/1	0.87	0.14	49,49,49,49	0
57	MG	1T	205	1/1	0.87	0.16	59,59,59,59	0
57	MG	1A	3419	1/1	0.87	0.13	31,31,31,31	0
57	MG	2B	216	1/1	0.87	0.09	77,77,77,77	0
57	MG	10	106	1/1	0.87	0.15	56,56,56,56	0
57	MG	2A	3514	1/1	0.87	0.15	61,61,61,61	0
57	MG	2A	3193	1/1	0.87	0.20	66,66,66,66	0
57	MG	2A	3197	1/1	0.87	0.28	49,49,49,49	0
57	MG	15	105	1/1	0.87	0.11	48,48,48,48	0
57	MG	2T	201	1/1	0.87	0.17	64,64,64,64	0
57	MG	2A	3210	1/1	0.87	0.11	60,60,60,60	0
57	MG	2T	204	1/1	0.87	0.17	56,56,56,56	0
57	MG	2A	3214	1/1	0.87	0.14	61,61,61,61	0
57	MG	1a	1781	1/1	0.87	0.25	71,71,71,71	0
57	MG	1a	1782	1/1	0.87	0.20	71,71,71,71	0
57	MG	1A	3751	1/1	0.87	0.10	26,26,26,26	0
57	MG	1A	3762	1/1	0.87	0.22	62,62,62,62	0
57	MG	2A	3550	1/1	0.87	0.15	62,62,62,62	0
57	MG	1A	3144	1/1	0.87	0.20	60,60,60,60	0
57	MG	1a	1616	1/1	0.87	0.19	59,59,59,59	0
57	MG	1A	3659	1/1	0.87	0.10	47,47,47,47	0
57	MG	1A	3367	1/1	0.87	0.19	72,72,72,72	0
57	MG	1a	1821	1/1	0.87	0.21	67,67,67,67	0
57	MG	1A	3948	1/1	0.87	0.09	24,24,24,24	0
57	MG	1A	3951	1/1	0.87	0.13	49,49,49,49	0
57	MG	1A	3088	1/1	0.87	0.16	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1a	1672	1/1	0.87	0.13	53,53,53,53	0
57	MG	1A	3974	1/1	0.87	0.11	50,50,50,50	0
57	MG	1A	3160	1/1	0.87	0.23	62,62,62,62	0
57	MG	2A	3366	1/1	0.87	0.13	58,58,58,58	0
57	MG	1A	3982	1/1	0.87	0.22	74,74,74,74	0
57	MG	2a	3110	1/1	0.87	0.29	77,77,77,77	0
57	MG	1A	3598	1/1	0.87	0.18	63,63,63,63	0
57	MG	1A	3397	1/1	0.87	0.10	44,44,44,44	0
57	MG	1a	1858	1/1	0.87	0.19	67,67,67,67	0
57	MG	2a	3127	1/1	0.87	0.12	62,62,62,62	0
57	MG	1A	3994	1/1	0.87	0.19	62,62,62,62	0
57	MG	1a	1704	1/1	0.87	0.24	62,62,62,62	0
57	MG	2a	3133	1/1	0.87	0.19	64,64,64,64	0
57	MG	2A	3415	1/1	0.87	0.12	37,37,37,37	0
57	MG	2a	3138	1/1	0.87	0.20	52,52,52,52	0
57	MG	2a	3144	1/1	0.87	0.14	65,65,65,65	0
57	MG	1e	202	1/1	0.87	0.15	65,65,65,65	0
57	MG	1A	3409	1/1	0.87	0.11	60,60,60,60	0
57	MG	1A	3447	1/1	0.87	0.12	64,64,64,64	0
57	MG	2A	3016	1/1	0.87	0.20	73,73,73,73	0
57	MG	1B	203	1/1	0.87	0.14	59,59,59,59	0
57	MG	1A	3456	1/1	0.87	0.13	55,55,55,55	0
57	MG	2A	3065	1/1	0.87	0.29	63,63,63,63	0
57	MG	2A	3446	1/1	0.87	0.12	57,57,57,57	0
57	MG	2j	202	1/1	0.87	0.10	80,80,80,80	0
57	MG	1A	3533	1/1	0.87	0.12	48,48,48,48	0
60	MPD	1A	4019	8/8	0.87	0.22	50,54,62,65	0
57	MG	1A	3870	1/1	0.87	0.16	58,58,58,58	0
60	MPD	2A	3748	8/8	0.87	0.22	56,60,66,66	0
60	MPD	2B	220	8/8	0.87	0.19	59,60,67,75	0
57	MG	2A	3664	1/1	0.88	0.10	57,57,57,57	0
57	MG	2A	3676	1/1	0.88	0.10	64,64,64,64	0
57	MG	2A	3678	1/1	0.88	0.10	68,68,68,68	0
57	MG	1a	1734	1/1	0.88	0.10	66,66,66,66	0
57	MG	2A	3390	1/1	0.88	0.14	48,48,48,48	0
57	MG	1y	202	1/1	0.88	0.38	71,71,71,71	0
57	MG	2A	3400	1/1	0.88	0.15	63,63,63,63	0
57	MG	2A	3716	1/1	0.88	0.17	69,69,69,69	0
57	MG	1A	3616	1/1	0.88	0.22	58,58,58,58	0
57	MG	1A	3459	1/1	0.88	0.21	45,45,45,45	0
57	MG	2A	3413	1/1	0.88	0.12	53,53,53,53	0
57	MG	1A	3825	1/1	0.88	0.27	35,35,35,35	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3055	1/1	0.88	0.21	63,63,63,63	0
57	MG	2A	3060	1/1	0.88	0.12	51,51,51,51	0
57	MG	1A	3377	1/1	0.88	0.12	54,54,54,54	0
57	MG	2A	3067	1/1	0.88	0.13	57,57,57,57	0
57	MG	1A	3851	1/1	0.88	0.10	52,52,52,52	0
57	MG	2A	3435	1/1	0.88	0.13	35,35,35,35	0
57	MG	1a	1759	1/1	0.88	0.22	64,64,64,64	0
57	MG	2A	3091	1/1	0.88	0.19	63,63,63,63	0
57	MG	1a	1767	1/1	0.88	0.17	63,63,63,63	0
57	MG	18	101	1/1	0.88	0.36	57,57,57,57	0
57	MG	1A	3199	1/1	0.88	0.30	51,51,51,51	0
57	MG	2G	202	1/1	0.88	0.18	66,66,66,66	0
57	MG	2A	3127	1/1	0.88	0.16	55,55,55,55	0
57	MG	1A	3466	1/1	0.88	0.11	63,63,63,63	0
57	MG	1a	1603	1/1	0.88	0.15	64,64,64,64	0
57	MG	1A	3422	1/1	0.88	0.10	61,61,61,61	0
57	MG	1A	3477	1/1	0.88	0.10	21,21,21,21	0
57	MG	1a	1780	1/1	0.88	0.23	71,71,71,71	0
57	MG	1A	3387	1/1	0.88	0.09	24,24,24,24	0
57	MG	2A	3165	1/1	0.88	0.18	58,58,58,58	0
57	MG	2A	3479	1/1	0.88	0.13	65,65,65,65	0
57	MG	2a	3005	1/1	0.88	0.17	62,62,62,62	0
57	MG	2A	3480	1/1	0.88	0.12	62,62,62,62	0
57	MG	2A	3490	1/1	0.88	0.09	61,61,61,61	0
57	MG	2a	3016	1/1	0.88	0.15	59,59,59,59	0
57	MG	1a	1637	1/1	0.88	0.20	73,73,73,73	0
57	MG	2A	3186	1/1	0.88	0.20	61,61,61,61	0
57	MG	2A	3192	1/1	0.88	0.12	58,58,58,58	0
57	MG	1A	3880	1/1	0.88	0.09	25,25,25,25	0
57	MG	2a	3035	1/1	0.88	0.37	72,72,72,72	0
57	MG	2a	3037	1/1	0.88	0.16	71,71,71,71	0
57	MG	2a	3041	1/1	0.88	0.21	65,65,65,65	0
57	MG	1A	3200	1/1	0.88	0.17	65,65,65,65	0
57	MG	2A	3523	1/1	0.88	0.15	63,63,63,63	0
57	MG	1A	3343	1/1	0.88	0.12	41,41,41,41	0
57	MG	2A	3209	1/1	0.88	0.20	63,63,63,63	0
57	MG	1A	3286	1/1	0.88	0.12	72,72,72,72	0
57	MG	1a	1675	1/1	0.88	0.16	80,80,80,80	0
57	MG	1a	1679	1/1	0.88	0.11	59,59,59,59	0
57	MG	1B	207	1/1	0.88	0.17	55,55,55,55	0
57	MG	2a	3067	1/1	0.88	0.29	69,69,69,69	0
57	MG	2A	3228	1/1	0.88	0.13	62,62,62,62	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3549	1/1	0.88	0.12	67,67,67,67	0
57	MG	2a	3084	1/1	0.88	0.22	75,75,75,75	0
57	MG	1A	3412	1/1	0.88	0.21	51,51,51,51	0
57	MG	2a	3090	1/1	0.88	0.14	68,68,68,68	0
57	MG	2a	3104	1/1	0.88	0.43	71,71,71,71	0
57	MG	2A	3551	1/1	0.88	0.15	68,68,68,68	0
57	MG	2A	3552	1/1	0.88	0.14	58,58,58,58	0
57	MG	2A	3240	1/1	0.88	0.22	58,58,58,58	0
57	MG	2A	3241	1/1	0.88	0.18	70,70,70,70	0
57	MG	2a	3122	1/1	0.88	0.18	75,75,75,75	0
57	MG	1a	1693	1/1	0.88	0.35	73,73,73,73	0
57	MG	1A	3758	1/1	0.88	0.15	54,54,54,54	0
57	MG	2A	3248	1/1	0.88	0.23	52,52,52,52	0
57	MG	1A	3903	1/1	0.88	0.11	25,25,25,25	0
57	MG	1A	3591	1/1	0.88	0.19	63,63,63,63	0
57	MG	2a	3137	1/1	0.88	0.15	65,65,65,65	0
57	MG	1A	3672	1/1	0.88	0.14	51,51,51,51	0
57	MG	2A	3296	1/1	0.88	0.34	67,67,67,67	0
57	MG	1A	3919	1/1	0.88	0.12	45,45,45,45	0
57	MG	2a	3162	1/1	0.88	0.15	59,59,59,59	0
57	MG	2A	3306	1/1	0.88	0.32	62,62,62,62	0
57	MG	1a	1708	1/1	0.88	0.26	45,45,45,45	0
57	MG	2a	3180	1/1	0.88	0.16	64,64,64,64	0
57	MG	1A	3303	1/1	0.88	0.17	66,66,66,66	0
57	MG	2A	3617	1/1	0.88	0.08	40,40,40,40	0
57	MG	2A	3319	1/1	0.88	0.12	34,34,34,34	0
57	MG	1A	3035	1/1	0.88	0.20	50,50,50,50	0
57	MG	1R	205	1/1	0.88	0.17	44,44,44,44	0
57	MG	1T	201	1/1	0.88	0.17	67,67,67,67	0
57	MG	1e	201	1/1	0.88	0.18	60,60,60,60	0
57	MG	1a	1726	1/1	0.88	0.14	60,60,60,60	0
57	MG	1h	202	1/1	0.88	0.15	63,63,63,63	0
57	MG	1A	3608	1/1	0.88	0.10	60,60,60,60	0
57	MG	2A	3385	1/1	0.88	0.12	75,75,75,75	0
57	MG	1A	3342	1/1	0.89	0.11	51,51,51,51	0
57	MG	2A	3143	1/1	0.89	0.18	63,63,63,63	0
57	MG	1a	1793	1/1	0.89	0.11	61,61,61,61	0
57	MG	2A	3717	1/1	0.89	0.24	44,44,44,44	0
57	MG	2A	3718	1/1	0.89	0.08	76,76,76,76	0
57	MG	2A	3425	1/1	0.89	0.12	45,45,45,45	0
57	MG	1a	1795	1/1	0.89	0.23	68,68,68,68	0
57	MG	2A	3159	1/1	0.89	0.08	44,44,44,44	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3435	1/1	0.89	0.13	66,66,66,66	0
57	MG	2A	3734	1/1	0.89	0.16	63,63,63,63	0
57	MG	2A	3172	1/1	0.89	0.16	64,64,64,64	0
57	MG	1a	1800	1/1	0.89	0.11	76,76,76,76	0
57	MG	2A	3447	1/1	0.89	0.15	54,54,54,54	0
57	MG	2A	3181	1/1	0.89	0.22	64,64,64,64	0
57	MG	2A	3185	1/1	0.89	0.25	51,51,51,51	0
57	MG	2A	3452	1/1	0.89	0.15	61,61,61,61	0
57	MG	1A	3817	1/1	0.89	0.16	62,62,62,62	0
57	MG	1A	3663	1/1	0.89	0.13	41,41,41,41	0
57	MG	2A	3458	1/1	0.89	0.13	51,51,51,51	0
57	MG	1A	3301	1/1	0.89	0.21	51,51,51,51	0
57	MG	2E	305	1/1	0.89	0.16	63,63,63,63	0
57	MG	2A	3194	1/1	0.89	0.16	64,64,64,64	0
57	MG	2A	3195	1/1	0.89	0.18	60,60,60,60	0
57	MG	1A	3735	1/1	0.89	0.14	54,54,54,54	0
57	MG	1a	1698	1/1	0.89	0.27	59,59,59,59	0
57	MG	1A	3670	1/1	0.89	0.09	57,57,57,57	0
57	MG	1A	3032	1/1	0.89	0.18	53,53,53,53	0
57	MG	1A	3311	1/1	0.89	0.30	49,49,49,49	0
57	MG	2A	3221	1/1	0.89	0.18	54,54,54,54	0
57	MG	1A	3684	1/1	0.89	0.14	71,71,71,71	0
57	MG	2Y	201	1/1	0.89	0.22	61,61,61,61	0
57	MG	2A	3501	1/1	0.89	0.11	55,55,55,55	0
57	MG	1A	3354	1/1	0.89	0.17	57,57,57,57	0
57	MG	2A	3508	1/1	0.89	0.14	53,53,53,53	0
57	MG	1A	3595	1/1	0.89	0.14	67,67,67,67	0
57	MG	1T	206	1/1	0.89	0.13	70,70,70,70	0
57	MG	2a	3014	1/1	0.89	0.17	69,69,69,69	0
57	MG	2A	3239	1/1	0.89	0.21	59,59,59,59	0
57	MG	1A	3976	1/1	0.89	0.13	53,53,53,53	0
57	MG	1a	1859	1/1	0.89	0.19	73,73,73,73	0
57	MG	2A	3242	1/1	0.89	0.25	62,62,62,62	0
57	MG	2A	3530	1/1	0.89	0.13	69,69,69,69	0
57	MG	2a	3034	1/1	0.89	0.24	63,63,63,63	0
57	MG	1A	3767	1/1	0.89	0.07	33,33,33,33	0
57	MG	1A	3883	1/1	0.89	0.10	47,47,47,47	0
57	MG	2A	3247	1/1	0.89	0.11	59,59,59,59	0
57	MG	2a	3043	1/1	0.89	0.30	59,59,59,59	0
57	MG	2a	3047	1/1	0.89	0.14	60,60,60,60	0
57	MG	1a	1731	1/1	0.89	0.11	48,48,48,48	0
57	MG	1A	3884	1/1	0.89	0.08	44,44,44,44	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3257	1/1	0.89	0.14	63,63,63,63	0
57	MG	2A	3260	1/1	0.89	0.14	57,57,57,57	0
57	MG	1g	202	1/1	0.89	0.14	61,61,61,61	0
57	MG	1A	3989	1/1	0.89	0.23	49,49,49,49	0
57	MG	2A	3273	1/1	0.89	0.17	57,57,57,57	0
57	MG	2A	3292	1/1	0.89	0.12	45,45,45,45	0
57	MG	1m	201	1/1	0.89	0.09	72,72,72,72	0
57	MG	2a	3071	1/1	0.89	0.13	59,59,59,59	0
57	MG	1a	1747	1/1	0.89	0.22	64,64,64,64	0
57	MG	1a	1749	1/1	0.89	0.11	60,60,60,60	0
57	MG	2a	3080	1/1	0.89	0.17	61,61,61,61	0
57	MG	2A	3574	1/1	0.89	0.10	52,52,52,52	0
57	MG	1A	3990	1/1	0.89	0.09	53,53,53,53	0
57	MG	1A	3487	1/1	0.89	0.11	54,54,54,54	0
57	MG	1A	3362	1/1	0.89	0.10	39,39,39,39	0
57	MG	1a	1611	1/1	0.89	0.29	66,66,66,66	0
57	MG	1A	4005	1/1	0.89	0.13	56,56,56,56	0
57	MG	1A	4010	1/1	0.89	0.19	66,66,66,66	0
57	MG	2A	3062	1/1	0.89	0.13	57,57,57,57	0
57	MG	1A	3887	1/1	0.89	0.14	53,53,53,53	0
57	MG	1A	3652	1/1	0.89	0.12	30,30,30,30	0
57	MG	1B	201	1/1	0.89	0.16	60,60,60,60	0
57	MG	2A	3621	1/1	0.89	0.10	53,53,53,53	0
57	MG	2A	3624	1/1	0.89	0.14	40,40,40,40	0
57	MG	2A	3082	1/1	0.89	0.10	69,69,69,69	0
57	MG	1a	1639	1/1	0.89	0.28	69,69,69,69	0
57	MG	1a	1642	1/1	0.89	0.24	63,63,63,63	0
57	MG	1B	202	1/1	0.89	0.13	49,49,49,49	0
57	MG	2A	3641	1/1	0.89	0.18	58,58,58,58	0
57	MG	2A	3393	1/1	0.89	0.14	62,62,62,62	0
57	MG	1a	1778	1/1	0.89	0.22	62,62,62,62	0
57	MG	1a	1660	1/1	0.89	0.18	62,62,62,62	0
57	MG	1A	3793	1/1	0.89	0.15	55,55,55,55	0
57	MG	2A	3408	1/1	0.89	0.12	61,61,61,61	0
57	MG	2A	3666	1/1	0.89	0.09	50,50,50,50	0
57	MG	2A	3670	1/1	0.89	0.13	37,37,37,37	0
57	MG	1B	206	1/1	0.89	0.11	47,47,47,47	0
57	MG	2A	3677	1/1	0.89	0.09	72,72,72,72	0
57	MG	2A	3414	1/1	0.89	0.10	34,34,34,34	0
57	MG	1A	3340	1/1	0.89	0.10	49,49,49,49	0
57	MG	2A	3695	1/1	0.89	0.12	41,41,41,41	0
57	MG	2A	3697	1/1	0.89	0.12	58,58,58,58	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
60	MPD	1a	1867	8/8	0.89	0.15	52,59,62,64	0
57	MG	2A	3708	1/1	0.89	0.11	51,51,51,51	0
57	MG	1a	1677	1/1	0.89	0.09	51,51,51,51	0
57	MG	2A	3731	1/1	0.90	0.25	51,51,51,51	0
57	MG	1A	3779	1/1	0.90	0.07	30,30,30,30	0
57	MG	2A	3467	1/1	0.90	0.14	45,45,45,45	0
57	MG	2A	3735	1/1	0.90	0.16	52,52,52,52	0
57	MG	2A	3738	1/1	0.90	0.15	64,64,64,64	0
57	MG	1A	3468	1/1	0.90	0.10	43,43,43,43	0
57	MG	1d	302	1/1	0.90	0.17	57,57,57,57	0
57	MG	1A	3943	1/1	0.90	0.14	62,62,62,62	0
57	MG	1A	3683	1/1	0.90	0.09	69,69,69,69	0
57	MG	1a	1733	1/1	0.90	0.12	41,41,41,41	0
57	MG	2B	202	1/1	0.90	0.09	71,71,71,71	0
57	MG	2B	206	1/1	0.90	0.13	61,61,61,61	0
57	MG	1A	3011	1/1	0.90	0.10	56,56,56,56	0
57	MG	2B	208	1/1	0.90	0.19	57,57,57,57	0
57	MG	2A	3243	1/1	0.90	0.15	52,52,52,52	0
57	MG	2A	3498	1/1	0.90	0.14	54,54,54,54	0
57	MG	2A	3500	1/1	0.90	0.17	68,68,68,68	0
57	MG	1A	3304	1/1	0.90	0.25	70,70,70,70	0
57	MG	2B	218	1/1	0.90	0.15	74,74,74,74	0
57	MG	13	102	1/1	0.90	0.11	59,59,59,59	0
57	MG	1A	3063	1/1	0.90	0.13	55,55,55,55	0
57	MG	2A	3511	1/1	0.90	0.12	61,61,61,61	0
57	MG	15	106	1/1	0.90	0.09	57,57,57,57	0
57	MG	2I	201	1/1	0.90	0.17	65,65,65,65	0
57	MG	1A	3969	1/1	0.90	0.15	47,47,47,47	0
57	MG	2A	3005	1/1	0.90	0.12	63,63,63,63	0
57	MG	1A	3973	1/1	0.90	0.10	52,52,52,52	0
57	MG	2A	3261	1/1	0.90	0.11	51,51,51,51	0
57	MG	1A	3552	1/1	0.90	0.09	37,37,37,37	0
57	MG	2A	3529	1/1	0.90	0.10	51,51,51,51	0
57	MG	2A	3265	1/1	0.90	0.17	55,55,55,55	0
57	MG	2A	3539	1/1	0.90	0.16	39,39,39,39	0
57	MG	2A	3032	1/1	0.90	0.34	59,59,59,59	0
57	MG	2A	3043	1/1	0.90	0.27	68,68,68,68	0
57	MG	2A	3279	1/1	0.90	0.13	50,50,50,50	0
57	MG	2A	3285	1/1	0.90	0.25	55,55,55,55	0
57	MG	2A	3047	1/1	0.90	0.10	68,68,68,68	0
57	MG	1A	3697	1/1	0.90	0.19	63,63,63,63	0
57	MG	2A	3299	1/1	0.90	0.27	61,61,61,61	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3698	1/1	0.90	0.11	53,53,53,53	0
57	MG	1a	1607	1/1	0.90	0.11	67,67,67,67	0
57	MG	2A	3308	1/1	0.90	0.26	65,65,65,65	0
57	MG	2a	3028	1/1	0.90	0.14	74,74,74,74	0
57	MG	2a	3029	1/1	0.90	0.17	62,62,62,62	0
57	MG	2a	3032	1/1	0.90	0.18	72,72,72,72	0
57	MG	1A	3833	1/1	0.90	0.11	40,40,40,40	0
57	MG	1A	3701	1/1	0.90	0.12	42,42,42,42	0
57	MG	1A	3077	1/1	0.90	0.13	62,62,62,62	0
57	MG	2a	3040	1/1	0.90	0.13	64,64,64,64	0
57	MG	2A	3078	1/1	0.90	0.17	55,55,55,55	0
57	MG	1A	3449	1/1	0.90	0.07	38,38,38,38	0
57	MG	2a	3044	1/1	0.90	0.14	71,71,71,71	0
57	MG	1A	3494	1/1	0.90	0.11	32,32,32,32	0
57	MG	1A	3645	1/1	0.90	0.15	59,59,59,59	0
57	MG	2A	3357	1/1	0.90	0.11	48,48,48,48	0
57	MG	2A	3587	1/1	0.90	0.11	43,43,43,43	0
57	MG	2a	3059	1/1	0.90	0.14	68,68,68,68	0
57	MG	1A	3863	1/1	0.90	0.07	62,62,62,62	0
57	MG	1A	3648	1/1	0.90	0.12	36,36,36,36	0
57	MG	1A	3715	1/1	0.90	0.10	38,38,38,38	0
57	MG	1A	3396	1/1	0.90	0.08	28,28,28,28	0
57	MG	2A	3120	1/1	0.90	0.20	72,72,72,72	0
57	MG	1A	3275	1/1	0.90	0.10	37,37,37,37	0
57	MG	1a	1791	1/1	0.90	0.14	61,61,61,61	0
57	MG	1A	3582	1/1	0.90	0.26	42,42,42,42	0
57	MG	1a	1674	1/1	0.90	0.10	55,55,55,55	0
57	MG	2A	3625	1/1	0.90	0.08	52,52,52,52	0
57	MG	1A	3461	1/1	0.90	0.07	31,31,31,31	0
57	MG	1B	204	1/1	0.90	0.08	48,48,48,48	0
57	MG	2A	3631	1/1	0.90	0.15	51,51,51,51	0
57	MG	1a	1798	1/1	0.90	0.13	62,62,62,62	0
57	MG	2a	3107	1/1	0.90	0.27	54,54,54,54	0
57	MG	2A	3635	1/1	0.90	0.14	49,49,49,49	0
57	MG	1A	3517	1/1	0.90	0.11	42,42,42,42	0
57	MG	2a	3113	1/1	0.90	0.11	73,73,73,73	0
57	MG	2a	3119	1/1	0.90	0.16	59,59,59,59	0
57	MG	2A	3640	1/1	0.90	0.14	54,54,54,54	0
57	MG	1a	1804	1/1	0.90	0.23	67,67,67,67	0
57	MG	2A	3642	1/1	0.90	0.19	54,54,54,54	0
57	MG	2a	3126	1/1	0.90	0.21	62,62,62,62	0
57	MG	1A	3165	1/1	0.90	0.10	41,41,41,41	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3416	1/1	0.90	0.12	50,50,50,50	0
57	MG	1a	1809	1/1	0.90	0.13	65,65,65,65	0
57	MG	1a	1812	1/1	0.90	0.21	56,56,56,56	0
57	MG	1A	3216	1/1	0.90	0.07	57,57,57,57	0
57	MG	1A	3754	1/1	0.90	0.23	57,57,57,57	0
57	MG	2A	3424	1/1	0.90	0.16	61,61,61,61	0
57	MG	1A	3434	1/1	0.90	0.11	38,38,38,38	0
57	MG	2A	3427	1/1	0.90	0.22	68,68,68,68	0
57	MG	2a	3150	1/1	0.90	0.09	55,55,55,55	0
57	MG	1A	3759	1/1	0.90	0.08	34,34,34,34	0
57	MG	1A	3531	1/1	0.90	0.09	56,56,56,56	0
57	MG	2a	3168	1/1	0.90	0.15	55,55,55,55	0
57	MG	1A	3763	1/1	0.90	0.14	42,42,42,42	0
57	MG	1D	301	1/1	0.90	0.17	59,59,59,59	0
57	MG	2A	3699	1/1	0.90	0.19	46,46,46,46	0
57	MG	2A	3196	1/1	0.90	0.18	71,71,71,71	0
57	MG	2a	3183	1/1	0.90	0.22	75,75,75,75	0
57	MG	1A	3673	1/1	0.90	0.08	36,36,36,36	0
57	MG	2a	3188	1/1	0.90	0.16	57,57,57,57	0
57	MG	1E	307	1/1	0.90	0.12	54,54,54,54	0
57	MG	2A	3201	1/1	0.90	0.27	59,59,59,59	0
57	MG	1A	3674	1/1	0.90	0.16	60,60,60,60	0
57	MG	2x	101	1/1	0.90	0.10	57,57,57,57	0
57	MG	1P	205	1/1	0.90	0.14	67,67,67,67	0
57	MG	1a	1856	1/1	0.90	0.23	68,68,68,68	0
57	MG	2A	3720	1/1	0.90	0.09	65,65,65,65	0
57	MG	1a	1857	1/1	0.90	0.08	65,65,65,65	0
57	MG	1A	3776	1/1	0.90	0.08	25,25,25,25	0
57	MG	2A	3225	1/1	0.90	0.18	65,65,65,65	0
57	MG	1V	205	1/1	0.91	0.13	57,57,57,57	0
57	MG	2A	3481	1/1	0.91	0.13	59,59,59,59	0
57	MG	2A	3486	1/1	0.91	0.20	47,47,47,47	0
57	MG	1A	3306	1/1	0.91	0.17	32,32,32,32	0
57	MG	1a	1719	1/1	0.91	0.11	57,57,57,57	0
57	MG	1a	1863	1/1	0.91	0.12	63,63,63,63	0
57	MG	1a	1864	1/1	0.91	0.20	62,62,62,62	0
57	MG	1Y	201	1/1	0.91	0.12	59,59,59,59	0
57	MG	1b	301	1/1	0.91	0.23	66,66,66,66	0
57	MG	10	101	1/1	0.91	0.16	39,39,39,39	0
57	MG	1A	3987	1/1	0.91	0.19	39,39,39,39	0
57	MG	1a	1729	1/1	0.91	0.10	54,54,54,54	0
57	MG	10	107	1/1	0.91	0.10	50,50,50,50	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2E	304	1/1	0.91	0.10	36,36,36,36	0
57	MG	2A	3518	1/1	0.91	0.15	44,44,44,44	0
57	MG	1f	202	1/1	0.91	0.14	49,49,49,49	0
57	MG	1g	201	1/1	0.91	0.12	47,47,47,47	0
57	MG	11	104	1/1	0.91	0.13	48,48,48,48	0
57	MG	1A	3475	1/1	0.91	0.08	20,20,20,20	0
57	MG	1A	3773	1/1	0.91	0.06	23,23,23,23	0
57	MG	1a	1742	1/1	0.91	0.13	61,61,61,61	0
57	MG	2Q	201	1/1	0.91	0.11	56,56,56,56	0
57	MG	1A	3205	1/1	0.91	0.07	52,52,52,52	0
57	MG	1A	3480	1/1	0.91	0.08	24,24,24,24	0
57	MG	1A	3390	1/1	0.91	0.08	40,40,40,40	0
57	MG	1A	3789	1/1	0.91	0.09	25,25,25,25	0
57	MG	1A	4007	1/1	0.91	0.10	59,59,59,59	0
57	MG	1A	4009	1/1	0.91	0.11	35,35,35,35	0
57	MG	2A	3034	1/1	0.91	0.19	65,65,65,65	0
57	MG	1A	3483	1/1	0.91	0.08	26,26,26,26	0
57	MG	1a	1608	1/1	0.91	0.12	58,58,58,58	0
57	MG	1a	1761	1/1	0.91	0.18	62,62,62,62	0
57	MG	1A	3610	1/1	0.91	0.19	42,42,42,42	0
57	MG	2A	3555	1/1	0.91	0.16	55,55,55,55	0
57	MG	2A	3556	1/1	0.91	0.15	65,65,65,65	0
57	MG	2a	3024	1/1	0.91	0.26	68,68,68,68	0
57	MG	1A	3668	1/1	0.91	0.10	50,50,50,50	0
57	MG	1a	1619	1/1	0.91	0.21	57,57,57,57	0
57	MG	2A	3563	1/1	0.91	0.13	32,32,32,32	0
57	MG	1A	3911	1/1	0.91	0.17	55,55,55,55	0
57	MG	2A	3322	1/1	0.91	0.08	48,48,48,48	0
57	MG	1a	1626	1/1	0.91	0.28	65,65,65,65	0
57	MG	1a	1627	1/1	0.91	0.33	67,67,67,67	0
57	MG	1A	3122	1/1	0.91	0.19	55,55,55,55	0
57	MG	1a	1631	1/1	0.91	0.15	63,63,63,63	0
57	MG	2A	3585	1/1	0.91	0.15	49,49,49,49	0
57	MG	1A	3801	1/1	0.91	0.09	48,48,48,48	0
57	MG	2a	3042	1/1	0.91	0.24	68,68,68,68	0
57	MG	1A	3217	1/1	0.91	0.09	54,54,54,54	0
57	MG	2A	3368	1/1	0.91	0.09	48,48,48,48	0
57	MG	1A	3809	1/1	0.91	0.12	23,23,23,23	0
57	MG	1A	3813	1/1	0.91	0.10	46,46,46,46	0
57	MG	2A	3604	1/1	0.91	0.12	55,55,55,55	0
57	MG	2A	3606	1/1	0.91	0.09	50,50,50,50	0
57	MG	2a	3054	1/1	0.91	0.26	62,62,62,62	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2a	3055	1/1	0.91	0.33	59,59,59,59	0
57	MG	2A	3607	1/1	0.91	0.09	48,48,48,48	0
57	MG	2A	3611	1/1	0.91	0.10	67,67,67,67	0
57	MG	2A	3612	1/1	0.91	0.09	63,63,63,63	0
57	MG	2A	3384	1/1	0.91	0.08	41,41,41,41	0
57	MG	2A	3098	1/1	0.91	0.17	57,57,57,57	0
57	MG	1B	208	1/1	0.91	0.33	66,66,66,66	0
57	MG	2a	3066	1/1	0.91	0.19	68,68,68,68	0
57	MG	2A	3116	1/1	0.91	0.17	72,72,72,72	0
57	MG	2a	3070	1/1	0.91	0.17	60,60,60,60	0
57	MG	1A	3729	1/1	0.91	0.14	58,58,58,58	0
57	MG	1a	1661	1/1	0.91	0.17	64,64,64,64	0
57	MG	1a	1662	1/1	0.91	0.29	59,59,59,59	0
57	MG	2a	3078	1/1	0.91	0.23	74,74,74,74	0
57	MG	1a	1794	1/1	0.91	0.14	59,59,59,59	0
57	MG	1A	3251	1/1	0.91	0.15	58,58,58,58	0
57	MG	2a	3085	1/1	0.91	0.11	60,60,60,60	0
57	MG	1A	3498	1/1	0.91	0.07	57,57,57,57	0
57	MG	2a	3089	1/1	0.91	0.24	63,63,63,63	0
57	MG	2A	3410	1/1	0.91	0.11	66,66,66,66	0
57	MG	2a	3091	1/1	0.91	0.12	66,66,66,66	0
57	MG	2a	3094	1/1	0.91	0.25	55,55,55,55	0
57	MG	2a	3097	1/1	0.91	0.42	71,71,71,71	0
57	MG	2a	3098	1/1	0.91	0.16	54,54,54,54	0
57	MG	1A	3676	1/1	0.91	0.07	61,61,61,61	0
57	MG	2A	3146	1/1	0.91	0.21	57,57,57,57	0
57	MG	1A	3842	1/1	0.91	0.09	54,54,54,54	0
57	MG	1A	3402	1/1	0.91	0.11	21,21,21,21	0
57	MG	2A	3153	1/1	0.91	0.13	47,47,47,47	0
57	MG	1A	3505	1/1	0.91	0.08	44,44,44,44	0
57	MG	2A	3420	1/1	0.91	0.10	40,40,40,40	0
57	MG	2A	3164	1/1	0.91	0.11	60,60,60,60	0
57	MG	2A	3663	1/1	0.91	0.08	66,66,66,66	0
57	MG	2a	3125	1/1	0.91	0.18	73,73,73,73	0
57	MG	1a	1683	1/1	0.91	0.18	63,63,63,63	0
57	MG	2A	3171	1/1	0.91	0.12	53,53,53,53	0
57	MG	1D	315	1/1	0.91	0.20	39,39,39,39	0
57	MG	2A	3674	1/1	0.91	0.07	75,75,75,75	0
57	MG	1A	3954	1/1	0.91	0.11	64,64,64,64	0
57	MG	1a	1689	1/1	0.91	0.21	64,64,64,64	0
57	MG	2A	3433	1/1	0.91	0.17	55,55,55,55	0
57	MG	2A	3682	1/1	0.91	0.10	64,64,64,64	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3958	1/1	0.91	0.11	49,49,49,49	0
57	MG	2A	3694	1/1	0.91	0.08	67,67,67,67	0
57	MG	1a	1825	1/1	0.91	0.13	74,74,74,74	0
57	MG	2a	3153	1/1	0.91	0.13	69,69,69,69	0
57	MG	2a	3160	1/1	0.91	0.12	68,68,68,68	0
57	MG	2A	3188	1/1	0.91	0.11	61,61,61,61	0
57	MG	1a	1827	1/1	0.91	0.13	59,59,59,59	0
57	MG	1A	3639	1/1	0.91	0.09	34,34,34,34	0
57	MG	1A	3972	1/1	0.91	0.10	46,46,46,46	0
57	MG	1A	3364	1/1	0.91	0.09	53,53,53,53	0
57	MG	1A	3572	1/1	0.91	0.14	45,45,45,45	0
57	MG	2A	3454	1/1	0.91	0.12	79,79,79,79	0
57	MG	1a	1838	1/1	0.91	0.09	49,49,49,49	0
57	MG	1A	3193	1/1	0.91	0.22	60,60,60,60	0
57	MG	1a	1702	1/1	0.91	0.18	63,63,63,63	0
57	MG	2A	3202	1/1	0.91	0.32	64,64,64,64	0
57	MG	2e	201	1/1	0.91	0.26	68,68,68,68	0
57	MG	2A	3725	1/1	0.91	0.18	52,52,52,52	0
57	MG	1A	3202	1/1	0.91	0.30	59,59,59,59	0
57	MG	1a	1705	1/1	0.91	0.21	57,57,57,57	0
57	MG	2A	3466	1/1	0.91	0.14	67,67,67,67	0
57	MG	1a	1851	1/1	0.91	0.16	55,55,55,55	0
57	MG	1a	1852	1/1	0.91	0.10	60,60,60,60	0
57	MG	2A	3222	1/1	0.91	0.11	56,56,56,56	0
57	MG	1a	1855	1/1	0.91	0.14	58,58,58,58	0
57	MG	1A	3980	1/1	0.91	0.06	65,65,65,65	0
57	MG	1A	3704	1/1	0.92	0.16	34,34,34,34	0
57	MG	1B	216	1/1	0.92	0.14	48,48,48,48	0
57	MG	1A	3606	1/1	0.92	0.13	37,37,37,37	0
57	MG	2A	3359	1/1	0.92	0.08	38,38,38,38	0
57	MG	2A	3689	1/1	0.92	0.14	73,73,73,73	0
57	MG	2A	3691	1/1	0.92	0.08	53,53,53,53	0
57	MG	2A	3363	1/1	0.92	0.11	39,39,39,39	0
57	MG	1a	1707	1/1	0.92	0.35	67,67,67,67	0
57	MG	2A	3367	1/1	0.92	0.08	33,33,33,33	0
57	MG	1y	201	1/1	0.92	0.12	57,57,57,57	0
57	MG	2A	3700	1/1	0.92	0.07	54,54,54,54	0
57	MG	2A	3702	1/1	0.92	0.10	51,51,51,51	0
57	MG	1A	3500	1/1	0.92	0.10	53,53,53,53	0
57	MG	2A	3374	1/1	0.92	0.07	33,33,33,33	0
57	MG	2A	3001	1/1	0.92	0.29	61,61,61,61	0
57	MG	1A	3872	1/1	0.92	0.09	49,49,49,49	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1a	1710	1/1	0.92	0.11	56,56,56,56	0
57	MG	1a	1715	1/1	0.92	0.16	72,72,72,72	0
57	MG	1A	3283	1/1	0.92	0.19	54,54,54,54	0
57	MG	2A	3719	1/1	0.92	0.14	67,67,67,67	0
57	MG	1A	3615	1/1	0.92	0.18	34,34,34,34	0
57	MG	2A	3039	1/1	0.92	0.14	60,60,60,60	0
57	MG	2A	3395	1/1	0.92	0.12	62,62,62,62	0
57	MG	2A	3727	1/1	0.92	0.10	64,64,64,64	0
57	MG	1A	3882	1/1	0.92	0.06	32,32,32,32	0
57	MG	1D	312	1/1	0.92	0.24	44,44,44,44	0
57	MG	2A	3048	1/1	0.92	0.13	62,62,62,62	0
57	MG	2A	3050	1/1	0.92	0.19	59,59,59,59	0
57	MG	2A	3733	1/1	0.92	0.10	51,51,51,51	0
57	MG	1A	3713	1/1	0.92	0.10	56,56,56,56	0
57	MG	1a	1727	1/1	0.92	0.23	57,57,57,57	0
57	MG	2A	3056	1/1	0.92	0.20	62,62,62,62	0
57	MG	1A	3285	1/1	0.92	0.08	63,63,63,63	0
57	MG	1E	306	1/1	0.92	0.10	24,24,24,24	0
57	MG	2A	3741	1/1	0.92	0.17	56,56,56,56	0
57	MG	2A	3064	1/1	0.92	0.14	51,51,51,51	0
57	MG	1A	3718	1/1	0.92	0.08	66,66,66,66	0
57	MG	2A	3744	1/1	0.92	0.25	69,69,69,69	0
57	MG	2A	3746	1/1	0.92	0.08	52,52,52,52	0
57	MG	1G	202	1/1	0.92	0.12	51,51,51,51	0
57	MG	2A	3075	1/1	0.92	0.12	63,63,63,63	0
57	MG	2B	204	1/1	0.92	0.18	70,70,70,70	0
57	MG	2B	205	1/1	0.92	0.24	68,68,68,68	0
57	MG	2A	3077	1/1	0.92	0.12	66,66,66,66	0
57	MG	1A	3155	1/1	0.92	0.19	46,46,46,46	0
57	MG	1a	1738	1/1	0.92	0.10	62,62,62,62	0
57	MG	2B	209	1/1	0.92	0.14	57,57,57,57	0
57	MG	1A	3512	1/1	0.92	0.12	28,28,28,28	0
57	MG	1A	3158	1/1	0.92	0.32	41,41,41,41	0
57	MG	2B	214	1/1	0.92	0.08	82,82,82,82	0
57	MG	1a	1746	1/1	0.92	0.11	61,61,61,61	0
57	MG	1A	3372	1/1	0.92	0.12	63,63,63,63	0
57	MG	1a	1748	1/1	0.92	0.07	62,62,62,62	0
57	MG	2D	304	1/1	0.92	0.15	51,51,51,51	0
57	MG	1A	3901	1/1	0.92	0.12	33,33,33,33	0
57	MG	1A	3629	1/1	0.92	0.10	43,43,43,43	0
57	MG	2A	3115	1/1	0.92	0.11	60,60,60,60	0
57	MG	2A	3448	1/1	0.92	0.08	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3906	1/1	0.92	0.10	27,27,27,27	0
57	MG	1T	207	1/1	0.92	0.19	60,60,60,60	0
57	MG	1U	203	1/1	0.92	0.16	60,60,60,60	0
57	MG	1A	3302	1/1	0.92	0.16	61,61,61,61	0
57	MG	1W	201	1/1	0.92	0.12	42,42,42,42	0
57	MG	1a	1763	1/1	0.92	0.23	71,71,71,71	0
57	MG	2R	201	1/1	0.92	0.12	40,40,40,40	0
57	MG	1A	3443	1/1	0.92	0.11	43,43,43,43	0
57	MG	2A	3139	1/1	0.92	0.14	63,63,63,63	0
57	MG	2A	3141	1/1	0.92	0.11	49,49,49,49	0
57	MG	2V	201	1/1	0.92	0.15	66,66,66,66	0
57	MG	1A	3748	1/1	0.92	0.18	57,57,57,57	0
57	MG	2A	3464	1/1	0.92	0.20	61,61,61,61	0
57	MG	1A	3379	1/1	0.92	0.09	39,39,39,39	0
57	MG	10	103	1/1	0.92	0.10	45,45,45,45	0
57	MG	1A	3031	1/1	0.92	0.13	50,50,50,50	0
57	MG	1A	3926	1/1	0.92	0.10	57,57,57,57	0
57	MG	2a	3012	1/1	0.92	0.30	67,67,67,67	0
57	MG	1A	3934	1/1	0.92	0.16	53,53,53,53	0
57	MG	1A	3106	1/1	0.92	0.08	42,42,42,42	0
57	MG	1a	1779	1/1	0.92	0.15	56,56,56,56	0
57	MG	2A	3169	1/1	0.92	0.20	69,69,69,69	0
57	MG	2A	3170	1/1	0.92	0.27	62,62,62,62	0
57	MG	2A	3488	1/1	0.92	0.11	59,59,59,59	0
57	MG	1A	3388	1/1	0.92	0.08	21,21,21,21	0
57	MG	2A	3491	1/1	0.92	0.08	57,57,57,57	0
57	MG	1A	3389	1/1	0.92	0.05	28,28,28,28	0
57	MG	2A	3495	1/1	0.92	0.10	67,67,67,67	0
57	MG	1A	3014	1/1	0.92	0.11	49,49,49,49	0
57	MG	2A	3177	1/1	0.92	0.18	56,56,56,56	0
57	MG	2A	3179	1/1	0.92	0.19	57,57,57,57	0
57	MG	2a	3039	1/1	0.92	0.13	72,72,72,72	0
57	MG	1a	1784	1/1	0.92	0.11	60,60,60,60	0
57	MG	2A	3184	1/1	0.92	0.10	52,52,52,52	0
57	MG	1A	3544	1/1	0.92	0.08	35,35,35,35	0
57	MG	1a	1788	1/1	0.92	0.14	70,70,70,70	0
57	MG	1A	3547	1/1	0.92	0.09	44,44,44,44	0
57	MG	2a	3045	1/1	0.92	0.14	64,64,64,64	0
57	MG	2a	3046	1/1	0.92	0.20	55,55,55,55	0
57	MG	1A	3229	1/1	0.92	0.22	42,42,42,42	0
57	MG	1A	3662	1/1	0.92	0.06	14,14,14,14	0
57	MG	2a	3049	1/1	0.92	0.20	65,65,65,65	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3521	1/1	0.92	0.10	62,62,62,62	0
57	MG	1A	3777	1/1	0.92	0.12	43,43,43,43	0
57	MG	2a	3052	1/1	0.92	0.33	59,59,59,59	0
57	MG	1A	3322	1/1	0.92	0.12	46,46,46,46	0
57	MG	1A	3960	1/1	0.92	0.18	72,72,72,72	0
57	MG	1A	3962	1/1	0.92	0.09	44,44,44,44	0
57	MG	2A	3198	1/1	0.92	0.18	57,57,57,57	0
57	MG	1a	1617	1/1	0.92	0.14	55,55,55,55	0
57	MG	1a	1799	1/1	0.92	0.16	65,65,65,65	0
57	MG	2A	3544	1/1	0.92	0.13	67,67,67,67	0
57	MG	1a	1618	1/1	0.92	0.13	56,56,56,56	0
57	MG	2A	3203	1/1	0.92	0.27	67,67,67,67	0
57	MG	1a	1803	1/1	0.92	0.13	54,54,54,54	0
57	MG	1A	3967	1/1	0.92	0.13	60,60,60,60	0
57	MG	2A	3213	1/1	0.92	0.23	65,65,65,65	0
57	MG	2a	3072	1/1	0.92	0.14	71,71,71,71	0
57	MG	1a	1805	1/1	0.92	0.15	59,59,59,59	0
57	MG	1A	3785	1/1	0.92	0.09	44,44,44,44	0
57	MG	1a	1808	1/1	0.92	0.13	59,59,59,59	0
57	MG	1A	3239	1/1	0.92	0.29	60,60,60,60	0
57	MG	1A	3558	1/1	0.92	0.12	46,46,46,46	0
57	MG	1A	3327	1/1	0.92	0.14	56,56,56,56	0
57	MG	1a	1817	1/1	0.92	0.08	56,56,56,56	0
57	MG	1A	3792	1/1	0.92	0.07	52,52,52,52	0
57	MG	2A	3235	1/1	0.92	0.26	54,54,54,54	0
57	MG	2A	3237	1/1	0.92	0.15	58,58,58,58	0
57	MG	2a	3092	1/1	0.92	0.31	69,69,69,69	0
57	MG	2A	3569	1/1	0.92	0.07	58,58,58,58	0
57	MG	2a	3096	1/1	0.92	0.28	68,68,68,68	0
57	MG	1A	3136	1/1	0.92	0.11	46,46,46,46	0
57	MG	1A	3979	1/1	0.92	0.08	33,33,33,33	0
57	MG	2A	3575	1/1	0.92	0.08	35,35,35,35	0
57	MG	1A	3189	1/1	0.92	0.12	49,49,49,49	0
57	MG	1a	1641	1/1	0.92	0.14	54,54,54,54	0
57	MG	1A	3258	1/1	0.92	0.08	41,41,41,41	0
57	MG	1a	1643	1/1	0.92	0.19	59,59,59,59	0
57	MG	2a	3115	1/1	0.92	0.12	63,63,63,63	0
57	MG	2a	3118	1/1	0.92	0.13	63,63,63,63	0
57	MG	1a	1648	1/1	0.92	0.25	68,68,68,68	0
57	MG	1A	3581	1/1	0.92	0.13	55,55,55,55	0
57	MG	1a	1655	1/1	0.92	0.09	61,61,61,61	0
57	MG	2A	3253	1/1	0.92	0.13	57,57,57,57	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3599	1/1	0.92	0.08	43,43,43,43	0
57	MG	1A	3806	1/1	0.92	0.09	50,50,50,50	0
57	MG	1A	3191	1/1	0.92	0.16	59,59,59,59	0
57	MG	1A	3682	1/1	0.92	0.08	60,60,60,60	0
57	MG	1a	1669	1/1	0.92	0.14	61,61,61,61	0
57	MG	1A	3587	1/1	0.92	0.07	38,38,38,38	0
57	MG	1A	3027	1/1	0.92	0.13	64,64,64,64	0
57	MG	2a	3136	1/1	0.92	0.22	61,61,61,61	0
57	MG	2A	3615	1/1	0.92	0.07	32,32,32,32	0
57	MG	1A	4004	1/1	0.92	0.16	50,50,50,50	0
57	MG	1A	3823	1/1	0.92	0.13	65,65,65,65	0
57	MG	1A	3040	1/1	0.92	0.13	56,56,56,56	0
57	MG	2a	3149	1/1	0.92	0.09	60,60,60,60	0
57	MG	2A	3280	1/1	0.92	0.13	49,49,49,49	0
57	MG	1A	3345	1/1	0.92	0.10	43,43,43,43	0
57	MG	2A	3287	1/1	0.92	0.18	58,58,58,58	0
57	MG	1a	1860	1/1	0.92	0.12	62,62,62,62	0
57	MG	2A	3627	1/1	0.92	0.10	49,49,49,49	0
57	MG	2A	3294	1/1	0.92	0.41	65,65,65,65	0
57	MG	2a	3172	1/1	0.92	0.15	68,68,68,68	0
57	MG	2A	3295	1/1	0.92	0.22	59,59,59,59	0
57	MG	1A	3834	1/1	0.92	0.07	41,41,41,41	0
57	MG	2A	3298	1/1	0.92	0.31	56,56,56,56	0
57	MG	1A	3835	1/1	0.92	0.09	25,25,25,25	0
57	MG	2A	3639	1/1	0.92	0.06	78,78,78,78	0
57	MG	1A	3278	1/1	0.92	0.13	57,57,57,57	0
57	MG	1A	3599	1/1	0.92	0.11	59,59,59,59	0
57	MG	2A	3307	1/1	0.92	0.18	55,55,55,55	0
57	MG	1a	1690	1/1	0.92	0.24	70,70,70,70	0
57	MG	1A	3848	1/1	0.92	0.11	27,27,27,27	0
57	MG	1A	3600	1/1	0.92	0.08	31,31,31,31	0
57	MG	1A	3700	1/1	0.92	0.11	40,40,40,40	0
57	MG	1A	3426	1/1	0.92	0.07	22,22,22,22	0
57	MG	1A	3859	1/1	0.92	0.10	46,46,46,46	0
57	MG	2A	3331	1/1	0.92	0.19	66,66,66,66	0
57	MG	1A	3603	1/1	0.92	0.11	37,37,37,37	0
57	MG	2A	3341	1/1	0.92	0.15	47,47,47,47	0
57	MG	2A	3344	1/1	0.92	0.14	59,59,59,59	0
57	MG	1A	3515	1/1	0.93	0.07	59,59,59,59	0
57	MG	1A	3213	1/1	0.93	0.09	54,54,54,54	0
57	MG	1A	3455	1/1	0.93	0.11	56,56,56,56	0
57	MG	2A	3453	1/1	0.93	0.21	51,51,51,51	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1a	1822	1/1	0.93	0.09	53,53,53,53	0
57	MG	2A	3737	1/1	0.93	0.12	67,67,67,67	0
57	MG	1A	3921	1/1	0.93	0.11	61,61,61,61	0
57	MG	1a	1681	1/1	0.93	0.10	59,59,59,59	0
57	MG	1A	3034	1/1	0.93	0.17	53,53,53,53	0
57	MG	1a	1685	1/1	0.93	0.10	53,53,53,53	0
57	MG	1A	3086	1/1	0.93	0.07	35,35,35,35	0
57	MG	1A	3529	1/1	0.93	0.07	37,37,37,37	0
57	MG	1A	3609	1/1	0.93	0.11	50,50,50,50	0
57	MG	1A	3695	1/1	0.93	0.09	54,54,54,54	0
57	MG	1a	1691	1/1	0.93	0.16	64,64,64,64	0
57	MG	1a	1840	1/1	0.93	0.07	58,58,58,58	0
57	MG	2A	3474	1/1	0.93	0.06	61,61,61,61	0
57	MG	1A	3404	1/1	0.93	0.07	25,25,25,25	0
57	MG	1F	315	1/1	0.93	0.08	33,33,33,33	0
57	MG	1a	1695	1/1	0.93	0.13	55,55,55,55	0
57	MG	2A	3207	1/1	0.93	0.13	53,53,53,53	0
57	MG	1A	3614	1/1	0.93	0.12	48,48,48,48	0
57	MG	2B	210	1/1	0.93	0.23	66,66,66,66	0
57	MG	1G	203	1/1	0.93	0.08	51,51,51,51	0
57	MG	2B	212	1/1	0.93	0.17	64,64,64,64	0
57	MG	1H	202	1/1	0.93	0.07	41,41,41,41	0
57	MG	1A	3407	1/1	0.93	0.09	45,45,45,45	0
57	MG	2A	3217	1/1	0.93	0.10	60,60,60,60	0
57	MG	2A	3492	1/1	0.93	0.12	48,48,48,48	0
57	MG	2A	3493	1/1	0.93	0.10	62,62,62,62	0
57	MG	2D	303	1/1	0.93	0.16	52,52,52,52	0
57	MG	1a	1701	1/1	0.93	0.18	59,59,59,59	0
57	MG	2D	307	1/1	0.93	0.08	35,35,35,35	0
57	MG	1O	201	1/1	0.93	0.09	54,54,54,54	0
57	MG	1P	204	1/1	0.93	0.12	39,39,39,39	0
57	MG	1A	3811	1/1	0.93	0.09	29,29,29,29	0
57	MG	1a	1862	1/1	0.93	0.12	60,60,60,60	0
57	MG	2A	3504	1/1	0.93	0.10	64,64,64,64	0
57	MG	1a	1706	1/1	0.93	0.12	56,56,56,56	0
57	MG	2N	201	1/1	0.93	0.11	70,70,70,70	0
57	MG	2O	201	1/1	0.93	0.10	62,62,62,62	0
57	MG	1Q	205	1/1	0.93	0.11	54,54,54,54	0
57	MG	1a	1865	1/1	0.93	0.12	60,60,60,60	0
57	MG	1R	204	1/1	0.93	0.11	48,48,48,48	0
57	MG	1A	3045	1/1	0.93	0.17	55,55,55,55	0
57	MG	2Q	203	1/1	0.93	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
57	MG	1A	3465	1/1	0.93	0.10	49,49,49,49	0
57	MG	2R	202	1/1	0.93	0.13	55,55,55,55	0
57	MG	1d	303	1/1	0.93	0.32	55,55,55,55	0
57	MG	1a	1711	1/1	0.93	0.14	59,59,59,59	0
57	MG	1a	1714	1/1	0.93	0.44	63,63,63,63	0
57	MG	2U	201	1/1	0.93	0.24	68,68,68,68	0
57	MG	1A	3154	1/1	0.93	0.10	38,38,38,38	0
57	MG	1a	1716	1/1	0.93	0.24	63,63,63,63	0
57	MG	20	102	1/1	0.93	0.16	69,69,69,69	0
57	MG	2A	3528	1/1	0.93	0.17	67,67,67,67	0
57	MG	23	101	1/1	0.93	0.13	59,59,59,59	0
57	MG	25	101	1/1	0.93	0.38	52,52,52,52	0
57	MG	1A	3621	1/1	0.93	0.12	18,18,18,18	0
57	MG	2a	3003	1/1	0.93	0.18	64,64,64,64	0
57	MG	1A	3240	1/1	0.93	0.21	53,53,53,53	0
57	MG	2a	3006	1/1	0.93	0.17	63,63,63,63	0
57	MG	2a	3009	1/1	0.93	0.07	66,66,66,66	0
57	MG	2A	3533	1/1	0.93	0.09	67,67,67,67	0
57	MG	2A	3534	1/1	0.93	0.09	60,60,60,60	0
57	MG	2A	3535	1/1	0.93	0.08	69,69,69,69	0
57	MG	2A	3250	1/1	0.93	0.10	59,59,59,59	0
57	MG	2a	3015	1/1	0.93	0.16	51,51,51,51	0
57	MG	2A	3251	1/1	0.93	0.22	48,48,48,48	0
57	MG	2a	3019	1/1	0.93	0.19	57,57,57,57	0
57	MG	1A	3010	1/1	0.93	0.13	51,51,51,51	0
57	MG	1l	201	1/1	0.93	0.13	54,54,54,54	0
57	MG	2A	3256	1/1	0.93	0.11	53,53,53,53	0
57	MG	1a	1723	1/1	0.93	0.21	64,64,64,64	0
57	MG	1A	3963	1/1	0.93	0.08	51,51,51,51	0
57	MG	1A	3966	1/1	0.93	0.09	37,37,37,37	0
57	MG	2A	3262	1/1	0.93	0.11	52,52,52,52	0
57	MG	1A	3626	1/1	0.93	0.12	53,53,53,53	0
57	MG	2a	3033	1/1	0.93	0.20	68,68,68,68	0
57	MG	1A	3627	1/1	0.93	0.06	26,26,26,26	0
57	MG	1A	3551	1/1	0.93	0.15	33,33,33,33	0
57	MG	1A	3365	1/1	0.93	0.08	21,21,21,21	0
57	MG	1A	3197	1/1	0.93	0.12	53,53,53,53	0
57	MG	10	105	1/1	0.93	0.07	39,39,39,39	0
57	MG	2A	3025	1/1	0.93	0.11	52,52,52,52	0
57	MG	1A	3641	1/1	0.93	0.10	33,33,33,33	0
57	MG	1a	1739	1/1	0.93	0.08	58,58,58,58	0
57	MG	1A	3257	1/1	0.93	0.11	63,63,63,63	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3423	1/1	0.93	0.11	27,27,27,27	0
57	MG	2A	3573	1/1	0.93	0.09	59,59,59,59	0
57	MG	1A	3373	1/1	0.93	0.14	52,52,52,52	0
57	MG	1A	3862	1/1	0.93	0.10	48,48,48,48	0
57	MG	1A	3984	1/1	0.93	0.07	24,24,24,24	0
57	MG	2A	3580	1/1	0.93	0.07	54,54,54,54	0
57	MG	2A	3301	1/1	0.93	0.19	53,53,53,53	0
57	MG	1A	3985	1/1	0.93	0.20	48,48,48,48	0
57	MG	2A	3305	1/1	0.93	0.31	63,63,63,63	0
57	MG	2A	3586	1/1	0.93	0.10	71,71,71,71	0
57	MG	1A	3738	1/1	0.93	0.08	30,30,30,30	0
57	MG	18	103	1/1	0.93	0.18	39,39,39,39	0
57	MG	1a	1755	1/1	0.93	0.19	61,61,61,61	0
57	MG	2A	3315	1/1	0.93	0.13	58,58,58,58	0
57	MG	2A	3598	1/1	0.93	0.10	58,58,58,58	0
57	MG	2a	3064	1/1	0.93	0.24	66,66,66,66	0
57	MG	1A	3742	1/1	0.93	0.14	49,49,49,49	0
57	MG	1A	3868	1/1	0.93	0.07	40,40,40,40	0
57	MG	1a	1602	1/1	0.93	0.15	70,70,70,70	0
57	MG	2a	3069	1/1	0.93	0.08	61,61,61,61	0
57	MG	1A	3869	1/1	0.93	0.08	38,38,38,38	0
57	MG	2A	3070	1/1	0.93	0.15	56,56,56,56	0
57	MG	2A	3072	1/1	0.93	0.13	51,51,51,51	0
57	MG	2A	3334	1/1	0.93	0.09	41,41,41,41	0
57	MG	2a	3075	1/1	0.93	0.13	59,59,59,59	0
57	MG	1A	3560	1/1	0.93	0.17	71,71,71,71	0
57	MG	1A	3562	1/1	0.93	0.10	53,53,53,53	0
57	MG	1A	3996	1/1	0.93	0.09	15,15,15,15	0
57	MG	2A	3079	1/1	0.93	0.08	49,49,49,49	0
57	MG	2A	3620	1/1	0.93	0.12	70,70,70,70	0
57	MG	2A	3080	1/1	0.93	0.14	54,54,54,54	0
57	MG	2A	3350	1/1	0.93	0.13	43,43,43,43	0
57	MG	1a	1614	1/1	0.93	0.10	65,65,65,65	0
57	MG	1A	3998	1/1	0.93	0.10	43,43,43,43	0
57	MG	2A	3083	1/1	0.93	0.16	61,61,61,61	0
57	MG	1A	4003	1/1	0.93	0.07	48,48,48,48	0
57	MG	1A	3879	1/1	0.93	0.09	44,44,44,44	0
57	MG	1A	3564	1/1	0.93	0.08	49,49,49,49	0
57	MG	1A	3374	1/1	0.93	0.12	45,45,45,45	0
57	MG	2a	3100	1/1	0.93	0.30	60,60,60,60	0
57	MG	1A	3319	1/1	0.93	0.14	52,52,52,52	0
57	MG	2a	3105	1/1	0.93	0.09	76,76,76,76	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3637	1/1	0.93	0.10	59,59,59,59	0
57	MG	2A	3379	1/1	0.93	0.11	41,41,41,41	0
57	MG	2a	3111	1/1	0.93	0.09	51,51,51,51	0
57	MG	2A	3382	1/1	0.93	0.07	43,43,43,43	0
57	MG	1A	3576	1/1	0.93	0.07	50,50,50,50	0
57	MG	2a	3114	1/1	0.93	0.11	68,68,68,68	0
57	MG	2A	3101	1/1	0.93	0.12	51,51,51,51	0
57	MG	1A	3661	1/1	0.93	0.09	46,46,46,46	0
57	MG	2A	3649	1/1	0.93	0.12	71,71,71,71	0
57	MG	1A	3101	1/1	0.93	0.15	37,37,37,37	0
57	MG	2A	3653	1/1	0.93	0.07	52,52,52,52	0
57	MG	2A	3657	1/1	0.93	0.11	55,55,55,55	0
57	MG	2a	3123	1/1	0.93	0.10	64,64,64,64	0
57	MG	2A	3388	1/1	0.93	0.07	43,43,43,43	0
57	MG	2A	3118	1/1	0.93	0.12	48,48,48,48	0
57	MG	2A	3119	1/1	0.93	0.14	55,55,55,55	0
57	MG	1a	1783	1/1	0.93	0.10	45,45,45,45	0
57	MG	2A	3122	1/1	0.93	0.12	50,50,50,50	0
57	MG	2A	3123	1/1	0.93	0.11	83,83,83,83	0
57	MG	2A	3402	1/1	0.93	0.09	50,50,50,50	0
57	MG	2a	3135	1/1	0.93	0.21	66,66,66,66	0
57	MG	1a	1634	1/1	0.93	0.17	58,58,58,58	0
57	MG	1a	1635	1/1	0.93	0.29	56,56,56,56	0
57	MG	2A	3406	1/1	0.93	0.07	32,32,32,32	0
57	MG	2a	3142	1/1	0.93	0.07	62,62,62,62	0
57	MG	2A	3681	1/1	0.93	0.10	56,56,56,56	0
57	MG	2A	3129	1/1	0.93	0.21	41,41,41,41	0
57	MG	1A	4016	1/1	0.93	0.10	42,42,42,42	0
57	MG	1A	3070	1/1	0.93	0.06	37,37,37,37	0
57	MG	2A	3690	1/1	0.93	0.09	65,65,65,65	0
57	MG	2a	3158	1/1	0.93	0.11	62,62,62,62	0
57	MG	1a	1790	1/1	0.93	0.15	67,67,67,67	0
57	MG	2a	3161	1/1	0.93	0.09	66,66,66,66	0
57	MG	1A	3268	1/1	0.93	0.11	45,45,45,45	0
57	MG	1a	1640	1/1	0.93	0.17	68,68,68,68	0
57	MG	1A	3038	1/1	0.93	0.07	37,37,37,37	0
57	MG	2a	3171	1/1	0.93	0.16	66,66,66,66	0
57	MG	1A	3273	1/1	0.93	0.07	55,55,55,55	0
57	MG	1B	205	1/1	0.93	0.07	47,47,47,47	0
57	MG	2A	3421	1/1	0.93	0.10	42,42,42,42	0
57	MG	2A	3704	1/1	0.93	0.10	34,34,34,34	0
57	MG	2A	3705	1/1	0.93	0.11	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3898	1/1	0.93	0.10	64,64,64,64	0
57	MG	1A	3180	1/1	0.93	0.22	49,49,49,49	0
57	MG	2a	3187	1/1	0.93	0.20	55,55,55,55	0
57	MG	2A	3154	1/1	0.93	0.13	56,56,56,56	0
57	MG	1A	3902	1/1	0.93	0.07	18,18,18,18	0
57	MG	2a	3190	1/1	0.93	0.14	67,67,67,67	0
57	MG	1a	1657	1/1	0.93	0.14	57,57,57,57	0
57	MG	2f	201	1/1	0.93	0.17	60,60,60,60	0
57	MG	1B	210	1/1	0.93	0.10	53,53,53,53	0
57	MG	1A	3211	1/1	0.93	0.28	68,68,68,68	0
57	MG	1B	215	1/1	0.93	0.11	54,54,54,54	0
57	MG	1a	1667	1/1	0.93	0.29	62,62,62,62	0
57	MG	2A	3442	1/1	0.93	0.06	38,38,38,38	0
57	MG	1A	3597	1/1	0.93	0.10	33,33,33,33	0
57	MG	1A	3448	1/1	0.93	0.14	54,54,54,54	0
57	MG	2A	3175	1/1	0.93	0.21	49,49,49,49	0
57	MG	1B	219	1/1	0.93	0.08	44,44,44,44	0
57	MG	2A	3167	1/1	0.94	0.25	64,64,64,64	0
57	MG	1a	1810	1/1	0.94	0.10	54,54,54,54	0
57	MG	2A	3450	1/1	0.94	0.12	61,61,61,61	0
57	MG	1A	3376	1/1	0.94	0.09	38,38,38,38	0
57	MG	1a	1670	1/1	0.94	0.19	53,53,53,53	0
57	MG	1a	1815	1/1	0.94	0.08	54,54,54,54	0
57	MG	1a	1816	1/1	0.94	0.09	64,64,64,64	0
57	MG	2A	3174	1/1	0.94	0.07	59,59,59,59	0
57	MG	1A	3501	1/1	0.94	0.08	55,55,55,55	0
57	MG	1B	220	1/1	0.94	0.07	30,30,30,30	0
57	MG	1A	3030	1/1	0.94	0.06	34,34,34,34	0
57	MG	2A	3461	1/1	0.94	0.11	62,62,62,62	0
57	MG	1A	3765	1/1	0.94	0.10	56,56,56,56	0
57	MG	1a	1824	1/1	0.94	0.10	67,67,67,67	0
57	MG	1B	228	1/1	0.94	0.16	70,70,70,70	0
57	MG	2A	3465	1/1	0.94	0.07	37,37,37,37	0
57	MG	1a	1826	1/1	0.94	0.12	52,52,52,52	0
57	MG	1A	3586	1/1	0.94	0.15	56,56,56,56	0
57	MG	2A	3469	1/1	0.94	0.06	58,58,58,58	0
57	MG	1a	1680	1/1	0.94	0.10	56,56,56,56	0
57	MG	2A	3473	1/1	0.94	0.15	59,59,59,59	0
57	MG	1A	3904	1/1	0.94	0.06	28,28,28,28	0
57	MG	1a	1830	1/1	0.94	0.15	62,62,62,62	0
57	MG	1a	1831	1/1	0.94	0.09	57,57,57,57	0
57	MG	2A	3478	1/1	0.94	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
57	MG	1A	3108	1/1	0.94	0.06	58,58,58,58	0
57	MG	1a	1833	1/1	0.94	0.09	59,59,59,59	0
57	MG	1A	3909	1/1	0.94	0.15	44,44,44,44	0
57	MG	2D	306	1/1	0.94	0.20	44,44,44,44	0
57	MG	2A	3483	1/1	0.94	0.17	53,53,53,53	0
57	MG	2A	3484	1/1	0.94	0.07	39,39,39,39	0
57	MG	1A	3770	1/1	0.94	0.06	25,25,25,25	0
57	MG	2F	301	1/1	0.94	0.21	41,41,41,41	0
57	MG	1A	3121	1/1	0.94	0.09	39,39,39,39	0
57	MG	1A	3774	1/1	0.94	0.08	43,43,43,43	0
57	MG	1A	3590	1/1	0.94	0.06	53,53,53,53	0
57	MG	2A	3206	1/1	0.94	0.09	46,46,46,46	0
57	MG	1A	3442	1/1	0.94	0.10	50,50,50,50	0
57	MG	1a	1844	1/1	0.94	0.08	57,57,57,57	0
57	MG	1F	317	1/1	0.94	0.18	47,47,47,47	0
57	MG	2P	201	1/1	0.94	0.11	57,57,57,57	0
57	MG	1A	3923	1/1	0.94	0.06	59,59,59,59	0
57	MG	1A	3384	1/1	0.94	0.12	53,53,53,53	0
57	MG	1G	204	1/1	0.94	0.10	41,41,41,41	0
57	MG	2A	3503	1/1	0.94	0.08	31,31,31,31	0
57	MG	2A	3220	1/1	0.94	0.07	46,46,46,46	0
57	MG	1A	3329	1/1	0.94	0.13	37,37,37,37	0
57	MG	1A	3064	1/1	0.94	0.09	45,45,45,45	0
57	MG	1A	3272	1/1	0.94	0.08	53,53,53,53	0
57	MG	2A	3512	1/1	0.94	0.12	25,25,25,25	0
57	MG	1A	3520	1/1	0.94	0.07	23,23,23,23	0
57	MG	2A	3516	1/1	0.94	0.14	56,56,56,56	0
57	MG	1A	3939	1/1	0.94	0.09	42,42,42,42	0
57	MG	1Q	202	1/1	0.94	0.08	31,31,31,31	0
57	MG	2A	3230	1/1	0.94	0.16	43,43,43,43	0
57	MG	2A	3232	1/1	0.94	0.07	48,48,48,48	0
57	MG	1Q	204	1/1	0.94	0.07	35,35,35,35	0
57	MG	25	102	1/1	0.94	0.15	45,45,45,45	0
57	MG	28	3800	1/1	0.94	0.09	55,55,55,55	0
57	MG	1A	3941	1/1	0.94	0.11	45,45,45,45	0
57	MG	1A	3791	1/1	0.94	0.07	29,29,29,29	0
57	MG	1A	3680	1/1	0.94	0.15	62,62,62,62	0
57	MG	1A	3601	1/1	0.94	0.08	40,40,40,40	0
57	MG	2a	3007	1/1	0.94	0.10	53,53,53,53	0
57	MG	2a	3008	1/1	0.94	0.15	53,53,53,53	0
57	MG	1d	301	1/1	0.94	0.11	65,65,65,65	0
57	MG	1A	3521	1/1	0.94	0.19	37,37,37,37	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3333	1/1	0.94	0.12	45,45,45,45	0
57	MG	1a	1712	1/1	0.94	0.36	55,55,55,55	0
57	MG	1a	1713	1/1	0.94	0.28	54,54,54,54	0
57	MG	1A	3799	1/1	0.94	0.07	31,31,31,31	0
57	MG	1f	201	1/1	0.94	0.33	74,74,74,74	0
57	MG	1A	3953	1/1	0.94	0.08	56,56,56,56	0
57	MG	2a	3020	1/1	0.94	0.23	67,67,67,67	0
57	MG	1U	201	1/1	0.94	0.20	47,47,47,47	0
57	MG	1A	3337	1/1	0.94	0.10	13,13,13,13	0
57	MG	1a	1718	1/1	0.94	0.34	62,62,62,62	0
57	MG	1V	204	1/1	0.94	0.09	47,47,47,47	0
57	MG	1l	202	1/1	0.94	0.10	67,67,67,67	0
57	MG	1A	3688	1/1	0.94	0.08	46,46,46,46	0
57	MG	1A	3168	1/1	0.94	0.10	47,47,47,47	0
57	MG	2a	3030	1/1	0.94	0.13	58,58,58,58	0
57	MG	1n	103	1/1	0.94	0.18	62,62,62,62	0
57	MG	1t	3101	1/1	0.94	0.10	50,50,50,50	0
57	MG	1A	3460	1/1	0.94	0.06	16,16,16,16	0
57	MG	2A	3557	1/1	0.94	0.09	62,62,62,62	0
57	MG	2A	3268	1/1	0.94	0.14	54,54,54,54	0
57	MG	1A	3174	1/1	0.94	0.13	50,50,50,50	0
57	MG	1A	3693	1/1	0.94	0.09	37,37,37,37	0
57	MG	2A	3566	1/1	0.94	0.07	61,61,61,61	0
57	MG	2A	3278	1/1	0.94	0.29	50,50,50,50	0
57	MG	1A	3534	1/1	0.94	0.11	48,48,48,48	0
57	MG	2A	3002	1/1	0.94	0.10	50,50,50,50	0
57	MG	1A	3818	1/1	0.94	0.08	23,23,23,23	0
57	MG	1A	3123	1/1	0.94	0.27	59,59,59,59	0
57	MG	2A	3291	1/1	0.94	0.11	51,51,51,51	0
57	MG	2A	3022	1/1	0.94	0.26	49,49,49,49	0
57	MG	2A	3023	1/1	0.94	0.20	58,58,58,58	0
57	MG	1A	3824	1/1	0.94	0.06	12,12,12,12	0
57	MG	2A	3582	1/1	0.94	0.11	57,57,57,57	0
57	MG	1A	3182	1/1	0.94	0.20	39,39,39,39	0
57	MG	2A	3027	1/1	0.94	0.11	60,60,60,60	0
57	MG	1a	1737	1/1	0.94	0.14	57,57,57,57	0
57	MG	1A	3830	1/1	0.94	0.13	47,47,47,47	0
57	MG	2A	3037	1/1	0.94	0.24	66,66,66,66	0
57	MG	2A	3591	1/1	0.94	0.07	50,50,50,50	0
57	MG	1A	3831	1/1	0.94	0.12	48,48,48,48	0
57	MG	1a	1740	1/1	0.94	0.12	62,62,62,62	0
57	MG	1A	3227	1/1	0.94	0.12	38,38,38,38	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3618	1/1	0.94	0.07	26,26,26,26	0
57	MG	1A	3125	1/1	0.94	0.14	51,51,51,51	0
57	MG	2A	3052	1/1	0.94	0.08	41,41,41,41	0
57	MG	1A	3620	1/1	0.94	0.06	41,41,41,41	0
57	MG	1A	3841	1/1	0.94	0.15	55,55,55,55	0
57	MG	19	103	1/1	0.94	0.08	54,54,54,54	0
57	MG	2A	3327	1/1	0.94	0.12	58,58,58,58	0
57	MG	2A	3059	1/1	0.94	0.22	50,50,50,50	0
57	MG	1A	3238	1/1	0.94	0.11	63,63,63,63	0
57	MG	1A	3844	1/1	0.94	0.11	42,42,42,42	0
57	MG	2A	3063	1/1	0.94	0.13	47,47,47,47	0
57	MG	2a	3079	1/1	0.94	0.12	47,47,47,47	0
57	MG	1A	3622	1/1	0.94	0.08	26,26,26,26	0
57	MG	2a	3081	1/1	0.94	0.34	56,56,56,56	0
57	MG	1a	1605	1/1	0.94	0.10	52,52,52,52	0
57	MG	2A	3623	1/1	0.94	0.07	39,39,39,39	0
57	MG	2A	3066	1/1	0.94	0.10	50,50,50,50	0
57	MG	2a	3087	1/1	0.94	0.23	59,59,59,59	0
57	MG	2A	3347	1/1	0.94	0.10	35,35,35,35	0
57	MG	1A	3850	1/1	0.94	0.12	51,51,51,51	0
57	MG	2A	3068	1/1	0.94	0.10	48,48,48,48	0
57	MG	2A	3355	1/1	0.94	0.07	52,52,52,52	0
57	MG	2A	3630	1/1	0.94	0.10	61,61,61,61	0
57	MG	2A	3356	1/1	0.94	0.11	38,38,38,38	0
57	MG	2A	3632	1/1	0.94	0.12	57,57,57,57	0
57	MG	1A	3357	1/1	0.94	0.07	26,26,26,26	0
57	MG	2a	3099	1/1	0.94	0.32	51,51,51,51	0
57	MG	1A	3710	1/1	0.94	0.07	49,49,49,49	0
57	MG	2A	3360	1/1	0.94	0.11	55,55,55,55	0
57	MG	2A	3361	1/1	0.94	0.08	45,45,45,45	0
57	MG	2A	3362	1/1	0.94	0.07	46,46,46,46	0
57	MG	2a	3108	1/1	0.94	0.41	63,63,63,63	0
57	MG	1A	3473	1/1	0.94	0.08	39,39,39,39	0
57	MG	1a	1764	1/1	0.94	0.07	49,49,49,49	0
57	MG	1a	1766	1/1	0.94	0.07	55,55,55,55	0
57	MG	1a	1615	1/1	0.94	0.14	61,61,61,61	0
57	MG	2A	3647	1/1	0.94	0.09	54,54,54,54	0
57	MG	2A	3370	1/1	0.94	0.09	33,33,33,33	0
57	MG	1A	3997	1/1	0.94	0.09	50,50,50,50	0
57	MG	1A	3358	1/1	0.94	0.06	20,20,20,20	0
57	MG	1a	1771	1/1	0.94	0.11	55,55,55,55	0
57	MG	2A	3380	1/1	0.94	0.12	73,73,73,73	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3999	1/1	0.94	0.10	63,63,63,63	0
57	MG	1a	1773	1/1	0.94	0.18	58,58,58,58	0
57	MG	1A	4002	1/1	0.94	0.07	24,24,24,24	0
57	MG	1A	3128	1/1	0.94	0.09	36,36,36,36	0
57	MG	2A	3668	1/1	0.94	0.08	54,54,54,54	0
57	MG	1A	3479	1/1	0.94	0.08	27,27,27,27	0
57	MG	1a	1777	1/1	0.94	0.20	55,55,55,55	0
57	MG	1A	3719	1/1	0.94	0.26	33,33,33,33	0
57	MG	1A	3865	1/1	0.94	0.09	35,35,35,35	0
57	MG	2A	3104	1/1	0.94	0.17	53,53,53,53	0
57	MG	2A	3111	1/1	0.94	0.15	53,53,53,53	0
57	MG	2A	3397	1/1	0.94	0.19	66,66,66,66	0
57	MG	1A	3632	1/1	0.94	0.08	21,21,21,21	0
57	MG	2a	3139	1/1	0.94	0.08	56,56,56,56	0
57	MG	2a	3141	1/1	0.94	0.13	63,63,63,63	0
57	MG	2A	3688	1/1	0.94	0.08	50,50,50,50	0
57	MG	1a	1632	1/1	0.94	0.08	42,42,42,42	0
57	MG	1a	1633	1/1	0.94	0.14	48,48,48,48	0
57	MG	1A	3047	1/1	0.94	0.15	43,43,43,43	0
57	MG	2A	3405	1/1	0.94	0.09	58,58,58,58	0
57	MG	1A	3728	1/1	0.94	0.09	43,43,43,43	0
57	MG	2a	3157	1/1	0.94	0.10	50,50,50,50	0
57	MG	1A	3094	1/1	0.94	0.11	44,44,44,44	0
57	MG	1A	3871	1/1	0.94	0.08	26,26,26,26	0
57	MG	1A	3640	1/1	0.94	0.09	29,29,29,29	0
57	MG	1A	3875	1/1	0.94	0.08	51,51,51,51	0
57	MG	1A	3255	1/1	0.94	0.08	43,43,43,43	0
57	MG	1A	3563	1/1	0.94	0.08	60,60,60,60	0
57	MG	2A	3706	1/1	0.94	0.09	56,56,56,56	0
57	MG	2A	3707	1/1	0.94	0.08	51,51,51,51	0
57	MG	2a	3174	1/1	0.94	0.09	64,64,64,64	0
57	MG	2a	3176	1/1	0.94	0.10	73,73,73,73	0
57	MG	1A	3370	1/1	0.94	0.07	24,24,24,24	0
57	MG	1A	3566	1/1	0.94	0.16	47,47,47,47	0
57	MG	2A	3711	1/1	0.94	0.09	46,46,46,46	0
57	MG	2A	3135	1/1	0.94	0.14	54,54,54,54	0
57	MG	2A	3137	1/1	0.94	0.10	51,51,51,51	0
57	MG	1A	3646	1/1	0.94	0.13	34,34,34,34	0
57	MG	1a	1654	1/1	0.94	0.09	56,56,56,56	0
57	MG	1A	3071	1/1	0.94	0.08	32,32,32,32	0
57	MG	2A	3144	1/1	0.94	0.11	51,51,51,51	0
57	MG	2A	3145	1/1	0.94	0.10	62,62,62,62	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3721	1/1	0.94	0.14	57,57,57,57	0
57	MG	1a	1656	1/1	0.94	0.23	51,51,51,51	0
57	MG	1A	3650	1/1	0.94	0.08	47,47,47,47	0
57	MG	1A	3752	1/1	0.94	0.17	42,42,42,42	0
57	MG	2r	101	1/1	0.94	0.13	74,74,74,74	0
57	MG	1B	212	1/1	0.94	0.06	51,51,51,51	0
57	MG	2A	3729	1/1	0.94	0.10	52,52,52,52	0
59	ARG	1B	231	12/12	0.94	0.10	29,39,47,50	0
57	MG	2A	3437	1/1	0.94	0.07	43,43,43,43	0
57	MG	1A	3316	1/1	0.94	0.10	45,45,45,45	0
60	MPD	18	104	8/8	0.94	0.13	30,35,42,46	0
57	MG	1a	1663	1/1	0.94	0.21	53,53,53,53	0
57	MG	1a	1665	1/1	0.94	0.14	50,50,50,50	0
57	MG	1A	3056	1/1	0.94	0.11	48,48,48,48	0
61	ZN	24	501	1/1	0.94	0.14	120,120,120,120	0
57	MG	1A	3368	1/1	0.95	0.10	37,37,37,37	0
57	MG	1A	3082	1/1	0.95	0.24	35,35,35,35	0
57	MG	2A	3389	1/1	0.95	0.11	32,32,32,32	0
57	MG	1A	3228	1/1	0.95	0.07	39,39,39,39	0
57	MG	1U	206	1/1	0.95	0.21	36,36,36,36	0
57	MG	2A	3712	1/1	0.95	0.07	51,51,51,51	0
57	MG	1A	3450	1/1	0.95	0.11	45,45,45,45	0
57	MG	1A	3927	1/1	0.95	0.08	35,35,35,35	0
57	MG	1A	3928	1/1	0.95	0.07	56,56,56,56	0
57	MG	2A	3084	1/1	0.95	0.08	46,46,46,46	0
57	MG	1W	202	1/1	0.95	0.07	41,41,41,41	0
57	MG	1A	3929	1/1	0.95	0.08	54,54,54,54	0
57	MG	1A	3931	1/1	0.95	0.10	45,45,45,45	0
57	MG	2A	3093	1/1	0.95	0.10	45,45,45,45	0
57	MG	1a	1758	1/1	0.95	0.18	59,59,59,59	0
57	MG	2A	3097	1/1	0.95	0.15	47,47,47,47	0
57	MG	2A	3409	1/1	0.95	0.07	48,48,48,48	0
57	MG	1A	3649	1/1	0.95	0.06	35,35,35,35	0
57	MG	10	102	1/1	0.95	0.15	36,36,36,36	0
57	MG	1A	3452	1/1	0.95	0.06	25,25,25,25	0
57	MG	1A	3454	1/1	0.95	0.08	51,51,51,51	0
57	MG	2A	3106	1/1	0.95	0.26	57,57,57,57	0
57	MG	2A	3417	1/1	0.95	0.07	50,50,50,50	0
57	MG	2A	3107	1/1	0.95	0.09	64,64,64,64	0
57	MG	1A	3305	1/1	0.95	0.32	40,40,40,40	0
57	MG	1A	3002	1/1	0.95	0.13	57,57,57,57	0
57	MG	10	108	1/1	0.95	0.08	54,54,54,54	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3117	1/1	0.95	0.18	49,49,49,49	0
57	MG	11	101	1/1	0.95	0.11	39,39,39,39	0
57	MG	1A	3308	1/1	0.95	0.07	38,38,38,38	0
57	MG	1A	3786	1/1	0.95	0.08	45,45,45,45	0
57	MG	1A	3657	1/1	0.95	0.20	47,47,47,47	0
57	MG	2A	3428	1/1	0.95	0.06	41,41,41,41	0
57	MG	2A	3745	1/1	0.95	0.30	59,59,59,59	0
57	MG	2A	3429	1/1	0.95	0.06	34,34,34,34	0
57	MG	1A	3176	1/1	0.95	0.10	52,52,52,52	0
57	MG	15	107	1/1	0.95	0.10	66,66,66,66	0
57	MG	1A	3315	1/1	0.95	0.17	36,36,36,36	0
57	MG	1A	3380	1/1	0.95	0.07	47,47,47,47	0
57	MG	1A	3567	1/1	0.95	0.06	46,46,46,46	0
57	MG	2A	3438	1/1	0.95	0.18	64,64,64,64	0
57	MG	2A	3440	1/1	0.95	0.14	66,66,66,66	0
57	MG	1A	3041	1/1	0.95	0.12	47,47,47,47	0
57	MG	2A	3443	1/1	0.95	0.11	48,48,48,48	0
57	MG	2A	3133	1/1	0.95	0.13	43,43,43,43	0
57	MG	1A	3957	1/1	0.95	0.11	51,51,51,51	0
57	MG	1A	3794	1/1	0.95	0.07	58,58,58,58	0
57	MG	1A	3666	1/1	0.95	0.07	48,48,48,48	0
57	MG	1A	3065	1/1	0.95	0.17	52,52,52,52	0
57	MG	2A	3140	1/1	0.95	0.28	61,61,61,61	0
57	MG	1a	1604	1/1	0.95	0.15	55,55,55,55	0
57	MG	1A	3797	1/1	0.95	0.07	74,74,74,74	0
57	MG	1A	3798	1/1	0.95	0.07	42,42,42,42	0
57	MG	1A	3669	1/1	0.95	0.06	50,50,50,50	0
57	MG	2A	3455	1/1	0.95	0.07	41,41,41,41	0
57	MG	2D	308	1/1	0.95	0.20	54,54,54,54	0
57	MG	1a	1610	1/1	0.95	0.22	52,52,52,52	0
57	MG	1A	3968	1/1	0.95	0.09	52,52,52,52	0
57	MG	1A	3573	1/1	0.95	0.11	46,46,46,46	0
57	MG	2F	303	1/1	0.95	0.12	52,52,52,52	0
57	MG	2A	3459	1/1	0.95	0.08	36,36,36,36	0
57	MG	1A	3970	1/1	0.95	0.07	22,22,22,22	0
57	MG	1A	3802	1/1	0.95	0.08	33,33,33,33	0
57	MG	2A	3156	1/1	0.95	0.08	69,69,69,69	0
57	MG	2A	3157	1/1	0.95	0.13	44,44,44,44	0
57	MG	1A	3805	1/1	0.95	0.06	44,44,44,44	0
57	MG	2A	3162	1/1	0.95	0.09	50,50,50,50	0
57	MG	1a	1796	1/1	0.95	0.13	58,58,58,58	0
57	MG	1A	3127	1/1	0.95	0.07	49,49,49,49	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3807	1/1	0.95	0.24	47,47,47,47	0
57	MG	1A	3577	1/1	0.95	0.09	22,22,22,22	0
57	MG	1a	1624	1/1	0.95	0.21	58,58,58,58	0
57	MG	1a	1801	1/1	0.95	0.09	55,55,55,55	0
57	MG	1a	1802	1/1	0.95	0.07	57,57,57,57	0
57	MG	1A	3066	1/1	0.95	0.09	33,33,33,33	0
57	MG	2T	202	1/1	0.95	0.09	60,60,60,60	0
57	MG	1A	3325	1/1	0.95	0.08	30,30,30,30	0
57	MG	1A	3981	1/1	0.95	0.10	43,43,43,43	0
57	MG	1a	1630	1/1	0.95	0.08	41,41,41,41	0
57	MG	2A	3178	1/1	0.95	0.09	52,52,52,52	0
57	MG	2V	203	1/1	0.95	0.15	62,62,62,62	0
57	MG	2W	201	1/1	0.95	0.24	49,49,49,49	0
57	MG	1A	3677	1/1	0.95	0.09	62,62,62,62	0
57	MG	1A	3678	1/1	0.95	0.07	37,37,37,37	0
57	MG	1A	3326	1/1	0.95	0.11	34,34,34,34	0
57	MG	2A	3487	1/1	0.95	0.07	66,66,66,66	0
57	MG	1a	1811	1/1	0.95	0.13	60,60,60,60	0
57	MG	1A	3820	1/1	0.95	0.09	36,36,36,36	0
57	MG	1A	3822	1/1	0.95	0.17	29,29,29,29	0
57	MG	2A	3191	1/1	0.95	0.13	44,44,44,44	0
57	MG	1A	3583	1/1	0.95	0.15	45,45,45,45	0
57	MG	1A	3584	1/1	0.95	0.12	51,51,51,51	0
57	MG	1A	3391	1/1	0.95	0.07	43,43,43,43	0
57	MG	2A	3496	1/1	0.95	0.11	53,53,53,53	0
57	MG	1A	3828	1/1	0.95	0.08	47,47,47,47	0
57	MG	1A	3392	1/1	0.95	0.06	30,30,30,30	0
57	MG	1A	3685	1/1	0.95	0.13	20,20,20,20	0
57	MG	1A	3478	1/1	0.95	0.07	28,28,28,28	0
57	MG	2A	3199	1/1	0.95	0.17	50,50,50,50	0
57	MG	2a	3013	1/1	0.95	0.09	50,50,50,50	0
57	MG	1a	1644	1/1	0.95	0.24	56,56,56,56	0
57	MG	1a	1646	1/1	0.95	0.14	41,41,41,41	0
57	MG	1A	3129	1/1	0.95	0.15	41,41,41,41	0
57	MG	1a	1649	1/1	0.95	0.14	63,63,63,63	0
57	MG	2A	3513	1/1	0.95	0.07	35,35,35,35	0
57	MG	2a	3021	1/1	0.95	0.10	53,53,53,53	0
57	MG	2A	3204	1/1	0.95	0.11	52,52,52,52	0
57	MG	1A	3395	1/1	0.95	0.10	24,24,24,24	0
57	MG	1a	1652	1/1	0.95	0.15	51,51,51,51	0
57	MG	1a	1653	1/1	0.95	0.11	36,36,36,36	0
57	MG	1A	3593	1/1	0.95	0.07	19,19,19,19	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3211	1/1	0.95	0.09	42,42,42,42	0
57	MG	2A	3212	1/1	0.95	0.09	57,57,57,57	0
57	MG	1A	3594	1/1	0.95	0.09	48,48,48,48	0
57	MG	2a	3031	1/1	0.95	0.13	55,55,55,55	0
57	MG	1A	3328	1/1	0.95	0.10	47,47,47,47	0
57	MG	2A	3215	1/1	0.95	0.22	57,57,57,57	0
57	MG	2A	3216	1/1	0.95	0.14	55,55,55,55	0
57	MG	1A	3190	1/1	0.95	0.10	43,43,43,43	0
57	MG	2A	3532	1/1	0.95	0.10	62,62,62,62	0
57	MG	2a	3038	1/1	0.95	0.08	63,63,63,63	0
57	MG	2A	3219	1/1	0.95	0.14	62,62,62,62	0
57	MG	1a	1658	1/1	0.95	0.09	60,60,60,60	0
57	MG	1a	1659	1/1	0.95	0.12	54,54,54,54	0
57	MG	2A	3536	1/1	0.95	0.07	52,52,52,52	0
57	MG	1A	3847	1/1	0.95	0.10	46,46,46,46	0
57	MG	1A	3398	1/1	0.95	0.06	33,33,33,33	0
57	MG	2A	3224	1/1	0.95	0.13	44,44,44,44	0
57	MG	1a	1843	1/1	0.95	0.15	49,49,49,49	0
57	MG	1A	3849	1/1	0.95	0.10	53,53,53,53	0
57	MG	1a	1845	1/1	0.95	0.14	62,62,62,62	0
57	MG	1A	3130	1/1	0.95	0.28	37,37,37,37	0
57	MG	1a	1848	1/1	0.95	0.07	35,35,35,35	0
57	MG	1A	3488	1/1	0.95	0.09	25,25,25,25	0
57	MG	1A	3702	1/1	0.95	0.14	43,43,43,43	0
57	MG	1a	1854	1/1	0.95	0.16	60,60,60,60	0
57	MG	1a	1668	1/1	0.95	0.13	52,52,52,52	0
57	MG	2a	3057	1/1	0.95	0.20	63,63,63,63	0
57	MG	2A	3554	1/1	0.95	0.08	51,51,51,51	0
57	MG	1A	3854	1/1	0.95	0.09	24,24,24,24	0
57	MG	1A	3491	1/1	0.95	0.07	63,63,63,63	0
57	MG	1A	3858	1/1	0.95	0.06	53,53,53,53	0
57	MG	1A	3331	1/1	0.95	0.07	23,23,23,23	0
57	MG	1A	3497	1/1	0.95	0.10	26,26,26,26	0
57	MG	2A	3561	1/1	0.95	0.07	44,44,44,44	0
57	MG	1A	3707	1/1	0.95	0.05	44,44,44,44	0
57	MG	1a	1676	1/1	0.95	0.11	46,46,46,46	0
57	MG	1A	3406	1/1	0.95	0.17	58,58,58,58	0
57	MG	1A	3864	1/1	0.95	0.07	28,28,28,28	0
57	MG	2A	3571	1/1	0.95	0.07	76,76,76,76	0
57	MG	1A	3192	1/1	0.95	0.09	59,59,59,59	0
57	MG	1A	3028	1/1	0.95	0.22	28,28,28,28	0
57	MG	1A	3711	1/1	0.95	0.08	27,27,27,27	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3096	1/1	0.95	0.11	33,33,33,33	0
57	MG	2A	3576	1/1	0.95	0.07	24,24,24,24	0
57	MG	1A	3270	1/1	0.95	0.09	44,44,44,44	0
57	MG	1A	3097	1/1	0.95	0.13	53,53,53,53	0
57	MG	1A	3148	1/1	0.95	0.12	47,47,47,47	0
57	MG	1A	3873	1/1	0.95	0.11	29,29,29,29	0
57	MG	2A	3263	1/1	0.95	0.24	58,58,58,58	0
57	MG	1B	226	1/1	0.95	0.08	32,32,32,32	0
57	MG	1a	1692	1/1	0.95	0.22	55,55,55,55	0
57	MG	1A	3020	1/1	0.95	0.26	30,30,30,30	0
57	MG	1A	3876	1/1	0.95	0.10	40,40,40,40	0
57	MG	2A	3272	1/1	0.95	0.15	30,30,30,30	0
57	MG	1A	3421	1/1	0.95	0.04	29,29,29,29	0
57	MG	1i	201	1/1	0.95	0.11	54,54,54,54	0
57	MG	2a	3095	1/1	0.95	0.07	53,53,53,53	0
57	MG	2A	3596	1/1	0.95	0.12	50,50,50,50	0
57	MG	1a	1696	1/1	0.95	0.37	57,57,57,57	0
57	MG	1A	3074	1/1	0.95	0.13	41,41,41,41	0
57	MG	1A	3022	1/1	0.95	0.10	38,38,38,38	0
57	MG	2A	3286	1/1	0.95	0.14	53,53,53,53	0
57	MG	2a	3101	1/1	0.95	0.42	62,62,62,62	0
57	MG	2a	3103	1/1	0.95	0.19	54,54,54,54	0
57	MG	1A	3349	1/1	0.95	0.10	25,25,25,25	0
57	MG	1A	3350	1/1	0.95	0.09	53,53,53,53	0
57	MG	2a	3106	1/1	0.95	0.17	64,64,64,64	0
57	MG	2A	3609	1/1	0.95	0.07	46,46,46,46	0
57	MG	1o	102	1/1	0.95	0.17	54,54,54,54	0
57	MG	2A	3293	1/1	0.95	0.25	52,52,52,52	0
57	MG	1D	319	1/1	0.95	0.07	61,61,61,61	0
57	MG	1A	3429	1/1	0.95	0.05	13,13,13,13	0
57	MG	1a	1703	1/1	0.95	0.38	62,62,62,62	0
57	MG	1A	3353	1/1	0.95	0.06	30,30,30,30	0
57	MG	1x	101	1/1	0.95	0.09	33,33,33,33	0
57	MG	2a	3116	1/1	0.95	0.07	49,49,49,49	0
57	MG	2a	3117	1/1	0.95	0.10	55,55,55,55	0
57	MG	1A	3740	1/1	0.95	0.06	24,24,24,24	0
57	MG	2A	3622	1/1	0.95	0.07	52,52,52,52	0
57	MG	1E	308	1/1	0.95	0.08	36,36,36,36	0
57	MG	1F	311	1/1	0.95	0.20	38,38,38,38	0
57	MG	2A	3008	1/1	0.95	0.07	37,37,37,37	0
57	MG	2A	3010	1/1	0.95	0.14	58,58,58,58	0
57	MG	1F	312	1/1	0.95	0.10	49,49,49,49	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3309	1/1	0.95	0.25	58,58,58,58	0
57	MG	2A	3017	1/1	0.95	0.12	56,56,56,56	0
57	MG	2a	3128	1/1	0.95	0.10	48,48,48,48	0
57	MG	2A	3019	1/1	0.95	0.28	49,49,49,49	0
57	MG	2a	3130	1/1	0.95	0.13	61,61,61,61	0
57	MG	1F	314	1/1	0.95	0.32	42,42,42,42	0
57	MG	1A	3113	1/1	0.95	0.14	37,37,37,37	0
57	MG	2A	3320	1/1	0.95	0.15	50,50,50,50	0
57	MG	1A	3114	1/1	0.95	0.19	31,31,31,31	0
57	MG	2A	3326	1/1	0.95	0.05	36,36,36,36	0
57	MG	1G	201	1/1	0.95	0.09	58,58,58,58	0
57	MG	1A	3896	1/1	0.95	0.06	43,43,43,43	0
57	MG	1A	3288	1/1	0.95	0.07	51,51,51,51	0
57	MG	1A	3289	1/1	0.95	0.10	52,52,52,52	0
57	MG	2A	3338	1/1	0.95	0.13	64,64,64,64	0
57	MG	1A	3900	1/1	0.95	0.08	54,54,54,54	0
57	MG	2a	3145	1/1	0.95	0.07	57,57,57,57	0
57	MG	2A	3648	1/1	0.95	0.06	64,64,64,64	0
57	MG	1N	202	1/1	0.95	0.11	36,36,36,36	0
57	MG	2A	3041	1/1	0.95	0.16	46,46,46,46	0
57	MG	2A	3651	1/1	0.95	0.08	60,60,60,60	0
57	MG	2A	3652	1/1	0.95	0.07	63,63,63,63	0
57	MG	2A	3042	1/1	0.95	0.05	25,25,25,25	0
57	MG	1N	203	1/1	0.95	0.06	48,48,48,48	0
57	MG	2A	3046	1/1	0.95	0.15	60,60,60,60	0
57	MG	1A	3750	1/1	0.95	0.10	28,28,28,28	0
57	MG	1a	1720	1/1	0.95	0.15	60,60,60,60	0
57	MG	1A	3635	1/1	0.95	0.10	45,45,45,45	0
57	MG	2a	3170	1/1	0.95	0.12	54,54,54,54	0
57	MG	1P	202	1/1	0.95	0.19	48,48,48,48	0
57	MG	2A	3667	1/1	0.95	0.10	47,47,47,47	0
57	MG	1A	3637	1/1	0.95	0.08	37,37,37,37	0
57	MG	2A	3669	1/1	0.95	0.12	36,36,36,36	0
57	MG	2a	3177	1/1	0.95	0.08	54,54,54,54	0
57	MG	1a	1725	1/1	0.95	0.18	54,54,54,54	0
57	MG	1A	3298	1/1	0.95	0.07	48,48,48,48	0
57	MG	2A	3057	1/1	0.95	0.14	50,50,50,50	0
57	MG	1A	3755	1/1	0.95	0.10	44,44,44,44	0
57	MG	1A	3907	1/1	0.95	0.05	26,26,26,26	0
57	MG	1A	3440	1/1	0.95	0.11	54,54,54,54	0
57	MG	1R	203	1/1	0.95	0.09	32,32,32,32	0
57	MG	2A	3684	1/1	0.95	0.07	40,40,40,40	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3369	1/1	0.95	0.10	38,38,38,38	0
57	MG	1A	3910	1/1	0.95	0.12	25,25,25,25	0
57	MG	2A	3372	1/1	0.95	0.11	50,50,50,50	0
57	MG	1A	3167	1/1	0.95	0.12	45,45,45,45	0
57	MG	1A	3219	1/1	0.95	0.12	46,46,46,46	0
57	MG	2A	3692	1/1	0.95	0.07	33,33,33,33	0
57	MG	2A	3377	1/1	0.95	0.14	63,63,63,63	0
57	MG	1A	3545	1/1	0.95	0.10	47,47,47,47	0
58	CLM	2A	3747	20/20	0.95	0.10	33,38,53,58	0
57	MG	1T	203	1/1	0.95	0.07	48,48,48,48	0
57	MG	2A	3698	1/1	0.95	0.07	62,62,62,62	0
57	MG	2A	3381	1/1	0.95	0.11	44,44,44,44	0
57	MG	2A	3069	1/1	0.95	0.30	57,57,57,57	0
57	MG	2A	3701	1/1	0.95	0.08	60,60,60,60	0
57	MG	1A	3764	1/1	0.95	0.06	27,27,27,27	0
57	MG	2A	3703	1/1	0.95	0.06	49,49,49,49	0
57	MG	1A	3920	1/1	0.95	0.06	54,54,54,54	0
57	MG	1a	1744	1/1	0.95	0.08	54,54,54,54	0
57	MG	2A	3723	1/1	0.96	0.23	51,51,51,51	0
57	MG	1A	3845	1/1	0.96	0.07	55,55,55,55	0
57	MG	2A	3726	1/1	0.96	0.07	38,38,38,38	0
57	MG	1a	1645	1/1	0.96	0.18	54,54,54,54	0
57	MG	2A	3434	1/1	0.96	0.07	56,56,56,56	0
57	MG	1A	3846	1/1	0.96	0.07	41,41,41,41	0
57	MG	2A	3158	1/1	0.96	0.28	55,55,55,55	0
57	MG	1A	4013	1/1	0.96	0.09	40,40,40,40	0
57	MG	1A	3401	1/1	0.96	0.05	17,17,17,17	0
57	MG	2A	3439	1/1	0.96	0.08	42,42,42,42	0
57	MG	2A	3163	1/1	0.96	0.05	62,62,62,62	0
57	MG	2A	3441	1/1	0.96	0.08	50,50,50,50	0
57	MG	1A	4015	1/1	0.96	0.07	50,50,50,50	0
57	MG	1a	1651	1/1	0.96	0.06	39,39,39,39	0
57	MG	2A	3444	1/1	0.96	0.07	46,46,46,46	0
57	MG	1A	3112	1/1	0.96	0.16	34,34,34,34	0
57	MG	1A	3589	1/1	0.96	0.07	44,44,44,44	0
57	MG	1A	3699	1/1	0.96	0.17	39,39,39,39	0
57	MG	1A	3089	1/1	0.96	0.10	32,32,32,32	0
57	MG	1A	3280	1/1	0.96	0.12	33,33,33,33	0
57	MG	1A	3482	1/1	0.96	0.08	44,44,44,44	0
57	MG	1A	3281	1/1	0.96	0.12	25,25,25,25	0
57	MG	1A	3484	1/1	0.96	0.09	26,26,26,26	0
57	MG	1A	3408	1/1	0.96	0.08	25,25,25,25	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2B	203	1/1	0.96	0.24	65,65,65,65	0
57	MG	1B	209	1/1	0.96	0.07	38,38,38,38	0
57	MG	1a	1835	1/1	0.96	0.09	55,55,55,55	0
57	MG	1a	1837	1/1	0.96	0.14	55,55,55,55	0
57	MG	1A	3132	1/1	0.96	0.27	40,40,40,40	0
57	MG	1A	3410	1/1	0.96	0.07	19,19,19,19	0
57	MG	1a	1664	1/1	0.96	0.24	55,55,55,55	0
57	MG	1A	3050	1/1	0.96	0.23	43,43,43,43	0
57	MG	2A	3189	1/1	0.96	0.13	59,59,59,59	0
57	MG	1a	1666	1/1	0.96	0.09	64,64,64,64	0
57	MG	1A	3347	1/1	0.96	0.05	38,38,38,38	0
57	MG	1A	3495	1/1	0.96	0.07	46,46,46,46	0
57	MG	1B	217	1/1	0.96	0.11	61,61,61,61	0
57	MG	1A	3866	1/1	0.96	0.10	40,40,40,40	0
57	MG	1A	3415	1/1	0.96	0.05	32,32,32,32	0
57	MG	1a	1849	1/1	0.96	0.07	55,55,55,55	0
57	MG	2A	3470	1/1	0.96	0.06	50,50,50,50	0
57	MG	1A	3604	1/1	0.96	0.17	56,56,56,56	0
57	MG	1B	222	1/1	0.96	0.09	42,42,42,42	0
57	MG	1A	3605	1/1	0.96	0.07	46,46,46,46	0
57	MG	2E	301	1/1	0.96	0.13	38,38,38,38	0
57	MG	1A	3716	1/1	0.96	0.20	27,27,27,27	0
57	MG	1A	3717	1/1	0.96	0.08	37,37,37,37	0
57	MG	1a	1678	1/1	0.96	0.20	55,55,55,55	0
57	MG	1A	3416	1/1	0.96	0.10	48,48,48,48	0
57	MG	1A	3607	1/1	0.96	0.15	31,31,31,31	0
57	MG	1A	3417	1/1	0.96	0.07	24,24,24,24	0
57	MG	2A	3482	1/1	0.96	0.06	51,51,51,51	0
57	MG	1A	3181	1/1	0.96	0.16	38,38,38,38	0
57	MG	1D	306	1/1	0.96	0.08	52,52,52,52	0
57	MG	1A	3726	1/1	0.96	0.06	71,71,71,71	0
57	MG	1a	1687	1/1	0.96	0.11	54,54,54,54	0
57	MG	1D	314	1/1	0.96	0.08	50,50,50,50	0
57	MG	1A	3727	1/1	0.96	0.07	35,35,35,35	0
57	MG	1D	316	1/1	0.96	0.13	49,49,49,49	0
57	MG	1A	3221	1/1	0.96	0.07	39,39,39,39	0
57	MG	1D	321	1/1	0.96	0.12	51,51,51,51	0
57	MG	1A	3611	1/1	0.96	0.17	27,27,27,27	0
57	MG	1A	3733	1/1	0.96	0.06	35,35,35,35	0
57	MG	1A	3734	1/1	0.96	0.08	50,50,50,50	0
57	MG	2A	3497	1/1	0.96	0.09	68,68,68,68	0
57	MG	1A	3613	1/1	0.96	0.10	26,26,26,26	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3499	1/1	0.96	0.11	58,58,58,58	0
57	MG	1F	308	1/1	0.96	0.12	34,34,34,34	0
57	MG	1F	309	1/1	0.96	0.07	36,36,36,36	0
57	MG	1A	3139	1/1	0.96	0.07	37,37,37,37	0
57	MG	2A	3226	1/1	0.96	0.06	46,46,46,46	0
57	MG	2W	202	1/1	0.96	0.17	50,50,50,50	0
57	MG	2X	101	1/1	0.96	0.08	47,47,47,47	0
57	MG	1h	201	1/1	0.96	0.20	49,49,49,49	0
57	MG	20	101	1/1	0.96	0.08	60,60,60,60	0
57	MG	2A	3507	1/1	0.96	0.12	66,66,66,66	0
57	MG	1A	3292	1/1	0.96	0.05	34,34,34,34	0
57	MG	1F	313	1/1	0.96	0.10	32,32,32,32	0
57	MG	1A	3739	1/1	0.96	0.07	45,45,45,45	0
57	MG	2A	3233	1/1	0.96	0.08	55,55,55,55	0
57	MG	25	103	1/1	0.96	0.09	55,55,55,55	0
57	MG	1A	3894	1/1	0.96	0.07	50,50,50,50	0
57	MG	28	3801	1/1	0.96	0.09	48,48,48,48	0
57	MG	1F	316	1/1	0.96	0.10	46,46,46,46	0
57	MG	2A	3236	1/1	0.96	0.09	39,39,39,39	0
57	MG	2a	3004	1/1	0.96	0.10	61,61,61,61	0
57	MG	1A	3509	1/1	0.96	0.08	57,57,57,57	0
57	MG	1F	318	1/1	0.96	0.12	46,46,46,46	0
57	MG	1o	101	1/1	0.96	0.10	49,49,49,49	0
57	MG	1A	3741	1/1	0.96	0.09	48,48,48,48	0
57	MG	1A	3356	1/1	0.96	0.05	22,22,22,22	0
57	MG	2A	3526	1/1	0.96	0.07	47,47,47,47	0
57	MG	1A	3899	1/1	0.96	0.09	54,54,54,54	0
57	MG	1A	3743	1/1	0.96	0.07	38,38,38,38	0
57	MG	1A	3744	1/1	0.96	0.17	54,54,54,54	0
57	MG	1A	3294	1/1	0.96	0.08	42,42,42,42	0
57	MG	1A	3514	1/1	0.96	0.05	34,34,34,34	0
57	MG	1A	3296	1/1	0.96	0.07	38,38,38,38	0
57	MG	2a	3017	1/1	0.96	0.07	58,58,58,58	0
57	MG	1A	3359	1/1	0.96	0.08	31,31,31,31	0
57	MG	2A	3252	1/1	0.96	0.31	44,44,44,44	0
57	MG	1A	3428	1/1	0.96	0.11	24,24,24,24	0
57	MG	2A	3537	1/1	0.96	0.11	53,53,53,53	0
57	MG	2A	3538	1/1	0.96	0.07	48,48,48,48	0
57	MG	1A	3908	1/1	0.96	0.06	19,19,19,19	0
57	MG	2A	3540	1/1	0.96	0.05	48,48,48,48	0
57	MG	2A	3255	1/1	0.96	0.13	39,39,39,39	0
57	MG	2A	3542	1/1	0.96	0.06	34,34,34,34	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3014	1/1	0.96	0.08	59,59,59,59	0
57	MG	1A	3361	1/1	0.96	0.09	46,46,46,46	0
57	MG	1A	3115	1/1	0.96	0.07	33,33,33,33	0
57	MG	2A	3018	1/1	0.96	0.19	36,36,36,36	0
57	MG	1A	3117	1/1	0.96	0.18	30,30,30,30	0
57	MG	2A	3021	1/1	0.96	0.05	34,34,34,34	0
57	MG	1A	3914	1/1	0.96	0.12	35,35,35,35	0
57	MG	1A	3757	1/1	0.96	0.06	37,37,37,37	0
57	MG	1A	3524	1/1	0.96	0.10	58,58,58,58	0
57	MG	1A	3628	1/1	0.96	0.08	53,53,53,53	0
57	MG	1A	3526	1/1	0.96	0.04	22,22,22,22	0
57	MG	1A	3231	1/1	0.96	0.16	38,38,38,38	0
57	MG	2A	3275	1/1	0.96	0.12	58,58,58,58	0
57	MG	1A	3232	1/1	0.96	0.12	27,27,27,27	0
57	MG	2A	3035	1/1	0.96	0.20	52,52,52,52	0
57	MG	2A	3559	1/1	0.96	0.06	54,54,54,54	0
57	MG	2A	3036	1/1	0.96	0.08	50,50,50,50	0
57	MG	2A	3281	1/1	0.96	0.12	41,41,41,41	0
57	MG	2A	3282	1/1	0.96	0.31	68,68,68,68	0
57	MG	1A	3436	1/1	0.96	0.08	48,48,48,48	0
57	MG	1A	3120	1/1	0.96	0.08	35,35,35,35	0
57	MG	1A	3369	1/1	0.96	0.05	26,26,26,26	0
57	MG	2A	3288	1/1	0.96	0.21	66,66,66,66	0
57	MG	2A	3289	1/1	0.96	0.15	54,54,54,54	0
57	MG	1A	3769	1/1	0.96	0.09	55,55,55,55	0
57	MG	2a	3056	1/1	0.96	0.13	58,58,58,58	0
57	MG	1A	3151	1/1	0.96	0.07	44,44,44,44	0
57	MG	2A	3045	1/1	0.96	0.09	59,59,59,59	0
57	MG	1A	3081	1/1	0.96	0.10	46,46,46,46	0
57	MG	1A	3642	1/1	0.96	0.16	34,34,34,34	0
57	MG	2A	3578	1/1	0.96	0.07	52,52,52,52	0
57	MG	2A	3579	1/1	0.96	0.07	61,61,61,61	0
57	MG	1A	3775	1/1	0.96	0.05	37,37,37,37	0
57	MG	2A	3049	1/1	0.96	0.12	55,55,55,55	0
57	MG	1A	3936	1/1	0.96	0.06	41,41,41,41	0
57	MG	2A	3300	1/1	0.96	0.10	51,51,51,51	0
57	MG	2a	3068	1/1	0.96	0.20	67,67,67,67	0
57	MG	2A	3051	1/1	0.96	0.11	48,48,48,48	0
57	MG	1A	3250	1/1	0.96	0.07	42,42,42,42	0
57	MG	2A	3303	1/1	0.96	0.14	43,43,43,43	0
57	MG	2A	3304	1/1	0.96	0.26	58,58,58,58	0
57	MG	1A	3539	1/1	0.96	0.08	51,51,51,51	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2a	3074	1/1	0.96	0.24	51,51,51,51	0
57	MG	2A	3054	1/1	0.96	0.15	57,57,57,57	0
57	MG	2a	3076	1/1	0.96	0.07	54,54,54,54	0
57	MG	1A	3540	1/1	0.96	0.05	23,23,23,23	0
57	MG	1A	3782	1/1	0.96	0.11	38,38,38,38	0
57	MG	2A	3597	1/1	0.96	0.09	39,39,39,39	0
57	MG	1A	3542	1/1	0.96	0.07	37,37,37,37	0
57	MG	2A	3311	1/1	0.96	0.09	51,51,51,51	0
57	MG	2a	3083	1/1	0.96	0.28	60,60,60,60	0
57	MG	1A	3647	1/1	0.96	0.12	65,65,65,65	0
57	MG	2A	3601	1/1	0.96	0.09	58,58,58,58	0
57	MG	1A	3947	1/1	0.96	0.11	25,25,25,25	0
57	MG	2A	3061	1/1	0.96	0.08	47,47,47,47	0
57	MG	2a	3088	1/1	0.96	0.10	55,55,55,55	0
57	MG	1a	1753	1/1	0.96	0.08	53,53,53,53	0
57	MG	1A	3543	1/1	0.96	0.06	32,32,32,32	0
57	MG	1A	3949	1/1	0.96	0.06	44,44,44,44	0
57	MG	2A	3324	1/1	0.96	0.07	36,36,36,36	0
57	MG	2a	3093	1/1	0.96	0.26	52,52,52,52	0
57	MG	1A	3445	1/1	0.96	0.15	40,40,40,40	0
57	MG	1A	3446	1/1	0.96	0.11	44,44,44,44	0
57	MG	1A	3546	1/1	0.96	0.08	31,31,31,31	0
57	MG	1A	3008	1/1	0.96	0.06	36,36,36,36	0
57	MG	2A	3332	1/1	0.96	0.07	54,54,54,54	0
57	MG	15	101	1/1	0.96	0.15	43,43,43,43	0
57	MG	2A	3335	1/1	0.96	0.06	41,41,41,41	0
57	MG	2A	3337	1/1	0.96	0.06	35,35,35,35	0
57	MG	2a	3102	1/1	0.96	0.08	55,55,55,55	0
57	MG	15	104	1/1	0.96	0.14	26,26,26,26	0
57	MG	2A	3339	1/1	0.96	0.09	49,49,49,49	0
57	MG	1A	3549	1/1	0.96	0.09	44,44,44,44	0
57	MG	2A	3073	1/1	0.96	0.07	32,32,32,32	0
57	MG	2A	3342	1/1	0.96	0.09	42,42,42,42	0
57	MG	1a	1765	1/1	0.96	0.10	52,52,52,52	0
57	MG	1A	3550	1/1	0.96	0.11	42,42,42,42	0
57	MG	2A	3346	1/1	0.96	0.16	52,52,52,52	0
57	MG	2A	3633	1/1	0.96	0.09	49,49,49,49	0
57	MG	1A	3312	1/1	0.96	0.17	30,30,30,30	0
57	MG	1A	3252	1/1	0.96	0.10	44,44,44,44	0
57	MG	1A	3553	1/1	0.96	0.06	49,49,49,49	0
57	MG	2A	3353	1/1	0.96	0.08	52,52,52,52	0
57	MG	2A	3638	1/1	0.96	0.07	50,50,50,50	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1a	1770	1/1	0.96	0.09	59,59,59,59	0
57	MG	1A	3378	1/1	0.96	0.09	48,48,48,48	0
57	MG	19	101	1/1	0.96	0.10	58,58,58,58	0
57	MG	1A	3556	1/1	0.96	0.12	53,53,53,53	0
57	MG	2A	3085	1/1	0.96	0.17	58,58,58,58	0
57	MG	2A	3645	1/1	0.96	0.08	67,67,67,67	0
57	MG	2a	3124	1/1	0.96	0.14	59,59,59,59	0
57	MG	2A	3087	1/1	0.96	0.36	47,47,47,47	0
57	MG	2A	3088	1/1	0.96	0.10	41,41,41,41	0
57	MG	1A	3253	1/1	0.96	0.06	45,45,45,45	0
57	MG	2A	3364	1/1	0.96	0.11	34,34,34,34	0
57	MG	1A	3453	1/1	0.96	0.09	58,58,58,58	0
57	MG	1A	3060	1/1	0.96	0.17	37,37,37,37	0
57	MG	1A	3194	1/1	0.96	0.10	34,34,34,34	0
57	MG	2A	3094	1/1	0.96	0.10	48,48,48,48	0
57	MG	2A	3095	1/1	0.96	0.18	65,65,65,65	0
57	MG	1A	3382	1/1	0.96	0.07	45,45,45,45	0
57	MG	1A	3196	1/1	0.96	0.13	48,48,48,48	0
57	MG	1A	3975	1/1	0.96	0.05	42,42,42,42	0
57	MG	2A	3099	1/1	0.96	0.06	53,53,53,53	0
57	MG	1A	3033	1/1	0.96	0.07	34,34,34,34	0
57	MG	1A	3977	1/1	0.96	0.05	48,48,48,48	0
57	MG	1A	3810	1/1	0.96	0.08	42,42,42,42	0
57	MG	1a	1613	1/1	0.96	0.10	49,49,49,49	0
57	MG	2A	3673	1/1	0.96	0.06	19,19,19,19	0
57	MG	2a	3146	1/1	0.96	0.09	71,71,71,71	0
57	MG	1a	1786	1/1	0.96	0.08	61,61,61,61	0
57	MG	2A	3108	1/1	0.96	0.08	52,52,52,52	0
57	MG	2A	3110	1/1	0.96	0.12	57,57,57,57	0
57	MG	2a	3152	1/1	0.96	0.06	56,56,56,56	0
57	MG	2A	3386	1/1	0.96	0.11	43,43,43,43	0
57	MG	2a	3154	1/1	0.96	0.05	65,65,65,65	0
57	MG	2a	3156	1/1	0.96	0.06	53,53,53,53	0
57	MG	1A	3565	1/1	0.96	0.09	56,56,56,56	0
57	MG	2A	3113	1/1	0.96	0.07	46,46,46,46	0
57	MG	2A	3683	1/1	0.96	0.08	58,58,58,58	0
57	MG	2A	3114	1/1	0.96	0.13	63,63,63,63	0
57	MG	1A	3675	1/1	0.96	0.17	38,38,38,38	0
57	MG	2a	3164	1/1	0.96	0.12	63,63,63,63	0
57	MG	1A	3260	1/1	0.96	0.21	33,33,33,33	0
57	MG	2A	3392	1/1	0.96	0.16	59,59,59,59	0
57	MG	1A	3262	1/1	0.96	0.13	25,25,25,25	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3983	1/1	0.96	0.06	55,55,55,55	0
57	MG	1A	3819	1/1	0.96	0.10	37,37,37,37	0
57	MG	2a	3173	1/1	0.96	0.07	64,64,64,64	0
57	MG	1a	1621	1/1	0.96	0.17	58,58,58,58	0
57	MG	1A	3569	1/1	0.96	0.07	14,14,14,14	0
57	MG	2A	3696	1/1	0.96	0.06	37,37,37,37	0
57	MG	1A	3679	1/1	0.96	0.07	55,55,55,55	0
57	MG	2A	3125	1/1	0.96	0.07	36,36,36,36	0
57	MG	1A	3463	1/1	0.96	0.12	54,54,54,54	0
57	MG	1A	3198	1/1	0.96	0.09	41,41,41,41	0
57	MG	1A	3265	1/1	0.96	0.10	39,39,39,39	0
57	MG	2a	3184	1/1	0.96	0.16	72,72,72,72	0
57	MG	1a	1629	1/1	0.96	0.13	47,47,47,47	0
57	MG	1A	3827	1/1	0.96	0.05	18,18,18,18	0
57	MG	2A	3411	1/1	0.96	0.11	61,61,61,61	0
57	MG	1A	3161	1/1	0.96	0.08	46,46,46,46	0
57	MG	1A	3829	1/1	0.96	0.07	38,38,38,38	0
57	MG	1A	3164	1/1	0.96	0.05	33,33,33,33	0
57	MG	2A	3136	1/1	0.96	0.14	58,58,58,58	0
57	MG	1A	3471	1/1	0.96	0.08	39,39,39,39	0
57	MG	2A	3710	1/1	0.96	0.06	64,64,64,64	0
57	MG	1A	3687	1/1	0.96	0.11	32,32,32,32	0
57	MG	2t	201	1/1	0.96	0.13	40,40,40,40	0
57	MG	1A	3087	1/1	0.96	0.11	37,37,37,37	0
57	MG	1a	1807	1/1	0.96	0.07	45,45,45,45	0
57	MG	2A	3714	1/1	0.96	0.08	47,47,47,47	0
57	MG	1A	3004	1/1	0.96	0.10	45,45,45,45	0
57	MG	1A	3474	1/1	0.96	0.07	52,52,52,52	0
57	MG	1A	3336	1/1	0.96	0.04	32,32,32,32	0
57	MG	1A	4006	1/1	0.96	0.17	32,32,32,32	0
57	MG	1A	3206	1/1	0.96	0.24	43,43,43,43	0
57	MG	2A	3150	1/1	0.96	0.10	50,50,50,50	0
57	MG	1A	3694	1/1	0.96	0.08	54,54,54,54	0
57	MG	1a	1814	1/1	0.96	0.15	58,58,58,58	0
57	MG	1A	3837	1/1	0.97	0.05	37,37,37,37	0
57	MG	2A	3044	1/1	0.97	0.14	44,44,44,44	0
57	MG	1a	1752	1/1	0.97	0.11	37,37,37,37	0
57	MG	1A	3839	1/1	0.97	0.06	43,43,43,43	0
57	MG	1A	3508	1/1	0.97	0.06	46,46,46,46	0
57	MG	1A	3204	1/1	0.97	0.09	36,36,36,36	0
57	MG	2A	3502	1/1	0.97	0.05	62,62,62,62	0
57	MG	2B	217	1/1	0.97	0.08	57,57,57,57	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3259	1/1	0.97	0.06	51,51,51,51	0
57	MG	2B	219	1/1	0.97	0.08	61,61,61,61	0
57	MG	2D	302	1/1	0.97	0.41	44,44,44,44	0
57	MG	17	102	1/1	0.97	0.05	31,31,31,31	0
57	MG	2A	3505	1/1	0.97	0.06	61,61,61,61	0
57	MG	2D	305	1/1	0.97	0.05	34,34,34,34	0
57	MG	1A	3714	1/1	0.97	0.05	30,30,30,30	0
57	MG	17	105	1/1	0.97	0.08	50,50,50,50	0
57	MG	1A	3039	1/1	0.97	0.09	37,37,37,37	0
57	MG	2A	3510	1/1	0.97	0.06	51,51,51,51	0
57	MG	2E	302	1/1	0.97	0.05	37,37,37,37	0
57	MG	2E	303	1/1	0.97	0.15	45,45,45,45	0
57	MG	1a	1760	1/1	0.97	0.11	60,60,60,60	0
57	MG	18	102	1/1	0.97	0.05	35,35,35,35	0
57	MG	2E	306	1/1	0.97	0.06	42,42,42,42	0
57	MG	2E	308	1/1	0.97	0.08	54,54,54,54	0
57	MG	2A	3266	1/1	0.97	0.15	39,39,39,39	0
57	MG	1A	3062	1/1	0.97	0.06	26,26,26,26	0
57	MG	2A	3270	1/1	0.97	0.16	44,44,44,44	0
57	MG	1A	3274	1/1	0.97	0.05	54,54,54,54	0
57	MG	1A	3348	1/1	0.97	0.08	50,50,50,50	0
57	MG	2A	3519	1/1	0.97	0.05	38,38,38,38	0
57	MG	2A	3058	1/1	0.97	0.10	38,38,38,38	0
57	MG	2A	3274	1/1	0.97	0.23	50,50,50,50	0
57	MG	2A	3522	1/1	0.97	0.04	59,59,59,59	0
57	MG	1A	3991	1/1	0.97	0.08	35,35,35,35	0
57	MG	2A	3276	1/1	0.97	0.14	40,40,40,40	0
57	MG	1A	3516	1/1	0.97	0.07	19,19,19,19	0
57	MG	1A	3720	1/1	0.97	0.17	47,47,47,47	0
57	MG	1A	3995	1/1	0.97	0.09	44,44,44,44	0
57	MG	1A	3208	1/1	0.97	0.07	33,33,33,33	0
57	MG	1A	3424	1/1	0.97	0.11	42,42,42,42	0
57	MG	2A	3531	1/1	0.97	0.10	44,44,44,44	0
57	MG	1a	1606	1/1	0.97	0.11	48,48,48,48	0
57	MG	1A	3853	1/1	0.97	0.06	28,28,28,28	0
57	MG	1A	3007	1/1	0.97	0.07	29,29,29,29	0
57	MG	1a	1609	1/1	0.97	0.10	55,55,55,55	0
57	MG	1A	3352	1/1	0.97	0.03	18,18,18,18	0
57	MG	2V	202	1/1	0.97	0.14	49,49,49,49	0
57	MG	1A	3856	1/1	0.97	0.13	35,35,35,35	0
57	MG	2A	3071	1/1	0.97	0.22	46,46,46,46	0
57	MG	1a	1612	1/1	0.97	0.12	28,28,28,28	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3427	1/1	0.97	0.07	26,26,26,26	0
57	MG	2A	3074	1/1	0.97	0.08	42,42,42,42	0
57	MG	1A	3001	1/1	0.97	0.06	29,29,29,29	0
57	MG	2A	3543	1/1	0.97	0.06	49,49,49,49	0
57	MG	2A	3297	1/1	0.97	0.12	40,40,40,40	0
57	MG	1A	3214	1/1	0.97	0.07	18,18,18,18	0
57	MG	1A	3355	1/1	0.97	0.07	31,31,31,31	0
57	MG	1A	3016	1/1	0.97	0.12	36,36,36,36	0
57	MG	1A	3284	1/1	0.97	0.10	49,49,49,49	0
57	MG	27	101	1/1	0.97	0.13	41,41,41,41	0
57	MG	1a	1785	1/1	0.97	0.05	64,64,64,64	0
57	MG	1A	3532	1/1	0.97	0.11	26,26,26,26	0
57	MG	2a	3001	1/1	0.97	0.06	40,40,40,40	0
57	MG	1A	3124	1/1	0.97	0.07	34,34,34,34	0
57	MG	1A	3630	1/1	0.97	0.07	29,29,29,29	0
57	MG	1a	1623	1/1	0.97	0.05	47,47,47,47	0
57	MG	1A	3090	1/1	0.97	0.15	25,25,25,25	0
57	MG	1a	1625	1/1	0.97	0.06	44,44,44,44	0
57	MG	1A	3287	1/1	0.97	0.11	31,31,31,31	0
57	MG	2A	3310	1/1	0.97	0.07	51,51,51,51	0
57	MG	2A	3090	1/1	0.97	0.04	38,38,38,38	0
57	MG	2A	3312	1/1	0.97	0.09	46,46,46,46	0
57	MG	2A	3313	1/1	0.97	0.06	52,52,52,52	0
57	MG	2A	3314	1/1	0.97	0.09	51,51,51,51	0
57	MG	2A	3562	1/1	0.97	0.08	37,37,37,37	0
57	MG	1A	3636	1/1	0.97	0.07	46,46,46,46	0
57	MG	2A	3564	1/1	0.97	0.09	58,58,58,58	0
57	MG	1A	3220	1/1	0.97	0.11	30,30,30,30	0
57	MG	1A	3745	1/1	0.97	0.07	50,50,50,50	0
57	MG	2a	3018	1/1	0.97	0.10	46,46,46,46	0
57	MG	1A	3170	1/1	0.97	0.11	34,34,34,34	0
57	MG	2A	3570	1/1	0.97	0.07	47,47,47,47	0
57	MG	1A	3222	1/1	0.97	0.15	40,40,40,40	0
57	MG	2A	3321	1/1	0.97	0.08	37,37,37,37	0
57	MG	2a	3023	1/1	0.97	0.10	50,50,50,50	0
57	MG	1A	3366	1/1	0.97	0.06	18,18,18,18	0
57	MG	1A	3878	1/1	0.97	0.10	59,59,59,59	0
57	MG	1A	3444	1/1	0.97	0.03	26,26,26,26	0
57	MG	1A	3293	1/1	0.97	0.08	53,53,53,53	0
57	MG	2A	3328	1/1	0.97	0.12	42,42,42,42	0
57	MG	1a	1636	1/1	0.97	0.06	38,38,38,38	0
57	MG	1A	3224	1/1	0.97	0.15	33,33,33,33	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3103	1/1	0.97	0.13	51,51,51,51	0
57	MG	1A	3126	1/1	0.97	0.06	66,66,66,66	0
57	MG	2A	3105	1/1	0.97	0.19	53,53,53,53	0
57	MG	2A	3336	1/1	0.97	0.05	33,33,33,33	0
57	MG	1A	3297	1/1	0.97	0.10	42,42,42,42	0
57	MG	2a	3036	1/1	0.97	0.07	43,43,43,43	0
57	MG	1A	3371	1/1	0.97	0.05	29,29,29,29	0
57	MG	1A	3005	1/1	0.97	0.09	26,26,26,26	0
57	MG	1A	3179	1/1	0.97	0.26	38,38,38,38	0
57	MG	1A	3761	1/1	0.97	0.10	47,47,47,47	0
57	MG	1A	3888	1/1	0.97	0.11	31,31,31,31	0
57	MG	2A	3593	1/1	0.97	0.05	60,60,60,60	0
57	MG	1A	3890	1/1	0.97	0.03	34,34,34,34	0
57	MG	2A	3595	1/1	0.97	0.03	44,44,44,44	0
57	MG	1A	3230	1/1	0.97	0.18	28,28,28,28	0
57	MG	1a	1647	1/1	0.97	0.12	54,54,54,54	0
57	MG	1A	3069	1/1	0.97	0.10	24,24,24,24	0
57	MG	1A	3036	1/1	0.97	0.07	24,24,24,24	0
57	MG	2A	3349	1/1	0.97	0.06	47,47,47,47	0
57	MG	1A	3235	1/1	0.97	0.17	34,34,34,34	0
57	MG	2A	3603	1/1	0.97	0.04	45,45,45,45	0
57	MG	1A	3766	1/1	0.97	0.10	34,34,34,34	0
57	MG	2a	3053	1/1	0.97	0.15	55,55,55,55	0
57	MG	2A	3121	1/1	0.97	0.06	45,45,45,45	0
57	MG	1a	1819	1/1	0.97	0.10	54,54,54,54	0
57	MG	1A	3053	1/1	0.97	0.17	30,30,30,30	0
57	MG	1A	3655	1/1	0.97	0.07	46,46,46,46	0
57	MG	2A	3126	1/1	0.97	0.10	40,40,40,40	0
57	MG	2A	3613	1/1	0.97	0.05	65,65,65,65	0
57	MG	1A	3307	1/1	0.97	0.13	26,26,26,26	0
57	MG	1D	303	1/1	0.97	0.14	35,35,35,35	0
57	MG	1A	3072	1/1	0.97	0.12	37,37,37,37	0
57	MG	1A	3184	1/1	0.97	0.10	54,54,54,54	0
57	MG	2A	3619	1/1	0.97	0.08	42,42,42,42	0
57	MG	1D	313	1/1	0.97	0.13	29,29,29,29	0
57	MG	1A	3660	1/1	0.97	0.04	20,20,20,20	0
57	MG	1A	3383	1/1	0.97	0.07	48,48,48,48	0
57	MG	1A	3241	1/1	0.97	0.15	33,33,33,33	0
57	MG	1D	317	1/1	0.97	0.16	32,32,32,32	0
57	MG	1D	318	1/1	0.97	0.06	53,53,53,53	0
57	MG	2A	3138	1/1	0.97	0.10	24,24,24,24	0
57	MG	1A	3385	1/1	0.97	0.10	35,35,35,35	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1D	320	1/1	0.97	0.07	47,47,47,47	0
57	MG	2A	3378	1/1	0.97	0.06	40,40,40,40	0
57	MG	1A	3244	1/1	0.97	0.14	46,46,46,46	0
57	MG	1E	302	1/1	0.97	0.18	39,39,39,39	0
57	MG	1A	3780	1/1	0.97	0.11	43,43,43,43	0
57	MG	1A	3781	1/1	0.97	0.16	33,33,33,33	0
57	MG	1A	3912	1/1	0.97	0.04	18,18,18,18	0
57	MG	1A	3467	1/1	0.97	0.06	45,45,45,45	0
57	MG	2a	3082	1/1	0.97	0.27	61,61,61,61	0
57	MG	2A	3149	1/1	0.97	0.19	46,46,46,46	0
57	MG	1F	305	1/1	0.97	0.10	35,35,35,35	0
57	MG	1a	1673	1/1	0.97	0.09	44,44,44,44	0
57	MG	2A	3152	1/1	0.97	0.14	41,41,41,41	0
57	MG	1A	3915	1/1	0.97	0.12	35,35,35,35	0
57	MG	1A	3784	1/1	0.97	0.11	42,42,42,42	0
57	MG	2A	3155	1/1	0.97	0.05	44,44,44,44	0
57	MG	1A	3667	1/1	0.97	0.10	24,24,24,24	0
57	MG	2A	3646	1/1	0.97	0.06	69,69,69,69	0
57	MG	1A	3246	1/1	0.97	0.16	34,34,34,34	0
57	MG	1A	3787	1/1	0.97	0.04	21,21,21,21	0
57	MG	2A	3396	1/1	0.97	0.06	49,49,49,49	0
57	MG	1A	3317	1/1	0.97	0.09	34,34,34,34	0
57	MG	2A	3160	1/1	0.97	0.10	49,49,49,49	0
57	MG	2A	3401	1/1	0.97	0.14	56,56,56,56	0
57	MG	2A	3161	1/1	0.97	0.13	46,46,46,46	0
57	MG	2A	3656	1/1	0.97	0.05	68,68,68,68	0
57	MG	1A	3249	1/1	0.97	0.09	42,42,42,42	0
57	MG	1A	3570	1/1	0.97	0.08	33,33,33,33	0
57	MG	2A	3659	1/1	0.97	0.10	45,45,45,45	0
57	MG	1A	3320	1/1	0.97	0.07	34,34,34,34	0
57	MG	1A	3321	1/1	0.97	0.08	26,26,26,26	0
57	MG	1A	3133	1/1	0.97	0.07	51,51,51,51	0
57	MG	2A	3665	1/1	0.97	0.06	56,56,56,56	0
57	MG	2A	3168	1/1	0.97	0.07	45,45,45,45	0
57	MG	1A	3574	1/1	0.97	0.15	33,33,33,33	0
57	MG	1A	3930	1/1	0.97	0.13	35,35,35,35	0
57	MG	1A	3575	1/1	0.97	0.12	53,53,53,53	0
57	MG	1H	201	1/1	0.97	0.08	53,53,53,53	0
57	MG	2A	3671	1/1	0.97	0.05	37,37,37,37	0
57	MG	2A	3672	1/1	0.97	0.06	33,33,33,33	0
57	MG	1A	3394	1/1	0.97	0.06	18,18,18,18	0
57	MG	1N	201	1/1	0.97	0.06	36,36,36,36	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3186	1/1	0.97	0.10	32,32,32,32	0
57	MG	1A	3104	1/1	0.97	0.09	34,34,34,34	0
57	MG	1A	3579	1/1	0.97	0.08	25,25,25,25	0
57	MG	1A	3105	1/1	0.97	0.13	30,30,30,30	0
57	MG	2A	3180	1/1	0.97	0.05	47,47,47,47	0
57	MG	1A	3141	1/1	0.97	0.07	36,36,36,36	0
57	MG	2A	3183	1/1	0.97	0.07	41,41,41,41	0
57	MG	1A	3803	1/1	0.97	0.14	31,31,31,31	0
57	MG	2A	3687	1/1	0.97	0.09	58,58,58,58	0
57	MG	1A	3804	1/1	0.97	0.07	51,51,51,51	0
57	MG	2A	3426	1/1	0.97	0.13	55,55,55,55	0
57	MG	1A	3399	1/1	0.97	0.07	18,18,18,18	0
57	MG	1A	3945	1/1	0.97	0.06	21,21,21,21	0
57	MG	1A	3400	1/1	0.97	0.08	25,25,25,25	0
57	MG	2a	3131	1/1	0.97	0.07	63,63,63,63	0
57	MG	2A	3693	1/1	0.97	0.07	64,64,64,64	0
57	MG	2A	3190	1/1	0.97	0.07	51,51,51,51	0
57	MG	1A	3585	1/1	0.97	0.12	38,38,38,38	0
57	MG	1A	3073	1/1	0.97	0.05	37,37,37,37	0
57	MG	1A	3145	1/1	0.97	0.06	38,38,38,38	0
57	MG	1A	3403	1/1	0.97	0.04	19,19,19,19	0
57	MG	1A	3054	1/1	0.97	0.08	34,34,34,34	0
57	MG	1A	3489	1/1	0.97	0.06	24,24,24,24	0
57	MG	1A	3955	1/1	0.97	0.12	42,42,42,42	0
57	MG	1A	3816	1/1	0.97	0.06	39,39,39,39	0
57	MG	1A	3490	1/1	0.97	0.06	31,31,31,31	0
57	MG	1n	101	1/1	0.97	0.29	56,56,56,56	0
57	MG	1A	3259	1/1	0.97	0.07	49,49,49,49	0
57	MG	1U	202	1/1	0.97	0.22	33,33,33,33	0
57	MG	2a	3148	1/1	0.97	0.08	62,62,62,62	0
57	MG	1A	3961	1/1	0.97	0.13	44,44,44,44	0
57	MG	1U	204	1/1	0.97	0.16	33,33,33,33	0
57	MG	2a	3151	1/1	0.97	0.07	53,53,53,53	0
57	MG	1A	3492	1/1	0.97	0.04	27,27,27,27	0
57	MG	1A	3493	1/1	0.97	0.06	22,22,22,22	0
57	MG	2A	3208	1/1	0.97	0.07	52,52,52,52	0
57	MG	2a	3155	1/1	0.97	0.06	60,60,60,60	0
57	MG	1A	3964	1/1	0.97	0.08	46,46,46,46	0
57	MG	1V	206	1/1	0.97	0.08	53,53,53,53	0
57	MG	1A	3821	1/1	0.97	0.12	36,36,36,36	0
57	MG	2a	3159	1/1	0.97	0.08	60,60,60,60	0
57	MG	1x	102	1/1	0.97	0.04	38,38,38,38	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3055	1/1	0.97	0.12	43,43,43,43	0
57	MG	1A	3150	1/1	0.97	0.06	40,40,40,40	0
57	MG	2A	3003	1/1	0.97	0.06	52,52,52,52	0
57	MG	2a	3166	1/1	0.97	0.05	69,69,69,69	0
57	MG	1X	101	1/1	0.97	0.10	33,33,33,33	0
57	MG	2A	3006	1/1	0.97	0.07	48,48,48,48	0
57	MG	2a	3169	1/1	0.97	0.05	51,51,51,51	0
57	MG	1A	3335	1/1	0.97	0.06	23,23,23,23	0
57	MG	1A	3263	1/1	0.97	0.07	47,47,47,47	0
57	MG	2A	3012	1/1	0.97	0.21	58,58,58,58	0
57	MG	2A	3724	1/1	0.97	0.08	38,38,38,38	0
57	MG	2A	3013	1/1	0.97	0.06	23,23,23,23	0
57	MG	2a	3175	1/1	0.97	0.07	71,71,71,71	0
57	MG	1A	3971	1/1	0.97	0.05	26,26,26,26	0
57	MG	1a	1728	1/1	0.97	0.15	52,52,52,52	0
57	MG	1A	3499	1/1	0.97	0.06	39,39,39,39	0
57	MG	10	104	1/1	0.97	0.08	57,57,57,57	0
57	MG	1A	3021	1/1	0.97	0.06	39,39,39,39	0
57	MG	1A	3705	1/1	0.97	0.08	55,55,55,55	0
57	MG	2A	3229	1/1	0.97	0.07	47,47,47,47	0
57	MG	2A	3471	1/1	0.97	0.07	61,61,61,61	0
57	MG	1A	3339	1/1	0.97	0.06	31,31,31,31	0
57	MG	2A	3231	1/1	0.97	0.07	54,54,54,54	0
57	MG	2A	3736	1/1	0.97	0.15	46,46,46,46	0
57	MG	1a	1735	1/1	0.97	0.06	56,56,56,56	0
57	MG	1A	3058	1/1	0.97	0.12	46,46,46,46	0
57	MG	1A	3503	1/1	0.97	0.06	44,44,44,44	0
57	MG	11	102	1/1	0.97	0.06	34,34,34,34	0
57	MG	2A	3030	1/1	0.97	0.05	18,18,18,18	0
57	MG	2A	3031	1/1	0.97	0.12	55,55,55,55	0
57	MG	11	103	1/1	0.97	0.08	43,43,43,43	0
57	MG	2A	3033	1/1	0.97	0.14	47,47,47,47	0
57	MG	1A	3084	1/1	0.97	0.33	38,38,38,38	0
57	MG	11	105	1/1	0.97	0.06	36,36,36,36	0
57	MG	13	101	1/1	0.97	0.11	31,31,31,31	0
57	MG	1A	3506	1/1	0.97	0.04	22,22,22,22	0
57	MG	2A	3245	1/1	0.97	0.06	51,51,51,51	0
57	MG	2A	3038	1/1	0.97	0.09	48,48,48,48	0
57	MG	13	103	1/1	0.97	0.06	40,40,40,40	0
57	MG	2A	3040	1/1	0.97	0.16	50,50,50,50	0
57	MG	2A	3249	1/1	0.97	0.21	59,59,59,59	0
57	MG	1A	3157	1/1	0.97	0.11	29,29,29,29	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
61	ZN	14	501	1/1	0.97	0.07	108,108,108,108	0
61	ZN	2Y	202	1/1	0.97	0.05	88,88,88,88	0
57	MG	15	103	1/1	0.97	0.13	30,30,30,30	0
57	MG	1A	3135	1/1	0.98	0.20	31,31,31,31	0
57	MG	2F	304	1/1	0.98	0.20	45,45,45,45	0
57	MG	1A	3555	1/1	0.98	0.07	41,41,41,41	0
57	MG	1A	3242	1/1	0.98	0.14	35,35,35,35	0
57	MG	1A	3080	1/1	0.98	0.09	26,26,26,26	0
57	MG	1A	3245	1/1	0.98	0.35	40,40,40,40	0
57	MG	1A	3654	1/1	0.98	0.10	38,38,38,38	0
57	MG	1B	213	1/1	0.98	0.04	36,36,36,36	0
57	MG	2A	3102	1/1	0.98	0.07	39,39,39,39	0
57	MG	1B	214	1/1	0.98	0.06	43,43,43,43	0
57	MG	1A	3137	1/1	0.98	0.07	45,45,45,45	0
57	MG	1A	3247	1/1	0.98	0.14	40,40,40,40	0
57	MG	1A	3889	1/1	0.98	0.04	33,33,33,33	0
57	MG	2A	3316	1/1	0.98	0.08	42,42,42,42	0
57	MG	1A	3138	1/1	0.98	0.20	42,42,42,42	0
57	MG	1A	3892	1/1	0.98	0.06	42,42,42,42	0
57	MG	1A	3658	1/1	0.98	0.04	34,34,34,34	0
57	MG	1B	221	1/1	0.98	0.06	35,35,35,35	0
57	MG	2A	3112	1/1	0.98	0.08	47,47,47,47	0
57	MG	1A	3107	1/1	0.98	0.14	35,35,35,35	0
57	MG	2A	3323	1/1	0.98	0.12	18,18,18,18	0
57	MG	1B	223	1/1	0.98	0.07	44,44,44,44	0
57	MG	1B	224	1/1	0.98	0.04	42,42,42,42	0
57	MG	1A	3188	1/1	0.98	0.07	41,41,41,41	0
57	MG	1A	3771	1/1	0.98	0.04	37,37,37,37	0
57	MG	1A	3049	1/1	0.98	0.28	44,44,44,44	0
57	MG	2W	203	1/1	0.98	0.05	54,54,54,54	0
57	MG	1a	1818	1/1	0.98	0.04	67,67,67,67	0
57	MG	1A	3142	1/1	0.98	0.05	28,28,28,28	0
57	MG	2A	3333	1/1	0.98	0.04	36,36,36,36	0
57	MG	2A	3565	1/1	0.98	0.06	47,47,47,47	0
57	MG	1a	1820	1/1	0.98	0.09	57,57,57,57	0
57	MG	2A	3567	1/1	0.98	0.07	56,56,56,56	0
57	MG	1A	3110	1/1	0.98	0.14	21,21,21,21	0
57	MG	1A	3568	1/1	0.98	0.16	38,38,38,38	0
57	MG	1A	3665	1/1	0.98	0.04	52,52,52,52	0
57	MG	1A	3778	1/1	0.98	0.05	26,26,26,26	0
57	MG	1D	305	1/1	0.98	0.06	39,39,39,39	0
57	MG	1A	3029	1/1	0.98	0.08	35,35,35,35	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1D	307	1/1	0.98	0.07	34,34,34,34	0
57	MG	2A	3130	1/1	0.98	0.12	46,46,46,46	0
57	MG	2A	3343	1/1	0.98	0.03	21,21,21,21	0
57	MG	1D	308	1/1	0.98	0.16	48,48,48,48	0
57	MG	1D	310	1/1	0.98	0.05	41,41,41,41	0
57	MG	1A	3037	1/1	0.98	0.10	45,45,45,45	0
57	MG	1A	3019	1/1	0.98	0.14	28,28,28,28	0
57	MG	1A	3195	1/1	0.98	0.12	33,33,33,33	0
57	MG	1A	3783	1/1	0.98	0.09	40,40,40,40	0
57	MG	2A	3583	1/1	0.98	0.06	54,54,54,54	0
57	MG	1A	3334	1/1	0.98	0.06	24,24,24,24	0
57	MG	2A	3351	1/1	0.98	0.10	49,49,49,49	0
57	MG	2A	3352	1/1	0.98	0.06	43,43,43,43	0
57	MG	1A	3671	1/1	0.98	0.04	43,43,43,43	0
57	MG	1a	1836	1/1	0.98	0.06	39,39,39,39	0
57	MG	2A	3589	1/1	0.98	0.04	47,47,47,47	0
57	MG	2A	3590	1/1	0.98	0.08	31,31,31,31	0
57	MG	1A	3149	1/1	0.98	0.16	30,30,30,30	0
57	MG	1A	3913	1/1	0.98	0.06	41,41,41,41	0
57	MG	2A	3142	1/1	0.98	0.08	39,39,39,39	0
57	MG	1A	3485	1/1	0.98	0.07	25,25,25,25	0
57	MG	1A	3261	1/1	0.98	0.20	36,36,36,36	0
57	MG	1A	3067	1/1	0.98	0.18	32,32,32,32	0
57	MG	1E	303	1/1	0.98	0.05	31,31,31,31	0
57	MG	1A	3917	1/1	0.98	0.05	51,51,51,51	0
57	MG	2A	3365	1/1	0.98	0.07	30,30,30,30	0
57	MG	2A	3148	1/1	0.98	0.08	36,36,36,36	0
57	MG	1A	3068	1/1	0.98	0.23	30,30,30,30	0
57	MG	2A	3602	1/1	0.98	0.04	46,46,46,46	0
57	MG	1A	3152	1/1	0.98	0.18	42,42,42,42	0
57	MG	1A	3411	1/1	0.98	0.03	35,35,35,35	0
57	MG	2A	3605	1/1	0.98	0.09	44,44,44,44	0
57	MG	1a	1847	1/1	0.98	0.07	59,59,59,59	0
57	MG	2A	3371	1/1	0.98	0.09	34,34,34,34	0
57	MG	1F	302	1/1	0.98	0.09	29,29,29,29	0
57	MG	2A	3610	1/1	0.98	0.07	67,67,67,67	0
57	MG	1F	303	1/1	0.98	0.14	25,25,25,25	0
57	MG	1F	304	1/1	0.98	0.10	35,35,35,35	0
57	MG	2A	3375	1/1	0.98	0.04	35,35,35,35	0
57	MG	2A	3376	1/1	0.98	0.04	36,36,36,36	0
57	MG	1A	3341	1/1	0.98	0.05	22,22,22,22	0
57	MG	1a	1853	1/1	0.98	0.04	58,58,58,58	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1F	306	1/1	0.98	0.09	35,35,35,35	0
57	MG	1F	307	1/1	0.98	0.12	27,27,27,27	0
57	MG	1A	3922	1/1	0.98	0.06	52,52,52,52	0
57	MG	1A	3153	1/1	0.98	0.26	36,36,36,36	0
57	MG	1F	310	1/1	0.98	0.06	31,31,31,31	0
57	MG	1A	3201	1/1	0.98	0.14	40,40,40,40	0
57	MG	1A	3119	1/1	0.98	0.07	29,29,29,29	0
57	MG	1a	1861	1/1	0.98	0.12	52,52,52,52	0
57	MG	2A	3166	1/1	0.98	0.13	49,49,49,49	0
57	MG	1A	3013	1/1	0.98	0.07	16,16,16,16	0
57	MG	1A	3496	1/1	0.98	0.07	53,53,53,53	0
57	MG	1A	3156	1/1	0.98	0.11	25,25,25,25	0
57	MG	1a	1682	1/1	0.98	0.13	42,42,42,42	0
57	MG	1A	3800	1/1	0.98	0.13	46,46,46,46	0
57	MG	1a	1684	1/1	0.98	0.10	44,44,44,44	0
57	MG	2a	3058	1/1	0.98	0.14	45,45,45,45	0
57	MG	1A	3009	1/1	0.98	0.06	30,30,30,30	0
57	MG	1A	3932	1/1	0.98	0.06	50,50,50,50	0
57	MG	1A	3933	1/1	0.98	0.10	58,58,58,58	0
57	MG	2A	3398	1/1	0.98	0.04	32,32,32,32	0
57	MG	1A	3207	1/1	0.98	0.13	37,37,37,37	0
57	MG	1A	3015	1/1	0.98	0.05	37,37,37,37	0
57	MG	1A	3592	1/1	0.98	0.15	49,49,49,49	0
57	MG	1A	3210	1/1	0.98	0.23	32,32,32,32	0
57	MG	1A	3938	1/1	0.98	0.04	61,61,61,61	0
57	MG	2A	3182	1/1	0.98	0.06	45,45,45,45	0
57	MG	2A	3644	1/1	0.98	0.05	53,53,53,53	0
57	MG	1A	3351	1/1	0.98	0.05	51,51,51,51	0
57	MG	1A	3940	1/1	0.98	0.10	41,41,41,41	0
57	MG	1A	3279	1/1	0.98	0.03	23,23,23,23	0
57	MG	1A	3596	1/1	0.98	0.04	34,34,34,34	0
57	MG	2A	3187	1/1	0.98	0.14	56,56,56,56	0
57	MG	2A	3412	1/1	0.98	0.04	52,52,52,52	0
57	MG	1A	3696	1/1	0.98	0.12	43,43,43,43	0
57	MG	1P	201	1/1	0.98	0.20	31,31,31,31	0
57	MG	1A	3504	1/1	0.98	0.05	43,43,43,43	0
57	MG	1A	3159	1/1	0.98	0.06	32,32,32,32	0
57	MG	1A	3946	1/1	0.98	0.03	27,27,27,27	0
57	MG	1A	3812	1/1	0.98	0.09	45,45,45,45	0
57	MG	1Q	203	1/1	0.98	0.08	46,46,46,46	0
57	MG	2A	3660	1/1	0.98	0.06	43,43,43,43	0
57	MG	2A	3661	1/1	0.98	0.10	58,58,58,58	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3212	1/1	0.98	0.20	28,28,28,28	0
57	MG	1A	3814	1/1	0.98	0.05	42,42,42,42	0
57	MG	1R	201	1/1	0.98	0.09	32,32,32,32	0
57	MG	1A	3950	1/1	0.98	0.07	35,35,35,35	0
57	MG	1A	3815	1/1	0.98	0.06	37,37,37,37	0
57	MG	1A	3282	1/1	0.98	0.21	41,41,41,41	0
57	MG	1A	3093	1/1	0.98	0.04	13,13,13,13	0
57	MG	1A	3059	1/1	0.98	0.08	37,37,37,37	0
57	MG	1A	3510	1/1	0.98	0.07	16,16,16,16	0
57	MG	1T	204	1/1	0.98	0.12	53,53,53,53	0
57	MG	2A	3205	1/1	0.98	0.06	46,46,46,46	0
57	MG	2A	3431	1/1	0.98	0.10	45,45,45,45	0
57	MG	2A	3432	1/1	0.98	0.05	35,35,35,35	0
57	MG	1A	3956	1/1	0.98	0.07	53,53,53,53	0
57	MG	2A	3004	1/1	0.98	0.06	38,38,38,38	0
57	MG	1A	3511	1/1	0.98	0.04	20,20,20,20	0
57	MG	2A	3679	1/1	0.98	0.05	55,55,55,55	0
57	MG	1A	3430	1/1	0.98	0.07	37,37,37,37	0
57	MG	2A	3007	1/1	0.98	0.06	40,40,40,40	0
57	MG	1A	3959	1/1	0.98	0.06	41,41,41,41	0
57	MG	1A	3215	1/1	0.98	0.06	25,25,25,25	0
57	MG	2A	3011	1/1	0.98	0.05	36,36,36,36	0
57	MG	1A	3162	1/1	0.98	0.07	27,27,27,27	0
57	MG	1A	3433	1/1	0.98	0.04	26,26,26,26	0
57	MG	2a	3109	1/1	0.98	0.04	64,64,64,64	0
57	MG	1A	3163	1/1	0.98	0.11	40,40,40,40	0
57	MG	1a	1722	1/1	0.98	0.12	47,47,47,47	0
57	MG	2A	3218	1/1	0.98	0.17	47,47,47,47	0
57	MG	1V	201	1/1	0.98	0.15	25,25,25,25	0
57	MG	1V	202	1/1	0.98	0.17	26,26,26,26	0
57	MG	1V	203	1/1	0.98	0.06	42,42,42,42	0
57	MG	2A	3020	1/1	0.98	0.17	39,39,39,39	0
57	MG	1A	3826	1/1	0.98	0.06	25,25,25,25	0
57	MG	1A	3965	1/1	0.98	0.04	27,27,27,27	0
57	MG	1A	3218	1/1	0.98	0.12	28,28,28,28	0
57	MG	1V	207	1/1	0.98	0.04	52,52,52,52	0
57	MG	1A	3518	1/1	0.98	0.04	51,51,51,51	0
57	MG	2A	3026	1/1	0.98	0.06	42,42,42,42	0
57	MG	1A	3612	1/1	0.98	0.13	32,32,32,32	0
57	MG	2A	3029	1/1	0.98	0.03	29,29,29,29	0
57	MG	1a	1732	1/1	0.98	0.06	33,33,33,33	0
57	MG	1A	3363	1/1	0.98	0.04	13,13,13,13	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3012	1/1	0.98	0.05	35,35,35,35	0
57	MG	1A	3291	1/1	0.98	0.07	16,16,16,16	0
57	MG	1Y	202	1/1	0.98	0.04	63,63,63,63	0
57	MG	1Z	301	1/1	0.98	0.11	60,60,60,60	0
57	MG	1A	3439	1/1	0.98	0.04	12,12,12,12	0
57	MG	2A	3238	1/1	0.98	0.20	44,44,44,44	0
57	MG	1A	3523	1/1	0.98	0.05	20,20,20,20	0
57	MG	1A	3061	1/1	0.98	0.04	36,36,36,36	0
57	MG	1a	1743	1/1	0.98	0.04	40,40,40,40	0
57	MG	1A	3525	1/1	0.98	0.06	42,42,42,42	0
57	MG	1A	3441	1/1	0.98	0.09	30,30,30,30	0
57	MG	1A	3840	1/1	0.98	0.04	41,41,41,41	0
57	MG	1A	3166	1/1	0.98	0.20	27,27,27,27	0
57	MG	2a	3140	1/1	0.98	0.08	51,51,51,51	0
57	MG	1A	3722	1/1	0.98	0.04	24,24,24,24	0
57	MG	2A	3475	1/1	0.98	0.04	53,53,53,53	0
57	MG	2a	3143	1/1	0.98	0.10	61,61,61,61	0
57	MG	1A	3843	1/1	0.98	0.04	19,19,19,19	0
57	MG	1a	1750	1/1	0.98	0.05	49,49,49,49	0
57	MG	1A	3075	1/1	0.98	0.20	29,29,29,29	0
57	MG	1A	3724	1/1	0.98	0.10	31,31,31,31	0
57	MG	1A	3725	1/1	0.98	0.05	39,39,39,39	0
57	MG	1A	3295	1/1	0.98	0.07	31,31,31,31	0
57	MG	1A	3223	1/1	0.98	0.08	33,33,33,33	0
57	MG	1A	3986	1/1	0.98	0.07	38,38,38,38	0
57	MG	1A	3098	1/1	0.98	0.26	37,37,37,37	0
57	MG	2A	3485	1/1	0.98	0.09	48,48,48,48	0
57	MG	1A	3225	1/1	0.98	0.23	37,37,37,37	0
57	MG	15	102	1/1	0.98	0.15	27,27,27,27	0
57	MG	2A	3258	1/1	0.98	0.12	45,45,45,45	0
57	MG	2A	3489	1/1	0.98	0.06	28,28,28,28	0
57	MG	1A	3731	1/1	0.98	0.07	49,49,49,49	0
57	MG	1A	3732	1/1	0.98	0.05	20,20,20,20	0
57	MG	1a	1762	1/1	0.98	0.06	52,52,52,52	0
57	MG	1A	3300	1/1	0.98	0.11	30,30,30,30	0
57	MG	1A	3992	1/1	0.98	0.05	47,47,47,47	0
57	MG	2a	3163	1/1	0.98	0.05	64,64,64,64	0
57	MG	1A	3226	1/1	0.98	0.05	29,29,29,29	0
57	MG	2a	3165	1/1	0.98	0.05	60,60,60,60	0
57	MG	17	101	1/1	0.98	0.07	34,34,34,34	0
57	MG	1A	3169	1/1	0.98	0.08	43,43,43,43	0
57	MG	2A	3267	1/1	0.98	0.04	37,37,37,37	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	17	103	1/1	0.98	0.12	38,38,38,38	0
57	MG	2A	3269	1/1	0.98	0.14	27,27,27,27	0
57	MG	1A	3736	1/1	0.98	0.10	37,37,37,37	0
57	MG	1A	3857	1/1	0.98	0.05	34,34,34,34	0
57	MG	1A	3631	1/1	0.98	0.07	33,33,33,33	0
57	MG	1A	3538	1/1	0.98	0.20	27,27,27,27	0
57	MG	1A	3860	1/1	0.98	0.11	41,41,41,41	0
57	MG	1A	4000	1/1	0.98	0.04	44,44,44,44	0
57	MG	1A	3633	1/1	0.98	0.08	45,45,45,45	0
57	MG	2a	3178	1/1	0.98	0.04	50,50,50,50	0
57	MG	2A	3277	1/1	0.98	0.04	29,29,29,29	0
57	MG	2A	3509	1/1	0.98	0.04	32,32,32,32	0
57	MG	1A	3634	1/1	0.98	0.05	37,37,37,37	0
57	MG	1A	3451	1/1	0.98	0.04	23,23,23,23	0
57	MG	1A	3100	1/1	0.98	0.04	46,46,46,46	0
57	MG	1A	3172	1/1	0.98	0.12	23,23,23,23	0
57	MG	2A	3076	1/1	0.98	0.09	46,46,46,46	0
57	MG	2a	3186	1/1	0.98	0.11	57,57,57,57	0
57	MG	2A	3284	1/1	0.98	0.13	53,53,53,53	0
57	MG	1A	3076	1/1	0.98	0.10	29,29,29,29	0
57	MG	1A	4008	1/1	0.98	0.14	34,34,34,34	0
57	MG	1A	3175	1/1	0.98	0.13	28,28,28,28	0
57	MG	1A	3131	1/1	0.98	0.12	25,25,25,25	0
57	MG	1A	3457	1/1	0.98	0.05	43,43,43,43	0
57	MG	2D	301	1/1	0.98	0.13	38,38,38,38	0
57	MG	2A	3290	1/1	0.98	0.06	44,44,44,44	0
57	MG	1A	4012	1/1	0.98	0.17	42,42,42,42	0
57	MG	2A	3524	1/1	0.98	0.05	30,30,30,30	0
57	MG	1A	3458	1/1	0.98	0.06	51,51,51,51	0
58	CLM	1A	4017	20/20	0.98	0.06	18,23,33,39	0
57	MG	1A	3548	1/1	0.98	0.12	34,34,34,34	0
57	MG	1A	3178	1/1	0.98	0.13	29,29,29,29	0
57	MG	2A	3086	1/1	0.98	0.05	39,39,39,39	0
57	MG	1A	3017	1/1	0.98	0.13	31,31,31,31	0
57	MG	1A	3753	1/1	0.98	0.10	39,39,39,39	0
57	MG	1A	3079	1/1	0.98	0.06	41,41,41,41	0
57	MG	1A	3877	1/1	0.98	0.04	25,25,25,25	0
57	MG	1A	3314	1/1	0.98	0.04	16,16,16,16	0
57	MG	1A	3756	1/1	0.98	0.04	39,39,39,39	0
57	MG	1A	3134	1/1	0.98	0.14	26,26,26,26	0
61	ZN	15	108	1/1	0.98	0.04	43,43,43,43	0
57	MG	1a	1620	1/1	0.98	0.05	39,39,39,39	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2F	302	1/1	0.98	0.05	40,40,40,40	0
61	ZN	29	501	1/1	0.98	0.05	65,65,65,65	0
61	ZN	2n	501	1/1	0.98	0.05	86,86,86,86	0
62	SF4	1d	305	8/8	0.98	0.05	59,64,67,72	0
62	SF4	2d	501	8/8	0.98	0.04	63,75,82,85	0
57	MG	1A	3530	1/1	0.99	0.04	25,25,25,25	0
57	MG	1a	1741	1/1	0.99	0.04	36,36,36,36	0
57	MG	1A	3209	1/1	0.99	0.12	36,36,36,36	0
57	MG	1A	3146	1/1	0.99	0.06	29,29,29,29	0
57	MG	2A	3685	1/1	0.99	0.04	34,34,34,34	0
57	MG	1A	3469	1/1	0.99	0.06	42,42,42,42	0
57	MG	1A	3470	1/1	0.99	0.03	31,31,31,31	0
57	MG	1D	302	1/1	0.99	0.18	33,33,33,33	0
57	MG	1A	3177	1/1	0.99	0.09	30,30,30,30	0
57	MG	1D	304	1/1	0.99	0.09	38,38,38,38	0
57	MG	1A	3299	1/1	0.99	0.14	31,31,31,31	0
57	MG	1A	3118	1/1	0.99	0.04	19,19,19,19	0
57	MG	2A	3354	1/1	0.99	0.04	46,46,46,46	0
57	MG	1A	3413	1/1	0.99	0.02	28,28,28,28	0
57	MG	1A	3891	1/1	0.99	0.03	40,40,40,40	0
57	MG	1D	309	1/1	0.99	0.04	16,16,16,16	0
57	MG	2A	3358	1/1	0.99	0.06	39,39,39,39	0
57	MG	2A	3468	1/1	0.99	0.05	32,32,32,32	0
57	MG	1A	3044	1/1	0.99	0.06	20,20,20,20	0
57	MG	1D	311	1/1	0.99	0.08	32,32,32,32	0
57	MG	1a	1850	1/1	0.99	0.07	51,51,51,51	0
57	MG	1A	3254	1/1	0.99	0.16	25,25,25,25	0
57	MG	1A	3541	1/1	0.99	0.03	28,28,28,28	0
57	MG	1A	3895	1/1	0.99	0.03	27,27,27,27	0
57	MG	1A	3018	1/1	0.99	0.07	27,27,27,27	0
57	MG	1A	3046	1/1	0.99	0.02	19,19,19,19	0
57	MG	1A	3006	1/1	0.99	0.02	21,21,21,21	0
57	MG	1A	3360	1/1	0.99	0.03	20,20,20,20	0
57	MG	1A	3749	1/1	0.99	0.05	23,23,23,23	0
57	MG	1A	3078	1/1	0.99	0.24	32,32,32,32	0
57	MG	1A	3048	1/1	0.99	0.09	41,41,41,41	0
57	MG	1E	301	1/1	0.99	0.09	25,25,25,25	0
57	MG	1A	3099	1/1	0.99	0.18	28,28,28,28	0
57	MG	1A	3309	1/1	0.99	0.07	19,19,19,19	0
57	MG	1A	3905	1/1	0.99	0.04	49,49,49,49	0
57	MG	1E	305	1/1	0.99	0.10	39,39,39,39	0
57	MG	1A	3310	1/1	0.99	0.06	35,35,35,35	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3023	1/1	0.99	0.18	32,32,32,32	0
57	MG	1A	3187	1/1	0.99	0.10	27,27,27,27	0
57	MG	1F	301	1/1	0.99	0.15	23,23,23,23	0
57	MG	1A	3686	1/1	0.99	0.03	33,33,33,33	0
57	MG	1A	3313	1/1	0.99	0.13	34,34,34,34	0
57	MG	2A	3176	1/1	0.99	0.09	42,42,42,42	0
57	MG	1A	3832	1/1	0.99	0.07	49,49,49,49	0
57	MG	1A	3024	1/1	0.99	0.06	15,15,15,15	0
57	MG	1A	3760	1/1	0.99	0.07	33,33,33,33	0
57	MG	2A	3608	1/1	0.99	0.06	34,34,34,34	0
57	MG	1A	3689	1/1	0.99	0.03	37,37,37,37	0
57	MG	1A	3102	1/1	0.99	0.09	29,29,29,29	0
57	MG	2A	3283	1/1	0.99	0.06	37,37,37,37	0
57	MG	1A	3103	1/1	0.99	0.20	26,26,26,26	0
57	MG	1A	3838	1/1	0.99	0.05	33,33,33,33	0
57	MG	2A	3614	1/1	0.99	0.04	50,50,50,50	0
57	MG	1A	3623	1/1	0.99	0.07	29,29,29,29	0
57	MG	1A	3266	1/1	0.99	0.14	23,23,23,23	0
57	MG	2A	3394	1/1	0.99	0.08	39,39,39,39	0
57	MG	1A	3318	1/1	0.99	0.04	36,36,36,36	0
57	MG	1A	4001	1/1	0.99	0.06	40,40,40,40	0
57	MG	1A	3267	1/1	0.99	0.17	30,30,30,30	0
57	MG	1A	3375	1/1	0.99	0.05	27,27,27,27	0
57	MG	2A	3399	1/1	0.99	0.04	36,36,36,36	0
57	MG	1A	3561	1/1	0.99	0.09	33,33,33,33	0
57	MG	1A	3051	1/1	0.99	0.13	30,30,30,30	0
57	MG	1A	3925	1/1	0.99	0.06	49,49,49,49	0
57	MG	1A	3083	1/1	0.99	0.19	34,34,34,34	0
57	MG	1A	3772	1/1	0.99	0.03	41,41,41,41	0
57	MG	2A	3628	1/1	0.99	0.03	21,21,21,21	0
57	MG	2A	3515	1/1	0.99	0.07	46,46,46,46	0
57	MG	1A	3052	1/1	0.99	0.14	30,30,30,30	0
57	MG	1A	3271	1/1	0.99	0.07	34,34,34,34	0
57	MG	2A	3407	1/1	0.99	0.06	49,49,49,49	0
57	MG	1A	3324	1/1	0.99	0.07	22,22,22,22	0
57	MG	1A	3025	1/1	0.99	0.14	33,33,33,33	0
57	MG	1A	3026	1/1	0.99	0.12	30,30,30,30	0
57	MG	1A	3109	1/1	0.99	0.14	31,31,31,31	0
57	MG	1A	3003	1/1	0.99	0.05	21,21,21,21	0
57	MG	1A	3276	1/1	0.99	0.20	40,40,40,40	0
57	MG	1A	3386	1/1	0.99	0.03	32,32,32,32	0
57	MG	1A	3277	1/1	0.99	0.03	27,27,27,27	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1P	203	1/1	0.99	0.17	23,23,23,23	0
57	MG	1A	3111	1/1	0.99	0.06	34,34,34,34	0
57	MG	1A	3233	1/1	0.99	0.03	32,32,32,32	0
57	MG	2A	3009	1/1	0.99	0.03	34,34,34,34	0
57	MG	1Q	201	1/1	0.99	0.03	36,36,36,36	0
57	MG	2A	3109	1/1	0.99	0.05	33,33,33,33	0
57	MG	1A	3234	1/1	0.99	0.05	33,33,33,33	0
57	MG	1A	3042	1/1	0.99	0.07	17,17,17,17	0
57	MG	1A	3236	1/1	0.99	0.20	27,27,27,27	0
57	MG	1A	3237	1/1	0.99	0.13	28,28,28,28	0
57	MG	2A	3015	1/1	0.99	0.14	33,33,33,33	0
57	MG	1A	3580	1/1	0.99	0.08	26,26,26,26	0
57	MG	1R	202	1/1	0.99	0.09	34,34,34,34	0
57	MG	2A	3655	1/1	0.99	0.08	35,35,35,35	0
57	MG	1A	3057	1/1	0.99	0.07	19,19,19,19	0
57	MG	1A	3338	1/1	0.99	0.09	37,37,37,37	0
57	MG	1A	3043	1/1	0.99	0.05	24,24,24,24	0
57	MG	1A	3091	1/1	0.99	0.04	36,36,36,36	0
57	MG	1A	3203	1/1	0.99	0.19	42,42,42,42	0
57	MG	2A	3325	1/1	0.99	0.04	40,40,40,40	0
57	MG	2E	307	1/1	0.99	0.08	33,33,33,33	0
57	MG	1A	3171	1/1	0.99	0.16	35,35,35,35	0
57	MG	1A	3243	1/1	0.99	0.15	28,28,28,28	0
57	MG	2A	3124	1/1	0.99	0.07	42,42,42,42	0
57	MG	2A	3329	1/1	0.99	0.18	47,47,47,47	0
57	MG	1A	3290	1/1	0.99	0.10	20,20,20,20	0
57	MG	1A	3143	1/1	0.99	0.03	22,22,22,22	0
57	MG	1A	3874	1/1	0.99	0.06	31,31,31,31	0
57	MG	2A	3028	1/1	0.99	0.03	27,27,27,27	0
57	MG	1A	3173	1/1	0.99	0.12	23,23,23,23	0
57	MG	1A	3116	1/1	0.99	0.11	31,31,31,31	0
57	MG	1A	3405	1/1	0.99	0.04	24,24,24,24	0
57	MG	1A	3527	1/1	0.99	0.21	20,20,20,20	0
57	MG	1U	205	1/1	0.99	0.12	26,26,26,26	0
61	ZN	16	501	1/1	0.99	0.05	39,39,39,39	0
61	ZN	19	104	1/1	0.99	0.04	40,40,40,40	0
61	ZN	1n	104	1/1	0.99	0.03	63,63,63,63	0
57	MG	2A	3675	1/1	0.99	0.06	50,50,50,50	0
57	MG	1a	1736	1/1	0.99	0.07	39,39,39,39	0
61	ZN	25	104	1/1	0.99	0.05	56,56,56,56	0
61	ZN	26	501	1/1	0.99	0.04	57,57,57,57	0
57	MG	1A	3730	1/1	0.99	0.07	24,24,24,24	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3092	1/1	0.99	0.08	28,28,28,28	0
57	MG	1A	3248	1/1	0.99	0.09	28,28,28,28	0
57	MG	2A	3680	1/1	0.99	0.03	35,35,35,35	0
57	MG	1A	3140	1/1	1.00	0.07	23,23,23,23	0
57	MG	2A	3654	1/1	1.00	0.05	37,37,37,37	0
61	ZN	1Y	203	1/1	1.00	0.03	56,56,56,56	0
57	MG	1A	3476	1/1	1.00	0.06	41,41,41,41	0

6.5 Other polymers (i)

There are no such residues in this entry.