



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 26, 2026 – 02:53 PM EDT

PDB ID : 7RQB / pdb_00007rqb
Title : Crystal structure of the *Thermus thermophilus* 70S ribosome in complex with protein Y, A-site aminoacyl-tRNA analog ACC-PMN, and P-site MAI-tripeptidyl-tRNA analog ACCA-IAM at 2.45Å resolution
Authors : Syroegin, E.A.; Flemmich, L.; Klepacki, D.; Vazquez-Laslop, N.; Micura, R.; Polikanov, Y.S.
Deposited on : 2021-08-06
Resolution : 2.45 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

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

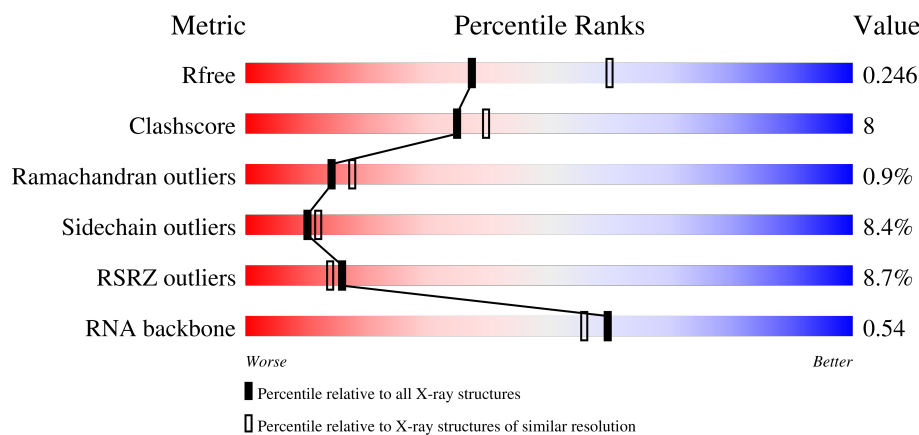
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.45 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	1190 (2.46-2.46)
Clashscore	190562	1229 (2.46-2.46)
Ramachandran outliers	187476	1218 (2.46-2.46)
Sidechain outliers	187428	1218 (2.46-2.46)
RSRZ outliers	180081	1190 (2.46-2.46)
RNA backbone	3983	1023 (2.72-2.20)

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 $\leq 5\%$. 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	
1	2A	2915	
2	1B	121	

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Mol	Chain	Length	Quality of chain
2	2B	121	 3% 65% 28% 6%
3	1D	276	 % 84% 13%
3	2D	276	 2% 82% 13%
4	1E	206	 % 84% 14%
4	2E	206	 % 81% 16%
5	1F	210	 2% 73% 21%
5	2F	210	 3% 66% 27%
6	1G	182	 8% 64% 30% 5%
6	2G	182	 37% 58% 36% 5%
7	1H	180	 3% 76% 18%
7	2H	180	 17% 63% 28%
8	1I	148	 7% 78% 16% 5%
8	2I	148	 14% 63% 30% 6%
9	1N	140	 79% 19%
9	2N	140	 4% 77% 20%
10	1O	122	 % 82% 16%
10	2O	122	 80% 17%
11	1P	150	 % 81% 17%
11	2P	150	 3% 78% 17%
12	1Q	141	 84% 14%
12	2Q	141	 6% 81% 18%
13	1R	118	 84% 15%
13	2R	118	 82% 16%
14	1S	112	 % 79% 18%
14	2S	112	 12% 66% 29%

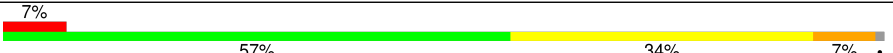
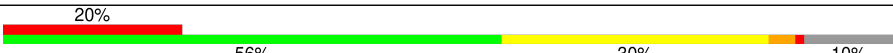
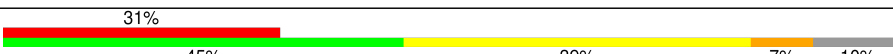
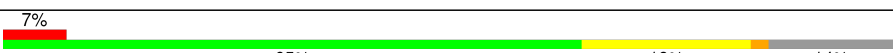
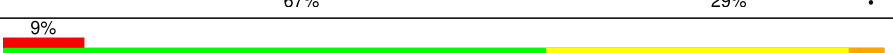
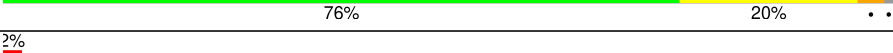
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Mol	Chain	Length	Quality of chain
15	1T	146	3% 68% 18% 10%
15	2T	146	3% 66% 21% 10%
16	1U	118	% 84% 14%
16	2U	118	75% 22%
17	1V	101	85% 14%
17	2V	101	3% 66% 31% 10%
18	1W	113	3% 86% 12%
18	2W	113	4% 83% 14%
19	1X	96	2% 74% 21%
19	2X	96	6% 74% 25%
20	1Y	110	2% 74% 21%
20	2Y	110	7% 65% 27% 5%
21	1Z	206	3% 76% 20%
21	2Z	206	16% 67% 29%
22	10	85	% 78% 20%
22	20	85	6% 82% 15%
23	11	98	% 77% 22%
23	21	98	2% 68% 26%
24	12	72	3% 78% 17%
24	22	72	6% 65% 29%
25	13	60	2% 73% 25%
25	23	60	5% 75% 22%
26	14	71	21% 56% 37%
26	24	71	49% 46% 41% 8%
27	15	60	2% 83% 13%

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Mol	Chain	Length	Quality of chain
27	25	60	
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	

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Mol	Chain	Length	Quality of chain
40	1i	128	
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	

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Mol	Chain	Length	Quality of chain
52	2u	27	
53	1y	113	
53	2y	113	
54	1w	4	
54	2w	4	
55	1x	4	
55	2x	4	
56	1v	3	
56	2v	3	

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	3576	-	-	-	X
57	MG	1A	3698	-	-	-	X
57	MG	1a	1702	-	-	-	X
57	MG	1a	1711	-	-	-	X
57	MG	1a	1822	-	-	-	X
57	MG	2A	3047	-	-	-	X
57	MG	2A	3159	-	-	-	X
57	MG	2a	3009	-	-	-	X
57	MG	2a	3045	-	-	-	X

2 Entry composition

There are 62 unique types of molecules in this entry. The entry contains 297350 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	C	N	O	S	0	0	0
			933	588	171	170	4			

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

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

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

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

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

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

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

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

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

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

- 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 Aminoacyl-tRNA Analog.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
54	1w	4	Total	C	N	O	P	0	0	1
			78	40	13	22	3			
54	2w	4	Total	C	N	O	P	0	0	1
			78	40	13	22	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	1013	Total	Mg	0	0
			1013	1013		
57	1B	30	Total	Mg	0	0
			30	30		
57	1D	17	Total	Mg	0	0
			17	17		
57	1E	8	Total	Mg	0	0
			8	8		
57	1F	17	Total	Mg	0	0
			17	17		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
57	1G	4	Total 4	Mg 4	0	0
57	1H	2	Total 2	Mg 2	0	0
57	1N	4	Total 4	Mg 4	0	0
57	1O	1	Total 1	Mg 1	0	0
57	1P	3	Total 3	Mg 3	0	0
57	1Q	5	Total 5	Mg 5	0	0
57	1R	7	Total 7	Mg 7	0	0
57	1T	7	Total 7	Mg 7	0	0
57	1U	5	Total 5	Mg 5	0	0
57	1V	7	Total 7	Mg 7	0	0
57	1W	3	Total 3	Mg 3	0	0
57	1Y	1	Total 1	Mg 1	0	0
57	1Z	1	Total 1	Mg 1	0	0
57	10	8	Total 8	Mg 8	0	0
57	11	5	Total 5	Mg 5	0	0
57	13	3	Total 3	Mg 3	0	0
57	15	7	Total 7	Mg 7	0	0
57	17	6	Total 6	Mg 6	0	0
57	18	3	Total 3	Mg 3	0	0
57	19	1	Total 1	Mg 1	0	0
57	1a	267	Total 267	Mg 267	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
57	1b	1	Total Mg 1 1	0	0
57	1d	5	Total Mg 5 5	0	0
57	1e	5	Total Mg 5 5	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	3	Total Mg 3 3	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	731	Total Mg 731 731	0	0
57	2B	19	Total Mg 19 19	0	0
57	2D	10	Total Mg 10 10	0	0
57	2E	6	Total Mg 6 6	0	0
57	2F	5	Total Mg 5 5	0	0
57	2G	2	Total Mg 2 2	0	0
57	2I	1	Total Mg 1 1	0	0

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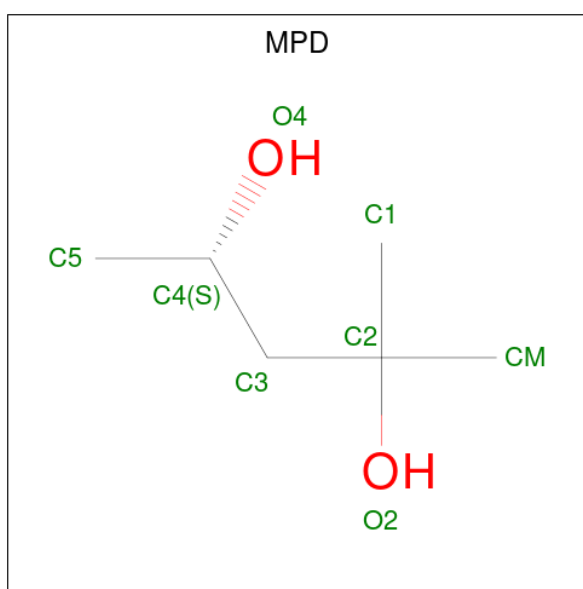
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
57	2O	2	Total 2	Mg 2	0	0
57	2P	1	Total 1	Mg 1	0	0
57	2Q	3	Total 3	Mg 3	0	0
57	2R	3	Total 3	Mg 3	0	0
57	2T	4	Total 4	Mg 4	0	0
57	2U	2	Total 2	Mg 2	0	0
57	2V	3	Total 3	Mg 3	0	0
57	2W	3	Total 3	Mg 3	0	0
57	2X	1	Total 1	Mg 1	0	0
57	2Y	1	Total 1	Mg 1	0	0
57	20	2	Total 2	Mg 2	0	0
57	23	1	Total 1	Mg 1	0	0
57	25	2	Total 2	Mg 2	0	0
57	27	2	Total 2	Mg 2	0	0
57	28	2	Total 2	Mg 2	0	0
57	29	1	Total 1	Mg 1	0	0
57	2a	183	Total 183	Mg 183	0	0
57	2e	1	Total 1	Mg 1	0	0
57	2f	2	Total 2	Mg 2	0	0
57	2j	1	Total 1	Mg 1	0	0
57	2k	1	Total 1	Mg 1	0	0

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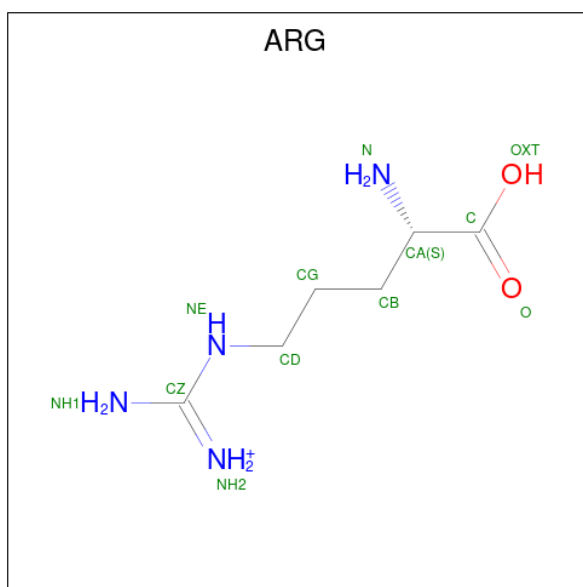
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
57	2p	1	Total	Mg	0	0
			1	1		
57	2r	1	Total	Mg	0	0
			1	1		
57	2t	1	Total	Mg	0	0
			1	1		
57	2x	2	Total	Mg	0	0
			2	2		

- Molecule 58 is (4S)-2-METHYL-2,4-PENTANEDIOL (CCD ID: MPD) (formula: C₆H₁₄O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
58	1A	1	Total	C	O	0	0
			8	6	2		
58	1T	1	Total	C	O	0	0
			8	6	2		
58	18	1	Total	C	O	0	0
			8	6	2		
58	1a	1	Total	C	O	0	0
			8	6	2		
58	2A	1	Total	C	O	0	0
			8	6	2		
58	2B	1	Total	C	O	0	0
			8	6	2		

- Molecule 59 is ARGinine (CCD ID: ARG) (formula: C₆H₁₅N₄O₂).



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

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

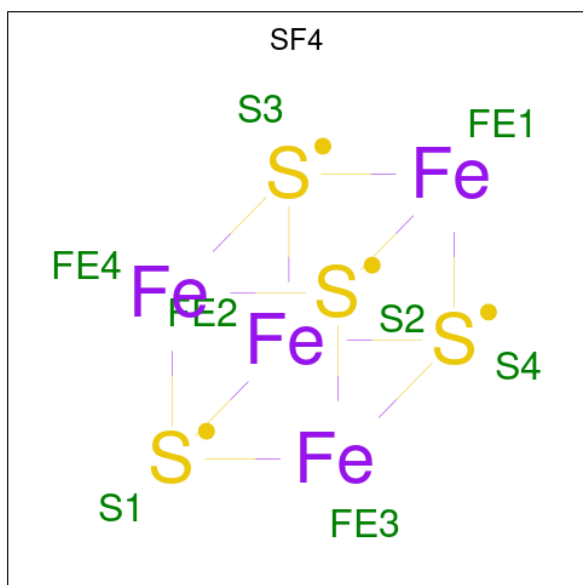
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
60	1Y	1	Total	Zn	0	0
			1	1		
60	14	1	Total	Zn	0	0
			1	1		
60	15	1	Total	Zn	0	0
			1	1		
60	16	1	Total	Zn	0	0
			1	1		
60	19	1	Total	Zn	0	0
			1	1		
60	1n	1	Total	Zn	0	0
			1	1		
60	2Y	1	Total	Zn	0	0
			1	1		
60	24	1	Total	Zn	0	0
			1	1		
60	25	1	Total	Zn	0	0
			1	1		
60	26	1	Total	Zn	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
60	29	1	Total	Zn	0	0
			1	1		
60	2n	1	Total	Zn	0	0
			1	1		

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



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
61	1d	1	Total	Fe	S	0	0
			8	4	4		
61	2d	1	Total	Fe	S	0	0
			8	4	4		

- Molecule 62 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
62	1A	3935	Total	O	0	0
			3935	3935		
62	1B	80	Total	O	0	0
			80	80		
62	1D	108	Total	O	0	0
			108	108		
62	1E	74	Total	O	0	0
			74	74		
62	1F	60	Total	O	0	0
			60	60		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
62	1G	16	Total	O	0	0
			16	16		
62	1H	15	Total	O	0	0
			15	15		
62	1I	5	Total	O	0	0
			5	5		
62	1N	54	Total	O	0	0
			54	54		
62	1O	21	Total	O	0	0
			21	21		
62	1P	63	Total	O	0	0
			63	63		
62	1Q	39	Total	O	0	0
			39	39		
62	1R	28	Total	O	0	0
			28	28		
62	1S	12	Total	O	0	0
			12	12		
62	1T	32	Total	O	0	0
			32	32		
62	1U	53	Total	O	0	0
			53	53		
62	1V	33	Total	O	0	0
			33	33		
62	1W	24	Total	O	0	0
			24	24		
62	1X	24	Total	O	0	0
			24	24		
62	1Y	15	Total	O	0	0
			15	15		
62	1Z	7	Total	O	0	0
			7	7		
62	10	23	Total	O	0	0
			23	23		
62	11	26	Total	O	0	0
			26	26		
62	12	10	Total	O	0	0
			10	10		
62	13	25	Total	O	0	0
			25	25		
62	14	2	Total	O	0	0
			2	2		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
62	15	18	Total 18	O 18	0	0
62	16	18	Total 18	O 18	0	0
62	17	17	Total 17	O 17	0	0
62	18	25	Total 25	O 25	0	0
62	19	5	Total 5	O 5	0	0
62	1a	424	Total 424	O 424	0	0
62	1b	1	Total 1	O 1	0	0
62	1d	8	Total 8	O 8	0	0
62	1e	2	Total 2	O 2	0	0
62	1f	2	Total 2	O 2	0	0
62	1g	1	Total 1	O 1	0	0
62	1h	1	Total 1	O 1	0	0
62	1l	2	Total 2	O 2	0	0
62	1o	4	Total 4	O 4	0	0
62	1p	1	Total 1	O 1	0	0
62	1t	1	Total 1	O 1	0	0
62	1y	2	Total 2	O 2	0	0
62	1w	6	Total 6	O 6	0	0
62	1x	2	Total 2	O 2	0	0
62	2A	2058	Total 2058	O 2058	0	0
62	2B	39	Total 39	O 39	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
62	2D	51	Total 51	O 51	0	0
62	2E	32	Total 32	O 32	0	0
62	2F	26	Total 26	O 26	0	0
62	2G	7	Total 7	O 7	0	0
62	2H	1	Total 1	O 1	0	0
62	2I	2	Total 2	O 2	0	0
62	2N	5	Total 5	O 5	0	0
62	2O	16	Total 16	O 16	0	0
62	2P	26	Total 26	O 26	0	0
62	2Q	14	Total 14	O 14	0	0
62	2R	17	Total 17	O 17	0	0
62	2S	3	Total 3	O 3	0	0
62	2T	7	Total 7	O 7	0	0
62	2U	15	Total 15	O 15	0	0
62	2V	3	Total 3	O 3	0	0
62	2W	17	Total 17	O 17	0	0
62	2X	8	Total 8	O 8	0	0
62	2Y	2	Total 2	O 2	0	0
62	2Z	6	Total 6	O 6	0	0
62	20	8	Total 8	O 8	0	0
62	21	15	Total 15	O 15	0	0

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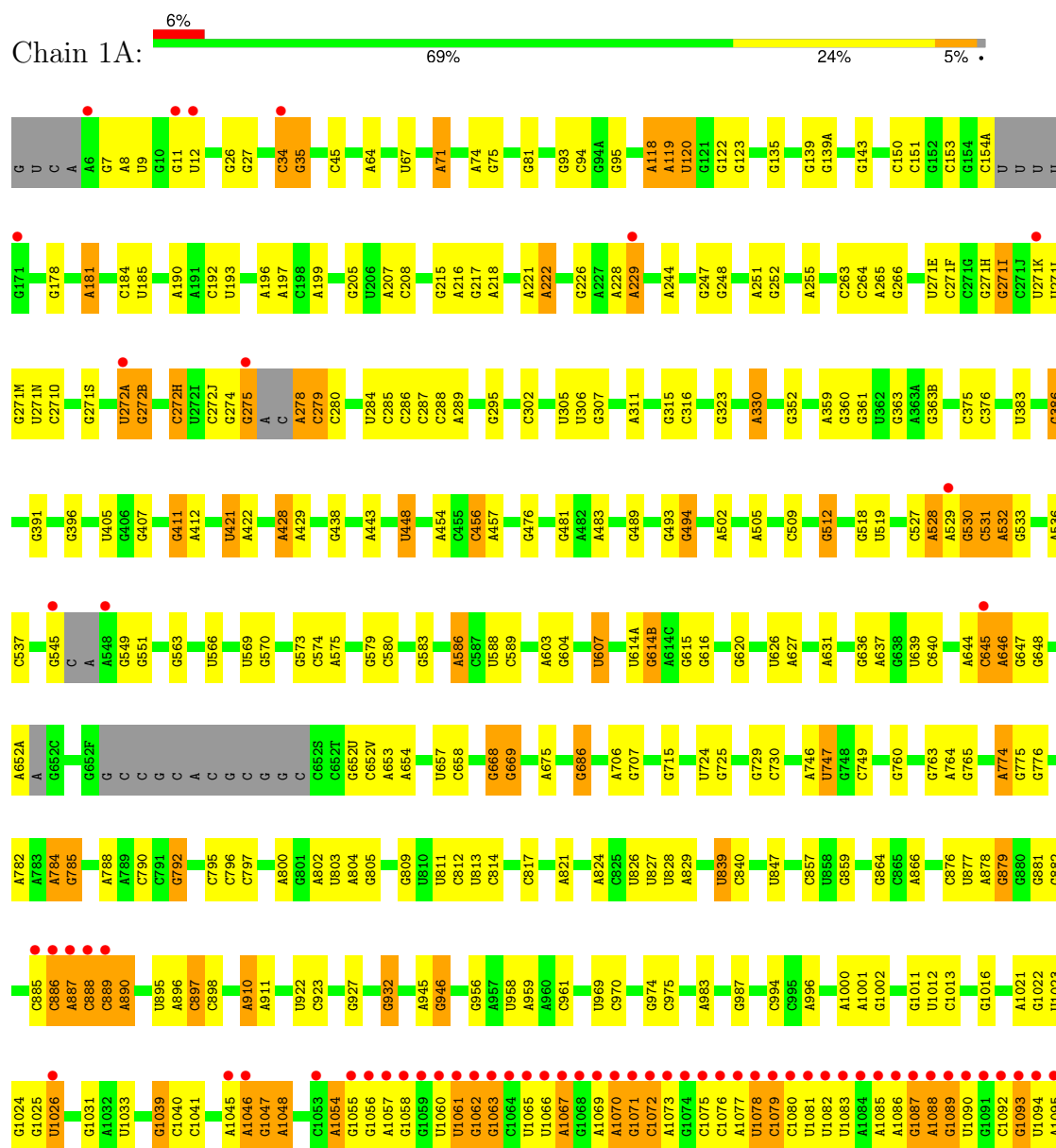
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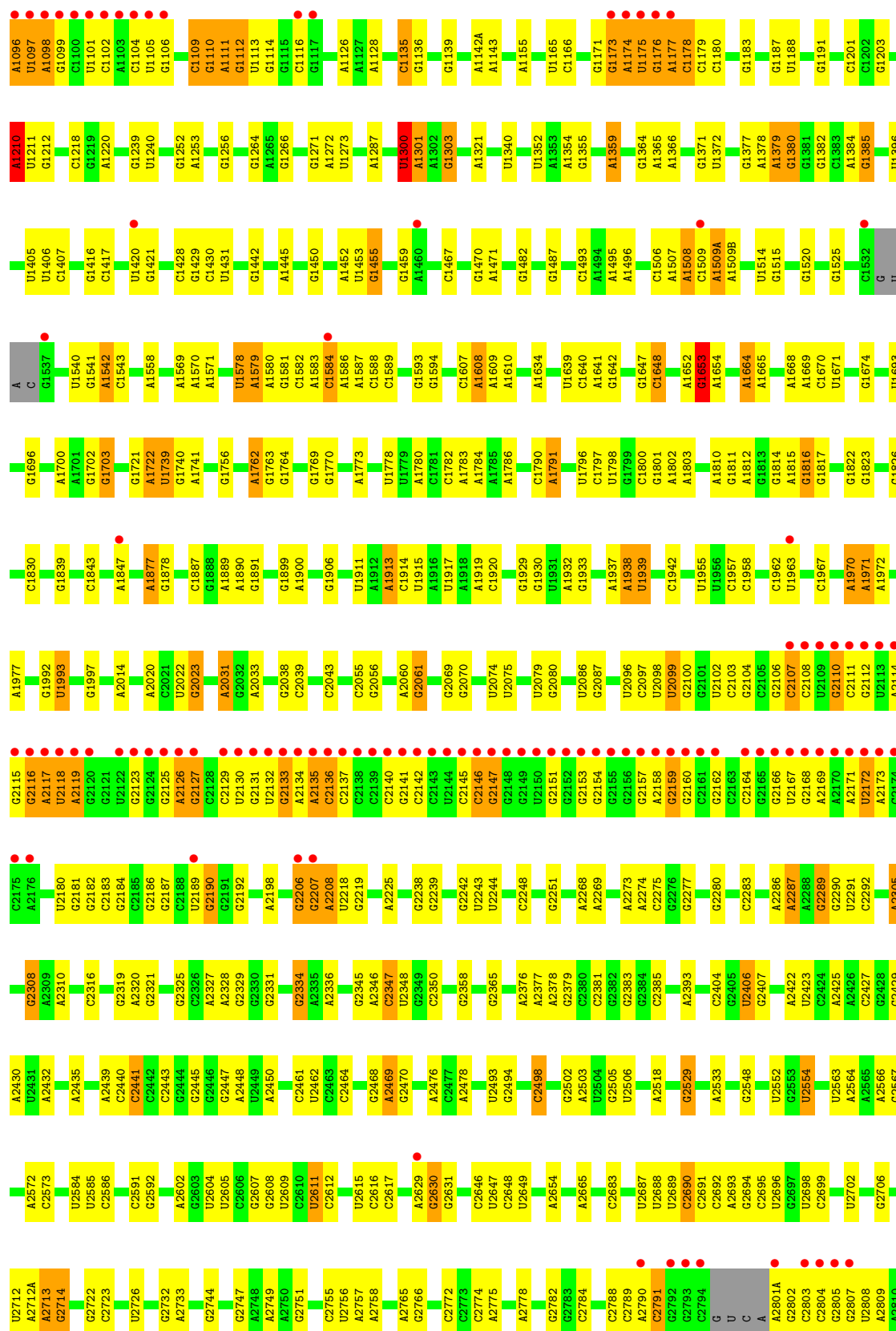
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
62	23	2	Total	O	0	0
			2	2		
62	25	11	Total	O	0	0
			11	11		
62	26	7	Total	O	0	0
			7	7		
62	27	5	Total	O	0	0
			5	5		
62	28	16	Total	O	0	0
			16	16		
62	2a	243	Total	O	0	0
			243	243		
62	2e	2	Total	O	0	0
			2	2		
62	2l	3	Total	O	0	0
			3	3		
62	2m	1	Total	O	0	0
			1	1		
62	2n	2	Total	O	0	0
			2	2		
62	2o	2	Total	O	0	0
			2	2		
62	2p	1	Total	O	0	0
			1	1		
62	2r	4	Total	O	0	0
			4	4		
62	2t	2	Total	O	0	0
			2	2		
62	2w	4	Total	O	0	0
			4	4		
62	2x	3	Total	O	0	0
			3	3		

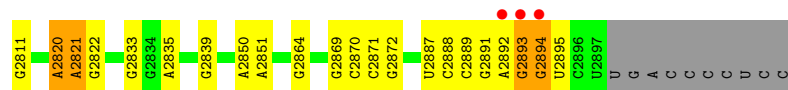
3 Residue-property plots

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.

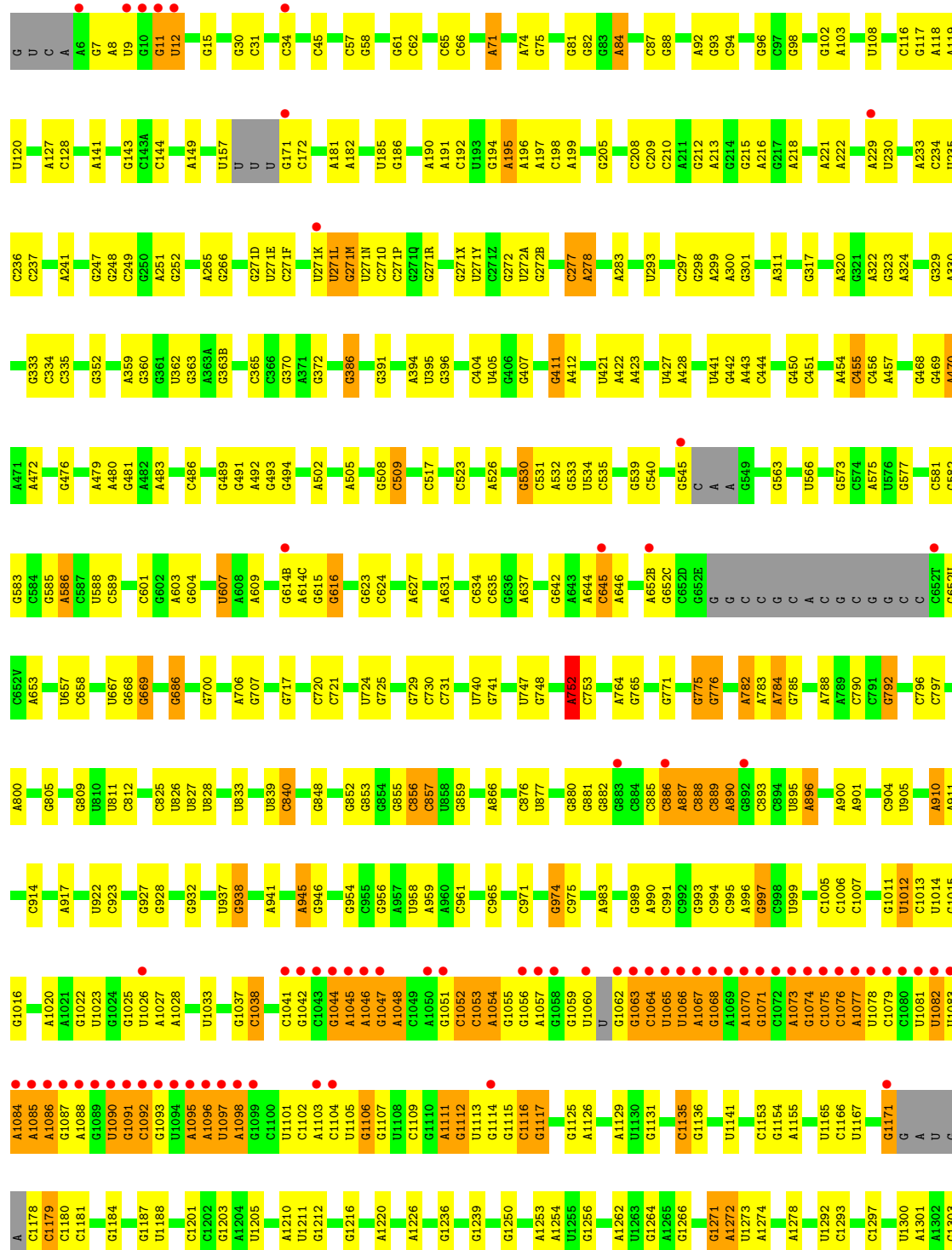
• Molecule 1: 23S Ribosomal RNA



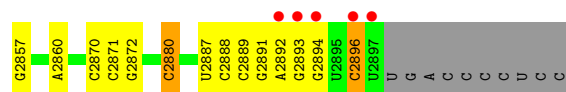




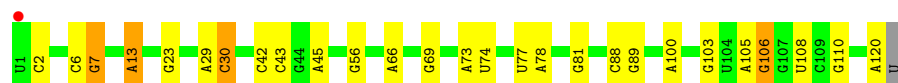
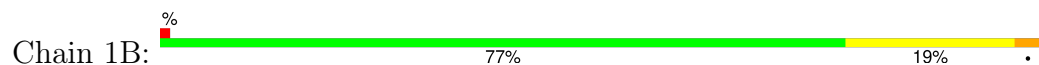
- Molecule 1: 23S Ribosomal RNA



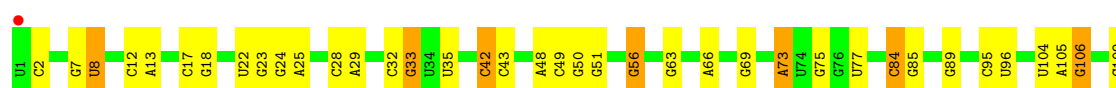
A2749	A2750	A2751	U2756	U2757	U2758	A2764	A2765	A2766	A2767	A2775	C2658	C2659	A2660	A2661	A2662	A2663	A2664	U2682	C2788	C2789	A	C	U	C	A	G	U	C	A	G	A2801A	C2802	C2803	C2804	C2805	C2807	U2808	A2809	A2810	G2818	G2819	A2820	A2821	A2822	A2823	G2833	G2834	U2835	U2836	C2837	C2742	G2838	C2743	C2839	C2840	U2847																																																																																																																																																																																																																																																																																																																																																																										
G2638	A2639	G2640	G2641	G2645	G2646	G2647	G2648	U2649	A2654	A2655	C2658	C2659	A2660	A2661	A2662	A2663	A2664	U2682	C2788	C2789	A	C	U	C	A	G	U	C	A	G	A2801A	C2802	C2803	C2804	C2805	C2807	U2808	A2809	A2810	G2818	G2819	A2820	A2821	A2822	A2823	G2833	G2834	U2835	U2836	C2837	C2742	G2838	C2743	C2839	C2840	U2847																																																																																																																																																																																																																																																																																																																																																																										
G2548	U2552	G2553	U2554	U2555	G2556	G2557	U2562	U2563	A2564	A2565	A2566	G2567	A2572	A2573	A2574	C2575	G2582	U2583	U2584	U2585	U2586	C2591	G2592	U2596	A2602	G2603	U2604	U2605	C2606	G2607	G2608	U2609	C2610	U2611	C2612	U2615	C2616	C2617	G2618	C2619	C2626	G2627	A2733	U2835	C2628	U2836	C2837	C2742	G2838	C2743	C2839	C2840	U2847																																																																																																																																																																																																																																																																																																																																																																													
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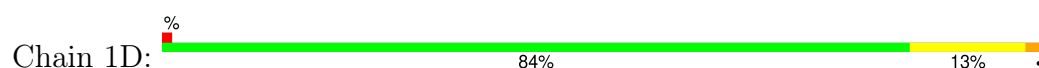
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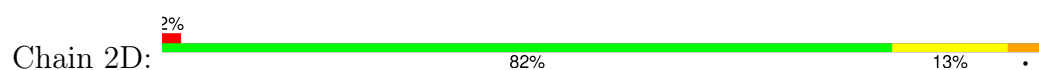
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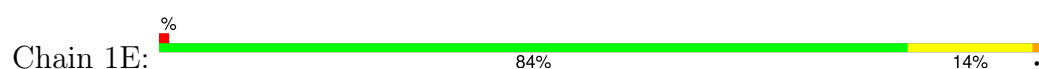
- Molecule 3: 50S ribosomal protein L2



- Molecule 3: 50S ribosomal protein L2

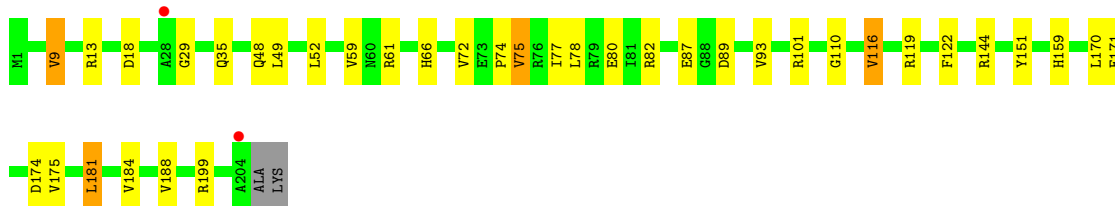
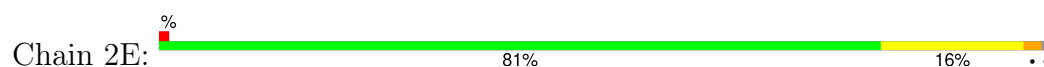


- Molecule 4: 50S ribosomal protein L3

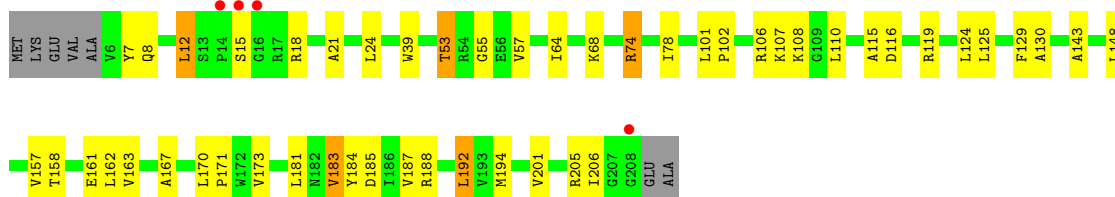
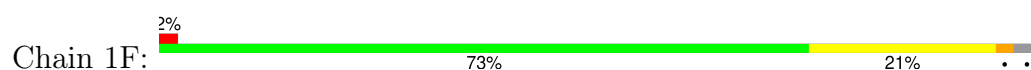




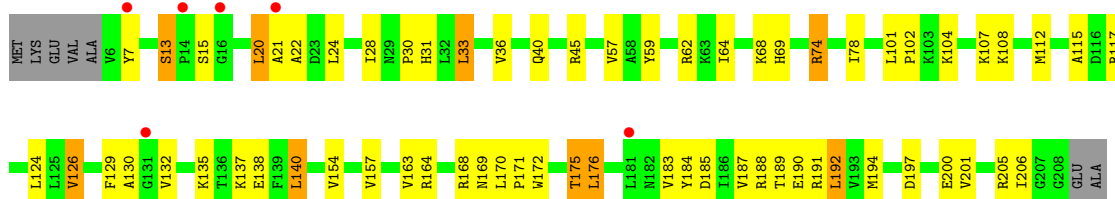
- Molecule 4: 50S ribosomal protein L3



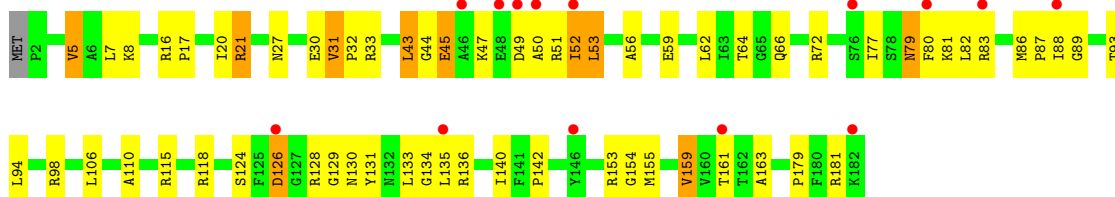
- Molecule 5: 50S ribosomal protein L4



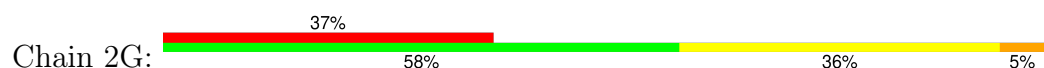
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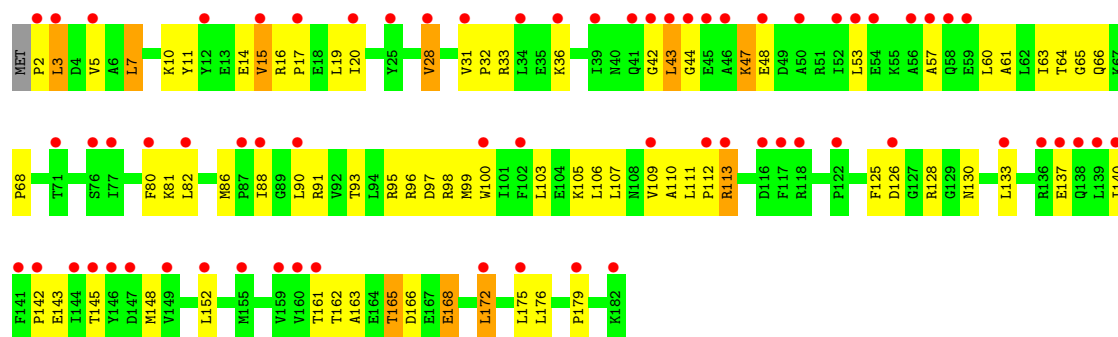


- Molecule 6: 50S ribosomal protein L5

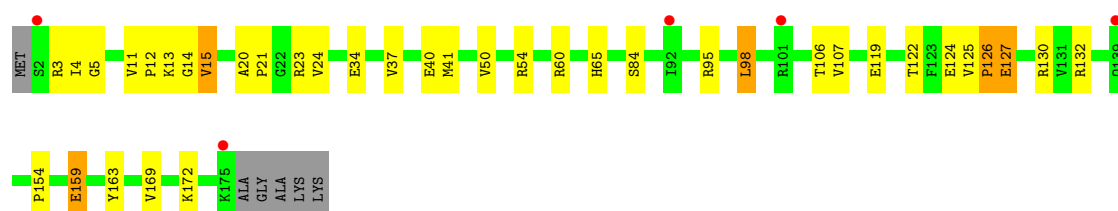
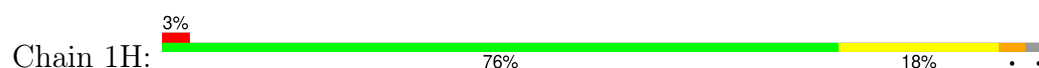


- Molecule 6: 50S ribosomal protein L5

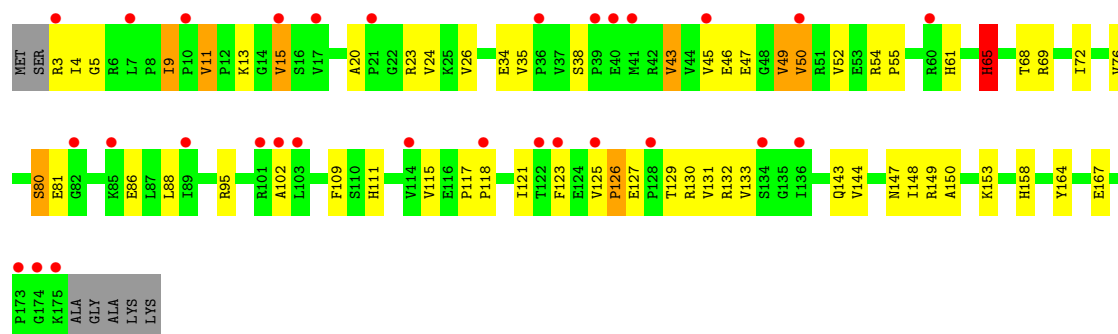




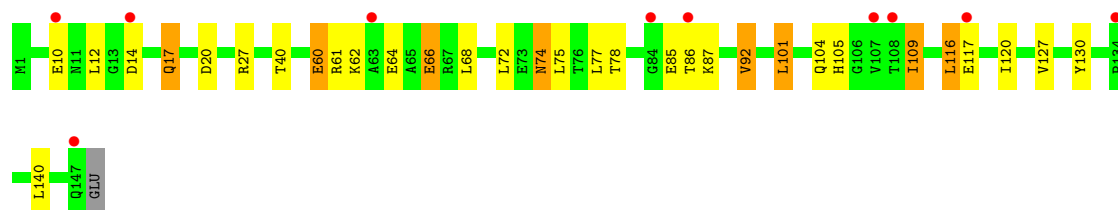
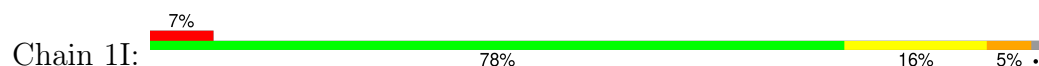
- Molecule 7: 50S ribosomal protein L6



- Molecule 7: 50S ribosomal protein L6

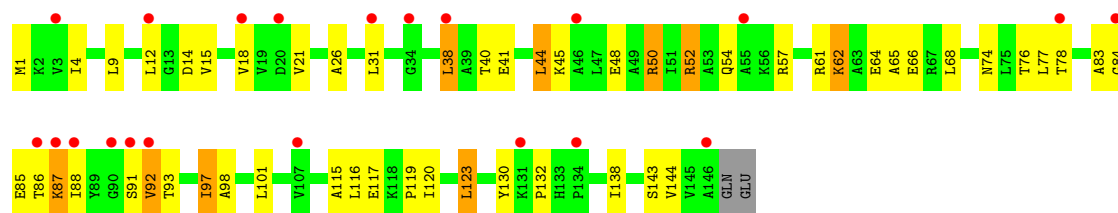


- Molecule 8: 50S ribosomal protein L9

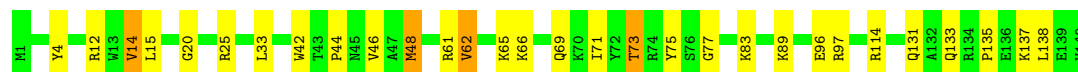
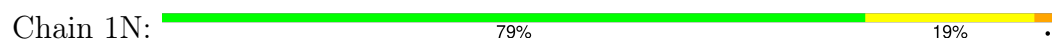


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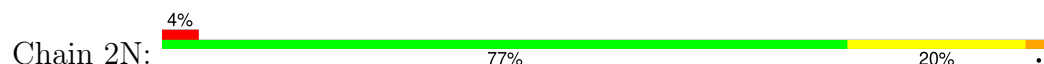




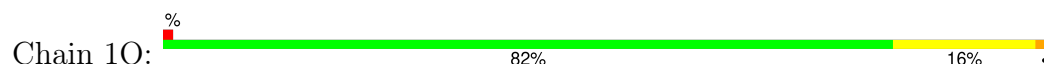
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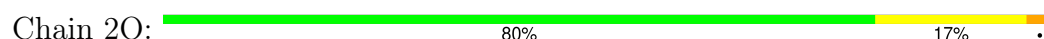
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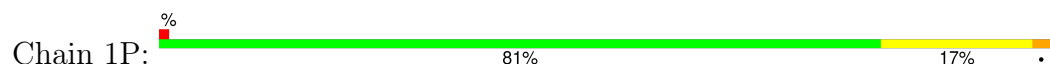
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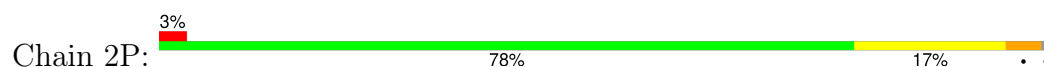
• Molecule 10: 50S ribosomal protein L14



• Molecule 11: 50S ribosomal protein L15

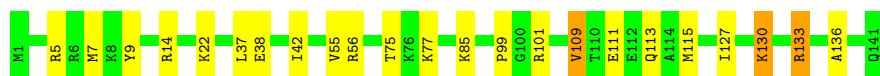


• Molecule 11: 50S ribosomal protein L15



- Molecule 12: 50S ribosomal protein L16

Chain 1Q:  84% 14% .



- Molecule 12: 50S ribosomal protein L16

Chain 2Q:  81% 18% 6% .



- Molecule 13: 50S ribosomal protein L17

Chain 1R:  84% 15% .



- Molecule 13: 50S ribosomal protein L17

Chain 2R:  82% 16% .



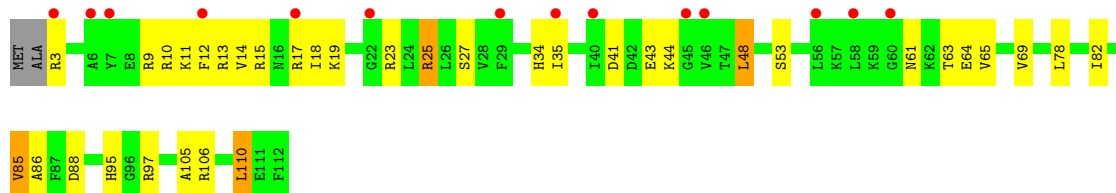
- Molecule 14: 50S ribosomal protein L18

Chain 1S:  79% 18% % .

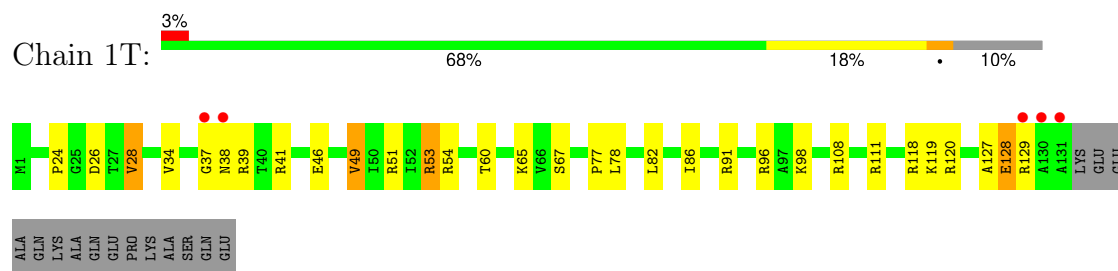


- Molecule 14: 50S ribosomal protein L18

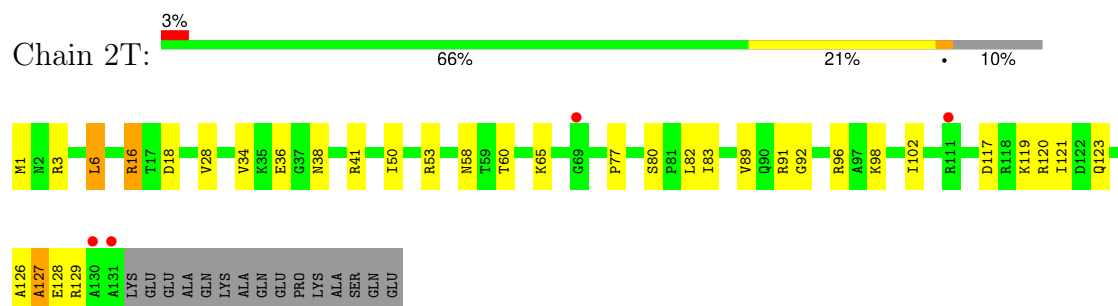
Chain 2S:  66% 29% 12% .



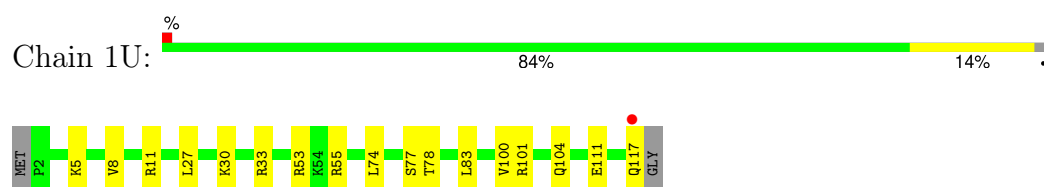
- Molecule 15: 50S ribosomal protein L19



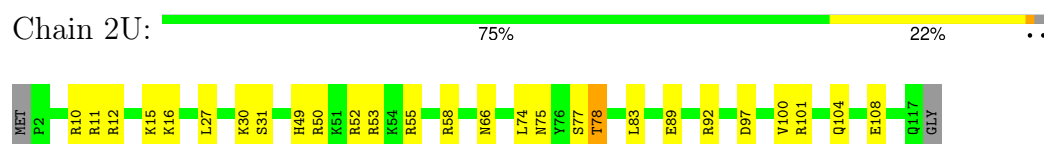
- Molecule 15: 50S ribosomal protein L19



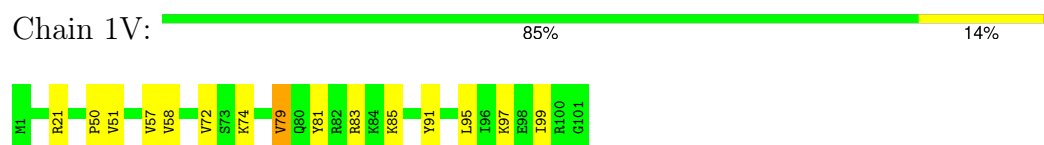
- Molecule 16: 50S ribosomal protein L20



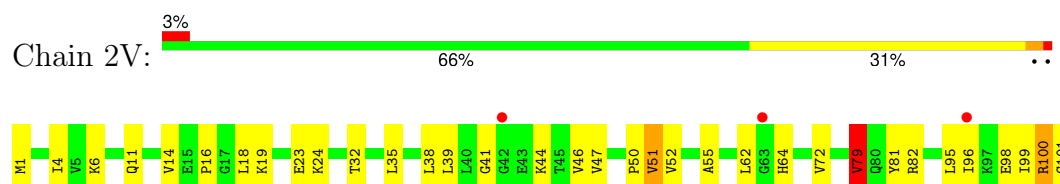
- Molecule 16: 50S ribosomal protein L20



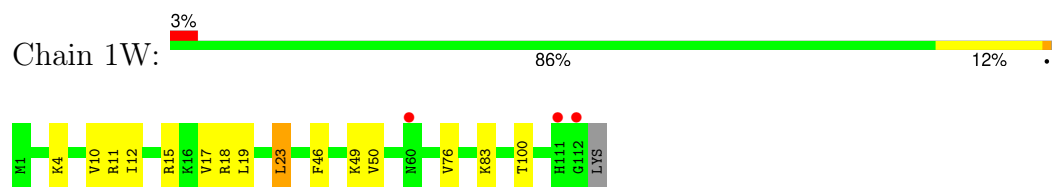
- Molecule 17: 50S ribosomal protein L21



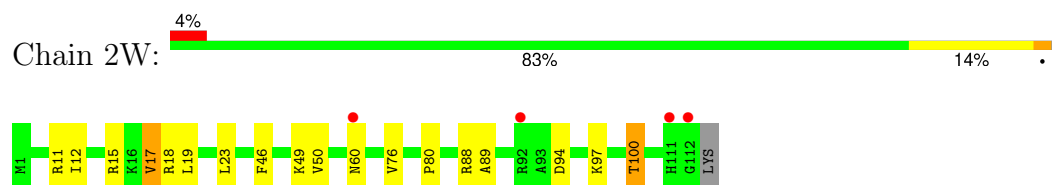
- Molecule 17: 50S ribosomal protein L21



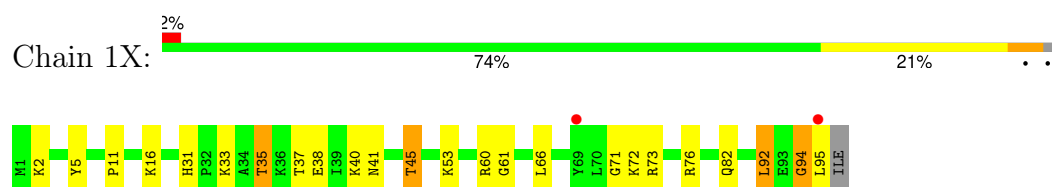
• Molecule 18: 50S ribosomal protein L22



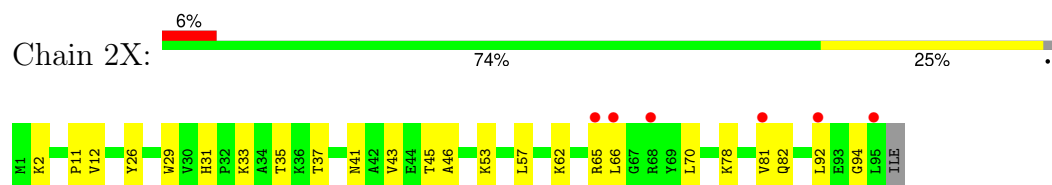
• Molecule 18: 50S ribosomal protein L22



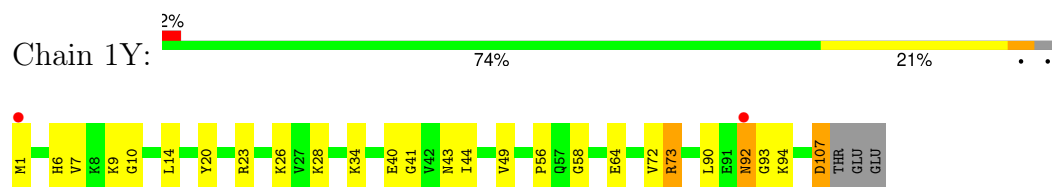
• Molecule 19: 50S ribosomal protein L23



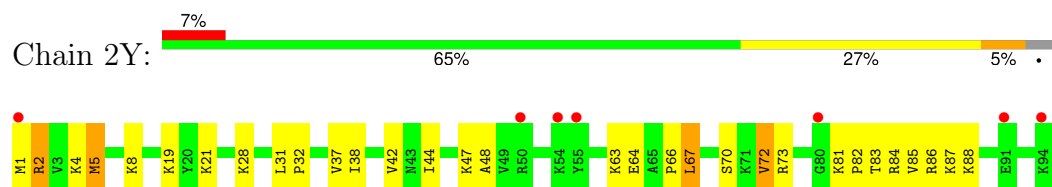
• Molecule 19: 50S ribosomal protein L23



• Molecule 20: 50S ribosomal protein L24

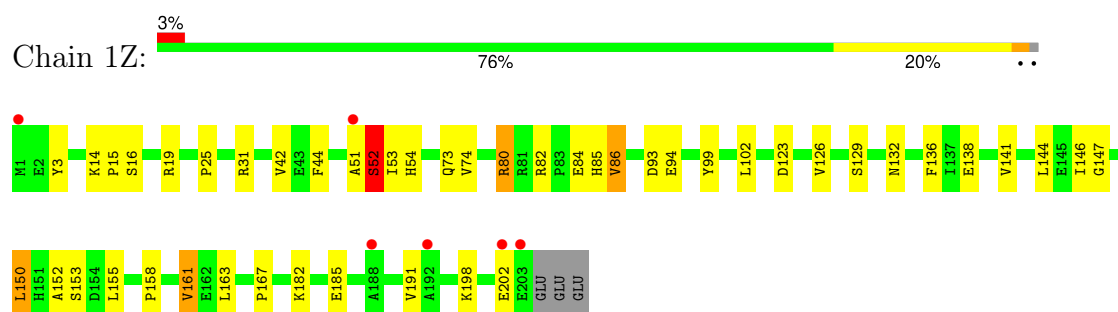


• Molecule 20: 50S ribosomal protein L24

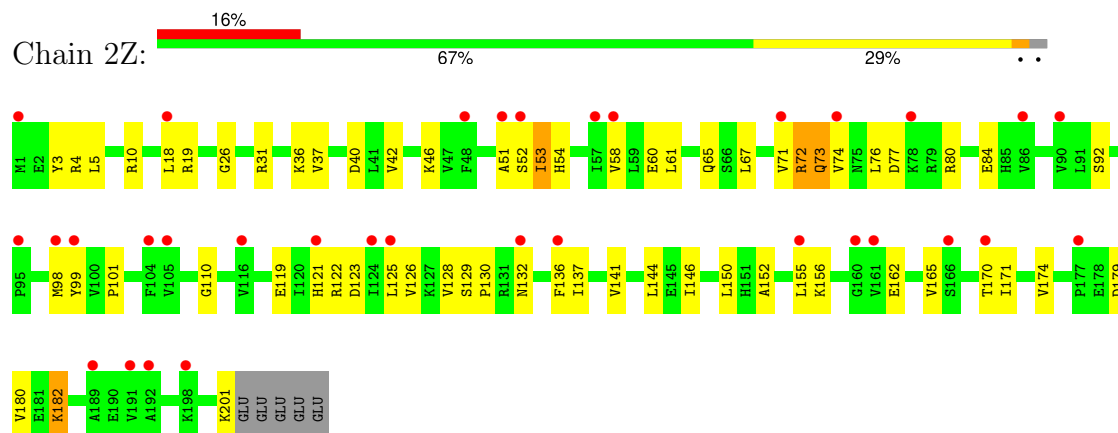


• Molecule 21: 50S ribosomal protein L25

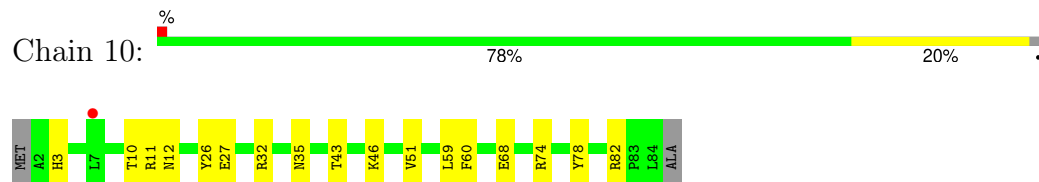




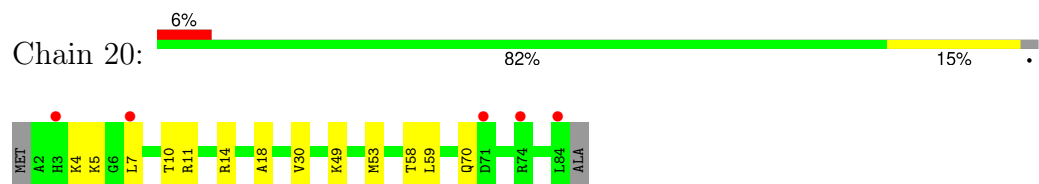
- Molecule 21: 50S ribosomal protein L25



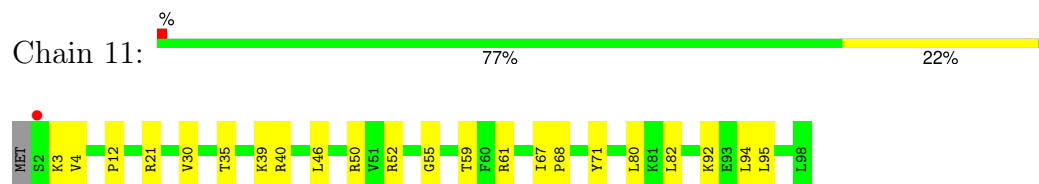
- Molecule 22: 50S ribosomal protein L27



- Molecule 22: 50S ribosomal protein L27



- Molecule 23: 50S ribosomal protein L28

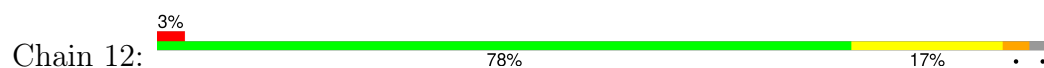


- Molecule 23: 50S ribosomal protein L28





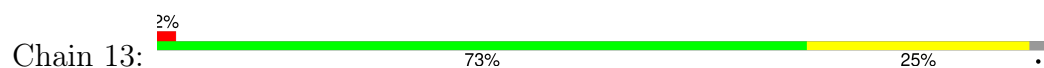
- Molecule 24: 50S ribosomal protein L29



- Molecule 24: 50S ribosomal protein L29



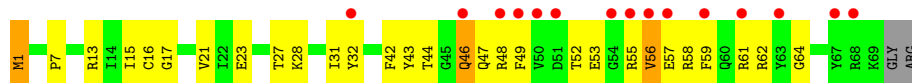
- Molecule 25: 50S ribosomal protein L30



- Molecule 25: 50S ribosomal protein L30

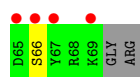


- Molecule 26: 50S ribosomal protein L31

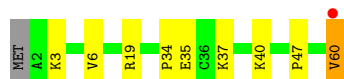
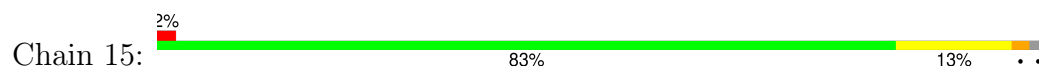


- Molecule 26: 50S ribosomal protein L31

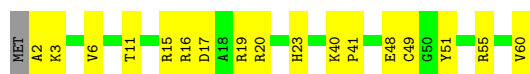




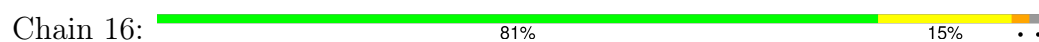
- Molecule 27: 50S ribosomal protein L32



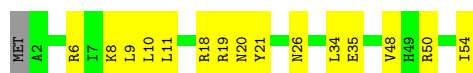
- Molecule 27: 50S ribosomal protein L32



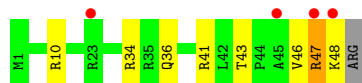
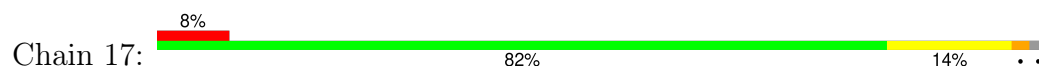
- Molecule 28: 50S ribosomal protein L33



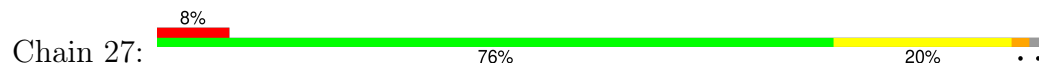
- Molecule 28: 50S ribosomal protein L33



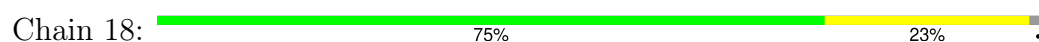
- Molecule 29: 50S ribosomal protein L34

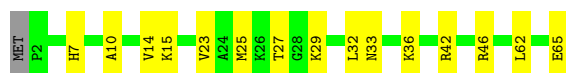


- Molecule 29: 50S ribosomal protein L34

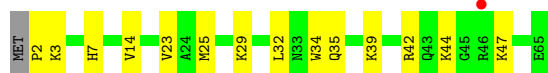
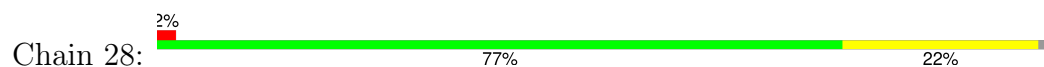


- Molecule 30: 50S ribosomal protein L35





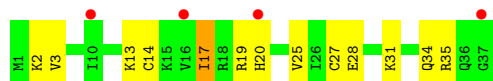
- Molecule 30: 50S ribosomal protein L35



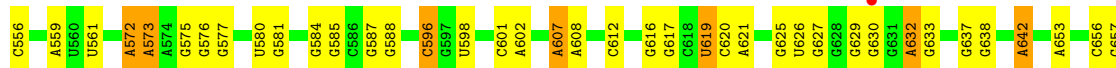
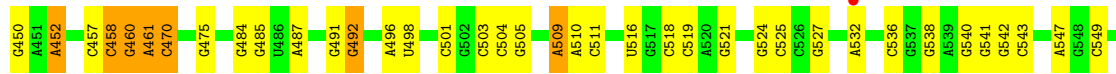
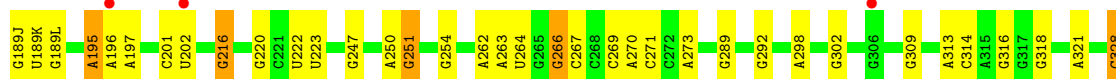
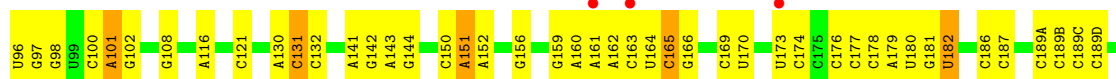
- Molecule 31: 50S ribosomal protein L36

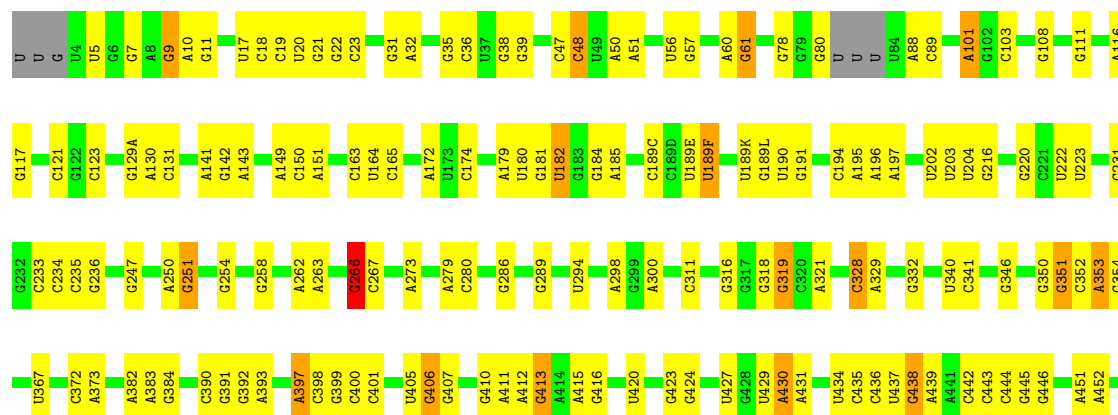
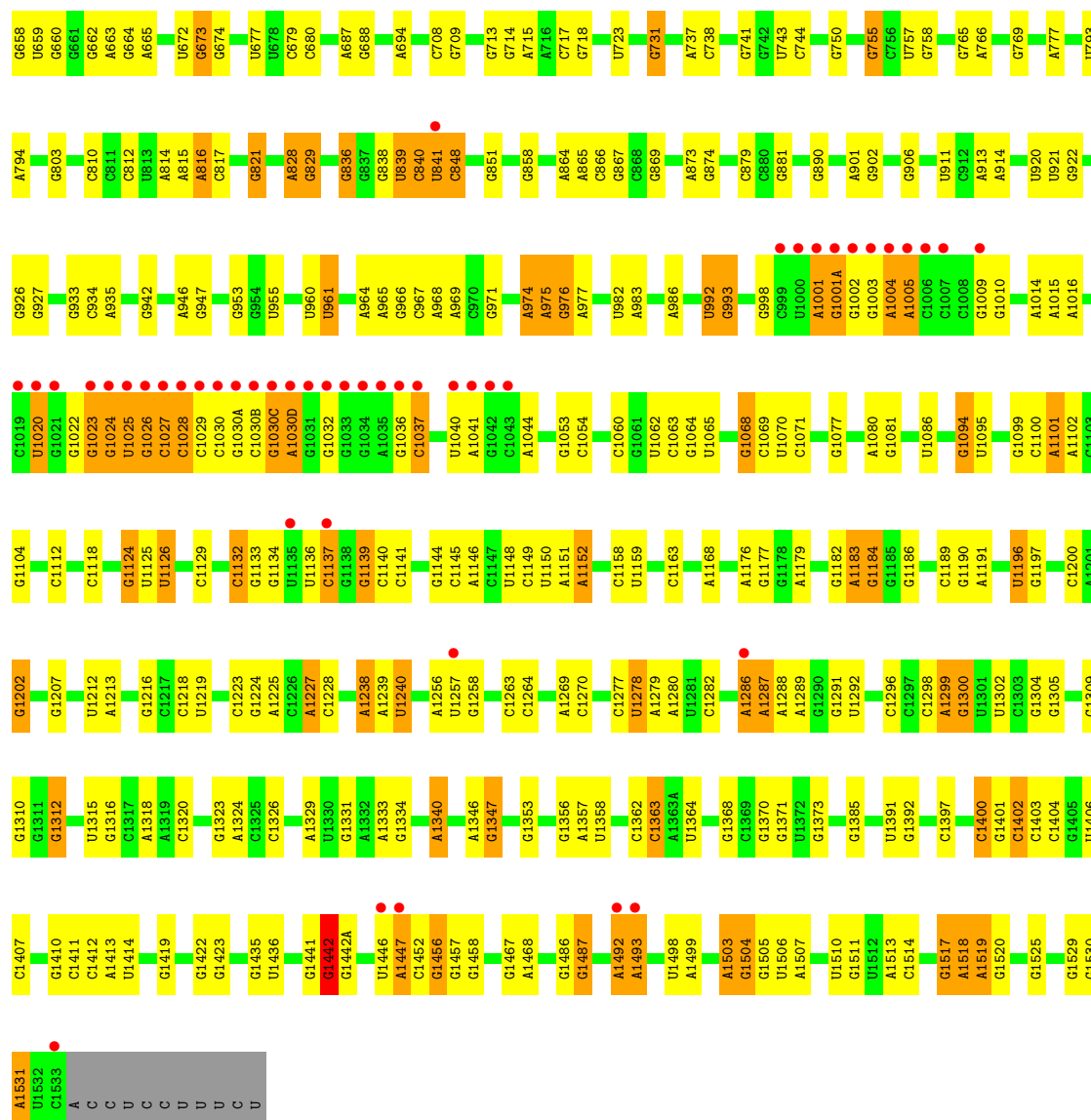


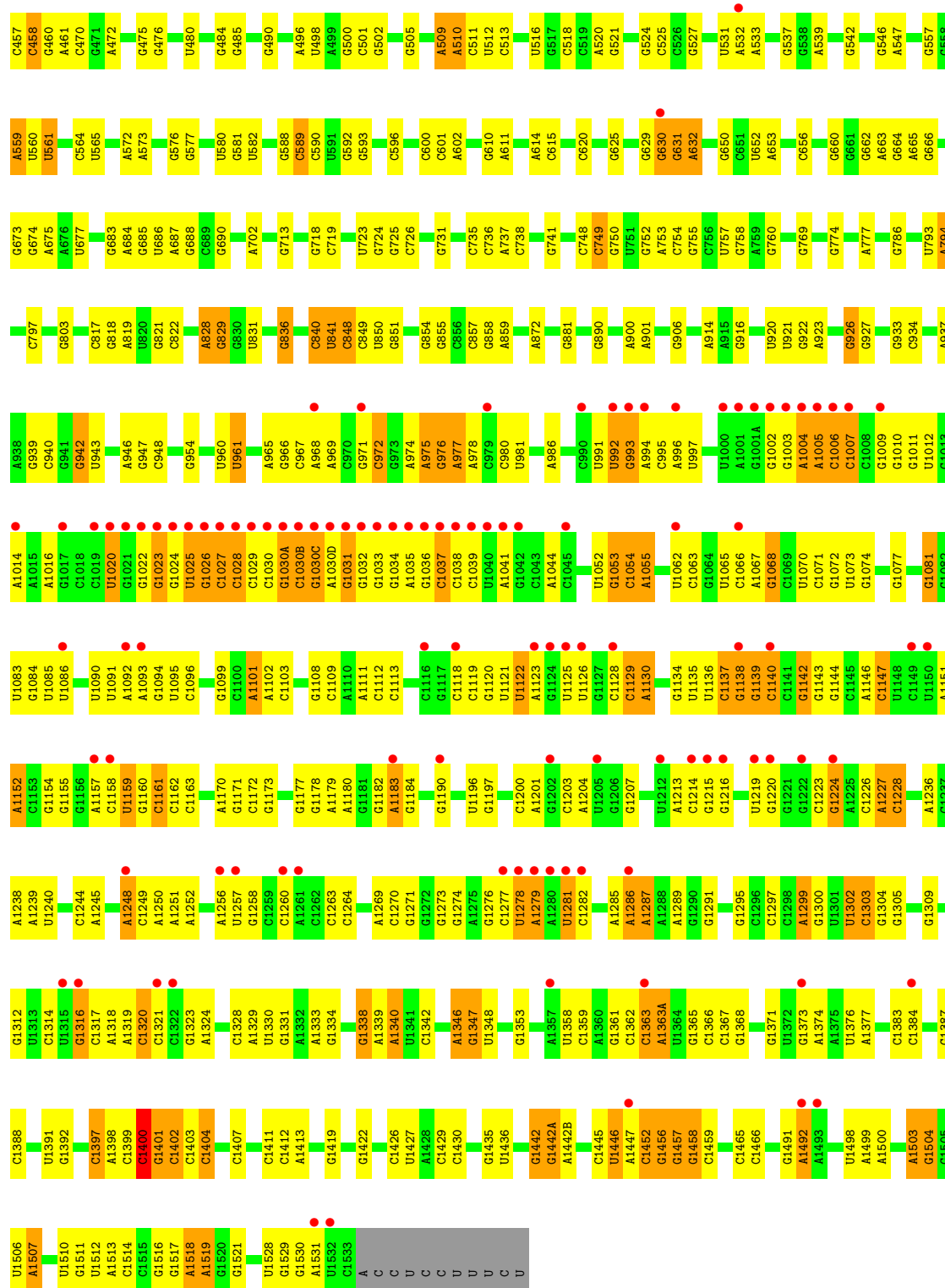
- Molecule 31: 50S ribosomal protein L36



- Molecule 32: 16S Ribosomal RNA

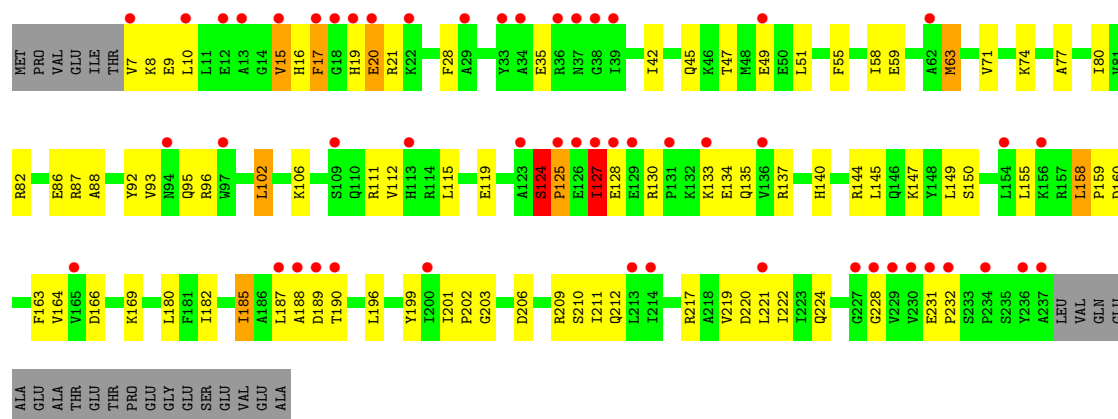




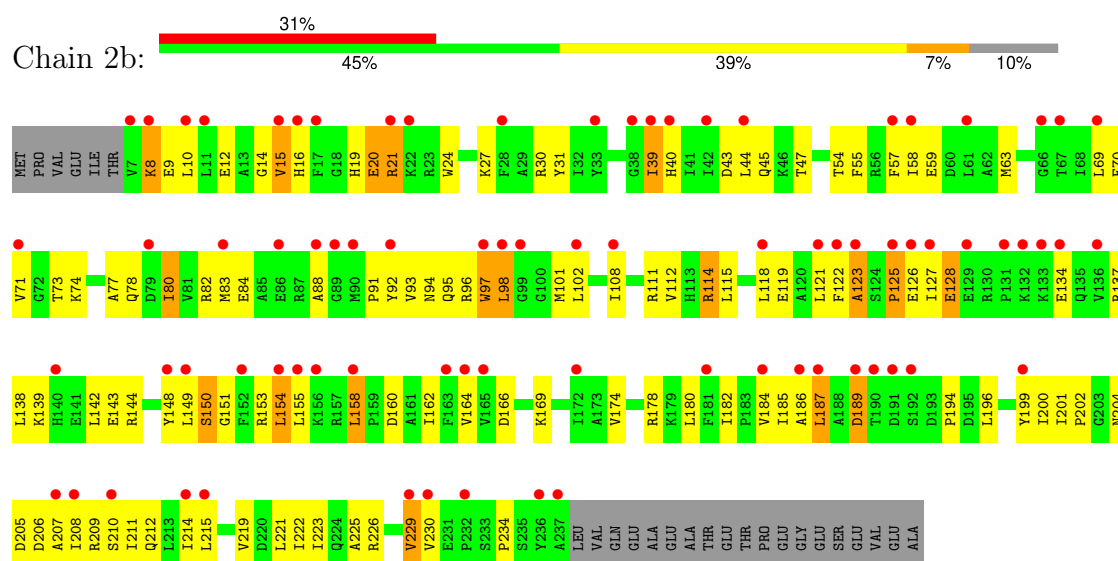


• Molecule 33: 30S ribosomal protein S2

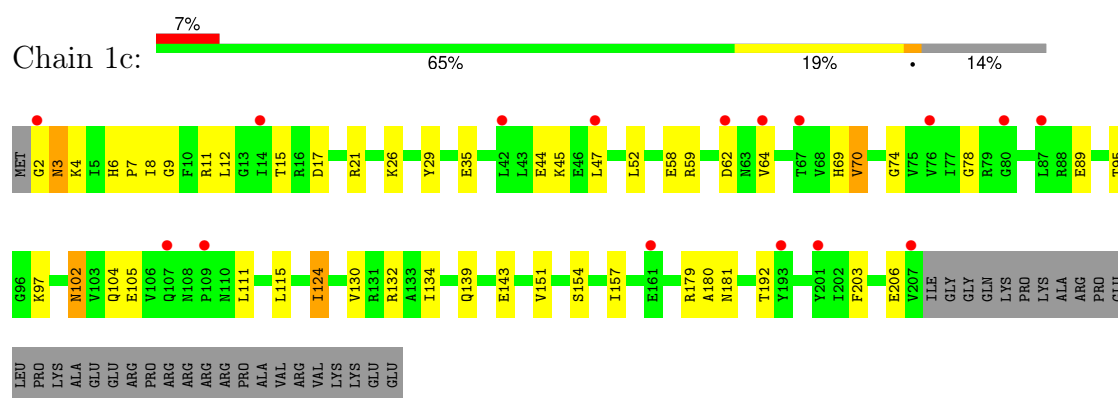




• Molecule 33: 30S ribosomal protein S2

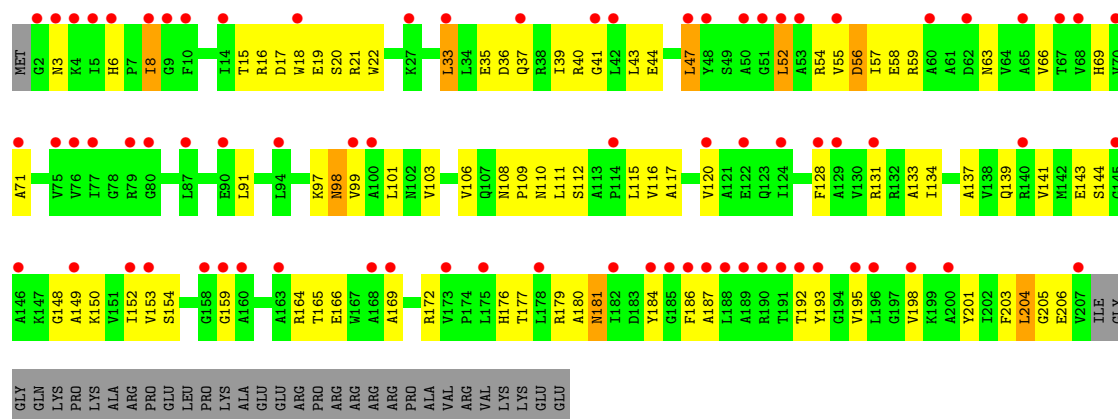


• Molecule 34: 30S ribosomal protein S3

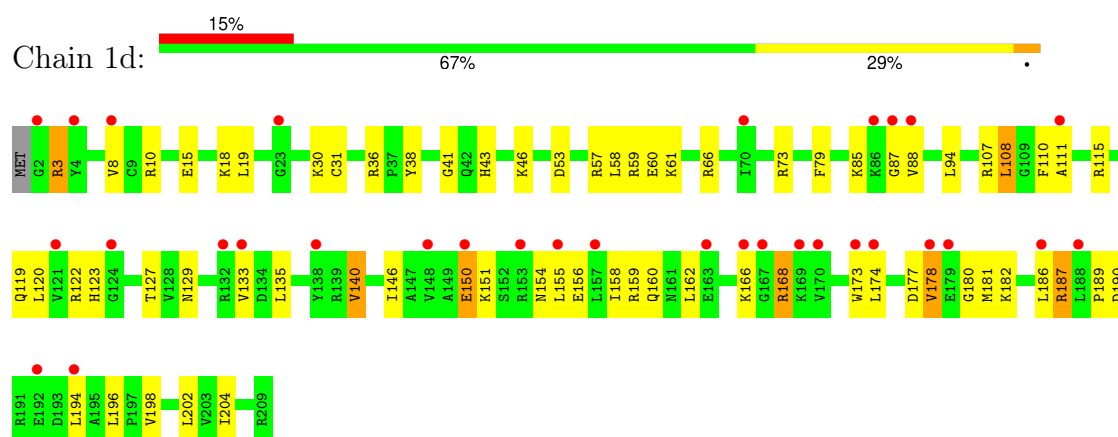


• Molecule 34: 30S ribosomal protein S3

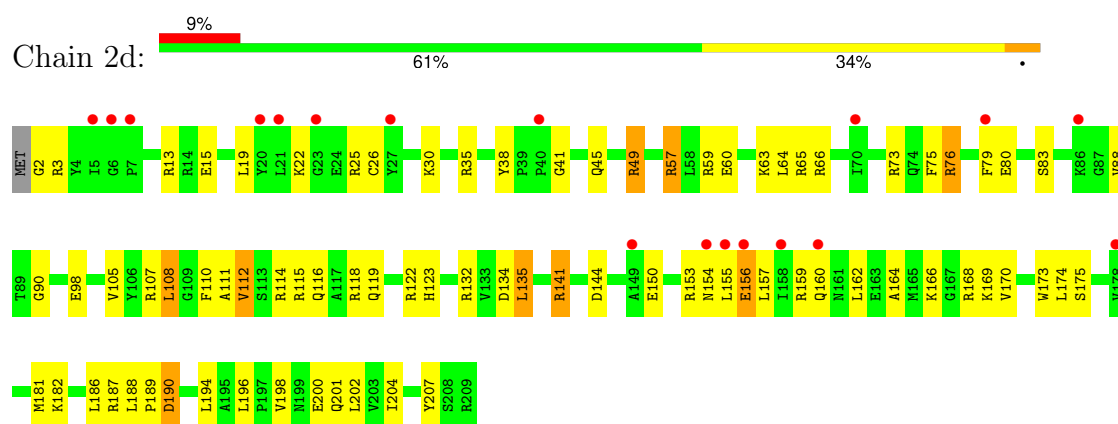




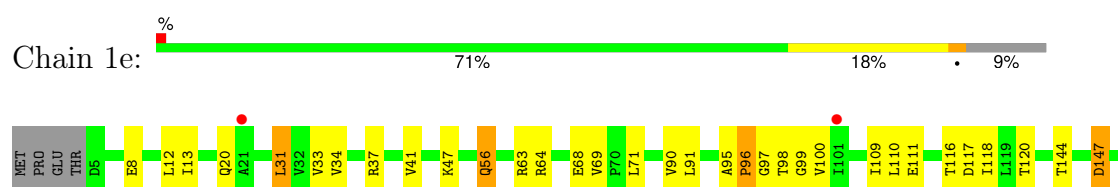
• Molecule 35: 30S ribosomal protein S4

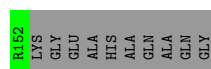


• Molecule 35: 30S ribosomal protein S4

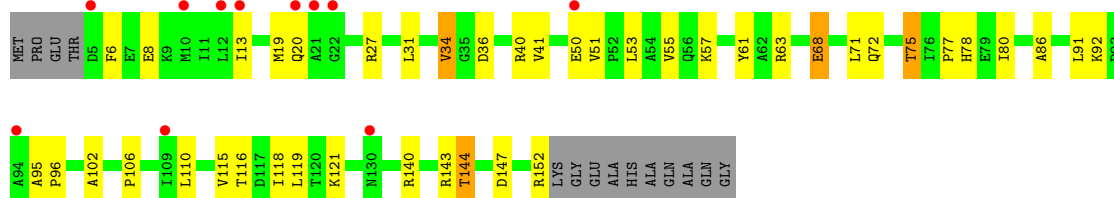


• Molecule 36: 30S ribosomal protein S5

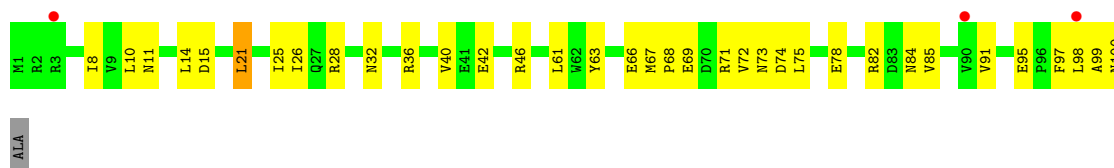




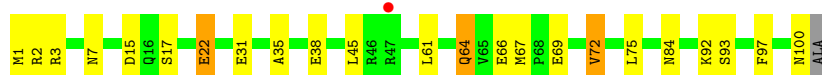
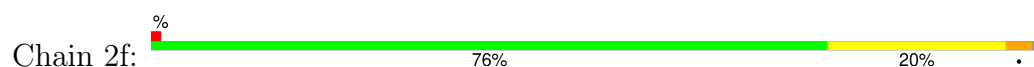
- Molecule 36: 30S ribosomal protein S5



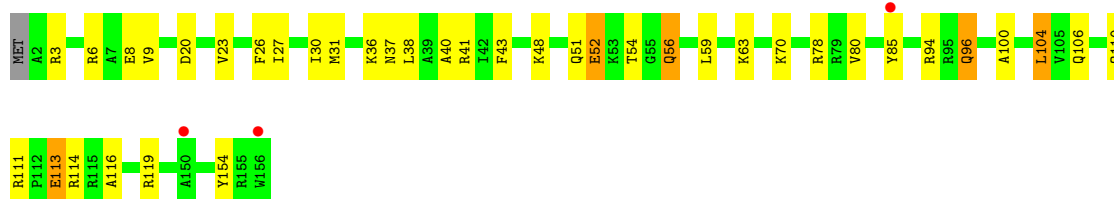
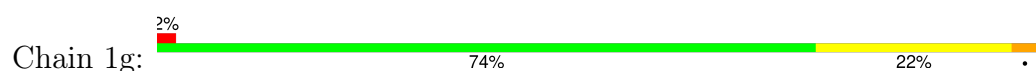
- Molecule 37: 30S ribosomal protein S6



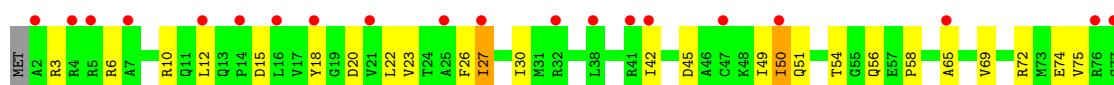
- Molecule 37: 30S ribosomal protein S6



- Molecule 38: 30S ribosomal protein S7

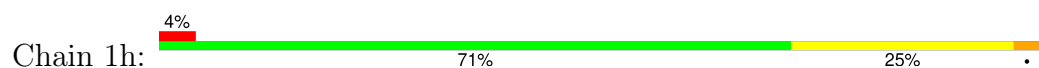


- Molecule 38: 30S ribosomal protein S7

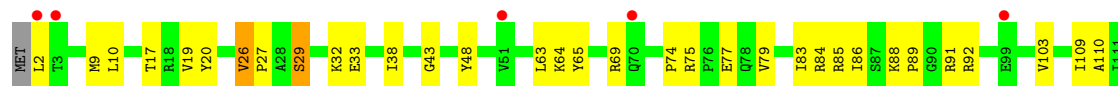
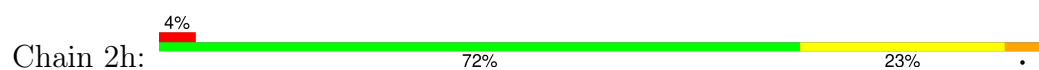




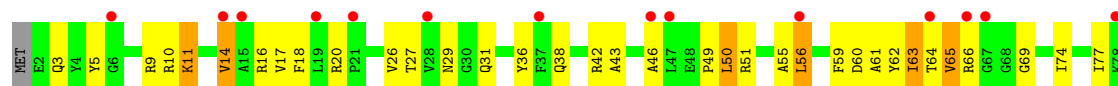
- Molecule 39: 30S ribosomal protein S8



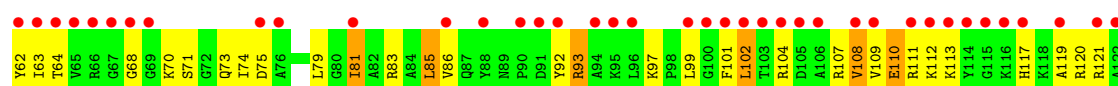
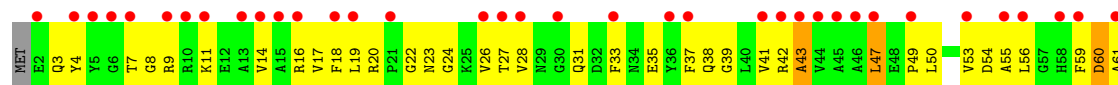
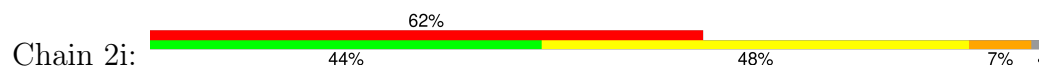
- Molecule 39: 30S ribosomal protein S8



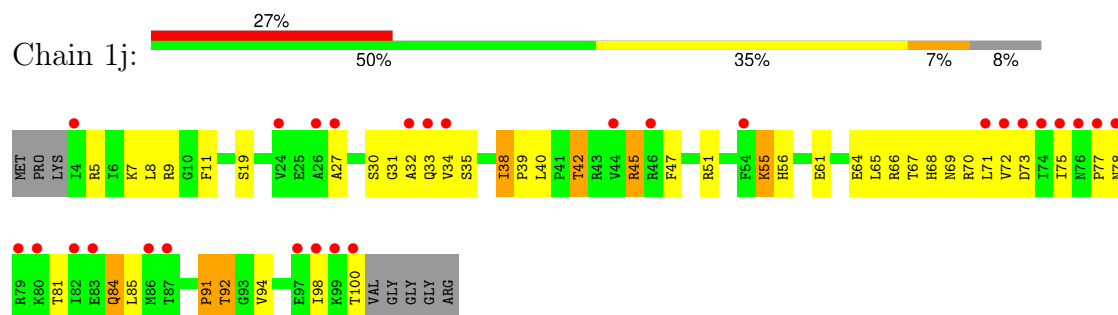
- Molecule 40: 30S ribosomal protein S9



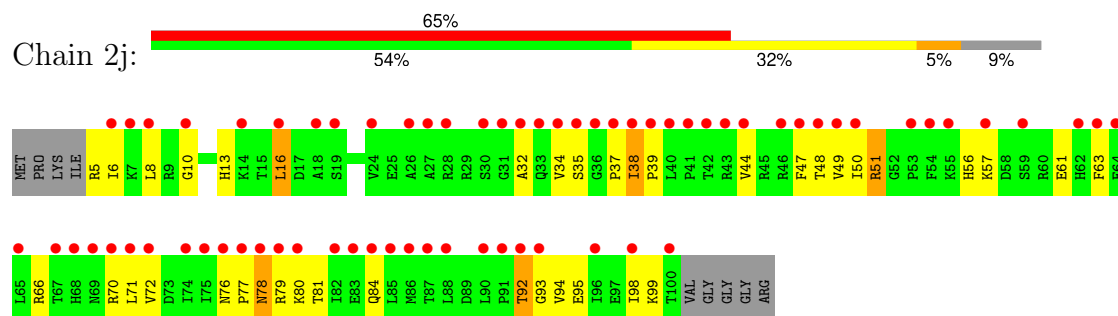
- Molecule 40: 30S ribosomal protein S9



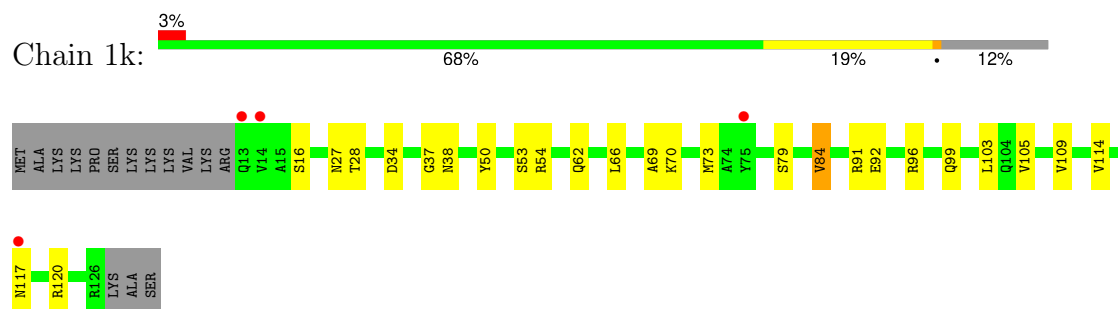
- Molecule 41: 30S ribosomal protein S10



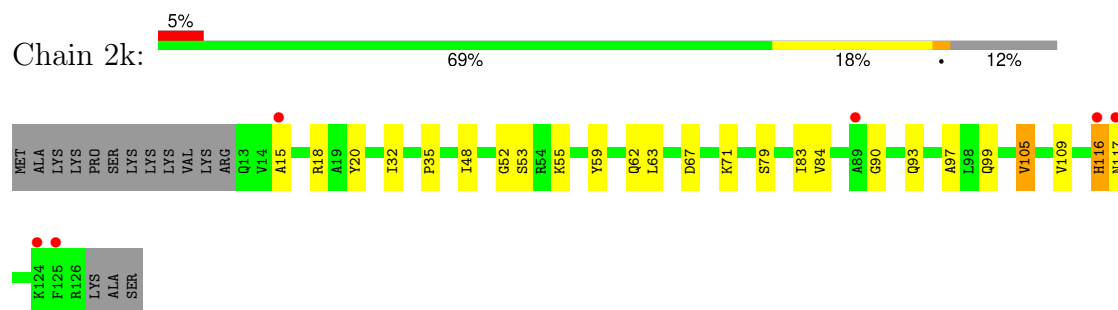
- Molecule 41: 30S ribosomal protein S10



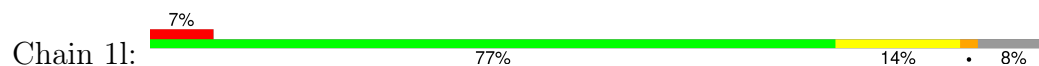
- Molecule 42: 30S ribosomal protein S11

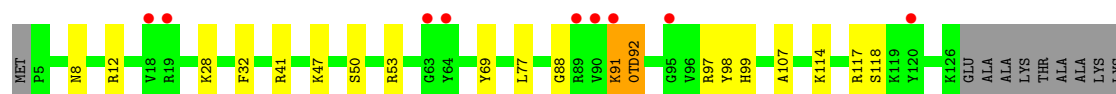


- Molecule 42: 30S ribosomal protein S11

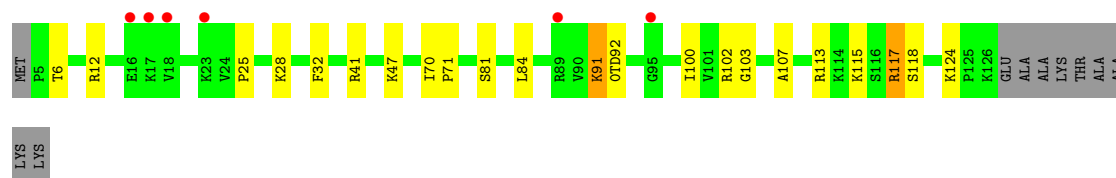
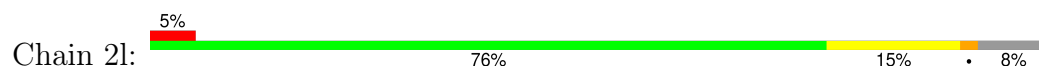


- Molecule 43: 30S ribosomal protein S12

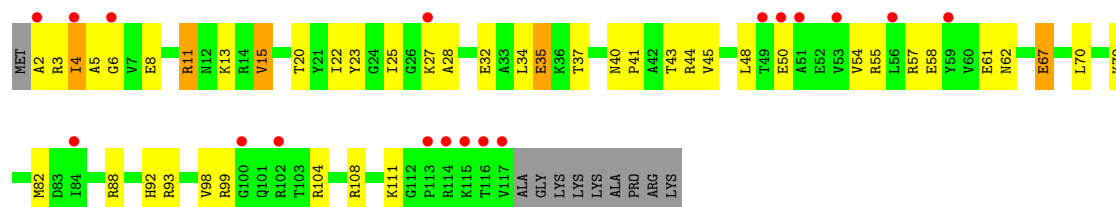




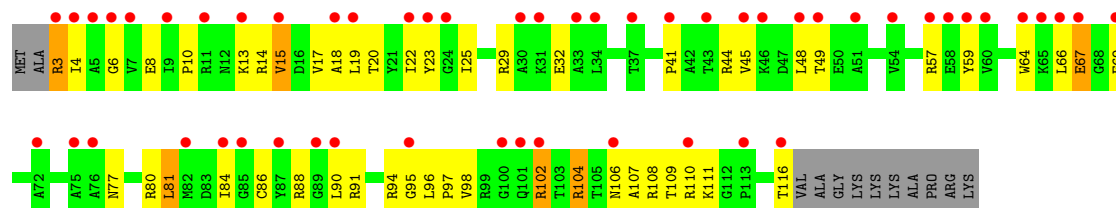
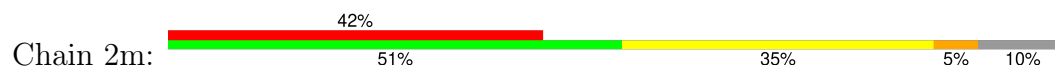
- Molecule 43: 30S ribosomal protein S12



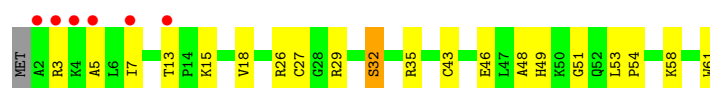
- Molecule 44: 30S ribosomal protein S13



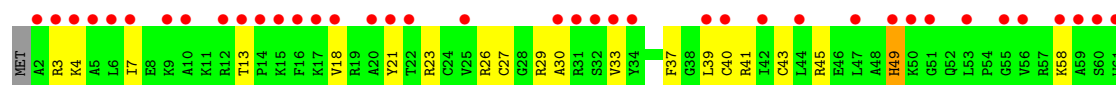
- Molecule 44: 30S ribosomal protein S13



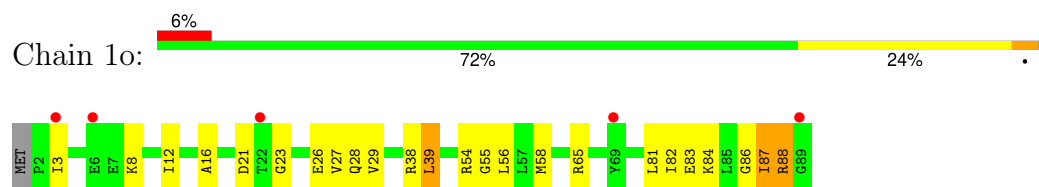
- Molecule 45: 30S ribosomal protein S14 type Z



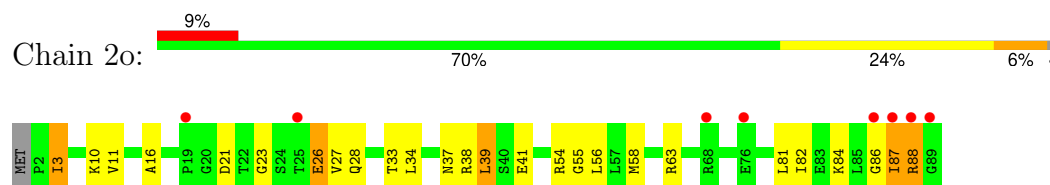
- Molecule 45: 30S ribosomal protein S14 type Z



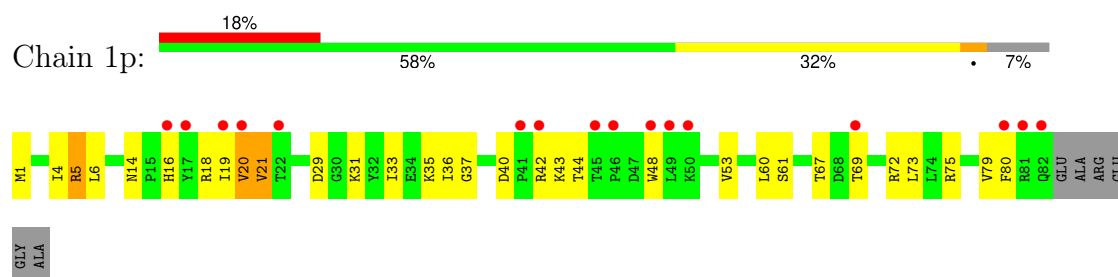
- Molecule 46: 30S ribosomal protein S15



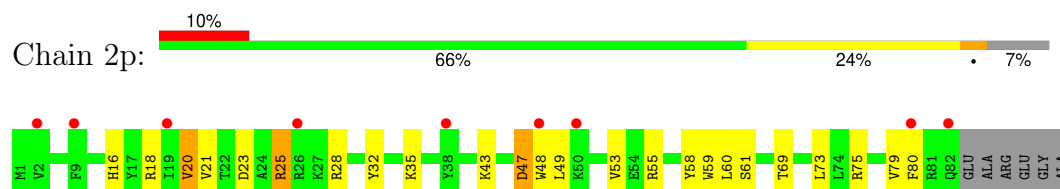
- Molecule 46: 30S ribosomal protein S15



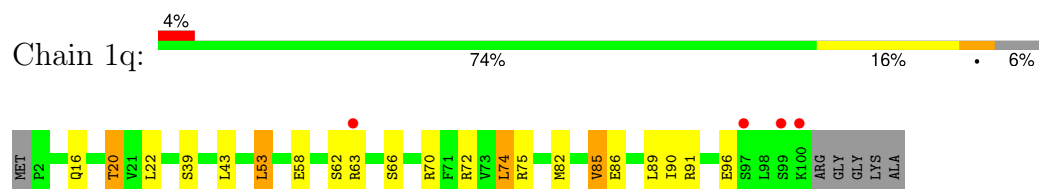
- Molecule 47: 30S ribosomal protein S16



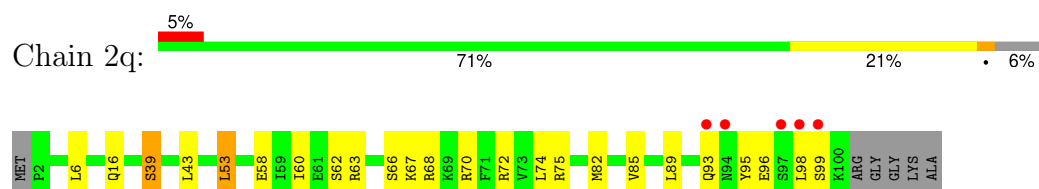
- Molecule 47: 30S ribosomal protein S16



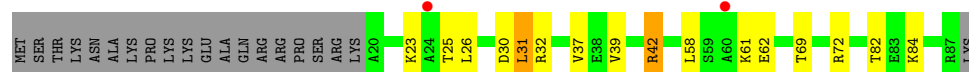
- Molecule 48: 30S ribosomal protein S17



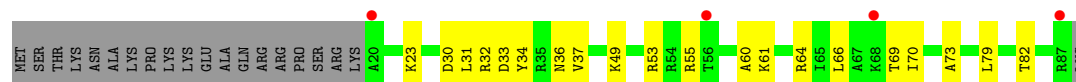
- Molecule 48: 30S ribosomal protein S17



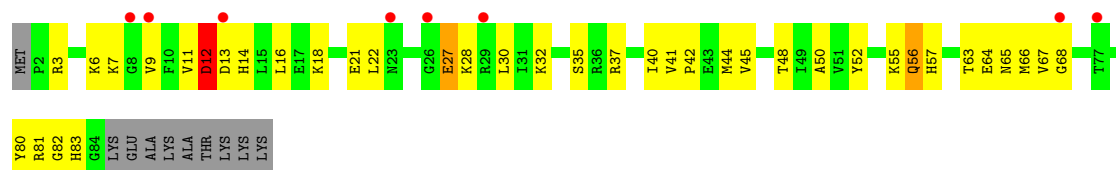
- Molecule 49: 30S ribosomal protein S18



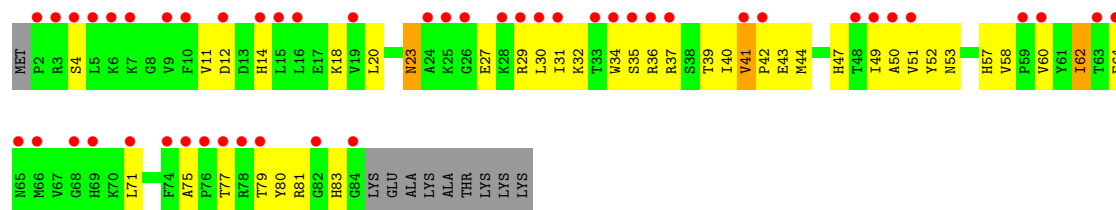
• Molecule 49: 30S ribosomal protein S18



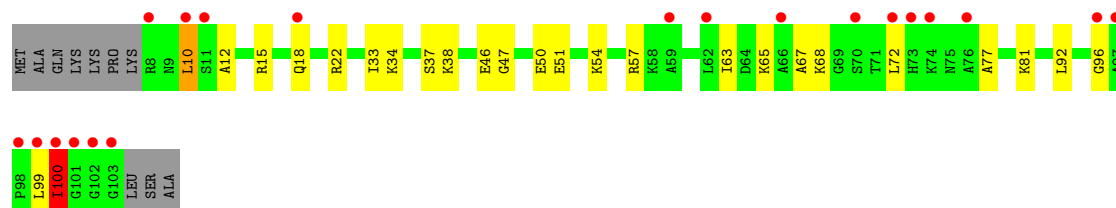
• Molecule 50: 30S ribosomal protein S19



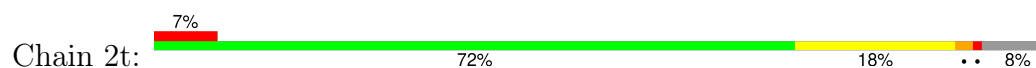
• Molecule 50: 30S ribosomal protein S19



• Molecule 51: 30S ribosomal protein S20

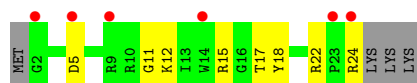


• Molecule 51: 30S ribosomal protein S20

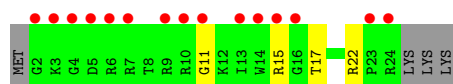




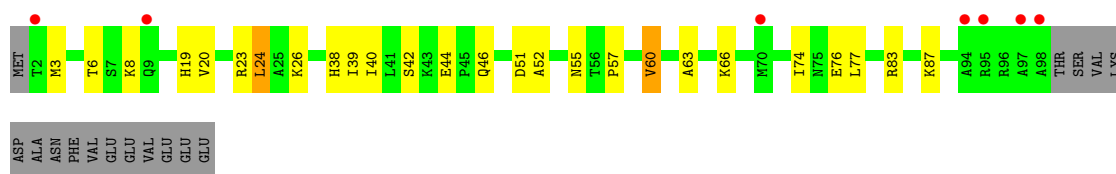
- Molecule 52: 30S ribosomal protein Thx



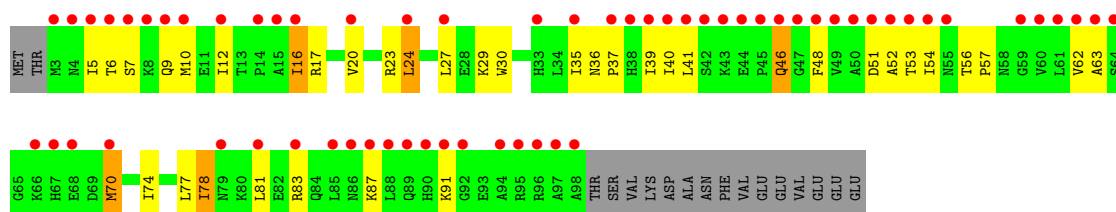
- Molecule 52: 30S ribosomal protein Thx



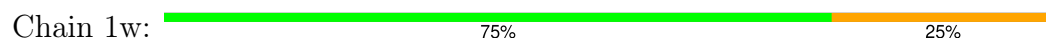
- Molecule 53: Ribosome-associated inhibitor A



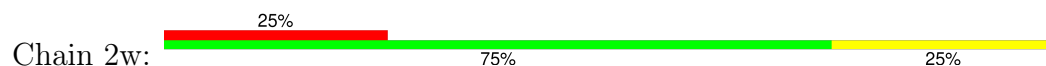
- Molecule 53: Ribosome-associated inhibitor A



- Molecule 54: A-site Aminoacyl-tRNA Analog



- Molecule 54: A-site Aminoacyl-tRNA Analog





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

Chain 1x:
75% 25%

A horizontal bar chart for Chain 1x. The bar is 75% green and 25% yellow.



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

Chain 2x:
25% 75% 25%

A horizontal bar chart for Chain 2x. The bar is 25% red, 75% green, and 25% orange.



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

Chain 1v:
100%

A horizontal bar chart for Chain 1v. The bar is 100% green.

There are no outlier residues recorded for this chain.

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

Chain 2v:
100%

A horizontal bar chart for Chain 2v. The bar is 100% green.

There are no outlier residues recorded for this chain.

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	209.61Å 448.45Å 618.45Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	187.31 – 2.45 187.31 – 2.45	Depositor EDS
% Data completeness (in resolution range)	99.9 (187.31-2.45) 99.9 (187.31-2.45)	Depositor EDS
R_{merge}	0.21	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.27 (at 2.45Å)	Xtriage
Refinement program	PHENIX 1.8.2	Depositor
R, R_{free}	0.205 , 0.244 0.207 , 0.246	Depositor DCC
R_{free} test set	105390 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	51.3	Xtriage
Anisotropy	0.140	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 59.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	297350	wwPDB-VP
Average B, all atoms (Å ²)	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.49% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ 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: 5MC, PPU, MPD, 5MU, 0TD, 4OC, SF4, 2MA, MG, M2G, 2MG, OMU, PSU, OMC, UR3, OMG, 8AN, MA6, G7M, ZN

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	0.29	0/69031	0.48	5/107754 (0.0%)
1	2A	0.23	0/68903	0.43	2/107552 (0.0%)
2	1B	0.23	0/2876	0.43	0/4486
2	2B	0.19	0/2878	0.36	0/4490
3	1D	0.29	0/2181	0.54	0/2940
3	2D	0.22	0/2186	0.47	0/2944
4	1E	0.25	0/1592	0.50	0/2149
4	2E	0.21	0/1592	0.45	0/2149
5	1F	0.26	0/1619	0.47	0/2193
5	2F	0.22	0/1615	0.46	0/2188
6	1G	0.20	0/1451	0.46	1/1961 (0.1%)
6	2G	0.22	0/1449	0.42	0/1957
7	1H	0.22	0/1356	0.41	0/1834
7	2H	0.20	0/1350	0.41	0/1826
8	1I	0.20	0/1109	0.44	0/1512
8	2I	0.18	0/1091	0.40	0/1490
9	1N	0.25	0/1148	0.47	0/1547
9	2N	0.19	0/1144	0.40	0/1543
10	1O	0.27	0/943	0.48	0/1269
10	2O	0.22	0/943	0.44	0/1269
11	1P	0.26	0/1152	0.54	0/1533
11	2P	0.21	0/1152	0.51	0/1533
12	1Q	0.29	0/1143	0.53	0/1527
12	2Q	0.21	0/1143	0.42	0/1527
13	1R	0.28	0/982	0.48	0/1312
13	2R	0.22	0/982	0.45	0/1312
14	1S	0.23	0/887	0.54	1/1180 (0.1%)
14	2S	0.20	0/880	0.44	0/1172
15	1T	0.25	0/1105	0.48	0/1477
15	2T	0.22	0/1097	0.45	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	0.20	0/977	0.41	0/1301
17	1V	0.25	0/786	0.47	0/1053
17	2V	0.19	0/782	0.43	0/1049
18	1W	0.28	0/897	0.49	0/1205
18	2W	0.22	0/897	0.43	0/1205
19	1X	0.27	0/764	0.49	0/1025
19	2X	0.21	0/764	0.42	0/1025
20	1Y	0.24	0/823	0.53	0/1099
20	2Y	0.19	0/823	0.47	0/1100
21	1Z	0.21	0/1620	0.44	0/2200
21	2Z	0.19	0/1590	0.40	0/2162
22	10	0.27	0/662	0.50	0/881
22	20	0.22	0/659	0.48	0/877
23	11	0.25	0/761	0.44	0/1013
23	21	0.24	0/766	0.43	0/1018
24	12	0.23	0/590	0.47	0/781
24	22	0.21	0/594	0.45	0/785
25	13	0.24	0/474	0.47	0/635
25	23	0.19	0/469	0.40	0/630
26	14	0.25	0/559	0.59	0/754
26	24	0.27	0/549	0.65	2/741 (0.3%)
27	15	0.26	0/473	0.52	0/639
27	25	0.21	0/469	0.45	0/635
28	16	0.25	0/460	0.49	0/613
28	26	0.21	0/456	0.42	0/608
29	17	0.29	0/426	0.55	0/561
29	27	0.24	0/426	0.51	0/561
30	18	0.26	0/525	0.50	0/691
30	28	0.21	0/525	0.43	0/691
31	19	0.29	0/310	0.48	0/407
31	29	0.21	0/310	0.41	0/407
32	1a	0.20	0/35795	0.39	1/55864 (0.0%)
32	2a	0.20	1/35890 (0.0%)	0.38	2/56012 (0.0%)
33	1b	0.22	0/1876	0.47	0/2533
33	2b	0.23	0/1860	0.48	0/2518
34	1c	0.19	0/1582	0.39	0/2137
34	2c	0.21	0/1566	0.39	0/2119
35	1d	0.20	0/1695	0.44	0/2274
35	2d	0.19	0/1698	0.42	0/2277
36	1e	0.21	0/1149	0.43	0/1548
36	2e	0.21	0/1149	0.42	0/1548
37	1f	0.20	0/827	0.38	0/1120
37	2f	0.19	0/829	0.40	0/1123

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
38	1g	0.18	0/1254	0.38	0/1683
38	2g	0.19	0/1248	0.36	0/1676
39	1h	0.19	0/1118	0.41	0/1506
39	2h	0.17	0/1108	0.40	0/1494
40	1i	0.20	0/1005	0.45	0/1351
40	2i	0.21	0/985	0.45	0/1329
41	1j	0.20	0/732	0.38	0/993
41	2j	0.22	0/723	0.49	0/984
42	1k	0.19	0/849	0.43	0/1150
42	2k	0.21	0/848	0.49	2/1149 (0.2%)
43	1l	0.20	0/937	0.44	0/1260
43	2l	0.20	0/937	0.43	0/1260
44	1m	0.20	0/924	0.45	0/1242
44	2m	0.23	0/905	0.48	0/1217
45	1n	0.20	0/501	0.41	0/664
45	2n	0.21	0/501	0.40	0/664
46	1o	0.21	0/739	0.39	0/985
46	2o	0.18	0/739	0.38	0/985
47	1p	0.21	0/697	0.50	0/939
47	2p	0.20	0/693	0.44	0/935
48	1q	0.19	0/836	0.40	0/1117
48	2q	0.18	0/836	0.37	0/1117
49	1r	0.19	0/560	0.43	0/746
49	2r	0.19	0/560	0.40	0/746
50	1s	0.18	0/663	0.42	0/895
50	2s	0.20	0/660	0.45	0/893
51	1t	0.20	0/734	0.45	0/969
51	2t	0.19	0/736	0.42	0/976
52	1u	0.20	0/203	0.43	0/266
52	2u	0.19	0/203	0.44	0/266
53	1y	0.18	0/776	0.40	0/1048
53	2y	0.19	0/761	0.36	0/1030
54	1w	0.30	0/44	0.39	0/67
54	2w	0.25	0/44	0.35	0/67
55	1x	0.38	0/44	0.57	0/67
55	2x	0.29	0/44	0.53	0/67
56	1v	0.18	0/20	0.32	0/25
56	2v	0.22	0/20	0.33	0/25
All	All	0.23	1/310246 (0.0%)	0.44	16/463673 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
32	2a	527	G7M	O3'-P	5.04	1.61	1.56

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	1S	60	GLY	N-CA-C	7.93	117.42	110.21
1	2A	1992	G	C2'-C3'-O3'	6.61	119.41	109.50
6	1G	89	GLY	N-CA-C	6.59	118.84	111.85
42	2k	116	HIS	CA-C-N	6.38	133.19	121.70
42	2k	116	HIS	C-N-CA	6.38	133.19	121.70
32	2a	266	G	C2'-C3'-O3'	6.30	118.96	109.50
1	1A	512	G	O4'-C1'-N9	5.72	116.78	108.20
1	1A	1653	G	C2'-C3'-O3'	5.39	117.59	109.50
32	2a	266	G	P-O3'-C3'	5.39	128.28	120.20
1	1A	1300	U	C4'-C3'-O3'	5.27	117.31	109.40
1	2A	752	A	C2'-C3'-O3'	5.17	117.25	109.50
1	1A	1210	A	C4'-C3'-O3'	5.13	117.10	109.40
32	1a	1442	G	P-O3'-C3'	5.11	125.84	119.70
1	1A	1300	U	P-O3'-C3'	5.09	127.84	120.20
26	24	61	ARG	CA-C-N	5.04	131.17	121.54
26	24	61	ARG	C-N-CA	5.04	131.17	121.54

There are no chirality outliers.

There are no planarity outliers.

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	31206	510	0
1	2A	61758	0	31154	637	0
2	1B	2572	0	1305	16	0
2	2B	2573	0	1306	31	0
3	1D	2131	0	2207	32	0
3	2D	2136	0	2218	31	0
4	1E	1559	0	1618	16	0
4	2E	1559	0	1618	20	0
5	1F	1584	0	1625	31	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	2F	1580	0	1619	49	0
6	1G	1426	0	1445	47	0
6	2G	1424	0	1441	47	0
7	1H	1330	0	1407	24	0
7	2H	1324	0	1402	41	0
8	1I	1094	0	1127	15	0
8	2I	1076	0	1094	27	0
9	1N	1121	0	1195	15	0
9	2N	1117	0	1184	21	0
10	1O	933	0	996	19	0
10	2O	933	0	996	15	0
11	1P	1135	0	1212	24	0
11	2P	1135	0	1212	27	0
12	1Q	1122	0	1177	15	0
12	2Q	1122	0	1177	17	0
13	1R	968	0	1033	13	0
13	2R	968	0	1033	16	0
14	1S	877	0	938	13	0
14	2S	870	0	923	25	0
15	1T	1091	0	1151	19	0
15	2T	1083	0	1136	22	0
16	1U	959	0	1019	12	0
16	2U	959	0	1019	17	0
17	1V	775	0	841	8	0
17	2V	771	0	830	19	0
18	1W	886	0	940	8	0
18	2W	886	0	940	10	0
19	1X	750	0	814	20	0
19	2X	750	0	814	18	0
20	1Y	810	0	892	15	0
20	2Y	810	0	887	22	0
21	1Z	1587	0	1598	26	0
21	2Z	1557	0	1564	40	0
22	10	653	0	674	12	0
22	20	650	0	665	7	0
23	11	754	0	823	15	0
23	21	759	0	837	20	0
24	12	588	0	643	8	0
24	22	592	0	654	12	0
25	13	469	0	518	10	0
25	23	464	0	514	9	0
26	14	546	0	522	26	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
26	24	536	0	514	30	0
27	15	459	0	476	5	0
27	25	455	0	465	12	0
28	16	453	0	473	3	0
28	26	449	0	469	10	0
29	17	418	0	467	7	0
29	27	418	0	467	7	0
30	18	517	0	582	10	0
30	28	517	0	582	9	0
31	19	307	0	335	1	0
31	29	307	0	335	9	0
32	1a	32246	0	16293	336	0
32	2a	32331	0	16338	412	0
33	1b	1842	0	1862	52	0
33	2b	1825	0	1828	80	0
34	1c	1558	0	1557	29	0
34	2c	1542	0	1517	64	0
35	1d	1665	0	1687	46	0
35	2d	1668	0	1703	57	0
36	1e	1133	0	1191	18	0
36	2e	1133	0	1191	29	0
37	1f	814	0	808	22	0
37	2f	816	0	808	14	0
38	1g	1235	0	1249	27	0
38	2g	1229	0	1238	29	0
39	1h	1098	0	1143	25	0
39	2h	1088	0	1126	20	0
40	1i	986	0	990	40	0
40	2i	966	0	953	51	0
41	1j	719	0	672	28	0
41	2j	710	0	661	26	0
42	1k	834	0	838	14	0
42	2k	833	0	836	12	0
43	1l	932	0	981	16	0
43	2l	932	0	981	15	0
44	1m	914	0	954	27	0
44	2m	895	0	920	33	0
45	1n	492	0	528	17	0
45	2n	492	0	529	14	0
46	1o	728	0	760	19	0
46	2o	728	0	760	13	0
47	1p	681	0	697	16	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
47	2p	677	0	686	17	0
48	1q	823	0	891	16	0
48	2q	823	0	891	17	0
49	1r	555	0	618	15	0
49	2r	555	0	618	11	0
50	1s	648	0	658	23	0
50	2s	645	0	635	33	0
51	1t	732	0	809	17	0
51	2t	733	0	795	14	0
52	1u	199	0	208	4	0
52	2u	199	0	208	2	0
53	1y	764	0	786	19	0
53	2y	749	0	757	27	0
54	1w	78	0	50	2	0
54	2w	78	0	50	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	6	0	0	0	0
57	18	3	0	0	0	0
57	19	1	0	0	0	0
57	1A	1013	0	0	0	0
57	1B	30	0	0	0	0
57	1D	17	0	0	0	0
57	1E	8	0	0	0	0
57	1F	17	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
57	1O	1	0	0	0	0
57	1P	3	0	0	0	0
57	1Q	5	0	0	0	0
57	1R	7	0	0	0	0
57	1T	7	0	0	0	0
57	1U	5	0	0	0	0
57	1V	7	0	0	0	0
57	1W	3	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
57	1Y	1	0	0	0	0
57	1Z	1	0	0	0	0
57	1a	267	0	0	0	0
57	1b	1	0	0	0	0
57	1d	5	0	0	0	0
57	1e	5	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	3	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	23	1	0	0	0	0
57	25	2	0	0	0	0
57	27	2	0	0	0	0
57	28	2	0	0	0	0
57	29	1	0	0	0	0
57	2A	731	0	0	0	0
57	2B	19	0	0	0	0
57	2D	10	0	0	0	0
57	2E	6	0	0	0	0
57	2F	5	0	0	0	0
57	2G	2	0	0	0	0
57	2I	1	0	0	0	0
57	2O	2	0	0	0	0
57	2P	1	0	0	0	0
57	2Q	3	0	0	0	0
57	2R	3	0	0	0	0
57	2T	4	0	0	0	0
57	2U	2	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	183	0	0	0	0
57	2e	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
57	2f	2	0	0	0	0
57	2j	1	0	0	0	0
57	2k	1	0	0	0	0
57	2p	1	0	0	0	0
57	2r	1	0	0	0	0
57	2t	1	0	0	0	0
57	2x	2	0	0	0	0
58	18	8	0	14	1	0
58	1A	8	0	14	0	0
58	1T	8	0	14	1	0
58	1a	8	0	12	4	0
58	2A	8	0	14	0	0
58	2B	8	0	14	0	0
59	1B	12	0	12	1	0
59	1F	12	0	12	0	0
60	14	1	0	0	0	0
60	15	1	0	0	0	0
60	16	1	0	0	0	0
60	19	1	0	0	0	0
60	1Y	1	0	0	0	0
60	1n	1	0	0	0	0
60	24	1	0	0	0	0
60	25	1	0	0	0	0
60	26	1	0	0	0	0
60	29	1	0	0	0	0
60	2Y	1	0	0	0	0
60	2n	1	0	0	0	0
61	1d	8	0	0	0	0
61	2d	8	0	0	0	0
62	10	23	0	0	1	0
62	11	26	0	0	0	0
62	12	10	0	0	2	0
62	13	25	0	0	0	0
62	14	2	0	0	0	0
62	15	18	0	0	0	0
62	16	18	0	0	1	0
62	17	17	0	0	1	0
62	18	25	0	0	1	0
62	19	5	0	0	0	0
62	1A	3935	0	0	72	0
62	1B	80	0	0	2	0
62	1D	108	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
62	1E	74	0	0	1	0
62	1F	60	0	0	1	0
62	1G	16	0	0	0	0
62	1H	15	0	0	0	0
62	1I	5	0	0	0	0
62	1N	54	0	0	1	0
62	1O	21	0	0	1	0
62	1P	63	0	0	2	0
62	1Q	39	0	0	2	0
62	1R	28	0	0	1	0
62	1S	12	0	0	0	0
62	1T	32	0	0	2	0
62	1U	53	0	0	4	0
62	1V	33	0	0	0	0
62	1W	24	0	0	1	0
62	1X	24	0	0	1	0
62	1Y	15	0	0	2	0
62	1Z	7	0	0	0	0
62	1a	424	0	0	17	0
62	1b	1	0	0	0	0
62	1d	8	0	0	1	0
62	1e	2	0	0	0	0
62	1f	2	0	0	0	0
62	1g	1	0	0	0	0
62	1h	1	0	0	0	0
62	1l	2	0	0	1	0
62	1o	4	0	0	0	0
62	1p	1	0	0	0	0
62	1t	1	0	0	0	0
62	1w	6	0	0	0	0
62	1x	2	0	0	0	0
62	1y	2	0	0	0	0
62	20	8	0	0	0	0
62	21	15	0	0	2	0
62	23	2	0	0	1	0
62	25	11	0	0	1	0
62	26	7	0	0	1	0
62	27	5	0	0	0	0
62	28	16	0	0	0	0
62	2A	2058	0	0	72	0
62	2B	39	0	0	2	0
62	2D	51	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
62	2E	32	0	0	3	0
62	2F	26	0	0	2	0
62	2G	7	0	0	0	0
62	2H	1	0	0	0	0
62	2I	2	0	0	1	0
62	2N	5	0	0	0	0
62	2O	16	0	0	0	0
62	2P	26	0	0	2	0
62	2Q	14	0	0	0	0
62	2R	17	0	0	3	0
62	2S	3	0	0	0	0
62	2T	7	0	0	0	0
62	2U	15	0	0	0	0
62	2V	3	0	0	1	0
62	2W	17	0	0	0	0
62	2X	8	0	0	0	0
62	2Y	2	0	0	0	0
62	2Z	6	0	0	0	0
62	2a	243	0	0	12	0
62	2e	2	0	0	0	0
62	2l	3	0	0	0	0
62	2m	1	0	0	0	0
62	2n	2	0	0	0	0
62	2o	2	0	0	0	0
62	2p	1	0	0	0	0
62	2r	4	0	0	0	0
62	2t	2	0	0	0	0
62	2w	4	0	0	0	0
62	2x	3	0	0	1	0
All	All	297350	0	194813	3545	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 8.

All (3545) 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	1.37	1.20
1:2A:2122:U:H3	1:2A:2176:A:N6	1.58	1.00
1:1A:1082:U:O4	1:1A:1086:A:N1	1.98	0.95
22:10:10:THR:HG22	22:10:12:ASN:H	1.27	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1003:G:H2'	32:1a:1004:A:H4'	1.46	0.95
1:2A:2319:G:H22	14:2S:3:ARG:HD3	1.30	0.94
1:2A:2427:C:OP1	62:2A:3803:HOH:O	1.88	0.90
10:2O:48:PRO:HB3	32:2a:1422:G:H5''	1.53	0.90
1:2A:2139:C:H42	1:2A:2152:G:H1	1.14	0.89
1:2A:2296:U:OP2	14:2S:9:ARG:NH2	2.06	0.87
1:1A:1359:A:H61	1:1A:1372:U:H3	1.23	0.87
1:1A:1798:U:H5'	3:1D:259:THR:HG22	1.56	0.86
1:1A:2822:G:OP2	62:1A:4101:HOH:O	1.93	0.86
32:1a:201:C:H42	32:1a:216:G:H1	1.23	0.86
32:2a:559:A:H4'	32:2a:560:U:H3'	1.58	0.85
1:1A:2137:C:N4	1:1A:2154:G:H1	1.73	0.85
26:24:16:CYS:SG	26:24:17:GLY:N	2.50	0.85
10:1O:48:PRO:HB3	32:1a:1422:G:H5''	1.58	0.84
8:1I:85:GLU:O	8:1I:87:LYS:N	2.10	0.84
1:2A:1647:G:OP1	62:2A:3804:HOH:O	1.95	0.84
5:1F:53:THR:HG22	5:1F:55:GLY:H	1.43	0.84
1:1A:1665:A:OP2	62:1A:4102:HOH:O	1.96	0.83
1:1A:2137:C:H42	1:1A:2154:G:H1	1.26	0.83
32:1a:1086:U:H3	32:1a:1099:G:H22	1.27	0.82
1:1A:1082:U:H3	1:1A:1086:A:H61	0.84	0.82
1:2A:1090:U:H2'	1:2A:1091:G:H8	1.43	0.82
1:2A:2139:C:N4	1:2A:2152:G:H1	1.78	0.82
1:1A:1669:A:OP2	62:1A:4104:HOH:O	1.97	0.82
1:1A:2464:C:O2'	62:1A:4103:HOH:O	1.96	0.81
1:2A:194:G:OP2	62:2A:3805:HOH:O	1.97	0.81
1:2A:2125:G:H22	1:2A:2172:U:H3'	1.46	0.81
1:2A:1798:U:H5'	3:2D:259:THR:HG22	1.63	0.80
40:2i:4:TYR:HB2	40:2i:19:LEU:HB2	1.62	0.80
41:1j:35:SER:HB3	41:1j:73:ASP:HB2	1.63	0.80
50:1s:50:ALA:HB1	50:1s:57:HIS:HB3	1.62	0.80
38:2g:50:ILE:HD11	38:2g:58:PRO:HA	1.64	0.80
33:2b:84:GLU:HB3	33:2b:219:VAL:HG21	1.63	0.80
34:1c:58:GLU:HB3	41:1j:92:THR:HG21	1.64	0.79
32:2a:1500:A:OP1	62:2a:3201:HOH:O	1.99	0.79
33:1b:59:GLU:HG3	33:1b:221:LEU:HD23	1.63	0.79
32:1a:812:C:N3	62:1a:1907:HOH:O	2.15	0.79
40:1i:50:LEU:HD13	40:1i:56:LEU:HA	1.65	0.79
51:2t:57:ARG:HH22	51:2t:100:ILE:HD12	1.46	0.79
55:2x:76:8AN:O2P	62:2x:201:HOH:O	2.00	0.79
32:2a:1226:C:OP2	44:2m:91:ARG:NH1	2.16	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:664:G:H22	32:1a:741:G:H1	1.30	0.78
42:2k:99:GLN:HG2	42:2k:105:VAL:HG21	1.65	0.78
16:1U:33:ARG:NH1	62:1U:301:HOH:O	2.16	0.78
22:20:11:ARG:O	22:20:14:ARG:NH2	2.17	0.78
1:1A:217:G:OP2	62:1A:4105:HOH:O	2.02	0.78
9:1N:46:VAL:HG23	9:1N:48:MET:HG2	1.66	0.78
1:1A:1143:A:OP1	9:1N:25:ARG:NH2	2.17	0.78
8:1I:92:VAL:HG13	8:1I:120:ILE:HB	1.66	0.78
1:2A:468:G:O2'	5:2F:62:ARG:NH2	2.17	0.77
8:2I:92:VAL:HG23	8:2I:120:ILE:HB	1.66	0.77
44:2m:94:ARG:HB3	44:2m:96:LEU:HD12	1.64	0.77
32:2a:1003:G:H2'	32:2a:1004:A:H4'	1.64	0.77
1:1A:2554:U:O4	62:1A:4108:HOH:O	2.03	0.77
46:2o:54:ARG:HG2	46:2o:58:MET:HE2	1.65	0.77
1:1A:1039:G:O6	1:1A:1116:C:N4	2.16	0.77
26:14:53:GLU:HB2	26:14:56:VAL:HG12	1.65	0.77
32:1a:501:C:OP1	43:1l:117:ARG:NH2	2.18	0.77
1:2A:2469:A:H4'	12:2Q:56:ARG:HG2	1.67	0.77
44:2m:107:ALA:HB3	44:2m:111:LYS:HD2	1.67	0.77
2:1B:81:G:N7	59:1B:231:ARG:NH1	2.33	0.77
1:2A:1602:U:O4	62:2A:3806:HOH:O	2.02	0.77
1:1A:2427:C:OP1	62:1A:4109:HOH:O	2.03	0.76
1:1A:2447:G:OP2	62:1A:4107:HOH:O	2.02	0.76
1:2A:994:C:OP1	16:2U:53:ARG:NH2	2.17	0.76
1:2A:2765:A:OP2	62:2A:3809:HOH:O	2.04	0.76
3:2D:134:ARG:NH1	3:2D:188:GLU:OE2	2.18	0.76
1:1A:123:G:OP2	62:1A:4106:HOH:O	2.02	0.76
1:1A:2821:A:OP2	62:1A:4101:HOH:O	2.03	0.76
1:1A:1023:U:OP2	62:1A:4110:HOH:O	2.04	0.76
6:1G:50:ALA:O	6:1G:52:ILE:N	2.19	0.76
1:2A:2122:U:H3	1:2A:2176:A:H61	0.81	0.76
32:1a:73:G:H1	32:1a:96:U:H3	1.33	0.75
1:2A:2141:G:O6	1:2A:2150:U:O2	2.05	0.75
1:2A:2683:C:OP1	15:2T:53:ARG:NH2	2.18	0.75
41:2j:49:VAL:HG23	45:2n:41:ARG:HB2	1.68	0.75
32:2a:427:U:OP1	35:2d:13:ARG:NH2	2.19	0.75
1:2A:1314:C:OP1	62:2A:3807:HOH:O	2.03	0.75
1:2A:2115:G:H21	1:2A:2171:A:H61	1.35	0.75
1:2A:2206:G:H3'	1:2A:2207:G:H8	1.52	0.75
15:2T:41:ARG:NH2	32:2a:346:G:OP1	2.20	0.75
1:1A:1300:U:H4'	1:1A:1301:A:H5'	1.69	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:986:A:N3	50:2s:52:TYR:OH	2.18	0.74
51:2t:50:GLU:HB2	51:2t:99:LEU:HD22	1.68	0.74
21:2Z:19:ARG:NH1	21:2Z:84:GLU:O	2.19	0.74
26:14:59:PHE:HZ	50:1s:45:VAL:HG21	1.51	0.74
28:16:13:CYS:SG	28:16:47:THR:HG21	2.27	0.74
1:2A:1064:C:H42	1:2A:1074:G:H1	1.35	0.74
5:2F:21:ALA:HB3	5:2F:22:ALA:HA	1.68	0.74
33:2b:223:ILE:HA	33:2b:226:ARG:HB2	1.70	0.74
1:2A:526:A:OP1	62:2A:3808:HOH:O	2.04	0.74
11:1P:141:ALA:HA	25:23:38:GLU:HG2	1.70	0.74
36:1e:37:ARG:HH12	36:1e:111:GLU:HG2	1.52	0.74
1:1A:1648:C:OP1	62:1A:4111:HOH:O	2.05	0.74
32:1a:975:A:H4'	32:1a:976:G:H5''	1.70	0.74
1:2A:2206:G:H3'	1:2A:2207:G:C8	2.22	0.74
32:2a:1086:U:H3	32:2a:1099:G:H22	1.33	0.74
34:2c:181:ASN:ND2	34:2c:205:GLY:O	2.21	0.74
50:2s:41:VAL:HG12	50:2s:44:MET:HG3	1.70	0.74
1:1A:1634:A:OP2	62:1A:4112:HOH:O	2.06	0.73
1:2A:1271:G:OP2	62:2A:3804:HOH:O	2.06	0.73
1:2A:2130:U:H2'	1:2A:2158:A:H61	1.54	0.73
1:1A:2137:C:N3	1:1A:2154:G:N2	2.37	0.73
21:1Z:52:SER:O	21:1Z:54:HIS:N	2.22	0.73
31:29:25:VAL:HB	31:29:34:GLN:HB2	1.69	0.73
1:2A:2584:U:O4	62:2A:3811:HOH:O	2.06	0.73
1:2A:2822:G:OP2	62:2A:3810:HOH:O	2.04	0.73
33:2b:144:ARG:NH1	33:2b:148:TYR:OH	2.21	0.73
15:2T:127:ALA:O	15:2T:129:ARG:N	2.22	0.73
1:2A:2807:G:H22	1:2A:2892:A:H62	1.35	0.73
1:1A:2690:C:OP1	13:1R:17:ARG:NH2	2.22	0.73
32:1a:612:C:O2	32:1a:629:G:N2	2.22	0.73
1:1A:1671:U:O4	62:1A:4104:HOH:O	2.07	0.72
47:1p:53:VAL:HG13	47:1p:79:VAL:HG12	1.70	0.72
48:2q:53:LEU:HD23	48:2q:82:MET:HE1	1.70	0.72
36:2e:50:GLU:HB2	36:2e:53:LEU:HD12	1.68	0.72
1:1A:2145:C:O2'	1:1A:2147:G:N2	2.22	0.72
53:2y:40:ILE:HB	53:2y:51:ASP:HB2	1.71	0.72
1:2A:450:G:OP2	62:2A:3812:HOH:O	2.06	0.72
62:1A:4101:HOH:O	13:1R:3:HIS:NE2	2.22	0.72
40:1i:16:ARG:HH11	40:1i:64:THR:HG21	1.54	0.72
1:2A:2137:C:O2	1:2A:2154:G:N1	2.22	0.72
1:1A:1016:G:N7	62:1A:4145:HOH:O	2.21	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1182:G:H4'	32:2a:1183:A:H3'	1.70	0.72
35:1d:18:LYS:NZ	35:1d:31:CYS:SG	2.63	0.72
44:1m:37:THR:O	44:1m:55:ARG:NH1	2.23	0.72
1:2A:1378:A:OP1	29:27:10:ARG:NH2	2.23	0.72
1:1A:826:U:OP1	62:1A:4109:HOH:O	2.06	0.72
1:1A:1762:A:N1	62:1A:4150:HOH:O	2.23	0.72
32:1a:376:G:H5''	47:1p:5:ARG:HD3	1.72	0.72
40:1i:46:ALA:HB2	40:1i:74:ILE:HG23	1.72	0.72
6:2G:179:PRO:HB2	26:24:42:PHE:HE2	1.55	0.72
1:1A:1024:G:OP2	62:1A:4110:HOH:O	2.07	0.72
6:2G:57:ALA:HB2	6:2G:90:LEU:HD13	1.70	0.72
33:2b:137:ARG:HH12	33:2b:138:LEU:HG	1.55	0.71
32:1a:38:G:H22	32:1a:397:A:H5'	1.55	0.71
44:1m:11:ARG:HA	44:1m:45:VAL:HB	1.72	0.71
49:1r:32:ARG:HA	49:1r:69:THR:HG21	1.72	0.71
1:2A:2126:A:H4'	1:2A:2127:G:O5'	1.89	0.71
1:1A:1047:G:H2'	1:1A:1110:G:H22	1.53	0.71
33:1b:15:VAL:HG22	33:1b:209:ARG:HB3	1.71	0.71
36:1e:147:ASP:OD1	36:1e:147:ASP:N	2.17	0.71
1:2A:2821:A:OP2	62:2R:301:HOH:O	2.08	0.71
6:2G:145:THR:H	6:2G:148:MET:HE3	1.56	0.71
1:1A:302:C:OP2	20:1Y:73:ARG:NH2	2.23	0.71
22:10:10:THR:HG22	22:10:12:ASN:N	2.04	0.71
32:1a:992:U:H4'	32:1a:993:G:H5'	1.72	0.71
32:1a:1300:G:N7	62:1a:1917:HOH:O	2.23	0.71
17:2V:98:GLU:OE1	17:2V:100:ARG:NH1	2.21	0.71
32:1a:1414:U:H3	32:1a:1486:G:H1	1.39	0.71
32:1a:1518:MA6:H93	32:1a:1519:MA6:H92	1.71	0.71
39:1h:10:LEU:HD22	39:1h:83:ILE:HD11	1.71	0.71
5:2F:188:ARG:HA	11:2P:3:LEU:HD11	1.73	0.71
9:2N:20:GLY:HA2	9:2N:61:ARG:HE	1.54	0.71
34:2c:139:GLN:HE21	34:2c:143:GLU:HG3	1.54	0.71
38:2g:72:ARG:HH22	38:2g:138:LYS:HZ1	1.38	0.71
32:1a:1189:C:OP1	41:1j:51:ARG:NH2	2.24	0.71
1:2A:2137:C:N3	1:2A:2154:G:O6	2.24	0.71
32:2a:117:G:OP2	62:2a:3202:HOH:O	2.09	0.71
1:1A:2646:C:OP2	1:1A:2732:G:O2'	2.09	0.71
3:1D:88:ARG:NH1	62:1D:402:HOH:O	2.24	0.71
15:1T:51:ARG:HG3	15:1T:98:LYS:HE3	1.72	0.71
1:2A:2107:C:H42	1:2A:2182:G:H1	1.38	0.71
1:1A:1070:A:O2'	1:1A:1098:A:OP1	2.08	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:1o:54:ARG:HG2	46:1o:58:MET:HE2	1.73	0.70
1:2A:585:G:OP2	62:2A:3816:HOH:O	2.08	0.70
23:21:54:ALA:HB1	23:21:83:GLU:HG3	1.71	0.70
1:2A:2839:G:H5'	13:2R:46:GLY:HA2	1.71	0.70
10:1O:64:ARG:HG2	10:1O:83:ALA:HB3	1.72	0.70
49:2r:32:ARG:HA	49:2r:69:THR:HG21	1.72	0.70
1:1A:493:G:OP2	62:1A:4114:HOH:O	2.10	0.70
1:1A:2242:G:OP1	62:1A:4113:HOH:O	2.09	0.70
1:2A:2134:A:N6	1:2A:2156:G:O2'	2.24	0.70
1:2A:2206:G:H8	1:2A:2207:G:N7	1.89	0.70
1:1A:330:A:H2	1:1A:1210:A:HO2'	1.38	0.70
1:1A:1041:C:H42	1:1A:1114:G:H1	1.39	0.70
42:1k:99:GLN:HG2	42:1k:105:VAL:HG21	1.73	0.70
1:2A:143:G:H4'	19:2X:35:THR:HG21	1.73	0.70
1:2A:2499:C:OP1	62:2A:3817:HOH:O	2.09	0.70
7:2H:11:VAL:HG12	7:2H:15:VAL:HG23	1.73	0.70
32:2a:977:A:N6	32:2a:1224:G:OP1	2.22	0.70
1:1A:1359:A:N6	1:1A:1372:U:H3	1.89	0.70
1:2A:530:G:O6	62:2A:3813:HOH:O	2.07	0.70
33:2b:63:MET:HG2	33:2b:225:ALA:HB1	1.74	0.70
1:2A:1356:G:O6	62:2A:3814:HOH:O	2.08	0.70
36:2e:143:ARG:NH1	39:2h:77:GLU:OE2	2.23	0.70
1:1A:2140:C:N3	1:1A:2151:G:O6	2.25	0.69
1:2A:991:C:OP2	62:2A:3815:HOH:O	2.08	0.69
32:2a:390:C:O3'	47:2p:28:ARG:NH2	2.25	0.69
33:2b:185:ILE:HG13	33:2b:199:TYR:HB2	1.74	0.69
41:2j:51:ARG:O	45:2n:45:ARG:NH1	2.25	0.69
51:1t:57:ARG:HH12	51:1t:100:ILE:HD12	1.57	0.69
1:2A:1771:C:OP1	62:2A:3818:HOH:O	2.10	0.69
32:2a:942:G:N2	40:2i:124:GLN:OE1	2.24	0.69
1:1A:2683:C:OP1	15:1T:53:ARG:NH2	2.26	0.69
1:1A:749:C:OP2	62:1A:4116:HOH:O	2.10	0.69
12:1Q:136:ALA:HB1	21:1Z:52:SER:HB2	1.75	0.69
1:1A:2292:C:OP1	14:1S:17:ARG:NH2	2.22	0.69
6:1G:21:ARG:O	6:1G:21:ARG:NH1	2.24	0.69
1:2A:1084:A:H3'	1:2A:1085:A:H4'	1.74	0.69
32:2a:1376:U:O4	38:2g:10:ARG:NH1	2.25	0.69
1:1A:120:U:OP2	62:1A:4115:HOH:O	2.10	0.69
32:1a:964:A:OP1	62:1a:1904:HOH:O	2.09	0.69
1:2A:1762:A:N1	62:2A:3861:HOH:O	2.25	0.69
4:2E:199:ARG:NH1	62:2E:403:HOH:O	2.26	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:2F:185:ASP:HA	5:2F:188:ARG:HD3	1.73	0.69
39:2h:64:LYS:HG2	39:2h:79:VAL:HG21	1.74	0.69
26:24:59:PHE:CE2	50:2s:64:GLU:HB2	2.27	0.69
19:2X:35:THR:HG22	19:2X:37:THR:H	1.58	0.69
1:2A:989:G:O2'	62:2A:3820:HOH:O	2.11	0.68
32:2a:1108:G:H5'	34:2c:176:HIS:HD2	1.57	0.68
1:2A:1023:U:OP2	62:2A:3819:HOH:O	2.11	0.68
1:2A:1090:U:H2'	1:2A:1091:G:C8	2.27	0.68
14:2S:35:ILE:HD11	14:2S:97:ARG:HE	1.58	0.68
32:2a:1518:MA6:H93	32:2a:1519:MA6:H102	1.73	0.68
1:2A:731:C:OP1	62:2A:3821:HOH:O	2.11	0.68
33:1b:74:LYS:NZ	33:1b:206:ASP:OD1	2.26	0.68
40:1i:17:VAL:HG23	40:1i:63:ILE:HG12	1.74	0.68
5:2F:20:LEU:HD23	5:2F:21:ALA:H	1.58	0.68
6:2G:137:GLU:HG3	6:2G:140:ILE:HG12	1.75	0.68
40:2i:7:THR:O	40:2i:83:ARG:NH1	2.27	0.68
1:2A:1105:U:H2'	1:2A:1106:G:C8	2.29	0.68
6:2G:7:LEU:HD23	6:2G:100:TRP:HE3	1.59	0.68
11:2P:35:HIS:O	62:2P:301:HOH:O	2.12	0.68
1:1A:1264:G:OP1	27:15:19:ARG:NH2	2.19	0.68
32:1a:573:A:OP2	62:1a:1905:HOH:O	2.12	0.68
1:2A:2237:G:OP1	62:2A:3823:HOH:O	2.12	0.68
7:2H:125:VAL:HG22	7:2H:131:VAL:HG22	1.76	0.68
24:22:1:MET:N	24:22:52:ASP:OD1	2.26	0.68
1:1A:1470:G:N2	1:1A:1520:G:OP2	2.20	0.68
3:1D:108:PRO:HD2	3:1D:111:LEU:HG	1.76	0.68
35:2d:175:SER:HB3	35:2d:186:LEU:HD21	1.76	0.68
32:1a:1385:G:N7	62:1a:1920:HOH:O	2.26	0.68
38:1g:27:ILE:HD12	38:1g:40:ALA:HA	1.76	0.68
38:1g:78:ARG:NH1	38:1g:154:TYR:O	2.26	0.68
1:2A:601:C:OP1	5:2F:108:LYS:NZ	2.25	0.68
1:2A:1365:A:O2'	23:21:11:ARG:NH1	2.26	0.68
2:2B:66:A:H61	2:2B:109:C:H5'	1.59	0.68
32:2a:664:G:H22	32:2a:741:G:H1	1.41	0.68
1:1A:2316:C:O2'	6:1G:128:ARG:NH2	2.27	0.68
32:1a:196:A:OP1	51:1t:68:LYS:NZ	2.27	0.68
32:1a:1003:G:C2'	32:1a:1004:A:H4'	2.22	0.68
40:2i:42:ARG:NH2	40:2i:71:SER:OG	2.24	0.68
37:1f:95:GLU:O	49:1r:32:ARG:NH1	2.27	0.67
23:21:31:GLY:O	62:21:101:HOH:O	2.11	0.67
1:1A:607:U:OP1	5:1F:102:PRO:HA	1.95	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1816:G:O6	3:1D:35:LYS:NZ	2.27	0.67
2:1B:6:C:H2'	2:1B:7:G:H5''	1.76	0.67
44:1m:15:VAL:HG11	44:1m:48:LEU:HD21	1.76	0.67
33:2b:8:LYS:HG2	33:2b:9:GLU:H	1.59	0.67
1:1A:1371:G:N7	62:1A:4176:HOH:O	2.27	0.67
1:1A:1970:A:OP1	62:1A:4118:HOH:O	2.11	0.67
33:1b:9:GLU:HG3	33:1b:217:ARG:HH22	1.58	0.67
1:2A:2575:C:OP2	62:2A:3822:HOH:O	2.12	0.67
32:2a:975:A:H4'	32:2a:976:G:H5''	1.76	0.67
33:2b:54:THR:HG23	33:2b:199:TYR:HB3	1.75	0.67
1:1A:1266:G:O5'	18:1W:15:ARG:NH2	2.27	0.67
1:1A:2114:A:H1'	1:1A:2168:G:H5'	1.76	0.67
51:1t:92:LEU:O	51:1t:96:GLY:N	2.26	0.67
40:1i:17:VAL:HG21	40:1i:81:ILE:HG22	1.77	0.67
40:1i:64:THR:HG23	40:1i:66:ARG:HH11	1.58	0.67
46:1o:82:ILE:HD12	46:1o:88:ARG:HB2	1.76	0.67
1:2A:2157:G:H5''	1:2A:2158:A:H5'	1.74	0.67
32:2a:1028:C:H2'	32:2a:1033:G:H22	1.58	0.67
1:1A:847:U:OP2	62:1A:4120:HOH:O	2.13	0.67
19:2X:53:LYS:HB3	19:2X:82:GLN:HB3	1.76	0.67
32:2a:937:A:OP2	62:2a:3203:HOH:O	2.13	0.67
40:2i:50:LEU:HB3	40:2i:56:LEU:HA	1.75	0.67
6:1G:83:ARG:H	6:1G:86:MET:HE3	1.59	0.67
21:1Z:158:PRO:HG2	21:1Z:161:VAL:HG11	1.76	0.67
36:2e:57:LYS:HG2	36:2e:61:TYR:HE2	1.60	0.67
32:1a:1356:G:H2'	32:1a:1357:A:C8	2.29	0.67
18:2W:18:ARG:NH1	18:2W:76:VAL:O	2.27	0.67
50:2s:20:LEU:HA	50:2s:23:ASN:HB2	1.76	0.67
1:1A:956:G:H5''	12:1Q:77:LYS:HD2	1.75	0.67
6:1G:44:GLY:HA2	6:1G:88:ILE:HG22	1.75	0.67
1:2A:775:G:O3'	62:2A:3825:HOH:O	2.12	0.67
1:1A:792:G:O2'	62:1A:4122:HOH:O	2.13	0.66
48:1q:53:LEU:HD23	48:1q:82:MET:HE1	1.77	0.66
1:2A:1264:G:OP1	27:25:19:ARG:NH2	2.22	0.66
32:2a:1401:G:N7	53:2y:83:ARG:NH1	2.41	0.66
1:1A:135:G:N7	62:1A:4177:HOH:O	2.28	0.66
1:1A:2379:G:O2'	14:1S:17:ARG:NH1	2.22	0.66
33:1b:82:ARG:NH1	33:1b:86:GLU:OE2	2.29	0.66
1:2A:7:G:H1	1:2A:2896:C:H42	1.43	0.66
46:2o:39:LEU:HD13	46:2o:56:LEU:HB2	1.76	0.66
1:1A:67:U:O4	62:1A:4117:HOH:O	2.11	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:438:G:N7	62:1A:4167:HOH:O	2.26	0.66
1:1A:803:U:OP2	62:1A:4123:HOH:O	2.13	0.66
1:1A:2470:G:OP2	62:1A:4121:HOH:O	2.13	0.66
1:2A:771:G:N7	62:2A:3874:HOH:O	2.28	0.66
32:1a:1179:A:OP2	40:1i:93:ARG:NH2	2.28	0.66
33:1b:112:VAL:HG12	33:1b:149:LEU:HD13	1.78	0.66
1:1A:1045:A:H5'	1:1A:1046:A:H5'	1.77	0.66
1:1A:1101:U:H2'	1:1A:1102:C:H6	1.60	0.66
1:1A:1721:G:H8	1:1A:1741:A:H62	1.44	0.66
11:1P:14:LYS:NZ	62:1P:302:HOH:O	2.25	0.66
39:1h:51:VAL:HG21	39:1h:60:ARG:HD2	1.77	0.66
33:2b:91:PRO:HG3	33:2b:155:LEU:HD13	1.78	0.66
41:2j:10:GLY:HA3	41:2j:16:LEU:HD21	1.77	0.66
1:1A:226:G:H21	1:1A:228:A:H62	1.43	0.66
1:2A:1364:G:OP2	23:21:3:LYS:HG3	1.95	0.66
32:2a:1142:G:H3'	32:2a:1143:G:H8	1.61	0.66
32:1a:1094:G:OP1	62:1a:1906:HOH:O	2.14	0.66
44:1m:58:GLU:O	44:1m:62:ASN:ND2	2.24	0.66
1:2A:2122:U:O2	1:2A:2176:A:N1	2.28	0.66
32:1a:1148:U:O2'	40:1i:66:ARG:NH2	2.29	0.65
48:1q:74:LEU:HD23	48:1q:75:ARG:HG2	1.75	0.65
32:2a:1004:A:H5''	32:2a:1025:U:C5	2.31	0.65
32:2a:1129:C:H2'	32:2a:1139:G:N7	2.11	0.65
1:2A:1076:C:H1'	1:2A:1077:A:H5'	1.78	0.65
1:2A:300:A:OP1	20:2Y:86:ARG:NH2	2.30	0.65
34:2c:109:PRO:HB3	34:2c:115:LEU:HD23	1.78	0.65
32:1a:976:G:N2	32:1a:1363:C:OP2	2.27	0.65
37:1f:36:ARG:NH2	37:1f:66:GLU:OE1	2.24	0.65
47:1p:75:ARG:HG3	47:1p:80:PHE:HD2	1.61	0.65
48:1q:66:SER:O	48:1q:70:ARG:NH1	2.30	0.65
1:1A:1452:A:OP2	62:1A:4125:HOH:O	2.15	0.65
1:1A:1321:A:N1	62:1A:4194:HOH:O	2.29	0.65
29:17:34:ARG:NH2	62:17:201:HOH:O	2.26	0.65
1:2A:1308:A:O2'	62:2A:3827:HOH:O	2.14	0.65
32:2a:411:A:OP1	35:2d:30:LYS:NZ	2.29	0.65
41:2j:81:THR:HA	41:2j:84:GLN:HB3	1.78	0.65
33:1b:134:GLU:HG3	33:1b:137:ARG:HH21	1.60	0.65
8:2I:115:ALA:O	62:2I:301:HOH:O	2.14	0.65
33:2b:88:ALA:HB2	33:2b:219:VAL:HG13	1.78	0.65
8:1I:68:LEU:HD21	8:1I:109:ILE:HD11	1.79	0.65
51:1t:33:ILE:O	51:1t:37:SER:OG	2.14	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:2G:80:PHE:O	6:2G:82:LEU:N	2.30	0.64
41:2j:8:LEU:HB2	41:2j:70:ARG:HB2	1.79	0.64
32:1a:1151:A:HO2'	32:1a:1152:A:H8	1.45	0.64
43:1l:77:LEU:HD21	43:1l:107:ALA:HA	1.79	0.64
6:2G:105:LYS:NZ	6:2G:143:GLU:OE2	2.25	0.64
33:2b:74:LYS:HD2	33:2b:166:ASP:HB2	1.80	0.64
33:2b:166:ASP:HB3	33:2b:169:LYS:HB3	1.79	0.64
34:2c:36:ASP:HA	34:2c:39:ILE:HD12	1.79	0.64
1:1A:1175:U:OP1	1:1A:1177:A:N6	2.30	0.64
12:1Q:111:GLU:OE2	12:1Q:133:ARG:NH2	2.26	0.64
36:1e:12:LEU:HB3	36:1e:31:LEU:HB2	1.79	0.64
1:2A:2574:G:OP1	62:2A:3822:HOH:O	2.15	0.64
32:2a:954:G:H21	32:2a:1227:A:H62	1.42	0.64
1:1A:279:C:H42	1:1A:361:G:H1	1.46	0.64
1:1A:1877:A:H5'	1:1A:1878:G:OP2	1.97	0.64
1:1A:2126:A:H4'	1:1A:2127:G:O5'	1.97	0.64
32:1a:572:A:OP2	62:1a:1905:HOH:O	2.15	0.64
3:2D:268:ARG:NE	62:2D:401:HOH:O	2.30	0.64
1:1A:278:A:O2'	1:1A:279:C:OP1	2.16	0.64
32:1a:538:G:H5''	43:1l:114:LYS:HB2	1.80	0.64
41:2j:38:ILE:HD13	41:2j:71:LEU:HD22	1.80	0.64
1:1A:1101:U:H2'	1:1A:1102:C:C6	2.33	0.64
1:1A:2115:G:H2'	1:1A:2117:A:N6	2.12	0.64
25:13:7:LYS:HE3	25:13:32:GLN:HE21	1.62	0.64
18:2W:12:ILE:HD13	18:2W:17:VAL:HG13	1.78	0.64
32:2a:1240:U:OP1	38:2g:119:ARG:NH2	2.30	0.64
1:1A:2308:G:O2'	1:1A:2310:A:N7	2.30	0.64
1:2A:1073:A:H2'	1:2A:1074:G:C8	2.33	0.64
1:1A:760:G:OP1	62:1A:4126:HOH:O	2.15	0.64
40:1i:121:ARG:NH1	40:1i:122:ALA:O	2.29	0.64
50:1s:32:LYS:HA	50:1s:50:ALA:HB3	1.78	0.64
1:2A:1057:A:N6	1:2A:1087:G:OP1	2.31	0.64
1:2A:2805:G:H2'	1:2A:2807:G:C8	2.32	0.64
33:1b:88:ALA:HB2	33:1b:219:VAL:HG13	1.79	0.64
1:2A:2079:U:OP1	23:21:21:ARG:NH2	2.31	0.64
24:22:65:ASN:OD1	24:22:69:ARG:NH1	2.31	0.64
32:2a:794:A:OP2	62:2a:3204:HOH:O	2.15	0.64
38:2g:54:THR:O	38:2g:56:GLN:NE2	2.31	0.64
1:1A:2548:G:O6	62:1A:4119:HOH:O	2.13	0.63
1:2A:993:G:OP1	16:2U:50:ARG:NH2	2.31	0.63
1:2A:1648:C:OP1	62:2A:3804:HOH:O	2.15	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2115:G:N3	1:1A:2117:A:N6	2.45	0.63
1:1A:2130:U:O2'	1:1A:2133:G:O2'	2.15	0.63
25:13:59:VAL:HG23	25:13:60:GLU:HG2	1.79	0.63
35:1d:162:LEU:HD13	35:1d:181:MET:HG2	1.79	0.63
1:2A:1073:A:H2'	1:2A:1074:G:H8	1.62	0.63
1:2A:1658:C:OP1	62:2E:401:HOH:O	2.14	0.63
7:2H:86:GLU:OE2	7:2H:132:ARG:NH2	2.29	0.63
32:2a:992:U:H4'	32:2a:993:G:O5'	1.97	0.63
41:2j:44:VAL:HG13	41:2j:66:ARG:HG2	1.80	0.63
2:1B:66:A:H61	2:1B:108:U:H2'	1.63	0.63
6:1G:126:ASP:N	6:1G:130:ASN:O	2.32	0.63
32:1a:953:G:N7	44:1m:104:ARG:NH2	2.46	0.63
1:2A:826:U:OP1	62:2A:3803:HOH:O	2.15	0.63
32:2a:1273:G:H3'	32:2a:1274:G:H8	1.63	0.63
1:1A:1173:G:N2	1:1A:1176:G:OP2	2.32	0.63
32:1a:1003:G:C2	32:1a:1004:A:H1'	2.34	0.63
1:1A:2820:A:OP2	13:1R:2:ARG:NH2	2.32	0.63
32:1a:1218:C:H2'	32:1a:1219:U:C6	2.34	0.63
35:2d:60:GLU:HG3	35:2d:202:LEU:HD12	1.80	0.63
16:1U:101:ARG:NH2	62:1U:302:HOH:O	2.32	0.62
32:2a:38:G:H22	32:2a:397:A:H5''	1.62	0.62
32:2a:1346:A:OP1	40:2i:120:ARG:NH1	2.31	0.62
34:2c:164:ARG:NH1	34:2c:166:GLU:OE1	2.32	0.62
44:2m:22:ILE:HB	44:2m:25:ILE:HD12	1.80	0.62
1:1A:1079:C:N4	1:1A:1088:A:OP1	2.24	0.62
32:1a:437:U:H5'	35:1d:155:LEU:HD11	1.81	0.62
32:2a:1271:G:O2'	62:2a:3205:HOH:O	2.15	0.62
32:1a:1015:A:H2'	32:1a:1016:A:C8	2.34	0.62
46:1o:39:LEU:HD13	46:1o:56:LEU:HB2	1.80	0.62
1:2A:668:G:H5'	1:2A:669:G:OP2	1.99	0.62
2:2B:75:G:H22	21:2Z:73:GLN:NE2	1.98	0.62
14:2S:15:ARG:HB3	14:2S:19:LYS:HE3	1.80	0.62
32:2a:17:U:H2'	32:2a:18:C:C6	2.34	0.62
1:1A:1830:C:OP2	62:1A:4128:HOH:O	2.16	0.62
1:2A:607:U:OP1	5:2F:102:PRO:HA	1.99	0.62
1:2A:2115:G:H22	1:2A:2119:A:H5'	1.64	0.62
26:24:59:PHE:HA	26:24:60:GLN:C	2.24	0.62
28:26:6:ARG:NH1	28:26:26:ASN:HB2	2.14	0.62
1:2A:2206:G:H5''	1:2A:2207:G:C8	2.34	0.62
32:2a:1401:G:O6	53:2y:83:ARG:NH2	2.32	0.62
26:14:55:ARG:H	26:14:56:VAL:HA	1.64	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1087:G:H1	1:2A:1102:C:H42	1.47	0.62
44:2m:29:ARG:HA	44:2m:32:GLU:HB3	1.82	0.62
44:2m:91:ARG:NE	44:2m:97:PRO:O	2.33	0.62
1:1A:1770:G:OP1	62:1A:4127:HOH:O	2.16	0.62
1:1A:2140:C:O2	1:1A:2151:G:N1	2.30	0.62
32:1a:222:U:H2'	32:1a:223:U:C6	2.35	0.62
33:1b:155:LEU:HD21	33:1b:159:PRO:HD3	1.81	0.62
26:24:59:PHE:HA	26:24:61:ARG:N	2.15	0.62
32:2a:1295:G:O2'	44:2m:14:ARG:NH1	2.33	0.62
8:1I:109:ILE:HG13	8:1I:130:TYR:CZ	2.34	0.62
32:1a:911:U:OP2	43:1I:97:ARG:NH2	2.31	0.62
7:2H:52:VAL:HG21	7:2H:69:ARG:HB2	1.82	0.62
32:2a:382:A:H2'	32:2a:383:A:C8	2.35	0.62
40:2i:16:ARG:HH11	40:2i:64:THR:HG21	1.65	0.62
15:1T:39:ARG:HH12	15:1T:41:ARG:HD3	1.64	0.62
3:2D:72:LYS:NZ	3:2D:99:ASP:OD2	2.28	0.62
32:2a:35:G:O2'	43:2I:118:SER:O	2.17	0.62
34:1c:15:THR:HG21	34:1c:181:ASN:HA	1.81	0.62
1:2A:2134:A:C8	1:2A:2157:G:H5'	2.35	0.62
34:2c:57:ILE:HG12	34:2c:66:VAL:HG13	1.81	0.62
32:2a:142:G:H2'	32:2a:143:A:H8	1.64	0.61
32:2a:769:G:H4'	32:2a:1513:A:H4'	1.82	0.61
32:1a:1278:U:H5'	32:1a:1279:A:O4'	2.00	0.61
41:1j:81:THR:O	41:1j:84:GLN:NE2	2.33	0.61
7:2H:46:GLU:HB2	7:2H:49:VAL:HG12	1.81	0.61
17:2V:16:PRO:HD3	17:2V:99:ILE:HD11	1.81	0.61
37:2f:1:MET:HE3	37:2f:66:GLU:HG2	1.82	0.61
32:1a:1441:G:H5''	32:1a:1442:G:H5'	1.83	0.61
1:2A:2150:U:H2'	1:2A:2151:G:C8	2.35	0.61
1:2A:2697:G:OP1	62:2A:3829:HOH:O	2.16	0.61
2:2B:77:U:OP1	21:2Z:19:ARG:NH2	2.33	0.61
5:2F:132:VAL:HG21	5:2F:163:VAL:HG22	1.82	0.61
30:28:23:VAL:HG22	30:28:47:LYS:HB3	1.82	0.61
2:1B:23:G:O6	62:1B:301:HOH:O	2.14	0.61
25:13:3:ARG:NH1	25:13:60:GLU:OE2	2.32	0.61
36:1e:110:LEU:HD13	36:1e:118:ILE:HG21	1.83	0.61
32:2a:1402:4OC:HM22	32:2a:1403:C:H5'	1.82	0.61
32:1a:1326:C:OP1	52:1u:12:LYS:NZ	2.34	0.61
32:2a:1151:A:O2'	32:2a:1152:A:H8	1.83	0.61
39:2h:121:ASP:OD1	39:2h:121:ASP:N	2.34	0.61
32:1a:100:C:H2'	32:1a:101:A:C8	2.35	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:262:A:H2'	32:1a:263:A:C8	2.34	0.61
1:2A:848:G:OP1	62:2A:3830:HOH:O	2.16	0.61
1:1A:2805:G:H2'	1:1A:2807:G:H8	1.65	0.61
44:1m:2:ALA:HB1	44:1m:6:GLY:HA2	1.82	0.61
32:2a:954:G:O6	44:2m:104:ARG:NH1	2.33	0.61
33:2b:119:GLU:HG3	33:2b:153:ARG:HH12	1.66	0.61
50:2s:50:ALA:HB1	50:2s:57:HIS:HB3	1.82	0.61
1:1A:383:U:O2'	62:1A:4130:HOH:O	2.16	0.61
11:1P:70:GLN:NE2	62:1P:303:HOH:O	2.33	0.61
15:1T:39:ARG:HH21	32:1a:345:C:H5''	1.66	0.61
7:2H:20:ALA:HB3	7:2H:23:ARG:HB2	1.82	0.61
32:2a:1249:C:O2'	40:2i:73:GLN:NE2	2.33	0.61
1:2A:1068:G:N1	1:2A:1095:A:N7	2.49	0.61
50:2s:41:VAL:HG13	50:2s:43:GLU:H	1.64	0.61
1:1A:1096:A:H3'	1:1A:1097:U:H5''	1.82	0.60
1:1A:2839:G:H5'	13:1R:46:GLY:HA2	1.82	0.60
5:1F:24:LEU:HD23	5:1F:115:ALA:HA	1.82	0.60
8:1I:104:GLN:HB2	8:1I:105:HIS:HD2	1.66	0.60
32:1a:1068:G:H8	32:1a:1068:G:OP2	1.84	0.60
2:2B:13:A:N1	2:2B:69:G:O2'	2.33	0.60
8:2I:85:GLU:H	8:2I:87:LYS:HE3	1.66	0.60
1:1A:1382:G:N7	62:1A:4207:HOH:O	2.31	0.60
1:1A:2404:C:OP2	62:1A:4131:HOH:O	2.16	0.60
20:1Y:92:ASN:N	20:1Y:93:GLY:HA2	2.14	0.60
24:12:59:ARG:NH2	62:12:102:HOH:O	2.34	0.60
6:2G:106:LEU:HA	6:2G:110:ALA:HB3	1.83	0.60
1:1A:588:U:H2'	1:1A:589:C:C6	2.35	0.60
1:1A:994:C:OP1	16:1U:53:ARG:NH2	2.34	0.60
35:1d:15:GLU:OE2	35:1d:66:ARG:NH1	2.34	0.60
41:1j:7:LYS:HE3	41:1j:9:ARG:HH12	1.65	0.60
1:2A:954:G:H5''	12:2Q:13:GLN:HB3	1.83	0.60
32:2a:539:A:OP2	43:2l:115:LYS:NZ	2.34	0.60
1:1A:1060:U:H4'	1:1A:1061:U:H5'	1.81	0.60
1:1A:1957:C:OP1	62:1A:4129:HOH:O	2.16	0.60
6:1G:79:ASN:OD1	6:1G:79:ASN:N	2.35	0.60
7:1H:11:VAL:HG21	7:1H:50:VAL:HG23	1.83	0.60
32:1a:1286:A:H2'	32:1a:1287:A:H4'	1.82	0.60
27:25:16:ARG:NH1	27:25:17:ASP:OD1	2.34	0.60
47:2p:75:ARG:HG3	47:2p:80:PHE:HD2	1.67	0.60
1:2A:956:G:H5''	12:2Q:77:LYS:HD2	1.83	0.60
32:2a:1492:A:H5''	43:2l:47:LYS:HD3	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:2o:16:ALA:HB1	46:2o:21:ASP:HB3	1.83	0.60
32:1a:450:G:OP1	47:1p:43:LYS:NZ	2.34	0.60
32:1a:1238:A:OP2	62:1a:1908:HOH:O	2.16	0.60
44:1m:40:ASN:HB3	44:1m:43:THR:HG23	1.84	0.60
4:2E:116:VAL:HG13	4:2E:122:PHE:HB2	1.83	0.60
32:2a:1027:C:H5'	32:2a:1028:C:C5	2.36	0.60
33:2b:211:ILE:O	33:2b:215:LEU:HB2	2.01	0.60
1:1A:330:A:H2	1:1A:1210:A:O2'	1.84	0.60
1:2A:1721:G:H8	1:2A:1741:A:H62	1.50	0.60
2:2B:84:C:OP1	25:23:15:TYR:OH	2.15	0.60
21:2Z:10:ARG:NH1	21:2Z:26:GLY:O	2.34	0.60
3:1D:164:GLN:OE1	3:1D:176:ARG:NH2	2.34	0.60
15:1T:91:ARG:NH2	62:1T:301:HOH:O	2.23	0.60
19:1X:41:ASN:O	19:1X:45:THR:HG23	2.01	0.60
32:2a:1244:C:H2'	32:2a:1245:A:H8	1.66	0.60
36:2e:144:THR:H	36:2e:147:ASP:HB2	1.66	0.60
1:1A:1670:C:OP2	62:1A:4104:HOH:O	2.16	0.60
5:1F:12:LEU:HD22	5:1F:124:LEU:HD21	1.84	0.60
1:2A:2139:C:N3	1:2A:2152:G:N2	2.46	0.60
1:2A:2379:G:O2'	14:2S:17:ARG:NH1	2.35	0.60
7:2H:3:ARG:HH11	7:2H:4:ILE:H	1.47	0.60
38:2g:114:ARG:HB2	38:2g:115:ARG:NH2	2.17	0.60
1:1A:2706:G:N7	62:1A:4212:HOH:O	2.32	0.60
1:1A:1026:U:OP1	62:1A:4110:HOH:O	2.15	0.59
1:1A:2611:U:H5'	1:1A:2611:U:H6	1.67	0.59
32:1a:159:G:N2	32:1a:162:A:OP2	2.35	0.59
41:2j:77:PRO:O	41:2j:81:THR:OG1	2.15	0.59
1:1A:763:G:OP1	62:1A:4133:HOH:O	2.17	0.59
1:1A:2751:G:H4'	7:1H:4:ILE:HD11	1.84	0.59
23:11:52:ARG:NH2	23:11:55:GLY:O	2.35	0.59
33:1b:77:ALA:HA	33:1b:80:ILE:HG22	1.84	0.59
1:2A:889:C:O2'	1:2A:890:A:O5'	2.20	0.59
21:2Z:42:VAL:O	21:2Z:46:LYS:NZ	2.35	0.59
40:2i:11:LYS:H	40:2i:104:ARG:HH12	1.51	0.59
1:1A:34:C:O2'	1:1A:35:G:H5'	2.02	0.59
1:1A:2805:G:H2'	1:1A:2807:G:C8	2.37	0.59
8:1I:60:GLU:OE2	8:1I:61:ARG:NH1	2.35	0.59
32:1a:1077:G:N2	32:1a:1080:A:OP2	2.33	0.59
1:2A:588:U:H2'	1:2A:589:C:C6	2.37	0.59
1:2A:1011:G:OP2	16:2U:66:ASN:ND2	2.35	0.59
1:2A:2218:U:O4'	23:21:52:ARG:NH2	2.34	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2250:G:OP1	12:2Q:85:LYS:NZ	2.35	0.59
23:21:3:LYS:HB2	23:21:61:ARG:HH12	1.67	0.59
1:1A:1054:A:H61	1:1A:1105:U:H3	1.50	0.59
1:1A:1179:C:H2'	1:1A:1180:C:H6	1.67	0.59
15:1T:24:PRO:HA	15:1T:49:VAL:HG22	1.84	0.59
26:14:58:ARG:HD2	50:1s:68:GLY:H	1.68	0.59
32:2a:1457:G:OP1	51:2t:39:LYS:NZ	2.35	0.59
1:2A:365:C:OP2	62:2A:3828:HOH:O	2.15	0.59
1:2A:2152:G:H2'	1:2A:2153:G:C8	2.37	0.59
1:1A:654:A:OP2	62:1A:4136:HOH:O	2.17	0.59
1:1A:2692:C:OP2	62:1A:4132:HOH:O	2.17	0.59
32:1a:1435:G:H2'	32:1a:1436:U:C6	2.38	0.59
33:1b:42:ILE:HD12	33:1b:203:GLY:HA2	1.82	0.59
32:2a:411:A:OP2	35:2d:25:ARG:NH2	2.33	0.59
32:2a:1305:G:N2	32:2a:1331:G:H1'	2.18	0.59
32:2a:1376:U:H2'	32:2a:1377:A:C8	2.37	0.59
1:1A:1173:G:O2'	1:1A:1174:A:O5'	2.20	0.59
1:1A:1803:A:O2'	3:1D:259:THR:HG21	2.02	0.59
1:1A:2243:U:H2'	1:1A:2244:U:C6	2.37	0.59
32:1a:626:U:H2'	32:1a:627:G:H8	1.66	0.59
41:1j:35:SER:N	41:1j:73:ASP:O	2.34	0.59
1:2A:1105:U:H2'	1:2A:1106:G:H8	1.67	0.59
7:2H:150:ALA:HA	7:2H:153:LYS:HG3	1.85	0.59
32:2a:1172:C:H2'	32:2a:1173:G:H8	1.68	0.59
32:2a:1285:A:H4'	32:2a:1286:A:H5'	1.85	0.59
32:2a:1435:G:H2'	32:2a:1436:U:C6	2.38	0.59
1:1A:1085:A:O2'	1:1A:1104:C:O2'	2.14	0.59
1:1A:1126:A:OP2	62:1A:4103:HOH:O	2.17	0.59
21:1Z:52:SER:C	21:1Z:54:HIS:H	2.10	0.59
1:2A:1688:U:O2	1:2A:1700:A:H5'	2.03	0.59
32:2a:164:U:H2'	32:2a:165:C:C6	2.37	0.59
53:2y:12:ILE:HG23	53:2y:16:ILE:HG12	1.85	0.59
31:29:14:CYS:HA	31:29:27:CYS:HB2	1.84	0.59
32:2a:222:U:H2'	32:2a:223:U:C6	2.38	0.59
39:2h:89:PRO:HA	39:2h:92:ARG:HE	1.66	0.59
32:1a:946:A:H2'	32:1a:947:G:C8	2.37	0.59
1:2A:2572:A:C8	4:2E:144:ARG:HD3	2.38	0.59
41:1j:5:ARG:NE	41:1j:73:ASP:OD1	2.32	0.58
41:1j:38:ILE:HG13	41:1j:71:LEU:HB3	1.85	0.58
32:2a:673:G:H2'	32:2a:674:G:C8	2.37	0.58
33:2b:16:HIS:CG	33:2b:210:SER:HB3	2.38	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:2j:78:ASN:O	41:2j:80:LYS:N	2.36	0.58
50:2s:36:ARG:HH12	50:2s:75:ALA:HB3	1.67	0.58
53:2y:53:THR:HG22	53:2y:62:VAL:HG12	1.85	0.58
1:1A:178:G:OP2	62:1A:4135:HOH:O	2.17	0.58
20:1Y:23:ARG:NH1	62:1Y:302:HOH:O	2.20	0.58
32:1a:1183:A:H3'	32:1a:1184:G:H5''	1.85	0.58
4:2E:110:GLY:O	62:2R:301:HOH:O	2.17	0.58
11:2P:98:GLU:HG3	11:2P:102:ARG:NH2	2.18	0.58
32:2a:111:G:OP2	62:2a:3206:HOH:O	2.17	0.58
32:2a:1291:G:O2'	40:2i:38:GLN:OE1	2.20	0.58
42:2k:18:ARG:NH2	42:2k:35:PRO:O	2.36	0.58
6:2G:19:LEU:HD11	6:2G:172:LEU:HB2	1.85	0.58
37:1f:11:ASN:HB3	37:1f:14:LEU:HG	1.84	0.58
1:2A:1266:G:O5'	18:2W:15:ARG:NH2	2.37	0.58
32:2a:662:G:H2'	32:2a:663:A:C8	2.38	0.58
32:2a:1159:U:O4'	32:2a:1182:G:N2	2.36	0.58
37:2f:35:ALA:HA	37:2f:67:MET:HB3	1.85	0.58
4:1E:116:VAL:HG13	4:1E:122:PHE:HB2	1.86	0.58
48:1q:58:GLU:OE2	48:1q:75:ARG:NH2	2.37	0.58
53:2y:12:ILE:HG22	53:2y:17:ARG:HG3	1.85	0.58
1:1A:644:A:H4'	1:1A:645:C:H5	1.69	0.58
10:1O:73:ASP:HB2	15:1T:82:LEU:HD13	1.85	0.58
12:1Q:127:ILE:O	62:1Q:301:HOH:O	2.16	0.58
5:2F:101:LEU:HD12	5:2F:102:PRO:HD2	1.86	0.58
32:2a:750:G:N3	46:2o:23:GLY:HA3	2.19	0.58
52:2u:17:THR:O	52:2u:22:ARG:NH1	2.34	0.58
1:2A:1355:G:O6	62:2A:3814:HOH:O	2.17	0.58
1:2A:2807:G:N2	1:2A:2893:G:O6	2.36	0.58
8:2I:78:THR:HG22	8:2I:143:SER:HB3	1.85	0.58
14:2S:15:ARG:O	14:2S:19:LYS:HG2	2.04	0.58
20:2Y:83:THR:HG21	20:2Y:99:CYS:HB2	1.85	0.58
33:2b:30:ARG:NH2	33:2b:194:PRO:HB2	2.19	0.58
34:2c:8:ILE:HD12	34:2c:16:ARG:HD2	1.86	0.58
1:1A:1340:U:OP1	19:1X:16:LYS:NZ	2.33	0.58
32:1a:1069:C:OP2	62:1a:1909:HOH:O	2.17	0.58
46:1o:55:GLY:HA2	46:1o:58:MET:HE3	1.85	0.58
7:2H:115:VAL:HG11	7:2H:148:ILE:HD11	1.86	0.58
14:2S:41:ASP:HB2	14:2S:48:LEU:HD21	1.85	0.58
32:2a:353:A:H5'	32:2a:353:A:H8	1.67	0.58
1:1A:153:C:OP2	23:11:92:LYS:NZ	2.36	0.58
1:1A:2023:G:H5'	1:1A:2617:C:H4'	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:1i:49:PRO:HB3	40:1i:96:LEU:HD11	1.85	0.58
1:2A:1153:C:OP1	16:2U:92:ARG:NH2	2.36	0.58
1:2A:2659:G:N2	1:2A:2662:A:OP2	2.30	0.58
19:2X:43:VAL:HG21	19:2X:81:VAL:HG11	1.86	0.58
26:24:47:GLN:O	26:24:49:PHE:N	2.34	0.58
1:1A:1098:A:H2'	1:1A:1099:G:O4'	2.03	0.58
34:1c:139:GLN:NE2	34:1c:143:GLU:OE2	2.34	0.58
1:2A:2130:U:H2'	1:2A:2158:A:N6	2.18	0.58
32:2a:748:C:H4'	32:2a:749:C:O5'	2.03	0.58
32:2a:976:G:H5'	32:2a:1358:U:O2'	2.04	0.58
33:2b:122:PHE:HA	33:2b:127:ILE:HG12	1.86	0.58
1:1A:1187:G:H5''	17:1V:81:TYR:CE1	2.39	0.57
40:1i:9:ARG:HG2	40:1i:14:VAL:HG13	1.86	0.57
35:2d:65:ARG:HG3	35:2d:75:PHE:CG	2.38	0.57
36:2e:102:ALA:HB1	36:2e:106:PRO:HG2	1.85	0.57
1:1A:1174:A:H1'	1:1A:1175:U:H5'	1.87	0.57
33:2b:139:LYS:HZ1	33:2b:143:GLU:HB2	1.69	0.57
1:1A:1379:A:H4'	1:1A:1380:G:OP2	2.05	0.57
4:1E:28:ALA:HB3	4:1E:93:VAL:HG13	1.86	0.57
51:1t:10:LEU:HB3	51:1t:12:ALA:H	1.68	0.57
1:2A:2788:C:N3	1:2A:2789:C:N4	2.51	0.57
2:2B:33:G:H5'	6:2G:2:PRO:HD3	1.85	0.57
20:2Y:5:MET:HE1	20:2Y:32:PRO:HA	1.86	0.57
32:2a:677:U:H3	32:2a:713:G:H22	1.50	0.57
32:2a:1030(A):G:H1'	32:2a:1030(C):G:C5	2.39	0.57
32:2a:1119:C:H2'	32:2a:1120:G:H8	1.68	0.57
33:2b:174:VAL:O	33:2b:178:ARG:HG2	2.04	0.57
1:1A:483:A:O2'	20:1Y:49:VAL:O	2.21	0.57
28:16:6:ARG:HD3	28:16:24:GLU:OE2	2.04	0.57
8:2I:1:MET:N	8:2I:21:VAL:O	2.36	0.57
32:2a:1244:C:H2'	32:2a:1245:A:C8	2.40	0.57
1:1A:2116:G:P	1:1A:2166:G:H21	2.27	0.57
35:1d:88:VAL:HA	36:1e:97:GLY:HA3	1.86	0.57
1:1A:2327:A:H2'	1:1A:2328:A:C8	2.39	0.57
33:1b:47:THR:HA	33:1b:202:PRO:HG2	1.86	0.57
1:2A:271(E):U:H2'	1:2A:271(F):C:C6	2.40	0.57
1:2A:2788:C:OP1	4:2E:61:ARG:NH2	2.38	0.57
32:2a:1123:A:H4'	41:2j:37:PRO:HD2	1.86	0.57
1:1A:2529:G:OP1	7:1H:172:LYS:NZ	2.38	0.57
1:1A:2801(A):A:H1'	1:1A:2895:U:H1'	1.87	0.57
5:1F:116:ASP:OD1	5:1F:119:ARG:NH2	2.37	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:185:U:H4'	1:2A:218:A:H4'	1.87	0.57
1:2A:1607:C:N4	1:2A:1622:G:OP2	2.30	0.57
1:2A:2112:G:H2'	1:2A:2113:U:H6	1.69	0.57
1:2A:2629:A:H1'	1:2A:2630:G:H5''	1.87	0.57
1:2A:2810:A:N6	1:2A:2891:G:O2'	2.37	0.57
3:2D:25:THR:HG21	3:2D:113:VAL:HG11	1.87	0.57
11:2P:7:ARG:NH1	62:2P:303:HOH:O	2.27	0.57
33:2b:15:VAL:HB	33:2b:209:ARG:HB3	1.87	0.57
34:2c:180:ALA:HB1	34:2c:203:PHE:CE1	2.39	0.57
32:1a:587:G:N7	62:1a:1929:HOH:O	2.33	0.57
32:1a:1318:A:H5''	50:1s:3:ARG:NH1	2.20	0.57
38:1g:111:ARG:NH1	38:1g:113:GLU:OE2	2.35	0.57
5:2F:184:TYR:CE2	5:2F:188:ARG:HD2	2.40	0.57
44:2m:15:VAL:O	44:2m:19:LEU:HG	2.05	0.57
26:14:59:PHE:CE1	50:1s:64:GLU:HG3	2.40	0.57
32:1a:922:G:H4'	36:1e:20:GLN:HA	1.87	0.57
33:1b:134:GLU:HG3	33:1b:137:ARG:NH2	2.20	0.57
34:1c:124:ILE:HG22	34:1c:130:VAL:HG22	1.87	0.57
1:2A:1778:U:OP2	62:2A:3831:HOH:O	2.17	0.57
1:2A:2635:C:O2'	4:2E:80:GLU:OE2	2.20	0.57
13:2R:103:ARG:NH1	13:2R:108:GLY:O	2.37	0.57
33:2b:101:MET:HA	33:2b:108:ILE:HG13	1.86	0.57
32:1a:330:C:OP2	62:1a:1910:HOH:O	2.18	0.57
32:1a:588:G:OP2	62:1a:1911:HOH:O	2.18	0.57
39:1h:111:ILE:HG22	39:1h:134:ILE:HD12	1.87	0.57
47:1p:18:ARG:HD3	47:1p:35:LYS:HD3	1.86	0.57
36:2e:140:ARG:O	36:2e:143:ARG:NH2	2.38	0.57
1:1A:2749:A:OP1	7:1H:3:ARG:NH1	2.38	0.56
3:1D:71:ASP:HB3	3:1D:103:ARG:HH12	1.70	0.56
6:1G:179:PRO:HG3	26:14:43:TYR:OH	2.05	0.56
32:1a:677:U:H3	32:1a:713:G:H22	1.51	0.56
32:1a:1010:G:H22	32:1a:1020:U:H1'	1.70	0.56
39:1h:41:ARG:NH2	39:1h:123:GLU:OE2	2.38	0.56
1:2A:958:U:O4	62:2A:3826:HOH:O	2.14	0.56
1:2A:1796:U:H2'	1:2A:1797:C:C6	2.40	0.56
1:2A:2611:U:C4	27:25:3:LYS:HG2	2.40	0.56
1:2A:2693:A:H2'	1:2A:2694:G:H8	1.70	0.56
33:2b:158:LEU:HD21	33:2b:180:LEU:HD13	1.86	0.56
40:2i:16:ARG:HB2	40:2i:64:THR:HG22	1.86	0.56
50:2s:49:ILE:O	50:2s:60:VAL:N	2.37	0.56
32:1a:757:U:H2'	32:1a:758:G:O4'	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2319:G:N2	14:2S:3:ARG:HD3	2.10	0.56
47:2p:43:LYS:HG2	47:2p:48:TRP:CD2	2.39	0.56
1:1A:969:U:H2'	1:1A:970:C:C6	2.40	0.56
1:1A:2273:A:H2'	1:1A:2274:A:C8	2.40	0.56
1:1A:2290:G:OP2	62:1A:4137:HOH:O	2.17	0.56
1:1A:2334:G:H5'	14:1S:9:ARG:HG2	1.87	0.56
4:1E:36:ARG:NH1	4:1E:85:ASN:OD1	2.38	0.56
32:1a:626:U:H2'	32:1a:627:G:C8	2.40	0.56
32:1a:1060:C:C5	34:1c:2:GLY:HA3	2.40	0.56
39:1h:14:ARG:O	39:1h:18:ARG:HG2	2.06	0.56
46:1o:3:ILE:HG13	46:1o:38:ARG:HE	1.70	0.56
1:2A:1184:G:OP1	25:23:30:ARG:NH1	2.38	0.56
1:2A:2291:U:OP1	1:2A:2380:C:O2'	2.23	0.56
6:2G:16:ARG:CZ	6:2G:31:VAL:HG21	2.36	0.56
7:2H:149:ARG:NH1	7:2H:167:GLU:OE2	2.38	0.56
8:2I:77:LEU:HD22	8:2I:101:LEU:HG	1.86	0.56
32:2a:405:U:O4	35:2d:2:GLY:N	2.38	0.56
34:2c:63:ASN:HB2	34:2c:98:ASN:HB2	1.86	0.56
40:2i:28:VAL:HA	40:2i:63:ILE:O	2.05	0.56
2:1B:77:U:OP1	21:1Z:19:ARG:NH2	2.39	0.56
33:1b:77:ALA:HB2	33:1b:211:ILE:HD13	1.88	0.56
1:2A:2405:G:O2'	1:2A:2406:U:OP1	2.18	0.56
20:2Y:73:ARG:HG2	20:2Y:73:ARG:HH11	1.70	0.56
32:2a:1002:G:N2	32:2a:1039:C:C2	2.74	0.56
1:1A:2683:C:O2	10:1O:70:LYS:NZ	2.29	0.56
1:2A:2203:U:H2'	1:2A:2205:C:C6	2.41	0.56
1:2A:2295:C:OP1	14:2S:10:ARG:NH1	2.39	0.56
9:2N:46:VAL:HG23	9:2N:48:MET:HG2	1.88	0.56
10:2O:24:VAL:HG13	10:2O:33:ALA:HB2	1.88	0.56
12:2Q:111:GLU:O	12:2Q:115:MET:HG2	2.05	0.56
31:29:2:LYS:NZ	31:29:31:LYS:O	2.30	0.56
32:1a:1129:C:O2'	32:1a:1139:G:N7	2.24	0.56
1:2A:2115:G:N2	1:2A:2171:A:H61	2.04	0.56
6:2G:19:LEU:HD13	6:2G:32:PRO:HD2	1.87	0.56
15:2T:60:THR:HG22	15:2T:77:PRO:HA	1.88	0.56
32:2a:56:U:H2'	32:2a:57:G:C8	2.40	0.56
32:2a:1030(A):G:H2'	32:2a:1030(B):C:H5''	1.88	0.56
1:1A:1429:G:H2'	1:1A:1430:C:C6	2.41	0.56
32:2a:251:G:N7	62:2a:3223:HOH:O	2.33	0.56
32:2a:946:A:O2'	32:2a:1333:A:N3	2.39	0.56
33:2b:229:VAL:HG12	33:2b:230:VAL:H	1.71	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:2m:13:LYS:HA	44:2m:44:ARG:HH11	1.70	0.56
53:2y:23:ARG:HG3	53:2y:78:ILE:HG13	1.88	0.56
1:1A:886:C:H3'	1:1A:887:A:H5''	1.87	0.56
1:1A:1786:A:H1'	1:1A:1938:A:N6	2.20	0.56
1:2A:2171:A:H4'	1:2A:2172:U:OP1	2.05	0.56
5:2F:192:LEU:HD13	5:2F:194:MET:HE2	1.88	0.56
22:20:53:MET:HG3	22:20:59:LEU:HD23	1.87	0.56
3:1D:71:ASP:CB	3:1D:103:ARG:HH12	2.19	0.56
20:1Y:28:LYS:HG3	20:1Y:40:GLU:HG2	1.87	0.56
32:1a:347:G:C8	58:1a:1868:MPD:H53	2.40	0.56
45:1n:26:ARG:HD3	45:1n:43:CYS:HB3	1.88	0.56
1:2A:881:G:H1	1:2A:895:U:H3	1.54	0.56
4:2E:75:VAL:HG13	4:2E:77:ILE:H	1.71	0.56
35:2d:173:TRP:CD1	35:2d:189:PRO:HG3	2.40	0.56
1:1A:631:A:OP1	11:1P:65:ARG:NH1	2.39	0.56
37:1f:68:PRO:HG2	37:1f:71:ARG:HD2	1.87	0.56
49:1r:26:LEU:HD22	49:1r:39:VAL:HG13	1.88	0.56
1:2A:1116:C:H2'	1:2A:1117:G:C8	2.41	0.56
21:2Z:125:LEU:HB3	21:2Z:165:VAL:HG13	1.86	0.56
32:2a:1030(A):G:H21	32:2a:1030(C):G:H3'	1.71	0.56
32:2a:1190:G:H5'	34:2c:176:HIS:CE1	2.41	0.56
33:2b:204:ASN:OD1	33:2b:205:ASP:N	2.39	0.56
36:2e:92:LYS:HB3	36:2e:119:LEU:HB2	1.88	0.56
5:1F:184:TYR:CE2	5:1F:188:ARG:HD2	2.42	0.55
30:18:33:ASN:HA	30:18:36:LYS:HD2	1.87	0.55
32:1a:1118:C:H1'	32:1a:1179:A:C4	2.41	0.55
1:2A:96:G:H4'	24:22:48:HIS:CD2	2.41	0.55
47:2p:20:VAL:HG23	47:2p:35:LYS:HA	1.88	0.55
1:1A:323:G:C8	5:1F:171:PRO:HG3	2.40	0.55
1:1A:2789:C:O2	1:1A:2894:G:N1	2.38	0.55
32:1a:141:A:H1'	32:1a:182:U:O2	2.06	0.55
32:1a:803:G:OP1	62:1a:1912:HOH:O	2.18	0.55
32:1a:1054:C:H41	53:1y:46:GLN:HE22	1.55	0.55
34:1c:17:ASP:OD2	34:1c:21:ARG:HD3	2.06	0.55
1:2A:1278:A:OP1	13:2R:36:THR:HG23	2.07	0.55
8:2I:93:THR:HG22	8:2I:119:PRO:HB3	1.87	0.55
11:2P:121:LYS:O	11:2P:123:LEU:N	2.40	0.55
32:2a:1190:G:O2'	34:2c:3:ASN:HB2	2.07	0.55
34:2c:150:LYS:HG3	34:2c:169:ALA:HB2	1.88	0.55
35:2d:76:ARG:NH2	35:2d:80:GLU:OE1	2.27	0.55
33:1b:102:LEU:HB3	33:1b:180:LEU:HD12	1.86	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2135:A:H4'	1:1A:2160:G:H5'	1.88	0.55
1:2A:1064:C:H3'	1:2A:1065:U:C5'	2.37	0.55
1:2A:2445:G:OP1	5:2F:74:ARG:NH2	2.38	0.55
1:2A:2870:C:H2'	1:2A:2871:C:O4'	2.06	0.55
28:26:8:LYS:NZ	62:26:603:HOH:O	2.38	0.55
32:2a:718:G:H5'	42:2k:117:ASN:OD1	2.05	0.55
32:2a:1273:G:H3'	32:2a:1274:G:C8	2.40	0.55
46:1o:88:ARG:HB3	46:1o:88:ARG:HH21	1.69	0.55
1:2A:2836:U:H2'	1:2A:2837:G:C8	2.42	0.55
2:2B:85:G:OP1	62:2B:302:HOH:O	2.18	0.55
28:26:10:LEU:HD13	28:26:19:ARG:HD3	1.89	0.55
32:2a:1146:A:H3'	32:2a:1147:C:H5''	1.88	0.55
40:2i:70:LYS:O	40:2i:74:ILE:HG13	2.06	0.55
1:1A:1203:G:O6	62:1A:4134:HOH:O	2.17	0.55
1:1A:2159:G:H2'	1:1A:2160:G:C8	2.41	0.55
5:1F:64:ILE:HG21	5:1F:78:ILE:HG23	1.88	0.55
24:12:22:GLU:OE2	24:12:68:ARG:NH2	2.36	0.55
33:1b:219:VAL:HA	33:1b:222:ILE:HD12	1.89	0.55
39:1h:51:VAL:HG12	39:1h:52:ASP:H	1.71	0.55
1:2A:1379:A:H4'	1:2A:1380:G:OP2	2.07	0.55
32:2a:189(F):U:O2	48:2q:63:ARG:NH2	2.30	0.55
33:2b:21:ARG:HA	33:2b:39:ILE:HA	1.87	0.55
41:2j:16:LEU:HD22	41:2j:94:VAL:HG13	1.89	0.55
32:1a:1148:U:H2'	32:1a:1149:C:O4'	2.06	0.55
1:2A:1525:G:H2'	1:2A:1526:G:C8	2.41	0.55
5:2F:64:ILE:HG21	5:2F:78:ILE:HG23	1.89	0.55
24:22:12:GLU:HA	24:22:15:LYS:HE2	1.89	0.55
33:2b:118:LEU:O	33:2b:122:PHE:HB3	2.05	0.55
17:1V:74:LYS:HB2	17:1V:83:ARG:HB2	1.87	0.55
32:1a:97:G:H2'	32:1a:98:G:O4'	2.07	0.55
32:1a:840:C:H4'	32:1a:841:U:OP2	2.06	0.55
33:1b:95:GLN:HG3	33:1b:147:LYS:O	2.07	0.55
37:1f:91:VAL:HG21	49:1r:72:ARG:NH1	2.21	0.55
13:2R:72:ASP:HB3	13:2R:75:LEU:HB3	1.88	0.55
35:2d:79:PHE:HE1	35:2d:204:ILE:HD13	1.71	0.55
1:1A:1664:A:OP1	62:1A:4102:HOH:O	2.18	0.55
48:1q:22:LEU:HD11	48:1q:39:SER:HB2	1.88	0.55
48:1q:86:GLU:O	48:1q:90:ILE:HG12	2.07	0.55
1:2A:1055:G:H3'	1:2A:1056:G:H8	1.72	0.55
32:2a:179:A:H2'	32:2a:180:U:H6	1.71	0.55
33:2b:70:PHE:O	33:2b:93:VAL:N	2.38	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:2h:20:TYR:HA	39:2h:65:TYR:CZ	2.41	0.55
32:1a:457:C:H2'	32:1a:458:C:H6	1.72	0.55
1:2A:2140:C:H2'	1:2A:2141:G:H8	1.72	0.55
15:2T:92:GLY:O	15:2T:120:ARG:NH2	2.40	0.55
32:2a:890:G:O2'	32:2a:906:G:O6	2.20	0.55
44:2m:13:LYS:O	44:2m:45:VAL:HG23	2.06	0.55
1:1A:796:C:H2'	1:1A:797:C:C6	2.42	0.54
32:1a:1305:G:N2	32:1a:1331:G:H1'	2.21	0.54
32:1a:1318:A:H5''	50:1s:3:ARG:HH12	1.71	0.54
1:2A:1074:G:C2	1:2A:1075:C:H1'	2.42	0.54
1:2A:1359:A:N3	1:2A:1359:A:H5'	2.22	0.54
1:2A:1651:G:OP1	13:2R:40:LYS:NZ	2.39	0.54
10:2O:64:ARG:HB2	10:2O:79:PHE:CD2	2.41	0.54
18:2W:80:PRO:O	18:2W:100:THR:HB	2.06	0.54
20:2Y:81:LYS:HG3	20:2Y:82:PRO:HD2	1.89	0.54
32:2a:1503:A:H5'	32:2a:1531:A:H1'	1.89	0.54
33:2b:82:ARG:HG3	33:2b:92:TYR:CZ	2.41	0.54
48:2q:60:ILE:HB	48:2q:74:LEU:HD12	1.88	0.54
1:1A:2791:C:H5'	1:1A:2893:G:N2	2.21	0.54
12:1Q:37:LEU:HD21	12:1Q:130:LYS:HE2	1.88	0.54
32:1a:1504:G:OP1	32:1a:1507:A:H4'	2.07	0.54
1:2A:2142:C:H2'	1:2A:2143:C:C6	2.43	0.54
8:2I:31:LEU:HD21	8:2I:38:LEU:HD12	1.89	0.54
38:2g:79:ARG:HA	38:2g:84:ASN:HA	1.88	0.54
38:2g:133:GLY:HA2	38:2g:136:LYS:HB2	1.90	0.54
2:1B:103:G:H21	21:1Z:73:GLN:HE22	1.56	0.54
5:1F:39:TRP:CH2	5:1F:106:ARG:HD3	2.42	0.54
26:14:57:GLU:HB2	26:14:58:ARG:HA	1.89	0.54
32:1a:17:U:H2'	32:1a:18:C:C6	2.42	0.54
34:1c:12:LEU:HD11	45:1n:51:GLY:HA2	1.88	0.54
17:2V:62:LEU:HD21	17:2V:95:LEU:HB2	1.87	0.54
32:2a:1054:C:H41	53:2y:46:GLN:NE2	2.05	0.54
36:2e:110:LEU:HD13	36:2e:118:ILE:HG21	1.89	0.54
46:2o:55:GLY:HA2	46:2o:58:MET:HE3	1.88	0.54
1:1A:1025:G:C4	1:1A:1135:C:H1'	2.43	0.54
6:1G:131:TYR:HB3	6:1G:159:VAL:HG13	1.89	0.54
26:24:48:ARG:HG3	26:24:52:THR:HG23	1.89	0.54
1:1A:2133:G:H3'	1:1A:2157:G:H21	1.72	0.54
32:1a:1182:G:H4'	32:1a:1183:A:H5'	1.89	0.54
32:1a:1391:U:H2'	32:1a:1392:G:C8	2.42	0.54
1:2A:1063:G:N2	1:2A:1076:C:O2'	2.41	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1065:U:O2'	1:2A:1066:U:OP2	2.24	0.54
1:2A:1171:G:N2	1:2A:1179:C:N3	2.55	0.54
6:2G:42:GLY:O	6:2G:44:GLY:N	2.39	0.54
32:2a:1030(B):C:H41	32:2a:1030(C):G:H21	1.55	0.54
47:2p:47:ASP:OD1	47:2p:47:ASP:N	2.37	0.54
1:1A:1919:A:O2'	32:1a:1517:G:N3	2.38	0.54
1:1A:2116:G:OP1	1:1A:2166:G:N2	2.36	0.54
1:1A:2207:G:O2'	1:1A:2208:A:OP1	2.24	0.54
5:1F:192:LEU:HD13	5:1F:194:MET:HE2	1.89	0.54
9:1N:4:TYR:CD2	16:1U:100:VAL:HG11	2.42	0.54
32:1a:1442:G:H2'	32:1a:1442:G:N3	2.22	0.54
1:2A:247:G:H4'	1:2A:386:G:C5	2.43	0.54
1:2A:2155:G:H2'	1:2A:2156:G:O4'	2.08	0.54
1:2A:2189:U:H2'	1:2A:2190:G:C8	2.43	0.54
1:2A:2892:A:H2'	1:2A:2893:G:H5'	1.89	0.54
6:2G:66:GLN:OE1	6:2G:98:ARG:NE	2.40	0.54
7:2H:144:VAL:O	7:2H:148:ILE:HG12	2.08	0.54
1:1A:1721:G:H5'	1:1A:1722:A:OP2	2.08	0.54
7:1H:3:ARG:NH1	7:1H:5:GLY:H	2.05	0.54
32:1a:177:C:OP1	51:1t:65:LYS:NZ	2.29	0.54
32:1a:1191:A:H5''	34:1c:4:LYS:HZ2	1.72	0.54
32:1a:1228:C:P	44:1m:108:ARG:HH22	2.30	0.54
35:1d:173:TRP:HA	35:1d:187:ARG:HE	1.73	0.54
19:2X:31:HIS:CD2	19:2X:33:LYS:H	2.26	0.54
1:1A:1178:C:H2'	1:1A:1179:C:C6	2.42	0.54
1:1A:2079:U:O3'	23:11:35:THR:OG1	2.26	0.54
19:1X:53:LYS:HB3	19:1X:82:GLN:HB3	1.90	0.54
25:13:39:ASP:OD2	25:13:44:ARG:NH2	2.40	0.54
1:2A:2391:G:OP1	62:2A:3832:HOH:O	2.18	0.54
1:2A:2805:G:H2'	1:2A:2807:G:H8	1.71	0.54
2:2B:106:G:H5'	21:2Z:31:ARG:HG2	1.90	0.54
32:2a:1154:G:H2'	32:2a:1155:G:C8	2.42	0.54
35:2d:88:VAL:HG22	36:2e:96:PRO:HB2	1.89	0.54
17:1V:72:VAL:HB	17:1V:85:LYS:HB3	1.90	0.54
32:1a:38:G:N2	32:1a:397:A:H5'	2.22	0.54
32:1a:328:C:OP1	62:1a:1913:HOH:O	2.19	0.54
38:1g:20:ASP:HB3	38:1g:23:VAL:HG23	1.90	0.54
46:1o:82:ILE:O	46:1o:86:GLY:N	2.40	0.54
1:2A:1102:C:H2'	1:2A:1103:A:H8	1.71	0.54
1:2A:1803:A:O2'	3:2D:259:THR:HG21	2.07	0.54
8:2I:50:ARG:O	8:2I:54:GLN:HG2	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:2Z:52:SER:C	21:2Z:54:HIS:H	2.15	0.54
25:23:7:LYS:HD3	25:23:34:GLU:HG2	1.88	0.54
32:2a:757:U:H2'	32:2a:758:G:O4'	2.07	0.54
32:2a:1038:C:H2'	32:2a:1039:C:H6	1.73	0.54
32:2a:1309:G:O2'	44:2m:77:ASN:ND2	2.35	0.54
1:1A:228:A:H8	1:1A:229:A:H5'	1.73	0.54
32:1a:656:C:O2'	46:1o:28:GLN:OE1	2.23	0.54
34:1c:35:GLU:OE1	34:1c:59:ARG:NH1	2.41	0.54
1:2A:265:A:N1	1:2A:427:U:O2'	2.40	0.54
1:2A:2490:G:O6	62:2A:3835:HOH:O	2.19	0.54
32:2a:401:C:OP2	35:2d:73:ARG:NH2	2.41	0.54
32:2a:1442:G:H2'	32:2a:1442:G:N3	2.23	0.54
32:2a:1521:G:N3	62:2a:3224:HOH:O	2.33	0.54
1:1A:620:G:N3	1:1A:620:G:H5'	2.23	0.53
1:1A:715:G:C2	46:1o:56:LEU:HD21	2.43	0.53
1:1A:1796:U:H2'	1:1A:1797:C:C6	2.43	0.53
1:1A:2206:G:H5''	1:1A:2207:G:C5	2.42	0.53
16:1U:33:ARG:NH2	62:1U:304:HOH:O	2.40	0.53
33:1b:115:LEU:O	33:1b:119:GLU:HG2	2.08	0.53
1:2A:1065:U:H4'	1:2A:1066:U:H5'	1.90	0.53
1:2A:1877:A:H5'	1:2A:1878:G:OP2	2.08	0.53
1:2A:2313:C:H2'	1:2A:2314:C:C6	2.43	0.53
1:2A:2756:U:H1'	1:2A:2757:A:H5''	1.90	0.53
19:2X:11:PRO:HB3	19:2X:92:LEU:HD11	1.89	0.53
27:25:15:ARG:NH1	62:25:201:HOH:O	2.18	0.53
32:2a:656:C:O2'	46:2o:28:GLN:OE1	2.17	0.53
1:1A:864:G:N7	12:1Q:22:LYS:NZ	2.56	0.53
1:1A:1155:A:OP1	16:1U:55:ARG:HD3	2.08	0.53
1:1A:1889:A:H2'	1:1A:1890:A:C8	2.44	0.53
32:1a:1291:G:OP1	38:1g:37:ASN:ND2	2.40	0.53
32:1a:1310:G:OP2	44:1m:88:ARG:NH2	2.42	0.53
32:1a:1373:G:H5''	38:1g:36:LYS:HD2	1.90	0.53
1:2A:1067:A:H4'	1:2A:1068:G:OP2	2.07	0.53
32:2a:266:G:N3	32:2a:266:G:H5''	2.23	0.53
38:2g:113:GLU:HG2	38:2g:119:ARG:HG3	1.89	0.53
1:1A:1048:A:OP2	1:1A:1109:C:N4	2.37	0.53
1:1A:2206:G:H2'	1:1A:2207:G:C2	2.43	0.53
1:1A:2564:A:C2	1:1A:2647:U:H4'	2.43	0.53
30:18:15:LYS:HB2	58:18:104:MPD:H11	1.88	0.53
32:1a:1001:A:H2'	32:1a:1001(A):G:H8	1.73	0.53
33:1b:163:PHE:HA	33:1b:185:ILE:HG12	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:1d:140:VAL:HG11	35:1d:146:ILE:HD11	1.90	0.53
1:2A:2419:U:OP1	62:2A:3836:HOH:O	2.19	0.53
8:2I:14:ASP:OD1	8:2I:15:VAL:N	2.41	0.53
26:24:46:GLN:HG2	26:24:48:ARG:HH12	1.74	0.53
32:2a:1338:G:H2'	32:2a:1339:A:C8	2.43	0.53
1:1A:1815:A:P	3:1D:54:ARG:HH22	2.31	0.53
22:10:3:HIS:HB3	62:10:220:HOH:O	2.08	0.53
32:1a:542:G:H5'	35:1d:41:GLY:HA3	1.91	0.53
36:1e:8:GLU:OE2	36:1e:63:ARG:NH2	2.41	0.53
17:2V:82:ARG:HH11	17:2V:82:ARG:HG3	1.73	0.53
32:2a:1071:C:H2'	32:2a:1072:G:H8	1.74	0.53
32:2a:1119:C:H2'	32:2a:1120:G:C8	2.43	0.53
32:2a:1170:A:C5	32:2a:1171:G:H1'	2.43	0.53
32:1a:189(B):C:H2'	32:1a:189(C):C:H6	1.74	0.53
32:1a:346:G:H5''	58:1a:1868:MPD:H4	1.90	0.53
52:1u:18:TYR:CD1	52:1u:24:ARG:HB3	2.44	0.53
1:2A:965:C:OP2	62:2A:3837:HOH:O	2.19	0.53
1:2A:1116:C:H2'	1:2A:1117:G:H8	1.74	0.53
1:2A:1250:G:H5''	62:2A:5120:HOH:O	2.09	0.53
1:2A:2376:A:N3	14:2S:106:ARG:NH2	2.51	0.53
6:2G:16:ARG:NH2	6:2G:28:VAL:HG13	2.23	0.53
32:2a:266:G:H3'	48:2q:67:LYS:HB2	1.89	0.53
32:2a:1316:G:N2	32:2a:1318:A:H3'	2.23	0.53
32:2a:1510:U:H2'	32:2a:1511:G:C8	2.42	0.53
44:2m:95:GLY:O	44:2m:110:ARG:HG3	2.09	0.53
50:2s:27:GLU:OE1	50:2s:47:HIS:NE2	2.35	0.53
1:1A:1176:G:H4'	1:1A:1177:A:OP1	2.08	0.53
32:1a:976:G:H5'	32:1a:1358:U:O2'	2.08	0.53
1:2A:971:C:OP2	62:2A:3839:HOH:O	2.19	0.53
1:2A:1803:A:H4'	3:2D:259:THR:HG23	1.89	0.53
6:2G:126:ASP:HB2	6:2G:130:ASN:HB2	1.91	0.53
21:2Z:54:HIS:HE2	21:2Z:123:ASP:HB3	1.74	0.53
23:21:53:VAL:HG22	23:21:74:VAL:HG13	1.89	0.53
33:2b:139:LYS:HZ1	33:2b:143:GLU:CB	2.21	0.53
38:2g:42:ILE:HD13	38:2g:116:ALA:HB3	1.91	0.53
40:2i:26:VAL:HG22	40:2i:61:ALA:HB3	1.91	0.53
1:1A:1070:A:C4	1:1A:1097:U:H4'	2.44	0.53
1:1A:1082:U:N3	1:1A:1086:A:N6	2.16	0.53
33:1b:82:ARG:NH1	33:1b:92:TYR:OH	2.42	0.53
37:1f:97:PHE:O	49:1r:31:LEU:N	2.36	0.53
50:1s:63:THR:OG1	50:1s:65:ASN:OD1	2.26	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1087:G:H22	1:2A:1102:C:N4	2.06	0.53
32:2a:1006:C:H2'	32:2a:1007:C:C6	2.44	0.53
35:2d:112:VAL:H	35:2d:116:GLN:NE2	2.06	0.53
10:1O:64:ARG:HB2	10:1O:79:PHE:CD2	2.44	0.53
32:1a:1003:G:N2	32:1a:1004:A:H1'	2.23	0.53
1:2A:1101:U:H2'	1:2A:1102:C:C6	2.43	0.53
1:2A:1420:U:O2'	1:2A:1421:G:OP1	2.25	0.53
1:2A:1993:U:OP2	62:2A:3838:HOH:O	2.19	0.53
50:2s:32:LYS:HG3	50:2s:57:HIS:CE1	2.44	0.53
1:1A:272(H):C:H42	1:1A:363(B):G:H1	1.57	0.53
7:1H:40:GLU:CD	7:1H:60:ARG:HH12	2.17	0.53
10:1O:107:ARG:HG3	10:1O:112:MET:HE1	1.89	0.53
34:1c:47:LEU:HB2	34:1c:52:LEU:HD22	1.91	0.53
1:2A:8:A:H2'	1:2A:9:U:C6	2.44	0.53
1:2A:776:G:P	62:2A:3825:HOH:O	2.67	0.53
1:2A:1092:C:H2'	1:2A:1092:C:O2	2.09	0.53
8:2I:87:LYS:H	8:2I:87:LYS:HD3	1.73	0.53
32:2a:286:G:N7	62:2a:3226:HOH:O	2.34	0.53
1:1A:636:G:OP1	11:1P:132:LYS:HE2	2.08	0.53
1:1A:889:C:O2'	1:1A:890:A:O5'	2.24	0.53
1:1A:1165:U:H2'	1:1A:1166:C:C6	2.43	0.53
1:1A:1509(A):A:H2'	1:1A:1509(B):A:O4'	2.09	0.53
32:1a:458:C:H2'	32:1a:460:G:O4'	2.09	0.53
32:1a:737:A:H2'	32:1a:738:C:C6	2.44	0.53
32:1a:1510:U:H2'	32:1a:1511:G:C8	2.44	0.53
35:1d:173:TRP:CD1	35:1d:173:TRP:H	2.27	0.53
1:2A:2023:G:H5'	1:2A:2617:C:H4'	1.90	0.53
17:2V:99:ILE:O	17:2V:101:GLY:N	2.42	0.53
19:2X:46:ALA:HB1	24:22:33:MET:HE1	1.90	0.53
23:21:4:VAL:HG11	23:21:11:ARG:NH2	2.24	0.53
33:2b:134:GLU:HA	33:2b:137:ARG:NH2	2.23	0.53
34:2c:180:ALA:HB1	34:2c:203:PHE:HE1	1.74	0.53
47:2p:53:VAL:HG13	47:2p:79:VAL:HG22	1.91	0.53
53:2y:7:SER:OG	53:2y:10:MET:O	2.26	0.53
1:2A:1639:U:H2'	1:2A:1640:C:H5''	1.91	0.52
4:2E:29:GLY:HA3	62:2E:405:HOH:O	2.09	0.52
7:2H:127:GLU:O	7:2H:129:THR:N	2.39	0.52
8:2I:130:TYR:HB3	8:2I:138:ILE:HB	1.91	0.52
32:2a:1090:U:H2'	32:2a:1091:U:C6	2.43	0.52
21:1Z:198:LYS:HB3	21:1Z:202:GLU:HB3	1.91	0.52
32:1a:176:C:H2'	32:1a:177:C:H6	1.73	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:316:G:OP2	32:1a:351:G:O2'	2.27	0.52
37:1f:46:ARG:NH2	49:1r:37:VAL:HG11	2.23	0.52
1:2A:271(D):G:H2'	1:2A:271(E):U:C6	2.43	0.52
1:2A:443:A:H1'	1:2A:1201:C:O4'	2.09	0.52
1:2A:1833:U:O2'	1:2A:1969:A:N1	2.36	0.52
2:2B:105:A:OP1	21:2Z:72:ARG:NH2	2.42	0.52
14:2S:35:ILE:HD11	14:2S:97:ARG:NE	2.21	0.52
32:2a:1129:C:N4	32:2a:1143:G:H1	2.08	0.52
33:2b:115:LEU:O	33:2b:119:GLU:N	2.39	0.52
33:2b:127:ILE:O	33:2b:128:GLU:HB2	2.09	0.52
33:2b:137:ARG:NH1	33:2b:138:LEU:HG	2.24	0.52
34:2c:58:GLU:HG2	41:2j:92:THR:HG21	1.91	0.52
37:2f:7:ASN:HD21	49:2r:34:TYR:HE1	1.55	0.52
48:2q:66:SER:O	48:2q:70:ARG:NH1	2.42	0.52
32:1a:102:G:O2'	32:1a:151:A:N3	2.41	0.52
32:1a:673:G:H2'	32:1a:674:G:C8	2.44	0.52
32:1a:714:G:H2'	32:1a:715:A:C8	2.45	0.52
32:1a:731:G:H5'	32:1a:766:A:H4'	1.91	0.52
32:1a:1277:C:H1'	32:1a:1282:C:O2	2.09	0.52
35:1d:60:GLU:HG3	35:1d:202:LEU:HD12	1.92	0.52
43:1l:117:ARG:HD3	62:1l:3202:HOH:O	2.09	0.52
1:2A:616:G:H5'	5:2F:205:ARG:HD3	1.90	0.52
12:2Q:42:ILE:HD13	12:2Q:97:VAL:HB	1.91	0.52
12:2Q:137:TYR:HB3	21:2Z:76:LEU:HD21	1.92	0.52
32:2a:179:A:H2'	32:2a:180:U:C6	2.44	0.52
32:2a:630:G:O2'	32:2a:631:G:H5'	2.09	0.52
32:2a:1263:C:H2'	32:2a:1264:C:H6	1.75	0.52
33:2b:139:LYS:HZ3	33:2b:139:LYS:C	2.16	0.52
1:1A:1040:C:H2'	1:1A:1041:C:O4'	2.09	0.52
32:1a:45:U:H2'	32:1a:46:G:C8	2.45	0.52
35:1d:155:LEU:HB3	35:1d:158:ILE:HG12	1.90	0.52
1:2A:1065:U:H3	1:2A:1073:A:H61	1.57	0.52
1:2A:2646:C:OP2	1:2A:2732:G:O2'	2.24	0.52
6:2G:63:ILE:HG22	6:2G:64:THR:HG23	1.91	0.52
37:2f:3:ARG:HD3	37:2f:64:GLN:NE2	2.25	0.52
1:1A:456:C:H4'	62:1A:4749:HOH:O	2.09	0.52
1:1A:1056:G:H5'	1:1A:1057:A:O4'	2.09	0.52
1:1A:1405:U:H2'	1:1A:1406:U:C6	2.44	0.52
11:1P:89:ALA:O	11:1P:121:LYS:NZ	2.36	0.52
19:1X:2:LYS:NZ	19:1X:38:GLU:OE2	2.36	0.52
34:1c:44:GLU:HA	34:1c:52:LEU:HD23	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:1d:79:PHE:HE1	35:1d:204:ILE:HD13	1.75	0.52
1:2A:1056:G:H5''	1:2A:1057:A:O4'	2.09	0.52
1:2A:2646:C:H2'	1:2A:2647:U:O4'	2.09	0.52
7:2H:55:PRO:HG2	7:2H:61:HIS:CE1	2.45	0.52
7:2H:164:TYR:HB2	7:2H:167:GLU:HB2	1.91	0.52
32:2a:316:G:OP2	32:2a:351:G:O2'	2.24	0.52
32:2a:546:G:OP1	35:2d:73:ARG:HG2	2.10	0.52
1:1A:247:G:H4'	1:1A:386:G:C5	2.44	0.52
1:1A:1080:C:H2'	1:1A:1081:U:C6	2.45	0.52
1:1A:2443:C:OP1	5:1F:68:LYS:HD3	2.09	0.52
1:1A:2646:C:H2'	1:1A:2647:U:O4'	2.10	0.52
18:1W:4:LYS:NZ	62:1W:301:HOH:O	2.33	0.52
32:1a:975:A:O2'	45:1n:32:SER:HB3	2.10	0.52
43:1l:91:LYS:HG3	43:1l:92:OTD:H8	1.91	0.52
1:2A:212:G:H2'	1:2A:213:A:O4'	2.10	0.52
8:2I:123:LEU:HD12	8:2I:144:VAL:HG12	1.91	0.52
32:1a:974:A:OP1	45:1n:29:ARG:NH2	2.42	0.52
40:1i:16:ARG:HB2	40:1i:64:THR:HG22	1.91	0.52
50:1s:22:LEU:O	50:1s:27:GLU:N	2.43	0.52
1:2A:990:A:OP2	62:2A:3815:HOH:O	2.19	0.52
14:2S:105:ALA:O	14:2S:110:LEU:HB2	2.10	0.52
24:22:19:VAL:O	24:22:23:LYS:HG2	2.10	0.52
32:2a:108:G:C6	51:2t:15:ARG:HG2	2.45	0.52
32:2a:611:A:H61	32:2a:629:G:H1	1.58	0.52
32:2a:1228:C:P	44:2m:108:ARG:HH22	2.32	0.52
32:2a:1286:A:H2'	32:2a:1287:A:H4'	1.90	0.52
34:2c:6:HIS:CD2	34:2c:8:ILE:H	2.27	0.52
1:1A:1252:G:N3	16:1U:33:ARG:HG2	2.25	0.52
7:1H:12:PRO:O	7:1H:15:VAL:HG13	2.09	0.52
32:1a:1140:C:H2'	32:1a:1141:C:H6	1.74	0.52
32:1a:1503:A:H5'	32:1a:1531:A:H1'	1.90	0.52
1:2A:1012:U:C5	9:2N:28:THR:HG21	2.45	0.52
1:2A:2138:C:H2'	1:2A:2139:C:O4'	2.09	0.52
2:2B:48:A:H4'	14:2S:95:HIS:HD2	1.74	0.52
8:2I:83:ALA:HA	8:2I:88:ILE:HA	1.92	0.52
35:2d:201:GLN:NE2	36:2e:116:THR:O	2.37	0.52
53:2y:87:LYS:O	53:2y:91:LYS:HB2	2.10	0.52
1:1A:2099:U:H3	1:1A:2190:G:H1	1.57	0.52
2:1B:43:C:H5''	26:14:1:MET:HG2	1.91	0.52
32:1a:407:G:H5''	35:1d:115:ARG:HB3	1.92	0.52
32:1a:1005:A:C2	32:1a:1025:U:H1'	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1298:C:P	38:1g:114:ARG:HH22	2.33	0.52
40:1i:3:GLN:HE21	40:1i:20:ARG:HE	1.58	0.52
44:1m:23:TYR:HB3	44:1m:67:GLU:HA	1.91	0.52
47:1p:21:VAL:HG22	47:1p:33:ILE:HB	1.91	0.52
53:1y:23:ARG:HH12	53:1y:26:LYS:HD2	1.74	0.52
1:2A:800:A:H8	1:2A:800:A:OP1	1.93	0.52
10:2O:88:ASN:HD21	10:2O:90:GLN:HB2	1.75	0.52
11:2P:94:GLU:HG3	11:2P:124:LYS:HD3	1.91	0.52
20:2Y:85:VAL:HG13	20:2Y:97:ARG:HB3	1.91	0.52
26:24:15:ILE:HG13	26:24:32:TYR:CE1	2.44	0.52
32:2a:881:G:P	43:2l:12:ARG:HH22	2.33	0.52
33:2b:74:LYS:NZ	33:2b:205:ASP:O	2.41	0.52
34:2c:19:GLU:HB3	34:2c:40:ARG:HH12	1.74	0.52
47:2p:21:VAL:HG21	47:2p:59:TRP:CD1	2.44	0.52
1:1A:1179:C:H2'	1:1A:1180:C:C6	2.45	0.52
1:1A:1541:G:O6	62:1A:4138:HOH:O	2.18	0.52
32:1a:769:G:H4'	32:1a:1513:A:H4'	1.92	0.52
35:1d:177:ASP:HB3	35:1d:182:LYS:HG3	1.92	0.52
1:2A:911:A:H2'	12:2Q:9:TYR:OH	2.10	0.52
33:2b:112:VAL:HG22	33:2b:149:LEU:HD13	1.91	0.52
34:2c:187:ALA:O	34:2c:198:VAL:HG22	2.09	0.52
41:2j:51:ARG:HG2	41:2j:61:GLU:HB2	1.92	0.52
1:1A:286:C:H2'	1:1A:287:C:C6	2.45	0.51
1:1A:527:C:H4'	1:1A:528:A:O5'	2.10	0.51
1:1A:2331:G:O2'	1:1A:2336:A:N1	2.40	0.51
1:1A:2469:A:H4'	12:1Q:56:ARG:HG2	1.92	0.51
3:1D:69:ARG:NH2	3:1D:128:GLY:O	2.43	0.51
21:1Z:14:LYS:HD2	21:1Z:16:SER:OG	2.09	0.51
22:10:27:GLU:HG3	22:10:68:GLU:HA	1.92	0.51
32:1a:90:U:H2'	32:1a:91:C:C6	2.44	0.51
32:1a:1240:U:OP2	38:1g:116:ALA:N	2.35	0.51
33:1b:115:LEU:HD13	33:1b:145:LEU:HB3	1.92	0.51
39:1h:95:VAL:HB	39:1h:99:GLU:HG3	1.92	0.51
1:2A:278:A:H61	1:2A:362:U:H3	1.56	0.51
1:2A:323:G:C8	5:2F:171:PRO:HG3	2.45	0.51
1:2A:577:G:O2'	1:2A:1254:A:OP1	2.25	0.51
1:2A:1062:G:N7	1:2A:1070:A:H1'	2.25	0.51
1:2A:1155:A:H5''	16:2U:55:ARG:HD3	1.92	0.51
1:2A:1794:U:H2'	1:2A:1795:C:C6	2.45	0.51
20:2Y:2:ARG:HH21	20:2Y:4:LYS:HD3	1.75	0.51
32:2a:1092:A:N3	32:2a:1183:A:N6	2.58	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1400:5MC:C2	53:2y:63:ALA:HA	2.45	0.51
34:2c:164:ARG:HG2	34:2c:165:THR:H	1.74	0.51
1:1A:1105:U:H2'	1:1A:1106:G:H8	1.75	0.51
6:1G:62:LEU:HD13	26:14:28:LYS:HE3	1.91	0.51
6:1G:161:THR:HG23	6:1G:163:ALA:H	1.74	0.51
1:2A:586:A:N1	1:2A:809:G:O2'	2.37	0.51
1:2A:2745:C:H2'	1:2A:2746:U:O4'	2.10	0.51
32:2a:757:U:OP1	32:2a:822:C:O2'	2.27	0.51
32:2a:1138:G:H2'	32:2a:1140:C:H5'	1.92	0.51
32:2a:1456:G:N1	51:2t:51:GLU:OE2	2.43	0.51
34:2c:134:ILE:HD11	34:2c:153:VAL:HG12	1.92	0.51
40:2i:71:SER:HA	40:2i:74:ILE:HD12	1.92	0.51
44:1m:79:LYS:HA	44:1m:82:MET:HE2	1.92	0.51
1:2A:1371:G:O6	62:2A:3833:HOH:O	2.19	0.51
1:2A:1778:U:H2'	1:2A:1784:A:N6	2.26	0.51
15:2T:120:ARG:HA	15:2T:123:GLN:HG2	1.92	0.51
32:2a:1014:A:C2	32:2a:1219:U:H1'	2.44	0.51
34:2c:54:ARG:HB2	34:2c:69:HIS:HB2	1.93	0.51
40:2i:26:VAL:HB	40:2i:33:PHE:HB2	1.92	0.51
1:1A:1086:A:H3'	1:1A:1086:A:N3	2.26	0.51
1:1A:1588:C:H2'	1:1A:1589:C:C6	2.45	0.51
2:1B:30:C:OP1	62:1B:302:HOH:O	2.18	0.51
27:15:47:PRO:O	27:15:60:VAL:HG21	2.09	0.51
32:1a:836:G:OP1	49:1r:61:LYS:NZ	2.44	0.51
1:2A:11:G:H2'	1:2A:12:U:H5'	1.92	0.51
1:2A:1721:G:N1	1:2A:1739:U:OP2	2.43	0.51
1:2A:2107:C:N4	1:2A:2182:G:H1	2.05	0.51
1:2A:2390:U:P	30:28:35:GLN:HE22	2.34	0.51
1:2A:2775:A:OP2	62:2A:3840:HOH:O	2.19	0.51
12:2Q:21:THR:HG21	12:2Q:25:ASP:HB3	1.92	0.51
23:21:80:LEU:HD23	23:21:82:LEU:HD21	1.91	0.51
32:2a:181:G:N2	32:2a:182:U:O4	2.35	0.51
32:2a:1009:G:H1	32:2a:1020:U:H3	1.59	0.51
1:1A:139:G:OP2	62:1A:4140:HOH:O	2.19	0.51
1:1A:2445:G:OP1	5:1F:74:ARG:NH2	2.39	0.51
3:1D:242:ARG:HG3	3:1D:242:ARG:HH11	1.75	0.51
7:1H:3:ARG:NH2	7:1H:65:HIS:HB3	2.26	0.51
32:1a:309:G:O2'	32:1a:607:A:N1	2.43	0.51
7:2H:117:PRO:HG3	7:2H:123:PHE:CE2	2.45	0.51
9:2N:30:ILE:HG22	9:2N:34:LEU:HD22	1.92	0.51
32:2a:7:G:H5'	32:2a:298:A:O4'	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:2d:15:GLU:OE2	35:2d:59:ARG:NH1	2.44	0.51
40:2i:4:TYR:N	40:2i:19:LEU:O	2.44	0.51
1:1A:927:G:N7	62:1A:4227:HOH:O	2.33	0.51
3:1D:148:GLU:HB2	3:1D:151:LYS:HD2	1.92	0.51
24:12:8:LYS:O	24:12:12:GLU:HG2	2.10	0.51
33:1b:185:ILE:HG22	33:1b:199:TYR:HB2	1.92	0.51
37:1f:69:GLU:H	37:1f:69:GLU:CD	2.19	0.51
1:2A:509:C:OP1	62:2A:3834:HOH:O	2.19	0.51
21:2Z:4:ARG:HG3	21:2Z:58:VAL:HB	1.92	0.51
34:2c:181:ASN:HD21	34:2c:205:GLY:H	1.57	0.51
38:2g:51:GLN:HB2	38:2g:58:PRO:HG3	1.92	0.51
40:2i:97:LYS:HA	40:2i:102:LEU:HD11	1.91	0.51
1:1A:886:C:C3'	1:1A:887:A:H5''	2.41	0.51
6:1G:16:ARG:HE	6:1G:31:VAL:HG21	1.76	0.51
13:1R:24:GLN:NE2	62:1R:301:HOH:O	2.43	0.51
26:14:15:ILE:HB	26:14:32:TYR:CD1	2.46	0.51
26:14:58:ARG:HG3	50:1s:67:VAL:HB	1.92	0.51
32:1a:347:G:H8	58:1a:1868:MPD:H53	1.74	0.51
37:1f:100:ASN:ND2	49:1r:23:LYS:HE2	2.26	0.51
1:2A:1028:A:N6	1:2A:1125:G:H2'	2.25	0.51
1:2A:1262:A:OP2	18:2W:97:LYS:NZ	2.43	0.51
1:2A:2206:G:C8	1:2A:2207:G:N7	2.74	0.51
16:2U:11:ARG:O	16:2U:15:LYS:HG3	2.10	0.51
19:2X:12:VAL:HG22	19:2X:29:TRP:CE2	2.45	0.51
33:2b:71:VAL:HG11	33:2b:97:TRP:HE1	1.76	0.51
35:2d:162:LEU:HD13	35:2d:181:MET:HG2	1.92	0.51
1:1A:1045:A:H1'	1:1A:1047:G:N3	2.26	0.51
1:1A:2887:U:H2'	1:1A:2888:C:C6	2.46	0.51
15:1T:127:ALA:C	15:1T:129:ARG:H	2.19	0.51
32:1a:60:A:H4'	32:1a:61:G:H5'	1.93	0.51
32:1a:189(A):C:H42	32:1a:189(J):G:H1	1.57	0.51
32:1a:1054:C:H41	53:1y:46:GLN:NE2	2.08	0.51
34:1c:6:HIS:CD2	34:1c:9:GLY:H	2.28	0.51
1:2A:2110:G:H5''	1:2A:2118:U:O2	2.11	0.51
2:2B:75:G:O3'	21:2Z:10:ARG:NH2	2.44	0.51
5:2F:135:LYS:HB3	5:2F:138:GLU:HG3	1.93	0.51
7:2H:80:SER:OG	7:2H:81:GLU:OE1	2.27	0.51
10:2O:115:VAL:HG13	10:2O:121:VAL:HG21	1.92	0.51
12:2Q:32:TYR:OH	12:2Q:111:GLU:OE2	2.20	0.51
32:2a:922:G:H4'	36:2e:20:GLN:HA	1.92	0.51
1:1A:1378:A:OP1	29:17:10:ARG:NH2	2.44	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2533:A:OP1	1:1A:2665:A:O2'	2.23	0.51
16:1U:33:ARG:NH2	62:1U:303:HOH:O	2.33	0.51
32:1a:1412:C:H2'	32:1a:1413:A:C8	2.46	0.51
33:1b:45:GLN:NE2	33:1b:49:GLU:OE2	2.43	0.51
37:1f:11:ASN:HD22	37:1f:84:ASN:ND2	2.09	0.51
41:1j:45:ARG:HG2	41:1j:47:PHE:CZ	2.46	0.51
1:2A:1514:U:H2'	1:2A:1515:G:H8	1.76	0.51
2:2B:63:G:OP1	62:2B:303:HOH:O	2.19	0.51
21:2Z:179:ASP:HB3	21:2Z:182:LYS:HE2	1.93	0.51
34:2c:181:ASN:ND2	34:2c:181:ASN:O	2.44	0.51
1:1A:2275:C:O2	12:1Q:85:LYS:HD2	2.11	0.51
1:1A:2328:A:H2'	1:1A:2329:G:C8	2.46	0.51
5:1F:116:ASP:OD2	11:1P:1:MET:HB3	2.10	0.51
6:1G:83:ARG:H	6:1G:86:MET:CE	2.24	0.51
19:1X:11:PRO:HB3	19:1X:92:LEU:HD11	1.93	0.51
25:13:3:ARG:HH11	25:13:60:GLU:CD	2.18	0.51
32:1a:96:U:H2'	32:1a:97:G:C8	2.46	0.51
1:2A:796:C:H2'	1:2A:797:C:C6	2.46	0.51
4:2E:9:VAL:HB	15:2T:3:ARG:HG2	1.93	0.51
40:2i:53:VAL:O	40:2i:55:ALA:N	2.44	0.51
41:2j:5:ARG:N	41:2j:99:LYS:O	2.44	0.51
1:1A:645:C:H5'	1:1A:646:A:OP2	2.11	0.50
1:1A:1359:A:N1	1:1A:1372:U:O4	2.44	0.50
1:1A:2110:G:OP1	1:1A:2118:U:N3	2.43	0.50
1:1A:2133:G:C2	1:1A:2157:G:H2'	2.46	0.50
6:1G:53:LEU:O	6:1G:56:ALA:N	2.43	0.50
7:1H:159:GLU:HG2	7:1H:169:VAL:HG11	1.93	0.50
18:1W:10:VAL:HG12	18:1W:12:ILE:HG22	1.93	0.50
21:1Z:3:TYR:CD2	21:1Z:51:ALA:HB2	2.46	0.50
26:14:59:PHE:HE2	50:1s:42:PRO:HB3	1.75	0.50
32:1a:750:G:N3	46:1o:23:GLY:HA3	2.26	0.50
33:1b:71:VAL:HB	33:1b:164:VAL:HG22	1.92	0.50
1:2A:2119:A:O2'	1:2A:2120:G:H5'	2.11	0.50
21:2Z:152:ALA:HA	21:2Z:155:LEU:HG	1.93	0.50
32:2a:56:U:H2'	32:2a:57:G:H8	1.76	0.50
35:2d:153:ARG:HH12	35:2d:181:MET:HB2	1.76	0.50
38:2g:65:ALA:HB1	38:2g:127:ALA:HB3	1.93	0.50
1:1A:1177:A:H2'	1:1A:1177:A:N3	2.26	0.50
1:1A:2153:G:H2'	1:1A:2154:G:C8	2.46	0.50
1:1A:2808:U:H5''	1:1A:2891:G:O6	2.11	0.50
6:1G:27:ASN:HB3	6:1G:30:GLU:HG3	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:11:3:LYS:HG3	23:11:4:VAL:H	1.77	0.50
23:11:50:ARG:HG2	23:11:59:THR:HG22	1.93	0.50
26:14:62:ARG:C	26:14:64:GLY:HA2	2.35	0.50
32:1a:79:G:N1	32:1a:90:U:N3	2.59	0.50
32:1a:108:G:N1	51:1t:15:ARG:HG2	2.26	0.50
39:1h:4:ASP:OD1	39:1h:85:ARG:NH1	2.43	0.50
1:2A:1053:C:H2'	1:2A:1054:A:H8	1.75	0.50
32:2a:1084:G:H5'	32:2a:1102:A:OP2	2.12	0.50
36:2e:8:GLU:HG2	36:2e:34:VAL:HG23	1.93	0.50
38:2g:22:LEU:HD11	38:2g:97:GLN:HG3	1.94	0.50
1:1A:987:G:O2'	1:1A:1000:A:N3	2.41	0.50
1:1A:1031:G:OP1	62:1A:4139:HOH:O	2.19	0.50
1:1A:1143:A:OP2	62:1A:4142:HOH:O	2.20	0.50
1:1A:1453:U:O2'	1:1A:1455:G:N7	2.39	0.50
8:1I:77:LEU:HD22	8:1I:101:LEU:HG	1.93	0.50
19:1X:31:HIS:CD2	19:1X:33:LYS:H	2.29	0.50
32:1a:1030(C):G:H2'	32:1a:1030(D):A:H8	1.75	0.50
32:1a:1492:A:H4'	32:1a:1493:A:C2	2.45	0.50
39:1h:17:THR:HG22	39:1h:63:LEU:HG	1.94	0.50
3:2D:108:PRO:HD2	3:2D:111:LEU:HD22	1.93	0.50
3:2D:206:LEU:HD22	3:2D:211:ARG:HG2	1.91	0.50
7:2H:43:VAL:HG12	7:2H:52:VAL:HG12	1.92	0.50
14:2S:65:VAL:O	14:2S:69:VAL:HG23	2.11	0.50
20:2Y:1:MET:HE3	20:2Y:2:ARG:HD3	1.93	0.50
21:2Z:77:ASP:OD2	21:2Z:80:ARG:NH1	2.43	0.50
30:28:34:TRP:CE2	30:28:35:GLN:HB3	2.46	0.50
32:2a:1323:G:H2'	32:2a:1324:A:C8	2.47	0.50
32:2a:1330:U:H4'	44:2m:23:TYR:CE1	2.47	0.50
39:2h:86:ILE:HG21	39:2h:133:LEU:HD13	1.91	0.50
1:1A:8:A:H2'	1:1A:9:U:C6	2.46	0.50
11:1P:63:PRO:HG2	30:18:25:MET:HB2	1.93	0.50
26:14:16:CYS:SG	26:14:17:GLY:N	2.84	0.50
46:1o:88:ARG:HB3	46:1o:88:ARG:NH2	2.26	0.50
1:2A:1178:C:H2'	1:2A:1179:C:C6	2.47	0.50
1:2A:2103:C:O2	1:2A:2187:G:N1	2.44	0.50
10:2O:64:ARG:HB2	10:2O:79:PHE:CG	2.46	0.50
32:2a:1010:G:H2'	32:2a:1011:G:C8	2.46	0.50
32:1a:1202:G:O4'	45:1n:29:ARG:NH1	2.43	0.50
1:2A:825:C:O2	11:2P:55:ARG:NH1	2.44	0.50
1:2A:1075:C:H2'	1:2A:1076:C:H5'	1.92	0.50
1:2A:2111:C:H42	1:2A:2147:G:H22	1.58	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2115:G:H2'	1:2A:2117:A:N6	2.26	0.50
5:2F:24:LEU:HD23	5:2F:115:ALA:HA	1.93	0.50
10:2O:87:ILE:HD12	10:2O:91:LEU:HA	1.93	0.50
33:2b:178:ARG:HH22	39:2h:74:PRO:HB3	1.77	0.50
33:2b:189:ASP:OD1	33:2b:189:ASP:N	2.40	0.50
1:1A:428:A:OP1	62:1A:4141:HOH:O	2.20	0.50
6:1G:59:GLU:CD	6:1G:153:ARG:HH22	2.20	0.50
14:1S:14:VAL:O	14:1S:18:ILE:HG12	2.11	0.50
26:14:13:ARG:NH1	26:14:23:GLU:OE2	2.45	0.50
28:16:2:ALA:N	62:16:602:HOH:O	2.44	0.50
41:1j:27:ALA:HA	41:1j:30:SER:HB3	1.94	0.50
1:2A:322:A:OP1	5:2F:168:ARG:NH1	2.44	0.50
1:2A:1007:C:H5''	9:2N:35:ARG:NH1	2.27	0.50
1:2A:2321:G:O2'	1:2A:2322:A:OP1	2.29	0.50
32:2a:557:G:OP1	62:2a:3208:HOH:O	2.19	0.50
32:2a:996:A:H2'	32:2a:997:U:C6	2.47	0.50
19:1X:5:TYR:CZ	24:12:30:ARG:HG3	2.47	0.50
32:1a:353:A:H5'	32:1a:353:A:H8	1.77	0.50
32:1a:1304:G:OP2	62:1a:1914:HOH:O	2.19	0.50
33:1b:185:ILE:HG22	33:1b:199:TYR:HD2	1.76	0.50
7:2H:102:ALA:HA	7:2H:117:PRO:HD3	1.93	0.50
7:2H:115:VAL:HG21	7:2H:148:ILE:HD12	1.93	0.50
15:2T:123:GLN:HA	15:2T:126:ALA:HB3	1.92	0.50
32:2a:662:G:H2'	32:2a:663:A:H8	1.75	0.50
32:2a:1070:U:H2'	32:2a:1071:C:H6	1.76	0.50
32:2a:1291:G:O3'	40:2i:39:GLY:HA3	2.11	0.50
33:2b:83:MET:SD	33:2b:234:PRO:HB2	2.51	0.50
38:2g:113:GLU:HG3	38:2g:118:VAL:HG12	1.94	0.50
50:2s:27:GLU:HB3	50:2s:47:HIS:CD2	2.46	0.50
5:1F:185:ASP:HA	5:1F:188:ARG:HD3	1.94	0.50
12:1Q:101:ARG:NH1	62:1Q:302:HOH:O	2.37	0.50
32:1a:865:A:H2'	32:1a:866:C:C6	2.46	0.50
40:1i:18:PHE:HB2	40:1i:62:TYR:HB3	1.93	0.50
1:2A:82:G:N1	1:2A:103:A:OP2	2.33	0.50
1:2A:2400:G:H4'	28:26:18:ARG:HG2	1.93	0.50
32:2a:719:C:O2'	49:2r:49:LYS:HB3	2.11	0.50
32:2a:1073:U:H2'	32:2a:1074:G:H8	1.77	0.50
32:2a:1314:C:OP2	50:2s:4:SER:OG	2.13	0.50
46:2o:37:ASN:O	46:2o:41:GLU:HG2	2.11	0.50
50:2s:51:VAL:HB	50:2s:75:ALA:HB2	1.92	0.50
1:1A:359:A:H2'	1:1A:360:G:O4'	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1083:U:H1'	1:1A:1086:A:N6	2.27	0.50
1:1A:2893:G:H4'	1:1A:2894:G:O5'	2.10	0.50
8:1I:116:LEU:HD11	8:1I:120:ILE:HG13	1.94	0.50
10:1O:118:ALA:O	58:1a:1868:MPD:H12	2.12	0.50
11:1P:138:LEU:HD23	11:1P:145:PRO:HB3	1.93	0.50
32:1a:131:C:H2'	32:1a:132:C:C6	2.46	0.50
32:1a:292:G:O2'	32:1a:608:A:N6	2.45	0.50
1:2A:236:C:H2'	1:2A:237:C:H6	1.76	0.50
1:2A:300:A:H2'	1:2A:334:C:H1'	1.92	0.50
2:2B:17:C:H2'	2:2B:18:G:O4'	2.12	0.50
6:2G:15:VAL:HB	6:2G:175:LEU:HB3	1.94	0.50
32:2a:184:G:H2'	32:2a:185:A:H8	1.77	0.50
32:2a:920:U:H2'	32:2a:921:U:C6	2.46	0.50
33:2b:187:LEU:HA	33:2b:201:ILE:HB	1.93	0.50
1:1A:251:A:C5	1:1A:252:G:H1'	2.46	0.49
1:1A:1048:A:N1	1:1A:1112:G:O2'	2.40	0.49
32:1a:130:A:H5'	48:1q:63:ARG:HH11	1.77	0.49
40:1i:5:TYR:H	40:1i:87:GLN:NE2	2.09	0.49
1:2A:530:G:N1	1:2A:2023:G:OP1	2.37	0.49
1:2A:1503:U:H2'	1:2A:1504:C:C6	2.47	0.49
1:2A:1786:A:H1'	1:2A:1938:A:N6	2.26	0.49
14:2S:14:VAL:O	14:2S:18:ILE:HG12	2.11	0.49
32:2a:1083:U:OP2	62:2a:3207:HOH:O	2.19	0.49
32:2a:1152:A:H4'	41:2j:13:HIS:CD2	2.47	0.49
32:2a:1154:G:H2'	32:2a:1155:G:H8	1.76	0.49
34:2c:120:VAL:HG21	34:2c:137:ALA:HB2	1.94	0.49
35:2d:141:ARG:N	35:2d:144:ASP:OD2	2.43	0.49
1:1A:551:G:O2'	1:1A:1220:A:N3	2.40	0.49
26:14:7:PRO:HB2	26:14:27:THR:HG21	1.94	0.49
32:1a:269:C:H2'	32:1a:270:A:C8	2.47	0.49
32:1a:1024:G:H2'	32:1a:1024:G:N3	2.27	0.49
41:1j:11:PHE:HE1	41:1j:67:THR:HG22	1.78	0.49
43:1l:53:ARG:HB3	43:1l:69:TYR:HE1	1.77	0.49
1:2A:271(L):U:H4'	1:2A:271(M):G:H5'	1.93	0.49
1:2A:1188:U:H4'	17:2V:79:VAL:HG22	1.94	0.49
1:2A:2285:C:OP2	28:26:6:ARG:NH1	2.45	0.49
26:24:53:GLU:H	26:24:53:GLU:CD	2.20	0.49
32:2a:410:G:OP1	35:2d:30:LYS:NZ	2.46	0.49
32:2a:411:A:O2'	32:2a:413:G:H5'	2.11	0.49
32:2a:434:U:H2'	32:2a:435:C:C6	2.46	0.49
40:2i:18:PHE:HB2	40:2i:62:TYR:HB3	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1401:G:O6	53:1y:83:ARG:NH2	2.45	0.49
34:1c:179:ARG:NH1	34:1c:206:GLU:OE1	2.44	0.49
35:1d:15:GLU:OE2	35:1d:59:ARG:NH1	2.43	0.49
41:1j:8:LEU:HB2	41:1j:70:ARG:HB2	1.95	0.49
44:1m:34:LEU:HD13	44:1m:41:PRO:HA	1.94	0.49
51:1t:57:ARG:HH22	51:1t:100:ILE:HD12	1.78	0.49
1:2A:876:C:H2'	1:2A:877:U:O4'	2.12	0.49
1:2A:2352:A:N6	1:2A:2365:G:O2'	2.46	0.49
1:2A:2390:U:O2'	1:2A:2391:G:H5'	2.12	0.49
14:2S:34:HIS:ND1	14:2S:53:SER:OG	2.40	0.49
32:2a:390:C:H2'	32:2a:391:G:C8	2.47	0.49
32:2a:1263:C:H2'	32:2a:1264:C:C6	2.47	0.49
53:2y:52:ALA:HB2	53:2y:77:LEU:HD21	1.94	0.49
10:1O:64:ARG:HB2	10:1O:79:PHE:CG	2.47	0.49
21:1Z:80:ARG:HB3	21:1Z:82:ARG:HG3	1.94	0.49
32:1a:1125:U:H4'	41:1j:5:ARG:NH2	2.27	0.49
37:1f:46:ARG:HH22	49:1r:37:VAL:HG11	1.78	0.49
38:1g:70:LYS:HB3	38:1g:96:GLN:HG2	1.95	0.49
38:1g:113:GLU:HG3	38:1g:119:ARG:HG2	1.95	0.49
1:2A:2748:A:H5'	7:2H:4:ILE:HD12	1.94	0.49
13:2R:87:TYR:OH	13:2R:117:VAL:O	2.24	0.49
32:2a:1030(A):G:N1	32:2a:1031:G:O6	2.46	0.49
32:2a:1513:A:H2'	32:2a:1514:C:C6	2.47	0.49
8:1I:27:ARG:HD2	23:11:71:TYR:CE2	2.47	0.49
32:1a:186:C:H2'	32:1a:187:C:C6	2.48	0.49
32:1a:501:C:H1'	32:1a:549:C:H1'	1.95	0.49
32:1a:955:U:O2'	50:1s:83:HIS:HD2	1.94	0.49
32:1a:1298:C:H2'	38:1g:114:ARG:HH21	1.76	0.49
39:1h:97:VAL:HG21	39:1h:128:GLY:HA2	1.94	0.49
1:2A:30:G:H2'	1:2A:31:C:C6	2.47	0.49
1:2A:236:C:H2'	1:2A:237:C:C6	2.47	0.49
6:2G:47:LYS:HG3	6:2G:48:GLU:H	1.77	0.49
6:2G:125:PHE:HB3	6:2G:166:ASP:CG	2.37	0.49
16:2U:75:ASN:OD1	16:2U:78:THR:OG1	2.30	0.49
32:2a:840:C:H4'	32:2a:841:U:OP2	2.13	0.49
45:2n:27:CYS:SG	45:2n:29:ARG:HB2	2.52	0.49
1:1A:530:G:N1	1:1A:2023:G:OP1	2.34	0.49
1:1A:1011:G:OP1	16:1U:77:SER:OG	2.28	0.49
2:1B:66:A:N6	2:1B:108:U:H2'	2.26	0.49
32:1a:273:A:H1'	48:1q:16:GLN:NE2	2.28	0.49
33:1b:106:LYS:H	33:1b:106:LYS:HD2	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:1c:130:VAL:HG21	34:1c:157:ILE:HG23	1.94	0.49
3:2D:175:LEU:HD12	3:2D:185:VAL:HG21	1.94	0.49
5:2F:108:LYS:O	5:2F:112:MET:HG3	2.11	0.49
5:2F:190:GLU:O	62:2F:401:HOH:O	2.19	0.49
26:24:35:VAL:HG11	26:24:40:HIS:HD2	1.77	0.49
32:2a:1248:A:N3	40:2i:70:LYS:NZ	2.55	0.49
32:2a:1347:G:N2	32:2a:1373:G:H2'	2.27	0.49
33:2b:201:ILE:HG21	33:2b:214:ILE:HG21	1.94	0.49
37:2f:15:ASP:OD1	37:2f:17:SER:OG	2.22	0.49
46:2o:26:GLU:HG3	46:2o:81:LEU:HD13	1.95	0.49
1:1A:2774:C:H2'	1:1A:2775:A:O4'	2.12	0.49
2:1B:13:A:N1	2:1B:69:G:O2'	2.44	0.49
7:1H:126:PRO:HG2	7:1H:130:ARG:HH21	1.78	0.49
32:1a:596:C:OP2	62:1a:1915:HOH:O	2.20	0.49
47:1p:40:ASP:HB3	47:1p:48:TRP:HB2	1.95	0.49
1:2A:62:C:OP1	62:2A:3844:HOH:O	2.20	0.49
1:2A:271(R):G:OP1	23:21:76:ARG:NH1	2.46	0.49
1:2A:1020:A:N1	1:2A:1141:U:O2'	2.45	0.49
1:2A:1153:C:H2'	1:2A:1154:G:O4'	2.12	0.49
1:2A:2693:A:H2'	1:2A:2694:G:C8	2.47	0.49
6:2G:11:TYR:HA	6:2G:15:VAL:HG22	1.94	0.49
20:2Y:44:ILE:HA	20:2Y:63:LYS:O	2.13	0.49
32:2a:620:C:C2	35:2d:135:LEU:HG	2.47	0.49
32:2a:1025:U:O2'	32:2a:1026:G:N7	2.45	0.49
36:2e:6:PHE:CE1	36:2e:36:ASP:HB3	2.48	0.49
37:2f:22:GLU:OE1	37:2f:84:ASN:HB2	2.13	0.49
53:2y:37:PRO:HB3	53:2y:54:ILE:HG23	1.95	0.49
1:1A:1430:C:H2'	1:1A:1431:U:C6	2.47	0.49
1:1A:1540:U:O4	62:1A:4124:HOH:O	2.15	0.49
35:1d:87:GLY:N	62:1d:402:HOH:O	2.46	0.49
35:1d:166:LYS:O	35:1d:168:ARG:NH1	2.44	0.49
1:2A:747:U:O2	1:2A:2014:A:H1'	2.12	0.49
1:2A:1071:G:N1	1:2A:1098:A:OP2	2.43	0.49
1:2A:2074:U:H2'	1:2A:2075:U:C6	2.48	0.49
1:2A:2659:G:O2'	1:2A:2661:G:N7	2.37	0.49
16:2U:27:LEU:HA	16:2U:30:LYS:HB2	1.94	0.49
21:2Z:3:TYR:CG	21:2Z:51:ALA:HB2	2.47	0.49
32:2a:1035:A:O2'	32:2a:1036:G:H8	1.95	0.49
32:2a:1179:A:H2'	32:2a:1180:A:O4'	2.13	0.49
29:17:34:ARG:NH1	29:17:41:ARG:O	2.46	0.49
32:1a:92:C:H2'	32:1a:93:G:C8	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:1p:19:ILE:HG22	47:1p:37:GLY:O	2.13	0.49
1:2A:404:C:OP1	62:2A:3845:HOH:O	2.20	0.49
1:2A:667:U:O2	30:28:2:PRO:HD2	2.13	0.49
1:2A:1816:G:O6	3:2D:35:LYS:NZ	2.31	0.49
1:2A:2531:A:H61	1:2A:2662:A:H61	1.59	0.49
14:2S:27:SER:HA	14:2S:88:ASP:HB3	1.95	0.49
32:2a:1030(C):G:H2'	32:2a:1030(D):A:C8	2.48	0.49
32:2a:1111:A:N1	34:2c:177:THR:OG1	2.40	0.49
44:2m:29:ARG:HD3	44:2m:64:TRP:CE2	2.47	0.49
1:1A:1087:G:H2'	1:1A:1089:G:O4'	2.13	0.49
1:1A:1385:G:O2'	1:1A:1396:U:O2	2.29	0.49
1:1A:2291:U:H2'	1:1A:2292:C:C6	2.48	0.49
32:1a:524:G:H2'	32:1a:525:C:C6	2.47	0.49
33:1b:16:HIS:HB3	33:1b:210:SER:HB2	1.95	0.49
34:1c:62:ASP:O	34:1c:97:LYS:HB2	2.12	0.49
37:1f:82:ARG:HB2	37:1f:85:VAL:HG23	1.95	0.49
1:2A:922:U:H2'	1:2A:923:C:C6	2.48	0.49
1:2A:1783:A:H5'	1:2A:2608:G:H4'	1.95	0.49
1:2A:2316:C:O2'	6:2G:128:ARG:NH2	2.45	0.49
9:2N:99:LEU:HD22	9:2N:103:VAL:HG23	1.95	0.49
13:2R:2:ARG:NH1	13:2R:5:LYS:O	2.45	0.49
21:2Z:144:LEU:HD11	21:2Z:150:LEU:HG	1.95	0.49
32:2a:149:A:H2'	32:2a:150:C:C6	2.47	0.49
32:2a:652:U:O4	32:2a:752:G:O2'	2.28	0.49
34:2c:37:GLN:O	34:2c:41:GLY:N	2.44	0.49
34:2c:71:ALA:HA	34:2c:106:VAL:HB	1.95	0.49
1:1A:2782:G:N7	62:1A:4253:HOH:O	2.35	0.48
7:1H:20:ALA:HB1	7:1H:21:PRO:HD2	1.95	0.48
32:1a:1149:C:H2'	32:1a:1150:U:C6	2.48	0.48
38:1g:48:LYS:O	38:1g:51:GLN:HB3	2.13	0.48
1:2A:1084:A:N6	1:2A:1086:A:N7	2.61	0.48
1:2A:1405:U:H2'	1:2A:1406:U:C6	2.47	0.48
1:2A:2111:C:N3	1:2A:2145:C:O2'	2.46	0.48
12:2Q:65:PHE:HB2	12:2Q:105:GLU:HB2	1.95	0.48
21:2Z:119:GLU:OE1	21:2Z:122:ARG:NH1	2.46	0.48
32:2a:279:A:N6	48:2q:98:LEU:O	2.46	0.48
32:2a:560:U:H4'	32:2a:561:U:O5'	2.13	0.48
32:2a:1003:G:C5	32:2a:1004:A:H1'	2.48	0.48
41:2j:32:ALA:O	41:2j:76:ASN:N	2.42	0.48
1:1A:1088:A:H5'	1:1A:1089:G:H5'	1.95	0.48
5:1F:53:THR:CG2	5:1F:55:GLY:H	2.20	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:165:C:H2'	32:1a:166:G:H8	1.78	0.48
32:1a:1323:G:H2'	32:1a:1324:A:C8	2.48	0.48
33:1b:55:PHE:HD1	33:1b:58:ILE:HD12	1.78	0.48
1:2A:1081:U:H2'	1:2A:1082:U:H5''	1.94	0.48
1:2A:1112:G:H2'	1:2A:1113:U:O4'	2.13	0.48
8:2I:48:GLU:OE2	8:2I:52:ARG:NH1	2.46	0.48
18:2W:88:ARG:NH1	18:2W:94:ASP:OD2	2.46	0.48
25:23:13:ILE:O	62:23:201:HOH:O	2.20	0.48
32:2a:1348:U:H4'	40:2i:120:ARG:HD2	1.95	0.48
33:2b:16:HIS:ND1	33:2b:16:HIS:O	2.45	0.48
33:2b:102:LEU:HD23	33:2b:182:ILE:HD12	1.95	0.48
1:1A:821:A:H2'	1:1A:946:G:H5''	1.94	0.48
1:1A:2167:U:H2'	1:1A:2168:G:C8	2.48	0.48
1:1A:2784:C:H1'	4:1E:37:ARG:HH12	1.78	0.48
22:10:32:ARG:H	22:10:35:ASN:ND2	2.11	0.48
32:1a:965:A:OP2	53:1y:8:LYS:NZ	2.44	0.48
32:1a:1492:A:P	43:1l:47:LYS:HE2	2.53	0.48
34:1c:134:ILE:HG23	34:1c:151:VAL:HB	1.96	0.48
1:2A:539:G:H2'	1:2A:540:C:C6	2.47	0.48
1:2A:2131:G:H5'	1:2A:2133:G:O5'	2.13	0.48
1:2A:2591:C:H2'	1:2A:2592:G:C8	2.48	0.48
19:2X:26:TYR:HB3	19:2X:92:LEU:HD22	1.94	0.48
32:2a:235:C:H2'	32:2a:236:G:H8	1.78	0.48
32:2a:961:U:OP2	32:2a:1223:C:O2'	2.15	0.48
34:2c:33:LEU:O	34:2c:37:GLN:HG2	2.14	0.48
36:2e:110:LEU:HD13	36:2e:118:ILE:HD13	1.95	0.48
1:1A:747:U:O2	1:1A:2014:A:H1'	2.12	0.48
1:1A:911:A:H2'	12:1Q:9:TYR:OH	2.13	0.48
1:1A:1041:C:N4	1:1A:1114:G:H1	2.10	0.48
1:1A:2086:U:H2'	1:1A:2087:G:C8	2.48	0.48
1:1A:2153:G:H2'	1:1A:2154:G:H8	1.79	0.48
1:1A:2693:A:H2'	1:1A:2694:G:H8	1.79	0.48
6:1G:118:ARG:O	6:1G:181:ARG:HB3	2.14	0.48
6:1G:129:GLY:O	6:1G:161:THR:HG22	2.13	0.48
19:1X:60:ARG:HH22	29:17:47:ARG:HH22	1.62	0.48
37:1f:21:LEU:O	37:1f:25:ILE:HG12	2.14	0.48
44:1m:22:ILE:HB	44:1m:25:ILE:HD13	1.94	0.48
1:2A:700:G:O2'	1:2A:1632:A:N3	2.43	0.48
1:2A:999:U:OP2	62:2A:3843:HOH:O	2.19	0.48
1:2A:1593:G:H2'	1:2A:1594:G:C8	2.48	0.48
3:2D:17:THR:O	3:2D:211:ARG:NH2	2.40	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:2V:52:VAL:CG2	17:2V:55:ALA:HB3	2.43	0.48
26:24:59:PHE:CZ	50:2s:64:GLU:HB2	2.47	0.48
32:2a:222:U:H2'	32:2a:223:U:H6	1.79	0.48
32:2a:921:U:O2	36:2e:19:MET:HB2	2.14	0.48
33:2b:200:ILE:HG22	33:2b:202:PRO:HD3	1.95	0.48
35:2d:15:GLU:OE1	35:2d:63:LYS:HG3	2.13	0.48
36:2e:6:PHE:HE1	36:2e:36:ASP:HB3	1.79	0.48
37:2f:38:GLU:HB2	37:2f:64:GLN:HG2	1.94	0.48
40:2i:26:VAL:HA	40:2i:61:ALA:O	2.13	0.48
40:2i:31:GLN:HE21	40:2i:35:GLU:HG2	1.77	0.48
40:2i:47:LEU:HD12	40:2i:50:LEU:HD12	1.94	0.48
43:2l:32:PHE:HB3	43:2l:84:LEU:HD11	1.96	0.48
44:2m:29:ARG:HD3	44:2m:64:TRP:CD2	2.48	0.48
1:1A:118:A:C8	1:1A:119:A:C8	3.01	0.48
1:1A:668:G:H5'	1:1A:669:G:OP2	2.13	0.48
1:1A:784:A:H5'	1:1A:785:G:OP1	2.14	0.48
1:1A:2377:A:H2'	1:1A:2378:A:C8	2.49	0.48
15:1T:108:ARG:HA	15:1T:111:ARG:NH1	2.29	0.48
32:1a:1003:G:N2	32:1a:1004:A:N3	2.61	0.48
32:1a:1402:4OC:HM22	32:1a:1403:C:H5'	1.94	0.48
1:2A:422:A:H2'	1:2A:423:A:C8	2.49	0.48
1:2A:2136:C:H42	1:2A:2156:G:N2	2.12	0.48
36:2e:57:LYS:HG2	36:2e:61:TYR:CE2	2.44	0.48
1:1A:1069:A:H5'	1:1A:1096:A:O2'	2.13	0.48
1:1A:2712:U:H2'	1:1A:2714:G:H5''	1.95	0.48
6:1G:106:LEU:HA	6:1G:110:ALA:HB3	1.94	0.48
9:1N:89:LYS:NZ	62:1N:301:HOH:O	2.35	0.48
32:1a:130:A:C8	48:1q:63:ARG:HG3	2.49	0.48
33:1b:124:SER:HA	33:1b:125:PRO:HA	1.66	0.48
40:1i:3:GLN:NE2	40:1i:20:ARG:HH21	2.11	0.48
51:1t:18:GLN:O	51:1t:22:ARG:HG3	2.13	0.48
1:2A:539:G:H2'	1:2A:540:C:H6	1.78	0.48
1:2A:1166:C:H2'	1:2A:1167:U:C6	2.48	0.48
1:2A:1525:G:H2'	1:2A:1526:G:H8	1.78	0.48
1:2A:2364:C:H2'	1:2A:2365:G:O4'	2.13	0.48
21:2Z:42:VAL:O	21:2Z:46:LYS:HG2	2.13	0.48
32:2a:101:A:H5'	51:2t:10:LEU:HD21	1.94	0.48
32:2a:123:C:OP1	32:2a:311:C:O2'	2.24	0.48
32:2a:1004:A:N7	32:2a:1037:C:H2'	2.28	0.48
33:2b:24:TRP:HB3	33:2b:40:HIS:CE1	2.48	0.48
40:2i:49:PRO:HD2	40:2i:81:ILE:HD11	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:2q:62:SER:OG	48:2q:72:ARG:NH1	2.46	0.48
21:1Z:152:ALA:HB1	21:1Z:163:LEU:HD21	1.96	0.48
25:13:3:ARG:HD3	25:13:60:GLU:HG3	1.95	0.48
32:1a:901:A:O2'	32:1a:1513:A:OP1	2.28	0.48
32:1a:1368:G:OP1	40:1i:111:ARG:NH2	2.43	0.48
1:2A:486:C:H4'	18:2W:60:ASN:ND2	2.29	0.48
1:2A:2262:U:H4'	1:2A:2328:A:C2	2.49	0.48
4:2E:18:ASP:HB3	15:2T:82:LEU:HD21	1.94	0.48
5:2F:30:PRO:HB3	11:2P:1:MET:HE1	1.96	0.48
8:2I:9:LEU:HD13	8:2I:12:LEU:HD12	1.95	0.48
9:2N:128:HIS:O	9:2N:131:GLN:NE2	2.46	0.48
10:2O:113:LYS:HB2	10:2O:113:LYS:HE3	1.63	0.48
27:25:49:CYS:SG	27:25:51:TYR:HB2	2.54	0.48
32:2a:972:C:O3'	41:2j:57:LYS:HD2	2.13	0.48
32:2a:1003:G:H3'	32:2a:1003:G:N3	2.29	0.48
32:2a:1023:G:H3'	32:2a:1024:G:H8	1.78	0.48
32:2a:1269:A:H2	32:2a:1312:G:N3	2.11	0.48
32:2a:1278:U:H5''	32:2a:1279:A:H5'	1.94	0.48
1:1A:286:C:H2'	1:1A:287:C:H6	1.79	0.48
1:1A:829:A:N7	1:1A:2248:C:H5'	2.28	0.48
1:1A:910:A:N1	1:1A:2277:G:H1'	2.29	0.48
1:1A:2870:C:H2'	1:1A:2871:C:O4'	2.13	0.48
5:1F:12:LEU:HD13	5:1F:124:LEU:HD11	1.95	0.48
39:1h:64:LYS:HG3	39:1h:79:VAL:HG21	1.95	0.48
1:2A:1047:G:O2'	1:2A:1048:A:H8	1.96	0.48
1:2A:1052:C:H2'	1:2A:1053:C:C6	2.48	0.48
1:2A:1469:A:H2'	1:2A:1470:G:O4'	2.13	0.48
1:2A:2131:G:OP1	1:2A:2132:U:H5'	2.14	0.48
1:2A:2137:C:C2	1:2A:2154:G:N1	2.72	0.48
3:2D:232:PRO:HB3	3:2D:244:ARG:CZ	2.44	0.48
7:2H:127:GLU:C	7:2H:129:THR:H	2.19	0.48
32:2a:1347:G:H5''	40:2i:107:ARG:HB3	1.94	0.48
40:2i:3:GLN:NE2	40:2i:20:ARG:HH21	2.11	0.48
47:2p:18:ARG:HD3	47:2p:35:LYS:HD2	1.95	0.48
1:1A:2336:A:H61	22:10:43:THR:CG2	2.26	0.48
5:1F:184:TYR:O	5:1F:188:ARG:HG3	2.13	0.48
32:1a:328:C:H4'	32:1a:329:A:H5''	1.95	0.48
32:1a:584:G:H5'	48:1q:91:ARG:NH2	2.29	0.48
32:1a:1070:U:H2'	32:1a:1071:C:C6	2.49	0.48
32:1a:1340:A:OP2	62:1a:1916:HOH:O	2.20	0.48
33:1b:16:HIS:CG	33:1b:17:PHE:N	2.82	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:811:U:H2'	11:2P:21:ARG:HA	1.95	0.48
1:2A:1799:G:O2'	3:2D:181:GLU:OE2	2.29	0.48
1:2A:2683:C:O2	10:2O:70:LYS:NZ	2.38	0.48
15:2T:80:SER:HB3	15:2T:83:ILE:HD12	1.95	0.48
26:24:13:ARG:HH12	26:24:23:GLU:HB3	1.79	0.48
32:2a:294:U:OP1	32:2a:610:G:O2'	2.26	0.48
32:2a:1002:G:C2	32:2a:1003:G:N7	2.82	0.48
32:2a:1052:U:O2'	32:2a:1055:A:OP2	2.26	0.48
32:2a:1239:A:H62	32:2a:1299:A:H62	1.61	0.48
33:2b:43:ASP:O	33:2b:47:THR:HG23	2.13	0.48
44:2m:10:PRO:HD2	44:2m:18:ALA:HB1	1.96	0.48
1:1A:2107:C:N3	1:1A:2182:G:O6	2.47	0.48
32:1a:457:C:H2'	32:1a:458:C:C6	2.49	0.48
32:1a:620:C:H2'	32:1a:621:A:O4'	2.14	0.48
32:1a:662:G:H2'	32:1a:663:A:C8	2.49	0.48
32:1a:890:G:O2'	32:1a:906:G:O6	2.24	0.48
2:2B:66:A:N6	2:2B:109:C:H5'	2.26	0.48
6:2G:3:LEU:HG	6:2G:97:ASP:OD2	2.14	0.48
11:2P:50:ARG:HD3	30:28:7:HIS:CD2	2.49	0.48
23:21:8:SER:HB3	23:21:66:HIS:CD2	2.49	0.48
32:2a:1005:A:H1'	32:2a:1025:U:O2	2.14	0.48
32:2a:1073:U:H2'	32:2a:1074:G:C8	2.49	0.48
50:2s:50:ALA:HA	50:2s:58:VAL:O	2.13	0.48
1:1A:813:U:H2'	1:1A:814:C:C6	2.49	0.47
1:1A:2461:C:H2'	1:1A:2462:U:C6	2.49	0.47
32:1a:6:G:H4'	32:1a:298:A:H4'	1.95	0.47
32:1a:1001:A:H2'	32:1a:1001(A):G:C8	2.49	0.47
40:1i:17:VAL:HB	40:1i:63:ILE:HG23	1.96	0.47
41:1j:39:PRO:HA	41:1j:70:ARG:HD3	1.95	0.47
45:1n:26:ARG:NH1	45:1n:46:GLU:OE1	2.44	0.47
51:1t:34:LYS:O	51:1t:38:LYS:HG2	2.14	0.47
1:2A:218:A:C2	1:2A:235:U:H4'	2.48	0.47
1:2A:301:G:OP2	20:2Y:84:ARG:NH2	2.46	0.47
1:2A:470:A:OP1	5:2F:59:TYR:HE1	1.96	0.47
1:2A:896:A:C6	21:2Z:146:ILE:HD12	2.49	0.47
1:2A:2319:G:N1	14:2S:3:ARG:HA	2.28	0.47
5:2F:124:LEU:HD23	5:2F:126:VAL:HG12	1.96	0.47
21:2Z:92:SER:O	21:2Z:130:PRO:HG2	2.14	0.47
32:2a:1038:C:H2'	32:2a:1039:C:C6	2.48	0.47
39:2h:69:ARG:HD3	39:2h:75:ARG:O	2.14	0.47
40:2i:85:LEU:HB3	40:2i:92:TYR:HD2	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:2k:20:TYR:CZ	42:2k:83:ILE:HD12	2.48	0.47
50:2s:52:TYR:HB2	50:2s:57:HIS:CE1	2.49	0.47
1:1A:2747:G:O6	1:1A:2755:C:H5'	2.14	0.47
62:1A:5984:HOH:O	3:1D:229:VAL:HG22	2.14	0.47
3:1D:221:VAL:HG22	3:1D:226:MET:HE3	1.95	0.47
32:1a:452:A:H4'	47:1p:72:ARG:CZ	2.44	0.47
32:1a:1070:U:H2'	32:1a:1071:C:H6	1.78	0.47
38:1g:54:THR:CB	38:1g:56:GLN:HE22	2.27	0.47
39:1h:81:HIS:N	39:1h:138:TRP:O	2.46	0.47
41:1j:61:GLU:OE2	45:1n:58:LYS:NZ	2.46	0.47
45:1n:3:ARG:HE	45:1n:7:ILE:HD11	1.79	0.47
1:2A:451:C:H5'	62:2A:3907:HOH:O	2.13	0.47
1:2A:1064:C:H3'	1:2A:1065:U:H5'	1.96	0.47
1:2A:1064:C:H1'	1:2A:1076:C:C6	2.49	0.47
1:2A:1453:U:P	13:2R:77:ARG:HH21	2.37	0.47
1:2A:2298:A:N6	1:2A:2318:G:C8	2.82	0.47
11:2P:121:LYS:HB3	11:2P:123:LEU:HD12	1.95	0.47
37:2f:100:ASN:ND2	49:2r:23:LYS:HE2	2.28	0.47
40:2i:9:ARG:HG2	40:2i:14:VAL:HG12	1.95	0.47
50:2s:32:LYS:HD3	50:2s:34:TRP:CH2	2.49	0.47
1:1A:1045:A:H8	1:1A:1111:A:C6	2.33	0.47
1:1A:1097:U:H2'	1:1A:1098:A:O4'	2.14	0.47
1:1A:2140:C:H2'	1:1A:2141:G:C8	2.49	0.47
5:1F:143:ALA:HB1	5:1F:148:LEU:HB2	1.95	0.47
33:1b:185:ILE:HG22	33:1b:199:TYR:CD2	2.49	0.47
35:1d:156:GLU:O	35:1d:160:GLN:HG2	2.14	0.47
38:1g:8:GLU:OE1	38:1g:8:GLU:N	2.43	0.47
1:2A:1843:C:H5'	3:2D:253:GLN:NE2	2.29	0.47
1:2A:2190:G:H2'	1:2A:2191:G:H8	1.79	0.47
1:2A:2582:G:OP2	62:2A:3842:HOH:O	2.19	0.47
1:2A:2749:A:OP1	7:2H:3:ARG:NH1	2.48	0.47
32:2a:142:G:H2'	32:2a:143:A:C8	2.47	0.47
32:2a:1142:G:H3'	32:2a:1143:G:C8	2.47	0.47
32:2a:1333:A:H2'	32:2a:1334:G:O4'	2.14	0.47
1:1A:639:U:H2'	1:1A:640:C:C6	2.49	0.47
1:1A:657:U:H2'	1:1A:658:C:C6	2.50	0.47
1:1A:1063:G:H2'	1:1A:1063:G:N3	2.29	0.47
1:1A:1817:G:OP1	3:1D:88:ARG:NH2	2.41	0.47
1:1A:1826:G:H4'	3:1D:242:ARG:CZ	2.44	0.47
32:1a:1400:5MC:C2	53:1y:63:ALA:HA	2.49	0.47
47:1p:4:ILE:HA	47:1p:20:VAL:O	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:171:G:H2'	1:2A:172:C:C6	2.50	0.47
1:2A:1939:5MU:OP1	1:2A:2604:U:O2'	2.25	0.47
1:2A:2243:U:H2'	1:2A:2244:U:C6	2.50	0.47
1:2A:2732:G:H3'	1:2A:2733:A:O4'	2.15	0.47
5:2F:164:ARG:HD2	5:2F:175:THR:HG23	1.95	0.47
6:2G:11:TYR:CZ	6:2G:16:ARG:HD3	2.49	0.47
6:2G:60:LEU:HD23	6:2G:68:PRO:HG3	1.96	0.47
8:2I:1:MET:HE2	8:2I:38:LEU:HD21	1.97	0.47
21:2Z:10:ARG:HD3	21:2Z:37:VAL:O	2.15	0.47
34:2c:43:LEU:HD22	34:2c:47:LEU:HD12	1.97	0.47
34:2c:112:SER:O	34:2c:116:VAL:HG23	2.14	0.47
38:2g:27:ILE:HA	38:2g:30:ILE:HD12	1.96	0.47
50:2s:41:VAL:HG22	50:2s:42:PRO:HD2	1.95	0.47
1:1A:2074:U:H2'	1:1A:2075:U:C6	2.49	0.47
5:1F:129:PHE:CD2	5:1F:163:VAL:HG21	2.49	0.47
6:1G:155:MET:HE2	6:1G:155:MET:HB3	1.78	0.47
7:1H:125:VAL:HG12	7:1H:127:GLU:O	2.15	0.47
14:1S:20:ARG:NH2	22:10:51:VAL:O	2.48	0.47
32:1a:1358:U:OP1	45:1n:35:ARG:HG2	2.14	0.47
34:1c:3:ASN:OD1	34:1c:3:ASN:N	2.47	0.47
1:2A:491:G:H2'	1:2A:492:A:C8	2.49	0.47
1:2A:1754:C:OP1	15:2T:96:ARG:NH1	2.47	0.47
1:2A:2562:U:OP2	62:2A:3846:HOH:O	2.20	0.47
32:2a:407:G:H1'	35:2d:119:GLN:HE22	1.79	0.47
32:2a:978:A:OP1	32:2a:1361:G:N1	2.40	0.47
34:2c:108:ASN:HD21	34:2c:144:SER:HB3	1.79	0.47
49:2r:73:ALA:HB3	49:2r:79:LEU:HD12	1.96	0.47
12:1Q:109:VAL:HG13	12:1Q:113:GLN:HB2	1.97	0.47
33:1b:166:ASP:HB3	33:1b:169:LYS:HB3	1.96	0.47
36:1e:37:ARG:HH12	36:1e:111:GLU:CG	2.24	0.47
36:1e:90:VAL:O	36:1e:120:THR:HA	2.14	0.47
1:2A:480:A:OP2	20:2Y:47:LYS:HD3	2.15	0.47
1:2A:856:C:H2'	1:2A:857:C:C6	2.50	0.47
1:2A:1053:C:H2'	1:2A:1054:A:C8	2.48	0.47
1:2A:1070:A:H2'	1:2A:1071:G:H5'	1.95	0.47
14:2S:23:ARG:HD2	14:2S:86:ALA:HB2	1.97	0.47
32:2a:382:A:H2'	32:2a:383:A:H8	1.80	0.47
32:2a:458:C:H2'	32:2a:460:G:O4'	2.13	0.47
32:2a:600:C:H2'	32:2a:601:C:C6	2.49	0.47
32:2a:675:A:N3	42:2k:116:HIS:HB2	2.29	0.47
32:2a:1010:G:H2'	32:2a:1011:G:H8	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1103:C:OP1	33:2b:96:ARG:NH2	2.47	0.47
33:2b:123:ALA:HB3	33:2b:125:PRO:HD2	1.97	0.47
39:2h:9:MET:HG3	39:2h:26:VAL:HG11	1.96	0.47
42:2k:52:GLY:H	42:2k:55:LYS:HZ3	1.63	0.47
1:1A:774:A:N3	1:1A:774:A:H2'	2.28	0.47
1:1A:2145:C:H5''	1:1A:2146:C:C5	2.49	0.47
1:1A:2319:G:H22	14:1S:3:ARG:CD	2.27	0.47
11:1P:63:PRO:HD3	30:18:27:THR:HG22	1.96	0.47
15:1T:37:GLY:HA2	15:1T:38:ASN:HA	1.54	0.47
20:1Y:107:ASP:OD1	20:1Y:107:ASP:N	2.48	0.47
21:1Z:153:SER:OG	21:1Z:167:PRO:O	2.31	0.47
23:11:67:ILE:N	23:11:68:PRO:HD2	2.30	0.47
32:1a:181:G:H4'	32:1a:182:U:H5'	1.97	0.47
32:1a:1182:G:C4'	32:1a:1183:A:H5'	2.44	0.47
1:2A:71:A:N7	19:2X:31:HIS:HE1	2.12	0.47
1:2A:623:G:H2'	1:2A:624:C:C6	2.50	0.47
1:2A:1818:U:O2'	3:2D:154:LYS:O	2.29	0.47
1:2A:1915:5MU:H2'	1:2A:1916:A:O4'	2.15	0.47
1:2A:2537:U:H2'	1:2A:2538:C:C6	2.50	0.47
2:2B:95:C:H2'	2:2B:96:U:C6	2.49	0.47
5:2F:107:LYS:HG3	5:2F:206:ILE:HA	1.97	0.47
6:2G:16:ARG:O	6:2G:20:ILE:HG13	2.14	0.47
7:2H:126:PRO:HB2	7:2H:127:GLU:OE1	2.15	0.47
11:2P:3:LEU:H	11:2P:3:LEU:HD12	1.80	0.47
21:2Z:99:TYR:HB3	21:2Z:123:ASP:HB2	1.97	0.47
21:2Z:179:ASP:O	21:2Z:182:LYS:HG2	2.15	0.47
32:2a:273:A:H1'	48:2q:16:GLN:HE21	1.80	0.47
32:2a:841:U:C5	32:2a:848:C:H1'	2.50	0.47
32:2a:1368:G:OP1	40:2i:111:ARG:NH2	2.47	0.47
34:2c:131:ARG:HD3	34:2c:166:GLU:OE2	2.15	0.47
53:2y:20:VAL:O	53:2y:24:LEU:HB2	2.15	0.47
53:2y:74:ILE:O	53:2y:78:ILE:HG12	2.14	0.47
1:1A:226:G:N2	1:1A:228:A:H62	2.09	0.47
1:1A:1406:U:H2'	1:1A:1407:C:C6	2.50	0.47
6:1G:5:VAL:HG22	6:1G:8:LYS:H	1.80	0.47
6:1G:32:PRO:HB3	6:1G:163:ALA:HB2	1.96	0.47
7:1H:40:GLU:OE2	7:1H:60:ARG:NH1	2.48	0.47
34:1c:58:GLU:CB	41:1j:92:THR:HG21	2.41	0.47
38:1g:9:VAL:HG22	38:1g:94:ARG:HE	1.79	0.47
41:1j:64:GLU:OE2	41:1j:66:ARG:HD2	2.14	0.47
1:2A:631:A:OP1	11:2P:65:ARG:NH1	2.45	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2462:U:H2'	1:2A:2463:C:C6	2.50	0.47
21:2Z:155:LEU:HD21	21:2Z:171:ILE:HD13	1.96	0.47
32:2a:407:G:OP1	35:2d:115:ARG:NH2	2.48	0.47
32:2a:1289:A:N1	32:2a:1371:G:O2'	2.38	0.47
32:2a:1376:U:H2'	32:2a:1377:A:H8	1.78	0.47
45:2n:37:PHE:HB3	45:2n:39:LEU:HD12	1.96	0.47
53:2y:48:PHE:HD2	53:2y:70:MET:HB2	1.78	0.47
1:1A:12:U:O2	1:1A:12:U:H2'	2.14	0.47
1:1A:244:A:C2	1:1A:255:A:C4	3.03	0.47
1:1A:1022:G:N7	9:1N:66:LYS:HE2	2.29	0.47
1:1A:2698:U:H2'	1:1A:2699:C:C6	2.50	0.47
4:1E:143:ASN:HD22	4:1E:147:PRO:HD3	1.80	0.47
7:1H:124:GLU:HG2	7:1H:132:ARG:HB3	1.97	0.47
11:1P:98:GLU:HG3	11:1P:102:ARG:HH21	1.80	0.47
32:1a:658:G:OP1	46:1o:8:LYS:NZ	2.42	0.47
32:1a:1010:G:N2	32:1a:1020:U:H1'	2.29	0.47
35:1d:178:VAL:C	35:1d:180:GLY:H	2.22	0.47
53:1y:24:LEU:HD11	53:1y:39:ILE:HD11	1.97	0.47
1:2A:1096:A:H8	1:2A:1097:U:H5''	1.80	0.47
1:2A:1583:A:OP1	1:2A:1584:C:H5	1.98	0.47
35:2d:98:GLU:OE2	35:2d:107:ARG:NH2	2.47	0.47
40:2i:11:LYS:H	40:2i:104:ARG:NH1	2.12	0.47
50:2s:31:ILE:HD12	50:2s:49:ILE:HD11	1.97	0.47
51:2t:33:ILE:O	51:2t:37:SER:OG	2.22	0.47
1:1A:185:U:H4'	1:1A:218:A:H4'	1.97	0.47
1:1A:278:A:H2'	1:1A:279:C:C6	2.50	0.47
1:1A:626:U:O4	11:1P:107:LYS:HE2	2.15	0.47
1:1A:1570:A:H2'	1:1A:1571:A:C8	2.50	0.47
1:1A:1810:A:H2'	1:1A:1811:G:O4'	2.15	0.47
1:1A:2070:G:OP2	62:1A:4143:HOH:O	2.20	0.47
1:1A:2129:C:N3	1:1A:2159:G:O6	2.48	0.47
10:1O:64:ARG:HD2	10:1O:81:ASP:OD1	2.14	0.47
11:1P:140:ALA:O	25:23:38:GLU:HG2	2.15	0.47
14:1S:110:LEU:HD12	14:1S:110:LEU:HA	1.81	0.47
1:2A:1864:U:OP1	1:2A:2410:G:O2'	2.31	0.47
16:2U:49:HIS:HA	16:2U:52:ARG:HG2	1.97	0.47
23:21:30:VAL:HG23	62:21:109:HOH:O	2.15	0.47
32:2a:103:C:O2'	32:2a:172:A:N1	2.44	0.47
32:2a:130:A:H1'	32:2a:263:A:O2'	2.14	0.47
32:2a:601:C:H2'	32:2a:602:A:C8	2.50	0.47
32:2a:841:U:H3'	32:2a:848:C:O4'	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1070:U:H2'	32:2a:1071:C:C6	2.50	0.47
1:1A:1070:A:H2'	1:1A:1097:U:O5'	2.14	0.46
1:1A:1113:U:H2'	1:1A:1114:G:C8	2.50	0.46
33:1b:189:ASP:OD1	33:1b:189:ASP:N	2.48	0.46
40:1i:106:ALA:O	40:1i:108:VAL:HG13	2.15	0.46
41:1j:33:GLN:O	41:1j:75:ILE:N	2.48	0.46
48:1q:62:SER:HB3	48:1q:72:ARG:HH11	1.80	0.46
1:2A:65:C:H2'	1:2A:66:C:H6	1.80	0.46
1:2A:1104:C:H2'	1:2A:1105:U:C6	2.50	0.46
1:2A:1514:U:H2'	1:2A:1515:G:C8	2.50	0.46
1:2A:2153:G:H2'	1:2A:2154:G:H8	1.80	0.46
1:2A:2658:C:H5''	7:2H:158:HIS:CD2	2.50	0.46
5:2F:169:ASN:O	5:2F:169:ASN:ND2	2.48	0.46
11:2P:91:PHE:O	11:2P:121:LYS:NZ	2.46	0.46
32:2a:9:G:OP2	36:2e:121:LYS:NZ	2.42	0.46
32:2a:1005:A:H1'	32:2a:1025:U:C2	2.50	0.46
34:2c:20:SER:HB2	34:2c:40:ARG:HH21	1.79	0.46
1:1A:493:G:H2'	1:1A:494:G:O4'	2.15	0.46
21:1Z:44:PHE:CZ	21:1Z:86:VAL:HG11	2.49	0.46
32:1a:946:A:O2'	32:1a:1333:A:N3	2.45	0.46
47:1p:4:ILE:HG22	47:1p:19:ILE:HD11	1.96	0.46
50:1s:80:TYR:CZ	50:1s:82:GLY:HA2	2.50	0.46
1:2A:2162:G:H1'	1:2A:2173:A:H1'	1.97	0.46
8:2I:62:LYS:O	8:2I:66:GLU:HB2	2.15	0.46
12:2Q:38:GLU:HG3	12:2Q:127:ILE:HG22	1.97	0.46
26:24:62:ARG:HD3	26:24:62:ARG:HA	1.65	0.46
32:2a:501:C:H2'	32:2a:502:G:C8	2.50	0.46
32:2a:980:C:H3'	32:2a:981:U:C6	2.50	0.46
32:2a:1303:C:H2'	32:2a:1304:G:H5'	1.97	0.46
32:2a:1346:A:C8	32:2a:1348:U:C2	3.03	0.46
34:2c:35:GLU:HG3	34:2c:59:ARG:HH22	1.80	0.46
37:2f:2:ARG:NE	37:2f:69:GLU:HG2	2.30	0.46
39:2h:112:LEU:HD11	39:2h:124:ALA:HB2	1.97	0.46
53:2y:29:LYS:HG2	53:2y:30:TRP:CE3	2.50	0.46
1:1A:391:G:H1'	1:1A:411:G:O4'	2.16	0.46
1:1A:489:G:N7	18:1W:49:LYS:NZ	2.62	0.46
1:1A:2286:A:H4'	1:1A:2287:A:O4'	2.16	0.46
1:1A:2811:G:N2	1:1A:2891:G:H1'	2.30	0.46
30:18:42:ARG:HD2	62:18:203:HOH:O	2.15	0.46
32:1a:178:C:H2'	32:1a:179:A:H8	1.81	0.46
35:1d:53:ASP:O	35:1d:57:ARG:HG3	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:1i:16:ARG:NH1	40:1i:64:THR:HG21	2.26	0.46
51:1t:67:ALA:HB2	51:1t:77:ALA:HB2	1.98	0.46
53:1y:6:THR:OG1	53:1y:38:HIS:HE1	1.99	0.46
1:2A:1012:U:H5	9:2N:28:THR:HG21	1.80	0.46
1:2A:1882:C:H2'	1:2A:1883:G:O4'	2.16	0.46
32:2a:397:A:H3'	32:2a:397:A:N3	2.31	0.46
32:2a:1220:G:O3'	50:2s:36:ARG:HD3	2.15	0.46
32:2a:1391:U:H2'	32:2a:1392:G:C8	2.50	0.46
32:2a:1491:G:O2'	32:2a:1492:A:OP1	2.29	0.46
34:2c:66:VAL:HB	34:2c:101:LEU:HD12	1.97	0.46
37:2f:97:PHE:CZ	49:2r:61:LYS:HE2	2.51	0.46
40:2i:99:LEU:HD23	40:2i:101:PHE:HE2	1.79	0.46
1:1A:644:A:H4'	1:1A:645:C:C5	2.50	0.46
1:1A:1364:G:N7	23:11:3:LYS:HE2	2.30	0.46
11:1P:59:LEU:HD11	30:18:10:ALA:HA	1.98	0.46
22:10:43:THR:O	22:10:43:THR:HG23	2.15	0.46
32:1a:1112:C:H1'	34:1c:179:ARG:HE	1.80	0.46
35:1d:173:TRP:C	35:1d:186:LEU:HB2	2.40	0.46
40:1i:26:VAL:HG13	40:1i:61:ALA:HB3	1.97	0.46
42:1k:34:ASP:OD1	42:1k:38:ASN:N	2.32	0.46
1:2A:297:C:OP1	20:2Y:87:LYS:HG3	2.15	0.46
1:2A:1371:G:O2'	1:2A:1372:U:H5	1.98	0.46
1:2A:2086:U:H2'	1:2A:2087:G:C8	2.50	0.46
1:2A:2118:U:OP2	1:2A:2147:G:O2'	2.28	0.46
8:2I:57:ARG:O	8:2I:61:ARG:HG2	2.16	0.46
28:26:10:LEU:HG	28:26:54:ILE:HG13	1.97	0.46
32:2a:1504:G:OP1	32:2a:1507:A:H4'	2.15	0.46
40:2i:108:VAL:HG12	40:2i:109:VAL:H	1.80	0.46
1:1A:1301:A:C8	1:1A:1303:G:C8	3.03	0.46
1:1A:1778:U:H2'	1:1A:1784:A:N6	2.31	0.46
3:1D:77:ALA:HB2	3:1D:97:TYR:CD1	2.51	0.46
10:1O:98:VAL:HG22	10:1O:118:ALA:HA	1.97	0.46
21:1Z:14:LYS:HD3	21:1Z:15:PRO:N	2.31	0.46
32:1a:540:G:H2'	32:1a:541:G:O4'	2.16	0.46
46:1o:16:ALA:HB1	46:1o:21:ASP:HB3	1.97	0.46
1:2A:657:U:H2'	1:2A:658:C:C6	2.51	0.46
1:2A:2022:U:O2'	1:2A:2617:C:H5'	2.15	0.46
1:2A:2280:G:H5'	21:2Z:201:LYS:HD3	1.97	0.46
1:2A:2544:G:H1'	1:2A:2646:C:H4'	1.96	0.46
8:2I:130:TYR:HD2	8:2I:138:ILE:HD12	1.80	0.46
13:2R:12:ARG:O	13:2R:17:ARG:NH1	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:129(A):G:C6	32:2a:189(E):U:H4'	2.51	0.46
32:2a:1226:C:N4	44:2m:104:ARG:HD3	2.31	0.46
45:2n:29:ARG:HD3	45:2n:40:CYS:SG	2.55	0.46
1:1A:1177:A:H3'	1:1A:1178:C:C6	2.51	0.46
7:1H:95:ARG:HG2	7:1H:106:THR:OG1	2.16	0.46
9:1N:75:TYR:CE2	9:1N:77:GLY:HA2	2.51	0.46
15:1T:60:THR:HG22	15:1T:77:PRO:HA	1.97	0.46
19:1X:94:GLY:HA3	19:1X:95:LEU:C	2.39	0.46
32:1a:411:A:OP1	35:1d:30:LYS:NZ	2.45	0.46
32:1a:585:G:N3	32:1a:879:C:H4'	2.30	0.46
33:1b:82:ARG:HD2	33:1b:92:TYR:CZ	2.50	0.46
36:1e:69:VAL:O	36:1e:71:LEU:N	2.48	0.46
1:2A:144:C:H5'	19:2X:2:LYS:HD2	1.96	0.46
1:2A:581:C:H2'	1:2A:582:G:C8	2.50	0.46
1:2A:945:A:C4	1:2A:2448:A:C2	3.04	0.46
1:2A:1807:G:OP1	62:2A:3847:HOH:O	2.20	0.46
1:2A:2115:G:H4'	1:2A:2166:G:O2'	2.14	0.46
1:2A:2320:A:N3	1:2A:2320:A:H2'	2.31	0.46
2:2B:73:A:C4	2:2B:105:A:C2	3.04	0.46
5:2F:176:LEU:HD23	5:2F:176:LEU:HA	1.77	0.46
6:2G:179:PRO:HG3	26:24:43:TYR:OH	2.16	0.46
33:2b:47:THR:HG22	33:2b:202:PRO:HG2	1.97	0.46
36:2e:51:VAL:O	36:2e:55:VAL:HG23	2.15	0.46
38:2g:45:ASP:O	38:2g:49:ILE:HG13	2.15	0.46
1:1A:529:A:OP2	9:1N:114:ARG:NH2	2.44	0.46
1:1A:1176:G:H21	1:1A:1178:C:P	2.38	0.46
1:1A:2713:A:OP1	13:1R:14:SER:OG	2.25	0.46
6:1G:45:GLU:H	6:1G:45:GLU:HG2	1.46	0.46
17:1V:57:VAL:HG22	17:1V:99:ILE:HG12	1.98	0.46
32:1a:1101:A:H4'	32:1a:1102:A:O5'	2.15	0.46
35:1d:196:LEU:O	35:1d:198:VAL:N	2.46	0.46
1:2A:1022:G:N7	9:2N:66:LYS:HE2	2.30	0.46
1:2A:1239:G:N7	62:2A:3933:HOH:O	2.36	0.46
1:2A:1274:A:N3	1:2A:1297:C:H1'	2.31	0.46
1:2A:2186:G:H5'	1:2A:2187:G:OP2	2.16	0.46
1:2A:2291:U:H2'	1:2A:2292:C:C6	2.51	0.46
4:2E:59:VAL:HG21	4:2E:74:PRO:HB3	1.98	0.46
5:2F:154:VAL:HG22	5:2F:191:ARG:HB2	1.98	0.46
20:2Y:2:ARG:NH2	20:2Y:4:LYS:HD3	2.30	0.46
32:2a:196:A:OP1	51:2t:68:LYS:NZ	2.48	0.46
32:2a:1053:G:N7	32:2a:1200:C:H5''	2.31	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1177:G:H2'	32:2a:1178:G:O4'	2.16	0.46
32:2a:1397:C:H4'	32:2a:1398:A:OP2	2.15	0.46
33:2b:30:ARG:HG3	33:2b:31:TYR:CD1	2.51	0.46
33:2b:98:LEU:HB2	33:2b:101:MET:HE3	1.97	0.46
40:2i:93:ARG:O	40:2i:97:LYS:N	2.45	0.46
43:2l:25:PRO:O	43:2l:28:LYS:HE3	2.15	0.46
43:2l:70:ILE:HG12	43:2l:100:ILE:HD12	1.97	0.46
47:2p:20:VAL:HG21	47:2p:32:TYR:CG	2.51	0.46
1:1A:1098:A:H8	1:1A:1098:A:OP2	1.97	0.46
1:1A:1506:C:H2'	1:1A:1507:A:H8	1.81	0.46
1:1A:2611:U:C4	27:15:3:LYS:HG2	2.50	0.46
32:1a:7:G:H5'	32:1a:298:A:O4'	2.16	0.46
32:1a:580:U:H2'	32:1a:581:G:O4'	2.16	0.46
33:1b:80:ILE:HD11	33:1b:212:GLN:HA	1.96	0.46
52:1u:17:THR:O	52:1u:22:ARG:NH1	2.49	0.46
53:1y:52:ALA:HB2	53:1y:77:LEU:HD21	1.97	0.46
1:2A:852:G:H2'	1:2A:853:G:C8	2.51	0.46
1:2A:1410:G:H2'	1:2A:1411:C:C6	2.50	0.46
1:2A:2117:A:H5'	1:2A:2147:G:O2'	2.15	0.46
5:2F:7:TYR:O	5:2F:22:ALA:N	2.49	0.46
9:2N:62:VAL:HG22	9:2N:66:LYS:HD2	1.98	0.46
21:2Z:110:GLY:HA3	21:2Z:174:VAL:HG11	1.98	0.46
23:21:75:GLU:O	23:21:78:LYS:HD3	2.16	0.46
32:2a:1005:A:O2'	32:2a:1036:G:N2	2.49	0.46
32:2a:1123:A:C2	41:2j:39:PRO:HD2	2.50	0.46
32:2a:1426:C:H2'	32:2a:1427:U:H6	1.81	0.46
33:2b:55:PHE:HD1	33:2b:58:ILE:HD11	1.81	0.46
35:2d:187:ARG:HH12	35:2d:190:ASP:CG	2.23	0.46
40:2i:22:GLY:HA3	40:2i:60:ASP:OD2	2.15	0.46
40:2i:99:LEU:HB3	40:2i:101:PHE:CE2	2.50	0.46
1:1A:11:G:H2'	1:1A:12:U:H5'	1.97	0.46
1:1A:574:C:N3	4:1E:145:LYS:NZ	2.53	0.46
8:1I:62:LYS:O	8:1I:66:GLU:HB2	2.16	0.46
32:1a:266:G:H2'	32:1a:266:G:N3	2.31	0.46
32:1a:1513:A:H2'	32:1a:1514:C:C6	2.51	0.46
36:1e:47:LYS:HB2	36:1e:47:LYS:HE3	1.72	0.46
44:1m:20:THR:C	44:1m:22:ILE:H	2.24	0.46
47:1p:19:ILE:HG23	47:1p:36:ILE:HG13	1.97	0.46
1:2A:1796:U:H2'	1:2A:1797:C:H6	1.78	0.46
1:2A:2370:G:C6	1:2A:2371:G:C6	3.04	0.46
5:2F:21:ALA:CB	5:2F:22:ALA:HA	2.44	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:2N:138:LEU:HD23	9:2N:138:LEU:HA	1.81	0.46
31:29:17:ILE:H	31:29:17:ILE:HD13	1.80	0.46
32:2a:9:G:H2'	32:2a:10:A:C8	2.51	0.46
32:2a:11:G:H1	32:2a:23:C:H42	1.64	0.46
32:2a:190:U:C2	32:2a:191:G:C8	3.03	0.46
32:2a:1215:G:C6	32:2a:1216:G:C5	3.03	0.46
33:2b:74:LYS:O	33:2b:78:GLN:N	2.49	0.46
44:2m:4:ILE:O	44:2m:4:ILE:HG13	2.15	0.46
44:2m:108:ARG:HD3	44:2m:108:ARG:HA	1.61	0.46
1:1A:207:A:H2'	1:1A:208:C:O4'	2.15	0.46
1:1A:1939:5MU:OP1	1:1A:2604:U:O2'	2.28	0.46
32:1a:1183:A:O2'	32:1a:1184:G:OP1	2.32	0.46
1:2A:359:A:H2'	1:2A:360:G:O4'	2.16	0.46
1:2A:724:U:H2'	1:2A:725:G:O4'	2.15	0.46
1:2A:886:C:H2'	1:2A:887:A:O4'	2.16	0.46
1:2A:1371:G:HO2'	1:2A:1372:U:H5	1.64	0.46
1:2A:1452:A:OP2	62:2A:3850:HOH:O	2.21	0.46
1:2A:2327:A:H2'	1:2A:2328:A:C8	2.50	0.46
7:2H:3:ARG:NH2	7:2H:65:HIS:HB3	2.31	0.46
9:2N:108:PRO:O	9:2N:113:GLY:HA3	2.16	0.46
10:2O:98:VAL:HG13	10:2O:117:LEU:HB2	1.98	0.46
17:2V:52:VAL:HG23	17:2V:55:ALA:HB3	1.96	0.46
26:24:62:ARG:HA	26:24:62:ARG:HH11	1.81	0.46
29:27:34:ARG:NH1	29:27:41:ARG:O	2.49	0.46
32:2a:184:G:H2'	32:2a:185:A:C8	2.51	0.46
32:2a:685:G:O2'	32:2a:686:U:H5'	2.16	0.46
32:2a:976:G:C8	32:2a:1358:U:C2	3.04	0.46
32:2a:1151:A:N3	41:2j:39:PRO:HG3	2.31	0.46
1:1A:274:G:H2'	1:1A:275:G:C8	2.51	0.45
1:1A:1210:A:H5''	1:1A:1212:G:O4'	2.16	0.45
6:1G:126:ASP:HB2	6:1G:130:ASN:H	1.80	0.45
10:1O:49:ARG:HH12	32:1a:1423:G:P	2.39	0.45
20:1Y:20:TYR:HB3	20:1Y:23:ARG:HG3	1.98	0.45
24:12:65:ASN:O	24:12:69:ARG:HG3	2.16	0.45
32:1a:201:C:H2'	32:1a:202:U:H2'	1.97	0.45
34:1c:29:TYR:OH	45:1n:54:PRO:O	2.29	0.45
42:1k:62:GLN:O	42:1k:66:LEU:HG	2.16	0.45
1:2A:234:C:H2'	1:2A:235:U:H6	1.81	0.45
5:2F:172:TRP:H	5:2F:172:TRP:CD1	2.33	0.45
21:2Z:136:PHE:O	21:2Z:137:ILE:HG13	2.16	0.45
32:2a:589:C:H2'	32:2a:590:C:H6	1.80	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:2g:23:VAL:O	38:2g:27:ILE:HG12	2.16	0.45
38:2g:132:GLY:O	38:2g:136:LYS:HG2	2.16	0.45
40:2i:110:GLU:HG2	40:2i:119:ALA:HB1	1.97	0.45
50:2s:40:ILE:HA	50:2s:44:MET:SD	2.56	0.45
1:1A:1056:G:O3'	1:1A:1057:A:H8	1.99	0.45
1:1A:1693:U:H1'	3:1D:14:ARG:NH1	2.30	0.45
1:1A:2183:C:H2'	1:1A:2184:G:C8	2.51	0.45
1:1A:2345:G:N3	1:1A:2381:C:H2'	2.31	0.45
16:1U:8:VAL:HG23	16:1U:11:ARG:NH2	2.31	0.45
21:1Z:146:ILE:HA	21:1Z:147:GLY:HA2	1.65	0.45
32:1a:164:U:H2'	32:1a:165:C:C6	2.51	0.45
32:1a:1062:U:H2'	32:1a:1063:C:C6	2.51	0.45
36:1e:33:VAL:HG21	36:1e:109:ILE:HA	1.99	0.45
39:1h:48:TYR:HA	39:1h:60:ARG:O	2.16	0.45
44:1m:57:ARG:O	44:1m:61:GLU:HG3	2.16	0.45
1:2A:84:A:H5''	20:2Y:8:LYS:HE3	1.98	0.45
1:2A:108:U:OP1	1:2A:293:U:O2'	2.34	0.45
1:2A:468:G:N7	29:27:39:ARG:NH2	2.58	0.45
1:2A:1076:C:H4'	1:2A:1077:A:OP1	2.15	0.45
1:2A:1686:C:H2'	1:2A:1687:G:O4'	2.15	0.45
1:2A:2103:C:N4	1:2A:2104:G:O6	2.49	0.45
5:2F:13:SER:C	5:2F:15:SER:H	2.24	0.45
7:2H:3:ARG:NH1	7:2H:4:ILE:H	2.12	0.45
20:2Y:21:LYS:HE3	20:2Y:21:LYS:HB2	1.81	0.45
21:2Z:61:LEU:HD11	21:2Z:67:LEU:HD12	1.98	0.45
32:2a:340:U:H2'	32:2a:341:C:C6	2.51	0.45
32:2a:664:G:N2	32:2a:741:G:H1	2.11	0.45
32:2a:737:A:H2'	32:2a:738:C:C6	2.50	0.45
32:2a:1286:A:C8	32:2a:1287:A:H4'	2.51	0.45
34:2c:56:ASP:OD1	34:2c:56:ASP:N	2.49	0.45
35:2d:90:GLY:HA3	35:2d:200:GLU:HG3	1.97	0.45
38:2g:108:ALA:HA	38:2g:111:ARG:HD2	1.97	0.45
44:2m:81:LEU:HA	44:2m:84:ILE:HG12	1.99	0.45
1:1A:811:U:H2'	11:1P:21:ARG:HA	1.98	0.45
1:1A:888:C:O5'	44:1m:93:ARG:HD2	2.16	0.45
1:1A:1071:G:H1'	1:1A:1089:G:H2'	1.98	0.45
1:1A:1769:G:O2'	1:1A:1958:C:OP1	2.31	0.45
23:11:3:LYS:O	23:11:12:PRO:HD3	2.16	0.45
32:1a:176:C:H2'	32:1a:177:C:C6	2.51	0.45
32:1a:841:U:H3'	32:1a:848:C:O4'	2.17	0.45
32:1a:1227:A:OP2	44:1m:111:LYS:NZ	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:297:C:H2'	1:2A:298:G:O4'	2.16	0.45
1:2A:443:A:N7	5:2F:45:ARG:HG2	2.32	0.45
1:2A:2291:U:O2'	1:2A:2374:C:O2	2.27	0.45
1:2A:2404:C:O3'	11:2P:77:ARG:NH2	2.49	0.45
1:2A:2548:G:O6	62:2A:3841:HOH:O	2.19	0.45
8:2I:26:ALA:O	8:2I:31:LEU:HB2	2.17	0.45
28:26:35:GLU:OE2	28:26:50:ARG:NH1	2.50	0.45
32:2a:818:G:O2'	32:2a:819:A:H5'	2.17	0.45
35:2d:108:LEU:HB3	35:2d:110:PHE:CE1	2.52	0.45
41:2j:6:ILE:HB	41:2j:72:VAL:HG23	1.97	0.45
50:2s:62:ILE:H	50:2s:62:ILE:HG12	1.51	0.45
1:1A:476:G:H4'	1:1A:502:A:N1	2.32	0.45
3:1D:146:GLU:HG2	3:1D:152:GLY:C	2.42	0.45
15:1T:65:LYS:HE3	15:1T:67:SER:HB2	1.96	0.45
32:1a:407:G:OP1	35:1d:3:ARG:NH2	2.45	0.45
32:1a:542:G:P	35:1d:10:ARG:HH22	2.39	0.45
32:1a:679:C:H2'	32:1a:680:C:C6	2.51	0.45
32:1a:1296:C:OP1	44:1m:44:ARG:NH2	2.48	0.45
34:1c:69:HIS:HA	34:1c:104:GLN:O	2.16	0.45
49:1r:58:LEU:HD22	49:1r:62:GLU:HB3	1.98	0.45
1:2A:1647:G:H3'	1:2A:1647:G:OP2	2.17	0.45
1:2A:1899:G:H2'	1:2A:1899:G:N3	2.31	0.45
1:2A:2840:C:O3'	13:2R:53:HIS:NE2	2.49	0.45
1:2A:2857:G:N2	1:2A:2860:A:OP2	2.34	0.45
1:2A:2889:C:H2'	1:2A:2891:G:O4'	2.16	0.45
6:2G:113:ARG:HD2	6:2G:140:ILE:HA	1.98	0.45
19:2X:31:HIS:HD2	19:2X:33:LYS:H	1.62	0.45
32:2a:434:U:H2'	32:2a:435:C:H6	1.81	0.45
1:1A:181:A:H5''	29:17:36:GLN:OE1	2.16	0.45
1:1A:222:A:H3'	1:1A:421:U:H5'	1.99	0.45
1:1A:1094:U:O2'	1:1A:1096:A:N7	2.42	0.45
1:1A:1587:A:H2'	1:1A:1588:C:C6	2.51	0.45
1:1A:2022:U:O2'	1:1A:2617:C:H5'	2.17	0.45
1:1A:2038:G:H2'	1:1A:2039:C:O4'	2.17	0.45
1:1A:2864:G:OP1	15:1T:119:LYS:HD2	2.16	0.45
21:1Z:141:VAL:HB	21:1Z:144:LEU:HD12	1.98	0.45
25:13:7:LYS:HE3	25:13:32:GLN:NE2	2.30	0.45
32:1a:1054:C:H41	53:1y:46:GLN:CD	2.24	0.45
35:1d:43:HIS:HB3	35:1d:46:LYS:HD2	1.99	0.45
36:1e:99:GLY:O	36:1e:117:ASP:HA	2.15	0.45
39:1h:86:ILE:HG13	39:1h:133:LEU:HD22	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:1j:40:LEU:HB2	41:1j:69:ASN:HB2	1.99	0.45
1:2A:251:A:C5	1:2A:252:G:H1'	2.51	0.45
1:2A:1014:U:H2'	1:2A:1015:G:H8	1.82	0.45
1:2A:2307:G:H4'	1:2A:2308:G:O5'	2.15	0.45
8:2I:93:THR:O	8:2I:97:ILE:HG13	2.17	0.45
12:2Q:85:LYS:HG3	22:20:7:LEU:CB	2.47	0.45
26:24:40:HIS:HB3	26:24:43:TYR:HD1	1.82	0.45
32:2a:923:A:O2'	32:2a:1399:C:OP2	2.32	0.45
32:2a:1295:G:H21	32:2a:1302:U:H3	1.64	0.45
33:2b:77:ALA:HB2	33:2b:211:ILE:HD13	1.99	0.45
34:2c:63:ASN:CB	34:2c:98:ASN:HB2	2.47	0.45
35:2d:79:PHE:CE1	35:2d:204:ILE:HD13	2.51	0.45
1:1A:307:G:H21	1:1A:330:A:H62	1.63	0.45
1:1A:330:A:H2	1:1A:1210:A:C2'	2.30	0.45
1:1A:579:G:H2'	1:1A:580:C:C6	2.52	0.45
1:1A:885:C:H2'	1:1A:886:C:O4'	2.17	0.45
1:1A:1814:G:H4'	3:1D:51:VAL:HG21	1.99	0.45
1:1A:2722:G:H2'	1:1A:2723:C:C6	2.52	0.45
1:1A:2889:C:H2'	1:1A:2891:G:O4'	2.16	0.45
2:1B:7:G:H5''	2:1B:7:G:H8	1.82	0.45
11:1P:50:ARG:HD3	30:18:7:HIS:CD2	2.51	0.45
16:1U:8:VAL:HG23	16:1U:11:ARG:HH21	1.82	0.45
32:1a:598:U:H4'	39:1h:94:TYR:CD2	2.52	0.45
32:1a:1239:A:H62	32:1a:1299:A:N6	2.15	0.45
35:1d:111:ALA:HB2	35:1d:120:LEU:HD12	1.98	0.45
1:2A:1497:U:H5''	1:2A:1498:C:H5	1.81	0.45
3:2D:69:ARG:NH2	3:2D:128:GLY:O	2.48	0.45
3:2D:148:GLU:HB2	3:2D:151:LYS:HD2	1.99	0.45
5:2F:36:VAL:O	5:2F:40:GLN:HG3	2.15	0.45
14:2S:110:LEU:HD12	14:2S:110:LEU:HA	1.86	0.45
32:2a:1084:G:C5	32:2a:1085:U:C4	3.04	0.45
32:2a:1161:C:H2'	32:2a:1162:C:C6	2.52	0.45
32:2a:1324:A:O4'	32:2a:1362:C:H4'	2.16	0.45
35:2d:15:GLU:OE2	35:2d:66:ARG:NH1	2.50	0.45
35:2d:122:ARG:NH1	35:2d:134:ASP:O	2.49	0.45
44:2m:81:LEU:HD13	44:2m:88:ARG:HG2	1.97	0.45
1:1A:878:A:H2'	1:1A:879:G:H5'	1.98	0.45
1:1A:1583:A:H5'	1:1A:1584:C:OP1	2.17	0.45
1:1A:1607:C:H4'	1:1A:1608:A:O5'	2.17	0.45
1:1A:1890:A:H2'	1:1A:1891:G:O4'	2.17	0.45
1:1A:2183:C:H2'	1:1A:2184:G:H8	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2591:C:H2'	1:1A:2592:G:C8	2.52	0.45
2:1B:105:A:H2'	2:1B:106:G:O4'	2.17	0.45
6:1G:47:LYS:HE3	6:1G:81:LYS:HE2	1.98	0.45
7:1H:13:LYS:HA	7:1H:14:GLY:HA2	1.57	0.45
42:1k:50:TYR:CD1	42:1k:54:ARG:HD3	2.51	0.45
44:1m:3:ARG:HG2	44:1m:8:GLU:HA	1.97	0.45
53:1y:87:LYS:HB2	53:1y:87:LYS:HE3	1.69	0.45
1:2A:65:C:H2'	1:2A:66:C:C6	2.52	0.45
1:2A:234:C:H2'	1:2A:235:U:C6	2.52	0.45
1:2A:881:G:H2'	1:2A:882:G:H8	1.82	0.45
1:2A:1056:G:H21	1:2A:1103:A:H62	1.64	0.45
1:2A:1657:C:H2'	1:2A:1658:C:C6	2.51	0.45
1:2A:2540:C:H2'	1:2A:2541:A:O4'	2.16	0.45
2:2B:24:G:N7	2:2B:56:G:H2'	2.32	0.45
11:2P:63:PRO:HG2	30:28:25:MET:HB2	1.99	0.45
16:2U:89:GLU:O	17:2V:11:GLN:NE2	2.44	0.45
34:2c:8:ILE:HG23	34:2c:16:ARG:HD3	1.99	0.45
40:2i:8:GLY:HA3	40:2i:79:LEU:HB3	1.97	0.45
1:1A:1652:A:O2'	1:1A:1653:G:H5'	2.17	0.45
1:1A:2687:U:H2'	1:1A:2688:U:O4'	2.15	0.45
20:1Y:9:LYS:HA	20:1Y:10:GLY:HA2	1.61	0.45
20:1Y:56:PRO:C	20:1Y:58:GLY:H	2.24	0.45
32:1a:384:G:H2'	32:1a:385:C:C6	2.52	0.45
39:1h:14:ARG:NH1	39:1h:83:ILE:O	2.49	0.45
39:1h:20:TYR:HA	39:1h:65:TYR:CZ	2.51	0.45
1:2A:1037:G:H2'	1:2A:1038:C:O4'	2.17	0.45
1:2A:2138:C:O5'	1:2A:2138:C:H6	2.00	0.45
8:2I:4:ILE:HD11	8:2I:44:LEU:HD12	1.97	0.45
24:22:24:LEU:O	24:22:28:LYS:HG3	2.17	0.45
32:2a:415:A:H2'	32:2a:416:G:O4'	2.17	0.45
32:2a:490:G:P	35:2d:132:ARG:HH22	2.40	0.45
33:2b:58:ILE:HD11	33:2b:221:LEU:HD23	1.98	0.45
39:2h:17:THR:HG22	39:2h:63:LEU:HD13	1.98	0.45
40:2i:23:ASN:OD1	40:2i:23:ASN:N	2.50	0.45
1:1A:228:A:C8	1:1A:229:A:H5'	2.52	0.45
1:1A:586:A:N1	1:1A:809:G:O2'	2.43	0.45
11:1P:59:LEU:HD21	30:18:10:ALA:HB2	1.99	0.45
15:1T:39:ARG:NH1	15:1T:41:ARG:HB3	2.31	0.45
17:1V:50:PRO:HG2	17:1V:51:VAL:HG23	1.99	0.45
36:1e:95:ALA:HB1	36:1e:96:PRO:HD2	1.98	0.45
50:1s:40:ILE:HA	50:1s:44:MET:SD	2.57	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:185:U:H2'	1:2A:186:G:C8	2.52	0.45
1:2A:887:A:O2'	1:2A:888:C:H3'	2.16	0.45
1:2A:1547:C:H2'	1:2A:1548:C:H6	1.82	0.45
1:2A:2173:A:H2'	1:2A:2173:A:N3	2.32	0.45
1:2A:2315:G:H2'	1:2A:2316:C:C6	2.52	0.45
3:2D:24:ILE:HD13	3:2D:84:TYR:HB2	1.97	0.45
29:27:5:TRP:CD1	29:27:7:PRO:HD3	2.52	0.45
32:2a:437:U:H5'	35:2d:155:LEU:HD11	1.98	0.45
32:2a:1226:C:H4'	50:2s:80:TYR:CZ	2.51	0.45
32:2a:1412:C:H2'	32:2a:1413:A:C8	2.52	0.45
32:2a:1516:G:N1	32:2a:1519:MA6:OP2	2.48	0.45
33:2b:19:HIS:CD2	33:2b:20:GLU:H	2.34	0.45
45:2n:58:LYS:HB3	45:2n:58:LYS:HE3	1.72	0.45
1:1A:263:C:H2'	1:1A:264:C:O4'	2.17	0.45
1:1A:1541:G:H5''	1:1A:1542:A:OP2	2.17	0.45
1:1A:1721:G:H2'	1:1A:1740:G:O6	2.17	0.45
6:1G:98:ARG:CZ	26:14:1:MET:HE3	2.47	0.45
7:1H:41:MET:HE2	7:1H:65:HIS:HA	1.98	0.45
8:1I:72:LEU:C	8:1I:74:ASN:H	2.25	0.45
32:1a:881:G:P	43:1l:12:ARG:HH22	2.39	0.45
32:1a:1124:G:N7	32:1a:1145:C:O2'	2.46	0.45
44:1m:11:ARG:C	44:1m:13:LYS:H	2.25	0.45
53:1y:3:MET:HE2	53:1y:3:MET:HB3	1.77	0.45
1:2A:81:G:N7	62:2A:3930:HOH:O	2.36	0.45
1:2A:644:A:H5''	1:2A:645:C:OP1	2.17	0.45
1:2A:1007:C:OP1	9:2N:35:ARG:NH1	2.49	0.45
1:2A:1065:U:H1'	1:2A:1066:U:O5'	2.17	0.45
1:2A:1467:C:C5	1:2A:1546:C:H2'	2.51	0.45
1:2A:2117:A:H4'	1:2A:2148:G:OP1	2.17	0.45
1:2A:2139:C:N4	1:2A:2152:G:N1	2.54	0.45
1:2A:2611:U:H6	1:2A:2611:U:H5'	1.82	0.45
15:2T:1:MET:HE2	15:2T:3:ARG:HG3	1.99	0.45
20:2Y:28:LYS:NZ	20:2Y:64:GLU:OE1	2.23	0.45
32:2a:831:U:H3	32:2a:855:G:H1	1.65	0.45
33:2b:16:HIS:HB2	33:2b:204:ASN:HB3	1.98	0.45
33:2b:27:LYS:HB3	33:2b:194:PRO:HD2	1.99	0.45
1:1A:1188:U:H4'	17:1V:79:VAL:HG22	1.98	0.44
1:1A:1377:G:H2'	62:1A:6871:HOH:O	2.17	0.44
32:1a:1023:G:H2'	32:1a:1024:G:C8	2.52	0.44
32:1a:1125:U:O2	32:1a:1126:U:O2'	2.33	0.44
34:1c:102:ASN:N	34:1c:102:ASN:OD1	2.49	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:299:A:N1	1:2A:322:A:O2'	2.39	0.44
1:2A:720:C:H2'	1:2A:721:C:H6	1.82	0.44
1:2A:995:C:O2	9:2N:3:THR:OG1	2.29	0.44
1:2A:1007:C:OP1	9:2N:37:LYS:NZ	2.50	0.44
1:2A:1115:G:H2'	1:2A:1116:C:C6	2.52	0.44
5:2F:129:PHE:CD2	5:2F:163:VAL:HG21	2.51	0.44
6:2G:96:ARG:O	6:2G:99:MET:HB3	2.17	0.44
17:2V:39:LEU:HD12	17:2V:47:VAL:HG22	1.99	0.44
27:25:16:ARG:HD2	27:25:20:ARG:NH1	2.32	0.44
32:2a:900:A:H2'	32:2a:901:A:C8	2.52	0.44
32:2a:1068:G:H8	32:2a:1068:G:OP2	1.99	0.44
32:2a:1458:G:H5''	51:2t:32:ALA:HB2	1.98	0.44
32:2a:1512:U:H2'	32:2a:1513:A:C8	2.53	0.44
33:2b:150:SER:OG	33:2b:151:GLY:N	2.50	0.44
34:2c:17:ASP:OD1	34:2c:21:ARG:HD3	2.16	0.44
1:1A:150:C:H2'	1:1A:151:C:C6	2.53	0.44
1:1A:800:A:H8	1:1A:800:A:OP1	1.99	0.44
1:1A:1993:U:H4'	4:1E:128:SER:OG	2.17	0.44
1:1A:2159:G:H2'	1:1A:2160:G:H8	1.81	0.44
1:1A:2693:A:H2'	1:1A:2694:G:C8	2.53	0.44
12:1Q:111:GLU:O	12:1Q:115:MET:HG2	2.17	0.44
20:1Y:44:ILE:H	20:1Y:44:ILE:HD12	1.81	0.44
31:19:25:VAL:O	31:19:33:LYS:HA	2.18	0.44
1:2A:98:G:H5'	24:22:3:LEU:HD23	1.98	0.44
1:2A:1401:G:H2'	1:2A:1402:C:O4'	2.17	0.44
1:2A:2331:G:O2'	1:2A:2336:A:N1	2.42	0.44
1:2A:2497:A:H5''	62:2A:4258:HOH:O	2.16	0.44
1:2A:2687:U:H2'	1:2A:2688:U:O4'	2.17	0.44
32:2a:353:A:H5'	32:2a:353:A:C8	2.50	0.44
32:2a:1162:C:H2'	32:2a:1163:C:C6	2.53	0.44
34:2c:97:LYS:O	34:2c:99:VAL:N	2.50	0.44
39:2h:33:GLU:HG2	39:2h:48:TYR:CE1	2.52	0.44
51:2t:54:LYS:HA	51:2t:57:ARG:CZ	2.48	0.44
1:1A:7:G:H2'	1:1A:8:A:O4'	2.18	0.44
1:1A:1593:G:H2'	1:1A:1594:G:C8	2.53	0.44
1:1A:2031:A:C6	1:1A:2498:C:H1'	2.52	0.44
1:1A:2206:G:OP2	1:1A:2206:G:H4'	2.16	0.44
19:1X:60:ARG:HH12	29:17:47:ARG:HH22	1.65	0.44
32:1a:632:A:H5'	32:1a:633:G:OP2	2.16	0.44
32:1a:642:A:N3	39:1h:113:SER:OG	2.39	0.44
32:1a:864:A:H2'	32:1a:865:A:C8	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:867:G:O2'	32:1a:873:A:N1	2.50	0.44
32:1a:1054:C:N4	53:1y:46:GLN:OE1	2.51	0.44
32:1a:1149:C:OP1	40:1i:9:ARG:NE	2.49	0.44
35:1d:154:ASN:HA	35:1d:159:ARG:HE	1.83	0.44
40:1i:3:GLN:HE21	40:1i:20:ARG:HH21	1.65	0.44
1:2A:1709:U:H2'	1:2A:1710:C:C6	2.52	0.44
2:2B:48:A:H2'	2:2B:49:C:C6	2.52	0.44
3:2D:145:VAL:HG12	3:2D:146:GLU:O	2.17	0.44
6:2G:106:LEU:O	6:2G:111:LEU:HG	2.17	0.44
6:2G:161:THR:HG22	6:2G:163:ALA:H	1.81	0.44
7:2H:109:PHE:C	7:2H:111:HIS:H	2.25	0.44
9:2N:4:TYR:CD2	16:2U:100:VAL:HG11	2.52	0.44
11:2P:106:LEU:HD13	11:2P:112:LEU:HD13	1.99	0.44
13:2R:2:ARG:HD2	62:2R:315:HOH:O	2.18	0.44
32:2a:1457:G:C2'	32:2a:1458:G:H5'	2.47	0.44
35:2d:76:ARG:HA	35:2d:76:ARG:HD2	1.61	0.44
48:2q:58:GLU:OE1	48:2q:75:ARG:NE	2.49	0.44
1:1A:1105:U:H2'	1:1A:1106:G:C8	2.52	0.44
1:1A:1300:U:H4'	1:1A:1301:A:C5'	2.44	0.44
32:1a:22:G:H2'	32:1a:23:C:C6	2.53	0.44
32:1a:986:A:N3	50:1s:52:TYR:OH	2.48	0.44
50:1s:41:VAL:HG22	50:1s:44:MET:HE3	2.00	0.44
1:2A:634:C:H2'	1:2A:635:C:C6	2.52	0.44
1:2A:1810:A:H2'	1:2A:1811:G:O4'	2.17	0.44
1:2A:2128:C:O2'	1:2A:2174:C:OP1	2.35	0.44
18:2W:46:PHE:O	18:2W:50:VAL:HG23	2.16	0.44
26:24:46:GLN:HE21	26:24:48:ARG:HH22	1.64	0.44
32:2a:662:G:O2'	32:2a:836:G:OP1	2.35	0.44
34:2c:63:ASN:HB3	34:2c:98:ASN:HD22	1.82	0.44
35:2d:76:ARG:HD3	35:2d:207:TYR:CE1	2.52	0.44
35:2d:164:ALA:O	35:2d:168:ARG:HD3	2.17	0.44
41:2j:47:PHE:N	41:2j:63:PHE:O	2.36	0.44
46:2o:11:VAL:HG21	46:2o:34:LEU:HD22	1.99	0.44
1:1A:2331:G:O2'	22:10:43:THR:HG22	2.18	0.44
26:14:55:ARG:N	26:14:56:VAL:HA	2.30	0.44
30:18:62:LEU:HB3	30:18:65:GLU:CG	2.47	0.44
32:1a:1347:G:H5''	40:1i:107:ARG:HB3	1.99	0.44
33:1b:19:HIS:CG	33:1b:20:GLU:N	2.86	0.44
37:1f:67:MET:HE1	37:1f:75:LEU:HD23	1.99	0.44
38:1g:48:LYS:O	38:1g:52:GLU:HG2	2.17	0.44
42:1k:34:ASP:OD1	42:1k:37:GLY:N	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:93:G:H2'	1:2A:94:C:C6	2.52	0.44
1:2A:372:G:H8	23:21:65:SER:O	2.00	0.44
1:2A:1111:A:O2'	1:2A:1112:G:H4'	2.17	0.44
1:2A:1359:A:H61	1:2A:1372:U:H3	1.64	0.44
1:2A:1417:C:H2'	1:2A:1418:G:O4'	2.18	0.44
1:2A:1876:A:H2'	1:2A:1877:A:C8	2.53	0.44
1:2A:2113:U:H2'	1:2A:2114:A:O4'	2.18	0.44
1:2A:2271:G:OP1	22:20:18:ALA:HB1	2.18	0.44
4:2E:101:ARG:CZ	4:2E:171:GLU:HB2	2.47	0.44
6:2G:10:LYS:HG3	6:2G:14:GLU:OE1	2.18	0.44
7:2H:3:ARG:NH1	7:2H:5:GLY:H	2.15	0.44
15:2T:91:ARG:HB2	15:2T:121:ILE:HG13	1.98	0.44
21:2Z:40:ASP:OD1	21:2Z:42:VAL:HG12	2.17	0.44
21:2Z:54:HIS:HB3	21:2Z:101:PRO:HD3	2.00	0.44
32:2a:392:G:H2'	32:2a:393:A:C8	2.53	0.44
32:2a:614:A:H2'	32:2a:615:C:C6	2.53	0.44
32:2a:1002:G:N3	32:2a:1003:G:N7	2.65	0.44
33:2b:14:GLY:O	33:2b:15:VAL:HG13	2.18	0.44
35:2d:155:LEU:HD12	35:2d:156:GLU:H	1.82	0.44
1:1A:264:C:O2'	1:1A:265:A:H2'	2.18	0.44
1:1A:1183:G:O2'	25:13:29:ARG:NH1	2.51	0.44
1:1A:2305:A:H5''	6:1G:134:GLY:HA3	1.98	0.44
4:1E:111:ARG:HA	13:1R:1:MET:SD	2.58	0.44
19:1X:31:HIS:HD2	19:1X:33:LYS:H	1.64	0.44
32:1a:179:A:H2'	32:1a:180:U:C6	2.53	0.44
32:1a:838:G:H5'	32:1a:839:U:OP2	2.16	0.44
32:1a:1014:A:C2	32:1a:1219:U:H1'	2.52	0.44
39:1h:105:ARG:HE	39:1h:105:ARG:HB2	1.57	0.44
51:1t:54:LYS:HE2	51:1t:54:LYS:HB3	1.88	0.44
1:2A:210:C:OP2	29:27:29:LYS:NZ	2.43	0.44
1:2A:1005:C:H2'	1:2A:1006:C:H6	1.83	0.44
1:2A:1991:U:H2'	1:2A:1992:G:H5''	1.99	0.44
1:2A:2391:G:O6	1:2A:2425:A:H8	2.00	0.44
1:2A:2663:G:C6	1:2A:2664:G:C4	3.06	0.44
7:2H:143:GLN:NE2	7:2H:147:ASN:OD1	2.51	0.44
10:2O:66:LYS:HE2	10:2O:66:LYS:HB3	1.76	0.44
11:2P:97:PRO:HD3	11:2P:126:VAL:O	2.18	0.44
11:2P:126:VAL:HG12	11:2P:148:LEU:HD11	1.99	0.44
21:2Z:53:ILE:HG22	21:2Z:71:VAL:HB	1.98	0.44
32:2a:991:U:H4'	32:2a:992:U:O5'	2.18	0.44
32:2a:1276:G:H2'	32:2a:1277:C:O4'	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1320:C:H2'	32:2a:1321:C:O4'	2.16	0.44
33:2b:59:GLU:HB2	33:2b:221:LEU:HD21	2.00	0.44
35:2d:196:LEU:H	35:2d:196:LEU:HD12	1.82	0.44
52:2u:11:GLY:O	52:2u:15:ARG:HG3	2.18	0.44
1:1A:184:C:H2'	1:1A:185:U:C6	2.52	0.44
1:1A:569:U:C4	1:1A:570:G:C6	3.05	0.44
1:1A:2406:U:H2'	1:1A:2406:U:OP2	2.18	0.44
7:1H:3:ARG:HH21	7:1H:65:HIS:HB3	1.82	0.44
26:14:46:GLN:O	26:14:48:ARG:N	2.50	0.44
32:1a:961:U:OP2	32:1a:1223:C:O2'	2.33	0.44
33:1b:15:VAL:HG12	33:1b:16:HIS:HD2	1.83	0.44
35:1d:155:LEU:HD12	35:1d:156:GLU:H	1.82	0.44
40:1i:43:ALA:HA	40:1i:74:ILE:HD13	1.99	0.44
42:1k:92:GLU:HG3	42:1k:96:ARG:NH1	2.33	0.44
49:1r:26:LEU:HG	49:1r:42:ARG:HH22	1.83	0.44
1:2A:1044:G:O2'	1:2A:1048:A:H1'	2.18	0.44
1:2A:1064:C:H5	1:2A:1065:U:C6	2.36	0.44
5:2F:74:ARG:HD2	62:2F:411:HOH:O	2.18	0.44
6:2G:36:LYS:HE3	6:2G:95:ARG:HH22	1.81	0.44
17:2V:6:LYS:HB2	17:2V:38:LEU:HD11	1.98	0.44
25:23:6:VAL:HG12	25:23:28:LEU:HD11	1.99	0.44
32:2a:1121:U:H2'	32:2a:1122:U:O4'	2.18	0.44
41:2j:10:GLY:N	41:2j:16:LEU:HD11	2.33	0.44
49:2r:33:ASP:OD2	49:2r:36:ASN:HB2	2.17	0.44
53:2y:48:PHE:CD2	53:2y:70:MET:HB2	2.51	0.44
1:1A:1175:U:H4'	1:1A:1176:G:OP2	2.15	0.44
1:1A:2166:G:N1	1:1A:2172:U:O4	2.44	0.44
10:1O:113:LYS:HE3	10:1O:113:LYS:HB2	1.65	0.44
32:1a:1304:G:C6	32:1a:1305:G:N1	2.86	0.44
1:2A:394:A:O2'	1:2A:395:U:H5'	2.18	0.44
1:2A:1180:C:H2'	1:2A:1181:C:C6	2.52	0.44
9:2N:14:VAL:HG11	9:2N:138:LEU:HD12	1.99	0.44
32:2a:582:U:C2	32:2a:760:G:C6	3.06	0.44
34:2c:17:ASP:OD1	34:2c:18:TRP:N	2.51	0.44
47:2p:58:TYR:O	47:2p:61:SER:OG	2.23	0.44
1:1A:64:A:O3'	19:1X:71:GLY:HA3	2.18	0.44
1:1A:1092:C:C2'	1:1A:1093:G:H5'	2.48	0.44
1:1A:1366:A:OP1	23:11:3:LYS:NZ	2.51	0.44
1:1A:1899:G:N3	1:1A:1899:G:H2'	2.32	0.44
2:1B:103:G:H21	21:1Z:73:GLN:NE2	2.15	0.44
17:1V:21:ARG:HD3	17:1V:91:TYR:CE1	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1124:G:H5''	41:1j:35:SER:OG	2.17	0.44
32:1a:1456:G:N1	51:1t:51:GLU:OE2	2.50	0.44
41:1j:42:THR:HG23	41:1j:68:HIS:HA	2.00	0.44
45:1n:48:ALA:HB2	45:1n:53:LEU:HD12	2.00	0.44
1:2A:904:C:H2'	1:2A:905:U:C6	2.53	0.44
1:2A:1047:G:H21	1:2A:1111:A:H62	1.66	0.44
1:2A:1359:A:N1	1:2A:1372:U:O4	2.51	0.44
1:2A:2141:G:O6	1:2A:2150:U:C2	2.71	0.44
1:2A:2607:G:H2'	1:2A:2608:G:O4'	2.18	0.44
17:2V:4:ILE:HD12	17:2V:39:LEU:HD22	1.99	0.44
24:22:23:LYS:HD3	24:22:26:ARG:HH12	1.83	0.44
32:2a:512:U:H2'	32:2a:513:C:C6	2.53	0.44
32:2a:954:G:H21	32:2a:1227:A:N6	2.12	0.44
32:2a:1071:C:H2'	32:2a:1072:G:C8	2.51	0.44
34:2c:6:HIS:NE2	34:2c:8:ILE:HB	2.33	0.44
44:2m:86:CYS:O	44:2m:90:LEU:HG	2.18	0.44
47:2p:49:LEU:HD11	47:2p:73:LEU:HB3	1.99	0.44
1:1A:1802:A:N1	1:1A:1822:G:H1'	2.32	0.43
9:1N:15:LEU:HB2	9:1N:135:PRO:HB2	2.00	0.43
10:1O:3:GLN:NE2	62:1O:306:HOH:O	2.50	0.43
15:1T:127:ALA:O	15:1T:128:GLU:HB3	2.18	0.43
26:14:59:PHE:HD2	26:14:62:ARG:HH21	1.66	0.43
32:1a:189(K):U:H2'	32:1a:189(L):G:C8	2.53	0.43
32:1a:428:G:OP2	35:1d:10:ARG:NH1	2.50	0.43
32:1a:601:C:H2'	32:1a:602:A:H8	1.83	0.43
32:1a:672:U:O2'	32:1a:673:G:O5'	2.36	0.43
34:1c:52:LEU:HA	34:1c:70:VAL:HG23	1.99	0.43
43:1l:97:ARG:HB2	43:1l:98:TYR:CE2	2.53	0.43
51:1t:50:GLU:O	51:1t:100:ILE:HD11	2.17	0.43
53:1y:20:VAL:HG22	53:1y:74:ILE:HD13	2.00	0.43
53:1y:40:ILE:HB	53:1y:51:ASP:HB2	2.00	0.43
1:2A:493:G:H2'	1:2A:494:G:O4'	2.17	0.43
1:2A:1025:G:C4	1:2A:1135:C:H1'	2.53	0.43
1:2A:2839:G:H5'	13:2R:46:GLY:CA	2.44	0.43
32:2a:254:G:OP1	48:2q:66:SER:OG	2.32	0.43
32:2a:500:G:H5''	43:2l:124:LYS:HE2	1.99	0.43
32:2a:947:G:H2'	32:2a:948:C:O4'	2.18	0.43
32:2a:1203:C:H2'	32:2a:1204:A:H8	1.83	0.43
36:2e:80:ILE:HG22	36:2e:91:LEU:HB2	1.99	0.43
50:2s:53:ASN:HB3	50:2s:75:ALA:HB1	1.98	0.43
51:2t:54:LYS:NZ	51:2t:54:LYS:HB3	2.32	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:295:G:OP1	20:1Y:1:MET:HB2	2.19	0.43
1:1A:2345:G:H4'	1:1A:2346:A:H5''	2.00	0.43
1:1A:2506:U:C2	1:1A:2585:U:O4	2.71	0.43
5:1F:107:LYS:HG3	5:1F:206:ILE:HA	2.00	0.43
6:1G:50:ALA:C	6:1G:52:ILE:H	2.21	0.43
9:1N:62:VAL:CG1	9:1N:66:LYS:HB2	2.49	0.43
21:1Z:136:PHE:HE1	21:1Z:138:GLU:HG3	1.83	0.43
32:1a:77:G:C2'	32:1a:78:G:H5'	2.48	0.43
32:1a:313:A:H2'	32:1a:314:C:C6	2.53	0.43
32:1a:1100:C:OP2	33:1b:96:ARG:HD2	2.17	0.43
32:1a:1137:C:H3'	32:1a:1137:C:H6	1.84	0.43
32:1a:1182:G:C3'	32:1a:1183:A:H5'	2.48	0.43
36:1e:98:THR:HB	36:1e:117:ASP:HB3	2.01	0.43
37:1f:98:LEU:HD23	49:1r:30:ASP:HA	2.01	0.43
38:1g:23:VAL:HG13	38:1g:43:PHE:CE2	2.52	0.43
46:1o:3:ILE:H	46:1o:3:ILE:HD12	1.83	0.43
51:1t:63:ILE:HG21	51:1t:81:LYS:HG3	2.01	0.43
1:2A:491:G:H2'	1:2A:492:A:H8	1.82	0.43
1:2A:997:G:OP2	16:2U:58:ARG:NH1	2.50	0.43
1:2A:1084:A:H3'	1:2A:1085:A:C4'	2.45	0.43
1:2A:1187:G:H5'	17:2V:81:TYR:CE1	2.54	0.43
1:2A:1450:G:H2'	1:2A:1450(A):C:H6	1.83	0.43
1:2A:1581:G:H2'	1:2A:1582:C:O4'	2.18	0.43
2:2B:8:U:H6	2:2B:8:U:H5''	1.83	0.43
2:2B:8:U:O3'	14:2S:25:ARG:NH2	2.50	0.43
2:2B:28:C:H2'	2:2B:29:A:O4'	2.18	0.43
5:2F:33:LEU:HD12	5:2F:33:LEU:HA	1.74	0.43
6:2G:152:LEU:H	6:2G:152:LEU:HD12	1.83	0.43
7:2H:76:VAL:O	7:2H:80:SER:HB3	2.18	0.43
25:23:46:ASN:O	25:23:50:VAL:HG22	2.18	0.43
32:2a:451:A:N6	32:2a:480:U:H2'	2.33	0.43
34:2c:22:TRP:HA	41:2j:93:GLY:HA2	1.99	0.43
34:2c:40:ARG:NH1	34:2c:55:VAL:O	2.51	0.43
38:2g:12:LEU:H	38:2g:12:LEU:HD12	1.83	0.43
38:2g:136:LYS:HD3	38:2g:139:GLU:OE2	2.17	0.43
50:2s:11:VAL:HG22	50:2s:39:THR:O	2.18	0.43
1:1A:1062:G:C4	1:1A:1088:A:C8	3.06	0.43
1:1A:2630:G:H2'	1:1A:2631:G:C8	2.53	0.43
7:1H:84:SER:OG	7:1H:132:ARG:NH1	2.50	0.43
7:1H:124:GLU:CG	7:1H:132:ARG:HB3	2.48	0.43
32:1a:743:U:H2'	32:1a:744:C:C6	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:1d:168:ARG:N	35:1d:168:ARG:HH11	2.15	0.43
1:2A:910:A:N1	1:2A:2277:G:H1'	2.33	0.43
1:2A:1068:G:N1	1:2A:1095:A:C8	2.87	0.43
1:2A:1131:G:O6	1:2A:2040:C:H1'	2.18	0.43
1:2A:1272:A:OP1	62:2A:3851:HOH:O	2.21	0.43
1:2A:1385:G:O2'	1:2A:1396:U:O2	2.34	0.43
1:2A:2410:G:N7	62:2A:3937:HOH:O	2.36	0.43
14:2S:43:GLU:OE1	22:20:49:LYS:NZ	2.47	0.43
15:2T:119:LYS:HB2	32:2a:1442(A):G:N2	2.33	0.43
17:2V:1:MET:HG3	17:2V:41:GLY:O	2.18	0.43
32:2a:683:G:H2'	32:2a:684:A:C8	2.53	0.43
32:2a:926:G:C6	53:2y:87:LYS:HG3	2.53	0.43
32:2a:1126:U:H4'	32:2a:1281:U:O2'	2.18	0.43
33:2b:71:VAL:CG1	33:2b:97:TRP:HE1	2.30	0.43
35:2d:173:TRP:CD1	35:2d:174:LEU:HG	2.53	0.43
1:1A:686:G:N2	1:1A:788:A:H61	2.15	0.43
1:1A:1803:A:H4'	3:1D:259:THR:HG23	1.99	0.43
1:1A:2106:G:C4	1:1A:2107:C:H1'	2.54	0.43
1:1A:2607:G:H2'	1:1A:2608:G:O4'	2.18	0.43
62:1A:5387:HOH:O	27:15:40:LYS:HE3	2.19	0.43
32:1a:1406:U:O2	32:1a:1517:G:N2	2.51	0.43
39:1h:6:ILE:O	39:1h:10:LEU:HG	2.18	0.43
39:1h:83:ILE:HA	39:1h:136:GLU:O	2.19	0.43
40:1i:77:ILE:O	40:1i:81:ILE:HG23	2.17	0.43
53:1y:55:ASN:OD1	53:1y:60:VAL:HG12	2.19	0.43
1:2A:272:G:N7	1:2A:421:U:H2'	2.32	0.43
1:2A:1055:G:H3'	1:2A:1056:G:C8	2.51	0.43
1:2A:1547:C:H2'	1:2A:1548:C:C6	2.54	0.43
1:2A:2133:G:H2'	1:2A:2157:G:H1'	1.99	0.43
1:2A:2205:C:H1'	1:2A:2220:G:N2	2.34	0.43
1:2A:2742:C:OP1	31:29:35:ARG:HD3	2.18	0.43
2:2B:75:G:H5''	21:2Z:36:LYS:HD3	2.00	0.43
5:2F:157:VAL:HB	5:2F:194:MET:HG2	2.00	0.43
20:2Y:38:ILE:HD13	20:2Y:66:PRO:HA	1.99	0.43
23:21:83:GLU:HA	23:21:84:GLY:HA2	1.65	0.43
25:23:15:TYR:CE2	25:23:53:LEU:HD21	2.54	0.43
32:2a:254:G:H21	48:2q:16:GLN:NE2	2.16	0.43
32:2a:457:C:H2'	32:2a:458:C:H6	1.84	0.43
32:2a:525:C:OP1	43:2l:91:LYS:HB2	2.19	0.43
32:2a:828:A:H2'	32:2a:829:G:O4'	2.18	0.43
32:2a:1457:G:H5'	51:2t:36:LEU:HD21	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:2t:43:LEU:HB3	51:2t:52:ALA:HB2	2.00	0.43
1:1A:71:A:N7	19:1X:31:HIS:HE1	2.16	0.43
1:1A:192:C:H2'	1:1A:193:U:H5'	2.01	0.43
1:1A:284:U:H2'	1:1A:285:C:C6	2.54	0.43
1:1A:566:U:H5''	11:1P:29:LYS:HE3	2.01	0.43
1:1A:2096:U:H2'	1:1A:2097:C:C6	2.54	0.43
1:1A:2162:G:H1'	1:1A:2173:A:H1'	2.01	0.43
1:1A:2493:U:H2'	1:1A:2494:G:O4'	2.19	0.43
2:1B:78:A:C2	2:1B:100:A:C4	3.06	0.43
5:1F:53:THR:HG22	5:1F:55:GLY:N	2.23	0.43
21:1Z:136:PHE:CE1	21:1Z:138:GLU:HG3	2.53	0.43
32:1a:1371:G:O3'	40:1i:69:GLY:HA3	2.18	0.43
35:1d:107:ARG:HG3	35:1d:173:TRP:HH2	1.83	0.43
36:1e:91:LEU:HB3	36:1e:118:ILE:HD11	2.01	0.43
38:1g:106:GLN:O	38:1g:110:GLN:HG2	2.18	0.43
39:1h:119:LEU:HB3	39:1h:123:GLU:HB2	2.00	0.43
1:2A:323:G:H1'	1:2A:1205:U:O2	2.18	0.43
1:2A:974:G:N2	62:2A:3820:HOH:O	2.19	0.43
1:2A:1664:A:H2	10:2O:1:MET:HE1	1.82	0.43
1:2A:1698:A:C8	1:2A:1700:A:O4'	2.72	0.43
1:2A:2619:C:H4'	4:2E:151:TYR:O	2.19	0.43
2:2B:24:G:H4'	2:2B:25:A:C8	2.53	0.43
6:2G:103:LEU:O	6:2G:107:LEU:HG	2.18	0.43
12:2Q:45:GLN:OE1	12:2Q:45:GLN:N	2.52	0.43
17:2V:1:MET:HE1	17:2V:44:LYS:H	1.82	0.43
21:2Z:129:SER:HB2	21:2Z:132:ASN:HD22	1.83	0.43
31:29:3:VAL:HA	31:29:35:ARG:O	2.18	0.43
32:2a:1157:A:H5'	32:2a:1158:C:C6	2.53	0.43
32:2a:1304:G:H1'	32:2a:1333:A:H61	1.83	0.43
34:2c:91:LEU:HD22	34:2c:101:LEU:HD13	2.00	0.43
38:2g:26:PHE:O	38:2g:30:ILE:HG13	2.18	0.43
44:2m:97:PRO:N	44:2m:110:ARG:HG2	2.32	0.43
45:2n:4:LYS:HE2	45:2n:4:LYS:HB2	1.89	0.43
50:2s:14:HIS:O	50:2s:18:LYS:HG3	2.18	0.43
53:2y:35:ILE:HG22	53:2y:36:ASN:HD22	1.83	0.43
1:1A:881:G:H2'	1:1A:882:G:O4'	2.18	0.43
1:1A:1039:G:N1	1:1A:1116:C:N3	2.52	0.43
1:1A:1287:A:H8	13:1R:104:ARG:HD3	1.83	0.43
5:1F:101:LEU:HD23	5:1F:106:ARG:HG2	1.99	0.43
18:1W:18:ARG:NH1	18:1W:76:VAL:O	2.51	0.43
21:1Z:19:ARG:NH1	21:1Z:84:GLU:O	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:250:A:H4'	32:1a:251:G:O5'	2.18	0.43
32:1a:509:A:N3	32:1a:543:C:O2'	2.45	0.43
32:1a:519:C:OP2	43:1l:50:SER:OG	2.34	0.43
32:1a:637:G:H2'	32:1a:638:G:H8	1.83	0.43
32:1a:920:U:H2'	32:1a:921:U:C6	2.54	0.43
33:1b:87:ARG:NH2	33:1b:220:ASP:OD1	2.29	0.43
33:1b:92:TYR:HH	33:1b:150:SER:HG	1.60	0.43
40:1i:10:ARG:O	40:1i:11:LYS:C	2.61	0.43
40:1i:82:ALA:HB1	40:1i:96:LEU:HD21	1.99	0.43
41:1j:5:ARG:HE	41:1j:73:ASP:CG	2.23	0.43
45:1n:27:CYS:SG	45:1n:29:ARG:HB2	2.59	0.43
1:2A:322:A:H3'	5:2F:169:ASN:OD1	2.19	0.43
1:2A:1338:G:N7	19:2X:62:LYS:NZ	2.65	0.43
1:2A:1798:U:H5'	3:2D:259:THR:CG2	2.41	0.43
1:2A:1920:OMC:HM22	1:2A:1921:G:H5'	2.00	0.43
1:2A:2032:G:OP2	1:2A:2454:G:O2'	2.31	0.43
1:2A:2099:U:H3	1:2A:2190:G:H1	1.66	0.43
1:2A:2596:U:OP1	62:2A:3853:HOH:O	2.22	0.43
3:2D:71:ASP:HB3	3:2D:103:ARG:HH22	1.83	0.43
3:2D:276:LYS:H	3:2D:276:LYS:HG3	1.31	0.43
11:2P:101:VAL:HA	11:2P:106:LEU:O	2.18	0.43
21:2Z:146:ILE:HA	21:2Z:174:VAL:HG12	2.01	0.43
32:2a:443:C:H2'	32:2a:444:C:C6	2.53	0.43
32:2a:625:G:H4'	47:2p:16:HIS:CD2	2.53	0.43
32:2a:675:A:H1'	42:2k:116:HIS:CG	2.53	0.43
32:2a:1004:A:H5''	32:2a:1025:U:C4	2.53	0.43
33:2b:98:LEU:HA	33:2b:98:LEU:HD23	1.67	0.43
47:2p:55:ARG:HA	47:2p:55:ARG:HD2	1.76	0.43
53:2y:24:LEU:HD23	53:2y:24:LEU:HA	1.78	0.43
1:1A:784:A:C8	1:1A:792:G:C5	3.07	0.43
1:1A:795:C:H2'	1:1A:796:C:C6	2.53	0.43
1:1A:1174:A:H4'	1:1A:1175:U:OP1	2.19	0.43
1:1A:2110:G:OP2	1:1A:2110:G:H8	2.02	0.43
62:1A:5362:HOH:O	11:1P:70:GLN:HG2	2.18	0.43
6:1G:72:ARG:NH1	6:1G:87:PRO:HG3	2.34	0.43
6:1G:142:PRO:HB2	26:14:31:ILE:HG21	1.99	0.43
19:1X:11:PRO:HD3	24:12:37:PHE:CE2	2.53	0.43
20:1Y:6:HIS:H	20:1Y:6:HIS:CD2	2.36	0.43
32:1a:1026:G:H2'	32:1a:1026:G:N3	2.34	0.43
32:1a:1132:C:H2'	32:1a:1133:G:C8	2.54	0.43
32:1a:1368:G:OP2	40:1i:112:LYS:HG3	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:1j:31:GLY:HA2	41:1j:32:ALA:HA	1.52	0.43
1:2A:833:U:O2	11:2P:55:ARG:NH2	2.51	0.43
1:2A:1557:C:H5''	1:2A:1558:A:OP2	2.18	0.43
1:2A:2641:G:H5''	9:2N:76:SER:HB3	2.00	0.43
8:2I:4:ILE:HG12	8:2I:18:VAL:HG22	1.99	0.43
19:2X:65:ARG:HE	19:2X:70:LEU:HD21	1.84	0.43
24:22:11:GLU:O	24:22:15:LYS:HG3	2.19	0.43
26:24:24:THR:OG1	26:24:25:TYR:N	2.48	0.43
32:2a:233:C:H2'	32:2a:234:C:H6	1.84	0.43
32:2a:1403:C:H2'	32:2a:1404:5MC:HM53	2.00	0.43
40:2i:24:GLY:HA2	40:2i:59:PHE:O	2.19	0.43
53:2y:27:LEU:HD11	53:2y:81:LEU:HD13	2.00	0.43
1:1A:706:A:H2'	1:1A:707:G:O4'	2.18	0.43
1:1A:1506:C:H2'	1:1A:1507:A:C8	2.54	0.43
1:1A:1977:A:OP2	62:1A:4144:HOH:O	2.21	0.43
1:1A:2287:A:C8	1:1A:2289:G:C8	3.06	0.43
6:1G:43:LEU:C	6:1G:45:GLU:H	2.27	0.43
7:1H:41:MET:HE1	7:1H:54:ARG:HB3	2.01	0.43
7:1H:154:PRO:HB3	7:1H:163:TYR:CZ	2.53	0.43
21:1Z:99:TYR:HB3	21:1Z:123:ASP:HB2	2.00	0.43
32:1a:77:G:H2'	32:1a:78:G:H5'	2.00	0.43
32:1a:254:G:H21	48:1q:16:GLN:NE2	2.16	0.43
32:1a:399:G:H2'	32:1a:400:C:C6	2.53	0.43
32:1a:448:A:H2'	32:1a:449:C:C6	2.54	0.43
32:1a:828:A:H2'	32:1a:829:G:O4'	2.18	0.43
32:1a:1002:G:C6	32:1a:1003:G:C2	3.07	0.43
32:1a:1004:A:C5	32:1a:1037:C:C2	3.07	0.43
33:1b:55:PHE:CD1	33:1b:58:ILE:HD12	2.53	0.43
34:1c:6:HIS:HD2	34:1c:8:ILE:H	1.65	0.43
1:2A:87:C:H5''	1:2A:88:G:H5'	1.99	0.43
1:2A:1106:G:H2'	1:2A:1107:G:O4'	2.19	0.43
1:2A:1165:U:H2'	1:2A:1166:C:C6	2.54	0.43
3:2D:38:LYS:HA	3:2D:38:LYS:HD2	1.51	0.43
6:2G:11:TYR:HB2	6:2G:176:LEU:HD21	2.01	0.43
21:2Z:4:ARG:HD3	21:2Z:60:GLU:OE2	2.18	0.43
27:25:40:LYS:NZ	27:25:41:PRO:O	2.52	0.43
32:2a:279:A:OP2	48:2q:95:TYR:OH	2.30	0.43
32:2a:399:G:H2'	32:2a:400:C:C6	2.53	0.43
32:2a:438:G:H5''	35:2d:123:HIS:HB3	2.00	0.43
32:2a:1108:G:H5'	34:2c:176:HIS:CD2	2.46	0.43
32:2a:1122:U:C4	32:2a:1123:A:N7	2.87	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:2f:69:GLU:O	37:2f:72:VAL:HG13	2.19	0.43
38:2g:74:GLU:OE2	38:2g:95:ARG:NE	2.44	0.43
44:2m:3:ARG:HD2	44:2m:8:GLU:CD	2.44	0.43
53:2y:5:ILE:HG23	53:2y:39:ILE:HB	2.00	0.43
1:1A:143:G:H1'	19:1X:37:THR:HG21	2.01	0.43
1:1A:287:C:O2'	1:1A:288:C:H5'	2.19	0.43
1:1A:2168:G:C2	1:1A:2171:A:C8	3.07	0.43
1:1A:2169:A:H8	1:1A:2169:A:OP1	2.02	0.43
1:1A:2447:G:N2	1:1A:2450:A:OP2	2.50	0.43
1:1A:2809:A:H62	1:1A:2891:G:H2'	1.84	0.43
5:1F:183:VAL:O	5:1F:187:VAL:HG23	2.19	0.43
6:1G:77:ILE:HG22	6:1G:80:PHE:H	1.84	0.43
17:1V:58:VAL:HG12	17:1V:97:LYS:HB2	1.99	0.43
32:1a:1026:G:H5''	32:1a:1027:C:H5	1.83	0.43
32:1a:1486:G:H2'	32:1a:1487:G:O4'	2.19	0.43
33:1b:187:LEU:HA	33:1b:201:ILE:HB	2.01	0.43
34:1c:95:THR:O	34:1c:97:LYS:HE3	2.18	0.43
38:1g:26:PHE:O	38:1g:30:ILE:HG13	2.18	0.43
43:1l:88:GLY:O	43:1l:99:HIS:HD2	2.00	0.43
46:1o:12:ILE:HG23	46:1o:27:VAL:HG21	2.00	0.43
1:2A:190:A:OP2	23:21:39:LYS:HE3	2.19	0.43
1:2A:517:C:OP1	27:25:16:ARG:NH2	2.51	0.43
1:2A:748:G:C8	18:2W:89:ALA:HB1	2.54	0.43
1:2A:839:U:H2'	1:2A:840:C:C6	2.53	0.43
1:2A:927:G:H2'	1:2A:928:G:O4'	2.19	0.43
1:2A:1479:G:H5''	1:2A:1560:G:H4'	2.00	0.43
1:2A:2059:A:O2'	5:2F:69:HIS:HD2	2.02	0.43
1:2A:2104:G:H2'	1:2A:2104:G:N3	2.34	0.43
1:2A:2162:G:O2'	1:2A:2172:U:O2'	2.34	0.43
2:2B:104:U:O2'	21:2Z:72:ARG:HG3	2.19	0.43
6:2G:91:ARG:CZ	6:2G:91:ARG:HB3	2.48	0.43
11:2P:6:LEU:HA	11:2P:6:LEU:HD23	1.81	0.43
32:2a:141:A:H1'	32:2a:182:U:O2	2.19	0.43
32:2a:1093:A:N3	32:2a:1109:C:O2'	2.48	0.43
32:2a:1151:A:O2'	32:2a:1152:A:O5'	2.33	0.43
33:2b:154:LEU:HD23	33:2b:154:LEU:HA	1.86	0.43
33:2b:164:VAL:HB	33:2b:186:ALA:HB2	2.01	0.43
39:2h:29:SER:HB3	39:2h:32:LYS:HD2	2.01	0.43
44:2m:66:LEU:HB3	44:2m:67:GLU:H	1.60	0.43
47:2p:75:ARG:HG3	47:2p:80:PHE:CD2	2.50	0.43
48:2q:85:VAL:O	48:2q:89:LEU:HG	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:2t:51:GLU:HG3	51:2t:54:LYS:NZ	2.34	0.43
1:1A:1668:A:H4'	1:1A:1669:A:O5'	2.18	0.43
21:1Z:14:LYS:HD3	21:1Z:16:SER:H	1.84	0.43
32:1a:708:C:H2'	32:1a:709:G:H8	1.84	0.43
32:1a:755:G:OP2	46:1o:65:ARG:HD2	2.19	0.43
33:1b:80:ILE:HD11	33:1b:212:GLN:CA	2.49	0.43
38:1g:52:GLU:HG2	38:1g:52:GLU:H	1.66	0.43
40:1i:56:LEU:HD23	40:1i:56:LEU:H	1.83	0.43
1:2A:1005:C:H2'	1:2A:1006:C:C6	2.54	0.43
1:2A:1086:A:OP1	1:2A:1104:C:O2'	2.36	0.43
1:2A:1087:G:H22	1:2A:1102:C:H42	1.67	0.43
1:2A:1216:G:P	16:2U:12:ARG:HH21	2.41	0.43
1:2A:1781:C:H5	29:27:1:MET:HE1	1.83	0.43
1:2A:1817:G:OP1	3:2D:88:ARG:NH2	2.44	0.43
62:2A:4269:HOH:O	5:2F:74:ARG:HG3	2.19	0.43
3:2D:12:SER:HB3	3:2D:208:LYS:HB3	2.00	0.43
7:2H:13:LYS:HE3	7:2H:13:LYS:HB3	1.90	0.43
26:24:46:GLN:O	26:24:48:ARG:N	2.51	0.43
27:25:20:ARG:HG2	27:25:23:HIS:CE1	2.53	0.43
28:26:11:LEU:HB2	28:26:21:TYR:HB2	2.00	0.43
31:29:19:ARG:HG2	31:29:20:HIS:ND1	2.34	0.43
32:2a:250:A:H4'	32:2a:251:G:O5'	2.19	0.43
38:2g:111:ARG:HB2	38:2g:119:ARG:HG2	2.01	0.43
40:2i:41:VAL:C	40:2i:43:ALA:H	2.27	0.43
1:1A:11:G:C2'	1:1A:12:U:H5'	2.49	0.42
1:1A:120:U:H5''	1:1A:122:G:OP2	2.19	0.42
1:1A:190:A:OP2	23:11:39:LYS:HE3	2.19	0.42
1:1A:652(V):C:H2'	1:1A:653:A:O4'	2.19	0.42
1:1A:1062:G:OP2	1:1A:1070:A:H4'	2.19	0.42
1:1A:1066:U:C2	1:1A:1067:A:N1	2.87	0.42
1:1A:1354:A:H2'	1:1A:1355:G:O4'	2.19	0.42
1:1A:1578:U:C2'	1:1A:1579:A:H5'	2.49	0.42
1:1A:2406:U:H2'	1:1A:2406:U:H6	1.66	0.42
3:1D:242:ARG:HD2	3:1D:246:PRO:HG3	2.01	0.42
8:1I:109:ILE:HD12	8:1I:109:ILE:HA	1.75	0.42
21:1Z:129:SER:HB3	21:1Z:132:ASN:HB2	2.01	0.42
27:15:34:PRO:HG2	27:15:35:GLU:OE1	2.19	0.42
32:1a:67:C:H2'	32:1a:68:G:C8	2.54	0.42
32:1a:659:U:H2'	32:1a:660:G:C8	2.54	0.42
32:1a:1277:C:O2'	32:1a:1279:A:H8	2.02	0.42
1:2A:889:C:O2'	1:2A:890:A:O4'	2.28	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1226:A:OP1	16:2U:16:LYS:NZ	2.47	0.42
1:2A:2637:U:OP1	4:2E:82:ARG:NH1	2.51	0.42
6:2G:33:ARG:NH2	6:2G:162:THR:HG21	2.34	0.42
12:2Q:1:MET:HE2	12:2Q:1:MET:HB3	1.73	0.42
32:2a:280:C:N3	48:2q:39:SER:OG	2.52	0.42
32:2a:537:G:H5''	43:2l:113:ARG:NH1	2.34	0.42
32:2a:1016:A:O5'	32:2a:1016:A:H8	2.02	0.42
34:2c:8:ILE:HG12	34:2c:184:TYR:HB3	2.00	0.42
48:2q:6:LEU:O	48:2q:58:GLU:HA	2.18	0.42
5:1F:181:LEU:O	5:1F:205:ARG:NH2	2.45	0.42
6:1G:59:GLU:OE1	6:1G:153:ARG:NH2	2.52	0.42
6:1G:64:THR:HB	6:1G:94:LEU:HD21	2.02	0.42
6:1G:131:TYR:HB3	6:1G:159:VAL:CG1	2.50	0.42
22:10:46:LYS:HB2	22:10:78:TYR:CD1	2.54	0.42
32:1a:858:G:O6	32:1a:869:G:H3'	2.19	0.42
32:1a:1027:C:H2'	32:1a:1028:C:C5	2.54	0.42
32:1a:1186:G:N2	45:1n:61:TRP:O	2.36	0.42
32:1a:1324:A:O4'	32:1a:1362:C:H4'	2.19	0.42
37:1f:28:ARG:O	37:1f:32:ASN:ND2	2.52	0.42
46:1o:82:ILE:HG13	46:1o:83:GLU:N	2.33	0.42
53:1y:44:GLU:OE1	53:1y:66:LYS:NZ	2.45	0.42
1:2A:479:A:H4'	1:2A:480:A:OP1	2.18	0.42
1:2A:2439:A:H5'	1:2A:2439:A:C8	2.55	0.42
1:2A:2648:C:H2'	1:2A:2649:U:C6	2.54	0.42
1:2A:2887:U:H2'	1:2A:2888:C:C6	2.54	0.42
5:2F:31:HIS:HB2	11:2P:9:ASN:OD1	2.19	0.42
16:2U:16:LYS:HE2	16:2U:16:LYS:HB3	1.82	0.42
28:26:9:LEU:HA	28:26:54:ILE:HB	1.99	0.42
32:2a:933:G:O6	38:2g:3:ARG:NH2	2.50	0.42
32:2a:1346:A:H61	32:2a:1374:A:H3'	1.84	0.42
33:2b:57:PHE:CE2	33:2b:185:ILE:HD11	2.54	0.42
33:2b:114:ARG:HA	33:2b:114:ARG:HD3	1.78	0.42
36:2e:27:ARG:HE	36:2e:27:ARG:HB2	1.66	0.42
40:2i:112:LYS:NZ	40:2i:113:LYS:O	2.48	0.42
42:2k:59:TYR:O	42:2k:63:LEU:HD12	2.19	0.42
49:2r:53:ARG:NH1	49:2r:60:ALA:HB2	2.33	0.42
1:1A:614(A):U:H4'	1:1A:614(B):G:H5''	2.01	0.42
6:1G:50:ALA:C	6:1G:52:ILE:N	2.76	0.42
10:1O:66:LYS:HE2	10:1O:66:LYS:HB3	1.78	0.42
32:1a:1333:A:H2'	32:1a:1334:G:O4'	2.20	0.42
1:2A:127:A:H5''	1:2A:128:C:C6	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:323:G:H2'	5:2F:169:ASN:ND2	2.34	0.42
1:2A:1580:A:H8	1:2A:1580:A:OP2	2.03	0.42
1:2A:2179:C:C4	1:2A:2180:U:C4	3.08	0.42
1:2A:2564:A:C2	1:2A:2647:U:H4'	2.53	0.42
1:2A:2887:U:H2'	1:2A:2888:C:H6	1.84	0.42
5:2F:117:ARG:NH2	5:2F:189:THR:O	2.51	0.42
20:2Y:67:LEU:HA	20:2Y:67:LEU:HD23	1.75	0.42
32:2a:445:G:H2'	32:2a:446:G:O4'	2.20	0.42
32:2a:475:G:H2'	32:2a:476:G:H8	1.84	0.42
32:2a:1005:A:H5''	32:2a:1006:C:C5	2.54	0.42
34:2c:148:GLY:HA3	34:2c:172:ARG:O	2.18	0.42
34:2c:159:GLY:HA2	34:2c:193:TYR:CE1	2.54	0.42
36:2e:40:ARG:NE	36:2e:68:GLU:OE2	2.53	0.42
38:2g:69:VAL:HG22	38:2g:135:VAL:HG12	2.02	0.42
45:2n:26:ARG:NH1	45:2n:43:CYS:SG	2.90	0.42
1:1A:448:U:O4	1:1A:583:G:H1'	2.19	0.42
1:1A:1932:A:H2'	1:1A:1933:G:O4'	2.19	0.42
1:1A:2080:G:OP1	23:11:35:THR:HG21	2.19	0.42
1:1A:2615:U:H2'	1:1A:2616:C:H6	1.85	0.42
1:1A:2887:U:H2'	1:1A:2888:C:H6	1.84	0.42
6:1G:43:LEU:O	6:1G:45:GLU:HG2	2.20	0.42
8:1I:75:LEU:HD13	8:1I:105:HIS:ND1	2.35	0.42
32:1a:418:C:H1'	32:1a:540:G:O2'	2.19	0.42
32:1a:1054:C:O2	32:1a:1196:U:O2'	2.32	0.42
34:1c:59:ARG:O	41:1j:92:THR:HG22	2.18	0.42
40:1i:29:ASN:OD1	40:1i:65:VAL:N	2.52	0.42
42:1k:92:GLU:HG3	42:1k:96:ARG:HH12	1.84	0.42
1:2A:686:G:N2	1:2A:788:A:H61	2.17	0.42
1:2A:1539:G:H2'	1:2A:1540:U:H6	1.84	0.42
1:2A:2417:C:OP1	11:2P:65:ARG:NH2	2.53	0.42
2:2B:89:G:OP2	2:2B:89:G:H8	2.03	0.42
6:2G:142:PRO:HG2	6:2G:143:GLU:OE1	2.20	0.42
32:2a:19:C:H5''	36:2e:86:ALA:HB3	2.01	0.42
33:2b:114:ARG:O	33:2b:118:LEU:HG	2.18	0.42
46:2o:82:ILE:O	46:2o:86:GLY:N	2.52	0.42
48:2q:43:LEU:HD22	48:2q:68:ARG:HH11	1.85	0.42
1:1A:724:U:H2'	1:1A:725:G:O4'	2.19	0.42
1:1A:1071:G:N3	1:1A:1089:G:O2'	2.42	0.42
1:1A:1702:G:H2'	1:1A:1703:G:O4'	2.19	0.42
1:1A:2100:G:C5	1:1A:2190:G:C6	3.07	0.42
5:1F:74:ARG:H	5:1F:74:ARG:HG3	1.43	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:1H:23:ARG:HD2	7:1H:34:GLU:OE1	2.19	0.42
12:1Q:38:GLU:HA	12:1Q:99:PRO:HG3	2.01	0.42
30:18:62:LEU:HB3	30:18:65:GLU:HG2	2.02	0.42
32:1a:448:A:C4	32:1a:487:A:C2	3.07	0.42
32:1a:1318:A:OP1	50:1s:7:LYS:NZ	2.49	0.42
32:1a:1329:A:P	44:1m:28:ALA:HB3	2.60	0.42
37:1f:8:ILE:HD12	37:1f:63:TYR:HE2	1.84	0.42
40:1i:31:GLN:HE21	40:1i:36:TYR:HD1	1.68	0.42
40:1i:55:ALA:HB1	40:1i:59:PHE:HD2	1.85	0.42
41:1j:61:GLU:OE2	45:1n:49:HIS:HE1	2.02	0.42
42:1k:69:ALA:HB1	42:1k:103:LEU:HD12	2.01	0.42
46:1o:29:VAL:HB	46:1o:81:LEU:HD21	2.01	0.42
52:1u:5:ASP:O	52:1u:11:GLY:HA3	2.18	0.42
1:2A:469:G:OP2	62:2A:3848:HOH:O	2.21	0.42
1:2A:1297:C:OP1	1:2A:2710:C:H4'	2.19	0.42
1:2A:1814:G:H4'	3:2D:51:VAL:HG21	2.02	0.42
1:2A:2165:G:H2'	1:2A:2166:G:O4'	2.18	0.42
6:2G:82:LEU:HA	6:2G:86:MET:SD	2.60	0.42
17:2V:14:VAL:HG12	17:2V:18:LEU:HD23	2.00	0.42
19:2X:65:ARG:HE	19:2X:70:LEU:CD2	2.32	0.42
32:2a:189(K):U:H2'	32:2a:189(L):G:C8	2.55	0.42
32:2a:273:A:H1'	48:2q:16:GLN:NE2	2.35	0.42
32:2a:736:C:H2'	32:2a:737:A:C8	2.55	0.42
32:2a:848:C:H2'	32:2a:849:C:H6	1.83	0.42
32:2a:1340:A:OP1	53:2y:57:PRO:HB3	2.19	0.42
33:2b:121:LEU:O	33:2b:127:ILE:HG12	2.18	0.42
35:2d:111:ALA:HB1	35:2d:116:GLN:HE21	1.84	0.42
5:1F:183:VAL:HG13	62:1F:439:HOH:O	2.18	0.42
6:1G:126:ASP:HB3	6:1G:128:ARG:H	1.84	0.42
32:1a:765:G:C6	32:1a:812:C:C2	3.07	0.42
32:1a:1015:A:O3'	45:1n:15:LYS:NZ	2.53	0.42
32:1a:1102:A:O3'	33:1b:96:ARG:NH2	2.46	0.42
32:1a:1410:G:H2'	32:1a:1411:C:C6	2.53	0.42
33:1b:130:ARG:NH2	33:1b:134:GLU:OE2	2.52	0.42
35:1d:59:ARG:HH22	35:1d:66:ARG:HH12	1.67	0.42
46:1o:87:ILE:O	46:1o:88:ARG:C	2.63	0.42
1:2A:185:U:H2'	1:2A:186:G:H8	1.83	0.42
1:2A:729:G:C6	3:2D:208:LYS:HB2	2.54	0.42
1:2A:2328:A:H2'	1:2A:2329:G:C8	2.54	0.42
1:2A:2626:C:H2'	1:2A:2627:G:O4'	2.19	0.42
6:2G:111:LEU:HB2	6:2G:112:PRO:HD3	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:2H:9:ILE:HB	7:2H:50:VAL:HG23	2.02	0.42
32:2a:1366:C:H2'	32:2a:1367:C:C6	2.54	0.42
32:2a:1387:G:H2'	32:2a:1388:C:C6	2.55	0.42
42:2k:48:ILE:HD13	42:2k:48:ILE:HA	1.81	0.42
1:1A:824:A:H1'	1:1A:2358:G:N7	2.35	0.42
1:1A:1588:C:H2'	1:1A:1589:C:H6	1.82	0.42
1:1A:2114:A:H2'	1:1A:2115:G:O4'	2.20	0.42
1:1A:2347:C:H2'	1:1A:2348:U:C6	2.55	0.42
1:1A:2820:A:P	13:1R:2:ARG:HH22	2.41	0.42
1:1A:2869:G:H2'	1:1A:2870:C:O4'	2.19	0.42
2:1B:29:A:H2'	2:1B:30:C:O4'	2.19	0.42
4:1E:119:ARG:HD2	4:1E:120:TRP:CE2	2.55	0.42
6:1G:16:ARG:O	6:1G:20:ILE:HG13	2.19	0.42
26:14:58:ARG:HB3	50:1s:64:GLU:O	2.19	0.42
32:1a:142:G:H2'	32:1a:143:A:H8	1.84	0.42
32:1a:160:A:H2'	32:1a:161:A:O4'	2.20	0.42
32:1a:718:G:H5'	42:1k:117:ASN:HB2	2.00	0.42
32:1a:1003:G:H8	32:1a:1003:G:O5'	2.03	0.42
32:1a:1151:A:O2'	32:1a:1152:A:H8	2.00	0.42
32:1a:1292:U:H5'	40:1i:38:GLN:OE1	2.20	0.42
1:2A:57:C:H2'	1:2A:58:G:O4'	2.20	0.42
1:2A:476:G:H4'	1:2A:502:A:N1	2.35	0.42
1:2A:489:G:N7	18:2W:49:LYS:NZ	2.68	0.42
1:2A:784:A:C8	1:2A:792:G:C5	3.07	0.42
1:2A:1053:C:H4'	1:2A:1054:A:OP1	2.19	0.42
1:2A:1057:A:N7	1:2A:1086:A:H2'	2.34	0.42
1:2A:1495:A:H2'	1:2A:1496:A:C8	2.54	0.42
1:2A:2031:A:C6	1:2A:2498:C:H1'	2.54	0.42
1:2A:2441:C:OP2	1:2A:2586:C:O2'	2.34	0.42
1:2A:2443:C:OP1	5:2F:68:LYS:HD3	2.20	0.42
1:2A:2543:G:H2'	1:2A:2544:G:C8	2.53	0.42
9:2N:75:TYR:CE2	9:2N:77:GLY:HA2	2.55	0.42
10:2O:101:PRO:HB3	10:2O:120:GLU:HB3	2.01	0.42
15:2T:117:ASP:OD2	15:2T:120:ARG:NE	2.36	0.42
24:22:51:ARG:O	24:22:55:ARG:HG3	2.19	0.42
27:25:11:THR:HG23	27:25:15:ARG:HB3	2.02	0.42
32:2a:1054:C:H4'	32:2a:1055:A:O5'	2.19	0.42
32:2a:1129:C:H1'	32:2a:1130:A:N7	2.34	0.42
32:2a:1226:C:H4'	50:2s:80:TYR:OH	2.18	0.42
32:2a:1323:G:H4'	32:2a:1363:C:C2	2.54	0.42
32:2a:1445:C:H2'	32:2a:1446:U:O4'	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:2b:73:THR:HA	33:2b:94:ASN:O	2.20	0.42
42:2k:59:TYR:CE2	42:2k:63:LEU:HD11	2.54	0.42
1:1A:288:C:H2'	1:1A:289:A:H8	1.85	0.42
1:1A:1508:A:H4'	1:1A:1509(A):A:C5	2.55	0.42
1:1A:1798:U:H5'	3:1D:259:THR:CG2	2.40	0.42
1:1A:2441:C:OP2	1:1A:2586:C:O2'	2.31	0.42
1:1A:2850:A:C2	1:1A:2851:A:C4	3.08	0.42
18:1W:23:LEU:HD12	18:1W:23:LEU:HA	1.88	0.42
24:12:55:ARG:NH1	62:12:101:HOH:O	2.22	0.42
32:1a:152:A:N6	32:1a:170:U:C2	2.88	0.42
32:1a:674:G:N2	32:1a:717:C:O2	2.52	0.42
32:1a:1269:A:H2	32:1a:1312:G:N3	2.17	0.42
32:1a:1316:G:N2	32:1a:1318:A:H3'	2.34	0.42
32:1a:1457:G:H2'	32:1a:1458:G:H8	1.85	0.42
33:1b:127:ILE:HG22	33:1b:130:ARG:HG2	2.01	0.42
35:1d:108:LEU:HD23	35:1d:110:PHE:CZ	2.54	0.42
35:1d:168:ARG:HD3	35:1d:168:ARG:HA	1.24	0.42
40:1i:5:TYR:HE1	40:1i:16:ARG:HB3	1.84	0.42
42:1k:84:VAL:HG11	42:1k:91:ARG:HD2	2.00	0.42
44:1m:4:ILE:HA	44:1m:5:ALA:HA	1.58	0.42
1:2A:195:A:H2'	1:2A:198:C:N4	2.35	0.42
1:2A:2706:G:N7	62:2A:3944:HOH:O	2.37	0.42
2:2B:22:U:H2'	2:2B:23:G:C8	2.55	0.42
13:2R:9:LYS:O	13:2R:17:ARG:HD3	2.20	0.42
23:21:80:LEU:HB3	23:21:82:LEU:HG	2.01	0.42
32:2a:664:G:P	49:2r:64:ARG:HH21	2.43	0.42
32:2a:685:G:C2	32:2a:686:U:C4	3.07	0.42
32:2a:1118:C:H1'	32:2a:1179:A:C4	2.55	0.42
33:2b:74:LYS:H	33:2b:74:LYS:HG3	1.63	0.42
35:2d:108:LEU:HD11	35:2d:174:LEU:HB3	2.00	0.42
44:2m:57:ARG:C	44:2m:59:TYR:H	2.27	0.42
50:2s:12:ASP:OD2	50:2s:35:SER:HB3	2.19	0.42
50:2s:31:ILE:HB	50:2s:49:ILE:HG13	2.02	0.42
1:1A:1364:G:OP2	23:11:3:LYS:HD3	2.20	0.42
1:1A:2784:C:H1'	4:1E:37:ARG:NH1	2.34	0.42
62:1A:4223:HOH:O	18:1W:83:LYS:NZ	2.50	0.42
6:1G:21:ARG:C	6:1G:21:ARG:HD3	2.45	0.42
9:1N:96:GLU:H	9:1N:96:GLU:CD	2.28	0.42
14:1S:3:ARG:HA	14:1S:3:ARG:HD3	1.82	0.42
14:1S:58:LEU:HA	14:1S:58:LEU:HD23	1.81	0.42
25:13:8:LEU:HG	25:13:31:LEU:HD23	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:694:A:OP1	42:1k:53:SER:OG	2.30	0.42
32:1a:933:G:OP2	38:1g:3:ARG:HB2	2.19	0.42
39:1h:25:ASP:OD1	39:1h:60:ARG:HG3	2.20	0.42
41:1j:55:LYS:HB2	41:1j:56:HIS:H	1.65	0.42
49:1r:31:LEU:HD12	49:1r:31:LEU:HA	1.93	0.42
50:1s:12:ASP:O	50:1s:14:HIS:N	2.45	0.42
50:1s:12:ASP:OD2	50:1s:37:ARG:HD2	2.20	0.42
1:2A:391:G:H1'	1:2A:411:G:O4'	2.20	0.42
1:2A:1203:G:O6	62:2A:3849:HOH:O	2.21	0.42
1:2A:2168:G:O2'	1:2A:2170:A:N7	2.42	0.42
1:2A:2169:A:H3'	1:2A:2170:A:C8	2.55	0.42
1:2A:2207:G:H2'	1:2A:2208:A:C2	2.55	0.42
1:2A:2507:C:H2'	1:2A:2508:G:O4'	2.20	0.42
5:2F:137:LYS:HA	5:2F:140:LEU:HB2	2.01	0.42
32:2a:31:G:O2'	32:2a:48:C:N4	2.52	0.42
32:2a:632:A:OP2	32:2a:632:A:H8	2.03	0.42
32:2a:975:A:N1	41:2j:48:THR:HB	2.35	0.42
32:2a:1328:C:H2'	32:2a:1329:A:O4'	2.20	0.42
32:2a:1363(A):A:H1'	32:2a:1365:G:N7	2.34	0.42
32:2a:1503:A:OP1	32:2a:1531:A:O2'	2.37	0.42
33:2b:119:GLU:OE1	33:2b:142:LEU:HD21	2.19	0.42
34:2c:111:LEU:HD12	34:2c:204:LEU:HD23	2.00	0.42
34:2c:117:ALA:HB1	34:2c:198:VAL:HG23	2.02	0.42
39:2h:10:LEU:HD22	39:2h:83:ILE:HD11	2.02	0.42
1:1A:272(A):U:H5'	1:1A:272(B):G:OP2	2.20	0.42
1:1A:1843:C:H5'	3:1D:253:GLN:NE2	2.34	0.42
1:1A:2061:G:O6	54:1w:76:PPU:HM3	2.20	0.42
1:1A:2772:C:OP1	4:1E:202:LYS:NZ	2.40	0.42
1:1A:2788:C:OP1	4:1E:61:ARG:NH2	2.53	0.42
4:1E:29:GLY:HA3	62:1E:409:HOH:O	2.19	0.42
10:1O:70:LYS:HB3	10:1O:70:LYS:HE2	1.86	0.42
15:1T:54:ARG:HG2	62:1T:311:HOH:O	2.20	0.42
19:1X:60:ARG:NH1	29:17:47:ARG:HH12	2.17	0.42
19:1X:76:ARG:NH1	62:1X:102:HOH:O	2.52	0.42
32:1a:35:G:H21	43:1l:118:SER:HB2	1.85	0.42
35:1d:36:ARG:HD2	35:1d:38:TYR:OH	2.20	0.42
47:1p:69:THR:O	47:1p:73:LEU:HG	2.20	0.42
48:1q:85:VAL:O	48:1q:89:LEU:HG	2.20	0.42
50:1s:11:VAL:HG11	50:1s:16:LEU:HB2	2.02	0.42
1:2A:171:G:H2'	1:2A:172:C:H6	1.85	0.42
1:2A:191:A:H2'	1:2A:192:C:C6	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1827:C:C2'	1:2A:1828:G:H5'	2.50	0.42
1:2A:1889:A:H2'	1:2A:1890:A:C8	2.55	0.42
1:2A:2286:A:H4'	1:2A:2287:A:O4'	2.20	0.42
1:2A:2365:G:N7	30:28:39:LYS:HE3	2.35	0.42
1:2A:2506:U:C2	1:2A:2585:U:O4	2.72	0.42
1:2A:2690:C:OP1	13:2R:17:ARG:NH2	2.53	0.42
3:2D:221:VAL:HG22	3:2D:226:MET:HE3	2.02	0.42
4:2E:13:ARG:HG2	15:2T:58:ASN:HD21	1.84	0.42
6:2G:36:LYS:HE3	6:2G:95:ARG:NH2	2.35	0.42
6:2G:61:ALA:O	6:2G:65:GLY:N	2.53	0.42
16:2U:97:ASP:OD1	16:2U:101:ARG:HD2	2.19	0.42
26:24:46:GLN:HG2	26:24:48:ARG:HH22	1.85	0.42
32:2a:1062:U:H2'	32:2a:1063:C:C6	2.55	0.42
35:2d:108:LEU:HB3	35:2d:110:PHE:CD1	2.55	0.42
53:2y:24:LEU:HD23	53:2y:78:ILE:HD12	2.01	0.42
53:2y:78:ILE:HG12	53:2y:78:ILE:H	1.64	0.42
1:1A:315:G:H2'	1:1A:316:C:C6	2.55	0.41
1:1A:839:U:H1'	1:1A:1191:G:H1'	2.01	0.41
1:1A:2097:C:H2'	1:1A:2098:U:O4'	2.20	0.41
1:1A:2171:A:H1'	1:1A:2172:U:C6	2.54	0.41
6:1G:124:SER:HB2	6:1G:131:TYR:CE1	2.55	0.41
15:1T:28:VAL:HG13	15:1T:86:ILE:HG23	2.02	0.41
21:1Z:182:LYS:HB3	21:1Z:182:LYS:HE2	1.79	0.41
26:14:15:ILE:HD12	26:14:21:VAL:HG22	2.02	0.41
32:1a:302:G:O2'	32:1a:556:C:H5''	2.20	0.41
32:1a:575:G:O2'	32:1a:821:G:H5'	2.20	0.41
32:1a:625:G:H2'	32:1a:626:U:C6	2.54	0.41
32:1a:1468:A:H8	32:1a:1468:A:O5'	2.03	0.41
33:1b:158:LEU:HG	33:1b:182:ILE:HD11	2.01	0.41
40:1i:50:LEU:HD12	40:1i:51:ARG:H	1.85	0.41
43:1l:8:ASN:O	43:1l:12:ARG:HG3	2.20	0.41
43:1l:28:LYS:HA	43:1l:28:LYS:HE2	2.02	0.41
1:2A:208:C:H2'	1:2A:209:C:C6	2.55	0.41
1:2A:1082:U:H6	1:2A:1082:U:H2'	1.64	0.41
1:2A:1592:C:H2'	1:2A:1593:G:C8	2.55	0.41
1:2A:2526:G:H5'	1:2A:2742:C:O2'	2.20	0.41
1:2A:2880:C:O3'	13:2R:90:ARG:NH1	2.53	0.41
26:24:46:GLN:C	26:24:48:ARG:H	2.27	0.41
31:29:13:LYS:HG2	31:29:28:GLU:OE2	2.20	0.41
32:2a:420:U:O2'	32:2a:423:G:O6	2.31	0.41
32:2a:524:G:H2'	32:2a:525:C:C6	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:803:G:OP1	62:2a:3210:HOH:O	2.22	0.41
33:2b:47:THR:HA	33:2b:202:PRO:HG2	2.01	0.41
34:2c:180:ALA:HA	34:2c:206:GLU:HA	2.01	0.41
37:2f:100:ASN:HD22	37:2f:100:ASN:HA	1.75	0.41
38:2g:78:ARG:HE	38:2g:80:VAL:HG21	1.85	0.41
39:2h:88:LYS:O	39:2h:92:ARG:HD3	2.21	0.41
50:2s:51:VAL:O	50:2s:57:HIS:HA	2.21	0.41
1:1A:93:G:H2'	1:1A:94:C:C6	2.55	0.41
1:1A:897:C:H2'	1:1A:898:C:C6	2.54	0.41
1:1A:2112:G:H8	1:1A:2112:G:OP2	2.03	0.41
1:1A:2615:U:H2'	1:1A:2616:C:C6	2.55	0.41
62:1A:5799:HOH:O	5:1F:74:ARG:HG3	2.20	0.41
6:1G:66:GLN:NE2	6:1G:93:THR:O	2.50	0.41
6:1G:77:ILE:H	6:1G:82:LEU:HB3	1.86	0.41
9:1N:20:GLY:HA2	9:1N:61:ARG:HG2	2.02	0.41
10:1O:49:ARG:NH1	32:1a:1422:G:O3'	2.53	0.41
32:1a:657:G:C2	32:1a:658:G:C8	3.08	0.41
40:1i:14:VAL:HB	40:1i:66:ARG:HH22	1.85	0.41
40:1i:66:ARG:NH2	40:1i:66:ARG:HB2	2.35	0.41
1:2A:271(P):C:OP1	8:2I:45:LYS:HD3	2.20	0.41
1:2A:271(X):G:C2	1:2A:271(Y):U:O4	2.73	0.41
1:2A:1410:G:H2'	1:2A:1411:C:H6	1.84	0.41
1:2A:2556:C:H2'	1:2A:2557:G:O4'	2.20	0.41
7:2H:117:PRO:HA	7:2H:118:PRO:HD3	1.83	0.41
12:2Q:58:PHE:C	12:2Q:60:ARG:H	2.28	0.41
17:2V:23:GLU:HB2	62:2V:302:HOH:O	2.19	0.41
32:2a:1157:A:H4'	32:2a:1158:C:O5'	2.20	0.41
32:2a:1279:A:N3	32:2a:1279:A:H2'	2.34	0.41
32:2a:1465:C:H2'	32:2a:1466:C:O4'	2.20	0.41
34:2c:40:ARG:O	34:2c:44:GLU:HG2	2.20	0.41
34:2c:149:ALA:HA	34:2c:201:TYR:O	2.20	0.41
43:2l:71:PRO:O	43:2l:102:ARG:NH1	2.51	0.41
44:2m:102:ARG:HB3	44:2m:102:ARG:HH11	1.85	0.41
46:2o:3:ILE:H	46:2o:3:ILE:HD12	1.85	0.41
1:1A:531:C:H4'	1:1A:532:A:H5''	2.02	0.41
1:1A:1843:C:H5'	3:1D:253:GLN:HE22	1.86	0.41
1:1A:2319:G:N1	14:1S:3:ARG:HA	2.35	0.41
1:1A:2691:C:O3'	1:1A:2871:C:H4'	2.20	0.41
1:1A:2695:C:H2'	1:1A:2696:U:C6	2.56	0.41
1:1A:2803:C:H2'	1:1A:2804:C:C6	2.55	0.41
13:1R:2:ARG:HG2	13:1R:5:LYS:HB2	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:1T:26:ASP:OD1	15:1T:120:ARG:NH2	2.44	0.41
58:1T:208:MPD:H11	58:1T:208:MPD:H4	1.82	0.41
32:1a:161:A:H8	32:1a:161:A:O5'	2.03	0.41
32:1a:390:C:H2'	32:1a:391:G:C8	2.56	0.41
32:1a:619:U:O2	35:1d:133:VAL:HA	2.20	0.41
32:1a:1158:C:O3'	33:1b:133:LYS:NZ	2.53	0.41
35:1d:173:TRP:CD1	35:1d:189:PRO:HB3	2.55	0.41
36:1e:56:GLN:HE21	36:1e:56:GLN:HB3	1.62	0.41
37:1f:21:LEU:HA	37:1f:21:LEU:HD13	1.82	0.41
1:2A:241:A:H5''	62:2A:5489:HOH:O	2.19	0.41
1:2A:277:C:O2	1:2A:277:C:H2'	2.20	0.41
1:2A:1091:G:N3	1:2A:1091:G:H2'	2.35	0.41
1:2A:1262:A:O2'	62:2A:3852:HOH:O	2.21	0.41
1:2A:1570:A:H2'	1:2A:1571:A:C8	2.55	0.41
1:2A:1826:G:H4'	3:2D:242:ARG:CZ	2.50	0.41
17:2V:24:LYS:HG3	17:2V:64:HIS:HD2	1.85	0.41
24:22:68:ARG:O	24:22:70:GLN:N	2.50	0.41
26:24:8:LYS:HE2	26:24:8:LYS:HB3	1.77	0.41
26:24:13:ARG:NH1	26:24:23:GLU:HB3	2.35	0.41
32:2a:60:A:H4'	32:2a:61:G:O5'	2.21	0.41
32:2a:786:G:C2	32:2a:797:C:C2	3.09	0.41
32:2a:1162:C:H2'	32:2a:1163:C:H6	1.85	0.41
33:2b:69:LEU:HD13	33:2b:91:PRO:HB2	2.01	0.41
35:2d:64:LEU:HB2	35:2d:198:VAL:HG11	2.02	0.41
36:2e:6:PHE:HB2	36:2e:63:ARG:HH12	1.84	0.41
44:2m:20:THR:HA	44:2m:25:ILE:O	2.20	0.41
47:2p:23:ASP:OD1	47:2p:25:ARG:HG3	2.20	0.41
50:2s:41:VAL:HG13	50:2s:43:GLU:N	2.33	0.41
1:1A:922:U:H2'	1:1A:923:C:C6	2.55	0.41
1:1A:2563:U:H4'	10:1O:28:SER:HA	2.03	0.41
1:1A:2630:G:H2'	1:1A:2631:G:H8	1.86	0.41
3:1D:34:VAL:HG12	3:1D:63:ARG:HG3	2.02	0.41
5:1F:8:GLN:HE22	5:1F:21:ALA:HB2	1.85	0.41
6:1G:16:ARG:HB2	6:1G:17:PRO:HD3	2.03	0.41
38:1g:100:ALA:O	38:1g:104:LEU:HD23	2.20	0.41
39:1h:73:ASP:OD1	39:1h:75:ARG:HG3	2.21	0.41
42:1k:27:ASN:OD1	42:1k:28:THR:N	2.51	0.41
1:2A:2140:C:H2'	1:2A:2141:G:C8	2.52	0.41
1:2A:2438:U:O2'	1:2A:2440:C:OP1	2.37	0.41
1:2A:2660:A:H2'	1:2A:2661:G:O4'	2.21	0.41
8:2I:65:ALA:HB1	8:2I:132:PRO:HG2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:2I:83:ALA:HB2	8:2I:88:ILE:HG22	2.03	0.41
9:2N:73:THR:HB	9:2N:82:LEU:HD11	2.02	0.41
32:2a:190:U:H2'	32:2a:191:G:H8	1.85	0.41
32:2a:413:G:O6	35:2d:35:ARG:HD2	2.19	0.41
32:2a:947:G:O3'	44:2m:109:THR:OG1	2.38	0.41
32:2a:1003:G:C6	32:2a:1004:A:H1'	2.56	0.41
32:2a:1178:G:N2	32:2a:1180:A:H3'	2.35	0.41
32:2a:1318:A:O2'	50:2s:37:ARG:HB3	2.20	0.41
32:2a:1366:C:H2'	32:2a:1367:C:H6	1.85	0.41
32:2a:1447:A:H5''	32:2a:1452:C:OP2	2.20	0.41
34:2c:131:ARG:HD2	34:2c:131:ARG:HA	1.87	0.41
35:2d:57:ARG:HG2	35:2d:202:LEU:O	2.21	0.41
39:2h:112:LEU:HB3	39:2h:133:LEU:HA	2.03	0.41
40:2i:37:PHE:CZ	40:2i:74:ILE:HG12	2.55	0.41
1:1A:81:G:HO2'	1:1A:295:G:HO2'	1.66	0.41
1:1A:443:A:H1'	1:1A:1201:C:O4'	2.21	0.41
1:1A:729:G:C5	3:1D:208:LYS:HB2	2.56	0.41
1:1A:1783:A:H5'	1:1A:2608:G:H4'	2.02	0.41
1:1A:2114:A:O2'	1:1A:2168:G:OP1	2.38	0.41
4:1E:3:GLY:HA3	4:1E:81:ILE:HD12	2.03	0.41
5:1F:188:ARG:HA	11:1P:3:LEU:CD1	2.50	0.41
6:1G:179:PRO:HB2	26:14:42:PHE:HE2	1.86	0.41
9:1N:42:TRP:CH2	9:1N:44:PRO:HB3	2.56	0.41
12:1Q:109:VAL:HG22	12:1Q:113:GLN:CD	2.46	0.41
15:1T:28:VAL:O	15:1T:46:GLU:HA	2.21	0.41
32:1a:1446:U:O2'	32:1a:1447:A:H3'	2.20	0.41
37:1f:61:LEU:HD13	37:1f:63:TYR:OH	2.21	0.41
38:1g:111:ARG:HD3	38:1g:113:GLU:OE2	2.21	0.41
1:2A:534:U:H2'	1:2A:535:C:C6	2.56	0.41
1:2A:782:A:H5'	1:2A:783:A:N7	2.35	0.41
1:2A:855:G:H2'	1:2A:856:C:C6	2.56	0.41
1:2A:1324:G:C4	1:2A:1328:G:O6	2.73	0.41
1:2A:1784:A:H4'	1:2A:1785:A:O5'	2.20	0.41
1:2A:2630:G:H2'	1:2A:2631:G:C8	2.55	0.41
2:2B:50:G:OP1	14:2S:63:THR:OG1	2.38	0.41
26:24:18:CYS:SG	26:24:39:CYS:HB3	2.60	0.41
32:2a:939:G:H2'	32:2a:940:C:C6	2.55	0.41
35:2d:182:LYS:HE2	35:2d:182:LYS:HB3	1.88	0.41
38:2g:111:ARG:NH1	38:2g:113:GLU:OE2	2.54	0.41
44:2m:15:VAL:HG23	44:2m:41:PRO:HA	2.02	0.41
1:1A:1060:U:C4	1:1A:1088:A:C5	3.08	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1B:88:C:H2'	2:1B:89:G:O4'	2.21	0.41
14:1S:27:SER:O	14:1S:37:ALA:HA	2.20	0.41
16:1U:78:THR:HG22	16:1U:117:GLN:HE22	1.86	0.41
23:11:80:LEU:HB3	23:11:82:LEU:HG	2.01	0.41
32:1a:33:A:N3	43:1l:32:PHE:HE2	2.19	0.41
32:1a:195:A:C6	32:1a:196:A:N1	2.89	0.41
32:1a:270:A:H2'	32:1a:271:C:C6	2.56	0.41
32:1a:1004:A:N7	32:1a:1036:G:N1	2.69	0.41
32:1a:1015:A:C6	32:1a:1016:A:C6	3.09	0.41
32:1a:1124:G:N2	32:1a:1125:U:O4	2.48	0.41
32:1a:1144:G:O2'	32:1a:1145:C:H5'	2.21	0.41
32:1a:1525:G:OP1	42:1k:120:ARG:NH2	2.54	0.41
33:1b:28:PHE:CD1	33:1b:190:THR:HA	2.55	0.41
36:1e:100:VAL:HG13	36:1e:118:ILE:HG22	2.03	0.41
50:1s:11:VAL:C	50:1s:13:ASP:H	2.29	0.41
1:2A:116:C:H2'	1:2A:117:G:O4'	2.21	0.41
1:2A:455:C:N3	1:2A:472:A:H2'	2.36	0.41
1:2A:483:A:O4'	20:2Y:48:ALA:HB1	2.20	0.41
1:2A:566:U:H5''	11:2P:29:LYS:HE3	2.03	0.41
1:2A:1316:U:H2'	1:2A:1317:A:C8	2.55	0.41
1:2A:1598:C:O3'	19:2X:35:THR:HG23	2.21	0.41
1:2A:1742:G:H2'	1:2A:1743:C:C6	2.55	0.41
1:2A:2028:U:H2'	1:2A:2029:G:O4'	2.21	0.41
1:2A:2206:G:H5''	1:2A:2207:G:N7	2.35	0.41
1:2A:2847:U:OP1	15:2T:98:LYS:NZ	2.50	0.41
2:2B:51:G:OP2	14:2S:61:ASN:HA	2.20	0.41
19:2X:57:LEU:HD11	19:2X:78:LYS:HE3	2.02	0.41
26:24:48:ARG:HB3	26:24:52:THR:HA	2.02	0.41
32:2a:300:A:H1'	32:2a:565:U:O2	2.21	0.41
32:2a:666:G:H5'	32:2a:726:C:H1'	2.03	0.41
32:2a:1143:G:H2'	32:2a:1144:G:H8	1.85	0.41
32:2a:1251:A:H2'	32:2a:1252:A:C8	2.55	0.41
32:2a:1305:G:H22	32:2a:1331:G:H1'	1.85	0.41
32:2a:1426:C:H2'	32:2a:1427:U:C6	2.55	0.41
36:2e:71:LEU:HD21	36:2e:115:VAL:HG22	2.02	0.41
36:2e:95:ALA:HB1	36:2e:96:PRO:HD2	2.02	0.41
36:2e:152:ARG:HB3	39:2h:43:GLY:O	2.21	0.41
42:2k:62:GLN:HG3	42:2k:97:ALA:HB2	2.03	0.41
42:2k:67:ASP:OD2	42:2k:71:LYS:NZ	2.41	0.41
1:1A:1054:A:N6	1:1A:1105:U:H3	2.16	0.41
1:1A:1790:C:H2'	1:1A:1791:A:C5	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2137:C:C2	1:1A:2154:G:N2	2.85	0.41
1:1A:2584:U:H5'	54:1w:76:PPU:H103	2.03	0.41
6:1G:115:ARG:HB3	6:1G:136:ARG:HH22	1.86	0.41
6:1G:135:LEU:O	6:1G:154:GLY:HA3	2.20	0.41
9:1N:14:VAL:HG22	9:1N:138:LEU:HG	2.02	0.41
19:1X:61:GLY:HA3	19:1X:73:ARG:O	2.21	0.41
21:1Z:25:PRO:O	21:1Z:85:HIS:HA	2.20	0.41
26:14:57:GLU:HB2	26:14:58:ARG:CA	2.51	0.41
32:1a:130:A:H5'	48:1q:63:ARG:NH1	2.36	0.41
32:1a:441:A:H8	32:1a:441:A:OP2	2.04	0.41
32:1a:491:G:H2'	32:1a:492:G:O4'	2.20	0.41
32:1a:744:C:O2'	32:1a:851:G:N2	2.53	0.41
32:1a:1288:A:H2'	32:1a:1289:A:O4'	2.21	0.41
33:1b:188:ALA:O	33:1b:202:PRO:HA	2.21	0.41
34:1c:74:GLY:O	34:1c:78:GLY:N	2.53	0.41
35:1d:59:ARG:HH11	35:1d:59:ARG:HD3	1.76	0.41
42:1k:70:LYS:HA	42:1k:73:MET:HE2	2.02	0.41
44:1m:35:GLU:H	44:1m:35:GLU:HG3	1.52	0.41
1:2A:752:A:H3'	29:27:1:MET:HE2	2.03	0.41
1:2A:885:C:H2'	1:2A:886:C:O4'	2.21	0.41
1:2A:1429:G:H2'	1:2A:1430:C:C6	2.56	0.41
1:2A:1827:C:O2'	1:2A:1970:A:N3	2.39	0.41
1:2A:1831:G:H2'	1:2A:1832:C:C6	2.56	0.41
1:2A:2484:G:C2	1:2A:2485:G:C8	3.08	0.41
1:2A:2658:C:H5''	7:2H:158:HIS:HD2	1.86	0.41
7:2H:86:GLU:OE1	7:2H:130:ARG:HD2	2.21	0.41
7:2H:118:PRO:HD2	7:2H:121:ILE:HB	2.02	0.41
15:2T:6:LEU:HD12	15:2T:6:LEU:HA	1.78	0.41
32:2a:20:U:H2'	32:2a:21:G:O4'	2.20	0.41
32:2a:1269:A:N1	32:2a:1312:G:O2'	2.42	0.41
35:2d:105:VAL:HG13	35:2d:110:PHE:HB2	2.03	0.41
35:2d:114:ARG:O	35:2d:118:ARG:N	2.48	0.41
39:2h:103:VAL:HG21	39:2h:110:ALA:HB2	2.02	0.41
1:1A:817:C:H4'	1:1A:932:G:C5	2.56	0.41
1:1A:1021:A:N3	1:1A:1021:A:H3'	2.36	0.41
1:1A:1071:G:C2	1:1A:1072:C:C2	3.08	0.41
1:1A:1582:C:H2'	1:1A:1583:A:O4'	2.21	0.41
1:1A:2376:A:H2'	1:1A:2377:A:O4'	2.21	0.41
3:1D:245:PRO:HA	3:1D:246:PRO:HD3	1.94	0.41
9:1N:73:THR:HA	9:1N:83:LYS:O	2.21	0.41
11:1P:98:GLU:HG3	11:1P:102:ARG:NH2	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:1R:38:VAL:HB	13:1R:39:PRO:HD3	2.03	0.41
23:11:3:LYS:HB3	23:11:61:ARG:HH22	1.86	0.41
33:1b:63:MET:HB2	33:1b:63:MET:HE2	1.84	0.41
37:1f:100:ASN:HD21	49:1r:23:LYS:HE2	1.85	0.41
38:1g:59:LEU:O	38:1g:63:LYS:HG3	2.21	0.41
45:1n:35:ARG:HE	45:1n:35:ARG:HB3	1.57	0.41
1:2A:1075:C:C2	1:2A:1076:C:H3'	2.55	0.41
1:2A:1889:A:N1	1:2A:2234:G:H1'	2.36	0.41
1:2A:2349:G:OP2	30:28:42:ARG:NE	2.44	0.41
1:2A:2660:A:H8	1:2A:2660:A:OP1	2.04	0.41
1:2A:2682:U:OP2	62:2A:3854:HOH:O	2.22	0.41
4:2E:174:ASP:OD1	4:2E:175:VAL:N	2.54	0.41
7:2H:80:SER:OG	7:2H:81:GLU:N	2.53	0.41
11:2P:80:TYR:CD1	11:2P:111:ARG:HB2	2.55	0.41
32:2a:392:G:H2'	32:2a:393:A:H8	1.84	0.41
32:2a:592:G:H2'	32:2a:593:G:H8	1.85	0.41
32:2a:849:C:H2'	32:2a:850:U:O4'	2.20	0.41
32:2a:981:U:H5'	45:2n:21:TYR:CE2	2.56	0.41
33:2b:16:HIS:ND1	33:2b:16:HIS:C	2.79	0.41
33:2b:80:ILE:HD11	33:2b:212:GLN:HA	2.02	0.41
35:2d:112:VAL:HG13	35:2d:116:GLN:HE22	1.85	0.41
41:2j:50:ILE:HB	45:2n:41:ARG:NH1	2.36	0.41
46:2o:33:THR:HG23	46:2o:63:ARG:NH1	2.36	0.41
1:1A:305:U:H2'	1:1A:306:U:C6	2.56	0.41
1:1A:1082:U:C4	1:1A:1086:A:N1	2.81	0.41
1:1A:1239:G:H2'	1:1A:1240:U:O4'	2.21	0.41
1:1A:1495:A:H2'	1:1A:1496:A:C8	2.56	0.41
1:1A:1641:A:H2'	1:1A:1642:G:O4'	2.21	0.41
1:1A:1721:G:N1	1:1A:1739:U:OP2	2.54	0.41
1:1A:2119:A:C6	1:1A:2171:A:C5	3.09	0.41
1:1A:2135:A:C2	1:1A:2136:C:H1'	2.56	0.41
1:1A:2648:C:H2'	1:1A:2649:U:C6	2.55	0.41
3:1D:3:VAL:HG13	3:1D:17:THR:HB	2.02	0.41
7:1H:98:LEU:HD12	7:1H:98:LEU:HA	1.86	0.41
8:1I:14:ASP:O	8:1I:17:GLN:HB3	2.20	0.41
8:1I:77:LEU:HD12	8:1I:77:LEU:HA	1.93	0.41
9:1N:69:GLN:O	9:1N:71:ILE:HD12	2.21	0.41
10:1O:64:ARG:NH2	10:1O:99:PHE:O	2.54	0.41
13:1R:28:LEU:HD23	13:1R:48:VAL:HG21	2.02	0.41
20:1Y:23:ARG:HD2	62:1Y:302:HOH:O	2.21	0.41
20:1Y:92:ASN:HB2	20:1Y:94:LYS:H	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:13:4:LEU:O	25:13:36:VAL:HA	2.21	0.41
32:1a:461:A:O2'	32:1a:470:C:H5'	2.19	0.41
32:1a:503:C:H2'	32:1a:504:C:H6	1.85	0.41
32:1a:637:G:H2'	32:1a:638:G:C8	2.56	0.41
35:1d:61:LYS:HE2	35:1d:61:LYS:HB3	1.90	0.41
37:1f:8:ILE:HD13	37:1f:26:ILE:HD13	2.02	0.41
37:1f:99:ALA:HB1	49:1r:23:LYS:HE3	2.02	0.41
39:1h:51:VAL:HG11	39:1h:60:ARG:NH1	2.35	0.41
41:1j:84:GLN:NE2	41:1j:85:LEU:HG	2.36	0.41
44:1m:50:GLU:O	44:1m:54:VAL:HG22	2.21	0.41
47:1p:42:ARG:HB3	47:1p:44:THR:HG23	2.03	0.41
48:1q:20:THR:HG23	48:1q:43:LEU:HD12	2.02	0.41
50:1s:55:LYS:HG2	50:1s:56:GLN:HG2	2.03	0.41
53:1y:19:HIS:O	53:1y:23:ARG:HG2	2.21	0.41
1:2A:9:U:O4	1:2A:2629:A:H2	2.04	0.41
1:2A:320:A:H4'	1:2A:322:A:N7	2.35	0.41
1:2A:468:G:HO2'	5:2F:62:ARG:HH22	1.60	0.41
1:2A:523:C:H4'	1:2A:540:C:O2	2.20	0.41
1:2A:642:G:N2	1:2A:644:A:H3'	2.36	0.41
1:2A:937:U:H2'	1:2A:938:G:O4'	2.21	0.41
1:2A:1027:A:C6	1:2A:1126:A:C4	3.09	0.41
1:2A:1045:A:H5''	1:2A:1046:A:OP1	2.21	0.41
1:2A:1062:G:H2'	1:2A:1062:G:N3	2.35	0.41
1:2A:1504:C:H2'	1:2A:1505:C:C6	2.56	0.41
1:2A:1799:G:N2	3:2D:155:LEU:HD12	2.36	0.41
1:2A:2111:C:N4	1:2A:2147:G:H22	2.18	0.41
1:2A:2282:G:H4'	1:2A:2389:G:O2'	2.21	0.41
1:2A:2612:C:OP2	27:25:2:ALA:N	2.54	0.41
2:2B:42:C:O2	6:2G:93:THR:N	2.42	0.41
6:2G:143:GLU:OE1	6:2G:143:GLU:N	2.54	0.41
7:2H:150:ALA:HA	7:2H:153:LYS:HE3	2.02	0.41
15:2T:16:ARG:HG3	15:2T:18:ASP:OD1	2.21	0.41
17:2V:50:PRO:HG2	17:2V:51:VAL:HG12	2.02	0.41
20:2Y:1:MET:HE2	20:2Y:1:MET:HB3	1.87	0.41
26:24:48:ARG:O	26:24:50:VAL:N	2.48	0.41
26:24:64:GLY:C	26:24:66:SER:H	2.28	0.41
32:2a:509:A:O2'	32:2a:510:A:OP1	2.34	0.41
32:2a:580:U:H2'	32:2a:581:G:O4'	2.20	0.41
32:2a:848:C:O2'	32:2a:849:C:H5'	2.20	0.41
32:2a:1005:A:H8	32:2a:1005:A:OP2	2.03	0.41
32:2a:1011:G:C6	32:2a:1012:U:C4	3.09	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1054:C:H5'	32:2a:1054:C:O2	2.21	0.41
32:2a:1112:C:O2	34:2c:179:ARG:N	2.42	0.41
32:2a:1161:C:H2'	32:2a:1162:C:H6	1.86	0.41
33:2b:19:HIS:HE1	33:2b:206:ASP:OD2	2.04	0.41
33:2b:215:LEU:O	33:2b:219:VAL:HG23	2.21	0.41
34:2c:47:LEU:HB3	34:2c:52:LEU:HG	2.02	0.41
35:2d:141:ARG:H	35:2d:141:ARG:HG3	1.52	0.41
36:2e:77:PRO:HG2	36:2e:78:HIS:HD2	1.85	0.41
37:2f:69:GLU:H	37:2f:69:GLU:CD	2.22	0.41
38:2g:18:TYR:C	38:2g:20:ASP:H	2.29	0.41
40:2i:117:HIS:HB2	40:2i:121:ARG:HG3	2.03	0.41
43:2l:28:LYS:HE2	43:2l:28:LYS:HA	2.03	0.41
43:2l:103:GLY:N	43:2l:107:ALA:O	2.53	0.41
44:2m:106:ASN:N	44:2m:106:ASN:OD1	2.54	0.41
49:2r:66:LEU:O	49:2r:70:ILE:HG13	2.21	0.41
5:1F:7:TYR:CD2	5:1F:24:LEU:HB2	2.56	0.41
32:1a:1140:C:H2'	32:1a:1141:C:C6	2.55	0.41
35:1d:150:GLU:HG3	35:1d:151:LYS:N	2.36	0.41
40:1i:111:ARG:HG2	40:1i:112:LYS:N	2.35	0.41
44:1m:13:LYS:C	44:1m:44:ARG:HD3	2.46	0.41
1:2A:885:C:H2'	1:2A:886:C:C4'	2.51	0.41
1:2A:1993:U:H2'	1:2A:1994:C:O4'	2.21	0.41
1:2A:2116:G:OP2	1:2A:2165:G:N2	2.54	0.41
1:2A:2304:G:H22	1:2A:2312:U:H3	1.69	0.41
1:2A:2716:U:O2'	1:2A:2717:G:H5'	2.21	0.41
4:2E:48:GLN:NE2	4:2E:78:LEU:HD13	2.35	0.41
6:2G:14:GLU:C	6:2G:17:PRO:HD2	2.45	0.41
10:2O:4:PRO:O	10:2O:5:GLN:HB2	2.21	0.41
13:2R:36:THR:HG22	13:2R:37:THR:H	1.86	0.41
23:21:67:ILE:N	23:21:68:PRO:HD2	2.35	0.41
32:2a:457:C:C2'	32:2a:458:C:H5'	2.51	0.41
32:2a:881:G:OP2	43:2l:12:ARG:NH2	2.53	0.41
32:2a:1095:U:H2'	32:2a:1096:C:C6	2.56	0.41
32:2a:1135:U:H2'	32:2a:1137:C:N3	2.36	0.41
34:2c:6:HIS:ND1	45:2n:49:HIS:HB3	2.36	0.41
34:2c:19:GLU:HG2	34:2c:54:ARG:CZ	2.51	0.41
34:2c:110:ASN:O	34:2c:141:VAL:HG22	2.21	0.41
45:2n:3:ARG:O	45:2n:7:ILE:HG13	2.21	0.41
47:2p:20:VAL:HG21	47:2p:32:TYR:CD2	2.56	0.41
1:1A:375:C:H2'	1:1A:376:C:C6	2.57	0.40
1:1A:857:C:H1'	22:10:26:TYR:CE1	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2365:G:H4'	22:10:60:PHE:CZ	2.56	0.40
32:1a:1040:U:H2'	32:1a:1041:A:H8	1.86	0.40
32:1a:1064:G:O2'	32:1a:1190:G:N2	2.55	0.40
32:1a:1309:G:N7	44:1m:99:ARG:NH2	2.59	0.40
32:1a:1340:A:OP1	53:1y:57:PRO:HB3	2.21	0.40
38:1g:80:VAL:HB	38:1g:85:TYR:CD2	2.56	0.40
51:1t:57:ARG:NH1	51:1t:100:ILE:HD12	2.29	0.40
51:1t:72:LEU:HD23	51:1t:72:LEU:HA	1.88	0.40
1:2A:335:C:H4'	20:2Y:73:ARG:NH1	2.36	0.40
1:2A:583:G:OP2	16:2U:10:ARG:HD2	2.21	0.40
1:2A:1916:A:H2'	1:2A:1917:PSU:O4'	2.21	0.40
1:2A:2238:G:H2'	1:2A:2238:G:N3	2.36	0.40
1:2A:2823:A:OP1	4:2E:159:HIS:NE2	2.49	0.40
2:2B:42:C:C4	2:2B:43:C:C4	3.09	0.40
4:2E:35:GLN:OE1	4:2E:66:HIS:HE1	2.04	0.40
6:2G:165:THR:HG23	6:2G:168:GLU:OE2	2.20	0.40
9:2N:73:THR:HA	9:2N:83:LYS:O	2.21	0.40
10:2O:73:ASP:HB2	15:2T:82:LEU:HD13	2.03	0.40
19:2X:41:ASN:O	19:2X:45:THR:HG23	2.22	0.40
20:2Y:37:VAL:HG21	20:2Y:72:VAL:HG21	2.03	0.40
27:25:48:GLU:O	27:25:60:VAL:HG11	2.22	0.40
32:2a:328:C:H4'	32:2a:329:A:H5'	2.02	0.40
32:2a:430:A:H2'	32:2a:431:A:O4'	2.21	0.40
32:2a:542:G:H5'	35:2d:41:GLY:HA3	2.02	0.40
32:2a:559:A:H5'	32:2a:559:A:N3	2.37	0.40
32:2a:857:C:H2'	32:2a:858:G:O4'	2.21	0.40
32:2a:1054:C:H41	53:2y:46:GLN:HG3	1.86	0.40
32:2a:1291:G:H5''	40:2i:39:GLY:O	2.22	0.40
32:2a:1411:C:H2'	32:2a:1412:C:H6	1.86	0.40
32:2a:1429:C:H2'	32:2a:1430:C:C6	2.56	0.40
1:1A:27:G:C2	1:1A:512:G:N3	2.90	0.40
1:1A:876:C:H2'	1:1A:877:U:O4'	2.21	0.40
1:1A:1815:A:OP2	3:1D:54:ARG:NH2	2.44	0.40
1:1A:1913:A:N3	32:1a:1493:A:H8	2.18	0.40
1:1A:1971:A:OP1	62:1A:4118:HOH:O	2.21	0.40
62:1A:6359:HOH:O	11:1P:68:GLN:HG3	2.20	0.40
3:1D:132:PRO:HG3	3:1D:190:TYR:CE2	2.57	0.40
4:1E:119:ARG:HG2	4:1E:160:TYR:CG	2.56	0.40
5:1F:167:ALA:HB1	5:1F:173:VAL:HG11	2.03	0.40
26:14:15:ILE:HB	26:14:32:TYR:HD1	1.86	0.40
32:1a:264:U:H4'	48:1q:63:ARG:HD2	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:441:A:H3'	32:1a:442:C:H6	1.86	0.40
32:1a:616:G:O2'	32:1a:617:G:H5'	2.21	0.40
32:1a:1002:G:N1	32:1a:1003:G:C2	2.89	0.40
32:1a:1053:G:N7	32:1a:1200:C:H5''	2.37	0.40
32:1a:1118:C:H1'	32:1a:1179:A:C5	2.57	0.40
32:1a:1176:A:H2'	32:1a:1177:G:C8	2.56	0.40
34:1c:7:PRO:O	34:1c:11:ARG:NH1	2.51	0.40
35:1d:119:GLN:HG3	35:1d:123:HIS:CE1	2.57	0.40
35:1d:122:ARG:HA	35:1d:122:ARG:HD2	1.75	0.40
35:1d:129:ASN:N	35:1d:129:ASN:HD22	2.19	0.40
35:1d:173:TRP:CE3	35:1d:174:LEU:HG	2.56	0.40
44:1m:92:HIS:CE1	44:1m:98:VAL:HG21	2.56	0.40
47:1p:14:ASN:OD1	47:1p:16:HIS:HE1	2.04	0.40
1:2A:581:C:H2'	1:2A:582:G:H8	1.86	0.40
1:2A:1041:C:H42	1:2A:1114:G:H1	1.69	0.40
1:2A:1322:A:N1	1:2A:1333:C:O2'	2.43	0.40
1:2A:1539:G:H2'	1:2A:1540:U:C6	2.56	0.40
1:2A:1762:A:N6	62:2A:4176:HOH:O	2.53	0.40
1:2A:2001:A:H2'	1:2A:2002:G:C8	2.56	0.40
1:2A:2095:C:H2'	1:2A:2096:U:O4'	2.22	0.40
2:2B:43:C:OP1	26:24:6:HIS:NE2	2.51	0.40
4:2E:181:LEU:HD11	15:2T:6:LEU:HG	2.04	0.40
5:2F:104:LYS:O	5:2F:108:LYS:HG3	2.21	0.40
7:2H:24:VAL:HG22	7:2H:35:VAL:HB	2.02	0.40
21:2Z:52:SER:C	21:2Z:54:HIS:N	2.80	0.40
32:2a:319:G:H8	32:2a:319:G:H5''	1.85	0.40
32:2a:472:A:OP1	47:2p:75:ARG:NH1	2.53	0.40
32:2a:674:G:O5'	32:2a:674:G:H8	2.04	0.40
32:2a:1359:C:O2'	32:2a:1361:G:N7	2.55	0.40
32:2a:1371:G:H5''	40:2i:68:GLY:HA2	2.02	0.40
34:2c:181:ASN:HD22	34:2c:181:ASN:N	2.18	0.40
34:2c:186:PHE:HD1	34:2c:198:VAL:O	2.04	0.40
35:2d:13:ARG:HD2	35:2d:38:TYR:O	2.21	0.40
35:2d:154:ASN:HA	35:2d:159:ARG:HH21	1.86	0.40
40:2i:17:VAL:HA	40:2i:63:ILE:HG12	2.03	0.40
45:2n:23:ARG:NH1	45:2n:30:ALA:HB2	2.35	0.40
46:2o:87:ILE:O	46:2o:88:ARG:C	2.64	0.40
1:1A:271(E):U:H2'	1:1A:271(F):C:C6	2.56	0.40
1:1A:518:G:H2'	1:1A:519:U:C6	2.56	0.40
1:1A:958:U:H5'	12:1Q:14:ARG:HD3	2.02	0.40
1:1A:1078:U:O4	1:1A:1088:A:H3'	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1514:U:H2'	1:1A:1515:G:C8	2.57	0.40
1:1A:1639:U:O2'	1:1A:1640:C:H5'	2.22	0.40
10:1O:16:ALA:HB2	10:1O:52:VAL:HG21	2.03	0.40
21:1Z:150:LEU:HD12	21:1Z:150:LEU:HA	1.92	0.40
32:1a:1263:C:H2'	32:1a:1264:C:C6	2.57	0.40
32:1a:1277:C:O2'	32:1a:1279:A:H1'	2.22	0.40
1:2A:441:U:H2'	1:2A:442:G:C8	2.56	0.40
1:2A:740:U:H2'	1:2A:741:G:C8	2.56	0.40
1:2A:1015:G:H2'	1:2A:1016:G:H8	1.85	0.40
1:2A:1056:G:N2	1:2A:1103:A:H62	2.19	0.40
1:2A:1292:U:H2'	1:2A:1293:C:C6	2.57	0.40
1:2A:2424:C:O2	1:2A:2429:G:O2'	2.27	0.40
1:2A:2461:C:H2'	1:2A:2462:U:C6	2.57	0.40
1:2A:2695:C:H2'	1:2A:2696:U:C6	2.57	0.40
1:2A:2785:C:H2'	1:2A:2786:U:C6	2.56	0.40
5:2F:187:VAL:HG12	11:2P:3:LEU:HG	2.02	0.40
12:2Q:81:VAL:HG12	22:20:5:LYS:HD3	2.02	0.40
14:2S:23:ARG:HD3	14:2S:85:VAL:C	2.46	0.40
22:20:53:MET:HA	22:20:58:THR:O	2.21	0.40
32:2a:436:C:H2'	32:2a:437:U:O4'	2.21	0.40
32:2a:942:G:C2	32:2a:1342:C:C2	3.09	0.40
32:2a:1026:G:N3	32:2a:1026:G:H2'	2.36	0.40
32:2a:1036:G:H3'	32:2a:1037:C:H6	1.86	0.40
32:2a:1401:G:C2	32:2a:1402:4OC:H1'	2.56	0.40
35:2d:22:LYS:HB2	35:2d:26:CYS:SG	2.61	0.40
35:2d:49:ARG:HE	35:2d:49:ARG:HB3	1.64	0.40
36:2e:72:GLN:O	36:2e:75:THR:HG22	2.21	0.40
40:2i:18:PHE:N	40:2i:62:TYR:O	2.45	0.40
41:2j:49:VAL:HG22	41:2j:50:ILE:O	2.22	0.40
45:2n:26:ARG:HD3	45:2n:43:CYS:HB3	2.03	0.40
1:1A:26:G:C6	1:1A:27:G:N1	2.90	0.40
1:1A:139(A):G:O6	19:1X:40:LYS:NZ	2.48	0.40
1:1A:143:G:H4'	19:1X:35:THR:HG21	2.02	0.40
1:1A:192:C:O2'	1:1A:802:A:N3	2.53	0.40
1:1A:271(H):G:HO2'	1:1A:271(I):G:H8	1.64	0.40
1:1A:675:A:C8	1:1A:804:A:C6	3.10	0.40
1:1A:1001:A:H2'	1:1A:1002:G:O4'	2.22	0.40
1:1A:1823:G:OP1	3:1D:54:ARG:NH1	2.54	0.40
1:1A:2572:A:N7	4:1E:145:LYS:HB2	2.35	0.40
11:1P:95:VAL:HG22	11:1P:125:VAL:HA	2.04	0.40
13:1R:9:LYS:O	13:1R:17:ARG:HD3	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:1S:74:ALA:HA	14:1S:110:LEU:HD22	2.04	0.40
18:1W:46:PHE:O	18:1W:50:VAL:HG23	2.21	0.40
32:1a:1216:G:H5''	45:1n:5:ALA:HB2	2.03	0.40
32:1a:1240:U:H1'	38:1g:38:LEU:HD21	2.04	0.40
33:1b:45:GLN:O	33:1b:49:GLU:HG2	2.22	0.40
34:1c:180:ALA:HB1	34:1c:203:PHE:CE1	2.56	0.40
41:1j:19:SER:OG	41:1j:91:PRO:HD2	2.22	0.40
1:2A:1052:C:H2'	1:2A:1053:C:H6	1.86	0.40
1:2A:1052:C:C6	1:2A:1053:C:H5	2.39	0.40
1:2A:2102:U:O2	1:2A:2187:G:O6	2.39	0.40
7:2H:54:ARG:HB2	7:2H:61:HIS:HB3	2.03	0.40
15:2T:50:ILE:HG22	15:2T:102:ILE:HD11	2.03	0.40
21:2Z:98:MET:HE2	21:2Z:98:MET:HB2	1.99	0.40
26:24:1:MET:HE2	26:24:6:HIS:CG	2.56	0.40
32:2a:36:C:O2'	43:2l:117:ARG:NH2	2.55	0.40
32:2a:443:C:H2'	32:2a:444:C:H6	1.87	0.40
32:2a:588:G:H4'	39:2h:2:LEU:HD23	2.03	0.40
32:2a:724:G:C2	32:2a:725:G:C8	3.09	0.40
32:2a:738:C:OP2	37:2f:92:LYS:HD2	2.21	0.40
32:2a:1067:A:H8	32:2a:1067:A:O5'	2.04	0.40
32:2a:1077:G:N1	32:2a:1081:G:C6	2.90	0.40
32:2a:1101:A:H4'	32:2a:1102:A:O5'	2.21	0.40
32:2a:1118:C:P	40:2i:104:ARG:HE	2.44	0.40
39:2h:26:VAL:HG23	39:2h:27:PRO:O	2.22	0.40
50:2s:39:THR:HG22	50:2s:40:ILE:O	2.20	0.40
1:1A:536:A:H2'	1:1A:537:C:C6	2.57	0.40
1:1A:647:G:H2'	1:1A:648:G:O4'	2.21	0.40
1:1A:1045:A:OP1	1:1A:1045:A:H4'	2.21	0.40
1:1A:1054:A:H5'	1:1A:1055:G:OP2	2.21	0.40
1:1A:1062:G:H2'	1:1A:1063:G:H8	1.86	0.40
1:1A:2319:G:H22	14:1S:3:ARG:HD3	1.86	0.40
11:1P:84:ASN:CG	11:1P:117:GLU:HB3	2.47	0.40
20:1Y:41:GLY:C	20:1Y:44:ILE:HD11	2.47	0.40
24:12:62:THR:O	24:12:66:GLU:HG3	2.22	0.40
32:1a:607:A:C2	47:1p:31:LYS:HD2	2.57	0.40
32:1a:731:G:OP1	32:1a:766:A:H1'	2.22	0.40
32:1a:814:A:H2'	32:1a:816:A:H5''	2.04	0.40
32:1a:1003:G:H2'	32:1a:1004:A:C4'	2.34	0.40
32:1a:1315:U:H2'	32:1a:1316:G:O4'	2.22	0.40
35:1d:73:ARG:HA	35:1d:73:ARG:HD2	1.81	0.40
38:1g:113:GLU:H	38:1g:113:GLU:HG2	1.32	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:407:G:H5''	62:2A:3913:HOH:O	2.21	0.40
1:2A:706:A:H2'	1:2A:707:G:O4'	2.21	0.40
1:2A:2100:G:H1	1:2A:2189:U:H3	1.70	0.40
1:2A:2639:A:H2'	1:2A:2640:G:O4'	2.22	0.40
1:2A:2645:G:N2	1:2A:2767:C:OP2	2.53	0.40
7:2H:24:VAL:HG21	7:2H:72:ILE:HG12	2.04	0.40
23:21:85:LEU:HB3	23:21:89:GLU:HB2	2.02	0.40
28:26:34:LEU:HD23	28:26:34:LEU:HA	1.91	0.40
30:28:29:LYS:HD3	30:28:44:LYS:O	2.21	0.40
31:29:2:LYS:HB2	31:29:34:GLN:HG2	2.04	0.40
32:2a:262:A:C6	32:2a:263:A:C6	3.09	0.40
32:2a:406:G:H21	35:2d:119:GLN:HE22	1.68	0.40
33:2b:162:ILE:HD11	33:2b:184:VAL:HG22	2.03	0.40
34:2c:120:VAL:HG13	34:2c:133:ALA:HB1	2.04	0.40
49:2r:30:ASP:HB3	49:2r:33:ASP:HB2	2.04	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%)	260 (95%)	13 (5%)	0	100	100
3	2D	273/276 (99%)	259 (95%)	14 (5%)	0	100	100
4	1E	202/206 (98%)	193 (96%)	8 (4%)	1 (0%)	24	32
4	2E	202/206 (98%)	192 (95%)	9 (4%)	1 (0%)	24	32
5	1F	201/210 (96%)	193 (96%)	7 (4%)	1 (0%)	24	32
5	2F	201/210 (96%)	192 (96%)	8 (4%)	1 (0%)	24	32
6	1G	179/182 (98%)	159 (89%)	18 (10%)	2 (1%)	11	12
6	2G	179/182 (98%)	157 (88%)	19 (11%)	3 (2%)	7	6

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	1H	172/180 (96%)	162 (94%)	8 (5%)	2 (1%)	10	11
7	2H	171/180 (95%)	148 (86%)	21 (12%)	2 (1%)	10	11
8	1I	145/148 (98%)	130 (90%)	14 (10%)	1 (1%)	18	24
8	2I	144/148 (97%)	128 (89%)	13 (9%)	3 (2%)	5	4
9	1N	138/140 (99%)	133 (96%)	5 (4%)	0	100	100
9	2N	138/140 (99%)	133 (96%)	5 (4%)	0	100	100
10	1O	120/122 (98%)	113 (94%)	6 (5%)	1 (1%)	16	20
10	2O	120/122 (98%)	114 (95%)	4 (3%)	2 (2%)	7	6
11	1P	147/150 (98%)	137 (93%)	9 (6%)	1 (1%)	18	24
11	2P	147/150 (98%)	139 (95%)	6 (4%)	2 (1%)	9	8
12	1Q	139/141 (99%)	133 (96%)	6 (4%)	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%)	102 (94%)	6 (6%)	0	100	100
14	2S	108/112 (96%)	102 (94%)	5 (5%)	1 (1%)	14	17
15	1T	129/146 (88%)	121 (94%)	8 (6%)	0	100	100
15	2T	129/146 (88%)	121 (94%)	6 (5%)	2 (2%)	7	7
16	1U	114/118 (97%)	114 (100%)	0	0	100	100
16	2U	114/118 (97%)	112 (98%)	2 (2%)	0	100	100
17	1V	99/101 (98%)	96 (97%)	3 (3%)	0	100	100
17	2V	99/101 (98%)	91 (92%)	6 (6%)	2 (2%)	6	4
18	1W	110/113 (97%)	110 (100%)	0	0	100	100
18	2W	110/113 (97%)	109 (99%)	1 (1%)	0	100	100
19	1X	93/96 (97%)	90 (97%)	2 (2%)	1 (1%)	11	12
19	2X	93/96 (97%)	90 (97%)	2 (2%)	1 (1%)	11	12
20	1Y	105/110 (96%)	97 (92%)	8 (8%)	0	100	100
20	2Y	105/110 (96%)	95 (90%)	10 (10%)	0	100	100
21	1Z	201/206 (98%)	187 (93%)	12 (6%)	2 (1%)	12	14
21	2Z	199/206 (97%)	186 (94%)	11 (6%)	2 (1%)	12	14
22	10	81/85 (95%)	79 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
22	20	81/85 (95%)	78 (96%)	2 (2%)	1 (1%)	10	11
23	11	95/98 (97%)	92 (97%)	3 (3%)	0	100	100
23	21	95/98 (97%)	92 (97%)	2 (2%)	1 (1%)	11	12
24	12	68/72 (94%)	67 (98%)	1 (2%)	0	100	100
24	22	68/72 (94%)	66 (97%)	2 (3%)	0	100	100
25	13	57/60 (95%)	56 (98%)	1 (2%)	0	100	100
25	23	57/60 (95%)	55 (96%)	2 (4%)	0	100	100
26	14	67/71 (94%)	47 (70%)	16 (24%)	4 (6%)	1	0
26	24	67/71 (94%)	47 (70%)	18 (27%)	2 (3%)	3	2
27	15	57/60 (95%)	56 (98%)	1 (2%)	0	100	100
27	25	57/60 (95%)	55 (96%)	2 (4%)	0	100	100
28	16	51/54 (94%)	49 (96%)	2 (4%)	0	100	100
28	26	51/54 (94%)	48 (94%)	3 (6%)	0	100	100
29	17	46/49 (94%)	45 (98%)	0	1 (2%)	5	3
29	27	46/49 (94%)	45 (98%)	1 (2%)	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%)	34 (97%)	1 (3%)	0	100	100
33	1b	229/256 (90%)	191 (83%)	28 (12%)	10 (4%)	2	0
33	2b	229/256 (90%)	199 (87%)	21 (9%)	9 (4%)	2	1
34	1c	204/239 (85%)	191 (94%)	12 (6%)	1 (0%)	24	32
34	2c	204/239 (85%)	179 (88%)	24 (12%)	1 (0%)	24	32
35	1d	206/209 (99%)	196 (95%)	10 (5%)	0	100	100
35	2d	206/209 (99%)	200 (97%)	6 (3%)	0	100	100
36	1e	146/162 (90%)	141 (97%)	4 (3%)	1 (1%)	18	24
36	2e	146/162 (90%)	141 (97%)	5 (3%)	0	100	100
37	1f	98/101 (97%)	94 (96%)	4 (4%)	0	100	100
37	2f	98/101 (97%)	96 (98%)	2 (2%)	0	100	100
38	1g	153/156 (98%)	146 (95%)	7 (5%)	0	100	100
38	2g	153/156 (98%)	144 (94%)	9 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
39	1h	135/138 (98%)	127 (94%)	7 (5%)	1 (1%)	18	24
39	2h	135/138 (98%)	126 (93%)	9 (7%)	0	100	100
40	1i	125/128 (98%)	114 (91%)	10 (8%)	1 (1%)	16	20
40	2i	124/128 (97%)	106 (86%)	15 (12%)	3 (2%)	4	3
41	1j	95/105 (90%)	82 (86%)	9 (10%)	4 (4%)	2	0
41	2j	94/105 (90%)	81 (86%)	9 (10%)	4 (4%)	2	0
42	1k	112/129 (87%)	104 (93%)	8 (7%)	0	100	100
42	2k	112/129 (87%)	106 (95%)	3 (3%)	3 (3%)	4	2
43	1l	119/132 (90%)	113 (95%)	5 (4%)	1 (1%)	16	20
43	2l	119/132 (90%)	111 (93%)	7 (6%)	1 (1%)	16	20
44	1m	114/126 (90%)	104 (91%)	9 (8%)	1 (1%)	14	17
44	2m	112/126 (89%)	96 (86%)	13 (12%)	3 (3%)	4	2
45	1n	58/61 (95%)	57 (98%)	1 (2%)	0	100	100
45	2n	58/61 (95%)	54 (93%)	4 (7%)	0	100	100
46	1o	86/89 (97%)	82 (95%)	2 (2%)	2 (2%)	5	3
46	2o	86/89 (97%)	81 (94%)	3 (4%)	2 (2%)	5	3
47	1p	80/88 (91%)	73 (91%)	7 (9%)	0	100	100
47	2p	80/88 (91%)	75 (94%)	5 (6%)	0	100	100
48	1q	97/105 (92%)	90 (93%)	7 (7%)	0	100	100
48	2q	97/105 (92%)	91 (94%)	6 (6%)	0	100	100
49	1r	66/88 (75%)	64 (97%)	2 (3%)	0	100	100
49	2r	66/88 (75%)	62 (94%)	4 (6%)	0	100	100
50	1s	81/93 (87%)	76 (94%)	3 (4%)	2 (2%)	4	3
50	2s	81/93 (87%)	70 (86%)	10 (12%)	1 (1%)	10	11
51	1t	94/106 (89%)	88 (94%)	3 (3%)	3 (3%)	3	1
51	2t	96/106 (91%)	89 (93%)	4 (4%)	3 (3%)	3	1
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%)	92 (97%)	3 (3%)	0	100	100
53	2y	94/113 (83%)	88 (94%)	6 (6%)	0	100	100
56	1v	1/3 (33%)	1 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
56	2v	1/3 (33%)	1 (100%)	0	0	100	100
All	All	11643/12360 (94%)	10886 (94%)	657 (6%)	100 (1%)	14	17

All (100) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	1F	130	ALA
6	1G	51	ARG
8	1I	86	THR
21	1Z	53	ILE
33	1b	21	ARG
33	1b	127	ILE
41	1j	55	LYS
43	1l	91	LYS
5	2F	130	ALA
6	2G	81	LYS
7	2H	126	PRO
15	2T	128	GLU
26	24	62	ARG
41	2j	56	HIS
41	2j	79	ARG
43	2l	91	LYS
46	2o	88	ARG
19	1X	94	GLY
26	14	47	GLN
26	14	61	ARG
40	1i	11	LYS
44	1m	67	GLU
6	2G	47	LYS
15	2T	127	ALA
17	2V	100	ARG
33	2b	10	LEU
33	2b	21	ARG
33	2b	128	GLU
40	2i	43	ALA
40	2i	54	ASP
50	2s	29	ARG
51	2t	100	ILE
4	1E	52	LEU
6	1G	49	ASP
26	14	44	THR
29	17	47	ARG

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Mol	Chain	Res	Type
33	1b	8	LYS
34	1c	3	ASN
41	1j	77	PRO
46	1o	88	ARG
50	1s	12	ASP
50	1s	27	GLU
51	1t	47	GLY
6	2G	43	LEU
7	2H	65	HIS
8	2I	97	ILE
10	2O	5	GLN
23	2I	3	LYS
33	2b	20	GLU
34	2c	98	ASN
44	2m	67	GLU
51	2t	95	ALA
7	1H	126	PRO
10	1O	5	GLN
33	1b	17	PHE
33	1b	20	GLU
41	1j	78	ASN
51	1t	99	LEU
4	2E	52	LEU
8	2I	98	ALA
10	2O	29	ASN
11	2P	29	LYS
11	2P	122	PRO
17	2V	79	VAL
33	2b	95	GLN
33	2b	123	ALA
33	2b	207	ALA
41	2j	35	SER
42	2k	15	ALA
44	2m	6	GLY
44	2m	80	ARG
33	1b	124	SER
39	1h	54	ASP
21	2Z	156	LYS
22	20	4	LYS
26	24	55	ARG
33	2b	125	PRO
33	2b	126	GLU

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Mol	Chain	Res	Type
40	2i	93	ARG
41	2j	78	ASN
42	2k	90	GLY
51	2t	47	GLY
7	1H	159	GLU
11	1P	29	LYS
21	1Z	52	SER
26	14	52	THR
33	1b	231	GLU
46	1o	87	ILE
51	1t	100	ILE
14	2S	82	ILE
33	1b	228	GLY
36	1e	96	PRO
21	2Z	53	ILE
33	1b	232	PRO
42	2k	105	VAL
46	2o	87	ILE
41	1j	91	PRO
8	2I	84	GLY
19	2X	94	GLY
33	1b	125	PRO

5.3.2 Protein sidechains ⓘ

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%)	198 (92%)	16 (8%)	12	16
3	2D	215/218 (99%)	197 (92%)	18 (8%)	10	12
4	1E	164/166 (99%)	151 (92%)	13 (8%)	11	14
4	2E	164/166 (99%)	151 (92%)	13 (8%)	11	14
5	1F	160/166 (96%)	143 (89%)	17 (11%)	6	6
5	2F	159/166 (96%)	143 (90%)	16 (10%)	7	7
6	1G	144/156 (92%)	130 (90%)	14 (10%)	8	8

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	2G	142/156 (91%)	128 (90%)	14 (10%)	7	7
7	1H	144/148 (97%)	136 (94%)	8 (6%)	19	27
7	2H	143/148 (97%)	126 (88%)	17 (12%)	5	4
8	1I	111/124 (90%)	94 (85%)	17 (15%)	3	2
8	2I	108/124 (87%)	90 (83%)	18 (17%)	2	1
9	1N	119/119 (100%)	108 (91%)	11 (9%)	8	9
9	2N	118/119 (99%)	109 (92%)	9 (8%)	12	15
10	1O	100/100 (100%)	95 (95%)	5 (5%)	22	32
10	2O	100/100 (100%)	95 (95%)	5 (5%)	22	32
11	1P	115/116 (99%)	110 (96%)	5 (4%)	26	38
11	2P	115/116 (99%)	107 (93%)	8 (7%)	14	18
12	1Q	111/111 (100%)	103 (93%)	8 (7%)	13	17
12	2Q	111/111 (100%)	104 (94%)	7 (6%)	16	23
13	1R	101/101 (100%)	95 (94%)	6 (6%)	18	26
13	2R	101/101 (100%)	96 (95%)	5 (5%)	22	32
14	1S	87/88 (99%)	75 (86%)	12 (14%)	3	3
14	2S	85/88 (97%)	75 (88%)	10 (12%)	5	4
15	1T	115/127 (91%)	107 (93%)	8 (7%)	14	18
15	2T	113/127 (89%)	105 (93%)	8 (7%)	13	18
16	1U	93/94 (99%)	86 (92%)	7 (8%)	12	16
16	2U	93/94 (99%)	86 (92%)	7 (8%)	12	16
17	1V	81/82 (99%)	79 (98%)	2 (2%)	42	56
17	2V	80/82 (98%)	72 (90%)	8 (10%)	7	7
18	1W	90/92 (98%)	85 (94%)	5 (6%)	19	27
18	2W	90/92 (98%)	85 (94%)	5 (6%)	19	27
19	1X	77/78 (99%)	72 (94%)	5 (6%)	15	21
19	2X	77/78 (99%)	76 (99%)	1 (1%)	61	73
20	1Y	86/91 (94%)	75 (87%)	11 (13%)	4	3
20	2Y	86/91 (94%)	74 (86%)	12 (14%)	3	3
21	1Z	169/179 (94%)	154 (91%)	15 (9%)	9	10
21	2Z	165/179 (92%)	151 (92%)	14 (8%)	10	11

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
22	10	65/67 (97%)	61 (94%)	4 (6%)	16	23
22	20	64/67 (96%)	61 (95%)	3 (5%)	23	35
23	11	79/83 (95%)	73 (92%)	6 (8%)	12	15
23	21	81/83 (98%)	72 (89%)	9 (11%)	6	5
24	12	65/67 (97%)	61 (94%)	4 (6%)	16	23
24	22	66/67 (98%)	60 (91%)	6 (9%)	9	10
25	13	51/52 (98%)	48 (94%)	3 (6%)	18	26
25	23	50/52 (96%)	46 (92%)	4 (8%)	11	13
26	14	58/63 (92%)	54 (93%)	4 (7%)	14	19
26	24	54/63 (86%)	43 (80%)	11 (20%)	1	0
27	15	51/52 (98%)	48 (94%)	3 (6%)	18	26
27	25	50/52 (96%)	48 (96%)	2 (4%)	28	41
28	16	51/52 (98%)	46 (90%)	5 (10%)	7	7
28	26	50/52 (96%)	48 (96%)	2 (4%)	28	41
29	17	41/42 (98%)	38 (93%)	3 (7%)	13	17
29	27	41/42 (98%)	37 (90%)	4 (10%)	7	7
30	18	54/55 (98%)	49 (91%)	5 (9%)	8	9
30	28	54/55 (98%)	51 (94%)	3 (6%)	19	27
31	19	34/34 (100%)	33 (97%)	1 (3%)	37	52
31	29	34/34 (100%)	33 (97%)	1 (3%)	37	52
33	1b	191/220 (87%)	171 (90%)	20 (10%)	6	6
33	2b	187/220 (85%)	166 (89%)	21 (11%)	6	5
34	1c	144/188 (77%)	131 (91%)	13 (9%)	9	10
34	2c	140/188 (74%)	126 (90%)	14 (10%)	7	7
35	1d	171/181 (94%)	155 (91%)	16 (9%)	8	8
35	2d	172/181 (95%)	151 (88%)	21 (12%)	5	4
36	1e	114/123 (93%)	104 (91%)	10 (9%)	9	10
36	2e	114/123 (93%)	107 (94%)	7 (6%)	17	24
37	1f	85/90 (94%)	76 (89%)	9 (11%)	6	6
37	2f	85/90 (94%)	77 (91%)	8 (9%)	8	8
38	1g	120/127 (94%)	112 (93%)	8 (7%)	15	20

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
38	2g	119/127 (94%)	113 (95%)	6 (5%)	22	32
39	1h	116/119 (98%)	111 (96%)	5 (4%)	26	38
39	2h	114/119 (96%)	103 (90%)	11 (10%)	8	8
40	1i	91/99 (92%)	81 (89%)	10 (11%)	6	5
40	2i	88/99 (89%)	78 (89%)	10 (11%)	5	5
41	1j	68/92 (74%)	57 (84%)	11 (16%)	2	1
41	2j	68/92 (74%)	61 (90%)	7 (10%)	7	6
42	1k	83/99 (84%)	78 (94%)	5 (6%)	17	26
42	2k	83/99 (84%)	77 (93%)	6 (7%)	13	17
43	1l	96/108 (89%)	95 (99%)	1 (1%)	68	77
43	2l	96/108 (89%)	92 (96%)	4 (4%)	26	39
44	1m	90/101 (89%)	83 (92%)	7 (8%)	11	14
44	2m	87/101 (86%)	76 (87%)	11 (13%)	4	4
45	1n	49/50 (98%)	46 (94%)	3 (6%)	17	24
45	2n	49/50 (98%)	45 (92%)	4 (8%)	10	13
46	1o	78/80 (98%)	75 (96%)	3 (4%)	29	43
46	2o	78/80 (98%)	71 (91%)	7 (9%)	9	10
47	1p	69/74 (93%)	60 (87%)	9 (13%)	4	3
47	2p	68/74 (92%)	63 (93%)	5 (7%)	13	16
48	1q	94/97 (97%)	89 (95%)	5 (5%)	20	30
48	2q	94/97 (97%)	89 (95%)	5 (5%)	20	30
49	1r	59/77 (77%)	54 (92%)	5 (8%)	10	11
49	2r	59/77 (77%)	55 (93%)	4 (7%)	14	20
50	1s	68/80 (85%)	56 (82%)	12 (18%)	2	1
50	2s	67/80 (84%)	58 (87%)	9 (13%)	4	3
51	1t	71/82 (87%)	68 (96%)	3 (4%)	26	39
51	2t	70/82 (85%)	63 (90%)	7 (10%)	7	7
52	1u	18/22 (82%)	17 (94%)	1 (6%)	19	27
52	2u	18/22 (82%)	18 (100%)	0	100	100
53	1y	82/98 (84%)	78 (95%)	4 (5%)	22	33
53	2y	79/98 (81%)	70 (89%)	9 (11%)	5	5

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
56	1v	2/2 (100%)	2 (100%)	0	100	100
56	2v	2/2 (100%)	2 (100%)	0	100	100
All	All	9535/10264 (93%)	8736 (92%)	799 (8%)	10	12

All (799) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	1D	3	VAL
3	1D	37	LEU
3	1D	39	LYS
3	1D	71	ASP
3	1D	94	LEU
3	1D	99	ASP
3	1D	111	LEU
3	1D	141	VAL
3	1D	155	LEU
3	1D	173	VAL
3	1D	193	VAL
3	1D	211	ARG
3	1D	221	VAL
3	1D	229	VAL
3	1D	242	ARG
3	1D	259	THR
4	1E	9	VAL
4	1E	49	LEU
4	1E	75	VAL
4	1E	93	VAL
4	1E	94	GLU
4	1E	116	VAL
4	1E	119	ARG
4	1E	163	GLU
4	1E	170	LEU
4	1E	181	LEU
4	1E	184	VAL
4	1E	188	VAL
4	1E	195	LEU
5	1F	12	LEU
5	1F	15	SER
5	1F	18	ARG
5	1F	53	THR
5	1F	57	VAL

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Mol	Chain	Res	Type
5	1F	74	ARG
5	1F	108	LYS
5	1F	110	LEU
5	1F	125	LEU
5	1F	157	VAL
5	1F	158	THR
5	1F	161	GLU
5	1F	162	LEU
5	1F	170	LEU
5	1F	183	VAL
5	1F	192	LEU
5	1F	201	VAL
6	1G	5	VAL
6	1G	7	LEU
6	1G	21	ARG
6	1G	31	VAL
6	1G	33	ARG
6	1G	43	LEU
6	1G	45	GLU
6	1G	52	ILE
6	1G	53	LEU
6	1G	79	ASN
6	1G	126	ASP
6	1G	133	LEU
6	1G	140	ILE
6	1G	159	VAL
7	1H	15	VAL
7	1H	24	VAL
7	1H	37	VAL
7	1H	98	LEU
7	1H	107	VAL
7	1H	119	GLU
7	1H	122	THR
7	1H	127	GLU
8	1I	10	GLU
8	1I	12	LEU
8	1I	17	GLN
8	1I	20	ASP
8	1I	40	THR
8	1I	60	GLU
8	1I	64	GLU
8	1I	66	GLU

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Mol	Chain	Res	Type
8	1I	74	ASN
8	1I	78	THR
8	1I	92	VAL
8	1I	101	LEU
8	1I	109	ILE
8	1I	116	LEU
8	1I	117	GLU
8	1I	127	VAL
8	1I	140	LEU
9	1N	12	ARG
9	1N	14	VAL
9	1N	33	LEU
9	1N	48	MET
9	1N	62	VAL
9	1N	65	LYS
9	1N	73	THR
9	1N	97	ARG
9	1N	131	GLN
9	1N	133	GLN
9	1N	137	LYS
10	1O	66	LYS
10	1O	69	ILE
10	1O	98	VAL
10	1O	108	GLU
10	1O	113	LYS
11	1P	1	MET
11	1P	75	ILE
11	1P	92	GLU
11	1P	95	VAL
11	1P	99	LEU
12	1Q	5	ARG
12	1Q	7	MET
12	1Q	42	ILE
12	1Q	55	VAL
12	1Q	75	THR
12	1Q	109	VAL
12	1Q	130	LYS
12	1Q	133	ARG
13	1R	6	SER
13	1R	14	SER
13	1R	29	LEU
13	1R	36	THR

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Mol	Chain	Res	Type
13	1R	100	LEU
13	1R	114	VAL
14	1S	3	ARG
14	1S	13	ARG
14	1S	43	GLU
14	1S	46	VAL
14	1S	48	LEU
14	1S	50	SER
14	1S	59	LYS
14	1S	73	LEU
14	1S	76	LYS
14	1S	78	LEU
14	1S	85	VAL
14	1S	110	LEU
15	1T	28	VAL
15	1T	34	VAL
15	1T	49	VAL
15	1T	53	ARG
15	1T	78	LEU
15	1T	96	ARG
15	1T	118	ARG
15	1T	128	GLU
16	1U	5	LYS
16	1U	27	LEU
16	1U	30	LYS
16	1U	74	LEU
16	1U	83	LEU
16	1U	104	GLN
16	1U	111	GLU
17	1V	79	VAL
17	1V	95	LEU
18	1W	11	ARG
18	1W	17	VAL
18	1W	19	LEU
18	1W	23	LEU
18	1W	100	THR
19	1X	35	THR
19	1X	45	THR
19	1X	66	LEU
19	1X	72	LYS
19	1X	92	LEU
20	1Y	7	VAL

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Mol	Chain	Res	Type
20	1Y	14	LEU
20	1Y	26	LYS
20	1Y	34	LYS
20	1Y	43	ASN
20	1Y	64	GLU
20	1Y	72	VAL
20	1Y	73	ARG
20	1Y	90	LEU
20	1Y	92	ASN
20	1Y	107	ASP
21	1Z	31	ARG
21	1Z	42	VAL
21	1Z	52	SER
21	1Z	74	VAL
21	1Z	80	ARG
21	1Z	86	VAL
21	1Z	93	ASP
21	1Z	94	GLU
21	1Z	102	LEU
21	1Z	126	VAL
21	1Z	150	LEU
21	1Z	155	LEU
21	1Z	161	VAL
21	1Z	185	GLU
21	1Z	191	VAL
22	10	11	ARG
22	10	59	LEU
22	10	74	ARG
22	10	82	ARG
23	11	21	ARG
23	11	30	VAL
23	11	40	ARG
23	11	46	LEU
23	11	94	LEU
23	11	95	LEU
24	12	1	MET
24	12	30	ARG
24	12	54	LYS
24	12	68	ARG
25	13	54	VAL
25	13	56	VAL
25	13	58	VAL

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Mol	Chain	Res	Type
26	14	1	MET
26	14	46	GLN
26	14	49	PHE
26	14	56	VAL
27	15	6	VAL
27	15	37	LYS
27	15	60	VAL
28	16	5	VAL
28	16	44	ARG
28	16	47	THR
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	32	LEU
30	18	46	ARG
31	19	17	ILE
33	1b	7	VAL
33	1b	10	LEU
33	1b	15	VAL
33	1b	35	GLU
33	1b	51	LEU
33	1b	63	MET
33	1b	93	VAL
33	1b	102	LEU
33	1b	111	ARG
33	1b	124	SER
33	1b	127	ILE
33	1b	128	GLU
33	1b	135	GLN
33	1b	140	HIS
33	1b	144	ARG
33	1b	158	LEU
33	1b	160	ASP
33	1b	185	ILE
33	1b	196	LEU
33	1b	224	GLN
34	1c	26	LYS

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Mol	Chain	Res	Type
34	1c	45	LYS
34	1c	64	VAL
34	1c	70	VAL
34	1c	89	GLU
34	1c	102	ASN
34	1c	105	GLU
34	1c	111	LEU
34	1c	115	LEU
34	1c	124	ILE
34	1c	132	ARG
34	1c	154	SER
34	1c	192	THR
35	1d	3	ARG
35	1d	8	VAL
35	1d	19	LEU
35	1d	58	LEU
35	1d	85	LYS
35	1d	94	LEU
35	1d	108	LEU
35	1d	127	THR
35	1d	135	LEU
35	1d	140	VAL
35	1d	150	GLU
35	1d	168	ARG
35	1d	178	VAL
35	1d	187	ARG
35	1d	190	ASP
35	1d	194	LEU
36	1e	13	ILE
36	1e	31	LEU
36	1e	34	VAL
36	1e	41	VAL
36	1e	56	GLN
36	1e	64	ARG
36	1e	68	GLU
36	1e	116	THR
36	1e	144	THR
36	1e	147	ASP
37	1f	10	LEU
37	1f	15	ASP
37	1f	21	LEU
37	1f	40	VAL

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Mol	Chain	Res	Type
37	1f	42	GLU
37	1f	72	VAL
37	1f	73	ASN
37	1f	74	ASP
37	1f	78	GLU
38	1g	6	ARG
38	1g	31	MET
38	1g	41	ARG
38	1g	52	GLU
38	1g	56	GLN
38	1g	96	GLN
38	1g	104	LEU
38	1g	113	GLU
39	1h	26	VAL
39	1h	51	VAL
39	1h	52	ASP
39	1h	63	LEU
39	1h	99	GLU
40	1i	14	VAL
40	1i	27	THR
40	1i	42	ARG
40	1i	50	LEU
40	1i	56	LEU
40	1i	60	ASP
40	1i	63	ILE
40	1i	65	VAL
40	1i	81	ILE
40	1i	92	TYR
41	1j	34	VAL
41	1j	38	ILE
41	1j	42	THR
41	1j	45	ARG
41	1j	65	LEU
41	1j	72	VAL
41	1j	84	GLN
41	1j	92	THR
41	1j	94	VAL
41	1j	98	ILE
41	1j	100	THR
42	1k	16	SER
42	1k	79	SER
42	1k	84	VAL

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Mol	Chain	Res	Type
42	1k	109	VAL
42	1k	114	VAL
43	1l	41	ARG
44	1m	4	ILE
44	1m	11	ARG
44	1m	15	VAL
44	1m	27	LYS
44	1m	32	GLU
44	1m	35	GLU
44	1m	70	LEU
45	1n	13	THR
45	1n	18	VAL
45	1n	32	SER
46	1o	26	GLU
46	1o	39	LEU
46	1o	84	LYS
47	1p	1	MET
47	1p	5	ARG
47	1p	6	LEU
47	1p	20	VAL
47	1p	21	VAL
47	1p	29	ASP
47	1p	60	LEU
47	1p	61	SER
47	1p	67	THR
48	1q	20	THR
48	1q	53	LEU
48	1q	74	LEU
48	1q	85	VAL
48	1q	96	GLU
49	1r	25	THR
49	1r	31	LEU
49	1r	42	ARG
49	1r	82	THR
49	1r	84	LYS
50	1s	6	LYS
50	1s	9	VAL
50	1s	12	ASP
50	1s	18	LYS
50	1s	21	GLU
50	1s	28	LYS
50	1s	30	LEU

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Mol	Chain	Res	Type
50	1s	35	SER
50	1s	48	THR
50	1s	56	GLN
50	1s	66	MET
50	1s	81	ARG
51	1t	10	LEU
51	1t	46	GLU
51	1t	100	ILE
52	1u	15	ARG
53	1y	24	LEU
53	1y	42	SER
53	1y	60	VAL
53	1y	76	GLU
3	2D	3	VAL
3	2D	32	SER
3	2D	38	LYS
3	2D	69	ARG
3	2D	94	LEU
3	2D	103	ARG
3	2D	113	VAL
3	2D	134	ARG
3	2D	142	VAL
3	2D	155	LEU
3	2D	173	VAL
3	2D	183	ARG
3	2D	211	ARG
3	2D	221	VAL
3	2D	229	VAL
3	2D	242	ARG
3	2D	259	THR
3	2D	276	LYS
4	2E	9	VAL
4	2E	49	LEU
4	2E	72	VAL
4	2E	75	VAL
4	2E	87	GLU
4	2E	89	ASP
4	2E	93	VAL
4	2E	116	VAL
4	2E	119	ARG
4	2E	170	LEU
4	2E	181	LEU

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Mol	Chain	Res	Type
4	2E	184	VAL
4	2E	188	VAL
5	2F	13	SER
5	2F	20	LEU
5	2F	28	ILE
5	2F	33	LEU
5	2F	57	VAL
5	2F	74	ARG
5	2F	126	VAL
5	2F	140	LEU
5	2F	170	LEU
5	2F	175	THR
5	2F	176	LEU
5	2F	183	VAL
5	2F	192	LEU
5	2F	197	ASP
5	2F	200	GLU
5	2F	201	VAL
6	2G	3	LEU
6	2G	5	VAL
6	2G	7	LEU
6	2G	15	VAL
6	2G	28	VAL
6	2G	43	LEU
6	2G	53	LEU
6	2G	88	ILE
6	2G	109	VAL
6	2G	113	ARG
6	2G	133	LEU
6	2G	165	THR
6	2G	168	GLU
6	2G	172	LEU
7	2H	9	ILE
7	2H	11	VAL
7	2H	15	VAL
7	2H	26	VAL
7	2H	34	GLU
7	2H	38	SER
7	2H	43	VAL
7	2H	45	VAL
7	2H	47	GLU
7	2H	49	VAL

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Mol	Chain	Res	Type
7	2H	50	VAL
7	2H	65	HIS
7	2H	68	THR
7	2H	80	SER
7	2H	88	LEU
7	2H	95	ARG
7	2H	133	VAL
8	2I	38	LEU
8	2I	40	THR
8	2I	41	GLU
8	2I	44	LEU
8	2I	50	ARG
8	2I	52	ARG
8	2I	62	LYS
8	2I	64	GLU
8	2I	68	LEU
8	2I	74	ASN
8	2I	76	THR
8	2I	86	THR
8	2I	87	LYS
8	2I	91	SER
8	2I	92	VAL
8	2I	116	LEU
8	2I	117	GLU
8	2I	123	LEU
9	2N	28	THR
9	2N	33	LEU
9	2N	34	LEU
9	2N	38	HIS
9	2N	48	MET
9	2N	67	LEU
9	2N	74	ARG
9	2N	99	LEU
9	2N	115	ARG
10	2O	1	MET
10	2O	52	VAL
10	2O	98	VAL
10	2O	113	LYS
10	2O	116	SER
11	2P	76	LYS
11	2P	98	GLU
11	2P	100	LEU

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Mol	Chain	Res	Type
11	2P	101	VAL
11	2P	106	LEU
11	2P	123	LEU
11	2P	126	VAL
11	2P	135	LEU
12	2Q	7	MET
12	2Q	55	VAL
12	2Q	75	THR
12	2Q	81	VAL
12	2Q	109	VAL
12	2Q	111	GLU
12	2Q	130	LYS
13	2R	29	LEU
13	2R	36	THR
13	2R	100	LEU
13	2R	114	VAL
13	2R	117	VAL
14	2S	11	LYS
14	2S	12	PHE
14	2S	13	ARG
14	2S	25	ARG
14	2S	44	LYS
14	2S	48	LEU
14	2S	64	GLU
14	2S	78	LEU
14	2S	85	VAL
14	2S	110	LEU
15	2T	6	LEU
15	2T	16	ARG
15	2T	28	VAL
15	2T	34	VAL
15	2T	36	GLU
15	2T	38	ASN
15	2T	65	LYS
15	2T	89	VAL
16	2U	31	SER
16	2U	74	LEU
16	2U	77	SER
16	2U	78	THR
16	2U	83	LEU
16	2U	104	GLN
16	2U	108	GLU

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Mol	Chain	Res	Type
17	2V	19	LYS
17	2V	32	THR
17	2V	35	LEU
17	2V	46	VAL
17	2V	51	VAL
17	2V	72	VAL
17	2V	79	VAL
17	2V	96	ILE
18	2W	11	ARG
18	2W	17	VAL
18	2W	19	LEU
18	2W	23	LEU
18	2W	100	THR
19	2X	66	LEU
20	2Y	2	ARG
20	2Y	5	MET
20	2Y	19	LYS
20	2Y	31	LEU
20	2Y	42	VAL
20	2Y	67	LEU
20	2Y	70	SER
20	2Y	72	VAL
20	2Y	88	LYS
20	2Y	96	ILE
20	2Y	98	VAL
20	2Y	99	CYS
21	2Z	5	LEU
21	2Z	18	LEU
21	2Z	65	GLN
21	2Z	72	ARG
21	2Z	73	GLN
21	2Z	74	VAL
21	2Z	121	HIS
21	2Z	126	VAL
21	2Z	128	VAL
21	2Z	141	VAL
21	2Z	162	GLU
21	2Z	170	THR
21	2Z	180	VAL
21	2Z	182	LYS
22	20	10	THR
22	20	30	VAL

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Mol	Chain	Res	Type
22	20	70	GLN
23	21	3	LYS
23	21	4	VAL
23	21	21	ARG
23	21	26	ARG
23	21	40	ARG
23	21	46	LEU
23	21	51	VAL
23	21	80	LEU
23	21	83	GLU
24	22	19	VAL
24	22	25	VAL
24	22	32	LEU
24	22	53	LEU
24	22	64	LEU
24	22	70	GLN
25	23	7	LYS
25	23	23	LEU
25	23	31	LEU
25	23	44	ARG
26	24	3	GLU
26	24	9	LEU
26	24	15	ILE
26	24	23	GLU
26	24	34	GLU
26	24	46	GLN
26	24	50	VAL
26	24	58	ARG
26	24	60	GLN
26	24	62	ARG
26	24	63	TYR
27	25	6	VAL
27	25	55	ARG
28	26	20	ASN
28	26	48	VAL
29	27	23	ARG
29	27	41	ARG
29	27	43	THR
29	27	46	VAL
30	28	3	LYS
30	28	14	VAL
30	28	32	LEU

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Mol	Chain	Res	Type
31	29	17	ILE
33	2b	8	LYS
33	2b	12	GLU
33	2b	15	VAL
33	2b	39	ILE
33	2b	44	LEU
33	2b	45	GLN
33	2b	80	ILE
33	2b	97	TRP
33	2b	98	LEU
33	2b	111	ARG
33	2b	114	ARG
33	2b	150	SER
33	2b	154	LEU
33	2b	158	LEU
33	2b	160	ASP
33	2b	187	LEU
33	2b	189	ASP
33	2b	196	LEU
33	2b	208	ILE
33	2b	222	ILE
33	2b	229	VAL
34	2c	8	ILE
34	2c	15	THR
34	2c	33	LEU
34	2c	47	LEU
34	2c	52	LEU
34	2c	56	ASP
34	2c	103	VAL
34	2c	128	PHE
34	2c	152	ILE
34	2c	154	SER
34	2c	181	ASN
34	2c	192	THR
34	2c	195	VAL
34	2c	204	LEU
35	2d	3	ARG
35	2d	19	LEU
35	2d	45	GLN
35	2d	49	ARG
35	2d	57	ARG
35	2d	76	ARG

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Mol	Chain	Res	Type
35	2d	83	SER
35	2d	108	LEU
35	2d	112	VAL
35	2d	135	LEU
35	2d	141	ARG
35	2d	150	GLU
35	2d	156	GLU
35	2d	157	LEU
35	2d	160	GLN
35	2d	166	LYS
35	2d	169	LYS
35	2d	170	VAL
35	2d	188	LEU
35	2d	190	ASP
35	2d	194	LEU
36	2e	13	ILE
36	2e	31	LEU
36	2e	34	VAL
36	2e	41	VAL
36	2e	68	GLU
36	2e	75	THR
36	2e	144	THR
37	2f	22	GLU
37	2f	31	GLU
37	2f	45	LEU
37	2f	61	LEU
37	2f	64	GLN
37	2f	72	VAL
37	2f	75	LEU
37	2f	93	SER
38	2g	6	ARG
38	2g	15	ASP
38	2g	27	ILE
38	2g	50	ILE
38	2g	75	VAL
38	2g	111	ARG
39	2h	19	VAL
39	2h	26	VAL
39	2h	29	SER
39	2h	38	ILE
39	2h	84	ARG
39	2h	85	ARG

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Mol	Chain	Res	Type
39	2h	91	ARG
39	2h	109	ILE
39	2h	112	LEU
39	2h	121	ASP
39	2h	133	LEU
40	2i	27	THR
40	2i	47	LEU
40	2i	60	ASP
40	2i	75	ASP
40	2i	81	ILE
40	2i	85	LEU
40	2i	86	VAL
40	2i	102	LEU
40	2i	108	VAL
40	2i	110	GLU
41	2j	16	LEU
41	2j	34	VAL
41	2j	38	ILE
41	2j	51	ARG
41	2j	92	THR
41	2j	95	GLU
41	2j	98	ILE
42	2k	32	ILE
42	2k	53	SER
42	2k	79	SER
42	2k	84	VAL
42	2k	93	GLN
42	2k	109	VAL
43	2l	6	THR
43	2l	41	ARG
43	2l	81	SER
43	2l	117	ARG
44	2m	3	ARG
44	2m	15	VAL
44	2m	17	VAL
44	2m	48	LEU
44	2m	49	THR
44	2m	69	GLU
44	2m	81	LEU
44	2m	98	VAL
44	2m	102	ARG
44	2m	104	ARG

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Mol	Chain	Res	Type
44	2m	116	THR
45	2n	13	THR
45	2n	18	VAL
45	2n	33	VAL
45	2n	49	HIS
46	2o	3	ILE
46	2o	10	LYS
46	2o	26	GLU
46	2o	27	VAL
46	2o	38	ARG
46	2o	39	LEU
46	2o	84	LYS
47	2p	20	VAL
47	2p	25	ARG
47	2p	47	ASP
47	2p	60	LEU
47	2p	69	THR
48	2q	39	SER
48	2q	53	LEU
48	2q	93	GLN
48	2q	96	GLU
48	2q	99	SER
49	2r	31	LEU
49	2r	37	VAL
49	2r	55	ARG
49	2r	82	THR
50	2s	23	ASN
50	2s	30	LEU
50	2s	41	VAL
50	2s	62	ILE
50	2s	71	LEU
50	2s	77	THR
50	2s	79	THR
50	2s	81	ARG
50	2s	83	HIS
51	2t	10	LEU
51	2t	11	SER
51	2t	24	LEU
51	2t	54	LYS
51	2t	55	ILE
51	2t	62	LEU
51	2t	100	ILE

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Mol	Chain	Res	Type
53	2y	6	THR
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	70	MET
53	2y	78	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (171) such sidechains are listed below:

Mol	Chain	Res	Type
3	1D	253	GLN
4	1E	55	ASN
4	1E	143	ASN
5	1F	8	GLN
5	1F	69	HIS
5	1F	133	ASN
5	1F	203	GLN
5	1F	204	ASN
6	1G	26	GLN
6	1G	132	ASN
8	1I	43	ASN
8	1I	54	GLN
8	1I	105	HIS
8	1I	139	GLN
9	1N	56	ASN
9	1N	133	GLN
10	1O	3	GLN
11	1P	84	ASN
13	1R	31	HIS
13	1R	50	HIS
13	1R	71	GLN
15	1T	58	ASN
15	1T	123	GLN
16	1U	72	HIS
16	1U	94	ASN
16	1U	117	GLN
19	1X	31	HIS
19	1X	82	GLN
21	1Z	55	HIS

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Mol	Chain	Res	Type
21	1Z	73	GLN
21	1Z	151	HIS
22	10	12	ASN
22	10	35	ASN
23	11	56	GLN
24	12	9	GLN
25	13	32	GLN
26	14	20	ASN
26	14	47	GLN
26	14	60	GLN
27	15	4	HIS
33	1b	78	GLN
34	1c	6	HIS
34	1c	31	HIS
34	1c	98	ASN
34	1c	104	GLN
34	1c	123	GLN
34	1c	162	GLN
35	1d	45	GLN
35	1d	77	ASN
35	1d	123	HIS
35	1d	129	ASN
35	1d	160	GLN
36	1e	20	GLN
36	1e	56	GLN
36	1e	141	GLN
37	1f	32	ASN
37	1f	73	ASN
37	1f	84	ASN
37	1f	100	ASN
38	1g	28	ASN
38	1g	56	GLN
38	1g	64	GLN
38	1g	86	GLN
38	1g	96	GLN
38	1g	97	GLN
40	1i	3	GLN
40	1i	31	GLN
41	1j	21	GLN
41	1j	56	HIS
41	1j	84	GLN
42	1k	22	HIS

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Mol	Chain	Res	Type
42	1k	93	GLN
42	1k	116	HIS
43	1l	99	HIS
44	1m	92	HIS
45	1n	49	HIS
46	1o	71	GLN
47	1p	16	HIS
47	1p	76	GLN
48	1q	16	GLN
50	1s	47	HIS
50	1s	56	GLN
50	1s	57	HIS
50	1s	69	HIS
50	1s	83	HIS
51	1t	16	HIS
51	1t	73	HIS
51	1t	75	ASN
53	1y	9	GLN
53	1y	38	HIS
3	2D	87	ASN
3	2D	126	GLN
3	2D	164	GLN
3	2D	253	GLN
4	2E	48	GLN
5	2F	69	HIS
5	2F	133	ASN
5	2F	169	ASN
6	2G	26	GLN
6	2G	41	GLN
6	2G	58	GLN
8	2I	43	ASN
8	2I	74	ASN
8	2I	105	HIS
8	2I	133	HIS
12	2Q	89	ASN
12	2Q	123	HIS
13	2R	50	HIS
15	2T	58	ASN
16	2U	81	HIS
16	2U	94	ASN
17	2V	64	HIS
19	2X	31	HIS

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Mol	Chain	Res	Type
19	2X	82	GLN
20	2Y	92	ASN
21	2Z	65	GLN
21	2Z	73	GLN
21	2Z	132	ASN
21	2Z	151	HIS
26	24	40	HIS
26	24	46	GLN
26	24	60	GLN
28	26	20	ASN
29	27	36	GLN
33	2b	19	HIS
33	2b	40	HIS
33	2b	135	GLN
34	2c	98	ASN
34	2c	110	ASN
34	2c	123	GLN
34	2c	136	GLN
34	2c	139	GLN
34	2c	176	HIS
34	2c	181	ASN
35	2d	45	GLN
35	2d	77	ASN
35	2d	116	GLN
35	2d	119	GLN
35	2d	123	HIS
35	2d	125	HIS
35	2d	129	ASN
35	2d	160	GLN
36	2e	56	GLN
37	2f	13	ASN
38	2g	13	GLN
38	2g	28	ASN
38	2g	56	GLN
38	2g	64	GLN
38	2g	109	ASN
39	2h	15	ASN
40	2i	3	GLN
40	2i	31	GLN
40	2i	73	GLN
40	2i	89	ASN
41	2j	33	GLN

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Mol	Chain	Res	Type
41	2j	62	HIS
41	2j	68	HIS
42	2k	93	GLN
43	2l	99	HIS
44	2m	77	ASN
46	2o	71	GLN
47	2p	16	HIS
48	2q	16	GLN
48	2q	93	GLN
50	2s	57	HIS
50	2s	83	HIS
53	2y	33	HIS
53	2y	36	ASN
53	2y	46	GLN
53	2y	84	GLN
53	2y	89	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1A	2865/2915 (98%)	389 (13%)	36 (1%)
1	2A	2858/2915 (98%)	457 (15%)	33 (1%)
2	1B	119/121 (98%)	12 (10%)	0
2	2B	119/121 (98%)	15 (12%)	0
32	1a	1497/1521 (98%)	232 (15%)	0
32	2a	1501/1521 (98%)	263 (17%)	0
54	1w	1/4 (25%)	0	0
54	2w	1/4 (25%)	0	0
55	1x	1/4 (25%)	0	0
55	2x	1/4 (25%)	0	0
All	All	8963/9130 (98%)	1368 (15%)	69 (0%)

All (1368) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1A	34	C
1	1A	35	G
1	1A	45	C
1	1A	71	A
1	1A	74	A
1	1A	75	G

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Mol	Chain	Res	Type
1	1A	95	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	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	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	271(S)	G
1	1A	272(A)	U
1	1A	272(B)	G
1	1A	272(H)	C
1	1A	272(J)	C
1	1A	275	G
1	1A	279	C
1	1A	280	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	407	G
1	1A	411	G
1	1A	412	A
1	1A	421	U
1	1A	422	A
1	1A	428	A

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Mol	Chain	Res	Type
1	1A	429	A
1	1A	448	U
1	1A	454	A
1	1A	456	C
1	1A	457	A
1	1A	481	G
1	1A	494	G
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	586	A
1	1A	603	A
1	1A	604	G
1	1A	607	U
1	1A	614(B)	G
1	1A	615	G
1	1A	616	G
1	1A	627	A
1	1A	637	A
1	1A	645	C
1	1A	646	A
1	1A	652(A)	A
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	764	A
1	1A	765	G
1	1A	774	A
1	1A	775	G

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Mol	Chain	Res	Type
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	879	G
1	1A	886	C
1	1A	887	A
1	1A	888	C
1	1A	889	C
1	1A	890	A
1	1A	896	A
1	1A	897	C
1	1A	910	A
1	1A	932	G
1	1A	945	A
1	1A	946	G
1	1A	959	A
1	1A	961	C
1	1A	974	G
1	1A	975	C
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	1046	A
1	1A	1047	G
1	1A	1048	A
1	1A	1054	A
1	1A	1058	G
1	1A	1061	U
1	1A	1062	G

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Mol	Chain	Res	Type
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	1075	C
1	1A	1076	C
1	1A	1077	A
1	1A	1078	U
1	1A	1079	C
1	1A	1087	G
1	1A	1088	A
1	1A	1089	G
1	1A	1090	U
1	1A	1093	G
1	1A	1095	A
1	1A	1096	A
1	1A	1097	U
1	1A	1098	A
1	1A	1109	C
1	1A	1110	G
1	1A	1111	A
1	1A	1112	G
1	1A	1128	A
1	1A	1135	C
1	1A	1136	G
1	1A	1139	G
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	1253	A
1	1A	1256	G
1	1A	1271	G

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Mol	Chain	Res	Type
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	1365	A
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	1455	G
1	1A	1459	G
1	1A	1467	C
1	1A	1471	A
1	1A	1482	G
1	1A	1487	G
1	1A	1493	C
1	1A	1508	A
1	1A	1509	C
1	1A	1509(A)	A
1	1A	1525	G
1	1A	1542	A
1	1A	1543	C
1	1A	1558	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

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Mol	Chain	Res	Type
1	1A	1647	G
1	1A	1648	C
1	1A	1653	G
1	1A	1654	A
1	1A	1664	A
1	1A	1674	G
1	1A	1696	G
1	1A	1700	A
1	1A	1703	G
1	1A	1722	A
1	1A	1739	U
1	1A	1756	G
1	1A	1762	A
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	1812	A
1	1A	1816	G
1	1A	1839	G
1	1A	1847	A
1	1A	1877	A
1	1A	1887	C
1	1A	1900	A
1	1A	1906	G
1	1A	1913	A
1	1A	1914	C
1	1A	1929	G
1	1A	1930	G
1	1A	1937	A
1	1A	1938	A
1	1A	1955	U
1	1A	1963	U
1	1A	1967	C
1	1A	1970	A
1	1A	1971	A
1	1A	1972	A
1	1A	1992	G

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Mol	Chain	Res	Type
1	1A	1993	U
1	1A	1997	G
1	1A	2020	A
1	1A	2023	G
1	1A	2031	A
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
1	1A	2099	U
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	2116	G
1	1A	2117	A
1	1A	2118	U
1	1A	2119	A
1	1A	2123	G
1	1A	2125	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	2136	C
1	1A	2142	C
1	1A	2146	C
1	1A	2147	G
1	1A	2158	A
1	1A	2159	G
1	1A	2164	C
1	1A	2172	U
1	1A	2180	U

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Mol	Chain	Res	Type
1	1A	2181	G
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	2218	U
1	1A	2219	G
1	1A	2225	A
1	1A	2238	G
1	1A	2239	G
1	1A	2268	A
1	1A	2269	A
1	1A	2280	G
1	1A	2283	C
1	1A	2287	A
1	1A	2289	G
1	1A	2305	A
1	1A	2308	G
1	1A	2320	A
1	1A	2321	G
1	1A	2325	G
1	1A	2334	G
1	1A	2347	C
1	1A	2350	C
1	1A	2383	G
1	1A	2385	C
1	1A	2393	A
1	1A	2406	U
1	1A	2407	G
1	1A	2422	A
1	1A	2423	U
1	1A	2425	A
1	1A	2429	G
1	1A	2430	A
1	1A	2432	A
1	1A	2435	A
1	1A	2439	A

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Mol	Chain	Res	Type
1	1A	2440	C
1	1A	2441	C
1	1A	2448	A
1	1A	2468	G
1	1A	2469	A
1	1A	2476	A
1	1A	2478	A
1	1A	2498	C
1	1A	2502	G
1	1A	2505	G
1	1A	2518	A
1	1A	2529	G
1	1A	2554	U
1	1A	2566	A
1	1A	2567	G
1	1A	2573	C
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	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	2757	A
1	1A	2758	A
1	1A	2765	A
1	1A	2766	G
1	1A	2778	A
1	1A	2790	A
1	1A	2791	C
1	1A	2802	G
1	1A	2820	A
1	1A	2821	A

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Mol	Chain	Res	Type
1	1A	2833	G
1	1A	2835	A
1	1A	2872	G
1	1A	2892	A
1	1A	2894	G
2	1B	2	C
2	1B	7	G
2	1B	13	A
2	1B	30	C
2	1B	42	C
2	1B	45	A
2	1B	56	G
2	1B	73	A
2	1B	74	U
2	1B	106	G
2	1B	110	G
2	1B	120	A
32	1a	7	G
32	1a	9	G
32	1a	32	A
32	1a	39	G
32	1a	48	C
32	1a	50	A
32	1a	51	A
32	1a	53	A
32	1a	61	G
32	1a	78	G
32	1a	79	G
32	1a	93	G
32	1a	101	A
32	1a	116	A
32	1a	121	C
32	1a	131	C
32	1a	144	G
32	1a	150	C
32	1a	151	A
32	1a	156	G
32	1a	163	C
32	1a	165	C
32	1a	169	C
32	1a	173	U
32	1a	174	C

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Mol	Chain	Res	Type
32	1a	182	U
32	1a	189(D)	C
32	1a	195	A
32	1a	197	A
32	1a	216	G
32	1a	220	G
32	1a	247	G
32	1a	251	G
32	1a	266	G
32	1a	267	C
32	1a	289	G
32	1a	318	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	353	A
32	1a	354	G
32	1a	356	A
32	1a	367	U
32	1a	372	C
32	1a	373	A
32	1a	384	G
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	452	A
32	1a	458	C
32	1a	460	G
32	1a	461	A
32	1a	470	C
32	1a	475	G
32	1a	484	G

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Mol	Chain	Res	Type
32	1a	485	G
32	1a	492	G
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	521	G
32	1a	532	A
32	1a	536	C
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	642	A
32	1a	653	A
32	1a	665	A
32	1a	673	G
32	1a	687	A
32	1a	688	G
32	1a	723	U
32	1a	731	G
32	1a	755	G
32	1a	777	A
32	1a	793	U
32	1a	794	A
32	1a	810	C
32	1a	815	A
32	1a	816	A
32	1a	817	C
32	1a	821	G
32	1a	828	A

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Mol	Chain	Res	Type
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	874	G
32	1a	902	G
32	1a	913	A
32	1a	914	A
32	1a	926	G
32	1a	927	G
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	982	U
32	1a	983	A
32	1a	992	U
32	1a	993	G
32	1a	998	G
32	1a	1001	A
32	1a	1001(A)	G
32	1a	1004	A
32	1a	1005	A
32	1a	1009	G
32	1a	1020	U
32	1a	1022	G
32	1a	1023	G
32	1a	1024	G
32	1a	1025	U
32	1a	1026	G
32	1a	1027	C
32	1a	1028	C

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Mol	Chain	Res	Type
32	1a	1029	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	1037	C
32	1a	1044	A
32	1a	1065	U
32	1a	1068	G
32	1a	1081	G
32	1a	1094	G
32	1a	1095	U
32	1a	1101	A
32	1a	1104	G
32	1a	1124	G
32	1a	1126	U
32	1a	1132	C
32	1a	1134	G
32	1a	1136	U
32	1a	1137	C
32	1a	1139	G
32	1a	1146	A
32	1a	1152	A
32	1a	1159	U
32	1a	1163	C
32	1a	1168	A
32	1a	1183	A
32	1a	1184	G
32	1a	1196	U
32	1a	1197	G
32	1a	1202	G
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	1240	U
32	1a	1256	A
32	1a	1257	U

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Mol	Chain	Res	Type
32	1a	1258	G
32	1a	1270	C
32	1a	1278	U
32	1a	1280	A
32	1a	1286	A
32	1a	1287	A
32	1a	1299	A
32	1a	1300	G
32	1a	1302	U
32	1a	1312	G
32	1a	1320	C
32	1a	1340	A
32	1a	1346	A
32	1a	1347	G
32	1a	1353	G
32	1a	1363	C
32	1a	1364	U
32	1a	1370	G
32	1a	1397	C
32	1a	1419	G
32	1a	1442	G
32	1a	1442(A)	G
32	1a	1447	A
32	1a	1452	C
32	1a	1456	G
32	1a	1467	G
32	1a	1487	G
32	1a	1492	A
32	1a	1493	A
32	1a	1499	A
32	1a	1503	A
32	1a	1504	G
32	1a	1505	G
32	1a	1506	U
32	1a	1517	G
32	1a	1520	G
32	1a	1529	G
32	1a	1530	G
32	1a	1531	A
1	2A	11	G
1	2A	12	U
1	2A	15	G

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Mol	Chain	Res	Type
1	2A	34	C
1	2A	45	C
1	2A	61	G
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	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	215	G
1	2A	216	A
1	2A	221	A
1	2A	222	A
1	2A	229	A
1	2A	230	U
1	2A	233	A
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

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Mol	Chain	Res	Type
1	2A	329	G
1	2A	330	A
1	2A	333	G
1	2A	352	G
1	2A	363	G
1	2A	363(B)	G
1	2A	370	G
1	2A	386	G
1	2A	396	G
1	2A	405	U
1	2A	411	G
1	2A	412	A
1	2A	428	A
1	2A	444	C
1	2A	454	A
1	2A	455	C
1	2A	456	C
1	2A	457	A
1	2A	470	A
1	2A	481	G
1	2A	505	A
1	2A	508	G
1	2A	509	C
1	2A	530	G
1	2A	531	C
1	2A	532	A
1	2A	533	G
1	2A	545	G
1	2A	563	G
1	2A	573	G
1	2A	575	A
1	2A	586	A
1	2A	603	A
1	2A	604	G
1	2A	607	U
1	2A	609	A
1	2A	614(B)	G
1	2A	614(C)	A
1	2A	615	G
1	2A	616	G
1	2A	627	A
1	2A	637	A

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Mol	Chain	Res	Type
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	717	G
1	2A	730	C
1	2A	752	A
1	2A	753	C
1	2A	764	A
1	2A	765	G
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	857	C
1	2A	859	G
1	2A	866	A
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	893	C
1	2A	896	A
1	2A	901	A
1	2A	910	A
1	2A	914	C
1	2A	917	A
1	2A	932	G
1	2A	938	G

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Mol	Chain	Res	Type
1	2A	941	A
1	2A	945	A
1	2A	946	G
1	2A	959	A
1	2A	961	C
1	2A	974	G
1	2A	975	C
1	2A	983	A
1	2A	996	A
1	2A	997	G
1	2A	1012	U
1	2A	1013	C
1	2A	1026	U
1	2A	1033	U
1	2A	1038	C
1	2A	1042	G
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	1059	G
1	2A	1060	U
1	2A	1063	G
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	1078	U
1	2A	1079	C
1	2A	1082	U
1	2A	1083	U

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Mol	Chain	Res	Type
1	2A	1084	A
1	2A	1085	A
1	2A	1086	A
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	1106	G
1	2A	1109	C
1	2A	1111	A
1	2A	1112	G
1	2A	1116	C
1	2A	1117	G
1	2A	1129	A
1	2A	1135	C
1	2A	1136	G
1	2A	1171	G
1	2A	1179	C
1	2A	1211	U
1	2A	1212	G
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	1273	U
1	2A	1300	U
1	2A	1301	A
1	2A	1303	G
1	2A	1314	C
1	2A	1321	A
1	2A	1352	U
1	2A	1359	A
1	2A	1360	A
1	2A	1365	A
1	2A	1368	G

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Mol	Chain	Res	Type
1	2A	1380	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	1453	U
1	2A	1459	G
1	2A	1467	C
1	2A	1471	A
1	2A	1482	G
1	2A	1493	C
1	2A	1494	A
1	2A	1497	U
1	2A	1508	A
1	2A	1509	C
1	2A	1509(A)	A
1	2A	1531	C
1	2A	1542	A
1	2A	1543	C
1	2A	1547	C
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	1595	G
1	2A	1608	A
1	2A	1609	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

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Mol	Chain	Res	Type
1	2A	1701	A
1	2A	1721	G
1	2A	1722	A
1	2A	1740	G
1	2A	1746	G
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	1786	A
1	2A	1791	A
1	2A	1800	C
1	2A	1801	G
1	2A	1816	G
1	2A	1828	G
1	2A	1829	A
1	2A	1835	G
1	2A	1847	A
1	2A	1848	A
1	2A	1877	A
1	2A	1878	G
1	2A	1889	A
1	2A	1900	A
1	2A	1906	G
1	2A	1913	A
1	2A	1914	C
1	2A	1919	A
1	2A	1929	G
1	2A	1930	G
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	1984	G
1	2A	1993	U
1	2A	1997	G

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Mol	Chain	Res	Type
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	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	2111	C
1	2A	2112	G
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	2121	G
1	2A	2123	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	2140	C
1	2A	2145	C
1	2A	2146	C
1	2A	2147	G
1	2A	2148	G

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Mol	Chain	Res	Type
1	2A	2150	U
1	2A	2151	G
1	2A	2153	G
1	2A	2155	G
1	2A	2157	G
1	2A	2158	A
1	2A	2159	G
1	2A	2161	C
1	2A	2162	G
1	2A	2163	C
1	2A	2164	C
1	2A	2165	G
1	2A	2166	G
1	2A	2167	U
1	2A	2172	U
1	2A	2173	A
1	2A	2174	C
1	2A	2175	C
1	2A	2176	A
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	2218	U
1	2A	2219	G
1	2A	2225	A
1	2A	2238	G
1	2A	2239	G
1	2A	2268	A
1	2A	2269	A
1	2A	2275	C
1	2A	2278	A
1	2A	2280	G
1	2A	2283	C
1	2A	2287	A

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Mol	Chain	Res	Type
1	2A	2289	G
1	2A	2305	A
1	2A	2308	G
1	2A	2312	U
1	2A	2320	A
1	2A	2321	G
1	2A	2322	A
1	2A	2325	G
1	2A	2334	G
1	2A	2336	A
1	2A	2347	C
1	2A	2350	C
1	2A	2383	G
1	2A	2384	G
1	2A	2385	C
1	2A	2406	U
1	2A	2410	G
1	2A	2422	A
1	2A	2423	U
1	2A	2424	C
1	2A	2425	A
1	2A	2429	G
1	2A	2430	A
1	2A	2435	A
1	2A	2439	A
1	2A	2440	C
1	2A	2441	C
1	2A	2448	A
1	2A	2468	G
1	2A	2474	C
1	2A	2476	A
1	2A	2491	U
1	2A	2502	G
1	2A	2505	G
1	2A	2518	A
1	2A	2529	G
1	2A	2554	U
1	2A	2566	A
1	2A	2567	G
1	2A	2573	C
1	2A	2585	U
1	2A	2602	A

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Mol	Chain	Res	Type
1	2A	2609	U
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	2689	U
1	2A	2690	C
1	2A	2702	U
1	2A	2712(A)	A
1	2A	2713	A
1	2A	2714	G
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	2778	A
1	2A	2779	U
1	2A	2789	C
1	2A	2802	G
1	2A	2818	G
1	2A	2820	A
1	2A	2821	A
1	2A	2833	G
1	2A	2835	A
1	2A	2872	G
1	2A	2880	C
1	2A	2894	G
1	2A	2896	C
2	2B	2	C
2	2B	7	G
2	2B	8	U
2	2B	12	C
2	2B	32	C
2	2B	33	G
2	2B	35	U
2	2B	42	C

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Mol	Chain	Res	Type
2	2B	56	G
2	2B	73	A
2	2B	84	C
2	2B	106	G
2	2B	110	G
2	2B	115	G
2	2B	120	A
32	2a	5	U
32	2a	9	G
32	2a	22	G
32	2a	32	A
32	2a	39	G
32	2a	47	C
32	2a	48	C
32	2a	50	A
32	2a	51	A
32	2a	61	G
32	2a	78	G
32	2a	80	G
32	2a	88	A
32	2a	89	C
32	2a	101	A
32	2a	116	A
32	2a	121	C
32	2a	131	C
32	2a	151	A
32	2a	163	C
32	2a	174	C
32	2a	182	U
32	2a	189(C)	C
32	2a	189(F)	U
32	2a	194	C
32	2a	195	A
32	2a	197	A
32	2a	202	U
32	2a	203	U
32	2a	204	U
32	2a	216	G
32	2a	220	G
32	2a	231	G
32	2a	247	G
32	2a	251	G

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Mol	Chain	Res	Type
32	2a	258	G
32	2a	266	G
32	2a	267	C
32	2a	289	G
32	2a	318	G
32	2a	319	G
32	2a	321	A
32	2a	328	C
32	2a	332	G
32	2a	350	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	384	G
32	2a	397	A
32	2a	398	C
32	2a	406	G
32	2a	412	A
32	2a	413	G
32	2a	424	G
32	2a	429	U
32	2a	430	A
32	2a	438	G
32	2a	439	A
32	2a	442	C
32	2a	452	A
32	2a	458	C
32	2a	461	A
32	2a	470	C
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

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Mol	Chain	Res	Type
32	2a	520	A
32	2a	521	G
32	2a	531	U
32	2a	532	A
32	2a	533	A
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	589	C
32	2a	596	C
32	2a	630	G
32	2a	631	G
32	2a	632	A
32	2a	650	G
32	2a	653	A
32	2a	660	G
32	2a	665	A
32	2a	687	A
32	2a	688	G
32	2a	690	G
32	2a	702	A
32	2a	723	U
32	2a	731	G
32	2a	735	C
32	2a	749	C
32	2a	753	A
32	2a	754	C
32	2a	755	G
32	2a	774	G
32	2a	777	A
32	2a	793	U
32	2a	794	A
32	2a	817	C
32	2a	821	G
32	2a	828	A
32	2a	829	G
32	2a	836	G

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Mol	Chain	Res	Type
32	2a	840	C
32	2a	841	U
32	2a	848	C
32	2a	851	G
32	2a	854	G
32	2a	859	A
32	2a	872	A
32	2a	914	A
32	2a	916	G
32	2a	926	G
32	2a	927	G
32	2a	934	C
32	2a	942	G
32	2a	943	U
32	2a	960	U
32	2a	961	U
32	2a	965	A
32	2a	968	A
32	2a	969	A
32	2a	971	G
32	2a	972	C
32	2a	974	A
32	2a	975	A
32	2a	976	G
32	2a	977	A
32	2a	992	U
32	2a	993	G
32	2a	994	A
32	2a	995	C
32	2a	1004	A
32	2a	1005	A
32	2a	1006	C
32	2a	1007	C
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	C

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Mol	Chain	Res	Type
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	1037	C
32	2a	1041	A
32	2a	1044	A
32	2a	1053	G
32	2a	1054	C
32	2a	1055	A
32	2a	1065	U
32	2a	1066	C
32	2a	1068	G
32	2a	1081	G
32	2a	1094	G
32	2a	1101	A
32	2a	1113	C
32	2a	1122	U
32	2a	1125	U
32	2a	1128	C
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
32	2a	1142	G
32	2a	1147	C
32	2a	1152	A
32	2a	1159	U
32	2a	1160	G
32	2a	1161	C
32	2a	1183	A
32	2a	1184	G
32	2a	1196	U
32	2a	1197	G
32	2a	1201	A
32	2a	1213	A

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Mol	Chain	Res	Type
32	2a	1214	C
32	2a	1224	G
32	2a	1227	A
32	2a	1228	C
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	1281	U
32	2a	1282	C
32	2a	1286	A
32	2a	1287	A
32	2a	1297	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	1338	G
32	2a	1340	A
32	2a	1346	A
32	2a	1347	G
32	2a	1353	G
32	2a	1363	C
32	2a	1363(A)	A
32	2a	1383	C
32	2a	1384	C
32	2a	1397	C
32	2a	1400	5MC
32	2a	1401	G
32	2a	1419	G
32	2a	1442	G

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Mol	Chain	Res	Type
32	2a	1442(A)	G
32	2a	1442(B)	A
32	2a	1446	U
32	2a	1452	C
32	2a	1456	G
32	2a	1457	G
32	2a	1458	G
32	2a	1459	C
32	2a	1492	A
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	1528	U
32	2a	1529	G
32	2a	1530	G

All (69) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1A	34	C
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	774	A
1	1A	776	G
1	1A	827	U
1	1A	839	U
1	1A	840	C
1	1A	888	C
1	1A	895	U
1	1A	974	G
1	1A	1047	G
1	1A	1067	A
1	1A	1142(A)	A
1	1A	1174	A

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Mol	Chain	Res	Type
1	1A	1175	U
1	1A	1210	A
1	1A	1300	U
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	249	C
1	2A	266	G
1	2A	271(M)	G
1	2A	277	C
1	2A	532	A
1	2A	752	A
1	2A	764	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	1379	A
1	2A	1420	U
1	2A	1442	G
1	2A	1491	G
1	2A	1992	G
1	2A	2126	A

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Mol	Chain	Res	Type
1	2A	2171	A
1	2A	2172	U
1	2A	2321	G
1	2A	2406	U
1	2A	2439	A
1	2A	2689	U
1	2A	2756	U

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

52 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	5MC	1A	1942	1,57	19,22,23	1.42	3 (15%)	26,32,35	1.09	2 (7%)
1	5MC	2A	1962	1,57	19,22,23	1.67	3 (15%)	26,32,35	1.11	2 (7%)
1	OMC	2A	1920	1	19,22,23	0.79	0	25,31,34	0.95	1 (4%)
1	OMU	1A	2552	1,57	19,22,23	1.26	3 (15%)	25,31,34	1.92	6 (24%)
32	4OC	1a	1402	32	20,23,24	0.72	0	25,32,35	1.01	1 (4%)
32	MA6	2a	1519	32	23,26,27	0.42	0	33,38,41	2.09	9 (27%)
1	5MU	1A	1915	1	19,22,23	1.47	4 (21%)	27,32,35	2.29	9 (33%)
32	5MC	2a	1400	32	19,22,23	1.56	3 (15%)	26,32,35	1.28	4 (15%)
1	5MC	1A	1962	1	19,22,23	1.71	3 (15%)	26,32,35	1.14	4 (15%)
1	PSU	1A	2605	1	18,21,22	1.36	3 (16%)	21,30,33	2.19	4 (19%)
54	PPU	1w	76	1,54	37,40,41	1.21	5 (13%)	47,57,60	1.93	11 (23%)
1	5MC	2A	1942	1	19,22,23	1.83	3 (15%)	26,32,35	1.19	2 (7%)
1	OMG	1A	2251	1,55	23,26,27	1.26	3 (13%)	32,38,41	2.01	5 (15%)
1	OMG	2A	2251	1,57,55	23,26,27	1.18	3 (13%)	32,38,41	1.93	6 (18%)
1	PSU	2A	1911	1	18,21,22	1.43	2 (11%)	21,30,33	2.01	3 (14%)
32	UR3	2a	1498	32	19,22,23	0.98	1 (5%)	26,32,35	1.75	3 (11%)
1	OMU	2A	2552	1,57	19,22,23	1.23	4 (21%)	25,31,34	1.97	6 (24%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
43	0TD	2l	92	43	8,9,10	4.37	2 (25%)	6,11,13	4.35	3 (50%)
32	MA6	2a	1518	32	23,26,27	0.38	0	33,38,41	2.03	9 (27%)
32	5MC	2a	1404	32	19,22,23	1.78	3 (15%)	26,32,35	1.24	4 (15%)
1	PSU	1A	1917	1	18,21,22	1.33	2 (11%)	21,30,33	2.00	4 (19%)
1	2MA	1A	2503	1,57	22,25,26	1.47	6 (27%)	32,37,40	2.29	7 (21%)
32	5MC	2a	1407	32	19,22,23	1.57	3 (15%)	26,32,35	1.13	3 (11%)
32	G7M	1a	527	32,57	23,26,27	1.49	3 (13%)	34,39,42	1.67	5 (14%)
32	2MG	1a	1207	32	23,26,27	1.23	3 (13%)	33,38,41	2.30	8 (24%)
32	M2G	1a	966	32	24,27,28	1.31	3 (12%)	33,40,43	1.84	5 (15%)
43	0TD	1l	92	43	8,9,10	4.78	2 (25%)	6,11,13	2.20	3 (50%)
1	5MU	2A	1915	1	19,22,23	1.46	4 (21%)	27,32,35	2.18	9 (33%)
1	PSU	2A	1917	1	18,21,22	1.34	2 (11%)	21,30,33	1.97	3 (14%)
32	MA6	1a	1519	32	23,26,27	0.44	0	33,38,41	1.99	9 (27%)
32	5MC	2a	967	32	19,22,23	1.83	2 (10%)	26,32,35	1.09	2 (7%)
32	PSU	1a	516	32,57	18,21,22	1.40	2 (11%)	21,30,33	1.93	3 (14%)
1	PSU	1A	1911	1	18,21,22	1.39	2 (11%)	21,30,33	1.96	4 (19%)
32	2MG	2a	1207	32	23,26,27	1.21	2 (8%)	33,38,41	2.20	7 (21%)
32	M2G	2a	966	32	24,27,28	1.28	3 (12%)	33,40,43	1.82	5 (15%)
32	G7M	2a	527	32,57	23,26,27	1.50	3 (13%)	34,39,42	1.68	5 (14%)
32	5MC	1a	1404	32	19,22,23	1.60	3 (15%)	26,32,35	1.08	2 (7%)
1	2MA	2A	2503	1,57	22,25,26	1.45	3 (13%)	32,37,40	2.44	9 (28%)
32	UR3	1a	1498	32	19,22,23	1.04	1 (5%)	26,32,35	1.89	4 (15%)
54	PPU	2w	76	1,54	37,40,41	1.23	3 (8%)	47,57,60	2.04	12 (25%)
32	5MC	1a	967	32	19,22,23	1.67	3 (15%)	26,32,35	1.10	2 (7%)
32	5MC	1a	1407	32	19,22,23	1.69	2 (10%)	26,32,35	1.14	3 (11%)
1	OMC	1A	1920	1	19,22,23	0.79	0	25,31,34	0.96	1 (4%)
32	4OC	2a	1402	32	20,23,24	0.76	0	25,32,35	0.93	1 (4%)
55	8AN	2x	76	57,55	21,24,25	1.42	3 (14%)	26,35,38	2.22	9 (34%)
32	MA6	1a	1518	32	23,26,27	0.37	0	33,38,41	1.96	9 (27%)
1	PSU	2A	2605	1	18,21,22	1.28	2 (11%)	21,30,33	2.07	4 (19%)
55	8AN	1x	76	57,55	21,24,25	1.35	3 (14%)	26,35,38	2.32	10 (38%)
1	5MU	1A	1939	1,57	19,22,23	1.38	5 (26%)	27,32,35	2.28	6 (22%)
1	5MU	2A	1939	1,57	19,22,23	1.44	6 (31%)	27,32,35	2.21	6 (22%)
32	5MC	1a	1400	32	19,22,23	1.76	3 (15%)	26,32,35	1.17	2 (7%)
32	PSU	2a	516	32,57	18,21,22	1.32	2 (11%)	21,30,33	2.02	5 (23%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	5MC	1A	1942	1,57	-	0/7/25/26	0/2/2/2
1	5MC	2A	1962	1,57	-	0/7/25/26	0/2/2/2
1	OMC	2A	1920	1	-	0/9/27/28	0/2/2/2
1	OMU	1A	2552	1,57	-	0/9/27/28	0/2/2/2
32	4OC	1a	1402	32	-	0/9/29/30	0/2/2/2
32	MA6	2a	1519	32	-	2/11/29/30	0/3/3/3
1	5MU	1A	1915	1	-	2/7/25/26	0/2/2/2
32	5MC	2a	1400	32	-	2/7/25/26	0/2/2/2
1	5MC	1A	1962	1	-	0/7/25/26	0/2/2/2
1	PSU	1A	2605	1	-	0/7/25/26	0/2/2/2
54	PPU	1w	76	1,54	-	0/25/43/44	0/4/4/4
1	5MC	2A	1942	1	-	0/7/25/26	0/2/2/2
1	OMG	1A	2251	1,55	-	0/9/27/28	0/3/3/3
1	OMG	2A	2251	1,57,55	-	1/9/27/28	0/3/3/3
1	PSU	2A	1911	1	-	0/7/25/26	0/2/2/2
32	UR3	2a	1498	32	-	0/7/25/26	0/2/2/2
1	OMU	2A	2552	1,57	-	0/9/27/28	0/2/2/2
43	0TD	2l	92	43	-	2/7/12/14	-
32	MA6	2a	1518	32	-	0/11/29/30	0/3/3/3
32	5MC	2a	1404	32	-	0/7/25/26	0/2/2/2
1	PSU	1A	1917	1	-	0/7/25/26	0/2/2/2
1	2MA	1A	2503	1,57	-	1/7/25/26	0/3/3/3
32	5MC	2a	1407	32	-	0/7/25/26	0/2/2/2
32	G7M	1a	527	32,57	-	2/7/25/26	0/3/3/3
32	2MG	1a	1207	32	-	0/9/27/28	0/3/3/3
32	M2G	1a	966	32	-	0/11/29/30	0/3/3/3
43	0TD	1l	92	43	-	2/7/12/14	-
1	5MU	2A	1915	1	-	2/7/25/26	0/2/2/2
1	PSU	2A	1917	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	967	32	-	0/7/25/26	0/2/2/2
32	PSU	1a	516	32,57	-	0/7/25/26	0/2/2/2
1	PSU	1A	1911	1	-	0/7/25/26	0/2/2/2
32	2MG	2a	1207	32	-	0/9/27/28	0/3/3/3
32	M2G	2a	966	32	-	0/11/29/30	0/3/3/3
32	G7M	2a	527	32,57	-	1/7/25/26	0/3/3/3
32	5MC	1a	1404	32	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	2MA	2A	2503	1,57	-	2/7/25/26	0/3/3/3
32	UR3	1a	1498	32	-	0/7/25/26	0/2/2/2
54	PPU	2w	76	1,54	-	2/25/43/44	0/4/4/4
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	OMC	1A	1920	1	-	1/9/27/28	0/2/2/2
32	4OC	2a	1402	32	-	0/9/29/30	0/2/2/2
55	8AN	2x	76	57,55	-	1/7/25/26	0/3/3/3
32	MA6	1a	1518	32	-	0/11/29/30	0/3/3/3
1	PSU	2A	2605	1	-	0/7/25/26	0/2/2/2
55	8AN	1x	76	57,55	-	1/7/25/26	0/3/3/3
1	5MU	1A	1939	1,57	-	0/7/25/26	0/2/2/2
1	5MU	2A	1939	1,57	-	0/7/25/26	0/2/2/2
32	5MC	1a	1400	32	-	0/7/25/26	0/2/2/2
32	PSU	2a	516	32,57	-	0/7/25/26	0/2/2/2

All (129) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
43	1l	92	0TD	CB-SB	-12.67	1.69	1.82
43	2l	92	0TD	CB-SB	-11.69	1.70	1.82
32	2a	967	5MC	C5-C4	6.91	1.49	1.44
1	2A	1942	5MC	C5-C4	6.85	1.49	1.44
32	2a	1404	5MC	C5-C4	6.60	1.49	1.44
32	1a	1400	5MC	C5-C4	6.39	1.49	1.44
1	1A	1962	5MC	C5-C4	6.27	1.48	1.44
32	1a	1407	5MC	C5-C4	6.11	1.48	1.44
32	1a	967	5MC	C5-C4	6.10	1.48	1.44
1	2A	1962	5MC	C5-C4	6.09	1.48	1.44
32	1a	1404	5MC	C5-C4	5.80	1.48	1.44
32	2a	1407	5MC	C5-C4	5.58	1.48	1.44
32	2a	1400	5MC	C5-C4	5.47	1.48	1.44
32	1a	527	G7M	C5-N7	-4.57	1.33	1.39
32	2a	527	G7M	C5-N7	-4.55	1.33	1.39
1	1A	1942	5MC	C5-C4	4.52	1.47	1.44
54	1w	76	PPU	C5-C4	4.43	1.47	1.39
54	2w	76	PPU	C5-C4	4.35	1.46	1.39
1	2A	2503	2MA	C5-C4	4.20	1.46	1.39
1	1A	2503	2MA	C5-C4	4.16	1.46	1.39
55	2x	76	8AN	C5-N7	-4.13	1.31	1.39
1	2A	1911	PSU	C6-C5	3.80	1.39	1.35
32	1a	516	PSU	C6-C5	3.57	1.39	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1A	1911	PSU	C6-C5	3.53	1.39	1.35
55	1x	76	8AN	C5-N7	-3.50	1.32	1.39
1	2A	1917	PSU	C6-C5	3.34	1.39	1.35
32	1a	527	G7M	C5-C4	3.31	1.46	1.38
32	1a	966	M2G	C5-C4	3.30	1.47	1.38
1	1A	1917	PSU	C6-C5	3.29	1.38	1.35
32	2a	966	M2G	C5-C4	3.28	1.47	1.38
32	2a	516	PSU	C6-C5	3.26	1.38	1.35
32	2a	527	G7M	C5-C4	3.21	1.46	1.38
43	1l	92	0TD	CB-CA	3.16	1.55	1.54
1	2A	2251	OMG	C5-C4	3.13	1.47	1.38
55	1x	76	8AN	C5-C4	-3.11	1.33	1.39
32	2a	1207	2MG	C5-C4	3.11	1.47	1.38
1	1A	1915	5MU	C2-N1	3.09	1.43	1.38
1	2A	1915	5MU	C2-N1	3.08	1.43	1.38
55	2x	76	8AN	C5-C4	-3.04	1.33	1.39
1	1A	2251	OMG	C5-C4	3.04	1.47	1.38
32	1a	1400	5MC	C6-C5	3.03	1.39	1.34
32	1a	1407	5MC	C6-C5	3.02	1.39	1.34
1	2A	1915	5MU	C6-C5	3.01	1.39	1.34
32	1a	1207	2MG	C5-C4	3.00	1.47	1.38
1	2A	1939	5MU	C6-C5	2.99	1.39	1.34
1	1A	2251	OMG	C6-N1	-2.97	1.33	1.38
1	1A	1939	5MU	C6-C5	2.93	1.39	1.34
32	2a	967	5MC	C6-C5	2.91	1.39	1.34
32	2a	1407	5MC	C6-C5	2.87	1.39	1.34
54	2w	76	PPU	C5-C6	2.87	1.48	1.41
1	1A	2605	PSU	C4-N3	-2.86	1.33	1.38
1	1A	1942	5MC	C6-C5	2.86	1.39	1.34
1	2A	1939	5MU	C4-N3	-2.86	1.33	1.38
1	2A	1942	5MC	C6-C5	2.82	1.39	1.34
32	1a	967	5MC	C6-C5	2.78	1.39	1.34
32	1a	1404	5MC	C6-C5	2.78	1.39	1.34
1	2A	1962	5MC	C6-C5	2.75	1.39	1.34
1	1A	2503	2MA	C5-N7	-2.73	1.34	1.39
32	2a	966	M2G	C2-N2	2.72	1.40	1.35
32	2a	1404	5MC	C6-C5	2.70	1.39	1.34
1	2A	2503	2MA	C5-C6	2.68	1.48	1.41
32	1a	966	M2G	C6-N1	-2.64	1.33	1.38
1	1A	1915	5MU	C4-N3	-2.64	1.33	1.38
1	2A	2605	PSU	C6-C5	2.63	1.38	1.35
32	1a	966	M2G	C2-N2	2.63	1.39	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
54	1w	76	PPU	C5-C6	2.61	1.48	1.41
1	1A	1915	5MU	C4-C5	2.60	1.49	1.44
1	1A	1911	PSU	C4-N3	-2.58	1.34	1.38
32	2a	1400	5MC	C6-C5	2.58	1.38	1.34
1	2A	1911	PSU	C4-N3	-2.58	1.34	1.38
1	1A	1915	5MU	C6-C5	2.57	1.38	1.34
32	1a	516	PSU	C4-N3	-2.56	1.34	1.38
1	1A	1939	5MU	C4-N3	-2.55	1.34	1.38
1	1A	1917	PSU	C4-N3	-2.54	1.34	1.38
1	2A	2552	OMU	C4-N3	-2.53	1.34	1.38
1	2A	1915	5MU	C4-N3	-2.53	1.34	1.38
54	2w	76	PPU	C5-N7	-2.52	1.34	1.39
1	1A	1942	5MC	C6-N1	-2.50	1.33	1.38
55	2x	76	8AN	C5-C6	-2.49	1.34	1.41
1	1A	2552	OMU	C4-N3	-2.49	1.34	1.38
32	2a	527	G7M	C6-N1	-2.49	1.34	1.38
55	1x	76	8AN	C5-C6	-2.48	1.34	1.41
1	2A	2251	OMG	C6-N1	-2.44	1.34	1.38
1	2A	2503	2MA	C8-N7	2.43	1.36	1.31
1	2A	1917	PSU	C4-N3	-2.43	1.34	1.38
1	2A	2605	PSU	C4-N3	-2.43	1.34	1.38
54	1w	76	PPU	C5-N7	-2.43	1.34	1.39
1	2A	1939	5MU	C4-C5	2.43	1.48	1.44
1	1A	2503	2MA	C8-N7	2.42	1.36	1.31
1	1A	1962	5MC	C6-N1	-2.41	1.33	1.38
32	2a	1400	5MC	C6-N1	-2.40	1.33	1.38
1	1A	2605	PSU	C6-C5	2.38	1.37	1.35
32	2a	516	PSU	C4-N3	-2.38	1.34	1.38
1	1A	1939	5MU	C6-N1	-2.37	1.34	1.38
1	1A	1962	5MC	C6-C5	2.37	1.38	1.34
1	1A	2552	OMU	C2-N1	2.36	1.42	1.38
1	2A	1915	5MU	C4-C5	2.36	1.48	1.44
32	1a	1400	5MC	C6-N1	-2.36	1.34	1.38
32	1a	1207	2MG	C6-N1	-2.35	1.34	1.38
43	2l	92	0TD	CB-CA	2.33	1.55	1.54
1	2A	1962	5MC	C6-N1	-2.30	1.34	1.38
32	2a	966	M2G	C6-N1	-2.29	1.34	1.38
1	1A	1939	5MU	C2-N3	-2.27	1.34	1.38
1	2A	1942	5MC	C6-N1	-2.24	1.34	1.38
32	2a	1404	5MC	C6-N1	-2.23	1.34	1.38
32	1a	527	G7M	C6-N1	-2.22	1.34	1.38
1	1A	2552	OMU	C5-C4	2.22	1.48	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1A	2503	2MA	C4-N9	-2.22	1.33	1.37
1	2A	2251	OMG	C5-N7	-2.20	1.34	1.39
1	1A	2251	OMG	C5-N7	-2.18	1.34	1.39
1	2A	1939	5MU	C2-N3	-2.18	1.34	1.38
1	1A	1939	5MU	C4-C5	2.17	1.48	1.44
1	2A	2552	OMU	C5-C4	2.16	1.48	1.43
1	2A	1939	5MU	C2-N1	2.15	1.41	1.38
32	2a	1498	UR3	C6-C5	2.15	1.40	1.35
1	1A	2503	2MA	C5-C6	2.12	1.46	1.41
1	2A	1939	5MU	C6-N1	-2.12	1.34	1.38
1	2A	2552	OMU	C2-N3	-2.11	1.34	1.38
1	1A	2503	2MA	C8-N9	-2.10	1.34	1.37
1	1A	2605	PSU	C2-N1	-2.09	1.33	1.36
32	1a	967	5MC	C6-N1	-2.08	1.34	1.38
32	1a	1404	5MC	C6-N1	-2.07	1.34	1.38
32	2a	1207	2MG	C6-N1	-2.06	1.35	1.38
54	1w	76	PPU	C8-N7	2.06	1.35	1.31
32	1a	1207	2MG	C4-N9	-2.05	1.32	1.38
32	1a	1498	UR3	C2-N1	2.05	1.41	1.38
32	2a	1407	5MC	C6-N1	-2.04	1.34	1.38
1	2A	2552	OMU	C2-N1	2.03	1.41	1.38
54	1w	76	PPU	C4-N9	-2.01	1.33	1.37

All (261) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
43	2l	92	0TD	CSB-SB-CB	-9.74	84.85	102.36
1	2A	2503	2MA	C5-C4-N3	-8.03	118.73	127.18
1	1A	2503	2MA	C5-C4-N3	-7.90	118.86	127.18
32	1a	1498	UR3	C4-N3-C2	-7.60	118.46	124.58
32	2a	1498	UR3	C4-N3-C2	-7.15	118.82	124.58
32	1a	1207	2MG	C2-N3-C4	7.02	120.78	112.00
32	2a	1207	2MG	C2-N3-C4	6.81	120.52	112.00
1	1A	2605	PSU	N1-C2-N3	6.60	122.14	115.17
1	2A	2503	2MA	N3-C4-N9	6.50	135.23	126.99
1	2A	1911	PSU	N1-C2-N3	6.35	121.87	115.17
1	1A	2503	2MA	N3-C4-N9	6.32	135.01	126.99
1	1A	2251	OMG	C5-C4-N3	-6.30	118.36	128.39
32	1a	966	M2G	C5-C4-N3	-6.18	118.55	128.39
1	2A	2605	PSU	N1-C2-N3	6.14	121.64	115.17
32	2a	516	PSU	N1-C2-N3	6.11	121.62	115.17
1	1A	1911	PSU	N1-C2-N3	6.11	121.61	115.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	2A	1917	PSU	N1-C2-N3	6.09	121.59	115.17
1	1A	1917	PSU	N1-C2-N3	6.08	121.58	115.17
1	2A	2251	OMG	C5-C4-N3	-5.96	118.90	128.39
32	1a	516	PSU	N1-C2-N3	5.83	121.32	115.17
55	1x	76	8AN	N1-C2-N3	-5.83	119.75	128.58
54	2w	76	PPU	C5-C4-N3	-5.79	118.74	126.72
32	2a	966	M2G	C5-C4-N3	-5.78	119.18	128.39
55	2x	76	8AN	N1-C2-N3	-5.76	119.86	128.58
54	1w	76	PPU	C5-C4-N3	-5.68	118.90	126.72
32	1a	1207	2MG	C5-C4-N3	-5.62	119.45	128.39
1	2A	1939	5MU	C4-N3-C2	-5.52	120.10	127.34
1	1A	1939	5MU	C4-N3-C2	-5.51	120.11	127.34
32	2a	1207	2MG	C5-C4-N3	-5.48	119.66	128.39
1	2A	1939	5MU	N3-C2-N1	5.44	121.97	114.89
1	1A	2552	OMU	N3-C2-N1	5.44	121.97	114.89
1	1A	2251	OMG	C2-N3-C4	5.39	121.58	112.30
32	1a	527	G7M	N9-C4-N3	5.31	136.57	125.95
55	1x	76	8AN	C5-C4-N3	-5.25	119.48	126.72
1	2A	2552	OMU	N3-C2-N1	5.25	121.72	114.89
32	2a	527	G7M	C5-C4-N3	-5.24	118.24	128.15
1	1A	1939	5MU	N3-C2-N1	5.18	121.64	114.89
32	2a	527	G7M	N9-C4-N3	5.13	136.21	125.95
32	1a	527	G7M	C5-C4-N3	-5.11	118.50	128.15
1	2A	1915	5MU	N3-C2-N1	5.08	121.50	114.89
1	2A	2251	OMG	C2-N3-C4	5.05	120.99	112.30
1	1A	1915	5MU	N3-C2-N1	4.99	121.39	114.89
1	2A	1939	5MU	C5-C4-N3	4.89	119.57	115.32
55	2x	76	8AN	C5-C4-N3	-4.82	120.07	126.72
1	2A	2552	OMU	C4-N3-C2	-4.81	120.64	126.61
1	1A	1939	5MU	C5-C4-N3	4.80	119.50	115.32
32	1a	1519	MA6	N1-C2-N3	-4.76	121.38	128.58
1	1A	2552	OMU	C4-N3-C2	-4.75	120.72	126.61
32	2a	1519	MA6	N1-C2-N3	-4.74	121.40	128.58
1	1A	1915	5MU	C4-N3-C2	-4.72	121.16	127.34
32	2a	1518	MA6	N1-C2-N3	-4.68	121.50	128.58
32	2a	527	G7M	C2-N3-C4	4.65	120.32	112.30
1	1A	2605	PSU	C4-N3-C2	-4.61	120.02	126.37
1	2A	1915	5MU	C4-N3-C2	-4.61	121.29	127.34
32	1a	527	G7M	C2-N3-C4	4.60	120.23	112.30
54	2w	76	PPU	N3-C4-N9	4.59	134.98	127.17
32	2a	1518	MA6	C5-C4-N3	-4.58	120.41	126.72
1	1A	1939	5MU	O4-C4-C5	-4.57	119.69	124.92

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1A	2251	OMG	N9-C4-N3	4.54	135.03	125.95
32	1a	1519	MA6	C5-C4-N3	-4.52	120.49	126.72
32	1a	1518	MA6	N1-C2-N3	-4.47	121.82	128.58
1	1A	1915	5MU	C1'-N1-C2	4.44	125.56	117.59
32	1a	966	M2G	N9-C4-N3	4.40	134.75	125.95
1	2A	2605	PSU	C4-N3-C2	-4.39	120.33	126.37
32	2a	966	M2G	C2-N3-C4	4.38	120.61	112.51
54	1w	76	PPU	N3-C4-N9	4.37	134.61	127.17
32	2a	1519	MA6	C5-C4-N3	-4.35	120.73	126.72
32	1a	966	M2G	C2-N3-C4	4.34	120.55	112.51
1	1A	2605	PSU	O2-C2-N1	-4.31	118.34	122.79
1	2A	2251	OMG	N9-C4-N3	4.30	134.56	125.95
54	1w	76	PPU	C2-N1-C6	4.25	122.21	111.83
1	1A	1915	5MU	C5-C4-N3	4.20	118.98	115.32
1	2A	1917	PSU	O2-C2-N1	-4.20	118.46	122.79
32	2a	516	PSU	C4-N3-C2	-4.18	120.61	126.37
1	1A	1917	PSU	C4-N3-C2	-4.18	120.61	126.37
32	2a	1519	MA6	C4-C5-N7	-4.14	105.84	110.58
1	1A	1939	5MU	C5-C6-N1	-4.08	118.88	123.31
54	2w	76	PPU	C2-N1-C6	4.07	121.78	111.83
32	1a	1518	MA6	C5-C4-N3	-4.05	121.14	126.72
32	1a	1518	MA6	C2-N1-C6	4.05	121.72	111.83
32	2a	1519	MA6	C5-N7-C8	4.05	109.81	103.45
32	2a	966	M2G	N9-C4-N3	4.01	133.97	125.95
1	2A	1911	PSU	C4-N3-C2	-4.01	120.85	126.37
1	1A	2503	2MA	N6-C6-N1	4.00	122.43	117.03
54	2w	76	PPU	C4-C5-N7	-3.99	106.02	110.58
32	1a	1207	2MG	C6-C5-N7	3.97	137.51	130.29
1	2A	1939	5MU	C5-C6-N1	-3.96	119.01	123.31
32	2a	1518	MA6	C2-N1-C6	3.95	121.49	111.83
32	2a	1519	MA6	C2-N1-C6	3.95	121.49	111.83
32	1a	516	PSU	C4-N3-C2	-3.94	120.95	126.37
1	2A	1942	5MC	C5-C6-N1	-3.92	119.06	123.31
32	1a	1400	5MC	C5-C6-N1	-3.91	119.07	123.31
1	2A	1915	5MU	C5-C4-N3	3.91	118.72	115.32
32	1a	1519	MA6	C2-N1-C6	3.89	121.33	111.83
1	1A	1911	PSU	C4-N3-C2	-3.88	121.03	126.37
1	2A	2503	2MA	C4-C5-N7	-3.86	106.17	110.58
1	2A	1915	5MU	O4-C4-C5	-3.84	120.52	124.92
1	2A	1915	5MU	C1'-N1-C2	3.84	124.49	117.59
1	2A	1939	5MU	O4-C4-C5	-3.84	120.53	124.92
32	2a	1207	2MG	C6-C5-N7	3.82	137.24	130.29

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	2a	1518	MA6	C4-C5-N7	-3.82	106.22	110.58
54	1w	76	PPU	C4-C5-N7	-3.81	106.22	110.58
32	1a	1207	2MG	N1-C2-N2	3.81	120.44	116.56
1	2A	2605	PSU	O2-C2-N1	-3.79	118.88	122.79
1	2A	2503	2MA	C4-N9-C8	3.79	109.72	105.74
32	2a	1518	MA6	C5-N7-C8	3.78	109.38	103.45
32	1a	1518	MA6	C5-N7-C8	3.76	109.36	103.45
1	1A	1915	5MU	C1'-N1-C6	-3.75	114.98	121.15
54	2w	76	PPU	C2-N3-C4	3.73	120.94	111.83
1	1A	1939	5MU	O2-C2-N1	-3.71	117.97	122.80
32	2a	1400	5MC	C5-C6-N1	-3.70	119.29	123.31
32	2a	516	PSU	O2-C2-N1	-3.67	119.01	122.79
1	1A	1942	5MC	C5-C6-N1	-3.66	119.34	123.31
1	2A	1962	5MC	C5-C6-N1	-3.66	119.34	123.31
1	2A	1917	PSU	C4-N3-C2	-3.66	121.33	126.37
32	2a	1207	2MG	N9-C4-N3	3.65	133.25	125.95
54	2w	76	PPU	N1-C6-N6	3.63	121.27	116.86
54	1w	76	PPU	C2-N3-C4	3.62	120.67	111.83
32	1a	1518	MA6	C4-C5-N7	-3.55	106.52	110.58
32	2a	966	M2G	C6-C5-N7	3.54	136.73	130.29
32	1a	1519	MA6	C4-C5-N7	-3.52	106.55	110.58
32	1a	1207	2MG	N9-C4-N3	3.52	132.99	125.95
32	2a	1404	5MC	C5-C4-N3	-3.52	118.15	121.75
1	1A	2251	OMG	C6-C5-N7	3.49	136.65	130.29
32	2a	1519	MA6	N9-C8-N7	-3.49	108.99	113.94
55	1x	76	8AN	C2-N3-C4	3.46	120.28	111.83
32	1a	967	5MC	C5-C6-N1	-3.45	119.56	123.31
55	2x	76	8AN	N9-C8-N7	-3.45	109.04	113.94
32	1a	1519	MA6	C5-N7-C8	3.45	108.87	103.45
32	2a	967	5MC	C5-C6-N1	-3.44	119.57	123.31
32	1a	1518	MA6	N9-C8-N7	-3.44	109.06	113.94
32	1a	1519	MA6	C2-N3-C4	3.42	120.19	111.83
1	1A	1915	5MU	O4-C4-C5	-3.42	121.01	124.92
55	1x	76	8AN	N9-C8-N7	-3.41	109.10	113.94
1	1A	1917	PSU	O2-C2-N1	-3.40	119.28	122.79
43	1l	92	0TD	OD2-CG-CB	3.38	120.45	113.15
32	2a	1518	MA6	C2-N3-C4	3.37	120.05	111.83
55	2x	76	8AN	C2-N3-C4	3.36	120.03	111.83
32	2a	1498	UR3	C5-C4-N3	3.36	119.46	115.04
32	2a	1207	2MG	N1-C2-N2	3.35	119.98	116.56
1	1A	1911	PSU	O2-C2-N1	-3.35	119.33	122.79
32	2a	1519	MA6	C2-N3-C4	3.35	120.00	111.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	2A	2251	OMG	C6-C5-N7	3.31	136.31	130.29
43	2l	92	0TD	OD2-CG-CB	3.30	120.28	113.15
32	1a	1407	5MC	C5-C6-N1	-3.28	119.75	123.31
54	2w	76	PPU	N3-C2-N1	-3.28	123.62	128.58
32	2a	1518	MA6	N9-C8-N7	-3.25	109.33	113.94
54	1w	76	PPU	N3-C2-N1	-3.25	123.67	128.58
32	1a	1404	5MC	C5-C6-N1	-3.23	119.81	123.31
1	2A	1911	PSU	O2-C2-N1	-3.23	119.46	122.79
1	2A	2552	OMU	C2'-C1'-N1	-3.23	108.12	114.24
32	1a	966	M2G	C6-C5-N7	3.19	136.09	130.29
1	2A	2552	OMU	C5-C4-N3	3.18	119.25	114.80
1	2A	2503	2MA	C5-N7-C8	3.18	108.44	103.45
54	2w	76	PPU	C5-N7-C8	3.16	108.42	103.45
32	1a	1498	UR3	C5-C4-N3	3.16	119.20	115.04
32	1a	516	PSU	O2-C2-N1	-3.16	119.53	122.79
43	1l	92	0TD	CSB-SB-CB	-3.14	96.72	102.36
32	1a	1207	2MG	C4-C5-N7	-3.06	105.83	110.67
54	1w	76	PPU	C10-N6-C6	-3.04	112.78	120.52
32	1a	1207	2MG	N2-C2-N3	-3.03	116.64	120.51
1	2A	2503	2MA	N9-C8-N7	-3.03	109.64	113.94
55	2x	76	8AN	C5-N7-C8	3.03	108.21	103.45
1	1A	2503	2MA	C4-C5-N7	-3.02	107.13	110.58
32	1a	1518	MA6	C2-N3-C4	3.02	119.20	111.83
1	2A	1915	5MU	C1'-N1-C6	-3.01	116.20	121.15
32	2a	1207	2MG	C4-C5-N7	-2.98	105.94	110.67
32	2a	1407	5MC	C5-C6-N1	-2.97	120.08	123.31
54	2w	76	PPU	C10-N6-C6	-2.97	112.96	120.52
32	1a	1400	5MC	C5-C4-N3	-2.94	118.74	121.75
1	1A	2552	OMU	O2-C2-N1	-2.93	118.98	122.80
55	1x	76	8AN	C5-N7-C8	2.92	108.03	103.45
1	2A	2503	2MA	N6-C6-N1	2.91	120.96	117.03
54	2w	76	PPU	C4-N9-C8	2.91	108.80	105.74
32	1a	1519	MA6	N9-C8-N7	-2.90	109.82	113.94
55	1x	76	8AN	C5-C4-N9	2.88	108.95	105.81
1	2A	2552	OMU	O4-C4-C5	-2.87	120.22	125.16
32	1a	1402	4OC	C6-C5-C4	2.84	120.42	117.00
1	1A	2503	2MA	C4-N9-C8	2.84	108.72	105.74
32	2a	1207	2MG	N2-C2-N3	-2.82	116.91	120.51
1	1A	2552	OMU	O4-C4-C5	-2.79	120.35	125.16
32	2a	966	M2G	C4-C5-N7	-2.78	106.26	110.67
1	1A	1962	5MC	C5-C6-N1	-2.77	120.30	123.31
54	1w	76	PPU	C5-N7-C8	2.77	107.81	103.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	2a	1407	5MC	C5-C4-N3	-2.76	118.92	121.75
32	2a	1404	5MC	C5-C6-N1	-2.74	120.34	123.31
32	2a	1518	MA6	N3-C4-N9	2.72	131.79	127.17
32	1a	1407	5MC	C5-C4-N3	-2.69	118.99	121.75
32	1a	966	M2G	C4-C5-N7	-2.69	106.41	110.67
32	1a	1519	MA6	N3-C4-N9	2.69	131.74	127.17
1	2A	2552	OMU	O2-C2-N1	-2.69	119.30	122.80
1	1A	1915	5MU	O2-C2-N3	-2.67	116.57	121.49
1	1A	2251	OMG	C4-C5-N7	-2.66	106.45	110.67
1	1A	1915	5MU	C5M-C5-C4	2.66	121.62	118.78
54	1w	76	PPU	C4-N9-C8	2.65	108.53	105.74
32	2a	1518	MA6	C4-C5-C6	2.65	118.65	115.91
54	1w	76	PPU	N1-C6-N6	2.63	120.06	116.86
55	1x	76	8AN	O4'-C1'-N9	2.62	113.12	108.09
1	1A	2552	OMU	C5-C4-N3	2.62	118.47	114.80
32	1a	1518	MA6	C4-C5-C6	2.60	118.59	115.91
32	1a	1404	5MC	C5-C4-N3	-2.59	119.10	121.75
32	1a	1518	MA6	N3-C4-N9	2.59	131.57	127.17
55	1x	76	8AN	N3-C4-N9	2.59	131.57	127.17
1	2A	1942	5MC	C5-C4-N3	-2.58	119.11	121.75
55	2x	76	8AN	N3-C4-N9	2.57	131.53	127.17
1	1A	1962	5MC	C5-C4-N3	-2.55	119.14	121.75
55	1x	76	8AN	C6-C5-C4	2.55	120.66	117.18
32	1a	967	5MC	C5-C4-N3	-2.54	119.15	121.75
1	1A	2552	OMU	C2'-C1'-N1	-2.52	109.46	114.24
1	2A	2251	OMG	C4-C5-N7	-2.51	106.69	110.67
1	2A	2503	2MA	C2-N1-C6	2.50	121.94	118.10
1	2A	1915	5MU	C5-C6-N1	-2.48	120.62	123.31
1	2A	1939	5MU	O2-C2-N1	-2.48	119.57	122.80
32	1a	1498	UR3	C3U-N3-C2	2.47	121.64	117.33
32	1a	1207	2MG	CM2-N2-C2	-2.47	118.35	123.65
1	2A	2503	2MA	C6-C5-N7	2.46	136.83	132.09
1	2A	1915	5MU	O2-C2-N3	-2.43	117.00	121.49
54	2w	76	PPU	N9-C8-N7	-2.43	110.49	113.94
32	2a	1519	MA6	N3-C4-N9	2.43	131.29	127.17
1	1A	1920	OMC	O2-C2-N3	-2.40	118.55	122.33
32	2a	967	5MC	C5-C4-N3	-2.40	119.30	121.75
1	1A	2503	2MA	C2-N1-C6	2.40	121.78	118.10
32	2a	1498	UR3	C3U-N3-C4	2.38	121.17	117.87
55	2x	76	8AN	C5-C4-N9	2.37	108.39	105.81
32	1a	1519	MA6	C4-C5-C6	2.36	118.36	115.91
32	2a	1404	5MC	O2-C2-N3	-2.36	118.61	122.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
55	2x	76	8AN	C4'-O4'-C1'	-2.35	104.28	109.47
43	2l	92	0TD	OD1-CG-CB	-2.35	117.52	122.44
54	2w	76	PPU	C5-C6-N6	-2.35	121.62	125.33
1	1A	2605	PSU	C5-C6-N1	-2.33	118.91	122.14
32	1a	527	G7M	O6-C6-C5	-2.31	122.85	128.01
1	1A	1915	5MU	C5-C6-N1	-2.31	120.81	123.31
32	2a	1400	5MC	C5-C4-N3	-2.30	119.39	121.75
32	1a	1498	UR3	C6-N1-C2	-2.29	119.92	121.80
32	2a	1407	5MC	O2-C2-N3	-2.29	118.72	122.33
55	1x	76	8AN	C4-C5-N7	-2.29	107.97	110.58
1	2A	1962	5MC	C5-C4-N3	-2.27	119.42	121.75
32	2a	1519	MA6	C4-C5-C6	2.27	118.26	115.91
1	2A	1920	OMC	O2-C2-N3	-2.27	118.75	122.33
1	1A	1962	5MC	C1'-N1-C6	-2.27	117.42	121.15
32	2a	1400	5MC	C1'-N1-C6	-2.26	117.42	121.15
32	1a	1407	5MC	O2-C2-N3	-2.22	118.83	122.33
32	2a	516	PSU	O4'-C1'-C2'	2.19	108.18	105.15
1	1A	2503	2MA	C5-N7-C8	2.17	106.86	103.45
43	1l	92	0TD	OD1-CG-CB	-2.17	117.90	122.44
32	2a	516	PSU	C5-C6-N1	-2.16	119.14	122.14
55	2x	76	8AN	O4'-C1'-N9	2.16	112.23	108.09
1	2A	2605	PSU	C5-C6-N1	-2.14	119.17	122.14
32	2a	1402	4OC	C6-C5-C4	2.13	119.57	117.00
32	2a	1404	5MC	CM5-C5-C6	-2.12	119.97	122.85
54	1w	76	PPU	N9-C8-N7	-2.11	110.94	113.94
1	1A	1942	5MC	C5-C4-N3	-2.11	119.59	121.75
1	1A	1917	PSU	C5-C6-N1	-2.11	119.22	122.14
1	2A	2251	OMG	O6-C6-C5	-2.09	121.02	126.53
32	2a	527	G7M	C5-C6-N1	2.09	116.16	111.84
1	1A	1962	5MC	CM5-C5-C6	-2.08	120.03	122.85
32	1a	527	G7M	C5-C6-N1	2.08	116.14	111.84
32	2a	1400	5MC	O2-C2-N3	-2.06	119.09	122.33
32	2a	527	G7M	O6-C6-C5	-2.06	123.42	128.01
1	2A	1915	5MU	C6-N1-C2	-2.03	119.28	121.30
1	1A	1911	PSU	O4'-C1'-C2'	2.01	107.94	105.15

There are no chirality outliers.

All (26) 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

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Mol	Chain	Res	Type	Atoms
43	1l	92	0TD	CA-CB-SB-CSB
43	1l	92	0TD	CG-CB-SB-CSB
1	2A	1915	5MU	O4'-C1'-N1-C2
1	2A	1915	5MU	O4'-C1'-N1-C6
1	2A	2251	OMG	C1'-C2'-O2'-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
54	2w	76	PPU	C3'-C4'-C5'-O5'
32	1a	1519	MA6	O4'-C4'-C5'-O5'
32	2a	1400	5MC	C3'-C4'-C5'-O5'
32	2a	1519	MA6	O4'-C4'-C5'-O5'
54	2w	76	PPU	O4'-C4'-C5'-O5'
32	2a	1400	5MC	O4'-C4'-C5'-O5'
55	2x	76	8AN	C4'-C5'-O5'-P
32	1a	1519	MA6	C3'-C4'-C5'-O5'
32	2a	1519	MA6	C3'-C4'-C5'-O5'
32	1a	527	G7M	C3'-C4'-C5'-O5'
32	2a	527	G7M	C3'-C4'-C5'-O5'
1	1A	2503	2MA	C4'-C5'-O5'-P
32	1a	527	G7M	C4'-C5'-O5'-P
1	2A	2503	2MA	C4'-C5'-O5'-P
1	1A	1920	OMC	C2'-C1'-N1-C2
1	2A	2503	2MA	O4'-C4'-C5'-O5'

There are no ring outliers.

17 monomers are involved in 18 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	2A	1920	OMC	1	0
32	1a	1402	4OC	1	0
32	2a	1519	MA6	2	0
32	2a	1400	5MC	1	0
54	1w	76	PPU	2	0
32	2a	1518	MA6	1	0
32	2a	1404	5MC	1	0
43	1l	92	0TD	1	0
1	2A	1915	5MU	1	0
1	2A	1917	PSU	1	0
32	1a	1519	MA6	1	0
32	2a	1402	4OC	2	0
55	2x	76	8AN	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
32	1a	1518	MA6	1	0
1	1A	1939	5MU	1	0
1	2A	1939	5MU	1	0
32	1a	1400	5MC	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2490 ligands modelled in this entry, 2480 are monoatomic - leaving 10 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	$\# Z > 2$
61	SF4	1d	306	35	0,12,12	-	-	-		
58	MPD	1a	1868	-	7,7,7	0.41	0	9,10,10	0.56	0
59	ARG	1F	318	-	10,11,11	0.73	1 (10%)	9,13,13	0.94	1 (11%)
58	MPD	1T	208	-	7,7,7	0.29	0	9,10,10	0.32	0
58	MPD	2B	220	-	7,7,7	0.34	0	9,10,10	0.28	0
61	SF4	2d	501	35	0,12,12	-	-	-		
58	MPD	2A	3732	-	7,7,7	0.38	0	9,10,10	0.22	0
58	MPD	18	104	-	7,7,7	0.30	0	9,10,10	0.30	0
59	ARG	1B	231	-	10,11,11	0.71	1 (10%)	9,13,13	0.93	1 (11%)
58	MPD	1A	4014	-	7,7,7	0.36	0	9,10,10	0.44	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
61	SF4	1d	306	35	-	-	0/6/5/5

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
58	MPD	1a	1868	-	-	4/5/5/5	-
59	ARG	1F	318	-	-	2/11/11/11	-
58	MPD	1T	208	-	-	5/5/5/5	-
58	MPD	2B	220	-	-	4/5/5/5	-
61	SF4	2d	501	35	-	-	0/6/5/5
58	MPD	2A	3732	-	-	2/5/5/5	-
58	MPD	18	104	-	-	1/5/5/5	-
59	ARG	1B	231	-	-	3/11/11/11	-
58	MPD	1A	4014	-	-	1/5/5/5	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
59	1F	318	ARG	OXT-C	-2.13	1.23	1.30
59	1B	231	ARG	OXT-C	-2.03	1.24	1.30

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
59	1F	318	ARG	OXT-C-O	-2.71	117.93	124.08
59	1B	231	ARG	OXT-C-O	-2.56	118.26	124.08

There are no chirality outliers.

All (22) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
58	1T	208	MPD	C1-C2-C3-C4
58	1a	1868	MPD	C2-C3-C4-O4
58	1a	1868	MPD	C2-C3-C4-C5
59	1B	231	ARG	C-CA-CB-CG
59	1F	318	ARG	NE-CD-CG-CB
59	1B	231	ARG	OXT-C-CA-N
58	1T	208	MPD	O2-C2-C3-C4
58	2B	220	MPD	C2-C3-C4-O4
58	1T	208	MPD	CM-C2-C3-C4
58	1a	1868	MPD	C1-C2-C3-C4
58	2A	3732	MPD	C1-C2-C3-C4
58	1A	4014	MPD	C2-C3-C4-C5
58	1T	208	MPD	C2-C3-C4-C5
58	2B	220	MPD	C2-C3-C4-C5

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Mol	Chain	Res	Type	Atoms
58	2B	220	MPD	O2-C2-C3-C4
58	1T	208	MPD	C2-C3-C4-O4
58	18	104	MPD	C2-C3-C4-O4
58	1a	1868	MPD	CM-C2-C3-C4
58	2A	3732	MPD	CM-C2-C3-C4
58	2B	220	MPD	C1-C2-C3-C4
59	1B	231	ARG	N-CA-CB-CG
59	1F	318	ARG	N-CA-CB-CG

There are no ring outliers.

4 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
58	1a	1868	MPD	4	0
58	1T	208	MPD	1	0
58	18	104	MPD	1	0
59	1B	231	ARG	1	0

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, 95th 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%)	-0.48	172 (6%) 27 24	22, 38, 90, 100	0
1	2A	2856/2915 (97%)	-0.00	185 (6%) 25 22	32, 55, 93, 102	0
2	1B	120/121 (99%)	-0.26	1 (0%) 82 83	34, 51, 67, 82	0
2	2B	120/121 (99%)	0.77	4 (3%) 49 50	59, 75, 82, 89	0
3	1D	275/276 (99%)	-0.20	4 (1%) 72 74	24, 37, 52, 71	0
3	2D	275/276 (99%)	0.14	5 (1%) 67 69	30, 49, 61, 81	0
4	1E	204/206 (99%)	-0.11	2 (0%) 79 80	22, 41, 61, 71	0
4	2E	204/206 (99%)	0.25	2 (0%) 79 80	33, 54, 68, 77	0
5	1F	203/210 (96%)	0.04	4 (1%) 65 66	23, 43, 68, 84	0
5	2F	203/210 (96%)	0.60	6 (2%) 52 53	33, 64, 76, 85	0
6	1G	181/182 (99%)	0.73	14 (7%) 19 17	49, 64, 75, 84	0
6	2G	181/182 (99%)	1.81	68 (37%) 1 0	70, 79, 85, 89	0
7	1H	174/180 (96%)	0.32	5 (2%) 53 55	40, 54, 66, 72	0
7	2H	173/180 (96%)	1.33	30 (17%) 4 3	65, 77, 83, 86	0
8	1I	147/148 (99%)	0.92	10 (6%) 23 21	42, 68, 78, 82	0
8	2I	146/148 (98%)	1.26	21 (14%) 6 4	56, 73, 81, 83	0
9	1N	140/140 (100%)	-0.06	0 100 100	29, 40, 59, 74	0
9	2N	140/140 (100%)	0.63	5 (3%) 46 46	45, 62, 73, 77	0
10	1O	122/122 (100%)	-0.13	1 (0%) 82 83	31, 41, 59, 64	0
10	2O	122/122 (100%)	0.25	0 100 100	43, 52, 64, 72	0
11	1P	149/150 (99%)	0.10	1 (0%) 84 86	23, 47, 67, 80	0
11	2P	149/150 (99%)	0.57	4 (2%) 56 57	39, 65, 78, 83	0
12	1Q	141/141 (100%)	-0.11	0 100 100	27, 40, 52, 68	0
12	2Q	141/141 (100%)	0.85	8 (5%) 29 26	41, 63, 72, 78	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
13	1R	118/118 (100%)	-0.23	0 100 100	27, 37, 54, 63	0
13	2R	118/118 (100%)	0.24	0 100 100	40, 50, 59, 71	0
14	1S	110/112 (98%)	0.28	1 (0%) 81 82	40, 51, 63, 69	0
14	2S	110/112 (98%)	1.33	14 (12%) 8 6	64, 71, 76, 79	0
15	1T	131/146 (89%)	0.09	5 (3%) 44 44	34, 45, 67, 79	0
15	2T	131/146 (89%)	0.38	4 (3%) 51 52	44, 56, 72, 81	0
16	1U	116/118 (98%)	-0.30	1 (0%) 81 82	25, 33, 48, 67	0
16	2U	116/118 (98%)	0.47	0 100 100	40, 58, 70, 75	0
17	1V	101/101 (100%)	-0.10	0 100 100	26, 43, 59, 68	0
17	2V	101/101 (100%)	0.70	3 (2%) 52 53	43, 68, 73, 80	0
18	1W	112/113 (99%)	-0.13	3 (2%) 56 57	28, 34, 53, 76	0
18	2W	112/113 (99%)	0.29	4 (3%) 46 46	38, 49, 65, 85	0
19	1X	95/96 (98%)	0.02	2 (2%) 63 65	30, 39, 61, 74	0
19	2X	95/96 (98%)	0.74	6 (6%) 26 23	45, 59, 72, 78	0
20	1Y	107/110 (97%)	0.33	2 (1%) 66 67	38, 50, 65, 75	0
20	2Y	107/110 (97%)	1.01	8 (7%) 20 17	58, 68, 76, 83	0
21	1Z	203/206 (98%)	0.56	6 (2%) 52 53	42, 59, 73, 82	0
21	2Z	201/206 (97%)	1.40	33 (16%) 4 3	63, 74, 81, 84	0
22	10	83/85 (97%)	-0.06	1 (1%) 76 78	30, 38, 50, 62	0
22	20	83/85 (97%)	0.97	5 (6%) 27 24	45, 60, 69, 74	0
23	11	97/98 (98%)	0.16	1 (1%) 79 80	29, 45, 67, 72	0
23	21	97/98 (98%)	0.45	2 (2%) 63 65	39, 55, 73, 77	0
24	12	70/72 (97%)	0.27	2 (2%) 53 55	39, 50, 59, 81	0
24	22	70/72 (97%)	0.89	4 (5%) 29 26	61, 67, 73, 77	0
25	13	59/60 (98%)	-0.06	1 (1%) 69 71	27, 38, 63, 74	0
25	23	59/60 (98%)	0.74	3 (5%) 33 31	51, 60, 77, 79	0
26	14	69/71 (97%)	1.22	15 (21%) 2 2	56, 76, 88, 95	0
26	24	69/71 (97%)	2.20	35 (50%) 0 0	78, 84, 90, 93	0
27	15	59/60 (98%)	-0.21	1 (1%) 69 71	25, 36, 54, 63	0
27	25	59/60 (98%)	0.11	0 100 100	35, 49, 65, 73	0
28	16	53/54 (98%)	-0.04	0 100 100	33, 43, 58, 60	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
28	26	53/54 (98%)	0.42	0 100 100	50, 59, 65, 71	0
29	17	48/49 (97%)	-0.14	4 (8%) 17 15	24, 31, 56, 61	0
29	27	48/49 (97%)	0.20	4 (8%) 17 15	35, 40, 64, 70	0
30	18	64/65 (98%)	-0.26	0 100 100	30, 36, 42, 53	0
30	28	64/65 (98%)	0.39	1 (1%) 70 73	45, 54, 61, 65	0
31	19	37/37 (100%)	0.07	0 100 100	33, 42, 54, 58	0
31	29	37/37 (100%)	0.96	4 (10%) 11 9	55, 64, 72, 74	0
32	1a	1488/1521 (97%)	0.28	62 (4%) 40 40	36, 67, 89, 100	0
32	2a	1492/1521 (98%)	0.62	106 (7%) 22 19	44, 73, 91, 102	0
33	1b	231/256 (90%)	1.41	52 (22%) 2 1	63, 75, 83, 88	0
33	2b	231/256 (90%)	1.77	79 (34%) 1 1	70, 80, 86, 91	0
34	1c	206/239 (86%)	0.95	16 (7%) 19 16	62, 70, 80, 84	0
34	2c	206/239 (86%)	1.85	77 (37%) 1 0	72, 81, 85, 92	0
35	1d	208/209 (99%)	1.10	32 (15%) 5 3	56, 69, 78, 84	0
35	2d	208/209 (99%)	1.13	18 (8%) 16 14	59, 69, 77, 82	0
36	1e	148/162 (91%)	0.65	2 (1%) 73 75	52, 63, 72, 80	0
36	2e	148/162 (91%)	1.08	11 (7%) 20 18	57, 70, 79, 85	0
37	1f	100/101 (99%)	0.67	3 (3%) 52 53	49, 64, 71, 79	0
37	2f	100/101 (99%)	0.71	1 (1%) 79 80	58, 67, 75, 82	0
38	1g	155/156 (99%)	0.68	3 (1%) 66 67	60, 69, 76, 81	0
38	2g	155/156 (99%)	1.54	39 (25%) 1 1	69, 79, 83, 87	0
39	1h	137/138 (99%)	0.71	5 (3%) 46 46	56, 66, 71, 78	0
39	2h	137/138 (99%)	0.95	6 (4%) 39 38	62, 71, 76, 79	0
40	1i	127/128 (99%)	1.39	23 (18%) 3 3	58, 75, 80, 82	0
40	2i	126/128 (98%)	2.40	79 (62%) 0 0	74, 82, 87, 89	0
41	1j	97/105 (92%)	1.58	28 (28%) 1 1	60, 75, 83, 89	0
41	2j	96/105 (91%)	2.66	68 (70%) 0 0	72, 82, 86, 91	0
42	1k	114/129 (88%)	0.60	4 (3%) 47 47	44, 62, 72, 77	0
42	2k	114/129 (88%)	0.86	6 (5%) 32 30	58, 70, 78, 81	0
43	1l	121/132 (91%)	0.68	9 (7%) 20 18	49, 59, 68, 76	0
43	2l	121/132 (91%)	0.74	6 (4%) 34 32	54, 63, 70, 75	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
44	1m	116/126 (92%)	1.11	18 (15%) 5 3	60, 72, 78, 80	0
44	2m	114/126 (90%)	1.99	53 (46%) 0 0	72, 81, 85, 87	0
45	1n	60/61 (98%)	1.12	6 (10%) 12 10	63, 68, 76, 79	0
45	2n	60/61 (98%)	2.48	39 (65%) 0 0	75, 80, 85, 89	0
46	1o	88/89 (98%)	0.86	5 (5%) 29 26	46, 63, 74, 76	0
46	2o	88/89 (98%)	1.03	8 (9%) 15 12	59, 69, 78, 81	0
47	1p	82/88 (93%)	1.41	16 (19%) 3 2	59, 69, 76, 83	0
47	2p	82/88 (93%)	1.26	9 (10%) 10 8	61, 68, 76, 79	0
48	1q	99/105 (94%)	1.02	4 (4%) 42 41	55, 67, 75, 80	0
48	2q	99/105 (94%)	0.73	5 (5%) 33 31	57, 67, 75, 79	0
49	1r	68/88 (77%)	0.62	2 (2%) 53 55	54, 61, 75, 82	0
49	2r	68/88 (77%)	0.91	4 (5%) 28 25	61, 69, 78, 85	0
50	1s	83/93 (89%)	1.17	8 (9%) 13 11	63, 74, 79, 82	0
50	2s	83/93 (89%)	2.26	48 (57%) 0 0	68, 82, 86, 89	0
51	1t	96/106 (90%)	1.34	20 (20%) 2 2	60, 70, 78, 82	0
51	2t	98/106 (92%)	0.97	7 (7%) 22 19	56, 67, 78, 80	0
52	1u	23/27 (85%)	1.51	6 (26%) 1 1	65, 69, 72, 74	0
52	2u	23/27 (85%)	2.48	15 (65%) 0 0	74, 79, 82, 82	0
53	1y	97/113 (85%)	0.68	7 (7%) 21 19	53, 62, 72, 76	0
53	2y	96/113 (84%)	2.39	62 (64%) 0 0	71, 80, 87, 89	0
54	1w	3/4 (75%)	0.19	0 100 100	30, 30, 40, 55	0
54	2w	3/4 (75%)	0.74	1 (33%) 1 1	41, 41, 48, 62	0
55	1x	3/4 (75%)	-0.45	0 100 100	28, 28, 30, 41	0
55	2x	3/4 (75%)	0.77	1 (33%) 1 1	37, 37, 40, 55	0
56	1v	3/3 (100%)	-0.46	0 100 100	25, 25, 27, 33	0
56	2v	3/3 (100%)	0.27	0 100 100	40, 40, 44, 51	0
All	All	20796/21490 (96%)	0.44	1806 (8%) 16 14	22, 62, 85, 102	0

All (1806) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
45	2n	2	ALA	9.3
1	1A	1087	G	7.6

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Mol	Chain	Res	Type	RSRZ
1	2A	2147	G	6.5
41	2j	37	PRO	6.1
45	1n	2	ALA	6.1
1	1A	1072	C	6.1
32	2a	1036	G	6.1
53	2y	98	ALA	6.1
51	1t	103	GLY	6.0
26	24	56	VAL	5.9
41	2j	34	VAL	5.7
1	1A	1071	G	5.7
1	1A	1070	A	5.7
26	14	56	VAL	5.7
53	1y	98	ALA	5.6
1	2A	2146	C	5.6
51	2t	6	PRO	5.6
40	2i	102	LEU	5.5
15	1T	37	GLY	5.5
44	2m	6	GLY	5.5
1	1A	1089	G	5.4
1	2A	2124	G	5.3
1	1A	1088	A	5.3
1	1A	1090	U	5.3
32	2a	1030(A)	G	5.3
1	2A	2139	C	5.3
7	1H	2	SER	5.3
44	2m	116	THR	5.3
6	2G	146	TYR	5.2
18	2W	60	ASN	5.2
1	2A	2125	G	5.1
26	14	63	TYR	5.1
41	1j	4	ILE	5.1
44	1m	2	ALA	5.1
3	1D	276	LYS	5.0
33	1b	229	VAL	5.0
32	1a	1036	G	5.0
40	2i	2	GLU	5.0
40	2i	43	ALA	4.8
1	2A	1536	C	4.8
1	2A	1067	A	4.8
21	1Z	51	ALA	4.8
1	1A	1093	G	4.7
26	24	49	PHE	4.7

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Mol	Chain	Res	Type	RSRZ
1	2A	2145	C	4.7
1	2A	2174	C	4.7
1	2A	1091	G	4.7
38	2g	5	ARG	4.7
45	2n	18	VAL	4.7
1	1A	1076	C	4.7
1	1A	1066	U	4.6
1	1A	1069	A	4.6
50	2s	2	PRO	4.6
6	2G	139	LEU	4.6
44	2m	102	ARG	4.6
1	2A	1046	A	4.6
1	2A	2793	G	4.6
34	2c	152	ILE	4.5
15	1T	131	ALA	4.5
20	1Y	1	MET	4.5
15	1T	130	ALA	4.5
33	2b	97	TRP	4.5
1	2A	2803	C	4.5
1	2A	2119	A	4.5
1	1A	1176	G	4.5
1	2A	2144	U	4.5
1	1A	2117	A	4.5
1	1A	1094	U	4.4
40	2i	56	LEU	4.4
51	1t	10	LEU	4.4
35	1d	2	GLY	4.4
44	2m	5	ALA	4.4
1	1A	1078	U	4.4
1	2A	2116	G	4.4
23	2l	2	SER	4.4
1	2A	2168	G	4.4
1	1A	1099	G	4.3
1	2A	1070	A	4.3
33	2b	165	VAL	4.3
40	2i	14	VAL	4.3
26	24	63	TYR	4.3
40	2i	101	PHE	4.3
1	2A	1089	G	4.3
40	2i	21	PRO	4.3
1	1A	2804	C	4.3
1	2A	2137	C	4.3

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Mol	Chain	Res	Type	RSRZ
1	2A	2152	G	4.3
1	1A	1065	U	4.3
29	27	48	LYS	4.3
33	2b	44	LEU	4.3
1	2A	2893	G	4.2
32	2a	1031	G	4.2
8	2I	146	ALA	4.2
32	2a	1030	C	4.2
1	2A	2169	A	4.2
6	2G	76	SER	4.2
1	2A	2165	G	4.2
41	2j	38	ILE	4.2
41	2j	74	ILE	4.2
33	1b	7	VAL	4.2
6	2G	50	ALA	4.2
41	1j	78	ASN	4.2
1	2A	2140	C	4.2
1	1A	1067	A	4.2
1	1A	1073	A	4.2
1	1A	1068	G	4.2
12	2Q	104	PHE	4.2
1	1A	1077	A	4.2
37	1f	90	VAL	4.2
52	2u	14	TRP	4.2
1	1A	2803	C	4.1
1	2A	1084	A	4.1
1	2A	1085	A	4.1
1	2A	2126	A	4.1
1	2A	2136	C	4.1
45	2n	33	VAL	4.1
1	2A	2109	U	4.1
1	2A	2153	G	4.1
1	2A	2802	G	4.1
1	2A	2111	C	4.1
40	2i	123	PRO	4.1
41	2j	76	ASN	4.1
41	2j	72	VAL	4.1
1	1A	1086	A	4.1
41	2j	32	ALA	4.1
23	11	2	SER	4.1
34	2c	77	ILE	4.1
1	1A	1058	G	4.1

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Mol	Chain	Res	Type	RSRZ
1	2A	2805	G	4.1
1	2A	2117	A	4.1
1	2A	2135	A	4.1
34	2c	128	PHE	4.1
55	2x	73	A	4.1
32	2a	1030(B)	C	4.0
1	1A	1081	U	4.0
1	2A	1066	U	4.0
5	1F	208	GLY	4.0
53	2y	40	ILE	4.0
1	1A	1074	G	4.0
41	2j	47	PHE	4.0
45	2n	14	PRO	4.0
47	2p	82	GLN	4.0
32	1a	1001	A	4.0
32	1a	1447	A	4.0
32	2a	1035	A	4.0
1	2A	2138	C	4.0
1	2A	2172	U	4.0
1	2A	2162	G	4.0
32	2a	1033	G	4.0
6	2G	136	ARG	4.0
1	2A	2173	A	4.0
1	1A	1075	C	4.0
1	2A	1064	C	4.0
40	2i	6	GLY	4.0
1	2A	2118	U	4.0
40	1i	66	ARG	4.0
45	2n	30	ALA	4.0
1	1A	1063	G	4.0
32	2a	1001(A)	G	4.0
1	1A	1095	A	4.0
52	2u	2	GLY	4.0
1	1A	888	C	4.0
33	2b	121	LEU	4.0
40	2i	7	THR	4.0
8	1I	147	GLN	4.0
45	2n	3	ARG	4.0
1	1A	1098	A	3.9
1	2A	1073	A	3.9
1	2A	2804	C	3.9
1	2A	2896	C	3.9

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Mol	Chain	Res	Type	RSRZ
1	2A	2133	G	3.9
1	2A	2148	G	3.9
40	2i	126	SER	3.9
41	2j	46	ARG	3.9
1	2A	2142	C	3.9
50	2s	76	PRO	3.9
6	1G	48	GLU	3.9
1	1A	1062	G	3.9
32	1a	1023	G	3.9
41	2j	77	PRO	3.9
1	1A	1102	C	3.9
26	14	59	PHE	3.9
41	2j	27	ALA	3.9
44	2m	24	GLY	3.9
32	2a	1286	A	3.9
40	1i	14	VAL	3.9
1	2A	1087	G	3.8
1	2A	2154	G	3.8
32	1a	1026	G	3.8
32	2a	1034	G	3.8
1	1A	1064	C	3.8
34	1c	107	GLN	3.8
53	2y	60	VAL	3.8
50	2s	34	TRP	3.8
40	2i	125	TYR	3.8
1	1A	1091	G	3.8
32	2a	1003	G	3.8
32	2a	1027	C	3.8
3	2D	276	LYS	3.8
33	2b	38	GLY	3.8
50	1s	13	ASP	3.8
1	2A	2113	U	3.8
33	2b	133	LYS	3.8
38	2g	7	ALA	3.8
40	2i	11	LYS	3.8
35	1d	167	GLY	3.8
1	2A	1092	C	3.8
53	2y	12	ILE	3.8
25	23	60	GLU	3.8
41	2j	91	PRO	3.8
41	2j	44	VAL	3.8
34	2c	5	ILE	3.8

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Mol	Chain	Res	Type	RSRZ
35	1d	157	LEU	3.8
41	2j	75	ILE	3.8
1	1A	2159	G	3.8
50	2s	4	SER	3.7
34	2c	187	ALA	3.7
32	2a	1257	U	3.7
1	2A	1072	C	3.7
1	1A	2793	G	3.7
45	1n	3	ARG	3.7
41	2j	54	PHE	3.7
1	1A	1097	U	3.7
41	2j	88	LEU	3.7
45	2n	7	ILE	3.7
1	1A	1085	A	3.7
40	2i	105	ASP	3.7
1	1A	2174	C	3.7
1	2A	1076	C	3.7
33	2b	230	VAL	3.7
41	2j	65	LEU	3.7
41	2j	90	LEU	3.7
2	2B	1	U	3.7
26	24	67	TYR	3.7
1	1A	2119	A	3.7
32	2a	1030(D)	A	3.7
14	2S	3	ARG	3.7
22	20	3	HIS	3.7
1	1A	1080	C	3.7
32	2a	1029	C	3.7
1	2A	2127	G	3.7
1	2A	2149	G	3.7
32	1a	1030(A)	G	3.7
53	2y	5	ILE	3.7
29	17	48	LYS	3.7
41	2j	78	ASN	3.7
41	2j	79	ARG	3.7
1	1A	2158	A	3.6
33	1b	19	HIS	3.6
33	2b	136	VAL	3.6
40	2i	27	THR	3.6
44	1m	117	VAL	3.6
45	2n	13	THR	3.6
53	2y	42	SER	3.6

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Mol	Chain	Res	Type	RSRZ
11	1P	149	GLU	3.6
32	1a	1030	C	3.6
33	1b	17	PHE	3.6
40	2i	67	GLY	3.6
38	2g	16	LEU	3.6
1	2A	2123	G	3.6
1	1A	2118	U	3.6
53	2y	38	HIS	3.6
34	2c	207	VAL	3.6
1	2A	2107	C	3.6
33	1b	10	LEU	3.6
48	2q	98	LEU	3.6
51	2t	103	GLY	3.6
25	23	2	PRO	3.6
1	2A	2150	U	3.6
1	1A	2805	G	3.6
1	2A	1071	G	3.6
1	2A	2104	G	3.6
1	2A	2106	G	3.6
32	1a	1024	G	3.6
6	1G	146	TYR	3.6
41	2j	100	THR	3.6
1	2A	2171	A	3.6
32	1a	1286	A	3.6
40	2i	127	LYS	3.6
20	2Y	1	MET	3.6
34	1c	2	GLY	3.6
53	2y	27	LEU	3.6
6	1G	88	ILE	3.6
1	2A	1509	C	3.6
1	2A	2105	C	3.6
41	2j	62	HIS	3.6
1	1A	1061	U	3.6
41	1j	83	GLU	3.6
33	2b	7	VAL	3.6
41	1j	87	THR	3.6
1	2A	2134	A	3.6
14	1S	3	ARG	3.6
26	14	55	ARG	3.6
40	2i	66	ARG	3.6
7	2H	136	ILE	3.6
26	24	51	ASP	3.6

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Mol	Chain	Res	Type	RSRZ
1	1A	1175	U	3.5
32	1a	1000	U	3.5
33	1b	236	TYR	3.5
41	2j	42	THR	3.5
26	24	66	SER	3.5
1	1A	2112	G	3.5
1	2A	2894	G	3.5
51	1t	96	GLY	3.5
53	2y	45	PRO	3.5
1	2A	34	C	3.5
1	2A	2143	C	3.5
51	2t	7	LYS	3.5
35	1d	179	GLU	3.5
1	1A	1101	U	3.5
1	1A	2167	U	3.5
45	2n	59	ALA	3.5
53	2y	97	ALA	3.5
44	2m	4	ILE	3.5
1	2A	2114	A	3.5
40	2i	18	PHE	3.5
21	2Z	170	THR	3.5
1	1A	2172	U	3.5
32	2a	1281	U	3.5
34	2c	2	GLY	3.5
1	1A	1057	A	3.5
1	1A	2116	G	3.5
32	1a	1033	G	3.5
26	24	50	VAL	3.5
1	1A	2794	C	3.5
1	2A	2175	C	3.5
2	1B	1	U	3.5
5	2F	21	ALA	3.5
53	2y	8	LYS	3.5
41	2j	64	GLU	3.4
1	2A	6	A	3.4
32	2a	1004	A	3.4
1	1A	1173	G	3.4
1	2A	2115	G	3.4
1	2A	2157	G	3.4
33	1b	230	VAL	3.4
44	1m	116	THR	3.4
41	2j	40	LEU	3.4

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Mol	Chain	Res	Type	RSRZ
1	1A	1079	C	3.4
40	2i	69	GLY	3.4
1	2A	2167	U	3.4
47	1p	19	ILE	3.4
53	2y	7	SER	3.4
47	1p	82	GLN	3.4
32	1a	1031	G	3.4
50	1s	9	VAL	3.4
41	2j	82	ILE	3.4
33	2b	236	TYR	3.4
53	2y	64	SER	3.4
1	1A	1100	C	3.4
1	2A	2129	C	3.4
32	1a	1028	C	3.4
44	2m	106	ASN	3.4
1	1A	1096	A	3.4
6	2G	145	THR	3.4
40	2i	96	LEU	3.4
41	1j	77	PRO	3.4
1	1A	2115	G	3.4
32	1a	1034	G	3.4
32	2a	1026	G	3.4
32	2a	1032	G	3.4
40	2i	9	ARG	3.4
50	2s	10	PHE	3.4
1	1A	2173	A	3.4
39	1h	2	LEU	3.4
6	2G	112	PRO	3.4
47	1p	46	PRO	3.4
40	2i	42	ARG	3.4
52	2u	24	ARG	3.4
1	1A	2125	G	3.3
1	2A	1062	G	3.3
1	2A	2166	G	3.3
32	1a	1001(A)	G	3.3
32	2a	1030(C)	G	3.3
1	1A	2144	U	3.3
32	1a	1037	C	3.3
41	2j	33	GLN	3.3
52	2u	23	PRO	3.3
32	2a	1001	A	3.3
40	2i	37	PHE	3.3

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Mol	Chain	Res	Type	RSRZ
45	2n	21	TYR	3.3
45	2n	34	TYR	3.3
1	1A	1082	U	3.3
1	1A	2130	U	3.3
1	1A	2893	G	3.3
33	2b	132	LYS	3.3
1	1A	1092	C	3.3
50	2s	5	LEU	3.3
7	2H	101	ARG	3.3
1	2A	652(B)	A	3.3
54	2w	73	A	3.3
26	24	59	PHE	3.3
53	2y	43	LYS	3.3
33	1b	33	TYR	3.3
40	2i	4	TYR	3.3
1	1A	2109	U	3.3
1	2A	1082	U	3.3
24	12	70	GLN	3.3
1	2A	2159	G	3.3
51	1t	99	LEU	3.3
40	2i	108	VAL	3.3
33	1b	97	TRP	3.3
33	1b	231	GLU	3.3
1	2A	2176	A	3.3
41	2j	30	SER	3.3
50	2s	12	ASP	3.3
6	2G	12	TYR	3.3
1	2A	1083	U	3.3
40	1i	56	LEU	3.3
40	1i	128	ARG	3.3
53	2y	88	LEU	3.3
1	1A	2168	G	3.3
32	1a	1003	G	3.3
41	2j	49	VAL	3.3
40	1i	64	THR	3.3
52	2u	11	GLY	3.3
6	2G	20	ILE	3.3
33	1b	200	ILE	3.3
1	1A	1084	A	3.2
1	1A	2169	A	3.2
1	2A	2801(A)	A	3.2
40	2i	36	TYR	3.2

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Mol	Chain	Res	Type	RSRZ
41	2j	69	ASN	3.2
1	2A	2130	U	3.2
19	1X	95	LEU	3.2
44	2m	54	VAL	3.2
53	2y	20	VAL	3.2
40	2i	63	ILE	3.2
1	1A	2145	C	3.2
1	1A	2147	G	3.2
1	1A	2792	G	3.2
1	1A	2894	G	3.2
32	1a	1027	C	3.2
32	2a	1002	G	3.2
32	2a	1037	C	3.2
32	2a	1124	G	3.2
41	2j	35	SER	3.2
1	2A	229	A	3.2
1	2A	1095	A	3.2
38	2g	76	ARG	3.2
33	1b	94	ASN	3.2
33	2b	15	VAL	3.2
38	2g	80	VAL	3.2
53	2y	62	VAL	3.2
5	1F	16	GLY	3.2
51	1t	100	ILE	3.2
53	2y	52	ALA	3.2
1	1A	2142	C	3.2
1	2A	2108	C	3.2
32	1a	1029	C	3.2
32	2a	1028	C	3.2
32	2a	1038	C	3.2
44	1m	102	ARG	3.2
32	2a	994	A	3.2
1	1A	1026	U	3.2
1	1A	2113	U	3.2
1	2A	2132	U	3.2
32	1a	1020	U	3.2
18	2W	112	GLY	3.2
35	1d	170	VAL	3.2
40	2i	115	GLY	3.2
45	2n	5	ALA	3.2
38	2g	156	TRP	3.2
1	2A	1075	C	3.2

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Mol	Chain	Res	Type	RSRZ
1	2A	2141	G	3.2
33	2b	22	LYS	3.2
40	1i	127	LYS	3.2
44	2m	113	PRO	3.2
1	1A	887	A	3.2
1	2A	2892	A	3.2
38	2g	154	TYR	3.2
47	2p	38	TYR	3.2
15	2T	69	GLY	3.2
26	14	54	GLY	3.2
1	2A	1090	U	3.2
41	1j	74	ILE	3.2
50	2s	63	THR	3.2
53	2y	6	THR	3.2
33	2b	21	ARG	3.1
52	2u	6	ARG	3.1
6	2G	117	PHE	3.1
26	14	49	PHE	3.1
33	2b	17	PHE	3.1
1	1A	889	C	3.1
1	2A	652(T)	C	3.1
33	2b	118	LEU	3.1
53	2y	3	MET	3.1
33	1b	37	ASN	3.1
41	1j	76	ASN	3.1
1	2A	2160	G	3.1
7	2H	45	VAL	3.1
26	24	43	TYR	3.1
34	2c	185	GLY	3.1
50	2s	41	VAL	3.1
6	2G	144	ILE	3.1
34	2c	124	ILE	3.1
1	1A	2150	U	3.1
1	2A	2897	U	3.1
15	2T	131	ALA	3.1
33	2b	207	ALA	3.1
38	2g	2	ALA	3.1
40	2i	45	ALA	3.1
40	2i	122	ALA	3.1
50	2s	3	ARG	3.1
6	2G	142	PRO	3.1
50	2s	42	PRO	3.1

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Mol	Chain	Res	Type	RSRZ
53	2y	4	ASN	3.1
8	2I	3	VAL	3.1
32	1a	630	G	3.1
50	2s	9	VAL	3.1
1	1A	2170	A	3.1
1	2A	1077	A	3.1
1	2A	1096	A	3.1
35	1d	70	ILE	3.1
33	2b	237	ALA	3.1
33	2b	152	PHE	3.1
44	2m	66	LEU	3.1
50	2s	16	LEU	3.1
51	1t	72	LEU	3.1
1	2A	2179	C	3.1
44	2m	100	GLY	3.1
34	2c	195	VAL	3.1
34	2c	48	TYR	3.1
43	1l	64	TYR	3.1
24	22	70	GLN	3.1
1	1A	6	A	3.1
1	1A	2152	G	3.1
1	2A	2110	G	3.1
32	1a	1005	A	3.1
32	2a	630	G	3.1
38	2g	117	ALA	3.1
1	1A	1083	U	3.1
1	2A	2180	U	3.1
32	1a	1257	U	3.1
53	2y	44	GLU	3.1
6	1G	80	PHE	3.1
34	2c	196	LEU	3.1
39	2h	2	LEU	3.1
15	1T	129	ARG	3.1
50	2s	29	ARG	3.1
41	2j	31	GLY	3.1
6	2G	28	VAL	3.1
34	2c	68	VAL	3.1
41	1j	98	ILE	3.1
41	2j	24	VAL	3.1
1	1A	2136	C	3.1
1	2A	645	C	3.1
1	2A	2164	C	3.1

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Mol	Chain	Res	Type	RSRZ
26	24	52	THR	3.0
41	2j	92	THR	3.0
33	1b	188	ALA	3.0
44	2m	87	TYR	3.0
1	2A	2158	A	3.0
1	2A	1094	U	3.0
1	1A	1056	G	3.0
1	2A	2112	G	3.0
1	2A	2151	G	3.0
21	2Z	95	PRO	3.0
21	2Z	125	LEU	3.0
34	2c	175	LEU	3.0
35	1d	23	GLY	3.0
53	2y	66	LYS	3.0
53	2y	54	ILE	3.0
40	2i	103	THR	3.0
1	2A	2163	C	3.0
1	2A	2183	C	3.0
32	1a	63	C	3.0
40	2i	119	ALA	3.0
40	2i	62	TYR	3.0
1	1A	1103	A	3.0
1	1A	2171	A	3.0
1	2A	1081	U	3.0
1	2A	2170	A	3.0
32	1a	1030(D)	A	3.0
33	1b	232	PRO	3.0
53	2y	14	PRO	3.0
22	20	7	LEU	3.0
39	1h	133	LEU	3.0
50	2s	30	LEU	3.0
6	1G	49	ASP	3.0
1	2A	2131	G	3.0
32	1a	1032	G	3.0
45	2n	61	TRP	3.0
50	2s	31	ILE	3.0
33	2b	123	ALA	3.0
34	2c	129	ALA	3.0
53	1y	97	ALA	3.0
40	2i	88	TYR	3.0
50	2s	69	HIS	3.0
1	1A	2107	C	3.0

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Mol	Chain	Res	Type	RSRZ
1	2A	2161	C	3.0
32	1a	1030(B)	C	3.0
44	2m	41	PRO	3.0
6	2G	152	LEU	3.0
19	2X	66	LEU	3.0
1	2A	1065	U	3.0
32	2a	1025	U	3.0
41	1j	99	LYS	3.0
1	1A	2153	G	3.0
1	2A	1074	G	3.0
32	1a	1021	G	3.0
38	2g	84	ASN	3.0
50	1s	68	GLY	3.0
8	1I	107	VAL	3.0
35	1d	178	VAL	3.0
6	2G	100	TRP	3.0
41	2j	26	ALA	3.0
44	2m	51	ALA	3.0
40	2i	90	PRO	3.0
52	1u	23	PRO	3.0
44	2m	59	TYR	3.0
1	1A	2146	C	3.0
1	2A	2178	C	3.0
50	2s	71	LEU	3.0
32	2a	1219	U	3.0
12	2Q	30	GLY	3.0
6	2G	52	ILE	2.9
6	2G	149	VAL	2.9
7	2H	89	ILE	2.9
6	2G	137	GLU	2.9
25	23	59	VAL	2.9
33	2b	164	VAL	2.9
40	2i	109	VAL	2.9
41	1j	100	THR	2.9
41	2j	48	THR	2.9
41	2j	67	THR	2.9
15	2T	130	ALA	2.9
34	2c	50	ALA	2.9
45	2n	49	HIS	2.9
11	2P	15	ARG	2.9
40	2i	10	ARG	2.9
33	2b	148	TYR	2.9

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Mol	Chain	Res	Type	RSRZ
33	2b	149	LEU	2.9
34	1c	62	ASP	2.9
40	2i	91	ASP	2.9
1	2A	1086	A	2.9
32	2a	1447	A	2.9
6	2G	159	VAL	2.9
21	2Z	191	VAL	2.9
26	24	40	HIS	2.9
1	1A	2123	G	2.9
1	2A	1047	G	2.9
1	2A	2121	G	2.9
6	1G	83	ARG	2.9
34	2c	189	ALA	2.9
35	2d	149	ALA	2.9
38	2g	103	TRP	2.9
35	1d	155	LEU	2.9
40	2i	5	TYR	2.9
40	1i	91	ASP	2.9
53	2y	48	PHE	2.9
1	1A	34	C	2.9
1	1A	271(K)	U	2.9
1	1A	1104	C	2.9
1	1A	2137	C	2.9
8	2I	34	GLY	2.9
21	2Z	1	MET	2.9
50	2s	68	GLY	2.9
50	2s	82	GLY	2.9
1	1A	2892	A	2.9
53	2y	35	ILE	2.9
41	1j	72	VAL	2.9
6	2G	71	THR	2.9
7	2H	128	PRO	2.9
29	27	45	ALA	2.9
33	2b	232	PRO	2.9
49	2r	20	ALA	2.9
50	2s	25	LYS	2.9
6	2G	43	LEU	2.9
26	24	9	LEU	2.9
1	2A	2207	G	2.9
32	1a	1030(C)	G	2.9
6	2G	138	GLN	2.9
44	2m	85	GLY	2.9

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Mol	Chain	Res	Type	RSRZ
1	1A	2132	U	2.9
1	1A	2139	C	2.9
1	1A	2161	C	2.9
32	2a	1116	C	2.9
32	2a	1260	C	2.9
34	2c	182	ILE	2.9
41	2j	6	ILE	2.9
32	2a	1005	A	2.9
40	2i	104	ARG	2.9
41	2j	87	THR	2.9
21	1Z	192	ALA	2.9
40	1i	106	ALA	2.9
45	2n	20	ALA	2.9
6	2G	3	LEU	2.9
40	1i	102	LEU	2.9
41	2j	85	LEU	2.9
45	2n	6	LEU	2.9
8	2I	20	ASP	2.9
1	1A	1059	G	2.9
1	1A	2148	G	2.9
1	2A	1044	G	2.9
1	2A	1063	G	2.9
1	2A	2120	G	2.9
32	2a	1224	G	2.9
38	1g	85	TYR	2.9
40	2i	59	PHE	2.9
6	2G	39	ILE	2.8
18	2W	92	ARG	2.8
34	2c	3	ASN	2.8
33	2b	16	HIS	2.8
41	2j	43	ARG	2.8
41	2j	70	ARG	2.8
53	1y	95	ARG	2.8
53	2y	39	ILE	2.8
9	2N	140	VAL	2.8
26	24	21	VAL	2.8
1	1A	1053	C	2.8
32	2a	1277	C	2.8
6	2G	87	PRO	2.8
36	1e	21	ALA	2.8
50	2s	24	ALA	2.8
34	2c	52	LEU	2.8

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Mol	Chain	Res	Type	RSRZ
6	2G	155	MET	2.8
12	2Q	59	ARG	2.8
33	1b	38	GLY	2.8
1	2A	1068	G	2.8
1	2A	2156	G	2.8
2	2B	118	G	2.8
15	1T	38	ASN	2.8
32	2a	1042	G	2.8
45	2n	32	SER	2.8
46	1o	3	ILE	2.8
32	1a	1040	U	2.8
34	2c	76	VAL	2.8
43	2l	18	VAL	2.8
33	1b	131	PRO	2.8
1	1A	2175	C	2.8
42	2k	89	ALA	2.8
53	2y	24	LEU	2.8
41	2j	86	MET	2.8
41	2j	63	PHE	2.8
14	2S	7	TYR	2.8
14	2S	35	ILE	2.8
44	2m	9	ILE	2.8
5	1F	15	SER	2.8
21	2Z	71	VAL	2.8
1	1A	1055	G	2.8
1	2A	11	G	2.8
40	2i	64	THR	2.8
19	2X	92	LEU	2.8
45	2n	39	LEU	2.8
26	24	39	CYS	2.8
19	2X	68	ARG	2.8
33	2b	156	LYS	2.8
41	2j	14	LYS	2.8
33	2b	189	ASP	2.8
41	2j	68	HIS	2.8
45	2n	16	PHE	2.8
6	1G	52	ILE	2.8
33	1b	127	ILE	2.8
6	2G	109	VAL	2.8
8	2I	107	VAL	2.8
33	1b	125	PRO	2.8
21	2Z	192	ALA	2.8

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Mol	Chain	Res	Type	RSRZ
33	1b	237	ALA	2.8
38	2g	116	ALA	2.8
40	1i	15	ALA	2.8
45	1n	5	ALA	2.8
50	2s	75	ALA	2.8
32	1a	1002	G	2.8
53	2y	70	MET	2.8
1	1A	2143	C	2.8
12	2Q	60	ARG	2.8
26	24	46	GLN	2.8
41	2j	36	GLY	2.7
46	1o	89	GLY	2.7
50	2s	49	ILE	2.7
38	2g	77	SER	2.7
53	2y	37	PRO	2.7
40	2i	53	VAL	2.7
5	2F	181	LEU	2.7
33	2b	67	THR	2.7
38	2g	38	LEU	2.7
44	2m	34	LEU	2.7
8	2I	46	ALA	2.7
21	1Z	1	MET	2.7
44	2m	65	LYS	2.7
1	1A	2110	G	2.7
2	2B	119	G	2.7
32	2a	1019	C	2.7
12	2Q	65	PHE	2.7
6	2G	140	ILE	2.7
34	2c	198	VAL	2.7
51	1t	11	SER	2.7
8	2I	38	LEU	2.7
34	2c	192	THR	2.7
40	2i	94	ALA	2.7
43	1l	91	LYS	2.7
44	2m	18	ALA	2.7
44	2m	31	LYS	2.7
45	2n	9	LYS	2.7
50	2s	66	MET	2.7
29	27	47	ARG	2.7
52	2u	15	ARG	2.7
41	2j	83	GLU	2.7
44	2m	58	GLU	2.7

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Mol	Chain	Res	Type	RSRZ
52	2u	5	ASP	2.7
1	2A	1171	G	2.7
1	2A	2184	G	2.7
1	1A	1046	A	2.7
1	1A	2138	C	2.7
1	1A	2140	C	2.7
1	2A	1088	A	2.7
6	2G	80	PHE	2.7
45	2n	55	GLY	2.7
51	1t	101	GLY	2.7
6	2G	77	ILE	2.7
32	2a	1128	C	2.7
35	2d	5	ILE	2.7
44	2m	7	VAL	2.7
53	2y	49	VAL	2.7
6	2G	90	LEU	2.7
33	2b	199	TYR	2.7
6	1G	50	ALA	2.7
21	1Z	188	ALA	2.7
33	1b	62	ALA	2.7
34	2c	200	ALA	2.7
38	2g	25	ALA	2.7
41	1j	27	ALA	2.7
52	1u	24	ARG	2.7
33	1b	128	GLU	2.7
46	2o	89	GLY	2.7
33	2b	57	PHE	2.7
41	2j	39	PRO	2.7
53	2y	16	ILE	2.7
1	1A	1045	A	2.7
1	1A	2108	C	2.7
1	2A	1057	A	2.7
1	2A	2789	C	2.7
1	2A	2794	C	2.7
45	2n	15	LYS	2.7
50	2s	28	LYS	2.7
51	1t	74	LYS	2.7
33	1b	36	ARG	2.7
33	2b	11	LEU	2.7
34	2c	173	VAL	2.7
40	2i	41	VAL	2.7
40	2i	99	LEU	2.7

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Mol	Chain	Res	Type	RSRZ
41	2j	16	LEU	2.7
46	2o	88	ARG	2.7
50	2s	35	SER	2.7
38	2g	85	TYR	2.7
6	2G	46	ALA	2.7
8	1I	108	THR	2.7
38	2g	83	ALA	2.7
44	2m	64	TRP	2.7
47	2p	48	TRP	2.7
40	2i	117	HIS	2.7
40	2i	75	ASP	2.6
26	24	45	GLY	2.6
34	1c	80	GLY	2.6
34	2c	158	GLY	2.6
52	2u	16	GLY	2.6
6	2G	88	ILE	2.6
7	2H	21	PRO	2.6
33	2b	127	ILE	2.6
33	2b	181	PHE	2.6
9	2N	115	ARG	2.6
53	2y	95	ARG	2.6
32	1a	1035	A	2.6
34	2c	178	LEU	2.6
40	2i	44	VAL	2.6
44	1m	56	LEU	2.6
1	1A	2124	G	2.6
1	2A	2155	G	2.6
32	2a	1006	C	2.6
45	2n	25	VAL	2.6
33	2b	33	TYR	2.6
38	2g	128	ALA	2.6
40	1i	125	TYR	2.6
40	2i	13	ALA	2.6
47	1p	48	TRP	2.6
6	2G	147	ASP	2.6
32	2a	1150	U	2.6
33	1b	18	GLY	2.6
41	2j	93	GLY	2.6
50	2s	6	LYS	2.6
33	2b	208	ILE	2.6
41	2j	50	ILE	2.6
50	2s	37	ARG	2.6

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Mol	Chain	Res	Type	RSRZ
14	2S	58	LEU	2.6
50	2s	15	LEU	2.6
53	2y	61	LEU	2.6
26	24	57	GLU	2.6
27	15	60	VAL	2.6
33	2b	71	VAL	2.6
1	2A	1098	A	2.6
1	2A	1079	C	2.6
6	2G	57	ALA	2.6
1	1A	2127	G	2.6
1	1A	2162	G	2.6
26	14	32	TYR	2.6
40	2i	92	TYR	2.6
20	2Y	94	LYS	2.6
26	24	54	GLY	2.6
44	1m	100	GLY	2.6
50	2s	26	GLY	2.6
1	1A	1060	U	2.6
1	2A	1026	U	2.6
6	2G	2	PRO	2.6
33	1b	234	PRO	2.6
36	2e	109	ILE	2.6
41	1j	75	ILE	2.6
6	2G	160	VAL	2.6
24	22	63	VAL	2.6
40	2i	86	VAL	2.6
42	2k	117	ASN	2.6
43	1l	18	VAL	2.6
50	2s	65	ASN	2.6
21	2Z	52	SER	2.6
48	1q	99	SER	2.6
53	2y	46	GLN	2.6
21	2Z	51	ALA	2.6
21	2Z	189	ALA	2.6
33	2b	186	ALA	2.6
34	2c	53	ALA	2.6
34	2c	60	ALA	2.6
34	2c	160	ALA	2.6
40	2i	46	ALA	2.6
1	1A	2126	A	2.6
1	1A	2790	A	2.6
46	2o	25	THR	2.6

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Mol	Chain	Res	Type	RSRZ
53	2y	33	HIS	2.6
1	2A	2128	C	2.6
33	2b	8	LYS	2.6
1	1A	171	G	2.6
1	1A	1537	G	2.6
1	1A	2141	G	2.6
1	1A	2151	G	2.6
1	1A	2154	G	2.6
1	2A	2319	G	2.6
32	2a	1190	G	2.6
18	1W	112	GLY	2.6
24	12	69	ARG	2.6
40	2i	49	PRO	2.6
48	1q	63	ARG	2.6
34	2c	8	ILE	2.6
36	2e	13	ILE	2.6
19	2X	95	LEU	2.6
21	2Z	18	LEU	2.6
35	1d	192	GLU	2.6
44	2m	90	LEU	2.6
53	2y	81	LEU	2.6
7	2H	15	VAL	2.6
41	1j	33	GLN	2.6
18	2W	111	HIS	2.6
34	2c	146	ALA	2.6
34	2c	163	ALA	2.6
40	2i	15	ALA	2.6
47	1p	16	HIS	2.6
50	2s	14	HIS	2.6
48	1q	100	LYS	2.6
35	2d	20	TYR	2.6
1	2A	2474	C	2.5
20	2Y	50	ARG	2.5
32	2a	1039	C	2.5
44	1m	114	ARG	2.5
44	2m	3	ARG	2.5
44	2m	57	ARG	2.5
5	1F	14	PRO	2.5
6	2G	44	GLY	2.5
31	29	37	GLY	2.5
40	2i	100	GLY	2.5
1	2A	2318	G	2.5

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Mol	Chain	Res	Type	RSRZ
32	1a	306	G	2.5
1	2A	1097	U	2.5
7	2H	103	LEU	2.5
38	2g	99	LEU	2.5
39	2h	70	GLN	2.5
4	2E	204	ALA	2.5
33	1b	123	ALA	2.5
34	2c	65	ALA	2.5
41	2j	55	LYS	2.5
45	2n	17	LYS	2.5
39	1h	24	THR	2.5
50	2s	79	THR	2.5
37	2f	47	ARG	2.5
45	2n	12	ARG	2.5
32	1a	1041	A	2.5
44	2m	23	TYR	2.5
26	24	65	ASP	2.5
41	2j	98	ILE	2.5
33	2b	129	GLU	2.5
33	1b	213	LEU	2.5
33	2b	10	LEU	2.5
33	2b	28	PHE	2.5
1	1A	2149	G	2.5
1	2A	1042	G	2.5
41	2j	8	LEU	2.5
41	2j	71	LEU	2.5
53	2y	9	GLN	2.5
3	2D	38	LYS	2.5
6	1G	182	LYS	2.5
7	2H	85	LYS	2.5
20	1Y	92	ASN	2.5
33	1b	133	LYS	2.5
33	2b	184	VAL	2.5
34	2c	149	ALA	2.5
40	1i	46	ALA	2.5
51	1t	76	ALA	2.5
51	2t	52	ALA	2.5
50	2s	77	THR	2.5
6	2G	118	ARG	2.5
26	24	55	ARG	2.5
1	1A	548	A	2.5
1	1A	2135	A	2.5

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Mol	Chain	Res	Type	RSRZ
32	2a	1093	A	2.5
32	2a	1256	A	2.5
32	2a	1531	A	2.5
33	2b	99	GLY	2.5
34	2c	80	GLY	2.5
46	2o	86	GLY	2.5
52	2u	4	GLY	2.5
33	2b	134	GLU	2.5
35	2d	70	ILE	2.5
47	2p	19	ILE	2.5
52	2u	13	ILE	2.5
1	1A	885	C	2.5
32	2a	979	C	2.5
32	2a	1149	C	2.5
32	2a	1384	C	2.5
11	2P	3	LEU	2.5
22	20	84	LEU	2.5
33	2b	122	PHE	2.5
35	2d	155	LEU	2.5
35	2d	86	LYS	2.5
41	1j	80	LYS	2.5
41	2j	57	LYS	2.5
1	1A	1105	U	2.5
1	2A	2122	U	2.5
9	2N	9	VAL	2.5
32	1a	1446	U	2.5
32	2a	1020	U	2.5
34	2c	70	VAL	2.5
41	1j	44	VAL	2.5
53	2y	67	HIS	2.5
1	1A	1117	G	2.5
1	2A	1099	G	2.5
1	2A	1537	G	2.5
1	2A	2807	G	2.5
6	1G	46	ALA	2.5
7	2H	3	ARG	2.5
8	1I	63	ALA	2.5
34	2c	190	ARG	2.5
52	1u	9	ARG	2.5
52	2u	7	ARG	2.5
44	2m	43	THR	2.5
53	2y	53	THR	2.5

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Mol	Chain	Res	Type	RSRZ
26	24	18	CYS	2.5
29	27	1	MET	2.5
38	2g	14	PRO	2.5
51	1t	98	PRO	2.5
6	2G	42	GLY	2.5
33	2b	86	GLU	2.5
40	2i	30	GLY	2.5
43	1l	63	GLY	2.5
43	1l	95	GLY	2.5
38	2g	18	TYR	2.5
43	2l	16	GLU	2.5
44	2m	67	GLU	2.5
22	20	71	ASP	2.5
1	2A	1050	A	2.5
32	2a	1279	A	2.5
14	2S	56	LEU	2.5
33	2b	154	LEU	2.5
34	2c	188	LEU	2.5
35	1d	194	LEU	2.5
43	2l	17	LYS	2.5
44	2m	19	LEU	2.5
45	1n	4	LYS	2.5
1	1A	2111	C	2.5
32	2a	1282	C	2.5
6	2G	5	VAL	2.5
14	2S	46	VAL	2.5
33	1b	165	VAL	2.5
44	2m	11	ARG	2.5
51	1t	8	ARG	2.5
51	2t	86	ARG	2.5
53	2y	83	ARG	2.5
29	17	45	ALA	2.5
33	1b	29	ALA	2.5
38	2g	65	ALA	2.5
1	1A	2166	G	2.5
1	1A	2207	G	2.5
40	1i	126	SER	2.5
41	2j	19	SER	2.5
35	2d	23	GLY	2.4
43	2l	95	GLY	2.4
6	2G	182	LYS	2.4
33	2b	214	ILE	2.4

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Mol	Chain	Res	Type	RSRZ
41	2j	80	LYS	2.4
45	2n	50	LYS	2.4
33	2b	69	LEU	2.4
34	2c	42	LEU	2.4
35	1d	188	LEU	2.4
44	2m	48	LEU	2.4
1	1A	229	A	2.4
32	1a	1493	A	2.4
42	1k	13	GLN	2.4
41	1j	54	PHE	2.4
47	2p	80	PHE	2.4
34	2c	79	ARG	2.4
38	1g	156	TRP	2.4
46	2o	68	ARG	2.4
52	2u	10	ARG	2.4
1	1A	1532	C	2.4
1	2A	1104	C	2.4
1	2A	2103	C	2.4
34	2c	75	VAL	2.4
40	2i	28	VAL	2.4
50	2s	19	VAL	2.4
50	2s	51	VAL	2.4
32	1a	1025	U	2.4
41	1j	32	ALA	2.4
7	2H	122	THR	2.4
44	2m	49	THR	2.4
21	2Z	177	PRO	2.4
38	2g	112	PRO	2.4
1	2A	10	G	2.4
1	2A	171	G	2.4
8	2I	90	GLY	2.4
32	1a	78	G	2.4
32	2a	1021	G	2.4
32	2a	1024	G	2.4
39	2h	131	GLY	2.4
41	2j	96	ILE	2.4
52	1u	5	ASP	2.4
6	2G	41	GLN	2.4
6	2G	172	LEU	2.4
11	2P	99	LEU	2.4
33	2b	187	LEU	2.4
34	1c	47	LEU	2.4

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Mol	Chain	Res	Type	RSRZ
35	1d	4	TYR	2.4
51	1t	18	GLN	2.4
33	2b	140	HIS	2.4
26	24	42	PHE	2.4
26	24	61	ARG	2.4
50	2s	78	ARG	2.4
1	1A	2114	A	2.4
1	1A	2801(A)	A	2.4
32	2a	968	A	2.4
21	2Z	86	VAL	2.4
1	1A	1509	C	2.4
1	1A	2129	C	2.4
1	2A	2177	C	2.4
4	2E	28	ALA	2.4
34	2c	168	ALA	2.4
41	2j	18	ALA	2.4
44	2m	76	ALA	2.4
33	2b	190	THR	2.4
44	1m	49	THR	2.4
7	2H	173	PRO	2.4
8	2I	131	LYS	2.4
21	1Z	202	GLU	2.4
33	1b	22	LYS	2.4
14	2S	22	GLY	2.4
21	2Z	160	GLY	2.4
53	2y	92	GLY	2.4
1	1A	2206	G	2.4
1	2A	2100	G	2.4
1	2A	2206	G	2.4
36	2e	20	GLN	2.4
45	2n	44	LEU	2.4
53	2y	85	LEU	2.4
43	1l	19	ARG	2.4
53	2y	96	ARG	2.4
33	1b	136	VAL	2.4
32	1a	196	A	2.4
32	2a	1092	A	2.4
36	2e	94	ALA	2.4
52	1u	14	TRP	2.4
3	1D	38	LYS	2.4
8	2I	134	PRO	2.4
33	1b	12	GLU	2.4

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Mol	Chain	Res	Type	RSRZ
35	1d	169	LYS	2.4
35	2d	156	GLU	2.4
41	2j	41	PRO	2.4
50	2s	59	PRO	2.4
50	2s	64	GLU	2.4
52	2u	3	LYS	2.4
1	1A	12	U	2.4
1	1A	2122	U	2.4
32	1a	1007	C	2.4
32	2a	1040	U	2.4
32	2a	1066	C	2.4
7	2H	82	GLY	2.4
33	1b	228	GLY	2.4
34	2c	41	GLY	2.4
35	1d	87	GLY	2.4
41	2j	10	GLY	2.4
18	1W	111	HIS	2.4
19	2X	65	ARG	2.4
30	28	46	ARG	2.4
33	2b	79	ASP	2.4
34	2c	140	ARG	2.4
35	1d	174	LEU	2.4
1	1A	1106	G	2.4
1	1A	2157	G	2.4
1	2A	892	G	2.4
1	2A	1051	G	2.4
1	2A	1058	G	2.4
21	2Z	136	PHE	2.4
32	2a	1316	G	2.4
26	24	35	VAL	2.4
45	2n	56	VAL	2.4
8	2I	87	LYS	2.4
40	2i	106	ALA	2.4
45	2n	4	LYS	2.4
50	2s	7	LYS	2.4
26	14	57	GLU	2.4
8	2I	86	THR	2.3
34	2c	67	THR	2.3
44	1m	113	PRO	2.3
53	1y	2	THR	2.3
32	1a	1135	U	2.3
32	2a	1126	U	2.3

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Mol	Chain	Res	Type	RSRZ
1	1A	886	C	2.3
7	2H	174	GLY	2.3
8	2I	84	GLY	2.3
17	2V	63	GLY	2.3
32	1a	1006	C	2.3
52	1u	2	GLY	2.3
15	2T	111	ARG	2.3
38	2g	41	ARG	2.3
33	1b	154	LEU	2.3
33	1b	214	ILE	2.3
38	2g	12	LEU	2.3
38	2g	42	ILE	2.3
6	2G	126	ASP	2.3
21	2Z	121	HIS	2.3
40	2i	114	TYR	2.3
33	1b	156	LYS	2.3
1	1A	2155	G	2.3
1	1A	2165	G	2.3
1	2A	1093	G	2.3
32	1a	1009	G	2.3
32	2a	1215	G	2.3
32	2a	1220	G	2.3
42	2k	15	ALA	2.3
53	2y	50	ALA	2.3
8	1I	86	THR	2.3
33	1b	190	THR	2.3
50	2s	48	THR	2.3
32	2a	1492	A	2.3
26	24	62	ARG	2.3
35	1d	124	GLY	2.3
40	2i	16	ARG	2.3
47	1p	81	ARG	2.3
51	1t	70	SER	2.3
32	2a	1000	U	2.3
32	2a	1532	U	2.3
21	2Z	124	ILE	2.3
22	10	7	LEU	2.3
33	1b	39	ILE	2.3
44	2m	101	GLN	2.3
40	1i	19	LEU	2.3
40	2i	19	LEU	2.3
51	1t	73	HIS	2.3

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Mol	Chain	Res	Type	RSRZ
26	14	51	ASP	2.3
32	2a	1045	C	2.3
9	2N	2	LYS	2.3
34	2c	4	LYS	2.3
35	2d	79	PHE	2.3
40	2i	33	PHE	2.3
47	1p	80	PHE	2.3
8	2I	18	VAL	2.3
26	14	67	TYR	2.3
33	2b	229	VAL	2.3
35	1d	88	VAL	2.3
35	1d	138	TYR	2.3
40	2i	26	VAL	2.3
20	2Y	91	GLU	2.3
34	2c	122	GLU	2.3
42	1k	117	ASN	2.3
48	2q	94	ASN	2.3
6	2G	56	ALA	2.3
33	2b	131	PRO	2.3
1	1A	2120	G	2.3
1	1A	2133	G	2.3
32	2a	1138	G	2.3
44	2m	37	THR	2.3
37	1f	3	ARG	2.3
38	2g	4	ARG	2.3
44	2m	110	ARG	2.3
6	1G	76	SER	2.3
14	2S	60	GLY	2.3
32	1a	532	A	2.3
33	1b	109	SER	2.3
35	1d	173	TRP	2.3
26	24	60	GLN	2.3
53	2y	59	GLY	2.3
33	2b	40	HIS	2.3
53	2y	90	HIS	2.3
8	2I	88	ILE	2.3
21	2Z	57	ILE	2.3
33	2b	39	ILE	2.3
33	2b	42	ILE	2.3
33	2b	58	ILE	2.3
1	2A	2808	U	2.3
32	2a	1212	U	2.3

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Mol	Chain	Res	Type	RSRZ
1	1A	1584	C	2.3
44	1m	115	LYS	2.3
35	1d	133	VAL	2.3
47	1p	17	TYR	2.3
50	2s	60	VAL	2.3
35	2d	154	ASN	2.3
44	2m	75	ALA	2.3
51	1t	66	ALA	2.3
53	2y	15	ALA	2.3
53	2y	55	ASN	2.3
53	2y	94	ALA	2.3
26	14	61	ARG	2.3
34	2c	191	THR	2.3
39	2h	3	THR	2.3
50	2s	33	THR	2.3
40	2i	58	HIS	2.3
40	2i	68	GLY	2.3
42	2k	116	HIS	2.3
51	1t	102	GLY	2.3
53	2y	47	GLY	2.3
1	2A	883	G	2.3
1	2A	1056	G	2.3
6	1G	135	LEU	2.3
6	2G	53	LEU	2.3
7	1H	92	ILE	2.3
32	2a	1009	G	2.3
33	2b	172	ILE	2.3
39	1h	112	LEU	2.3
45	1n	7	ILE	2.3
45	2n	53	LEU	2.3
32	2a	1280	A	2.3
36	2e	5	ASP	2.3
40	2i	113	LYS	2.3
44	2m	13	LYS	2.3
53	2y	87	LYS	2.3
1	1A	1116	C	2.3
1	1A	2164	C	2.3
1	2A	1041	C	2.3
7	2H	123	PHE	2.3
8	1I	10	GLU	2.3
26	24	30	GLU	2.3
32	2a	1322	C	2.3

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Mol	Chain	Res	Type	RSRZ
33	1b	20	GLU	2.3
40	1i	37	PHE	2.3
33	1b	15	VAL	2.3
35	1d	8	VAL	2.3
40	1i	28	VAL	2.3
44	2m	15	VAL	2.3
44	2m	45	VAL	2.3
5	2F	14	PRO	2.3
7	2H	39	PRO	2.3
45	2n	40	CYS	2.3
46	2o	19	PRO	2.3
34	1c	201	TYR	2.3
44	1m	59	TYR	2.3
49	2r	87	ARG	2.3
51	1t	59	ALA	2.2
11	2P	116	GLY	2.2
36	2e	22	GLY	2.2
48	2q	93	GLN	2.2
50	2s	84	GLY	2.2
8	2I	12	LEU	2.2
8	2I	91	SER	2.2
20	2Y	106	LEU	2.2
26	24	14	ILE	2.2
33	2b	61	LEU	2.2
34	2c	14	ILE	2.2
34	2c	33	LEU	2.2
41	2j	59	SER	2.2
53	2y	41	LEU	2.2
32	2a	1183	A	2.2
1	1A	545	G	2.2
1	2A	1533	G	2.2
1	2A	2181	G	2.2
1	2A	2187	G	2.2
32	2a	971	G	2.2
32	2a	993	G	2.2
1	1A	272(A)	U	2.2
1	2A	1060	U	2.2
1	2A	1078	U	2.2
32	2a	992	U	2.2
6	2G	48	GLU	2.2
7	2H	10	PRO	2.2
7	2H	125	VAL	2.2

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Mol	Chain	Res	Type	RSRZ
8	2I	92	VAL	2.2
14	2S	17	ARG	2.2
34	1c	207	VAL	2.2
34	2c	55	VAL	2.2
40	2i	65	VAL	2.2
44	2m	60	VAL	2.2
50	2s	36	ARG	2.2
40	2i	55	ALA	2.2
44	1m	51	ALA	2.2
34	1c	193	TYR	2.2
6	1G	161	THR	2.2
26	24	69	LYS	2.2
34	2c	27	LYS	2.2
42	2k	124	LYS	2.2
6	2G	82	LEU	2.2
34	2c	87	LEU	2.2
34	2c	94	LEU	2.2
7	2H	134	SER	2.2
3	2D	71	ASP	2.2
41	1j	73	ASP	2.2
21	1Z	203	GLU	2.2
1	1A	2189	U	2.2
1	2A	1114	G	2.2
1	2A	2321	G	2.2
26	14	68	ARG	2.2
32	2a	1216	G	2.2
34	2c	131	ARG	2.2
35	1d	132	ARG	2.2
43	1l	89	ARG	2.2
21	2Z	104	PHE	2.2
34	2c	10	PHE	2.2
42	2k	125	PHE	2.2
34	2c	99	VAL	2.2
34	2c	114	PRO	2.2
35	1d	121	VAL	2.2
39	2h	51	VAL	2.2
42	1k	14	VAL	2.2
47	2p	2	VAL	2.2
21	2Z	132	ASN	2.2
38	2g	147	ALA	2.2
21	2Z	198	LYS	2.2
3	2D	259	THR	2.2

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Mol	Chain	Res	Type	RSRZ
26	24	32	TYR	2.2
40	1i	78	LYS	2.2
40	2i	116	LYS	2.2
44	2m	82	MET	2.2
45	1n	13	THR	2.2
45	2n	22	THR	2.2
47	1p	22	THR	2.2
6	2G	34	LEU	2.2
33	2b	89	GLY	2.2
33	2b	158	LEU	2.2
50	1s	26	GLY	2.2
51	1t	62	LEU	2.2
14	2S	40	ILE	2.2
38	2g	27	ILE	2.2
33	2b	192	SER	2.2
48	2q	97	SER	2.2
33	1b	189	ASP	2.2
33	2b	191	ASP	2.2
33	1b	126	GLU	2.2
39	2h	99	GLU	2.2
44	1m	50	GLU	2.2
34	2c	18	TRP	2.2
35	1d	153	ARG	2.2
38	2g	149	ARG	2.2
41	2j	28	ARG	2.2
1	2A	271(K)	U	2.2
1	2A	1045	A	2.2
2	2B	120	A	2.2
7	2H	36	PRO	2.2
32	1a	173	U	2.2
32	1a	202	U	2.2
32	2a	532	A	2.2
32	2a	1261	A	2.2
47	2p	9	PHE	2.2
7	2H	50	VAL	2.2
34	2c	120	VAL	2.2
43	1l	90	VAL	2.2
1	1A	2156	G	2.2
7	1H	175	LYS	2.2
32	2a	1202	G	2.2
18	1W	60	ASN	2.2
33	1b	34	ALA	2.2

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Mol	Chain	Res	Type	RSRZ
44	1m	27	LYS	2.2
44	2m	72	ALA	2.2
45	2n	10	ALA	2.2
50	1s	23	ASN	2.2
7	1H	139	GLN	2.2
53	1y	70	MET	2.2
5	2F	7	TYR	2.2
6	2G	161	THR	2.2
33	2b	92	TYR	2.2
43	1l	120	TYR	2.2
50	1s	77	THR	2.2
14	2S	45	GLY	2.2
26	24	19	GLY	2.2
34	2c	145	GLY	2.2
40	2i	47	LEU	2.2
3	1D	106	ILE	2.2
31	29	10	ILE	2.2
34	1c	14	ILE	2.2
38	2g	50	ILE	2.2
40	2i	81	ILE	2.2
44	2m	84	ILE	2.2
48	2q	99	SER	2.2
6	2G	116	ASP	2.2
8	1I	14	ASP	2.2
10	1O	108	GLU	2.2
44	2m	69	GLU	2.2
46	1o	6	GLU	2.2
53	2y	68	GLU	2.2
47	1p	42	ARG	2.2
35	2d	7	PRO	2.2
1	1A	1963	U	2.2
1	1A	2629	A	2.1
1	2A	9	U	2.2
7	2H	114	VAL	2.1
21	2Z	90	VAL	2.1
21	2Z	161	VAL	2.1
32	1a	1492	A	2.1
32	2a	1014	A	2.1
53	2y	91	LYS	2.2
38	2g	21	VAL	2.1
16	1U	117	GLN	2.1
33	1b	13	ALA	2.1

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Mol	Chain	Res	Type	RSRZ
33	2b	83	MET	2.1
34	2c	169	ALA	2.1
36	2e	21	ALA	2.1
53	2y	63	ALA	2.1
1	1A	2131	G	2.1
1	1A	2160	G	2.1
1	2A	2792	G	2.1
32	1a	79	G	2.1
32	2a	1022	G	2.1
33	2b	66	GLY	2.1
33	2b	155	LEU	2.1
34	1c	67	THR	2.1
34	2c	51	GLY	2.1
36	2e	12	LEU	2.1
40	1i	6	GLY	2.1
40	1i	47	LEU	2.1
44	2m	95	GLY	2.1
45	2n	51	GLY	2.1
17	2V	96	ILE	2.1
19	1X	69	TYR	2.1
34	2c	193	TYR	2.1
44	1m	4	ILE	2.1
46	2o	87	ILE	2.1
51	2t	100	ILE	2.1
1	2A	1043	C	2.1
32	1a	91	C	2.1
32	1a	999	C	2.1
32	1a	1043	C	2.1
32	1a	1137	C	2.1
32	1a	1533	C	2.1
6	2G	59	GLU	2.1
12	2Q	5	ARG	2.1
22	20	74	ARG	2.1
33	1b	129	GLU	2.1
34	2c	90	GLU	2.1
43	2l	89	ARG	2.1
45	2n	31	ARG	2.1
45	2n	60	SER	2.1
50	1s	29	ARG	2.1
12	2Q	135	ASP	2.1
34	2c	62	ASP	2.1
6	2G	179	PRO	2.1

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Mol	Chain	Res	Type	RSRZ
21	2Z	78	LYS	2.1
35	1d	166	LYS	2.1
40	2i	112	LYS	2.1
47	1p	41	PRO	2.1
6	2G	141	PHE	2.1
14	2S	12	PHE	2.1
21	2Z	105	VAL	2.1
26	14	50	VAL	2.1
7	2H	41	MET	2.1
31	29	20	HIS	2.1
1	1A	1174	A	2.1
1	1A	1177	A	2.1
6	2G	58	GLN	2.1
33	2b	90	MET	2.1
41	1j	86	MET	2.1
32	1a	1004	A	2.1
32	2a	1357	A	2.1
53	2y	89	GLN	2.1
33	2b	88	ALA	2.1
40	1i	84	ALA	2.1
49	1r	24	ALA	2.1
50	2s	50	ALA	2.1
53	1y	94	ALA	2.1
6	2G	133	LEU	2.1
8	2I	31	LEU	2.1
20	2Y	80	GLY	2.1
33	2b	102	LEU	2.1
33	2b	215	LEU	2.1
34	1c	87	LEU	2.1
47	1p	45	THR	2.1
41	1j	82	ILE	2.1
6	2G	45	GLU	2.1
21	2Z	99	TYR	2.1
41	1j	79	ARG	2.1
1	1A	645	C	2.1
1	2A	886	C	2.1
32	2a	1140	C	2.1
20	2Y	54	LYS	2.1
45	2n	58	LYS	2.1
6	2G	17	PRO	2.1
34	2c	6	HIS	2.1
36	2e	10	MET	2.1

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Mol	Chain	Res	Type	RSRZ
38	2g	153	HIS	2.1
21	2Z	116	VAL	2.1
31	29	16	VAL	2.1
34	1c	64	VAL	2.1
34	1c	76	VAL	2.1
35	1d	148	VAL	2.1
35	2d	178	VAL	2.1
41	1j	24	VAL	2.1
41	1j	34	VAL	2.1
44	1m	53	VAL	2.1
47	1p	20	VAL	2.1
1	2A	12	U	2.1
8	2I	55	ALA	2.1
32	1a	65	U	2.1
32	2a	1315	U	2.1
34	2c	100	ALA	2.1
53	2y	79	ASN	2.1
53	2y	86	ASN	2.1
1	2A	1460	A	2.1
6	2G	175	LEU	2.1
32	2a	1041	A	2.1
32	2a	1493	A	2.1
34	1c	42	LEU	2.1
34	2c	47	LEU	2.1
37	1f	98	LEU	2.1
41	1j	71	LEU	2.1
8	2I	78	THR	2.1
26	24	27	THR	2.1
44	1m	6	GLY	2.1
6	2G	113	ARG	2.1
40	1i	107	ARG	2.1
33	1b	49	GLU	2.1
41	1j	97	GLU	2.1
6	2G	25	TYR	2.1
34	2c	184	TYR	2.1
40	2i	95	LYS	2.1
44	2m	46	LYS	2.1
47	1p	50	LYS	2.1
38	2g	47	CYS	2.1
48	1q	97	SER	2.1
1	1A	275	G	2.1
32	2a	1017	G	2.1

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Mol	Chain	Res	Type	RSRZ
32	2a	1222	G	2.1
1	2A	1080	C	2.1
32	1a	163	C	2.1
32	1a	1019	C	2.1
32	2a	990	C	2.1
32	2a	1118	C	2.1
33	1b	113	HIS	2.1
33	2b	163	PHE	2.1
34	2c	37	GLN	2.1
41	2j	84	GLN	2.1
4	1E	75	VAL	2.1
21	2Z	58	VAL	2.1
3	1D	2	ALA	2.1
7	2H	102	ALA	2.1
38	1g	150	ALA	2.1
44	2m	33	ALA	2.1
7	1H	101	ARG	2.1
21	2Z	155	LEU	2.1
32	2a	1278	U	2.1
33	1b	221	LEU	2.1
45	2n	47	LEU	2.1
47	1p	49	LEU	2.1
17	2V	42	GLY	2.1
51	2t	25	ARG	2.1
7	2H	40	GLU	2.1
26	24	3	GLU	2.1
36	2e	50	GLU	2.1
46	1o	22	THR	2.1
1	1A	529	A	2.1
32	2a	1123	A	2.1
32	2a	1157	A	2.1
44	1m	84	ILE	2.1
44	2m	22	ILE	2.1
6	2G	36	LYS	2.1
7	2H	175	LYS	2.1
41	2j	7	LYS	2.1
43	2l	23	LYS	2.1
20	2Y	55	TYR	2.1
53	2y	51	ASP	2.1
6	2G	122	PRO	2.1
35	2d	40	PRO	2.1
41	2j	53	PRO	2.1

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Mol	Chain	Res	Type	RSRZ
1	2A	2101	G	2.0
32	1a	380	G	2.0
32	2a	1007	C	2.1
32	2a	1321	C	2.1
35	2d	160	GLN	2.0
53	1y	9	GLN	2.0
6	2G	31	VAL	2.0
9	2N	5	VAL	2.0
14	2S	29	PHE	2.0
19	2X	81	VAL	2.0
21	2Z	48	PHE	2.0
21	2Z	74	VAL	2.0
3	2D	2	ALA	2.0
26	14	48	ARG	2.0
29	17	23	ARG	2.0
29	17	47	ARG	2.0
38	2g	32	ARG	2.0
38	2g	95	ARG	2.0
40	2i	76	ALA	2.0
40	2i	121	ARG	2.0
41	1j	26	ALA	2.0
41	1j	46	ARG	2.0
44	2m	30	ALA	2.0
47	2p	26	ARG	2.0
52	2u	9	ARG	2.0
24	22	3	LEU	2.0
33	1b	187	LEU	2.0
35	1d	186	LEU	2.0
8	1I	117	GLU	2.0
23	21	83	GLU	2.0
33	2b	126	GLU	2.0
34	2c	159	GLY	2.0
35	1d	150	GLU	2.0
35	1d	163	GLU	2.0
38	2g	81	GLY	2.0
44	2m	89	GLY	2.0
46	2o	76	GLU	2.0
1	1A	1420	U	2.0
12	2Q	22	LYS	2.0
32	2a	1125	U	2.0
35	1d	86	LYS	2.0
49	2r	56	THR	2.0

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Mol	Chain	Res	Type	RSRZ
1	1A	1460	A	2.0
1	1A	2176	A	2.0
1	2A	1103	A	2.0
6	1G	126	ASP	2.0
8	1I	134	PRO	2.0
21	2Z	166	SER	2.0
25	13	2	PRO	2.0
26	24	11	PRO	2.0
33	2b	125	PRO	2.0
35	2d	27	TYR	2.0
40	1i	21	PRO	2.0
42	1k	75	TYR	2.0
46	1o	69	TYR	2.0
38	2g	125	MET	2.0
26	14	46	GLN	2.0
6	2G	15	VAL	2.0
6	2G	102	PHE	2.0
7	2H	17	VAL	2.0
7	2H	60	ARG	2.0
24	22	51	ARG	2.0
26	24	10	VAL	2.0
32	2a	1158	C	2.0
32	2a	1214	C	2.0
32	2a	1363	C	2.0
34	2c	153	VAL	2.0
34	2c	186	PHE	2.0
40	2i	111	ARG	2.0
50	2s	74	PHE	2.0
1	1A	11	G	2.0
1	1A	2807	G	2.0
1	2A	545	G	2.0
1	2A	614(B)	G	2.0
1	2A	2751	G	2.0
32	1a	1042	G	2.0
32	2a	1023	G	2.0
32	2a	1373	G	2.0
7	2H	7	LEU	2.0
14	2S	6	ALA	2.0
33	2b	98	LEU	2.0
34	2c	71	ALA	2.0
35	1d	111	ALA	2.0
34	1c	161	GLU	2.0

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Mol	Chain	Res	Type	RSRZ
35	2d	21	LEU	2.0
40	2i	61	ALA	2.0
49	1r	60	ALA	2.0
51	1t	97	ALA	2.0
4	1E	57	LYS	2.0
6	2G	54	GLU	2.0
5	2F	16	GLY	2.0
5	2F	131	GLY	2.0
8	1I	84	GLY	2.0
33	1b	227	GLY	2.0
34	2c	9	GLY	2.0
35	2d	6	GLY	2.0
36	2e	130	ASN	2.0
38	2g	133	GLY	2.0
40	1i	67	GLY	2.0
47	2p	50	LYS	2.0
49	2r	68	LYS	2.0
50	1s	8	GLY	2.0
33	2b	108	ILE	2.0
35	2d	158	ILE	2.0
36	1e	101	ILE	2.0
45	2n	42	ILE	2.0
47	1p	69	THR	2.0
32	1a	90	U	2.0
32	1a	841	U	2.0
32	2a	1062	U	2.0
32	2a	1086	U	2.0
32	2a	1205	U	2.0
1	1A	1847	A	2.0
1	1A	2134	A	2.0
1	2A	1069	A	2.0
7	2H	118	PRO	2.0
32	1a	161	A	2.0
32	2a	996	A	2.0
32	2a	1248	A	2.0
21	2Z	98	MET	2.0
34	1c	109	PRO	2.0
39	1h	72	PRO	2.0
53	2y	10	MET	2.0
33	2b	210	SER	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, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
1	5MU	2A	1915	21/22	0.82	0.12	79,87,90,101	0
32	M2G	2a	966	25/26	0.86	0.16	63,71,84,97	0
1	5MU	1A	1915	21/22	0.88	0.12	74,79,83,87	0
32	2MG	2a	1207	24/25	0.88	0.12	77,81,86,93	0
1	PSU	2A	1911	20/21	0.89	0.10	67,72,77,80	0
1	PSU	2A	1917	20/21	0.89	0.10	73,77,92,95	0
43	0TD	2l	92	10/11	0.90	0.12	59,66,69,74	0
1	PSU	1A	1917	20/21	0.91	0.11	65,69,75,77	0
32	5MC	2a	967	21/22	0.91	0.15	66,72,78,80	0
43	0TD	1l	92	10/11	0.92	0.13	49,59,64,67	0
32	PSU	2a	516	20/21	0.92	0.10	66,72,76,79	0
1	OMC	2A	1920	21/22	0.93	0.10	65,68,71,76	0
1	PSU	1A	1911	20/21	0.93	0.09	57,64,69,70	0
32	5MC	2a	1404	21/22	0.93	0.10	54,61,64,66	0
32	5MC	1a	967	21/22	0.93	0.11	57,66,73,82	0
32	5MC	2a	1400	21/22	0.94	0.13	62,75,78,80	0
32	4OC	2a	1402	22/23	0.94	0.11	59,64,71,73	0
32	G7M	2a	527	24/25	0.94	0.10	60,67,70,72	0
32	UR3	2a	1498	21/22	0.94	0.10	52,62,66,69	0
32	M2G	1a	966	25/26	0.94	0.10	55,61,68,71	0
32	5MC	2a	1407	21/22	0.95	0.10	56,64,67,69	0
32	2MG	1a	1207	24/25	0.95	0.09	62,70,74,78	0
32	MA6	2a	1518	24/25	0.95	0.10	58,64,68,69	0
32	PSU	1a	516	20/21	0.95	0.08	60,64,67,71	0
32	G7M	1a	527	24/25	0.96	0.10	48,55,59,67	0
1	OMC	1A	1920	21/22	0.96	0.09	50,57,61,63	0
32	5MC	1a	1400	21/22	0.96	0.10	49,57,60,65	0
32	4OC	1a	1402	22/23	0.96	0.09	46,53,56,64	0
32	5MC	1a	1407	21/22	0.96	0.09	44,54,58,63	0
1	5MC	2A	1942	21/22	0.96	0.09	44,49,54,60	0
32	UR3	1a	1498	21/22	0.96	0.08	42,50,53,59	0
32	MA6	1a	1518	24/25	0.96	0.10	43,47,52,53	0
32	MA6	2a	1519	24/25	0.96	0.12	49,63,67,69	0
32	MA6	1a	1519	24/25	0.96	0.10	42,48,52,54	0
32	5MC	1a	1404	21/22	0.97	0.08	45,48,51,56	0
1	5MU	2A	1939	21/22	0.97	0.08	35,39,42,46	0
1	2MA	1A	2503	23/24	0.97	0.07	20,24,27,29	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
1	OMG	2A	2251	24/25	0.97	0.08	38,40,43,45	0
1	2MA	2A	2503	23/24	0.97	0.08	29,34,37,39	0
1	5MC	1A	1942	21/22	0.97	0.08	33,39,44,47	0
1	5MC	1A	1962	21/22	0.98	0.07	30,36,40,48	0
1	OMU	2A	2552	21/22	0.98	0.07	33,40,43,46	0
1	PSU	2A	2605	20/21	0.98	0.08	32,38,43,44	0
1	OMG	1A	2251	24/25	0.98	0.07	22,28,32,43	0
1	5MU	1A	1939	21/22	0.98	0.07	27,31,36,39	0
1	OMU	1A	2552	21/22	0.98	0.06	26,31,33,35	0
1	5MC	2A	1962	21/22	0.98	0.07	33,46,53,56	0
1	PSU	1A	2605	20/21	0.98	0.07	27,30,33,36	0
54	PPU	1w	76	37/38	0.98	0.07	21,26,30,30	0
54	PPU	2w	76	37/38	0.98	0.07	30,36,41,44	0
55	8AN	1x	76	22/23	0.98	0.06	19,26,28,32	0
55	8AN	2x	76	22/23	0.98	0.07	33,36,39,44	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1A	3741	1/1	0.43	0.21	71,71,71,71	0
57	MG	2A	3542	1/1	0.49	0.32	70,70,70,70	0
57	MG	1a	1822	1/1	0.52	0.40	89,89,89,89	0
57	MG	1A	3968	1/1	0.53	0.21	40,40,40,40	0
57	MG	1A	3683	1/1	0.55	0.17	79,79,79,79	0
57	MG	2a	3176	1/1	0.55	0.36	74,74,74,74	0
57	MG	1A	3319	1/1	0.56	0.33	83,83,83,83	0
57	MG	1a	1802	1/1	0.58	0.34	76,76,76,76	0
57	MG	2A	3707	1/1	0.60	0.23	86,86,86,86	0
57	MG	1A	3506	1/1	0.60	0.29	76,76,76,76	0
57	MG	2a	3128	1/1	0.61	0.23	74,74,74,74	0
57	MG	2A	3399	1/1	0.61	0.20	79,79,79,79	0
57	MG	1a	1835	1/1	0.63	0.31	67,67,67,67	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1A	3637	1/1	0.64	0.29	79,79,79,79	0
57	MG	2A	3121	1/1	0.64	0.34	79,79,79,79	0
57	MG	1a	1702	1/1	0.64	0.44	79,79,79,79	0
57	MG	2a	3131	1/1	0.64	0.23	76,76,76,76	0
57	MG	2A	3511	1/1	0.64	0.14	75,75,75,75	0
57	MG	1A	3874	1/1	0.65	0.25	45,45,45,45	0
57	MG	2A	3414	1/1	0.65	0.24	70,70,70,70	0
57	MG	2A	3474	1/1	0.65	0.22	64,64,64,64	0
57	MG	2A	3326	1/1	0.66	0.27	72,72,72,72	0
57	MG	2A	3540	1/1	0.66	0.17	70,70,70,70	0
57	MG	2G	202	1/1	0.66	0.26	80,80,80,80	0
57	MG	1A	3857	1/1	0.67	0.19	71,71,71,71	0
57	MG	1a	1867	1/1	0.68	0.23	76,76,76,76	0
57	MG	2A	3433	1/1	0.68	0.28	69,69,69,69	0
57	MG	2a	3089	1/1	0.68	0.37	83,83,83,83	0
57	MG	2A	3304	1/1	0.69	0.32	73,73,73,73	0
57	MG	1a	1798	1/1	0.69	0.16	77,77,77,77	0
57	MG	2a	3099	1/1	0.69	0.33	75,75,75,75	0
57	MG	1A	3981	1/1	0.69	0.27	73,73,73,73	0
57	MG	1a	1784	1/1	0.69	0.22	79,79,79,79	0
57	MG	2A	3172	1/1	0.69	0.27	80,80,80,80	0
57	MG	2A	3164	1/1	0.70	0.28	86,86,86,86	0
57	MG	1A	3501	1/1	0.70	0.23	69,69,69,69	0
57	MG	1a	1841	1/1	0.70	0.25	74,74,74,74	0
57	MG	1A	3518	1/1	0.70	0.15	58,58,58,58	0
57	MG	2A	3116	1/1	0.70	0.25	91,91,91,91	0
57	MG	1A	3554	1/1	0.70	0.28	65,65,65,65	0
57	MG	1A	3596	1/1	0.71	0.16	47,47,47,47	0
57	MG	1A	3602	1/1	0.71	0.22	71,71,71,71	0
57	MG	1a	1740	1/1	0.71	0.24	91,91,91,91	0
57	MG	1A	3913	1/1	0.71	0.24	64,64,64,64	0
57	MG	1A	3613	1/1	0.71	0.23	72,72,72,72	0
57	MG	2A	3467	1/1	0.72	0.21	66,66,66,66	0
57	MG	2a	3025	1/1	0.72	0.19	69,69,69,69	0
57	MG	1t	202	1/1	0.72	0.20	74,74,74,74	0
57	MG	1a	1612	1/1	0.72	0.34	90,90,90,90	0
57	MG	1a	1795	1/1	0.72	0.15	69,69,69,69	0
57	MG	1A	3589	1/1	0.72	0.23	66,66,66,66	0
57	MG	1A	3690	1/1	0.72	0.18	70,70,70,70	0
57	MG	2B	214	1/1	0.73	0.19	65,65,65,65	0
57	MG	1a	1718	1/1	0.73	0.34	77,77,77,77	0
57	MG	2a	3019	1/1	0.73	0.25	85,85,85,85	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1d	303	1/1	0.73	0.31	77,77,77,77	0
57	MG	2A	3502	1/1	0.73	0.23	58,58,58,58	0
57	MG	1O	201	1/1	0.73	0.16	61,61,61,61	0
57	MG	2a	3120	1/1	0.73	0.30	80,80,80,80	0
57	MG	1a	1773	1/1	0.73	0.20	75,75,75,75	0
57	MG	1A	3433	1/1	0.73	0.20	51,51,51,51	0
57	MG	1A	3528	1/1	0.73	0.18	57,57,57,57	0
57	MG	2B	218	1/1	0.74	0.20	85,85,85,85	0
57	MG	1A	3572	1/1	0.74	0.23	51,51,51,51	0
57	MG	2a	3009	1/1	0.74	0.51	81,81,81,81	0
57	MG	2A	3311	1/1	0.74	0.20	79,79,79,79	0
57	MG	1A	3327	1/1	0.74	0.18	61,61,61,61	0
57	MG	1A	3695	1/1	0.74	0.26	65,65,65,65	0
57	MG	1A	3698	1/1	0.74	0.45	45,45,45,45	0
57	MG	2A	3675	1/1	0.74	0.14	64,64,64,64	0
57	MG	2A	3698	1/1	0.74	0.25	65,65,65,65	0
57	MG	1A	3413	1/1	0.74	0.17	70,70,70,70	0
57	MG	1A	3674	1/1	0.74	0.21	69,69,69,69	0
57	MG	2A	3132	1/1	0.75	0.24	65,65,65,65	0
57	MG	2A	3159	1/1	0.75	0.44	59,59,59,59	0
57	MG	1a	1792	1/1	0.75	0.30	83,83,83,83	0
57	MG	2A	3047	1/1	0.75	0.44	79,79,79,79	0
57	MG	2A	3663	1/1	0.75	0.13	71,71,71,71	0
57	MG	2A	3445	1/1	0.75	0.36	76,76,76,76	0
57	MG	2A	3691	1/1	0.75	0.19	50,50,50,50	0
57	MG	1a	1678	1/1	0.75	0.33	78,78,78,78	0
57	MG	2A	3703	1/1	0.75	0.14	67,67,67,67	0
57	MG	1A	3380	1/1	0.75	0.17	57,57,57,57	0
57	MG	2a	3164	1/1	0.75	0.19	82,82,82,82	0
57	MG	2A	3491	1/1	0.75	0.28	72,72,72,72	0
57	MG	1A	3924	1/1	0.76	0.15	61,61,61,61	0
57	MG	2A	3726	1/1	0.76	0.24	64,64,64,64	0
57	MG	1A	3846	1/1	0.76	0.15	62,62,62,62	0
57	MG	1A	3708	1/1	0.76	0.18	41,41,41,41	0
57	MG	1A	3531	1/1	0.76	0.14	50,50,50,50	0
57	MG	2A	3032	1/1	0.76	0.33	80,80,80,80	0
57	MG	1T	202	1/1	0.76	0.25	69,69,69,69	0
57	MG	2A	3075	1/1	0.76	0.32	74,74,74,74	0
57	MG	2a	3037	1/1	0.76	0.17	77,77,77,77	0
57	MG	2a	3043	1/1	0.76	0.24	74,74,74,74	0
57	MG	2a	3047	1/1	0.76	0.30	82,82,82,82	0
57	MG	2A	3655	1/1	0.76	0.12	77,77,77,77	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2A	3397	1/1	0.76	0.17	66,66,66,66	0
57	MG	2a	3109	1/1	0.76	0.25	85,85,85,85	0
57	MG	2A	3671	1/1	0.76	0.16	58,58,58,58	0
57	MG	2A	3082	1/1	0.76	0.21	78,78,78,78	0
57	MG	2A	3085	1/1	0.76	0.38	77,77,77,77	0
57	MG	1a	1827	1/1	0.76	0.20	77,77,77,77	0
57	MG	1A	3762	1/1	0.76	0.18	62,62,62,62	0
57	MG	2f	202	1/1	0.76	0.19	75,75,75,75	0
57	MG	1A	3618	1/1	0.77	0.15	43,43,43,43	0
57	MG	1A	3419	1/1	0.77	0.17	76,76,76,76	0
57	MG	2A	3495	1/1	0.77	0.20	71,71,71,71	0
57	MG	1a	1746	1/1	0.77	0.20	67,67,67,67	0
57	MG	2A	3403	1/1	0.77	0.19	78,78,78,78	0
57	MG	2A	3704	1/1	0.77	0.19	64,64,64,64	0
57	MG	2A	3525	1/1	0.77	0.22	75,75,75,75	0
57	MG	1a	1855	1/1	0.77	0.21	79,79,79,79	0
57	MG	1A	3783	1/1	0.77	0.23	67,67,67,67	0
57	MG	2A	3572	1/1	0.77	0.21	50,50,50,50	0
57	MG	2A	3624	1/1	0.77	0.19	71,71,71,71	0
57	MG	1A	3785	1/1	0.77	0.16	66,66,66,66	0
57	MG	2a	3178	1/1	0.77	0.34	69,69,69,69	0
57	MG	1n	101	1/1	0.77	0.36	78,78,78,78	0
57	MG	2j	201	1/1	0.77	0.23	79,79,79,79	0
57	MG	2A	3473	1/1	0.78	0.21	71,71,71,71	0
57	MG	1A	3799	1/1	0.78	0.21	30,30,30,30	0
57	MG	2A	3481	1/1	0.78	0.34	51,51,51,51	0
57	MG	1y	201	1/1	0.78	0.14	70,70,70,70	0
57	MG	2A	3345	1/1	0.78	0.21	67,67,67,67	0
57	MG	2A	3127	1/1	0.78	0.37	78,78,78,78	0
57	MG	2A	3699	1/1	0.78	0.22	65,65,65,65	0
57	MG	2a	3093	1/1	0.78	0.39	69,69,69,69	0
57	MG	2A	3700	1/1	0.78	0.19	70,70,70,70	0
57	MG	1a	1611	1/1	0.78	0.35	69,69,69,69	0
57	MG	2A	3146	1/1	0.78	0.25	70,70,70,70	0
57	MG	2a	3121	1/1	0.78	0.17	77,77,77,77	0
57	MG	1a	1787	1/1	0.78	0.30	75,75,75,75	0
57	MG	2A	3722	1/1	0.78	0.31	75,75,75,75	0
57	MG	2A	3541	1/1	0.78	0.23	79,79,79,79	0
57	MG	2a	3174	1/1	0.78	0.28	66,66,66,66	0
57	MG	1A	3556	1/1	0.78	0.14	56,56,56,56	0
57	MG	1d	305	1/1	0.78	0.12	85,85,85,85	0
57	MG	1A	3661	1/1	0.78	0.16	64,64,64,64	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2O	202	1/1	0.78	0.28	76,76,76,76	0
58	MPD	2B	220	8/8	0.78	0.28	63,66,74,77	0
59	ARG	1F	318	12/12	0.78	0.22	58,66,77,78	0
57	MG	2A	3551	1/1	0.79	0.15	61,61,61,61	0
57	MG	2Q	203	1/1	0.79	0.34	62,62,62,62	0
57	MG	1A	3121	1/1	0.79	0.31	62,62,62,62	0
57	MG	2A	3620	1/1	0.79	0.15	79,79,79,79	0
57	MG	2A	3415	1/1	0.79	0.16	53,53,53,53	0
57	MG	1A	3179	1/1	0.79	0.23	77,77,77,77	0
57	MG	1A	3424	1/1	0.79	0.19	53,53,53,53	0
57	MG	1A	3821	1/1	0.79	0.19	62,62,62,62	0
57	MG	2A	3471	1/1	0.79	0.16	69,69,69,69	0
57	MG	1A	3280	1/1	0.79	0.11	80,80,80,80	0
57	MG	1A	3986	1/1	0.79	0.19	52,52,52,52	0
57	MG	1a	1743	1/1	0.79	0.22	74,74,74,74	0
57	MG	1a	1831	1/1	0.79	0.26	80,80,80,80	0
57	MG	1B	217	1/1	0.79	0.14	63,63,63,63	0
57	MG	1A	3853	1/1	0.79	0.11	69,69,69,69	0
57	MG	2A	3377	1/1	0.79	0.17	72,72,72,72	0
57	MG	2A	3711	1/1	0.79	0.22	78,78,78,78	0
57	MG	2A	3517	1/1	0.79	0.24	77,77,77,77	0
57	MG	2A	3089	1/1	0.79	0.26	76,76,76,76	0
57	MG	2B	212	1/1	0.79	0.26	68,68,68,68	0
57	MG	1a	1775	1/1	0.79	0.27	72,72,72,72	0
57	MG	1A	3576	1/1	0.79	0.46	46,46,46,46	0
57	MG	2D	304	1/1	0.79	0.24	58,58,58,58	0
57	MG	2A	3413	1/1	0.79	0.21	77,77,77,77	0
57	MG	1A	3952	1/1	0.80	0.15	49,49,49,49	0
57	MG	1A	3160	1/1	0.80	0.19	52,52,52,52	0
57	MG	1A	3430	1/1	0.80	0.22	62,62,62,62	0
57	MG	1a	1642	1/1	0.80	0.21	67,67,67,67	0
57	MG	2A	3670	1/1	0.80	0.17	69,69,69,69	0
57	MG	1A	3038	1/1	0.80	0.17	53,53,53,53	0
57	MG	2a	3045	1/1	0.80	0.43	71,71,71,71	0
57	MG	1A	4009	1/1	0.80	0.22	68,68,68,68	0
57	MG	2a	3060	1/1	0.80	0.40	75,75,75,75	0
57	MG	2a	3080	1/1	0.80	0.19	62,62,62,62	0
57	MG	2A	3163	1/1	0.80	0.18	74,74,74,74	0
57	MG	1a	1711	1/1	0.80	0.41	76,76,76,76	0
57	MG	1A	3611	1/1	0.80	0.28	61,61,61,61	0
57	MG	2A	3193	1/1	0.80	0.41	73,73,73,73	0
57	MG	2A	3209	1/1	0.80	0.28	73,73,73,73	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2A	3219	1/1	0.80	0.25	69,69,69,69	0
57	MG	2A	3250	1/1	0.80	0.17	68,68,68,68	0
57	MG	1A	3781	1/1	0.80	0.21	59,59,59,59	0
57	MG	2a	3162	1/1	0.80	0.24	78,78,78,78	0
57	MG	2A	3045	1/1	0.80	0.13	67,67,67,67	0
57	MG	1a	1824	1/1	0.80	0.31	76,76,76,76	0
57	MG	1R	207	1/1	0.80	0.25	53,53,53,53	0
57	MG	1T	201	1/1	0.80	0.23	68,68,68,68	0
57	MG	1a	1758	1/1	0.80	0.31	71,71,71,71	0
57	MG	1a	1838	1/1	0.80	0.22	71,71,71,71	0
57	MG	2A	3111	1/1	0.80	0.20	58,58,58,58	0
57	MG	2A	3598	1/1	0.80	0.18	74,74,74,74	0
57	MG	1a	1675	1/1	0.81	0.20	60,60,60,60	0
57	MG	1A	3673	1/1	0.81	0.22	69,69,69,69	0
57	MG	2A	3723	1/1	0.81	0.23	57,57,57,57	0
57	MG	1A	3514	1/1	0.81	0.15	65,65,65,65	0
57	MG	2B	201	1/1	0.81	0.31	79,79,79,79	0
57	MG	1a	1703	1/1	0.81	0.20	72,72,72,72	0
57	MG	1A	3997	1/1	0.81	0.34	42,42,42,42	0
57	MG	1A	3646	1/1	0.81	0.17	54,54,54,54	0
57	MG	1a	1722	1/1	0.81	0.21	76,76,76,76	0
57	MG	1A	3873	1/1	0.81	0.11	57,57,57,57	0
57	MG	1a	1863	1/1	0.81	0.18	57,57,57,57	0
57	MG	2A	3516	1/1	0.81	0.10	79,79,79,79	0
57	MG	2A	3179	1/1	0.81	0.17	73,73,73,73	0
57	MG	2A	3182	1/1	0.81	0.29	73,73,73,73	0
57	MG	2a	3021	1/1	0.81	0.29	74,74,74,74	0
57	MG	2a	3023	1/1	0.81	0.40	79,79,79,79	0
57	MG	2A	3539	1/1	0.81	0.19	73,73,73,73	0
57	MG	1A	3211	1/1	0.81	0.14	64,64,64,64	0
57	MG	1P	202	1/1	0.81	0.22	43,43,43,43	0
57	MG	2A	3212	1/1	0.81	0.28	66,66,66,66	0
57	MG	1a	1748	1/1	0.81	0.30	72,72,72,72	0
57	MG	2A	3571	1/1	0.81	0.17	44,44,44,44	0
57	MG	1e	205	1/1	0.81	0.15	70,70,70,70	0
57	MG	2A	3577	1/1	0.81	0.31	60,60,60,60	0
57	MG	1A	3816	1/1	0.81	0.26	37,37,37,37	0
57	MG	1a	1772	1/1	0.81	0.12	69,69,69,69	0
57	MG	1A	3691	1/1	0.81	0.20	73,73,73,73	0
57	MG	1A	3943	1/1	0.81	0.19	74,74,74,74	0
57	MG	2A	3037	1/1	0.81	0.29	69,69,69,69	0
57	MG	1A	3835	1/1	0.81	0.14	61,61,61,61	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1A	3953	1/1	0.81	0.15	71,71,71,71	0
57	MG	2a	3154	1/1	0.81	0.30	80,80,80,80	0
57	MG	2A	3051	1/1	0.81	0.22	68,68,68,68	0
57	MG	1A	3842	1/1	0.81	0.15	71,71,71,71	0
57	MG	1a	1647	1/1	0.81	0.27	70,70,70,70	0
57	MG	1a	1651	1/1	0.81	0.29	72,72,72,72	0
57	MG	2A	3419	1/1	0.81	0.15	62,62,62,62	0
57	MG	2A	3701	1/1	0.81	0.17	55,55,55,55	0
57	MG	2A	3426	1/1	0.81	0.19	68,68,68,68	0
57	MG	1a	1662	1/1	0.81	0.22	75,75,75,75	0
57	MG	1a	1819	1/1	0.81	0.27	80,80,80,80	0
57	MG	2A	3683	1/1	0.82	0.27	57,57,57,57	0
57	MG	2A	3381	1/1	0.82	0.19	55,55,55,55	0
57	MG	2A	3697	1/1	0.82	0.19	84,84,84,84	0
57	MG	2A	3026	1/1	0.82	0.21	70,70,70,70	0
57	MG	1A	3868	1/1	0.82	0.17	67,67,67,67	0
57	MG	1A	3632	1/1	0.82	0.28	45,45,45,45	0
57	MG	2A	3405	1/1	0.82	0.17	72,72,72,72	0
57	MG	1a	1603	1/1	0.82	0.22	72,72,72,72	0
57	MG	1A	3634	1/1	0.82	0.20	48,48,48,48	0
57	MG	1A	3752	1/1	0.82	0.21	69,69,69,69	0
57	MG	1A	3636	1/1	0.82	0.13	75,75,75,75	0
57	MG	1A	3567	1/1	0.82	0.20	50,50,50,50	0
57	MG	1A	3946	1/1	0.82	0.18	65,65,65,65	0
57	MG	2A	3441	1/1	0.82	0.18	70,70,70,70	0
57	MG	2A	3442	1/1	0.82	0.31	75,75,75,75	0
57	MG	1A	3366	1/1	0.82	0.26	77,77,77,77	0
57	MG	2A	3447	1/1	0.82	0.23	62,62,62,62	0
57	MG	2A	3449	1/1	0.82	0.18	92,92,92,92	0
57	MG	1A	3178	1/1	0.82	0.18	55,55,55,55	0
57	MG	1A	3663	1/1	0.82	0.12	52,52,52,52	0
57	MG	1A	3977	1/1	0.82	0.26	55,55,55,55	0
57	MG	1a	1830	1/1	0.82	0.23	77,77,77,77	0
57	MG	2U	201	1/1	0.82	0.16	62,62,62,62	0
57	MG	1A	3582	1/1	0.82	0.16	37,37,37,37	0
57	MG	2A	3134	1/1	0.82	0.20	68,68,68,68	0
57	MG	1A	3985	1/1	0.82	0.18	72,72,72,72	0
57	MG	1a	1713	1/1	0.82	0.36	60,60,60,60	0
57	MG	1A	3323	1/1	0.82	0.39	74,74,74,74	0
57	MG	2a	3026	1/1	0.82	0.36	75,75,75,75	0
57	MG	2A	3514	1/1	0.82	0.18	68,68,68,68	0
57	MG	1a	1842	1/1	0.82	0.18	88,88,88,88	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1a	1719	1/1	0.82	0.18	58,58,58,58	0
57	MG	1a	1857	1/1	0.82	0.23	59,59,59,59	0
57	MG	2a	3053	1/1	0.82	0.20	67,67,67,67	0
57	MG	1A	3444	1/1	0.82	0.15	42,42,42,42	0
57	MG	1A	3458	1/1	0.82	0.21	42,42,42,42	0
57	MG	2A	3204	1/1	0.82	0.33	67,67,67,67	0
57	MG	1A	3544	1/1	0.82	0.12	48,48,48,48	0
57	MG	2A	3544	1/1	0.82	0.12	64,64,64,64	0
57	MG	2A	3545	1/1	0.82	0.21	78,78,78,78	0
57	MG	2A	3549	1/1	0.82	0.28	65,65,65,65	0
57	MG	1B	220	1/1	0.82	0.17	69,69,69,69	0
57	MG	1e	201	1/1	0.82	0.22	76,76,76,76	0
57	MG	1e	202	1/1	0.82	0.36	73,73,73,73	0
57	MG	2A	3573	1/1	0.82	0.14	47,47,47,47	0
57	MG	2A	3289	1/1	0.82	0.35	65,65,65,65	0
57	MG	2A	3292	1/1	0.82	0.33	76,76,76,76	0
57	MG	2a	3171	1/1	0.82	0.24	75,75,75,75	0
57	MG	2A	3298	1/1	0.82	0.47	78,78,78,78	0
57	MG	1e	204	1/1	0.82	0.22	70,70,70,70	0
57	MG	2a	3177	1/1	0.82	0.34	61,61,61,61	0
57	MG	1A	3467	1/1	0.82	0.14	52,52,52,52	0
57	MG	1a	1750	1/1	0.82	0.15	82,82,82,82	0
57	MG	2A	3334	1/1	0.82	0.19	64,64,64,64	0
58	MPD	1T	208	8/8	0.82	0.22	68,70,74,81	0
58	MPD	1a	1868	8/8	0.82	0.17	53,64,70,74	0
57	MG	1A	3027	1/1	0.82	0.13	70,70,70,70	0
57	MG	1A	3865	1/1	0.82	0.12	51,51,51,51	0
57	MG	2B	207	1/1	0.83	0.14	67,67,67,67	0
57	MG	1A	3775	1/1	0.83	0.18	45,45,45,45	0
57	MG	2A	3069	1/1	0.83	0.37	65,65,65,65	0
57	MG	2B	216	1/1	0.83	0.15	83,83,83,83	0
57	MG	2A	3307	1/1	0.83	0.18	65,65,65,65	0
57	MG	2A	3531	1/1	0.83	0.19	77,77,77,77	0
57	MG	1R	203	1/1	0.83	0.29	47,47,47,47	0
57	MG	2A	3312	1/1	0.83	0.15	39,39,39,39	0
57	MG	1a	1714	1/1	0.83	0.20	72,72,72,72	0
57	MG	1a	1717	1/1	0.83	0.28	81,81,81,81	0
57	MG	1A	3776	1/1	0.83	0.19	45,45,45,45	0
57	MG	1A	3508	1/1	0.83	0.20	62,62,62,62	0
57	MG	2A	3379	1/1	0.83	0.18	70,70,70,70	0
57	MG	2A	3550	1/1	0.83	0.13	73,73,73,73	0
57	MG	1A	3511	1/1	0.83	0.14	35,35,35,35	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1a	1732	1/1	0.83	0.15	85,85,85,85	0
57	MG	18	102	1/1	0.83	0.24	40,40,40,40	0
57	MG	1A	3641	1/1	0.83	0.14	45,45,45,45	0
57	MG	1A	3448	1/1	0.83	0.11	49,49,49,49	0
57	MG	1A	3992	1/1	0.83	0.16	60,60,60,60	0
57	MG	1a	1632	1/1	0.83	0.27	63,63,63,63	0
57	MG	1a	1638	1/1	0.83	0.26	67,67,67,67	0
57	MG	2a	3063	1/1	0.83	0.25	78,78,78,78	0
57	MG	1a	1761	1/1	0.83	0.20	70,70,70,70	0
57	MG	2A	3420	1/1	0.83	0.20	55,55,55,55	0
57	MG	2a	3091	1/1	0.83	0.33	69,69,69,69	0
57	MG	1A	3656	1/1	0.83	0.21	75,75,75,75	0
57	MG	2A	3178	1/1	0.83	0.21	65,65,65,65	0
57	MG	1A	4002	1/1	0.83	0.16	71,71,71,71	0
57	MG	2A	3677	1/1	0.83	0.32	56,56,56,56	0
57	MG	1A	3252	1/1	0.83	0.14	47,47,47,47	0
57	MG	1a	1658	1/1	0.83	0.14	69,69,69,69	0
57	MG	1A	3376	1/1	0.83	0.11	65,65,65,65	0
57	MG	1A	3434	1/1	0.83	0.26	63,63,63,63	0
57	MG	2a	3157	1/1	0.83	0.19	73,73,73,73	0
57	MG	2A	3456	1/1	0.83	0.17	78,78,78,78	0
57	MG	1E	304	1/1	0.83	0.14	28,28,28,28	0
57	MG	2A	3217	1/1	0.83	0.12	69,69,69,69	0
57	MG	1a	1701	1/1	0.83	0.25	72,72,72,72	0
57	MG	1G	202	1/1	0.83	0.13	60,60,60,60	0
57	MG	2A	3253	1/1	0.83	0.27	75,75,75,75	0
57	MG	2A	3259	1/1	0.83	0.29	57,57,57,57	0
57	MG	1A	3263	1/1	0.83	0.48	77,77,77,77	0
57	MG	2A	3290	1/1	0.83	0.47	68,68,68,68	0
57	MG	1a	1709	1/1	0.83	0.21	60,60,60,60	0
57	MG	2A	3729	1/1	0.83	0.18	69,69,69,69	0
57	MG	2A	3295	1/1	0.83	0.38	65,65,65,65	0
57	MG	2B	202	1/1	0.83	0.16	75,75,75,75	0
57	MG	1e	203	1/1	0.84	0.14	61,61,61,61	0
57	MG	2G	201	1/1	0.84	0.21	77,77,77,77	0
57	MG	1A	3660	1/1	0.84	0.29	36,36,36,36	0
57	MG	2A	3546	1/1	0.84	0.23	66,66,66,66	0
57	MG	1A	3465	1/1	0.84	0.12	62,62,62,62	0
57	MG	1A	3875	1/1	0.84	0.23	62,62,62,62	0
57	MG	2a	3004	1/1	0.84	0.19	76,76,76,76	0
57	MG	15	105	1/1	0.84	0.23	35,35,35,35	0
57	MG	2a	3010	1/1	0.84	0.38	81,81,81,81	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1A	3525	1/1	0.84	0.21	64,64,64,64	0
57	MG	1a	1810	1/1	0.84	0.20	72,72,72,72	0
57	MG	1a	1816	1/1	0.84	0.12	73,73,73,73	0
57	MG	2A	3034	1/1	0.84	0.16	58,58,58,58	0
57	MG	1A	3321	1/1	0.84	0.38	70,70,70,70	0
57	MG	2A	3612	1/1	0.84	0.18	44,44,44,44	0
57	MG	2A	3614	1/1	0.84	0.16	38,38,38,38	0
57	MG	2A	3232	1/1	0.84	0.27	69,69,69,69	0
57	MG	2A	3249	1/1	0.84	0.33	69,69,69,69	0
57	MG	1A	3926	1/1	0.84	0.13	69,69,69,69	0
57	MG	1B	206	1/1	0.84	0.12	53,53,53,53	0
57	MG	1B	207	1/1	0.84	0.24	69,69,69,69	0
57	MG	2a	3073	1/1	0.84	0.40	71,71,71,71	0
57	MG	2A	3451	1/1	0.84	0.20	64,64,64,64	0
57	MG	2A	3452	1/1	0.84	0.17	58,58,58,58	0
57	MG	2A	3454	1/1	0.84	0.32	82,82,82,82	0
57	MG	2A	3286	1/1	0.84	0.31	67,67,67,67	0
57	MG	2A	3461	1/1	0.84	0.18	56,56,56,56	0
57	MG	2a	3107	1/1	0.84	0.31	80,80,80,80	0
57	MG	1A	3063	1/1	0.84	0.13	52,52,52,52	0
57	MG	2a	3117	1/1	0.84	0.15	69,69,69,69	0
57	MG	1A	3677	1/1	0.84	0.14	83,83,83,83	0
57	MG	1D	313	1/1	0.84	0.25	33,33,33,33	0
57	MG	1A	3272	1/1	0.84	0.13	67,67,67,67	0
57	MG	1a	1657	1/1	0.84	0.12	72,72,72,72	0
57	MG	2A	3483	1/1	0.84	0.18	64,64,64,64	0
57	MG	2A	3301	1/1	0.84	0.21	70,70,70,70	0
57	MG	2A	3492	1/1	0.84	0.19	78,78,78,78	0
57	MG	2A	3105	1/1	0.84	0.22	65,65,65,65	0
57	MG	1A	3856	1/1	0.84	0.13	45,45,45,45	0
57	MG	1N	203	1/1	0.84	0.13	61,61,61,61	0
57	MG	1A	3454	1/1	0.84	0.15	55,55,55,55	0
57	MG	1A	3330	1/1	0.84	0.13	58,58,58,58	0
57	MG	1a	1866	1/1	0.84	0.29	72,72,72,72	0
57	MG	2a	3181	1/1	0.84	0.26	70,70,70,70	0
57	MG	1a	1769	1/1	0.84	0.13	69,69,69,69	0
57	MG	1a	1691	1/1	0.84	0.30	69,69,69,69	0
57	MG	1a	1692	1/1	0.84	0.40	64,64,64,64	0
57	MG	1a	1697	1/1	0.84	0.27	69,69,69,69	0
57	MG	2A	3394	1/1	0.84	0.16	75,75,75,75	0
57	MG	1A	3463	1/1	0.84	0.13	46,46,46,46	0
57	MG	1A	3476	1/1	0.85	0.10	24,24,24,24	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2A	3206	1/1	0.85	0.17	67,67,67,67	0
57	MG	1B	210	1/1	0.85	0.16	60,60,60,60	0
57	MG	2A	3728	1/1	0.85	0.15	56,56,56,56	0
57	MG	2A	3468	1/1	0.85	0.14	65,65,65,65	0
57	MG	1B	213	1/1	0.85	0.25	69,69,69,69	0
57	MG	1a	1768	1/1	0.85	0.17	62,62,62,62	0
57	MG	2B	204	1/1	0.85	0.21	75,75,75,75	0
57	MG	2B	205	1/1	0.85	0.32	72,72,72,72	0
57	MG	1a	1652	1/1	0.85	0.32	74,74,74,74	0
57	MG	2B	210	1/1	0.85	0.13	66,66,66,66	0
57	MG	2A	3228	1/1	0.85	0.46	73,73,73,73	0
57	MG	1A	3823	1/1	0.85	0.14	50,50,50,50	0
57	MG	1A	3442	1/1	0.85	0.13	55,55,55,55	0
57	MG	1D	309	1/1	0.85	0.33	47,47,47,47	0
57	MG	1a	1674	1/1	0.85	0.18	69,69,69,69	0
57	MG	2A	3499	1/1	0.85	0.20	78,78,78,78	0
57	MG	1A	3093	1/1	0.85	0.17	57,57,57,57	0
57	MG	2A	3505	1/1	0.85	0.11	71,71,71,71	0
57	MG	2A	3264	1/1	0.85	0.35	60,60,60,60	0
57	MG	1A	3206	1/1	0.85	0.26	68,68,68,68	0
57	MG	1E	307	1/1	0.85	0.14	62,62,62,62	0
57	MG	1A	3852	1/1	0.85	0.14	41,41,41,41	0
57	MG	2A	3521	1/1	0.85	0.24	66,66,66,66	0
57	MG	1A	3010	1/1	0.85	0.16	52,52,52,52	0
57	MG	1A	3568	1/1	0.85	0.17	52,52,52,52	0
57	MG	2A	3532	1/1	0.85	0.16	67,67,67,67	0
57	MG	1A	3151	1/1	0.85	0.25	62,62,62,62	0
57	MG	2A	3300	1/1	0.85	0.27	66,66,66,66	0
57	MG	2a	3034	1/1	0.85	0.39	68,68,68,68	0
57	MG	2A	3058	1/1	0.85	0.15	67,67,67,67	0
57	MG	2a	3039	1/1	0.85	0.18	76,76,76,76	0
57	MG	2A	3062	1/1	0.85	0.15	56,56,56,56	0
57	MG	1A	3863	1/1	0.85	0.17	35,35,35,35	0
57	MG	1a	1821	1/1	0.85	0.14	68,68,68,68	0
57	MG	1a	1708	1/1	0.85	0.37	70,70,70,70	0
57	MG	2a	3058	1/1	0.85	0.26	79,79,79,79	0
57	MG	2A	3084	1/1	0.85	0.32	74,74,74,74	0
57	MG	1A	3982	1/1	0.85	0.21	50,50,50,50	0
57	MG	2a	3064	1/1	0.85	0.26	71,71,71,71	0
57	MG	1A	3155	1/1	0.85	0.29	71,71,71,71	0
57	MG	2A	3373	1/1	0.85	0.15	44,44,44,44	0
57	MG	1A	3040	1/1	0.85	0.18	64,64,64,64	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1l	104	1/1	0.85	0.15	64,64,64,64	0
57	MG	2a	3092	1/1	0.85	0.20	60,60,60,60	0
57	MG	1A	3786	1/1	0.85	0.23	65,65,65,65	0
57	MG	2A	3385	1/1	0.85	0.15	78,78,78,78	0
57	MG	2a	3101	1/1	0.85	0.25	61,61,61,61	0
57	MG	2a	3102	1/1	0.85	0.30	66,66,66,66	0
57	MG	2A	3389	1/1	0.85	0.18	76,76,76,76	0
57	MG	2A	3120	1/1	0.85	0.16	65,65,65,65	0
57	MG	2A	3619	1/1	0.85	0.17	59,59,59,59	0
57	MG	1A	3035	1/1	0.85	0.15	54,54,54,54	0
57	MG	1A	4001	1/1	0.85	0.17	34,34,34,34	0
57	MG	2A	3651	1/1	0.85	0.12	76,76,76,76	0
57	MG	1A	3529	1/1	0.85	0.11	56,56,56,56	0
57	MG	2a	3148	1/1	0.85	0.14	69,69,69,69	0
57	MG	1a	1844	1/1	0.85	0.12	69,69,69,69	0
57	MG	2A	3139	1/1	0.85	0.21	55,55,55,55	0
57	MG	1a	1846	1/1	0.85	0.21	64,64,64,64	0
57	MG	2A	3150	1/1	0.85	0.34	63,63,63,63	0
57	MG	2a	3167	1/1	0.85	0.21	72,72,72,72	0
57	MG	2A	3155	1/1	0.85	0.10	66,66,66,66	0
57	MG	1a	1724	1/1	0.85	0.20	63,63,63,63	0
57	MG	1A	3876	1/1	0.85	0.16	55,55,55,55	0
57	MG	1a	1861	1/1	0.85	0.21	74,74,74,74	0
57	MG	1a	1621	1/1	0.85	0.25	61,61,61,61	0
57	MG	2A	3175	1/1	0.85	0.17	56,56,56,56	0
57	MG	1A	4011	1/1	0.85	0.23	59,59,59,59	0
57	MG	1a	1635	1/1	0.85	0.29	65,65,65,65	0
57	MG	2r	101	1/1	0.85	0.18	67,67,67,67	0
57	MG	1b	301	1/1	0.85	0.27	78,78,78,78	0
57	MG	2A	3191	1/1	0.85	0.37	71,71,71,71	0
58	MPD	2A	3732	8/8	0.85	0.22	51,60,66,69	0
57	MG	1A	3890	1/1	0.85	0.27	37,37,37,37	0
57	MG	2A	3199	1/1	0.85	0.13	59,59,59,59	0
57	MG	1A	3659	1/1	0.86	0.12	51,51,51,51	0
57	MG	1a	1694	1/1	0.86	0.40	67,67,67,67	0
57	MG	2A	3500	1/1	0.86	0.19	63,63,63,63	0
57	MG	1F	314	1/1	0.86	0.10	42,42,42,42	0
57	MG	1A	3372	1/1	0.86	0.17	74,74,74,74	0
57	MG	1A	3585	1/1	0.86	0.18	72,72,72,72	0
57	MG	1A	3373	1/1	0.86	0.21	53,53,53,53	0
57	MG	1a	1706	1/1	0.86	0.31	62,62,62,62	0
57	MG	1A	3672	1/1	0.86	0.16	69,69,69,69	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1A	3485	1/1	0.86	0.10	24,24,24,24	0
57	MG	2A	3108	1/1	0.86	0.21	72,72,72,72	0
57	MG	2A	3308	1/1	0.86	0.21	64,64,64,64	0
57	MG	1A	3535	1/1	0.86	0.24	78,78,78,78	0
57	MG	1a	1840	1/1	0.86	0.13	76,76,76,76	0
57	MG	2A	3325	1/1	0.86	0.19	65,65,65,65	0
57	MG	1A	3223	1/1	0.86	0.15	54,54,54,54	0
57	MG	1A	3549	1/1	0.86	0.11	39,39,39,39	0
57	MG	2A	3335	1/1	0.86	0.14	65,65,65,65	0
57	MG	2a	3032	1/1	0.86	0.25	73,73,73,73	0
57	MG	2A	3340	1/1	0.86	0.17	75,75,75,75	0
57	MG	1W	201	1/1	0.86	0.28	55,55,55,55	0
57	MG	1A	3824	1/1	0.86	0.11	54,54,54,54	0
57	MG	2a	3040	1/1	0.86	0.33	72,72,72,72	0
57	MG	2A	3133	1/1	0.86	0.34	65,65,65,65	0
57	MG	13	102	1/1	0.86	0.12	73,73,73,73	0
57	MG	2A	3553	1/1	0.86	0.13	39,39,39,39	0
57	MG	2A	3380	1/1	0.86	0.14	47,47,47,47	0
57	MG	1A	3120	1/1	0.86	0.24	55,55,55,55	0
57	MG	1a	1858	1/1	0.86	0.26	77,77,77,77	0
57	MG	1A	3326	1/1	0.86	0.17	45,45,45,45	0
57	MG	1A	3558	1/1	0.86	0.14	55,55,55,55	0
57	MG	2A	3600	1/1	0.86	0.14	53,53,53,53	0
57	MG	2a	3077	1/1	0.86	0.36	69,69,69,69	0
57	MG	1A	3849	1/1	0.86	0.10	57,57,57,57	0
57	MG	2a	3082	1/1	0.86	0.38	66,66,66,66	0
57	MG	2A	3398	1/1	0.86	0.17	66,66,66,66	0
57	MG	1A	3417	1/1	0.86	0.11	22,22,22,22	0
57	MG	1a	1618	1/1	0.86	0.14	62,62,62,62	0
57	MG	2A	3165	1/1	0.86	0.18	60,60,60,60	0
57	MG	2A	3640	1/1	0.86	0.13	41,41,41,41	0
57	MG	1A	3281	1/1	0.86	0.19	46,46,46,46	0
57	MG	2A	3173	1/1	0.86	0.12	52,52,52,52	0
57	MG	2a	3105	1/1	0.86	0.30	65,65,65,65	0
57	MG	1A	3713	1/1	0.86	0.11	44,44,44,44	0
57	MG	1a	1754	1/1	0.86	0.28	67,67,67,67	0
57	MG	1A	3715	1/1	0.86	0.17	59,59,59,59	0
57	MG	1A	3730	1/1	0.86	0.12	54,54,54,54	0
57	MG	2A	3183	1/1	0.86	0.34	78,78,78,78	0
57	MG	2a	3127	1/1	0.86	0.15	68,68,68,68	0
57	MG	1A	3317	1/1	0.86	0.20	52,52,52,52	0
57	MG	2a	3130	1/1	0.86	0.29	73,73,73,73	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1A	3746	1/1	0.86	0.23	50,50,50,50	0
57	MG	2a	3134	1/1	0.86	0.22	77,77,77,77	0
57	MG	1A	3575	1/1	0.86	0.14	54,54,54,54	0
57	MG	2A	3446	1/1	0.86	0.26	47,47,47,47	0
57	MG	2a	3156	1/1	0.86	0.14	84,84,84,84	0
57	MG	1n	102	1/1	0.86	0.15	53,53,53,53	0
57	MG	1n	103	1/1	0.86	0.29	67,67,67,67	0
57	MG	1A	3756	1/1	0.86	0.24	68,68,68,68	0
57	MG	2A	3210	1/1	0.86	0.31	65,65,65,65	0
57	MG	1A	3759	1/1	0.86	0.15	59,59,59,59	0
57	MG	2A	3001	1/1	0.86	0.34	65,65,65,65	0
57	MG	2A	3016	1/1	0.86	0.29	76,76,76,76	0
57	MG	2A	3463	1/1	0.86	0.16	41,41,41,41	0
57	MG	1B	218	1/1	0.86	0.17	53,53,53,53	0
57	MG	2A	3230	1/1	0.86	0.23	67,67,67,67	0
57	MG	1A	3652	1/1	0.86	0.10	43,43,43,43	0
57	MG	1a	1669	1/1	0.86	0.17	66,66,66,66	0
57	MG	1D	301	1/1	0.86	0.17	65,65,65,65	0
57	MG	2A	3480	1/1	0.86	0.16	56,56,56,56	0
57	MG	1A	3193	1/1	0.86	0.42	64,64,64,64	0
57	MG	1A	3892	1/1	0.86	0.13	28,28,28,28	0
57	MG	1A	3907	1/1	0.86	0.14	29,29,29,29	0
57	MG	2A	3272	1/1	0.86	0.25	78,78,78,78	0
57	MG	1a	1860	1/1	0.87	0.21	68,68,68,68	0
57	MG	1F	316	1/1	0.87	0.20	53,53,53,53	0
57	MG	2F	301	1/1	0.87	0.15	66,66,66,66	0
57	MG	1A	3124	1/1	0.87	0.21	63,63,63,63	0
57	MG	1A	3446	1/1	0.87	0.13	83,83,83,83	0
57	MG	2I	201	1/1	0.87	0.14	74,74,74,74	0
57	MG	1a	1663	1/1	0.87	0.13	61,61,61,61	0
57	MG	2A	3529	1/1	0.87	0.14	75,75,75,75	0
57	MG	2R	201	1/1	0.87	0.26	51,51,51,51	0
57	MG	1a	1759	1/1	0.87	0.21	67,67,67,67	0
57	MG	29	101	1/1	0.87	0.14	66,66,66,66	0
57	MG	2A	3336	1/1	0.87	0.21	60,60,60,60	0
57	MG	2A	3533	1/1	0.87	0.21	68,68,68,68	0
57	MG	1A	3171	1/1	0.87	0.19	68,68,68,68	0
57	MG	2a	3016	1/1	0.87	0.27	80,80,80,80	0
57	MG	1a	1763	1/1	0.87	0.19	65,65,65,65	0
57	MG	2A	3366	1/1	0.87	0.18	64,64,64,64	0
57	MG	2A	3161	1/1	0.87	0.27	74,74,74,74	0
57	MG	1A	3083	1/1	0.87	0.13	55,55,55,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1A	3062	1/1	0.87	0.20	68,68,68,68	0
57	MG	1a	1770	1/1	0.87	0.26	67,67,67,67	0
57	MG	2A	3547	1/1	0.87	0.17	80,80,80,80	0
57	MG	2A	3170	1/1	0.87	0.14	52,52,52,52	0
57	MG	1A	3246	1/1	0.87	0.12	68,68,68,68	0
57	MG	1a	1681	1/1	0.87	0.32	72,72,72,72	0
57	MG	2A	3391	1/1	0.87	0.16	65,65,65,65	0
57	MG	2A	3561	1/1	0.87	0.09	63,63,63,63	0
57	MG	1l	3101	1/1	0.87	0.17	73,73,73,73	0
57	MG	1a	1686	1/1	0.87	0.24	72,72,72,72	0
57	MG	2a	3055	1/1	0.87	0.14	68,68,68,68	0
57	MG	2a	3056	1/1	0.87	0.28	77,77,77,77	0
57	MG	2a	3057	1/1	0.87	0.30	68,68,68,68	0
57	MG	1a	1688	1/1	0.87	0.18	63,63,63,63	0
57	MG	1A	3431	1/1	0.87	0.12	32,32,32,32	0
57	MG	1o	101	1/1	0.87	0.27	73,73,73,73	0
57	MG	2A	3186	1/1	0.87	0.20	74,74,74,74	0
57	MG	2a	3065	1/1	0.87	0.12	65,65,65,65	0
57	MG	2a	3066	1/1	0.87	0.30	65,65,65,65	0
57	MG	2A	3406	1/1	0.87	0.12	74,74,74,74	0
57	MG	2a	3074	1/1	0.87	0.12	75,75,75,75	0
57	MG	1A	3700	1/1	0.87	0.24	60,60,60,60	0
57	MG	1A	3891	1/1	0.87	0.09	20,20,20,20	0
57	MG	2a	3081	1/1	0.87	0.37	75,75,75,75	0
57	MG	2A	3196	1/1	0.87	0.21	64,64,64,64	0
57	MG	2A	3418	1/1	0.87	0.21	56,56,56,56	0
57	MG	1a	1796	1/1	0.87	0.09	80,80,80,80	0
57	MG	2A	3012	1/1	0.87	0.18	68,68,68,68	0
57	MG	10	107	1/1	0.87	0.17	65,65,65,65	0
57	MG	2a	3098	1/1	0.87	0.18	63,63,63,63	0
57	MG	2A	3024	1/1	0.87	0.11	51,51,51,51	0
57	MG	2A	3668	1/1	0.87	0.20	57,57,57,57	0
57	MG	1A	3378	1/1	0.87	0.14	44,44,44,44	0
57	MG	1a	1808	1/1	0.87	0.23	72,72,72,72	0
57	MG	2A	3444	1/1	0.87	0.24	70,70,70,70	0
57	MG	1A	3296	1/1	0.87	0.18	66,66,66,66	0
57	MG	2a	3110	1/1	0.87	0.12	69,69,69,69	0
57	MG	2a	3114	1/1	0.87	0.15	59,59,59,59	0
57	MG	1A	3480	1/1	0.87	0.15	39,39,39,39	0
57	MG	2A	3222	1/1	0.87	0.12	65,65,65,65	0
57	MG	1a	1704	1/1	0.87	0.30	66,66,66,66	0
57	MG	17	105	1/1	0.87	0.19	59,59,59,59	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1A	3408	1/1	0.87	0.14	68,68,68,68	0
57	MG	1a	1601	1/1	0.87	0.13	80,80,80,80	0
57	MG	1A	3740	1/1	0.87	0.17	65,65,65,65	0
57	MG	1a	1829	1/1	0.87	0.12	46,46,46,46	0
57	MG	1A	3490	1/1	0.87	0.09	71,71,71,71	0
57	MG	1A	3546	1/1	0.87	0.17	58,58,58,58	0
57	MG	2a	3155	1/1	0.87	0.24	66,66,66,66	0
57	MG	2A	3270	1/1	0.87	0.16	64,64,64,64	0
57	MG	2A	3713	1/1	0.87	0.25	68,68,68,68	0
57	MG	2a	3161	1/1	0.87	0.17	70,70,70,70	0
57	MG	2A	3719	1/1	0.87	0.21	58,58,58,58	0
57	MG	1B	225	1/1	0.87	0.09	53,53,53,53	0
57	MG	2A	3278	1/1	0.87	0.14	55,55,55,55	0
57	MG	2a	3169	1/1	0.87	0.21	72,72,72,72	0
57	MG	1A	3667	1/1	0.87	0.18	72,72,72,72	0
57	MG	2A	3288	1/1	0.87	0.39	62,62,62,62	0
57	MG	1A	3548	1/1	0.87	0.27	40,40,40,40	0
57	MG	2A	3090	1/1	0.87	0.30	66,66,66,66	0
57	MG	2A	3093	1/1	0.87	0.10	57,57,57,57	0
57	MG	2a	3179	1/1	0.87	0.29	77,77,77,77	0
57	MG	1A	3757	1/1	0.87	0.17	50,50,50,50	0
57	MG	1a	1723	1/1	0.87	0.30	68,68,68,68	0
57	MG	1D	315	1/1	0.87	0.18	74,74,74,74	0
57	MG	2p	101	1/1	0.87	0.26	61,61,61,61	0
57	MG	1A	3500	1/1	0.87	0.12	58,58,58,58	0
57	MG	2x	101	1/1	0.87	0.15	44,44,44,44	0
57	MG	1A	3979	1/1	0.87	0.13	85,85,85,85	0
57	MG	2B	213	1/1	0.87	0.29	74,74,74,74	0
57	MG	1F	312	1/1	0.87	0.13	37,37,37,37	0
57	MG	2B	215	1/1	0.87	0.14	68,68,68,68	0
57	MG	1A	3760	1/1	0.87	0.17	50,50,50,50	0
57	MG	1A	3958	1/1	0.88	0.12	50,50,50,50	0
57	MG	2Q	202	1/1	0.88	0.38	65,65,65,65	0
57	MG	2A	3060	1/1	0.88	0.30	54,54,54,54	0
57	MG	1A	3963	1/1	0.88	0.13	60,60,60,60	0
57	MG	1A	3130	1/1	0.88	0.13	60,60,60,60	0
57	MG	1a	1805	1/1	0.88	0.28	71,71,71,71	0
57	MG	2A	3078	1/1	0.88	0.35	63,63,63,63	0
57	MG	2a	3005	1/1	0.88	0.31	73,73,73,73	0
57	MG	1A	3361	1/1	0.88	0.11	39,39,39,39	0
57	MG	1H	201	1/1	0.88	0.10	72,72,72,72	0
57	MG	1A	3850	1/1	0.88	0.12	49,49,49,49	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2A	3088	1/1	0.88	0.16	65,65,65,65	0
57	MG	2A	3535	1/1	0.88	0.18	37,37,37,37	0
57	MG	1A	3980	1/1	0.88	0.18	58,58,58,58	0
57	MG	2A	3310	1/1	0.88	0.15	64,64,64,64	0
57	MG	1A	3287	1/1	0.88	0.18	54,54,54,54	0
57	MG	2a	3031	1/1	0.88	0.21	69,69,69,69	0
57	MG	1a	1695	1/1	0.88	0.30	66,66,66,66	0
57	MG	2a	3033	1/1	0.88	0.32	64,64,64,64	0
57	MG	2A	3321	1/1	0.88	0.16	61,61,61,61	0
57	MG	2a	3036	1/1	0.88	0.19	67,67,67,67	0
57	MG	1A	3474	1/1	0.88	0.09	28,28,28,28	0
57	MG	2a	3038	1/1	0.88	0.23	65,65,65,65	0
57	MG	1a	1825	1/1	0.88	0.11	67,67,67,67	0
57	MG	1A	3184	1/1	0.88	0.15	55,55,55,55	0
57	MG	1A	3479	1/1	0.88	0.12	30,30,30,30	0
57	MG	1A	3987	1/1	0.88	0.22	77,77,77,77	0
57	MG	2a	3046	1/1	0.88	0.22	73,73,73,73	0
57	MG	2A	3339	1/1	0.88	0.19	73,73,73,73	0
57	MG	2A	3552	1/1	0.88	0.10	59,59,59,59	0
57	MG	1V	204	1/1	0.88	0.20	64,64,64,64	0
57	MG	1A	3603	1/1	0.88	0.14	59,59,59,59	0
57	MG	2A	3348	1/1	0.88	0.18	61,61,61,61	0
57	MG	2A	3130	1/1	0.88	0.14	54,54,54,54	0
57	MG	2a	3059	1/1	0.88	0.37	70,70,70,70	0
57	MG	1A	3993	1/1	0.88	0.26	70,70,70,70	0
57	MG	1A	3312	1/1	0.88	0.19	64,64,64,64	0
57	MG	1A	3866	1/1	0.88	0.12	40,40,40,40	0
57	MG	1A	3676	1/1	0.88	0.11	74,74,74,74	0
57	MG	2A	3608	1/1	0.88	0.13	36,36,36,36	0
57	MG	2a	3070	1/1	0.88	0.37	62,62,62,62	0
57	MG	1A	3059	1/1	0.88	0.21	44,44,44,44	0
57	MG	1a	1716	1/1	0.88	0.13	70,70,70,70	0
57	MG	2A	3617	1/1	0.88	0.12	82,82,82,82	0
57	MG	2A	3618	1/1	0.88	0.14	31,31,31,31	0
57	MG	1A	3197	1/1	0.88	0.34	68,68,68,68	0
57	MG	1B	203	1/1	0.88	0.17	68,68,68,68	0
57	MG	2A	3623	1/1	0.88	0.15	66,66,66,66	0
57	MG	1a	1602	1/1	0.88	0.18	74,74,74,74	0
57	MG	1a	1859	1/1	0.88	0.33	71,71,71,71	0
57	MG	1A	3685	1/1	0.88	0.17	72,72,72,72	0
57	MG	1A	3626	1/1	0.88	0.12	23,23,23,23	0
57	MG	1A	3200	1/1	0.88	0.27	63,63,63,63	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2A	3171	1/1	0.88	0.15	53,53,53,53	0
57	MG	1a	1615	1/1	0.88	0.13	63,63,63,63	0
57	MG	1a	1735	1/1	0.88	0.23	70,70,70,70	0
57	MG	1a	1736	1/1	0.88	0.20	72,72,72,72	0
57	MG	1B	212	1/1	0.88	0.28	72,72,72,72	0
57	MG	1A	3555	1/1	0.88	0.20	60,60,60,60	0
57	MG	1A	3788	1/1	0.88	0.20	64,64,64,64	0
57	MG	2A	3694	1/1	0.88	0.26	65,65,65,65	0
57	MG	1A	3898	1/1	0.88	0.17	57,57,57,57	0
57	MG	1A	3383	1/1	0.88	0.17	62,62,62,62	0
57	MG	2A	3429	1/1	0.88	0.23	69,69,69,69	0
57	MG	1a	1753	1/1	0.88	0.16	67,67,67,67	0
57	MG	1a	1639	1/1	0.88	0.41	74,74,74,74	0
57	MG	2A	3194	1/1	0.88	0.16	62,62,62,62	0
57	MG	1h	202	1/1	0.88	0.15	67,67,67,67	0
57	MG	1a	1755	1/1	0.88	0.14	47,47,47,47	0
57	MG	1A	3808	1/1	0.88	0.18	73,73,73,73	0
57	MG	1B	230	1/1	0.88	0.10	72,72,72,72	0
57	MG	1A	3014	1/1	0.88	0.27	62,62,62,62	0
57	MG	1A	3279	1/1	0.88	0.09	75,75,75,75	0
57	MG	2A	3211	1/1	0.88	0.32	70,70,70,70	0
57	MG	1o	102	1/1	0.88	0.24	68,68,68,68	0
57	MG	2a	3163	1/1	0.88	0.19	81,81,81,81	0
57	MG	1a	1653	1/1	0.88	0.29	70,70,70,70	0
57	MG	2a	3165	1/1	0.88	0.24	67,67,67,67	0
57	MG	1A	3711	1/1	0.88	0.35	40,40,40,40	0
57	MG	1A	3208	1/1	0.88	0.11	58,58,58,58	0
57	MG	2a	3170	1/1	0.88	0.27	59,59,59,59	0
57	MG	1A	3459	1/1	0.88	0.08	23,23,23,23	0
57	MG	2A	3229	1/1	0.88	0.17	65,65,65,65	0
57	MG	1A	3461	1/1	0.88	0.20	63,63,63,63	0
57	MG	1a	1664	1/1	0.88	0.26	68,68,68,68	0
57	MG	2B	208	1/1	0.88	0.18	69,69,69,69	0
57	MG	2A	3235	1/1	0.88	0.19	72,72,72,72	0
57	MG	1a	1777	1/1	0.88	0.18	75,75,75,75	0
57	MG	2a	3183	1/1	0.88	0.21	70,70,70,70	0
57	MG	1a	1667	1/1	0.88	0.39	65,65,65,65	0
57	MG	1a	1668	1/1	0.88	0.16	58,58,58,58	0
57	MG	2A	3035	1/1	0.88	0.28	70,70,70,70	0
57	MG	1a	1791	1/1	0.88	0.17	66,66,66,66	0
57	MG	1E	308	1/1	0.88	0.09	36,36,36,36	0
57	MG	1a	1793	1/1	0.88	0.18	66,66,66,66	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2A	3276	1/1	0.88	0.30	69,69,69,69	0
57	MG	2A	3050	1/1	0.88	0.15	61,61,61,61	0
57	MG	1F	311	1/1	0.88	0.12	55,55,55,55	0
59	ARG	1B	231	12/12	0.88	0.14	40,47,58,61	0
57	MG	2A	3508	1/1	0.88	0.17	71,71,71,71	0
57	MG	1a	1727	1/1	0.89	0.13	54,54,54,54	0
57	MG	2A	3189	1/1	0.89	0.14	48,48,48,48	0
57	MG	1a	1728	1/1	0.89	0.16	77,77,77,77	0
57	MG	1A	3533	1/1	0.89	0.14	69,69,69,69	0
57	MG	2A	3458	1/1	0.89	0.32	64,64,64,64	0
57	MG	1A	3623	1/1	0.89	0.12	53,53,53,53	0
57	MG	2E	304	1/1	0.89	0.13	43,43,43,43	0
57	MG	1A	3728	1/1	0.89	0.11	64,64,64,64	0
57	MG	2F	303	1/1	0.89	0.10	49,49,49,49	0
57	MG	1A	3534	1/1	0.89	0.33	57,57,57,57	0
57	MG	1a	1741	1/1	0.89	0.16	67,67,67,67	0
57	MG	1B	204	1/1	0.89	0.21	60,60,60,60	0
57	MG	2O	201	1/1	0.89	0.14	66,66,66,66	0
57	MG	1a	1624	1/1	0.89	0.20	60,60,60,60	0
57	MG	1i	201	1/1	0.89	0.18	68,68,68,68	0
57	MG	2A	3475	1/1	0.89	0.30	60,60,60,60	0
57	MG	1a	1630	1/1	0.89	0.37	67,67,67,67	0
57	MG	2T	202	1/1	0.89	0.22	68,68,68,68	0
57	MG	1A	3328	1/1	0.89	0.16	62,62,62,62	0
57	MG	2A	3216	1/1	0.89	0.14	62,62,62,62	0
57	MG	2A	3485	1/1	0.89	0.12	59,59,59,59	0
57	MG	1A	3542	1/1	0.89	0.09	36,36,36,36	0
57	MG	1A	3870	1/1	0.89	0.09	27,27,27,27	0
57	MG	1A	3871	1/1	0.89	0.08	37,37,37,37	0
57	MG	2a	3011	1/1	0.89	0.18	65,65,65,65	0
57	MG	2a	3015	1/1	0.89	0.23	61,61,61,61	0
57	MG	2A	3223	1/1	0.89	0.12	62,62,62,62	0
57	MG	1a	1640	1/1	0.89	0.21	69,69,69,69	0
57	MG	1A	3267	1/1	0.89	0.14	76,76,76,76	0
57	MG	1a	1645	1/1	0.89	0.30	63,63,63,63	0
57	MG	1a	1646	1/1	0.89	0.27	60,60,60,60	0
57	MG	1a	1765	1/1	0.89	0.14	61,61,61,61	0
57	MG	2A	3239	1/1	0.89	0.23	58,58,58,58	0
57	MG	1a	1767	1/1	0.89	0.18	53,53,53,53	0
57	MG	2A	3017	1/1	0.89	0.15	56,56,56,56	0
57	MG	2A	3252	1/1	0.89	0.17	65,65,65,65	0
57	MG	1A	3298	1/1	0.89	0.30	82,82,82,82	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1a	1648	1/1	0.89	0.26	68,68,68,68	0
57	MG	2A	3530	1/1	0.89	0.13	72,72,72,72	0
57	MG	2A	3261	1/1	0.89	0.13	53,53,53,53	0
57	MG	1A	3639	1/1	0.89	0.16	39,39,39,39	0
57	MG	2A	3266	1/1	0.89	0.46	63,63,63,63	0
57	MG	2a	3044	1/1	0.89	0.33	71,71,71,71	0
57	MG	2A	3033	1/1	0.89	0.30	68,68,68,68	0
57	MG	1A	3421	1/1	0.89	0.10	67,67,67,67	0
57	MG	1A	3645	1/1	0.89	0.10	29,29,29,29	0
57	MG	1A	3232	1/1	0.89	0.21	76,76,76,76	0
57	MG	2A	3281	1/1	0.89	0.29	72,72,72,72	0
57	MG	1A	3369	1/1	0.89	0.10	32,32,32,32	0
57	MG	2A	3046	1/1	0.89	0.20	63,63,63,63	0
57	MG	1A	3002	1/1	0.89	0.11	52,52,52,52	0
57	MG	1D	311	1/1	0.89	0.21	43,43,43,43	0
57	MG	1a	1790	1/1	0.89	0.16	74,74,74,74	0
57	MG	2a	3062	1/1	0.89	0.12	83,83,83,83	0
57	MG	2A	3053	1/1	0.89	0.26	73,73,73,73	0
57	MG	1A	3482	1/1	0.89	0.11	32,32,32,32	0
57	MG	2A	3299	1/1	0.89	0.34	75,75,75,75	0
57	MG	1a	1666	1/1	0.89	0.27	74,74,74,74	0
57	MG	2a	3068	1/1	0.89	0.17	71,71,71,71	0
57	MG	2A	3061	1/1	0.89	0.10	46,46,46,46	0
57	MG	2a	3071	1/1	0.89	0.22	69,69,69,69	0
57	MG	1A	3778	1/1	0.89	0.17	63,63,63,63	0
57	MG	1A	3318	1/1	0.89	0.31	65,65,65,65	0
57	MG	2A	3074	1/1	0.89	0.19	55,55,55,55	0
57	MG	1A	3560	1/1	0.89	0.13	57,57,57,57	0
57	MG	2A	3582	1/1	0.89	0.18	63,63,63,63	0
57	MG	1A	3929	1/1	0.89	0.12	44,44,44,44	0
57	MG	1a	1801	1/1	0.89	0.24	58,58,58,58	0
57	MG	1A	3247	1/1	0.89	0.18	64,64,64,64	0
57	MG	1A	3944	1/1	0.89	0.11	57,57,57,57	0
57	MG	1A	3377	1/1	0.89	0.14	63,63,63,63	0
57	MG	2a	3097	1/1	0.89	0.33	60,60,60,60	0
57	MG	1A	3187	1/1	0.89	0.31	68,68,68,68	0
57	MG	1a	1811	1/1	0.89	0.25	70,70,70,70	0
57	MG	1A	3504	1/1	0.89	0.09	53,53,53,53	0
57	MG	2A	3099	1/1	0.89	0.37	66,66,66,66	0
57	MG	1A	3956	1/1	0.89	0.12	48,48,48,48	0
57	MG	1a	1820	1/1	0.89	0.11	60,60,60,60	0
57	MG	1A	3282	1/1	0.89	0.19	67,67,67,67	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2A	3352	1/1	0.89	0.12	51,51,51,51	0
57	MG	2a	3111	1/1	0.89	0.16	71,71,71,71	0
57	MG	2A	3112	1/1	0.89	0.22	63,63,63,63	0
57	MG	2A	3662	1/1	0.89	0.20	58,58,58,58	0
57	MG	2a	3118	1/1	0.89	0.12	62,62,62,62	0
57	MG	2A	3113	1/1	0.89	0.27	72,72,72,72	0
57	MG	1A	3962	1/1	0.89	0.11	54,54,54,54	0
57	MG	2a	3122	1/1	0.89	0.15	63,63,63,63	0
57	MG	1A	3283	1/1	0.89	0.11	62,62,62,62	0
57	MG	1a	1696	1/1	0.89	0.37	71,71,71,71	0
57	MG	1A	3449	1/1	0.89	0.15	51,51,51,51	0
57	MG	2A	3676	1/1	0.89	0.14	65,65,65,65	0
57	MG	2a	3132	1/1	0.89	0.22	62,62,62,62	0
57	MG	2A	3384	1/1	0.89	0.15	49,49,49,49	0
57	MG	2A	3678	1/1	0.89	0.07	77,77,77,77	0
57	MG	2A	3682	1/1	0.89	0.14	59,59,59,59	0
57	MG	1a	1698	1/1	0.89	0.39	68,68,68,68	0
57	MG	1a	1699	1/1	0.89	0.20	70,70,70,70	0
57	MG	1A	3452	1/1	0.89	0.14	71,71,71,71	0
57	MG	1A	3591	1/1	0.89	0.12	39,39,39,39	0
57	MG	2A	3136	1/1	0.89	0.20	66,66,66,66	0
57	MG	1a	1837	1/1	0.89	0.29	72,72,72,72	0
57	MG	1A	3832	1/1	0.89	0.12	53,53,53,53	0
57	MG	1T	206	1/1	0.89	0.09	71,71,71,71	0
57	MG	2A	3153	1/1	0.89	0.41	62,62,62,62	0
57	MG	2A	3154	1/1	0.89	0.18	52,52,52,52	0
57	MG	1A	3386	1/1	0.89	0.11	29,29,29,29	0
57	MG	1A	3837	1/1	0.89	0.17	56,56,56,56	0
57	MG	1A	3838	1/1	0.89	0.11	37,37,37,37	0
57	MG	2a	3175	1/1	0.89	0.12	65,65,65,65	0
57	MG	10	108	1/1	0.89	0.13	64,64,64,64	0
57	MG	1a	1848	1/1	0.89	0.17	65,65,65,65	0
57	MG	1a	1850	1/1	0.89	0.21	70,70,70,70	0
57	MG	2A	3422	1/1	0.89	0.20	78,78,78,78	0
57	MG	2A	3727	1/1	0.89	0.19	69,69,69,69	0
57	MG	1A	3600	1/1	0.89	0.15	31,31,31,31	0
57	MG	1A	3456	1/1	0.89	0.12	53,53,53,53	0
57	MG	2A	3730	1/1	0.89	0.29	68,68,68,68	0
57	MG	1A	3387	1/1	0.89	0.08	24,24,24,24	0
57	MG	1A	3610	1/1	0.89	0.11	56,56,56,56	0
57	MG	1A	3996	1/1	0.89	0.12	58,58,58,58	0
57	MG	1A	3405	1/1	0.89	0.23	69,69,69,69	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1A	3999	1/1	0.89	0.09	47,47,47,47	0
57	MG	1A	3174	1/1	0.89	0.42	62,62,62,62	0
57	MG	2B	209	1/1	0.89	0.30	71,71,71,71	0
57	MG	1a	1604	1/1	0.89	0.29	72,72,72,72	0
57	MG	2A	3185	1/1	0.89	0.25	66,66,66,66	0
57	MG	2A	3493	1/1	0.90	0.18	60,60,60,60	0
57	MG	1A	3435	1/1	0.90	0.13	54,54,54,54	0
57	MG	1a	1605	1/1	0.90	0.16	64,64,64,64	0
57	MG	1A	3436	1/1	0.90	0.08	61,61,61,61	0
57	MG	1a	1712	1/1	0.90	0.25	63,63,63,63	0
57	MG	1A	3764	1/1	0.90	0.10	27,27,27,27	0
57	MG	1A	3886	1/1	0.90	0.10	63,63,63,63	0
57	MG	2A	3510	1/1	0.90	0.13	55,55,55,55	0
57	MG	20	101	1/1	0.90	0.16	63,63,63,63	0
57	MG	25	101	1/1	0.90	0.18	62,62,62,62	0
57	MG	25	102	1/1	0.90	0.18	70,70,70,70	0
57	MG	1A	3584	1/1	0.90	0.11	47,47,47,47	0
57	MG	1A	3437	1/1	0.90	0.24	68,68,68,68	0
57	MG	1A	3588	1/1	0.90	0.12	49,49,49,49	0
57	MG	2a	3006	1/1	0.90	0.12	55,55,55,55	0
57	MG	2A	3092	1/1	0.90	0.21	68,68,68,68	0
57	MG	1A	3530	1/1	0.90	0.12	30,30,30,30	0
57	MG	2A	3097	1/1	0.90	0.28	58,58,58,58	0
57	MG	2A	3098	1/1	0.90	0.36	72,72,72,72	0
57	MG	1A	3290	1/1	0.90	0.16	61,61,61,61	0
57	MG	2a	3018	1/1	0.90	0.29	68,68,68,68	0
57	MG	2A	3291	1/1	0.90	0.39	65,65,65,65	0
57	MG	1A	3592	1/1	0.90	0.12	69,69,69,69	0
57	MG	1A	3915	1/1	0.90	0.14	55,55,55,55	0
57	MG	2A	3110	1/1	0.90	0.23	63,63,63,63	0
57	MG	2A	3536	1/1	0.90	0.10	67,67,67,67	0
57	MG	1A	3918	1/1	0.90	0.12	63,63,63,63	0
57	MG	1A	3595	1/1	0.90	0.10	47,47,47,47	0
57	MG	1A	3411	1/1	0.90	0.22	56,56,56,56	0
57	MG	1a	1643	1/1	0.90	0.19	59,59,59,59	0
57	MG	1A	3793	1/1	0.90	0.11	43,43,43,43	0
57	MG	1a	1738	1/1	0.90	0.15	67,67,67,67	0
57	MG	2A	3125	1/1	0.90	0.18	85,85,85,85	0
57	MG	1A	3680	1/1	0.90	0.13	37,37,37,37	0
57	MG	2A	3548	1/1	0.90	0.25	73,73,73,73	0
57	MG	2a	3041	1/1	0.90	0.31	61,61,61,61	0
57	MG	2a	3042	1/1	0.90	0.22	78,78,78,78	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1A	3322	1/1	0.90	0.26	62,62,62,62	0
57	MG	2A	3313	1/1	0.90	0.30	66,66,66,66	0
57	MG	1A	3811	1/1	0.90	0.20	48,48,48,48	0
57	MG	2A	3322	1/1	0.90	0.18	75,75,75,75	0
57	MG	1a	1745	1/1	0.90	0.17	66,66,66,66	0
57	MG	2a	3049	1/1	0.90	0.37	66,66,66,66	0
57	MG	2a	3052	1/1	0.90	0.16	74,74,74,74	0
57	MG	1A	3947	1/1	0.90	0.15	63,63,63,63	0
57	MG	1A	3684	1/1	0.90	0.13	68,68,68,68	0
57	MG	2A	3137	1/1	0.90	0.09	45,45,45,45	0
57	MG	2A	3138	1/1	0.90	0.12	63,63,63,63	0
57	MG	1A	3819	1/1	0.90	0.10	57,57,57,57	0
57	MG	2A	3143	1/1	0.90	0.25	57,57,57,57	0
57	MG	2A	3588	1/1	0.90	0.15	50,50,50,50	0
57	MG	1A	3447	1/1	0.90	0.18	58,58,58,58	0
57	MG	2A	3148	1/1	0.90	0.12	69,69,69,69	0
57	MG	2A	3602	1/1	0.90	0.10	68,68,68,68	0
57	MG	1d	301	1/1	0.90	0.23	73,73,73,73	0
57	MG	2A	3355	1/1	0.90	0.14	65,65,65,65	0
57	MG	1F	313	1/1	0.90	0.30	45,45,45,45	0
57	MG	2A	3367	1/1	0.90	0.19	70,70,70,70	0
57	MG	1a	1661	1/1	0.90	0.17	58,58,58,58	0
57	MG	2A	3376	1/1	0.90	0.09	40,40,40,40	0
57	MG	1A	3144	1/1	0.90	0.09	69,69,69,69	0
57	MG	2A	3378	1/1	0.90	0.09	40,40,40,40	0
57	MG	2A	3157	1/1	0.90	0.13	64,64,64,64	0
57	MG	2A	3629	1/1	0.90	0.18	71,71,71,71	0
57	MG	1A	3543	1/1	0.90	0.11	52,52,52,52	0
57	MG	2a	3086	1/1	0.90	0.27	78,78,78,78	0
57	MG	2A	3644	1/1	0.90	0.12	68,68,68,68	0
57	MG	2a	3090	1/1	0.90	0.45	67,67,67,67	0
57	MG	1A	3486	1/1	0.90	0.08	57,57,57,57	0
57	MG	2A	3162	1/1	0.90	0.24	65,65,65,65	0
57	MG	1a	1762	1/1	0.90	0.09	60,60,60,60	0
57	MG	1a	1665	1/1	0.90	0.25	65,65,65,65	0
57	MG	1G	204	1/1	0.90	0.23	65,65,65,65	0
57	MG	2A	3169	1/1	0.90	0.21	56,56,56,56	0
57	MG	1a	1766	1/1	0.90	0.20	71,71,71,71	0
57	MG	1A	3696	1/1	0.90	0.19	44,44,44,44	0
57	MG	2a	3103	1/1	0.90	0.16	61,61,61,61	0
57	MG	1l	3102	1/1	0.90	0.18	75,75,75,75	0
57	MG	1A	3418	1/1	0.90	0.13	28,28,28,28	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2a	3108	1/1	0.90	0.12	52,52,52,52	0
57	MG	1A	3493	1/1	0.90	0.12	34,34,34,34	0
57	MG	2A	3679	1/1	0.90	0.12	77,77,77,77	0
57	MG	1a	1671	1/1	0.90	0.21	62,62,62,62	0
57	MG	2A	3409	1/1	0.90	0.10	56,56,56,56	0
57	MG	1A	3705	1/1	0.90	0.10	60,60,60,60	0
57	MG	1A	3499	1/1	0.90	0.11	63,63,63,63	0
57	MG	1R	205	1/1	0.90	0.17	56,56,56,56	0
57	MG	1a	1679	1/1	0.90	0.17	77,77,77,77	0
57	MG	1a	1680	1/1	0.90	0.11	63,63,63,63	0
57	MG	2a	3124	1/1	0.90	0.14	77,77,77,77	0
57	MG	2A	3187	1/1	0.90	0.26	53,53,53,53	0
57	MG	2A	3188	1/1	0.90	0.17	63,63,63,63	0
57	MG	2A	3423	1/1	0.90	0.23	77,77,77,77	0
57	MG	1A	3550	1/1	0.90	0.11	58,58,58,58	0
57	MG	1a	1788	1/1	0.90	0.13	66,66,66,66	0
57	MG	2a	3133	1/1	0.90	0.12	66,66,66,66	0
57	MG	2A	3710	1/1	0.90	0.19	62,62,62,62	0
57	MG	2a	3142	1/1	0.90	0.09	51,51,51,51	0
57	MG	2A	3430	1/1	0.90	0.14	59,59,59,59	0
57	MG	2a	3150	1/1	0.90	0.20	71,71,71,71	0
57	MG	2a	3153	1/1	0.90	0.15	60,60,60,60	0
57	MG	2A	3431	1/1	0.90	0.14	41,41,41,41	0
57	MG	2A	3718	1/1	0.90	0.36	63,63,63,63	0
57	MG	1a	1682	1/1	0.90	0.23	68,68,68,68	0
57	MG	1A	3094	1/1	0.90	0.10	57,57,57,57	0
57	MG	1A	3191	1/1	0.90	0.14	61,61,61,61	0
57	MG	2A	3724	1/1	0.90	0.19	69,69,69,69	0
57	MG	2A	3031	1/1	0.90	0.26	56,56,56,56	0
57	MG	2A	3201	1/1	0.90	0.32	74,74,74,74	0
57	MG	1a	1689	1/1	0.90	0.27	65,65,65,65	0
57	MG	1A	3315	1/1	0.90	0.17	58,58,58,58	0
57	MG	2a	3168	1/1	0.90	0.28	64,64,64,64	0
57	MG	2A	3207	1/1	0.90	0.36	53,53,53,53	0
57	MG	1A	3234	1/1	0.90	0.29	57,57,57,57	0
57	MG	1A	3268	1/1	0.90	0.10	62,62,62,62	0
57	MG	2B	203	1/1	0.90	0.21	77,77,77,77	0
57	MG	1A	3153	1/1	0.90	0.28	52,52,52,52	0
57	MG	2A	3039	1/1	0.90	0.17	49,49,49,49	0
57	MG	2A	3041	1/1	0.90	0.31	72,72,72,72	0
57	MG	1A	3643	1/1	0.90	0.13	56,56,56,56	0
57	MG	1A	3512	1/1	0.90	0.10	24,24,24,24	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1A	3753	1/1	0.90	0.12	44,44,44,44	0
57	MG	1A	3571	1/1	0.90	0.11	22,22,22,22	0
57	MG	2e	201	1/1	0.90	0.25	73,73,73,73	0
57	MG	1A	4003	1/1	0.90	0.10	29,29,29,29	0
57	MG	1a	1813	1/1	0.90	0.21	70,70,70,70	0
57	MG	2A	3057	1/1	0.90	0.12	61,61,61,61	0
57	MG	1A	3320	1/1	0.90	0.25	64,64,64,64	0
57	MG	1a	1818	1/1	0.90	0.14	68,68,68,68	0
58	MPD	1A	4014	8/8	0.90	0.27	55,58,65,69	0
57	MG	2A	3237	1/1	0.90	0.16	46,46,46,46	0
57	MG	1A	3464	1/1	0.90	0.16	57,57,57,57	0
57	MG	1A	4012	1/1	0.90	0.17	64,64,64,64	0
57	MG	2A	3489	1/1	0.90	0.10	73,73,73,73	0
57	MG	2A	3065	1/1	0.90	0.42	48,48,48,48	0
57	MG	1B	202	1/1	0.90	0.22	60,60,60,60	0
57	MG	23	101	1/1	0.91	0.14	59,59,59,59	0
57	MG	1A	3266	1/1	0.91	0.12	56,56,56,56	0
57	MG	1B	221	1/1	0.91	0.09	50,50,50,50	0
57	MG	2A	3303	1/1	0.91	0.25	67,67,67,67	0
57	MG	1A	3803	1/1	0.91	0.09	40,40,40,40	0
57	MG	1B	228	1/1	0.91	0.08	58,58,58,58	0
57	MG	2A	3128	1/1	0.91	0.21	60,60,60,60	0
57	MG	1a	1739	1/1	0.91	0.10	60,60,60,60	0
57	MG	1a	1862	1/1	0.91	0.27	67,67,67,67	0
57	MG	1A	3382	1/1	0.91	0.24	61,61,61,61	0
57	MG	1A	3709	1/1	0.91	0.12	44,44,44,44	0
57	MG	1a	1644	1/1	0.91	0.22	61,61,61,61	0
57	MG	1A	3815	1/1	0.91	0.08	16,16,16,16	0
57	MG	1A	3932	1/1	0.91	0.08	44,44,44,44	0
57	MG	1A	3352	1/1	0.91	0.07	36,36,36,36	0
57	MG	1A	3353	1/1	0.91	0.18	62,62,62,62	0
57	MG	1A	3133	1/1	0.91	0.11	51,51,51,51	0
57	MG	1A	3722	1/1	0.91	0.14	60,60,60,60	0
57	MG	1A	3657	1/1	0.91	0.11	26,26,26,26	0
57	MG	1a	1655	1/1	0.91	0.21	60,60,60,60	0
57	MG	1A	3826	1/1	0.91	0.08	47,47,47,47	0
57	MG	1f	201	1/1	0.91	0.37	72,72,72,72	0
57	MG	2A	3562	1/1	0.91	0.20	57,57,57,57	0
57	MG	1g	202	1/1	0.91	0.21	68,68,68,68	0
57	MG	1h	201	1/1	0.91	0.28	59,59,59,59	0
57	MG	2A	3362	1/1	0.91	0.11	48,48,48,48	0
57	MG	1A	3401	1/1	0.91	0.15	29,29,29,29	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1A	3731	1/1	0.91	0.15	55,55,55,55	0
57	MG	1A	3959	1/1	0.91	0.14	55,55,55,55	0
57	MG	2A	3590	1/1	0.91	0.08	46,46,46,46	0
57	MG	1A	3738	1/1	0.91	0.20	52,52,52,52	0
57	MG	2A	3599	1/1	0.91	0.10	41,41,41,41	0
57	MG	1A	3363	1/1	0.91	0.08	52,52,52,52	0
57	MG	2A	3166	1/1	0.91	0.17	68,68,68,68	0
57	MG	2A	3603	1/1	0.91	0.13	59,59,59,59	0
57	MG	2a	3051	1/1	0.91	0.27	69,69,69,69	0
57	MG	1A	3964	1/1	0.91	0.12	58,58,58,58	0
57	MG	1A	3841	1/1	0.91	0.20	59,59,59,59	0
57	MG	1A	3973	1/1	0.91	0.20	52,52,52,52	0
57	MG	2A	3383	1/1	0.91	0.11	34,34,34,34	0
57	MG	1A	3974	1/1	0.91	0.15	44,44,44,44	0
57	MG	1A	3141	1/1	0.91	0.18	64,64,64,64	0
57	MG	1P	203	1/1	0.91	0.16	72,72,72,72	0
57	MG	1A	3742	1/1	0.91	0.21	59,59,59,59	0
57	MG	2A	3003	1/1	0.91	0.11	64,64,64,64	0
57	MG	2A	3396	1/1	0.91	0.28	70,70,70,70	0
57	MG	2A	3638	1/1	0.91	0.14	58,58,58,58	0
57	MG	1A	3604	1/1	0.91	0.17	35,35,35,35	0
57	MG	1a	1778	1/1	0.91	0.15	72,72,72,72	0
57	MG	2A	3184	1/1	0.91	0.10	60,60,60,60	0
57	MG	1a	1782	1/1	0.91	0.16	71,71,71,71	0
57	MG	2A	3659	1/1	0.91	0.25	79,79,79,79	0
57	MG	2A	3660	1/1	0.91	0.11	42,42,42,42	0
57	MG	1A	3751	1/1	0.91	0.08	50,50,50,50	0
57	MG	1A	3609	1/1	0.91	0.15	32,32,32,32	0
57	MG	2A	3667	1/1	0.91	0.18	54,54,54,54	0
57	MG	1A	3669	1/1	0.91	0.08	61,61,61,61	0
57	MG	2A	3669	1/1	0.91	0.12	53,53,53,53	0
57	MG	2A	3411	1/1	0.91	0.10	35,35,35,35	0
57	MG	2a	3088	1/1	0.91	0.44	74,74,74,74	0
57	MG	1A	3755	1/1	0.91	0.11	59,59,59,59	0
57	MG	2A	3190	1/1	0.91	0.16	74,74,74,74	0
57	MG	1A	3367	1/1	0.91	0.09	42,42,42,42	0
57	MG	2A	3192	1/1	0.91	0.16	66,66,66,66	0
57	MG	1A	3858	1/1	0.91	0.09	45,45,45,45	0
57	MG	1W	203	1/1	0.91	0.14	48,48,48,48	0
57	MG	1Y	201	1/1	0.91	0.18	57,57,57,57	0
57	MG	2A	3198	1/1	0.91	0.35	75,75,75,75	0
57	MG	2A	3688	1/1	0.91	0.19	55,55,55,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	10	101	1/1	0.91	0.10	43,43,43,43	0
57	MG	1a	1797	1/1	0.91	0.20	70,70,70,70	0
57	MG	2A	3042	1/1	0.91	0.20	48,48,48,48	0
57	MG	2A	3044	1/1	0.91	0.16	67,67,67,67	0
57	MG	10	102	1/1	0.91	0.29	47,47,47,47	0
57	MG	2A	3435	1/1	0.91	0.21	76,76,76,76	0
57	MG	1a	1693	1/1	0.91	0.26	70,70,70,70	0
57	MG	10	104	1/1	0.91	0.11	59,59,59,59	0
57	MG	1A	3860	1/1	0.91	0.10	58,58,58,58	0
57	MG	1A	3240	1/1	0.91	0.13	50,50,50,50	0
57	MG	2A	3052	1/1	0.91	0.23	66,66,66,66	0
57	MG	1a	1809	1/1	0.91	0.12	60,60,60,60	0
57	MG	2A	3712	1/1	0.91	0.29	68,68,68,68	0
57	MG	2A	3448	1/1	0.91	0.35	61,61,61,61	0
57	MG	2A	3054	1/1	0.91	0.25	65,65,65,65	0
57	MG	11	101	1/1	0.91	0.17	44,44,44,44	0
57	MG	11	102	1/1	0.91	0.18	59,59,59,59	0
57	MG	1A	3371	1/1	0.91	0.15	64,64,64,64	0
57	MG	1a	1700	1/1	0.91	0.41	60,60,60,60	0
57	MG	1A	3532	1/1	0.91	0.14	53,53,53,53	0
57	MG	2A	3064	1/1	0.91	0.17	57,57,57,57	0
57	MG	1A	3761	1/1	0.91	0.07	29,29,29,29	0
57	MG	17	104	1/1	0.91	0.14	53,53,53,53	0
57	MG	2a	3145	1/1	0.91	0.10	52,52,52,52	0
57	MG	1A	3619	1/1	0.91	0.10	57,57,57,57	0
57	MG	2A	3731	1/1	0.91	0.14	63,63,63,63	0
57	MG	2A	3469	1/1	0.91	0.08	62,62,62,62	0
57	MG	1A	3621	1/1	0.91	0.08	24,24,24,24	0
57	MG	18	103	1/1	0.91	0.08	54,54,54,54	0
57	MG	1A	3773	1/1	0.91	0.17	45,45,45,45	0
57	MG	1A	3297	1/1	0.91	0.28	65,65,65,65	0
57	MG	2a	3159	1/1	0.91	0.09	70,70,70,70	0
57	MG	2B	206	1/1	0.91	0.22	65,65,65,65	0
57	MG	2A	3476	1/1	0.91	0.12	63,63,63,63	0
57	MG	1A	3123	1/1	0.91	0.19	54,54,54,54	0
57	MG	2A	3086	1/1	0.91	0.13	51,51,51,51	0
57	MG	2A	3263	1/1	0.91	0.16	64,64,64,64	0
57	MG	1A	3076	1/1	0.91	0.16	55,55,55,55	0
57	MG	1A	3577	1/1	0.91	0.26	65,65,65,65	0
57	MG	2A	3267	1/1	0.91	0.20	54,54,54,54	0
57	MG	1a	1607	1/1	0.91	0.09	63,63,63,63	0
57	MG	2A	3271	1/1	0.91	0.29	61,61,61,61	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2a	3172	1/1	0.91	0.25	68,68,68,68	0
57	MG	2a	3173	1/1	0.91	0.26	65,65,65,65	0
57	MG	1a	1836	1/1	0.91	0.10	58,58,58,58	0
57	MG	1A	3889	1/1	0.91	0.12	57,57,57,57	0
57	MG	1A	3635	1/1	0.91	0.19	39,39,39,39	0
57	MG	1A	3537	1/1	0.91	0.11	56,56,56,56	0
57	MG	2A	3504	1/1	0.91	0.10	55,55,55,55	0
57	MG	1A	3001	1/1	0.91	0.09	36,36,36,36	0
57	MG	1A	3194	1/1	0.91	0.29	65,65,65,65	0
57	MG	2a	3182	1/1	0.91	0.17	59,59,59,59	0
57	MG	1A	3900	1/1	0.91	0.14	63,63,63,63	0
57	MG	2A	3109	1/1	0.91	0.27	74,74,74,74	0
57	MG	1a	1726	1/1	0.91	0.17	57,57,57,57	0
57	MG	1A	3379	1/1	0.91	0.18	53,53,53,53	0
57	MG	1A	3797	1/1	0.91	0.09	60,60,60,60	0
57	MG	2A	3297	1/1	0.91	0.42	60,60,60,60	0
57	MG	2R	203	1/1	0.91	0.14	62,62,62,62	0
57	MG	2A	3522	1/1	0.91	0.26	71,71,71,71	0
57	MG	1a	1852	1/1	0.91	0.07	61,61,61,61	0
57	MG	2V	201	1/1	0.91	0.18	69,69,69,69	0
57	MG	2V	203	1/1	0.91	0.27	72,72,72,72	0
57	MG	2X	101	1/1	0.91	0.12	52,52,52,52	0
57	MG	2Y	201	1/1	0.91	0.23	64,64,64,64	0
57	MG	1a	1729	1/1	0.91	0.15	53,53,53,53	0
60	ZN	24	501	1/1	0.91	0.17	129,129,129,129	0
57	MG	1A	3594	1/1	0.92	0.09	42,42,42,42	0
57	MG	2A	3342	1/1	0.92	0.18	42,42,42,42	0
57	MG	1A	3923	1/1	0.92	0.14	47,47,47,47	0
57	MG	2A	3346	1/1	0.92	0.16	58,58,58,58	0
57	MG	1a	1800	1/1	0.92	0.09	68,68,68,68	0
57	MG	2a	3008	1/1	0.92	0.11	68,68,68,68	0
57	MG	1a	1705	1/1	0.92	0.27	63,63,63,63	0
57	MG	1A	3654	1/1	0.92	0.10	59,59,59,59	0
57	MG	2A	3357	1/1	0.92	0.11	51,51,51,51	0
57	MG	1A	3087	1/1	0.92	0.09	56,56,56,56	0
57	MG	1a	1806	1/1	0.92	0.18	82,82,82,82	0
57	MG	1B	227	1/1	0.92	0.20	66,66,66,66	0
57	MG	1A	3269	1/1	0.92	0.08	45,45,45,45	0
57	MG	2A	3374	1/1	0.92	0.19	70,70,70,70	0
57	MG	2A	3375	1/1	0.92	0.13	43,43,43,43	0
57	MG	1A	3597	1/1	0.92	0.20	39,39,39,39	0
57	MG	1a	1626	1/1	0.92	0.19	57,57,57,57	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2a	3027	1/1	0.92	0.15	73,73,73,73	0
57	MG	2a	3029	1/1	0.92	0.23	70,70,70,70	0
57	MG	1a	1812	1/1	0.92	0.21	70,70,70,70	0
57	MG	1A	3937	1/1	0.92	0.07	26,26,26,26	0
57	MG	2A	3580	1/1	0.92	0.12	52,52,52,52	0
57	MG	2A	3043	1/1	0.92	0.14	61,61,61,61	0
57	MG	2A	3585	1/1	0.92	0.14	58,58,58,58	0
57	MG	1A	3553	1/1	0.92	0.09	41,41,41,41	0
57	MG	1A	3364	1/1	0.92	0.14	27,27,27,27	0
57	MG	2A	3595	1/1	0.92	0.09	70,70,70,70	0
57	MG	1A	3825	1/1	0.92	0.11	31,31,31,31	0
57	MG	1A	3241	1/1	0.92	0.17	38,38,38,38	0
57	MG	2A	3387	1/1	0.92	0.23	63,63,63,63	0
57	MG	1A	3948	1/1	0.92	0.12	48,48,48,48	0
57	MG	1A	3388	1/1	0.92	0.06	29,29,29,29	0
57	MG	2A	3606	1/1	0.92	0.17	38,38,38,38	0
57	MG	1A	3392	1/1	0.92	0.09	38,38,38,38	0
57	MG	2A	3610	1/1	0.92	0.11	50,50,50,50	0
57	MG	2a	3048	1/1	0.92	0.35	69,69,69,69	0
57	MG	2A	3395	1/1	0.92	0.14	61,61,61,61	0
57	MG	2A	3613	1/1	0.92	0.10	60,60,60,60	0
57	MG	1A	3058	1/1	0.92	0.15	49,49,49,49	0
57	MG	2A	3203	1/1	0.92	0.11	63,63,63,63	0
57	MG	1A	3192	1/1	0.92	0.12	48,48,48,48	0
57	MG	1A	3840	1/1	0.92	0.12	51,51,51,51	0
57	MG	2A	3401	1/1	0.92	0.07	36,36,36,36	0
57	MG	2A	3402	1/1	0.92	0.13	64,64,64,64	0
57	MG	1A	3022	1/1	0.92	0.08	49,49,49,49	0
57	MG	1A	3614	1/1	0.92	0.07	44,44,44,44	0
57	MG	1a	1833	1/1	0.92	0.09	68,68,68,68	0
57	MG	1A	3845	1/1	0.92	0.13	30,30,30,30	0
57	MG	2A	3410	1/1	0.92	0.07	32,32,32,32	0
57	MG	1A	3966	1/1	0.92	0.12	62,62,62,62	0
57	MG	2A	3412	1/1	0.92	0.12	48,48,48,48	0
57	MG	2A	3657	1/1	0.92	0.12	45,45,45,45	0
57	MG	2A	3214	1/1	0.92	0.31	72,72,72,72	0
57	MG	1a	1737	1/1	0.92	0.10	67,67,67,67	0
57	MG	1A	3316	1/1	0.92	0.12	60,60,60,60	0
57	MG	1A	3847	1/1	0.92	0.15	39,39,39,39	0
57	MG	2A	3220	1/1	0.92	0.21	67,67,67,67	0
57	MG	1A	3758	1/1	0.92	0.08	33,33,33,33	0
57	MG	1A	3975	1/1	0.92	0.19	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1a	1843	1/1	0.92	0.08	56,56,56,56	0
57	MG	1A	3483	1/1	0.92	0.09	29,29,29,29	0
57	MG	1A	3573	1/1	0.92	0.06	23,23,23,23	0
57	MG	2A	3231	1/1	0.92	0.45	74,74,74,74	0
57	MG	1A	3080	1/1	0.92	0.19	55,55,55,55	0
57	MG	2A	3234	1/1	0.92	0.17	66,66,66,66	0
57	MG	1a	1747	1/1	0.92	0.11	66,66,66,66	0
57	MG	2A	3436	1/1	0.92	0.08	53,53,53,53	0
57	MG	2a	3096	1/1	0.92	0.20	63,63,63,63	0
57	MG	2A	3440	1/1	0.92	0.12	53,53,53,53	0
57	MG	1R	206	1/1	0.92	0.20	53,53,53,53	0
57	MG	1a	1854	1/1	0.92	0.17	67,67,67,67	0
57	MG	2A	3243	1/1	0.92	0.15	47,47,47,47	0
57	MG	2A	3696	1/1	0.92	0.13	70,70,70,70	0
57	MG	2A	3245	1/1	0.92	0.19	57,57,57,57	0
57	MG	2a	3104	1/1	0.92	0.33	61,61,61,61	0
57	MG	2A	3248	1/1	0.92	0.12	55,55,55,55	0
57	MG	1A	3375	1/1	0.92	0.08	38,38,38,38	0
57	MG	1A	3763	1/1	0.92	0.12	60,60,60,60	0
57	MG	1A	3984	1/1	0.92	0.10	16,16,16,16	0
57	MG	2A	3450	1/1	0.92	0.10	45,45,45,45	0
57	MG	1A	3630	1/1	0.92	0.17	57,57,57,57	0
57	MG	2A	3705	1/1	0.92	0.18	76,76,76,76	0
57	MG	2a	3116	1/1	0.92	0.20	71,71,71,71	0
57	MG	2A	3256	1/1	0.92	0.29	62,62,62,62	0
57	MG	2A	3708	1/1	0.92	0.18	62,62,62,62	0
57	MG	1a	1756	1/1	0.92	0.09	58,58,58,58	0
57	MG	1A	3631	1/1	0.92	0.15	49,49,49,49	0
57	MG	2A	3457	1/1	0.92	0.11	61,61,61,61	0
57	MG	1A	3345	1/1	0.92	0.14	42,42,42,42	0
57	MG	2a	3126	1/1	0.92	0.09	76,76,76,76	0
57	MG	2A	3459	1/1	0.92	0.10	43,43,43,43	0
57	MG	1a	1673	1/1	0.92	0.27	63,63,63,63	0
57	MG	1A	3349	1/1	0.92	0.17	60,60,60,60	0
57	MG	2A	3466	1/1	0.92	0.16	71,71,71,71	0
57	MG	1A	3583	1/1	0.92	0.14	60,60,60,60	0
57	MG	2A	3725	1/1	0.92	0.17	56,56,56,56	0
57	MG	1a	1677	1/1	0.92	0.14	66,66,66,66	0
57	MG	2a	3137	1/1	0.92	0.08	63,63,63,63	0
57	MG	1A	3455	1/1	0.92	0.12	52,52,52,52	0
57	MG	2a	3144	1/1	0.92	0.13	67,67,67,67	0
57	MG	1A	3782	1/1	0.92	0.08	26,26,26,26	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2A	3275	1/1	0.92	0.37	58,58,58,58	0
57	MG	1A	3701	1/1	0.92	0.14	69,69,69,69	0
57	MG	10	105	1/1	0.92	0.14	56,56,56,56	0
57	MG	1A	3196	1/1	0.92	0.19	56,56,56,56	0
57	MG	2A	3282	1/1	0.92	0.34	58,58,58,58	0
57	MG	2A	3283	1/1	0.92	0.29	56,56,56,56	0
57	MG	1A	3044	1/1	0.92	0.34	68,68,68,68	0
57	MG	1A	3545	1/1	0.92	0.26	56,56,56,56	0
57	MG	2A	3487	1/1	0.92	0.19	52,52,52,52	0
57	MG	1a	1774	1/1	0.92	0.15	69,69,69,69	0
57	MG	1A	3789	1/1	0.92	0.08	43,43,43,43	0
57	MG	1f	202	1/1	0.92	0.14	51,51,51,51	0
57	MG	1g	201	1/1	0.92	0.31	67,67,67,67	0
57	MG	2A	3494	1/1	0.92	0.13	57,57,57,57	0
57	MG	1A	3882	1/1	0.92	0.13	59,59,59,59	0
57	MG	2A	3296	1/1	0.92	0.45	69,69,69,69	0
57	MG	1A	3791	1/1	0.92	0.22	52,52,52,52	0
57	MG	1a	1779	1/1	0.92	0.10	50,50,50,50	0
57	MG	1A	4013	1/1	0.92	0.11	61,61,61,61	0
57	MG	1A	3792	1/1	0.92	0.10	51,51,51,51	0
57	MG	2D	308	1/1	0.92	0.12	69,69,69,69	0
57	MG	2A	3507	1/1	0.92	0.12	44,44,44,44	0
57	MG	1a	1785	1/1	0.92	0.14	75,75,75,75	0
57	MG	1a	1786	1/1	0.92	0.14	68,68,68,68	0
57	MG	1A	3710	1/1	0.92	0.07	62,62,62,62	0
57	MG	1A	3796	1/1	0.92	0.11	56,56,56,56	0
57	MG	2a	3180	1/1	0.92	0.29	72,72,72,72	0
57	MG	1a	1789	1/1	0.92	0.14	78,78,78,78	0
57	MG	1A	3356	1/1	0.92	0.10	33,33,33,33	0
57	MG	1t	201	1/1	0.92	0.12	57,57,57,57	0
57	MG	1A	3460	1/1	0.92	0.09	30,30,30,30	0
57	MG	1A	3801	1/1	0.92	0.10	30,30,30,30	0
57	MG	2A	3526	1/1	0.92	0.13	45,45,45,45	0
57	MG	2A	3527	1/1	0.92	0.08	72,72,72,72	0
57	MG	2A	3320	1/1	0.92	0.10	51,51,51,51	0
57	MG	2t	201	1/1	0.92	0.16	46,46,46,46	0
57	MG	1y	202	1/1	0.92	0.10	84,84,84,84	0
57	MG	2U	202	1/1	0.92	0.11	84,84,84,84	0
57	MG	1x	101	1/1	0.92	0.13	47,47,47,47	0
57	MG	1x	102	1/1	0.92	0.12	32,32,32,32	0
57	MG	1A	3593	1/1	0.92	0.12	67,67,67,67	0
57	MG	1A	3719	1/1	0.92	0.09	33,33,33,33	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2A	3005	1/1	0.92	0.09	63,63,63,63	0
57	MG	2A	3010	1/1	0.92	0.15	65,65,65,65	0
57	MG	1A	3810	1/1	0.92	0.18	36,36,36,36	0
57	MG	1a	1710	1/1	0.93	0.34	64,64,64,64	0
57	MG	1A	3127	1/1	0.93	0.14	40,40,40,40	0
57	MG	1A	3976	1/1	0.93	0.13	59,59,59,59	0
57	MG	2R	202	1/1	0.93	0.20	62,62,62,62	0
57	MG	1A	3526	1/1	0.93	0.13	54,54,54,54	0
57	MG	2T	201	1/1	0.93	0.21	73,73,73,73	0
57	MG	2A	3515	1/1	0.93	0.14	56,56,56,56	0
57	MG	1A	3829	1/1	0.93	0.08	45,45,45,45	0
57	MG	2A	3124	1/1	0.93	0.41	47,47,47,47	0
57	MG	1a	1715	1/1	0.93	0.42	63,63,63,63	0
57	MG	2A	3126	1/1	0.93	0.19	49,49,49,49	0
57	MG	2W	202	1/1	0.93	0.20	56,56,56,56	0
57	MG	2A	3524	1/1	0.93	0.10	73,73,73,73	0
57	MG	1A	3440	1/1	0.93	0.10	46,46,46,46	0
57	MG	1A	3606	1/1	0.93	0.32	42,42,42,42	0
57	MG	15	102	1/1	0.93	0.20	51,51,51,51	0
57	MG	1A	3607	1/1	0.93	0.19	35,35,35,35	0
57	MG	1a	1721	1/1	0.93	0.33	69,69,69,69	0
57	MG	28	102	1/1	0.93	0.24	62,62,62,62	0
57	MG	2A	3314	1/1	0.93	0.07	37,37,37,37	0
57	MG	2A	3315	1/1	0.93	0.07	50,50,50,50	0
57	MG	1A	3245	1/1	0.93	0.13	54,54,54,54	0
57	MG	1A	3011	1/1	0.93	0.11	60,60,60,60	0
57	MG	17	106	1/1	0.93	0.10	58,58,58,58	0
57	MG	1a	1725	1/1	0.93	0.24	66,66,66,66	0
57	MG	1A	3185	1/1	0.93	0.30	60,60,60,60	0
57	MG	1a	1865	1/1	0.93	0.21	59,59,59,59	0
57	MG	1A	3251	1/1	0.93	0.09	69,69,69,69	0
57	MG	2A	3543	1/1	0.93	0.13	59,59,59,59	0
57	MG	1A	3988	1/1	0.93	0.11	53,53,53,53	0
57	MG	1A	3186	1/1	0.93	0.21	78,78,78,78	0
57	MG	2A	3151	1/1	0.93	0.07	43,43,43,43	0
57	MG	2A	3341	1/1	0.93	0.17	59,59,59,59	0
57	MG	1A	3615	1/1	0.93	0.12	24,24,24,24	0
57	MG	1A	3253	1/1	0.93	0.12	55,55,55,55	0
57	MG	1A	3030	1/1	0.93	0.08	31,31,31,31	0
57	MG	1A	3733	1/1	0.93	0.06	45,45,45,45	0
57	MG	2a	3030	1/1	0.93	0.10	58,58,58,58	0
57	MG	2A	3351	1/1	0.93	0.10	37,37,37,37	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1a	1608	1/1	0.93	0.11	61,61,61,61	0
57	MG	2A	3556	1/1	0.93	0.15	34,34,34,34	0
57	MG	2A	3354	1/1	0.93	0.08	39,39,39,39	0
57	MG	1A	4000	1/1	0.93	0.24	42,42,42,42	0
57	MG	2A	3564	1/1	0.93	0.09	32,32,32,32	0
57	MG	2A	3568	1/1	0.93	0.10	75,75,75,75	0
57	MG	1A	3453	1/1	0.93	0.10	61,61,61,61	0
57	MG	2A	3358	1/1	0.93	0.12	35,35,35,35	0
57	MG	1A	3032	1/1	0.93	0.34	62,62,62,62	0
57	MG	1a	1617	1/1	0.93	0.12	67,67,67,67	0
57	MG	1A	3855	1/1	0.93	0.08	36,36,36,36	0
57	MG	2A	3368	1/1	0.93	0.09	32,32,32,32	0
57	MG	1a	1620	1/1	0.93	0.08	55,55,55,55	0
57	MG	2A	3167	1/1	0.93	0.15	42,42,42,42	0
57	MG	1A	3034	1/1	0.93	0.08	50,50,50,50	0
57	MG	1A	3628	1/1	0.93	0.08	43,43,43,43	0
57	MG	1A	3148	1/1	0.93	0.11	56,56,56,56	0
57	MG	1a	1629	1/1	0.93	0.22	72,72,72,72	0
57	MG	1A	3747	1/1	0.93	0.08	52,52,52,52	0
57	MG	1A	3750	1/1	0.93	0.07	50,50,50,50	0
57	MG	2A	3177	1/1	0.93	0.12	65,65,65,65	0
57	MG	1A	3095	1/1	0.93	0.09	41,41,41,41	0
57	MG	1A	3105	1/1	0.93	0.10	68,68,68,68	0
57	MG	1A	3547	1/1	0.93	0.27	55,55,55,55	0
57	MG	2A	3386	1/1	0.93	0.20	62,62,62,62	0
57	MG	1A	3389	1/1	0.93	0.08	40,40,40,40	0
57	MG	1A	3118	1/1	0.93	0.11	38,38,38,38	0
57	MG	1A	3395	1/1	0.93	0.08	31,31,31,31	0
57	MG	1a	1764	1/1	0.93	0.18	70,70,70,70	0
57	MG	1A	3551	1/1	0.93	0.13	51,51,51,51	0
57	MG	1A	3396	1/1	0.93	0.07	41,41,41,41	0
57	MG	2a	3067	1/1	0.93	0.24	71,71,71,71	0
57	MG	1A	3400	1/1	0.93	0.08	26,26,26,26	0
57	MG	2a	3069	1/1	0.93	0.35	70,70,70,70	0
57	MG	1B	219	1/1	0.93	0.11	66,66,66,66	0
57	MG	2A	3626	1/1	0.93	0.06	54,54,54,54	0
57	MG	1A	3331	1/1	0.93	0.12	30,30,30,30	0
57	MG	2A	3631	1/1	0.93	0.09	44,44,44,44	0
57	MG	2A	3636	1/1	0.93	0.07	60,60,60,60	0
57	MG	2a	3079	1/1	0.93	0.10	59,59,59,59	0
57	MG	2A	3002	1/1	0.93	0.19	53,53,53,53	0
57	MG	1a	1649	1/1	0.93	0.14	44,44,44,44	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1A	3473	1/1	0.93	0.15	63,63,63,63	0
57	MG	2A	3647	1/1	0.93	0.07	66,66,66,66	0
57	MG	2A	3650	1/1	0.93	0.08	45,45,45,45	0
57	MG	1B	224	1/1	0.93	0.19	65,65,65,65	0
57	MG	1A	3403	1/1	0.93	0.09	29,29,29,29	0
57	MG	1A	3332	1/1	0.93	0.10	26,26,26,26	0
57	MG	2A	3658	1/1	0.93	0.08	70,70,70,70	0
57	MG	1a	1776	1/1	0.93	0.18	59,59,59,59	0
57	MG	2a	3094	1/1	0.93	0.33	67,67,67,67	0
57	MG	2a	3095	1/1	0.93	0.48	71,71,71,71	0
57	MG	2A	3019	1/1	0.93	0.25	48,48,48,48	0
57	MG	2A	3022	1/1	0.93	0.24	44,44,44,44	0
57	MG	1A	3769	1/1	0.93	0.07	44,44,44,44	0
57	MG	1A	3655	1/1	0.93	0.06	16,16,16,16	0
57	MG	1a	1660	1/1	0.93	0.17	64,64,64,64	0
57	MG	2A	3416	1/1	0.93	0.08	43,43,43,43	0
57	MG	2A	3417	1/1	0.93	0.08	50,50,50,50	0
57	MG	1A	3341	1/1	0.93	0.10	55,55,55,55	0
57	MG	1A	3899	1/1	0.93	0.12	30,30,30,30	0
57	MG	1A	3343	1/1	0.93	0.09	30,30,30,30	0
57	MG	1A	3570	1/1	0.93	0.08	63,63,63,63	0
57	MG	1D	314	1/1	0.93	0.09	69,69,69,69	0
57	MG	1A	3909	1/1	0.93	0.08	63,63,63,63	0
57	MG	2A	3680	1/1	0.93	0.10	76,76,76,76	0
57	MG	1A	3779	1/1	0.93	0.13	55,55,55,55	0
57	MG	2a	3115	1/1	0.93	0.18	66,66,66,66	0
57	MG	1E	306	1/1	0.93	0.09	25,25,25,25	0
57	MG	1A	3156	1/1	0.93	0.15	56,56,56,56	0
57	MG	1A	3416	1/1	0.93	0.07	27,27,27,27	0
57	MG	2a	3119	1/1	0.93	0.14	65,65,65,65	0
57	MG	1A	3205	1/1	0.93	0.29	38,38,38,38	0
57	MG	1A	3157	1/1	0.93	0.09	36,36,36,36	0
57	MG	2A	3437	1/1	0.93	0.08	48,48,48,48	0
57	MG	1A	3668	1/1	0.93	0.25	41,41,41,41	0
57	MG	1a	1676	1/1	0.93	0.18	58,58,58,58	0
57	MG	1A	3787	1/1	0.93	0.17	69,69,69,69	0
57	MG	1F	315	1/1	0.93	0.12	60,60,60,60	0
57	MG	1A	3070	1/1	0.93	0.09	38,38,38,38	0
57	MG	1A	3934	1/1	0.93	0.09	72,72,72,72	0
57	MG	2A	3055	1/1	0.93	0.14	47,47,47,47	0
57	MG	2A	3706	1/1	0.93	0.14	66,66,66,66	0
57	MG	2A	3241	1/1	0.93	0.10	54,54,54,54	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2a	3135	1/1	0.93	0.14	62,62,62,62	0
57	MG	1A	3671	1/1	0.93	0.09	55,55,55,55	0
57	MG	2A	3244	1/1	0.93	0.10	60,60,60,60	0
57	MG	1A	3940	1/1	0.93	0.13	57,57,57,57	0
57	MG	1a	1683	1/1	0.93	0.15	59,59,59,59	0
57	MG	1a	1684	1/1	0.93	0.12	56,56,56,56	0
57	MG	1A	3420	1/1	0.93	0.07	32,32,32,32	0
57	MG	1a	1687	1/1	0.93	0.10	45,45,45,45	0
57	MG	2A	3720	1/1	0.93	0.15	77,77,77,77	0
57	MG	2A	3721	1/1	0.93	0.13	73,73,73,73	0
57	MG	1A	3497	1/1	0.93	0.07	62,62,62,62	0
57	MG	2A	3068	1/1	0.93	0.13	54,54,54,54	0
57	MG	1A	3286	1/1	0.93	0.17	50,50,50,50	0
57	MG	1A	3163	1/1	0.93	0.27	58,58,58,58	0
57	MG	1a	1817	1/1	0.93	0.07	83,83,83,83	0
57	MG	1A	3425	1/1	0.93	0.13	29,29,29,29	0
57	MG	1R	204	1/1	0.93	0.13	39,39,39,39	0
57	MG	1A	3426	1/1	0.93	0.09	25,25,25,25	0
57	MG	2a	3166	1/1	0.93	0.14	70,70,70,70	0
57	MG	1A	3505	1/1	0.93	0.08	25,25,25,25	0
57	MG	2A	3472	1/1	0.93	0.21	55,55,55,55	0
57	MG	1A	3167	1/1	0.93	0.15	33,33,33,33	0
57	MG	1A	3071	1/1	0.93	0.30	54,54,54,54	0
57	MG	2A	3273	1/1	0.93	0.27	55,55,55,55	0
57	MG	1A	3686	1/1	0.93	0.14	46,46,46,46	0
57	MG	2A	3477	1/1	0.93	0.20	64,64,64,64	0
57	MG	2A	3478	1/1	0.93	0.19	58,58,58,58	0
57	MG	1A	3054	1/1	0.93	0.13	44,44,44,44	0
57	MG	1A	3055	1/1	0.93	0.14	58,58,58,58	0
57	MG	1A	3693	1/1	0.93	0.18	56,56,56,56	0
57	MG	1W	202	1/1	0.93	0.17	52,52,52,52	0
57	MG	2A	3486	1/1	0.93	0.06	59,59,59,59	0
57	MG	1A	3303	1/1	0.93	0.17	49,49,49,49	0
57	MG	2A	3488	1/1	0.93	0.12	74,74,74,74	0
57	MG	2A	3284	1/1	0.93	0.29	67,67,67,67	0
57	MG	2A	3285	1/1	0.93	0.25	53,53,53,53	0
57	MG	1A	3516	1/1	0.93	0.08	53,53,53,53	0
57	MG	2f	201	1/1	0.93	0.16	58,58,58,58	0
57	MG	2D	303	1/1	0.93	0.29	45,45,45,45	0
57	MG	2A	3287	1/1	0.93	0.49	70,70,70,70	0
57	MG	2D	305	1/1	0.93	0.14	55,55,55,55	0
57	MG	1A	3969	1/1	0.93	0.11	49,49,49,49	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2D	309	1/1	0.93	0.08	35,35,35,35	0
57	MG	2A	3106	1/1	0.93	0.18	62,62,62,62	0
57	MG	2x	102	1/1	0.93	0.17	52,52,52,52	0
57	MG	2A	3496	1/1	0.93	0.09	56,56,56,56	0
57	MG	2F	302	1/1	0.93	0.30	47,47,47,47	0
58	MPD	18	104	8/8	0.93	0.14	32,40,42,51	0
57	MG	2A	3107	1/1	0.93	0.14	62,62,62,62	0
57	MG	1A	3971	1/1	0.93	0.06	49,49,49,49	0
57	MG	1a	1707	1/1	0.93	0.43	64,64,64,64	0
57	MG	2A	3293	1/1	0.93	0.10	55,55,55,55	0
57	MG	1A	3307	1/1	0.93	0.23	45,45,45,45	0
57	MG	1A	3519	1/1	0.93	0.08	24,24,24,24	0
57	MG	1Q	204	1/1	0.94	0.10	39,39,39,39	0
57	MG	2A	3356	1/1	0.94	0.08	49,49,49,49	0
57	MG	1Q	205	1/1	0.94	0.14	55,55,55,55	0
57	MG	1A	3665	1/1	0.94	0.13	49,49,49,49	0
57	MG	1A	3970	1/1	0.94	0.13	50,50,50,50	0
57	MG	20	102	1/1	0.94	0.11	64,64,64,64	0
57	MG	2A	3363	1/1	0.94	0.10	43,43,43,43	0
57	MG	2A	3364	1/1	0.94	0.08	35,35,35,35	0
57	MG	1A	3666	1/1	0.94	0.07	41,41,41,41	0
57	MG	27	102	1/1	0.94	0.15	42,42,42,42	0
57	MG	1A	3844	1/1	0.94	0.08	37,37,37,37	0
57	MG	1A	3165	1/1	0.94	0.15	29,29,29,29	0
57	MG	1A	3262	1/1	0.94	0.09	55,55,55,55	0
57	MG	1A	3212	1/1	0.94	0.11	56,56,56,56	0
57	MG	2A	3554	1/1	0.94	0.09	47,47,47,47	0
57	MG	1A	3502	1/1	0.94	0.11	52,52,52,52	0
57	MG	1T	207	1/1	0.94	0.14	58,58,58,58	0
57	MG	1a	1794	1/1	0.94	0.12	59,59,59,59	0
57	MG	1U	205	1/1	0.94	0.25	38,38,38,38	0
57	MG	2a	3013	1/1	0.94	0.26	71,71,71,71	0
57	MG	1V	203	1/1	0.94	0.10	42,42,42,42	0
57	MG	2A	3569	1/1	0.94	0.10	71,71,71,71	0
57	MG	2A	3038	1/1	0.94	0.16	49,49,49,49	0
57	MG	1a	1685	1/1	0.94	0.17	56,56,56,56	0
57	MG	1A	3978	1/1	0.94	0.19	40,40,40,40	0
57	MG	2A	3576	1/1	0.94	0.11	58,58,58,58	0
57	MG	2a	3024	1/1	0.94	0.17	65,65,65,65	0
57	MG	1a	1799	1/1	0.94	0.07	66,66,66,66	0
57	MG	1V	207	1/1	0.94	0.08	59,59,59,59	0
57	MG	2A	3205	1/1	0.94	0.21	61,61,61,61	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2a	3028	1/1	0.94	0.12	57,57,57,57	0
57	MG	2A	3583	1/1	0.94	0.07	48,48,48,48	0
57	MG	1A	3552	1/1	0.94	0.08	52,52,52,52	0
57	MG	1A	3503	1/1	0.94	0.07	49,49,49,49	0
57	MG	2A	3390	1/1	0.94	0.08	53,53,53,53	0
57	MG	2A	3593	1/1	0.94	0.07	61,61,61,61	0
57	MG	1A	3300	1/1	0.94	0.14	54,54,54,54	0
57	MG	1A	3333	1/1	0.94	0.15	51,51,51,51	0
57	MG	1Z	301	1/1	0.94	0.13	62,62,62,62	0
57	MG	1A	3983	1/1	0.94	0.16	57,57,57,57	0
57	MG	1A	3339	1/1	0.94	0.09	35,35,35,35	0
57	MG	1A	3767	1/1	0.94	0.07	32,32,32,32	0
57	MG	1A	3507	1/1	0.94	0.10	51,51,51,51	0
57	MG	1A	3681	1/1	0.94	0.06	49,49,49,49	0
57	MG	1A	3616	1/1	0.94	0.10	27,27,27,27	0
57	MG	2A	3221	1/1	0.94	0.10	52,52,52,52	0
57	MG	2A	3404	1/1	0.94	0.09	50,50,50,50	0
57	MG	1A	3301	1/1	0.94	0.24	35,35,35,35	0
57	MG	1A	3046	1/1	0.94	0.26	51,51,51,51	0
57	MG	2A	3224	1/1	0.94	0.17	60,60,60,60	0
57	MG	2A	3227	1/1	0.94	0.22	51,51,51,51	0
57	MG	2a	3050	1/1	0.94	0.22	57,57,57,57	0
57	MG	1A	3422	1/1	0.94	0.14	31,31,31,31	0
57	MG	2A	3622	1/1	0.94	0.07	57,57,57,57	0
57	MG	1A	3622	1/1	0.94	0.09	52,52,52,52	0
57	MG	13	103	1/1	0.94	0.09	45,45,45,45	0
57	MG	1A	3423	1/1	0.94	0.11	38,38,38,38	0
57	MG	1A	3625	1/1	0.94	0.09	37,37,37,37	0
57	MG	15	107	1/1	0.94	0.12	71,71,71,71	0
57	MG	2A	3073	1/1	0.94	0.08	51,51,51,51	0
57	MG	2A	3637	1/1	0.94	0.10	53,53,53,53	0
57	MG	2A	3236	1/1	0.94	0.22	59,59,59,59	0
57	MG	1a	1826	1/1	0.94	0.08	65,65,65,65	0
57	MG	2A	3238	1/1	0.94	0.08	60,60,60,60	0
57	MG	2A	3646	1/1	0.94	0.08	61,61,61,61	0
57	MG	1A	3227	1/1	0.94	0.18	36,36,36,36	0
57	MG	1A	3627	1/1	0.94	0.17	71,71,71,71	0
57	MG	2A	3080	1/1	0.94	0.41	50,50,50,50	0
57	MG	1A	3169	1/1	0.94	0.18	64,64,64,64	0
57	MG	2A	3656	1/1	0.94	0.07	52,52,52,52	0
57	MG	1A	3629	1/1	0.94	0.15	56,56,56,56	0
57	MG	1A	4010	1/1	0.94	0.20	51,51,51,51	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2A	3432	1/1	0.94	0.08	51,51,51,51	0
57	MG	2a	3075	1/1	0.94	0.13	50,50,50,50	0
57	MG	2a	3076	1/1	0.94	0.23	69,69,69,69	0
57	MG	1a	1834	1/1	0.94	0.12	60,60,60,60	0
57	MG	1A	3233	1/1	0.94	0.29	66,66,66,66	0
57	MG	1A	3790	1/1	0.94	0.10	33,33,33,33	0
57	MG	1A	3522	1/1	0.94	0.10	62,62,62,62	0
57	MG	2A	3091	1/1	0.94	0.17	53,53,53,53	0
57	MG	2a	3083	1/1	0.94	0.16	67,67,67,67	0
57	MG	1A	3049	1/1	0.94	0.19	44,44,44,44	0
57	MG	2a	3087	1/1	0.94	0.17	55,55,55,55	0
57	MG	2A	3260	1/1	0.94	0.11	32,32,32,32	0
57	MG	2A	3443	1/1	0.94	0.06	61,61,61,61	0
57	MG	1A	3470	1/1	0.94	0.07	33,33,33,33	0
57	MG	2A	3262	1/1	0.94	0.27	50,50,50,50	0
57	MG	1A	3795	1/1	0.94	0.12	59,59,59,59	0
57	MG	1B	205	1/1	0.94	0.10	50,50,50,50	0
57	MG	1a	1609	1/1	0.94	0.09	60,60,60,60	0
57	MG	2A	3103	1/1	0.94	0.18	67,67,67,67	0
57	MG	2A	3269	1/1	0.94	0.12	45,45,45,45	0
57	MG	1a	1610	1/1	0.94	0.29	60,60,60,60	0
57	MG	2A	3685	1/1	0.94	0.11	59,59,59,59	0
57	MG	2A	3686	1/1	0.94	0.06	43,43,43,43	0
57	MG	2a	3100	1/1	0.94	0.37	63,63,63,63	0
57	MG	1A	3471	1/1	0.94	0.12	55,55,55,55	0
57	MG	2A	3690	1/1	0.94	0.10	46,46,46,46	0
57	MG	2A	3453	1/1	0.94	0.07	37,37,37,37	0
57	MG	2A	3693	1/1	0.94	0.17	57,57,57,57	0
57	MG	1A	3274	1/1	0.94	0.19	39,39,39,39	0
57	MG	2A	3695	1/1	0.94	0.13	62,62,62,62	0
57	MG	2A	3455	1/1	0.94	0.11	65,65,65,65	0
57	MG	1A	3390	1/1	0.94	0.09	40,40,40,40	0
57	MG	2A	3274	1/1	0.94	0.22	51,51,51,51	0
57	MG	1A	3102	1/1	0.94	0.12	38,38,38,38	0
57	MG	1A	3911	1/1	0.94	0.10	66,66,66,66	0
57	MG	2A	3277	1/1	0.94	0.10	50,50,50,50	0
57	MG	2A	3702	1/1	0.94	0.09	47,47,47,47	0
57	MG	1A	3640	1/1	0.94	0.08	65,65,65,65	0
57	MG	2A	3279	1/1	0.94	0.11	53,53,53,53	0
57	MG	2A	3280	1/1	0.94	0.11	61,61,61,61	0
57	MG	1A	3807	1/1	0.94	0.09	48,48,48,48	0
57	MG	1a	1731	1/1	0.94	0.15	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1a	1623	1/1	0.94	0.15	54,54,54,54	0
57	MG	2A	3709	1/1	0.94	0.09	65,65,65,65	0
57	MG	2A	3118	1/1	0.94	0.17	37,37,37,37	0
57	MG	1a	1733	1/1	0.94	0.07	56,56,56,56	0
57	MG	1A	3721	1/1	0.94	0.12	46,46,46,46	0
57	MG	2a	3129	1/1	0.94	0.22	69,69,69,69	0
57	MG	1a	1625	1/1	0.94	0.09	58,58,58,58	0
57	MG	2A	3714	1/1	0.94	0.19	67,67,67,67	0
57	MG	1A	3919	1/1	0.94	0.16	45,45,45,45	0
57	MG	1a	1628	1/1	0.94	0.41	65,65,65,65	0
57	MG	1A	3809	1/1	0.94	0.12	27,27,27,27	0
57	MG	2A	3479	1/1	0.94	0.10	46,46,46,46	0
57	MG	2a	3136	1/1	0.94	0.13	67,67,67,67	0
57	MG	1A	3073	1/1	0.94	0.18	51,51,51,51	0
57	MG	2A	3129	1/1	0.94	0.19	66,66,66,66	0
57	MG	2A	3482	1/1	0.94	0.08	71,71,71,71	0
57	MG	1A	3158	1/1	0.94	0.12	45,45,45,45	0
57	MG	2A	3484	1/1	0.94	0.09	35,35,35,35	0
57	MG	1A	3813	1/1	0.94	0.20	35,35,35,35	0
57	MG	2a	3151	1/1	0.94	0.16	54,54,54,54	0
57	MG	1a	1636	1/1	0.94	0.44	65,65,65,65	0
57	MG	1A	3930	1/1	0.94	0.09	54,54,54,54	0
57	MG	1B	229	1/1	0.94	0.19	77,77,77,77	0
57	MG	1A	3814	1/1	0.94	0.15	75,75,75,75	0
57	MG	1a	1641	1/1	0.94	0.15	69,69,69,69	0
57	MG	1a	1752	1/1	0.94	0.07	55,55,55,55	0
57	MG	2A	3140	1/1	0.94	0.12	50,50,50,50	0
57	MG	1A	3933	1/1	0.94	0.09	62,62,62,62	0
57	MG	1A	3644	1/1	0.94	0.10	59,59,59,59	0
57	MG	1A	3590	1/1	0.94	0.07	48,48,48,48	0
57	MG	1A	3938	1/1	0.94	0.11	49,49,49,49	0
57	MG	1A	3183	1/1	0.94	0.16	72,72,72,72	0
57	MG	2A	3501	1/1	0.94	0.16	60,60,60,60	0
57	MG	1A	3734	1/1	0.94	0.06	22,22,22,22	0
57	MG	2B	211	1/1	0.94	0.09	69,69,69,69	0
57	MG	1A	3822	1/1	0.94	0.10	53,53,53,53	0
57	MG	1A	3945	1/1	0.94	0.08	62,62,62,62	0
57	MG	2A	3156	1/1	0.94	0.13	66,66,66,66	0
57	MG	2A	3318	1/1	0.94	0.13	38,38,38,38	0
57	MG	1A	3159	1/1	0.94	0.07	35,35,35,35	0
57	MG	1A	3248	1/1	0.94	0.07	43,43,43,43	0
57	MG	2A	3512	1/1	0.94	0.12	40,40,40,40	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1A	3126	1/1	0.94	0.17	43,43,43,43	0
57	MG	1A	3950	1/1	0.94	0.13	82,82,82,82	0
57	MG	2D	307	1/1	0.94	0.22	49,49,49,49	0
57	MG	1A	3488	1/1	0.94	0.07	30,30,30,30	0
57	MG	2A	3330	1/1	0.94	0.09	42,42,42,42	0
57	MG	2E	303	1/1	0.94	0.50	49,49,49,49	0
57	MG	1A	3827	1/1	0.94	0.21	58,58,58,58	0
57	MG	1A	3406	1/1	0.94	0.13	47,47,47,47	0
57	MG	2A	3523	1/1	0.94	0.19	64,64,64,64	0
57	MG	1A	3830	1/1	0.94	0.10	52,52,52,52	0
57	MG	2A	3337	1/1	0.94	0.13	46,46,46,46	0
57	MG	1G	201	1/1	0.94	0.11	65,65,65,65	0
57	MG	1A	3407	1/1	0.94	0.07	27,27,27,27	0
57	MG	2A	3528	1/1	0.94	0.10	63,63,63,63	0
57	MG	1A	3834	1/1	0.94	0.10	49,49,49,49	0
57	MG	1A	3748	1/1	0.94	0.09	54,54,54,54	0
57	MG	2A	3343	1/1	0.94	0.12	58,58,58,58	0
57	MG	1A	3598	1/1	0.94	0.12	56,56,56,56	0
57	MG	1A	3494	1/1	0.94	0.07	48,48,48,48	0
57	MG	1A	3967	1/1	0.94	0.06	62,62,62,62	0
57	MG	1A	3066	1/1	0.94	0.21	41,41,41,41	0
57	MG	2A	3537	1/1	0.94	0.11	37,37,37,37	0
57	MG	1a	1781	1/1	0.94	0.08	72,72,72,72	0
57	MG	2A	3353	1/1	0.94	0.12	47,47,47,47	0
57	MG	2A	3006	1/1	0.94	0.15	51,51,51,51	0
57	MG	1A	3539	1/1	0.95	0.07	37,37,37,37	0
57	MG	1A	3112	1/1	0.95	0.26	41,41,41,41	0
57	MG	2A	3197	1/1	0.95	0.10	53,53,53,53	0
57	MG	1Q	203	1/1	0.95	0.10	53,53,53,53	0
57	MG	2A	3559	1/1	0.95	0.09	69,69,69,69	0
57	MG	1a	1670	1/1	0.95	0.32	61,61,61,61	0
57	MG	1A	3703	1/1	0.95	0.07	29,29,29,29	0
57	MG	2A	3563	1/1	0.95	0.07	59,59,59,59	0
57	MG	1A	3275	1/1	0.95	0.25	36,36,36,36	0
57	MG	2A	3382	1/1	0.95	0.05	40,40,40,40	0
57	MG	28	101	1/1	0.95	0.09	65,65,65,65	0
57	MG	1R	201	1/1	0.95	0.17	41,41,41,41	0
57	MG	1A	3276	1/1	0.95	0.25	43,43,43,43	0
57	MG	2a	3001	1/1	0.95	0.07	46,46,46,46	0
57	MG	2a	3003	1/1	0.95	0.08	56,56,56,56	0
57	MG	1A	3278	1/1	0.95	0.13	47,47,47,47	0
57	MG	1A	3620	1/1	0.95	0.15	54,54,54,54	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2A	3574	1/1	0.95	0.08	54,54,54,54	0
57	MG	1A	3117	1/1	0.95	0.12	37,37,37,37	0
57	MG	1A	3712	1/1	0.95	0.19	38,38,38,38	0
57	MG	1A	3346	1/1	0.95	0.11	50,50,50,50	0
57	MG	2A	3581	1/1	0.95	0.09	48,48,48,48	0
57	MG	1A	3478	1/1	0.95	0.06	28,28,28,28	0
57	MG	2a	3014	1/1	0.95	0.23	57,57,57,57	0
57	MG	1T	205	1/1	0.95	0.08	57,57,57,57	0
57	MG	1A	3716	1/1	0.95	0.06	33,33,33,33	0
57	MG	1A	3624	1/1	0.95	0.09	30,30,30,30	0
57	MG	1A	3347	1/1	0.95	0.10	52,52,52,52	0
57	MG	2A	3591	1/1	0.95	0.08	50,50,50,50	0
57	MG	1A	3061	1/1	0.95	0.07	35,35,35,35	0
57	MG	1A	3724	1/1	0.95	0.10	57,57,57,57	0
57	MG	2A	3597	1/1	0.95	0.07	37,37,37,37	0
57	MG	1V	205	1/1	0.95	0.07	55,55,55,55	0
57	MG	2A	3056	1/1	0.95	0.15	55,55,55,55	0
57	MG	1A	3078	1/1	0.95	0.23	44,44,44,44	0
57	MG	2A	3226	1/1	0.95	0.14	54,54,54,54	0
57	MG	1a	1690	1/1	0.95	0.17	57,57,57,57	0
57	MG	2A	3605	1/1	0.95	0.07	44,44,44,44	0
57	MG	1A	3972	1/1	0.95	0.06	20,20,20,20	0
57	MG	1A	3214	1/1	0.95	0.13	49,49,49,49	0
57	MG	1A	3354	1/1	0.95	0.05	34,34,34,34	0
57	MG	2a	3035	1/1	0.95	0.12	41,41,41,41	0
57	MG	2A	3611	1/1	0.95	0.06	26,26,26,26	0
57	MG	1A	3732	1/1	0.95	0.10	30,30,30,30	0
57	MG	1A	3839	1/1	0.95	0.18	40,40,40,40	0
57	MG	1A	3218	1/1	0.95	0.06	39,39,39,39	0
57	MG	2A	3615	1/1	0.95	0.12	59,59,59,59	0
57	MG	2A	3616	1/1	0.95	0.19	64,64,64,64	0
57	MG	1A	3487	1/1	0.95	0.15	29,29,29,29	0
57	MG	2A	3072	1/1	0.95	0.21	51,51,51,51	0
57	MG	1A	3012	1/1	0.95	0.10	41,41,41,41	0
57	MG	1A	3633	1/1	0.95	0.17	33,33,33,33	0
57	MG	1A	3226	1/1	0.95	0.24	38,38,38,38	0
57	MG	2A	3240	1/1	0.95	0.30	44,44,44,44	0
57	MG	2A	3076	1/1	0.95	0.15	58,58,58,58	0
57	MG	2A	3242	1/1	0.95	0.09	60,60,60,60	0
57	MG	1A	3559	1/1	0.95	0.07	63,63,63,63	0
57	MG	2A	3630	1/1	0.95	0.08	57,57,57,57	0
57	MG	1A	3745	1/1	0.95	0.08	26,26,26,26	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2A	3427	1/1	0.95	0.09	48,48,48,48	0
57	MG	1A	3288	1/1	0.95	0.09	33,33,33,33	0
57	MG	1A	3563	1/1	0.95	0.08	52,52,52,52	0
57	MG	2A	3639	1/1	0.95	0.14	33,33,33,33	0
57	MG	11	105	1/1	0.95	0.09	43,43,43,43	0
57	MG	1A	3851	1/1	0.95	0.07	63,63,63,63	0
57	MG	2A	3251	1/1	0.95	0.31	65,65,65,65	0
57	MG	2a	3061	1/1	0.95	0.32	74,74,74,74	0
57	MG	2A	3434	1/1	0.95	0.10	38,38,38,38	0
57	MG	2A	3649	1/1	0.95	0.07	42,42,42,42	0
57	MG	1A	3638	1/1	0.95	0.12	62,62,62,62	0
57	MG	1A	3564	1/1	0.95	0.18	45,45,45,45	0
57	MG	2A	3654	1/1	0.95	0.12	69,69,69,69	0
57	MG	15	104	1/1	0.95	0.21	38,38,38,38	0
57	MG	2A	3439	1/1	0.95	0.14	56,56,56,56	0
57	MG	1A	3122	1/1	0.95	0.09	46,46,46,46	0
57	MG	1A	3495	1/1	0.95	0.17	60,60,60,60	0
57	MG	1A	3042	1/1	0.95	0.09	18,18,18,18	0
57	MG	1A	3368	1/1	0.95	0.09	33,33,33,33	0
57	MG	1A	3084	1/1	0.95	0.09	51,51,51,51	0
57	MG	1A	3861	1/1	0.95	0.06	25,25,25,25	0
57	MG	1A	3085	1/1	0.95	0.10	37,37,37,37	0
57	MG	2A	3104	1/1	0.95	0.14	47,47,47,47	0
57	MG	2a	3078	1/1	0.95	0.41	65,65,65,65	0
57	MG	2A	3268	1/1	0.95	0.31	61,61,61,61	0
57	MG	1A	3238	1/1	0.95	0.23	44,44,44,44	0
57	MG	1A	3653	1/1	0.95	0.06	23,23,23,23	0
57	MG	2A	3673	1/1	0.95	0.16	54,54,54,54	0
57	MG	1a	1845	1/1	0.95	0.16	77,77,77,77	0
57	MG	1A	3064	1/1	0.95	0.27	54,54,54,54	0
57	MG	1A	3374	1/1	0.95	0.12	38,38,38,38	0
57	MG	1a	1849	1/1	0.95	0.12	58,58,58,58	0
57	MG	1A	3581	1/1	0.95	0.11	47,47,47,47	0
57	MG	1a	1851	1/1	0.95	0.09	44,44,44,44	0
57	MG	2A	3681	1/1	0.95	0.08	70,70,70,70	0
57	MG	1a	1606	1/1	0.95	0.24	57,57,57,57	0
57	MG	2A	3115	1/1	0.95	0.23	50,50,50,50	0
57	MG	2A	3684	1/1	0.95	0.07	40,40,40,40	0
57	MG	1A	3872	1/1	0.95	0.09	49,49,49,49	0
57	MG	2A	3460	1/1	0.95	0.12	62,62,62,62	0
57	MG	1A	3008	1/1	0.95	0.06	38,38,38,38	0
57	MG	1A	3658	1/1	0.95	0.06	47,47,47,47	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1A	3439	1/1	0.95	0.18	55,55,55,55	0
57	MG	2A	3122	1/1	0.95	0.25	44,44,44,44	0
57	MG	1A	3768	1/1	0.95	0.08	50,50,50,50	0
57	MG	1A	3242	1/1	0.95	0.22	47,47,47,47	0
57	MG	2A	3470	1/1	0.95	0.06	56,56,56,56	0
57	MG	1A	3772	1/1	0.95	0.05	30,30,30,30	0
57	MG	1A	3131	1/1	0.95	0.29	32,32,32,32	0
57	MG	1B	208	1/1	0.95	0.35	65,65,65,65	0
57	MG	1a	1864	1/1	0.95	0.29	57,57,57,57	0
57	MG	1a	1619	1/1	0.95	0.13	55,55,55,55	0
57	MG	1A	3587	1/1	0.95	0.06	23,23,23,23	0
57	MG	1A	3313	1/1	0.95	0.15	60,60,60,60	0
57	MG	1A	3777	1/1	0.95	0.08	39,39,39,39	0
57	MG	2A	3135	1/1	0.95	0.09	37,37,37,37	0
57	MG	1A	3893	1/1	0.95	0.07	35,35,35,35	0
57	MG	1A	3896	1/1	0.95	0.06	32,32,32,32	0
57	MG	1A	3445	1/1	0.95	0.09	51,51,51,51	0
57	MG	1A	3513	1/1	0.95	0.06	37,37,37,37	0
57	MG	1A	3056	1/1	0.95	0.14	28,28,28,28	0
57	MG	1B	222	1/1	0.95	0.08	35,35,35,35	0
57	MG	2A	3144	1/1	0.95	0.20	45,45,45,45	0
57	MG	2A	3145	1/1	0.95	0.13	47,47,47,47	0
57	MG	2A	3305	1/1	0.95	0.11	52,52,52,52	0
57	MG	2A	3716	1/1	0.95	0.11	66,66,66,66	0
57	MG	1a	1631	1/1	0.95	0.12	43,43,43,43	0
57	MG	2A	3490	1/1	0.95	0.11	69,69,69,69	0
57	MG	1A	3902	1/1	0.95	0.05	46,46,46,46	0
57	MG	1A	3903	1/1	0.95	0.21	41,41,41,41	0
57	MG	1a	1751	1/1	0.95	0.15	42,42,42,42	0
57	MG	2A	3152	1/1	0.95	0.18	61,61,61,61	0
57	MG	1A	3138	1/1	0.95	0.12	43,43,43,43	0
57	MG	1a	1637	1/1	0.95	0.09	44,44,44,44	0
57	MG	2A	3497	1/1	0.95	0.08	35,35,35,35	0
57	MG	2A	3498	1/1	0.95	0.07	67,67,67,67	0
57	MG	2a	3139	1/1	0.95	0.07	58,58,58,58	0
57	MG	2a	3140	1/1	0.95	0.07	77,77,77,77	0
57	MG	2a	3141	1/1	0.95	0.09	72,72,72,72	0
57	MG	1A	3009	1/1	0.95	0.07	32,32,32,32	0
57	MG	1A	3142	1/1	0.95	0.10	53,53,53,53	0
57	MG	1A	3097	1/1	0.95	0.20	42,42,42,42	0
57	MG	1A	3145	1/1	0.95	0.12	51,51,51,51	0
57	MG	1A	3254	1/1	0.95	0.20	36,36,36,36	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2A	3324	1/1	0.95	0.19	55,55,55,55	0
57	MG	2A	3506	1/1	0.95	0.15	28,28,28,28	0
57	MG	1A	3147	1/1	0.95	0.09	40,40,40,40	0
57	MG	1A	3099	1/1	0.95	0.12	47,47,47,47	0
57	MG	2A	3327	1/1	0.95	0.10	61,61,61,61	0
57	MG	1A	3150	1/1	0.95	0.08	41,41,41,41	0
57	MG	2A	3332	1/1	0.95	0.06	36,36,36,36	0
57	MG	2A	3333	1/1	0.95	0.14	58,58,58,58	0
57	MG	1A	3925	1/1	0.95	0.10	54,54,54,54	0
57	MG	1A	3072	1/1	0.95	0.06	39,39,39,39	0
57	MG	1A	3927	1/1	0.95	0.06	58,58,58,58	0
57	MG	2A	3519	1/1	0.95	0.10	62,62,62,62	0
57	MG	2A	3168	1/1	0.95	0.15	51,51,51,51	0
57	MG	1A	3103	1/1	0.95	0.12	45,45,45,45	0
57	MG	1A	3794	1/1	0.95	0.17	40,40,40,40	0
57	MG	1A	3398	1/1	0.95	0.10	27,27,27,27	0
57	MG	2B	219	1/1	0.95	0.08	69,69,69,69	0
57	MG	2D	301	1/1	0.95	0.22	39,39,39,39	0
57	MG	1A	3048	1/1	0.95	0.23	51,51,51,51	0
57	MG	1a	1771	1/1	0.95	0.14	60,60,60,60	0
57	MG	2A	3174	1/1	0.95	0.11	38,38,38,38	0
57	MG	1A	3687	1/1	0.95	0.08	59,59,59,59	0
57	MG	2A	3347	1/1	0.95	0.16	59,59,59,59	0
57	MG	1a	1656	1/1	0.95	0.28	58,58,58,58	0
57	MG	2A	3350	1/1	0.95	0.08	52,52,52,52	0
57	MG	1A	3936	1/1	0.95	0.08	34,34,34,34	0
57	MG	1A	3689	1/1	0.95	0.20	50,50,50,50	0
57	MG	2A	3180	1/1	0.95	0.08	55,55,55,55	0
57	MG	2A	3181	1/1	0.95	0.07	46,46,46,46	0
57	MG	1A	3608	1/1	0.95	0.10	46,46,46,46	0
57	MG	2A	3538	1/1	0.95	0.12	57,57,57,57	0
57	MG	1A	3270	1/1	0.95	0.22	43,43,43,43	0
57	MG	1A	3942	1/1	0.95	0.07	60,60,60,60	0
57	MG	2A	3014	1/1	0.95	0.10	54,54,54,54	0
57	MG	2P	201	1/1	0.95	0.09	61,61,61,61	0
57	MG	2A	3361	1/1	0.95	0.10	37,37,37,37	0
57	MG	1A	3536	1/1	0.95	0.26	31,31,31,31	0
57	MG	1a	1780	1/1	0.95	0.17	64,64,64,64	0
57	MG	1A	3109	1/1	0.95	0.18	44,44,44,44	0
57	MG	2A	3365	1/1	0.95	0.08	37,37,37,37	0
57	MG	1A	3612	1/1	0.95	0.11	33,33,33,33	0
57	MG	2A	3023	1/1	0.95	0.20	61,61,61,61	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2T	203	1/1	0.95	0.13	68,68,68,68	0
57	MG	2T	204	1/1	0.95	0.09	59,59,59,59	0
57	MG	1a	1783	1/1	0.95	0.10	79,79,79,79	0
57	MG	1A	3538	1/1	0.95	0.05	26,26,26,26	0
57	MG	2A	3027	1/1	0.95	0.05	36,36,36,36	0
57	MG	2V	202	1/1	0.95	0.25	49,49,49,49	0
57	MG	1A	3182	1/1	0.96	0.09	51,51,51,51	0
57	MG	1A	3143	1/1	0.96	0.09	41,41,41,41	0
57	MG	2A	3344	1/1	0.96	0.07	56,56,56,56	0
57	MG	1A	3243	1/1	0.96	0.17	44,44,44,44	0
57	MG	1A	3784	1/1	0.96	0.09	35,35,35,35	0
57	MG	1A	3662	1/1	0.96	0.07	54,54,54,54	0
57	MG	1A	3569	1/1	0.96	0.13	52,52,52,52	0
57	MG	2A	3349	1/1	0.96	0.06	51,51,51,51	0
57	MG	1A	3928	1/1	0.96	0.06	22,22,22,22	0
57	MG	1A	3477	1/1	0.96	0.06	28,28,28,28	0
57	MG	2A	3160	1/1	0.96	0.23	45,45,45,45	0
57	MG	1A	3108	1/1	0.96	0.15	44,44,44,44	0
57	MG	2W	203	1/1	0.96	0.07	54,54,54,54	0
57	MG	1A	3931	1/1	0.96	0.08	48,48,48,48	0
57	MG	1A	3081	1/1	0.96	0.20	46,46,46,46	0
57	MG	1A	3391	1/1	0.96	0.09	37,37,37,37	0
57	MG	2A	3557	1/1	0.96	0.06	54,54,54,54	0
57	MG	1A	3481	1/1	0.96	0.11	47,47,47,47	0
57	MG	1A	3935	1/1	0.96	0.07	29,29,29,29	0
57	MG	1T	203	1/1	0.96	0.11	58,58,58,58	0
57	MG	1T	204	1/1	0.96	0.07	63,63,63,63	0
57	MG	1d	302	1/1	0.96	0.12	71,71,71,71	0
57	MG	1A	3110	1/1	0.96	0.11	56,56,56,56	0
57	MG	1d	304	1/1	0.96	0.07	70,70,70,70	0
57	MG	1A	3082	1/1	0.96	0.33	48,48,48,48	0
57	MG	2a	3002	1/1	0.96	0.26	60,60,60,60	0
57	MG	1A	3578	1/1	0.96	0.07	52,52,52,52	0
57	MG	1U	203	1/1	0.96	0.18	37,37,37,37	0
57	MG	1U	204	1/1	0.96	0.23	29,29,29,29	0
57	MG	2A	3176	1/1	0.96	0.11	65,65,65,65	0
57	MG	2a	3007	1/1	0.96	0.24	56,56,56,56	0
57	MG	1A	3484	1/1	0.96	0.10	34,34,34,34	0
57	MG	1V	201	1/1	0.96	0.23	36,36,36,36	0
57	MG	1A	3941	1/1	0.96	0.07	58,58,58,58	0
57	MG	1A	3250	1/1	0.96	0.10	48,48,48,48	0
57	MG	2a	3012	1/1	0.96	0.08	50,50,50,50	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1A	3188	1/1	0.96	0.15	37,37,37,37	0
57	MG	1V	206	1/1	0.96	0.11	59,59,59,59	0
57	MG	1A	3798	1/1	0.96	0.22	46,46,46,46	0
57	MG	2A	3589	1/1	0.96	0.13	49,49,49,49	0
57	MG	2a	3017	1/1	0.96	0.13	49,49,49,49	0
57	MG	1A	3189	1/1	0.96	0.15	42,42,42,42	0
57	MG	1a	1720	1/1	0.96	0.13	50,50,50,50	0
57	MG	1A	3800	1/1	0.96	0.08	48,48,48,48	0
57	MG	1A	3325	1/1	0.96	0.06	37,37,37,37	0
57	MG	1A	3802	1/1	0.96	0.09	59,59,59,59	0
57	MG	1A	3586	1/1	0.96	0.20	56,56,56,56	0
57	MG	1A	3489	1/1	0.96	0.07	38,38,38,38	0
57	MG	1A	3402	1/1	0.96	0.07	27,27,27,27	0
57	MG	10	103	1/1	0.96	0.07	47,47,47,47	0
57	MG	1A	3955	1/1	0.96	0.05	28,28,28,28	0
57	MG	2A	3604	1/1	0.96	0.08	46,46,46,46	0
57	MG	1A	3190	1/1	0.96	0.19	61,61,61,61	0
57	MG	10	106	1/1	0.96	0.07	44,44,44,44	0
57	MG	2A	3607	1/1	0.96	0.06	65,65,65,65	0
57	MG	1A	3047	1/1	0.96	0.21	41,41,41,41	0
57	MG	1A	3257	1/1	0.96	0.08	54,54,54,54	0
57	MG	1A	3496	1/1	0.96	0.09	27,27,27,27	0
57	MG	2A	3400	1/1	0.96	0.13	65,65,65,65	0
57	MG	1A	3329	1/1	0.96	0.13	30,30,30,30	0
57	MG	2A	3202	1/1	0.96	0.29	65,65,65,65	0
57	MG	1A	3069	1/1	0.96	0.06	35,35,35,35	0
57	MG	1A	3965	1/1	0.96	0.15	56,56,56,56	0
57	MG	1A	3409	1/1	0.96	0.05	22,22,22,22	0
57	MG	1A	3818	1/1	0.96	0.05	23,23,23,23	0
57	MG	2A	3407	1/1	0.96	0.16	61,61,61,61	0
57	MG	15	101	1/1	0.96	0.09	41,41,41,41	0
57	MG	2A	3621	1/1	0.96	0.14	60,60,60,60	0
57	MG	2A	3208	1/1	0.96	0.17	59,59,59,59	0
57	MG	1A	3119	1/1	0.96	0.09	41,41,41,41	0
57	MG	1A	3820	1/1	0.96	0.11	53,53,53,53	0
57	MG	1A	3697	1/1	0.96	0.14	57,57,57,57	0
57	MG	1A	3020	1/1	0.96	0.23	38,38,38,38	0
57	MG	2A	3213	1/1	0.96	0.09	53,53,53,53	0
57	MG	2A	3018	1/1	0.96	0.39	44,44,44,44	0
57	MG	2A	3634	1/1	0.96	0.07	49,49,49,49	0
57	MG	2A	3635	1/1	0.96	0.10	60,60,60,60	0
57	MG	2A	3215	1/1	0.96	0.11	52,52,52,52	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	17	103	1/1	0.96	0.16	38,38,38,38	0
57	MG	1a	1749	1/1	0.96	0.06	54,54,54,54	0
57	MG	1A	3414	1/1	0.96	0.06	37,37,37,37	0
57	MG	2A	3421	1/1	0.96	0.10	41,41,41,41	0
57	MG	2A	3641	1/1	0.96	0.07	41,41,41,41	0
57	MG	1A	3599	1/1	0.96	0.09	62,62,62,62	0
57	MG	1A	3004	1/1	0.96	0.09	41,41,41,41	0
57	MG	2A	3424	1/1	0.96	0.09	37,37,37,37	0
57	MG	2A	3425	1/1	0.96	0.10	37,37,37,37	0
57	MG	18	101	1/1	0.96	0.07	42,42,42,42	0
57	MG	2A	3030	1/1	0.96	0.16	60,60,60,60	0
57	MG	2A	3652	1/1	0.96	0.10	62,62,62,62	0
57	MG	2A	3428	1/1	0.96	0.05	33,33,33,33	0
57	MG	1A	3704	1/1	0.96	0.10	67,67,67,67	0
57	MG	2a	3072	1/1	0.96	0.09	64,64,64,64	0
57	MG	1A	3601	1/1	0.96	0.21	35,35,35,35	0
57	MG	1A	3334	1/1	0.96	0.08	30,30,30,30	0
57	MG	1a	1757	1/1	0.96	0.21	55,55,55,55	0
57	MG	1A	3335	1/1	0.96	0.07	26,26,26,26	0
57	MG	1A	3831	1/1	0.96	0.18	54,54,54,54	0
57	MG	2A	3661	1/1	0.96	0.05	44,44,44,44	0
57	MG	1A	3336	1/1	0.96	0.04	31,31,31,31	0
57	MG	1A	3088	1/1	0.96	0.15	35,35,35,35	0
57	MG	2A	3664	1/1	0.96	0.09	56,56,56,56	0
57	MG	2A	3666	1/1	0.96	0.09	32,32,32,32	0
57	MG	2A	3233	1/1	0.96	0.14	65,65,65,65	0
57	MG	2a	3085	1/1	0.96	0.24	51,51,51,51	0
57	MG	1A	3199	1/1	0.96	0.11	41,41,41,41	0
57	MG	1A	3342	1/1	0.96	0.09	35,35,35,35	0
57	MG	1A	3051	1/1	0.96	0.15	32,32,32,32	0
57	MG	1A	3344	1/1	0.96	0.13	47,47,47,47	0
57	MG	2A	3672	1/1	0.96	0.06	62,62,62,62	0
57	MG	1A	3204	1/1	0.96	0.14	39,39,39,39	0
57	MG	1A	3720	1/1	0.96	0.12	60,60,60,60	0
57	MG	1A	3517	1/1	0.96	0.05	56,56,56,56	0
57	MG	1A	3990	1/1	0.96	0.04	38,38,38,38	0
57	MG	1a	1616	1/1	0.96	0.14	65,65,65,65	0
57	MG	1A	3843	1/1	0.96	0.06	67,67,67,67	0
57	MG	1A	3053	1/1	0.96	0.07	41,41,41,41	0
57	MG	1A	3427	1/1	0.96	0.09	34,34,34,34	0
57	MG	2A	3246	1/1	0.96	0.25	46,46,46,46	0
57	MG	2A	3247	1/1	0.96	0.06	59,59,59,59	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1A	3074	1/1	0.96	0.22	37,37,37,37	0
57	MG	1A	3162	1/1	0.96	0.12	45,45,45,45	0
57	MG	1A	3351	1/1	0.96	0.07	31,31,31,31	0
57	MG	1A	3096	1/1	0.96	0.12	47,47,47,47	0
57	MG	2A	3689	1/1	0.96	0.17	63,63,63,63	0
57	MG	2A	3059	1/1	0.96	0.14	44,44,44,44	0
57	MG	1A	3075	1/1	0.96	0.13	39,39,39,39	0
57	MG	2A	3692	1/1	0.96	0.09	39,39,39,39	0
57	MG	1A	3166	1/1	0.96	0.33	42,42,42,42	0
57	MG	1A	4004	1/1	0.96	0.10	56,56,56,56	0
57	MG	2a	3112	1/1	0.96	0.07	50,50,50,50	0
57	MG	1A	4005	1/1	0.96	0.09	53,53,53,53	0
57	MG	2A	3462	1/1	0.96	0.12	39,39,39,39	0
57	MG	1A	4008	1/1	0.96	0.15	68,68,68,68	0
57	MG	1A	3735	1/1	0.96	0.06	46,46,46,46	0
57	MG	1A	3854	1/1	0.96	0.10	31,31,31,31	0
57	MG	2A	3070	1/1	0.96	0.26	48,48,48,48	0
57	MG	1a	1633	1/1	0.96	0.10	40,40,40,40	0
57	MG	1a	1634	1/1	0.96	0.10	49,49,49,49	0
57	MG	1A	3023	1/1	0.96	0.19	34,34,34,34	0
57	MG	1A	3357	1/1	0.96	0.11	26,26,26,26	0
57	MG	2a	3125	1/1	0.96	0.12	58,58,58,58	0
57	MG	1A	3219	1/1	0.96	0.14	38,38,38,38	0
57	MG	1B	201	1/1	0.96	0.16	61,61,61,61	0
57	MG	1A	3441	1/1	0.96	0.08	53,53,53,53	0
57	MG	2A	3081	1/1	0.96	0.09	43,43,43,43	0
57	MG	1A	3221	1/1	0.96	0.10	38,38,38,38	0
57	MG	1A	3101	1/1	0.96	0.12	39,39,39,39	0
57	MG	1A	3862	1/1	0.96	0.05	56,56,56,56	0
57	MG	1A	3224	1/1	0.96	0.16	40,40,40,40	0
57	MG	2A	3087	1/1	0.96	0.12	52,52,52,52	0
57	MG	1A	3135	1/1	0.96	0.23	47,47,47,47	0
57	MG	2A	3715	1/1	0.96	0.19	63,63,63,63	0
57	MG	1A	3289	1/1	0.96	0.07	42,42,42,42	0
57	MG	2a	3138	1/1	0.96	0.08	75,75,75,75	0
57	MG	1A	3867	1/1	0.96	0.08	29,29,29,29	0
57	MG	1A	3541	1/1	0.96	0.08	36,36,36,36	0
57	MG	1A	3039	1/1	0.96	0.17	41,41,41,41	0
57	MG	1B	214	1/1	0.96	0.07	57,57,57,57	0
57	MG	1A	3370	1/1	0.96	0.07	33,33,33,33	0
57	MG	1A	3294	1/1	0.96	0.18	41,41,41,41	0
57	MG	2a	3147	1/1	0.96	0.11	77,77,77,77	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1A	3295	1/1	0.96	0.23	58,58,58,58	0
57	MG	2a	3149	1/1	0.96	0.08	75,75,75,75	0
57	MG	1A	3230	1/1	0.96	0.15	37,37,37,37	0
57	MG	1A	3175	1/1	0.96	0.21	41,41,41,41	0
57	MG	1A	3177	1/1	0.96	0.07	52,52,52,52	0
57	MG	1A	3299	1/1	0.96	0.34	44,44,44,44	0
57	MG	1a	1659	1/1	0.96	0.23	50,50,50,50	0
57	MG	1a	1815	1/1	0.96	0.07	66,66,66,66	0
57	MG	1A	3079	1/1	0.96	0.13	37,37,37,37	0
57	MG	1A	3887	1/1	0.96	0.07	63,63,63,63	0
57	MG	2a	3160	1/1	0.96	0.06	71,71,71,71	0
57	MG	1A	3888	1/1	0.96	0.05	57,57,57,57	0
57	MG	1A	3235	1/1	0.96	0.24	40,40,40,40	0
57	MG	1A	3065	1/1	0.96	0.13	43,43,43,43	0
57	MG	2A	3114	1/1	0.96	0.12	49,49,49,49	0
57	MG	1A	3462	1/1	0.96	0.12	57,57,57,57	0
57	MG	1D	302	1/1	0.96	0.25	34,34,34,34	0
57	MG	2A	3117	1/1	0.96	0.10	54,54,54,54	0
57	MG	1D	305	1/1	0.96	0.24	44,44,44,44	0
57	MG	1D	307	1/1	0.96	0.05	39,39,39,39	0
57	MG	1A	3766	1/1	0.96	0.05	38,38,38,38	0
57	MG	1A	3239	1/1	0.96	0.19	33,33,33,33	0
57	MG	1a	1828	1/1	0.96	0.08	51,51,51,51	0
57	MG	2A	3513	1/1	0.96	0.07	35,35,35,35	0
57	MG	1A	3895	1/1	0.96	0.10	31,31,31,31	0
57	MG	1a	1672	1/1	0.96	0.18	69,69,69,69	0
57	MG	1A	3381	1/1	0.96	0.10	48,48,48,48	0
57	MG	1A	3897	1/1	0.96	0.09	26,26,26,26	0
57	MG	1A	3649	1/1	0.96	0.10	53,53,53,53	0
57	MG	1A	3771	1/1	0.96	0.07	42,42,42,42	0
57	MG	1A	3308	1/1	0.96	0.21	33,33,33,33	0
57	MG	1A	3180	1/1	0.96	0.15	33,33,33,33	0
57	MG	1A	3774	1/1	0.96	0.11	42,42,42,42	0
57	MG	1a	1839	1/1	0.96	0.06	44,44,44,44	0
57	MG	1A	3904	1/1	0.96	0.20	43,43,43,43	0
57	MG	2D	310	1/1	0.96	0.14	66,66,66,66	0
57	MG	2E	302	1/1	0.96	0.08	60,60,60,60	0
57	MG	1A	3905	1/1	0.96	0.05	55,55,55,55	0
57	MG	2A	3329	1/1	0.96	0.07	33,33,33,33	0
57	MG	1A	3384	1/1	0.96	0.08	36,36,36,36	0
57	MG	2A	3331	1/1	0.96	0.10	32,32,32,32	0
57	MG	1A	3908	1/1	0.96	0.11	46,46,46,46	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2F	304	1/1	0.96	0.15	53,53,53,53	0
57	MG	1A	3385	1/1	0.96	0.08	32,32,32,32	0
57	MG	1A	3561	1/1	0.96	0.06	53,53,53,53	0
57	MG	2A	3534	1/1	0.96	0.07	57,57,57,57	0
57	MG	1A	3912	1/1	0.96	0.07	56,56,56,56	0
57	MG	1A	3562	1/1	0.96	0.21	62,62,62,62	0
57	MG	1A	3472	1/1	0.96	0.10	42,42,42,42	0
57	MG	1H	202	1/1	0.96	0.06	53,53,53,53	0
57	MG	2A	3149	1/1	0.96	0.18	51,51,51,51	0
57	MG	1A	3780	1/1	0.96	0.06	30,30,30,30	0
57	MG	1A	3989	1/1	0.97	0.11	54,54,54,54	0
57	MG	2A	3020	1/1	0.97	0.11	40,40,40,40	0
57	MG	1A	3220	1/1	0.97	0.16	36,36,36,36	0
57	MG	1A	3521	1/1	0.97	0.11	23,23,23,23	0
57	MG	1A	3304	1/1	0.97	0.22	56,56,56,56	0
57	MG	2A	3025	1/1	0.97	0.08	46,46,46,46	0
57	MG	1A	3994	1/1	0.97	0.11	37,37,37,37	0
57	MG	2A	3323	1/1	0.97	0.11	43,43,43,43	0
57	MG	1A	3995	1/1	0.97	0.05	61,61,61,61	0
57	MG	2A	3029	1/1	0.97	0.15	31,31,31,31	0
57	MG	1A	3258	1/1	0.97	0.07	53,53,53,53	0
57	MG	1A	3725	1/1	0.97	0.08	30,30,30,30	0
57	MG	1A	3726	1/1	0.97	0.05	35,35,35,35	0
57	MG	1A	3259	1/1	0.97	0.10	38,38,38,38	0
57	MG	1A	3647	1/1	0.97	0.24	49,49,49,49	0
57	MG	1A	3311	1/1	0.97	0.12	35,35,35,35	0
57	MG	1A	3650	1/1	0.97	0.28	48,48,48,48	0
57	MG	2A	3674	1/1	0.97	0.06	51,51,51,51	0
57	MG	1A	3906	1/1	0.97	0.04	54,54,54,54	0
57	MG	1A	3410	1/1	0.97	0.04	38,38,38,38	0
57	MG	2A	3040	1/1	0.97	0.06	23,23,23,23	0
57	MG	1A	3360	1/1	0.97	0.06	45,45,45,45	0
57	MG	2A	3338	1/1	0.97	0.06	30,30,30,30	0
57	MG	1A	3146	1/1	0.97	0.23	37,37,37,37	0
57	MG	1A	3910	1/1	0.97	0.09	57,57,57,57	0
57	MG	1A	3736	1/1	0.97	0.10	50,50,50,50	0
57	MG	1A	3737	1/1	0.97	0.15	44,44,44,44	0
57	MG	1A	3222	1/1	0.97	0.11	37,37,37,37	0
57	MG	1A	3739	1/1	0.97	0.07	61,61,61,61	0
57	MG	2A	3048	1/1	0.97	0.15	48,48,48,48	0
57	MG	2A	3687	1/1	0.97	0.05	67,67,67,67	0
57	MG	1A	3916	1/1	0.97	0.05	31,31,31,31	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2A	3195	1/1	0.97	0.09	51,51,51,51	0
57	MG	1A	3917	1/1	0.97	0.04	50,50,50,50	0
57	MG	1A	3415	1/1	0.97	0.06	48,48,48,48	0
57	MG	1A	3314	1/1	0.97	0.05	30,30,30,30	0
57	MG	13	101	1/1	0.97	0.07	35,35,35,35	0
57	MG	1A	3921	1/1	0.97	0.09	62,62,62,62	0
57	MG	1A	3264	1/1	0.97	0.19	45,45,45,45	0
57	MG	1A	3744	1/1	0.97	0.13	42,42,42,42	0
57	MG	1A	3013	1/1	0.97	0.06	19,19,19,19	0
57	MG	15	103	1/1	0.97	0.21	33,33,33,33	0
57	MG	1B	211	1/1	0.97	0.09	39,39,39,39	0
57	MG	1A	3125	1/1	0.97	0.05	31,31,31,31	0
57	MG	2A	3520	1/1	0.97	0.06	44,44,44,44	0
57	MG	2A	3359	1/1	0.97	0.12	34,34,34,34	0
57	MG	15	106	1/1	0.97	0.04	52,52,52,52	0
57	MG	1A	3225	1/1	0.97	0.22	36,36,36,36	0
57	MG	17	102	1/1	0.97	0.11	35,35,35,35	0
57	MG	2A	3067	1/1	0.97	0.06	22,22,22,22	0
57	MG	1A	3041	1/1	0.97	0.09	29,29,29,29	0
57	MG	1A	3173	1/1	0.97	0.12	37,37,37,37	0
57	MG	1a	1832	1/1	0.97	0.15	70,70,70,70	0
57	MG	1A	3229	1/1	0.97	0.12	40,40,40,40	0
57	MG	2A	3370	1/1	0.97	0.06	46,46,46,46	0
57	MG	2A	3371	1/1	0.97	0.20	64,64,64,64	0
57	MG	1A	3031	1/1	0.97	0.07	42,42,42,42	0
57	MG	1A	3231	1/1	0.97	0.12	30,30,30,30	0
57	MG	2A	3218	1/1	0.97	0.10	53,53,53,53	0
57	MG	2a	3084	1/1	0.97	0.33	59,59,59,59	0
57	MG	1A	3754	1/1	0.97	0.07	36,36,36,36	0
57	MG	2A	3717	1/1	0.97	0.16	48,48,48,48	0
57	MG	1A	3324	1/1	0.97	0.09	30,30,30,30	0
57	MG	2A	3077	1/1	0.97	0.09	52,52,52,52	0
57	MG	19	101	1/1	0.97	0.07	62,62,62,62	0
57	MG	1A	3021	1/1	0.97	0.08	36,36,36,36	0
57	MG	1A	3670	1/1	0.97	0.11	59,59,59,59	0
57	MG	1A	3605	1/1	0.97	0.26	35,35,35,35	0
57	MG	2A	3083	1/1	0.97	0.05	43,43,43,43	0
57	MG	1A	3277	1/1	0.97	0.18	49,49,49,49	0
57	MG	1A	3939	1/1	0.97	0.06	46,46,46,46	0
57	MG	1A	3111	1/1	0.97	0.14	36,36,36,36	0
57	MG	1A	3057	1/1	0.97	0.09	47,47,47,47	0
57	MG	1A	3033	1/1	0.97	0.10	46,46,46,46	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1a	1847	1/1	0.97	0.08	55,55,55,55	0
57	MG	1D	303	1/1	0.97	0.08	41,41,41,41	0
57	MG	1A	3491	1/1	0.97	0.05	32,32,32,32	0
57	MG	1A	3203	1/1	0.97	0.14	44,44,44,44	0
57	MG	1A	3848	1/1	0.97	0.04	41,41,41,41	0
57	MG	2A	3094	1/1	0.97	0.09	53,53,53,53	0
57	MG	2A	3095	1/1	0.97	0.12	46,46,46,46	0
57	MG	2A	3096	1/1	0.97	0.15	52,52,52,52	0
57	MG	1a	1613	1/1	0.97	0.09	29,29,29,29	0
57	MG	2A	3558	1/1	0.97	0.06	73,73,73,73	0
57	MG	1a	1853	1/1	0.97	0.08	52,52,52,52	0
57	MG	2A	3560	1/1	0.97	0.07	65,65,65,65	0
57	MG	1A	3007	1/1	0.97	0.07	33,33,33,33	0
57	MG	2a	3113	1/1	0.97	0.07	62,62,62,62	0
57	MG	2A	3102	1/1	0.97	0.05	33,33,33,33	0
57	MG	1a	1730	1/1	0.97	0.05	32,32,32,32	0
57	MG	1A	3181	1/1	0.97	0.17	37,37,37,37	0
57	MG	2A	3566	1/1	0.97	0.05	23,23,23,23	0
57	MG	1A	3438	1/1	0.97	0.07	15,15,15,15	0
57	MG	1A	3100	1/1	0.97	0.20	36,36,36,36	0
57	MG	1D	316	1/1	0.97	0.07	57,57,57,57	0
57	MG	1D	317	1/1	0.97	0.05	45,45,45,45	0
57	MG	2D	302	1/1	0.97	0.14	50,50,50,50	0
57	MG	2a	3123	1/1	0.97	0.12	57,57,57,57	0
57	MG	1E	301	1/1	0.97	0.07	36,36,36,36	0
57	MG	1E	302	1/1	0.97	0.15	37,37,37,37	0
57	MG	2A	3575	1/1	0.97	0.07	31,31,31,31	0
57	MG	1A	3770	1/1	0.97	0.11	28,28,28,28	0
57	MG	2A	3254	1/1	0.97	0.12	42,42,42,42	0
57	MG	2A	3255	1/1	0.97	0.10	40,40,40,40	0
57	MG	1E	305	1/1	0.97	0.12	50,50,50,50	0
57	MG	2E	301	1/1	0.97	0.18	42,42,42,42	0
57	MG	2A	3258	1/1	0.97	0.14	42,42,42,42	0
57	MG	1A	3015	1/1	0.97	0.10	32,32,32,32	0
57	MG	1A	3954	1/1	0.97	0.09	45,45,45,45	0
57	MG	2E	305	1/1	0.97	0.05	54,54,54,54	0
57	MG	2A	3586	1/1	0.97	0.05	57,57,57,57	0
57	MG	1A	3210	1/1	0.97	0.12	33,33,33,33	0
57	MG	1F	301	1/1	0.97	0.10	34,34,34,34	0
57	MG	1F	305	1/1	0.97	0.16	36,36,36,36	0
57	MG	2F	305	1/1	0.97	0.28	50,50,50,50	0
57	MG	1A	3244	1/1	0.97	0.10	44,44,44,44	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2A	3265	1/1	0.97	0.03	23,23,23,23	0
57	MG	2A	3594	1/1	0.97	0.06	59,59,59,59	0
57	MG	2A	3119	1/1	0.97	0.09	36,36,36,36	0
57	MG	2a	3146	1/1	0.97	0.14	52,52,52,52	0
57	MG	1A	3337	1/1	0.97	0.10	15,15,15,15	0
57	MG	1A	3161	1/1	0.97	0.17	29,29,29,29	0
57	MG	2Q	201	1/1	0.97	0.08	52,52,52,52	0
57	MG	1A	3960	1/1	0.97	0.07	30,30,30,30	0
57	MG	2A	3123	1/1	0.97	0.18	43,43,43,43	0
57	MG	1A	3859	1/1	0.97	0.08	40,40,40,40	0
57	MG	1A	3692	1/1	0.97	0.23	41,41,41,41	0
57	MG	1F	317	1/1	0.97	0.06	51,51,51,51	0
57	MG	1A	3293	1/1	0.97	0.17	39,39,39,39	0
57	MG	1A	3016	1/1	0.97	0.23	34,34,34,34	0
57	MG	1G	203	1/1	0.97	0.12	44,44,44,44	0
57	MG	1A	3565	1/1	0.97	0.08	22,22,22,22	0
57	MG	1A	3566	1/1	0.97	0.07	48,48,48,48	0
57	MG	2A	3438	1/1	0.97	0.10	46,46,46,46	0
57	MG	1A	3213	1/1	0.97	0.15	34,34,34,34	0
57	MG	1N	202	1/1	0.97	0.17	45,45,45,45	0
57	MG	1A	3394	1/1	0.97	0.10	27,27,27,27	0
57	MG	1A	3029	1/1	0.97	0.07	41,41,41,41	0
57	MG	1A	3702	1/1	0.97	0.06	48,48,48,48	0
57	MG	1m	201	1/1	0.97	0.07	67,67,67,67	0
57	MG	1A	3509	1/1	0.97	0.07	21,21,21,21	0
57	MG	1a	1650	1/1	0.97	0.14	49,49,49,49	0
57	MG	1Q	202	1/1	0.97	0.07	34,34,34,34	0
57	MG	1A	3215	1/1	0.97	0.16	38,38,38,38	0
57	MG	1A	3397	1/1	0.97	0.06	42,42,42,42	0
57	MG	1a	1654	1/1	0.97	0.07	41,41,41,41	0
57	MG	27	101	1/1	0.97	0.18	46,46,46,46	0
57	MG	1A	3707	1/1	0.97	0.04	38,38,38,38	0
57	MG	1A	3216	1/1	0.97	0.07	52,52,52,52	0
57	MG	2A	3627	1/1	0.97	0.08	37,37,37,37	0
57	MG	1R	202	1/1	0.97	0.11	39,39,39,39	0
57	MG	2A	3294	1/1	0.97	0.07	40,40,40,40	0
57	MG	1A	3574	1/1	0.97	0.11	36,36,36,36	0
57	MG	2A	3633	1/1	0.97	0.09	56,56,56,56	0
57	MG	1A	3877	1/1	0.97	0.12	30,30,30,30	0
57	MG	1A	3878	1/1	0.97	0.07	50,50,50,50	0
57	MG	1A	3217	1/1	0.97	0.13	36,36,36,36	0
57	MG	1A	3515	1/1	0.97	0.10	22,22,22,22	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1A	3348	1/1	0.97	0.09	26,26,26,26	0
57	MG	2k	201	1/1	0.97	0.10	57,57,57,57	0
57	MG	1A	3164	1/1	0.97	0.08	47,47,47,47	0
57	MG	2A	3302	1/1	0.97	0.25	46,46,46,46	0
57	MG	2A	3008	1/1	0.97	0.12	41,41,41,41	0
57	MG	2A	3009	1/1	0.97	0.06	47,47,47,47	0
57	MG	1A	3714	1/1	0.97	0.08	29,29,29,29	0
57	MG	2A	3306	1/1	0.97	0.10	65,65,65,65	0
57	MG	1A	3579	1/1	0.97	0.08	40,40,40,40	0
57	MG	1A	3580	1/1	0.97	0.10	60,60,60,60	0
57	MG	2A	3309	1/1	0.97	0.06	39,39,39,39	0
57	MG	1A	3718	1/1	0.97	0.06	72,72,72,72	0
57	MG	2A	3653	1/1	0.97	0.07	43,43,43,43	0
57	MG	2a	3020	1/1	0.97	0.07	49,49,49,49	0
57	MG	1A	3104	1/1	0.97	0.18	41,41,41,41	0
60	ZN	2Y	202	1/1	0.97	0.06	93,93,93,93	0
57	MG	1U	201	1/1	0.97	0.15	38,38,38,38	0
60	ZN	2n	501	1/1	0.97	0.05	95,95,95,95	0
57	MG	2A	3079	1/1	0.98	0.11	44,44,44,44	0
57	MG	1A	3176	1/1	0.98	0.22	38,38,38,38	0
57	MG	1A	3019	1/1	0.98	0.19	29,29,29,29	0
57	MG	1A	3836	1/1	0.98	0.05	46,46,46,46	0
57	MG	1A	3260	1/1	0.98	0.26	34,34,34,34	0
57	MG	1A	3261	1/1	0.98	0.31	35,35,35,35	0
57	MG	2A	3225	1/1	0.98	0.13	41,41,41,41	0
57	MG	1A	3090	1/1	0.98	0.05	45,45,45,45	0
57	MG	1A	3113	1/1	0.98	0.08	43,43,43,43	0
57	MG	1A	3749	1/1	0.98	0.08	44,44,44,44	0
57	MG	1A	3114	1/1	0.98	0.13	38,38,38,38	0
57	MG	1D	304	1/1	0.98	0.05	40,40,40,40	0
57	MG	1A	3664	1/1	0.98	0.08	46,46,46,46	0
57	MG	1D	306	1/1	0.98	0.07	22,22,22,22	0
57	MG	1A	3265	1/1	0.98	0.07	42,42,42,42	0
57	MG	1D	308	1/1	0.98	0.19	38,38,38,38	0
57	MG	1A	3116	1/1	0.98	0.09	23,23,23,23	0
57	MG	1D	310	1/1	0.98	0.16	35,35,35,35	0
57	MG	1A	3025	1/1	0.98	0.16	40,40,40,40	0
57	MG	1D	312	1/1	0.98	0.10	54,54,54,54	0
57	MG	1A	3060	1/1	0.98	0.04	34,34,34,34	0
57	MG	1A	3949	1/1	0.98	0.09	45,45,45,45	0
57	MG	2A	3100	1/1	0.98	0.11	71,71,71,71	0
57	MG	1A	3524	1/1	0.98	0.06	31,31,31,31	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1a	1734	1/1	0.98	0.08	45,45,45,45	0
57	MG	1A	3951	1/1	0.98	0.17	43,43,43,43	0
57	MG	1a	1614	1/1	0.98	0.07	54,54,54,54	0
57	MG	1A	3149	1/1	0.98	0.21	44,44,44,44	0
57	MG	1A	3451	1/1	0.98	0.05	26,26,26,26	0
57	MG	1A	3527	1/1	0.98	0.05	30,30,30,30	0
57	MG	1E	303	1/1	0.98	0.11	35,35,35,35	0
57	MG	1A	3003	1/1	0.98	0.04	23,23,23,23	0
57	MG	1A	3271	1/1	0.98	0.06	39,39,39,39	0
57	MG	1A	3957	1/1	0.98	0.09	54,54,54,54	0
57	MG	1A	3050	1/1	0.98	0.14	31,31,31,31	0
57	MG	1A	3273	1/1	0.98	0.06	32,32,32,32	0
57	MG	2A	3555	1/1	0.98	0.09	31,31,31,31	0
57	MG	1A	3678	1/1	0.98	0.11	29,29,29,29	0
57	MG	1F	302	1/1	0.98	0.11	37,37,37,37	0
57	MG	2A	3408	1/1	0.98	0.04	68,68,68,68	0
57	MG	1a	1627	1/1	0.98	0.06	49,49,49,49	0
57	MG	1A	3152	1/1	0.98	0.17	34,34,34,34	0
57	MG	1F	306	1/1	0.98	0.17	39,39,39,39	0
57	MG	1F	307	1/1	0.98	0.13	37,37,37,37	0
57	MG	1F	308	1/1	0.98	0.16	35,35,35,35	0
57	MG	1F	309	1/1	0.98	0.11	34,34,34,34	0
57	MG	2A	3565	1/1	0.98	0.05	63,63,63,63	0
57	MG	1F	310	1/1	0.98	0.08	30,30,30,30	0
57	MG	1A	3077	1/1	0.98	0.22	40,40,40,40	0
57	MG	1A	3682	1/1	0.98	0.04	43,43,43,43	0
57	MG	2A	3570	1/1	0.98	0.07	56,56,56,56	0
57	MG	1A	3228	1/1	0.98	0.05	42,42,42,42	0
57	MG	1A	3098	1/1	0.98	0.25	35,35,35,35	0
57	MG	1A	3393	1/1	0.98	0.09	26,26,26,26	0
57	MG	1A	3005	1/1	0.98	0.08	23,23,23,23	0
57	MG	1A	3052	1/1	0.98	0.26	42,42,42,42	0
57	MG	2A	3131	1/1	0.98	0.10	30,30,30,30	0
57	MG	1A	3688	1/1	0.98	0.04	53,53,53,53	0
57	MG	1A	3017	1/1	0.98	0.21	34,34,34,34	0
57	MG	1o	103	1/1	0.98	0.04	61,61,61,61	0
57	MG	1A	3540	1/1	0.98	0.05	33,33,33,33	0
57	MG	1A	3869	1/1	0.98	0.07	41,41,41,41	0
57	MG	2B	217	1/1	0.98	0.07	68,68,68,68	0
57	MG	2A	3584	1/1	0.98	0.04	58,58,58,58	0
57	MG	1A	3043	1/1	0.98	0.17	17,17,17,17	0
57	MG	1A	3466	1/1	0.98	0.05	47,47,47,47	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1A	3067	1/1	0.98	0.29	33,33,33,33	0
57	MG	1A	3694	1/1	0.98	0.14	50,50,50,50	0
57	MG	2A	3141	1/1	0.98	0.07	37,37,37,37	0
57	MG	2A	3142	1/1	0.98	0.18	49,49,49,49	0
57	MG	2D	306	1/1	0.98	0.04	37,37,37,37	0
57	MG	2A	3592	1/1	0.98	0.07	34,34,34,34	0
57	MG	1A	3399	1/1	0.98	0.10	26,26,26,26	0
57	MG	1P	201	1/1	0.98	0.28	37,37,37,37	0
57	MG	1A	3340	1/1	0.98	0.08	26,26,26,26	0
57	MG	1A	3195	1/1	0.98	0.18	39,39,39,39	0
57	MG	2A	3147	1/1	0.98	0.06	40,40,40,40	0
57	MG	1Q	201	1/1	0.98	0.07	36,36,36,36	0
57	MG	1A	3236	1/1	0.98	0.18	34,34,34,34	0
57	MG	2A	3601	1/1	0.98	0.05	42,42,42,42	0
57	MG	1A	3237	1/1	0.98	0.06	35,35,35,35	0
57	MG	1A	3404	1/1	0.98	0.04	24,24,24,24	0
57	MG	1A	3128	1/1	0.98	0.24	34,34,34,34	0
57	MG	1A	3129	1/1	0.98	0.26	39,39,39,39	0
57	MG	2A	3015	1/1	0.98	0.22	40,40,40,40	0
57	MG	1A	3068	1/1	0.98	0.15	33,33,33,33	0
57	MG	1A	3291	1/1	0.98	0.15	44,44,44,44	0
57	MG	1A	3706	1/1	0.98	0.10	39,39,39,39	0
57	MG	2A	3158	1/1	0.98	0.15	46,46,46,46	0
57	MG	1A	3292	1/1	0.98	0.05	49,49,49,49	0
57	MG	1A	3036	1/1	0.98	0.04	32,32,32,32	0
57	MG	2A	3021	1/1	0.98	0.04	35,35,35,35	0
57	MG	1A	3991	1/1	0.98	0.04	57,57,57,57	0
57	MG	1A	3201	1/1	0.98	0.19	41,41,41,41	0
57	MG	1A	3557	1/1	0.98	0.10	42,42,42,42	0
57	MG	1A	3412	1/1	0.98	0.04	27,27,27,27	0
57	MG	1A	3202	1/1	0.98	0.14	41,41,41,41	0
57	MG	1A	3106	1/1	0.98	0.20	33,33,33,33	0
57	MG	2A	3028	1/1	0.98	0.05	44,44,44,44	0
57	MG	1A	3134	1/1	0.98	0.06	49,49,49,49	0
57	MG	1A	3998	1/1	0.98	0.05	54,54,54,54	0
57	MG	1A	3355	1/1	0.98	0.06	25,25,25,25	0
57	MG	2A	3625	1/1	0.98	0.03	44,44,44,44	0
57	MG	2A	3464	1/1	0.98	0.04	53,53,53,53	0
57	MG	2A	3465	1/1	0.98	0.04	54,54,54,54	0
57	MG	1U	202	1/1	0.98	0.24	40,40,40,40	0
57	MG	2W	201	1/1	0.98	0.31	48,48,48,48	0
57	MG	1A	3045	1/1	0.98	0.04	23,23,23,23	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1A	3717	1/1	0.98	0.05	52,52,52,52	0
57	MG	2a	3152	1/1	0.98	0.06	59,59,59,59	0
57	MG	2A	3316	1/1	0.98	0.12	23,23,23,23	0
57	MG	1A	3168	1/1	0.98	0.14	28,28,28,28	0
57	MG	2A	3319	1/1	0.98	0.05	39,39,39,39	0
57	MG	2A	3036	1/1	0.98	0.14	50,50,50,50	0
57	MG	1A	3804	1/1	0.98	0.04	38,38,38,38	0
57	MG	1V	202	1/1	0.98	0.30	35,35,35,35	0
57	MG	1a	1804	1/1	0.98	0.07	60,60,60,60	0
57	MG	1A	3805	1/1	0.98	0.05	47,47,47,47	0
57	MG	1A	3806	1/1	0.98	0.10	50,50,50,50	0
57	MG	2A	3642	1/1	0.98	0.04	22,22,22,22	0
57	MG	1a	1807	1/1	0.98	0.08	62,62,62,62	0
57	MG	1A	4006	1/1	0.98	0.07	35,35,35,35	0
57	MG	1A	4007	1/1	0.98	0.04	48,48,48,48	0
57	MG	1A	3358	1/1	0.98	0.10	32,32,32,32	0
57	MG	1A	3359	1/1	0.98	0.04	22,22,22,22	0
57	MG	1A	3136	1/1	0.98	0.05	37,37,37,37	0
57	MG	1A	3209	1/1	0.98	0.04	22,22,22,22	0
57	MG	2A	3049	1/1	0.98	0.04	40,40,40,40	0
57	MG	1A	3723	1/1	0.98	0.07	26,26,26,26	0
57	MG	1A	3812	1/1	0.98	0.20	39,39,39,39	0
57	MG	1A	3362	1/1	0.98	0.05	14,14,14,14	0
57	MG	1A	3170	1/1	0.98	0.14	32,32,32,32	0
57	MG	1A	3498	1/1	0.98	0.06	46,46,46,46	0
57	MG	1A	3727	1/1	0.98	0.07	55,55,55,55	0
57	MG	1A	3086	1/1	0.98	0.10	41,41,41,41	0
57	MG	1A	3920	1/1	0.98	0.11	47,47,47,47	0
57	MG	1A	3729	1/1	0.98	0.13	36,36,36,36	0
57	MG	1A	3365	1/1	0.98	0.06	17,17,17,17	0
57	MG	2A	3200	1/1	0.98	0.11	48,48,48,48	0
57	MG	2A	3665	1/1	0.98	0.04	51,51,51,51	0
57	MG	1B	209	1/1	0.98	0.06	41,41,41,41	0
57	MG	1A	3306	1/1	0.98	0.13	38,38,38,38	0
57	MG	1I	103	1/1	0.98	0.06	52,52,52,52	0
57	MG	2a	3022	1/1	0.98	0.10	58,58,58,58	0
57	MG	2A	3063	1/1	0.98	0.07	48,48,48,48	0
57	MG	1A	3429	1/1	0.98	0.07	44,44,44,44	0
57	MG	1A	3648	1/1	0.98	0.06	54,54,54,54	0
57	MG	1A	3139	1/1	0.98	0.06	33,33,33,33	0
57	MG	1A	3140	1/1	0.98	0.05	34,34,34,34	0
57	MG	1B	215	1/1	0.98	0.12	49,49,49,49	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1A	3651	1/1	0.98	0.07	30,30,30,30	0
57	MG	2A	3071	1/1	0.98	0.06	50,50,50,50	0
57	MG	2A	3509	1/1	0.98	0.07	54,54,54,54	0
57	MG	1A	3432	1/1	0.98	0.04	30,30,30,30	0
57	MG	1A	3310	1/1	0.98	0.07	14,14,14,14	0
57	MG	1A	3255	1/1	0.98	0.25	37,37,37,37	0
57	MG	2A	3360	1/1	0.98	0.10	31,31,31,31	0
57	MG	1A	3256	1/1	0.98	0.06	27,27,27,27	0
60	ZN	14	501	1/1	0.98	0.07	105,105,105,105	0
60	ZN	15	108	1/1	0.98	0.03	49,49,49,49	0
57	MG	1A	3037	1/1	0.98	0.07	48,48,48,48	0
57	MG	1B	223	1/1	0.98	0.12	45,45,45,45	0
60	ZN	26	501	1/1	0.98	0.04	62,62,62,62	0
60	ZN	29	102	1/1	0.98	0.04	71,71,71,71	0
57	MG	17	101	1/1	0.98	0.05	45,45,45,45	0
61	SF4	1d	306	8/8	0.98	0.06	63,67,73,74	0
61	SF4	2d	501	8/8	0.98	0.05	68,78,79,82	0
57	MG	1A	3922	1/1	0.99	0.04	62,62,62,62	0
57	MG	1A	3137	1/1	0.99	0.03	23,23,23,23	0
57	MG	1N	204	1/1	0.99	0.03	51,51,51,51	0
57	MG	2A	3011	1/1	0.99	0.06	33,33,33,33	0
57	MG	1A	3024	1/1	0.99	0.03	17,17,17,17	0
57	MG	2A	3388	1/1	0.99	0.08	41,41,41,41	0
57	MG	2A	3643	1/1	0.99	0.04	49,49,49,49	0
57	MG	2A	3013	1/1	0.99	0.05	22,22,22,22	0
57	MG	2A	3645	1/1	0.99	0.05	34,34,34,34	0
57	MG	1A	3743	1/1	0.99	0.03	25,25,25,25	0
57	MG	1A	3492	1/1	0.99	0.06	21,21,21,21	0
57	MG	2A	3648	1/1	0.99	0.04	60,60,60,60	0
57	MG	2A	3392	1/1	0.99	0.04	31,31,31,31	0
57	MG	2A	3393	1/1	0.99	0.06	38,38,38,38	0
57	MG	1A	3828	1/1	0.99	0.04	41,41,41,41	0
57	MG	1A	3207	1/1	0.99	0.38	32,32,32,32	0
57	MG	1A	3107	1/1	0.99	0.18	30,30,30,30	0
57	MG	1A	3338	1/1	0.99	0.08	40,40,40,40	0
57	MG	1A	3091	1/1	0.99	0.12	39,39,39,39	0
57	MG	1A	3092	1/1	0.99	0.05	14,14,14,14	0
57	MG	1A	3879	1/1	0.99	0.04	34,34,34,34	0
57	MG	1A	3880	1/1	0.99	0.04	45,45,45,45	0
57	MG	1A	3881	1/1	0.99	0.08	45,45,45,45	0
57	MG	2A	3567	1/1	0.99	0.06	56,56,56,56	0
57	MG	1A	3154	1/1	0.99	0.16	37,37,37,37	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1A	3883	1/1	0.99	0.04	51,51,51,51	0
57	MG	1A	3884	1/1	0.99	0.06	31,31,31,31	0
57	MG	2A	3101	1/1	0.99	0.04	51,51,51,51	0
57	MG	1a	1856	1/1	0.99	0.05	61,61,61,61	0
57	MG	1A	3885	1/1	0.99	0.05	42,42,42,42	0
57	MG	2a	3143	1/1	0.99	0.09	53,53,53,53	0
57	MG	2A	3328	1/1	0.99	0.04	37,37,37,37	0
57	MG	1A	3018	1/1	0.99	0.14	29,29,29,29	0
57	MG	1A	3469	1/1	0.99	0.07	26,26,26,26	0
57	MG	1A	3026	1/1	0.99	0.17	34,34,34,34	0
57	MG	2A	3578	1/1	0.99	0.03	52,52,52,52	0
57	MG	2A	3579	1/1	0.99	0.02	46,46,46,46	0
57	MG	2E	306	1/1	0.99	0.10	33,33,33,33	0
57	MG	2a	3054	1/1	0.99	0.08	49,49,49,49	0
57	MG	1A	3675	1/1	0.99	0.04	62,62,62,62	0
57	MG	1A	3198	1/1	0.99	0.18	41,41,41,41	0
57	MG	2A	3257	1/1	0.99	0.11	23,23,23,23	0
57	MG	1A	3132	1/1	0.99	0.21	32,32,32,32	0
57	MG	1A	3443	1/1	0.99	0.03	24,24,24,24	0
57	MG	1A	3679	1/1	0.99	0.04	38,38,38,38	0
57	MG	2a	3158	1/1	0.99	0.03	55,55,55,55	0
57	MG	1A	3894	1/1	0.99	0.03	65,65,65,65	0
57	MG	2A	3587	1/1	0.99	0.03	49,49,49,49	0
57	MG	1A	3642	1/1	0.99	0.07	37,37,37,37	0
57	MG	1A	3006	1/1	0.99	0.03	23,23,23,23	0
57	MG	1A	3475	1/1	0.99	0.08	44,44,44,44	0
57	MG	1A	3302	1/1	0.99	0.15	30,30,30,30	0
57	MG	1a	1803	1/1	0.99	0.03	69,69,69,69	0
57	MG	1A	3249	1/1	0.99	0.12	29,29,29,29	0
57	MG	1A	3284	1/1	0.99	0.11	23,23,23,23	0
57	MG	1A	3901	1/1	0.99	0.04	15,15,15,15	0
57	MG	2A	3596	1/1	0.99	0.03	51,51,51,51	0
57	MG	1a	1742	1/1	0.99	0.04	37,37,37,37	0
57	MG	1A	3765	1/1	0.99	0.05	43,43,43,43	0
57	MG	1a	1744	1/1	0.99	0.05	42,42,42,42	0
57	MG	1A	3510	1/1	0.99	0.07	21,21,21,21	0
57	MG	1a	1622	1/1	0.99	0.05	49,49,49,49	0
57	MG	1A	3350	1/1	0.99	0.04	52,52,52,52	0
57	MG	1F	303	1/1	0.99	0.07	32,32,32,32	0
57	MG	1a	1814	1/1	0.99	0.07	73,73,73,73	0
57	MG	2A	3518	1/1	0.99	0.06	30,30,30,30	0
57	MG	1F	304	1/1	0.99	0.16	33,33,33,33	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1A	3305	1/1	0.99	0.08	22,22,22,22	0
57	MG	1A	3450	1/1	0.99	0.07	26,26,26,26	0
57	MG	2A	3609	1/1	0.99	0.04	44,44,44,44	0
57	MG	1A	3961	1/1	0.99	0.04	37,37,37,37	0
57	MG	1A	3285	1/1	0.99	0.07	17,17,17,17	0
57	MG	1A	3617	1/1	0.99	0.09	32,32,32,32	0
57	MG	1A	3172	1/1	0.99	0.15	33,33,33,33	0
57	MG	1A	3028	1/1	0.99	0.22	30,30,30,30	0
57	MG	1a	1823	1/1	0.99	0.04	74,74,74,74	0
57	MG	1A	3309	1/1	0.99	0.11	34,34,34,34	0
57	MG	1A	3428	1/1	0.99	0.03	14,14,14,14	0
57	MG	2A	3066	1/1	0.99	0.04	44,44,44,44	0
57	MG	1A	3817	1/1	0.99	0.07	29,29,29,29	0
57	MG	1a	1760	1/1	0.99	0.03	55,55,55,55	0
57	MG	2A	3369	1/1	0.99	0.04	33,33,33,33	0
57	MG	1A	3914	1/1	0.99	0.03	49,49,49,49	0
57	MG	1A	3089	1/1	0.99	0.21	33,33,33,33	0
57	MG	2A	3372	1/1	0.99	0.07	42,42,42,42	0
57	MG	1A	3520	1/1	0.99	0.04	33,33,33,33	0
57	MG	1A	3864	1/1	0.99	0.04	34,34,34,34	0
57	MG	1A	3457	1/1	0.99	0.08	52,52,52,52	0
57	MG	2A	3628	1/1	0.99	0.03	38,38,38,38	0
60	ZN	1Y	202	1/1	0.99	0.04	60,60,60,60	0
57	MG	1B	216	1/1	0.99	0.06	44,44,44,44	0
57	MG	1A	3699	1/1	0.99	0.02	40,40,40,40	0
60	ZN	19	102	1/1	0.99	0.05	44,44,44,44	0
60	ZN	1n	104	1/1	0.99	0.03	68,68,68,68	0
57	MG	2a	3106	1/1	0.99	0.06	67,67,67,67	0
57	MG	1A	3115	1/1	0.99	0.21	36,36,36,36	0
60	ZN	25	103	1/1	0.99	0.04	57,57,57,57	0
57	MG	2A	3632	1/1	0.99	0.06	48,48,48,48	0
57	MG	2A	3004	1/1	0.99	0.02	33,33,33,33	0
57	MG	1A	3523	1/1	0.99	0.05	44,44,44,44	0
57	MG	1N	201	1/1	0.99	0.05	41,41,41,41	0
57	MG	2A	3007	1/1	0.99	0.04	42,42,42,42	0
57	MG	2A	3317	1/1	1.00	0.05	59,59,59,59	0
60	ZN	16	501	1/1	1.00	0.05	44,44,44,44	0
57	MG	1A	3468	1/1	1.00	0.05	52,52,52,52	0
57	MG	2A	3503	1/1	1.00	0.04	37,37,37,37	0
57	MG	1B	226	1/1	1.00	0.01	47,47,47,47	0
57	MG	1A	3833	1/1	1.00	0.04	22,22,22,22	0

6.5 Other polymers [i](#)

There are no such residues in this entry.