



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 20, 2026 – 05:32 AM UTC

PDB ID : 8FC3 / pdb_00008fc3
Title : Crystal structure of the Thermus thermophilus 70S ribosome in complex with protein Y, hygromycin A, and telithromycin at 2.60Å resolution
Authors : Chen, C.-W.; Syroegin, E.A.; Svetlov, M.S.; Polikanov, Y.S.
Deposited on : 2022-12-01
Resolution : 2.60 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

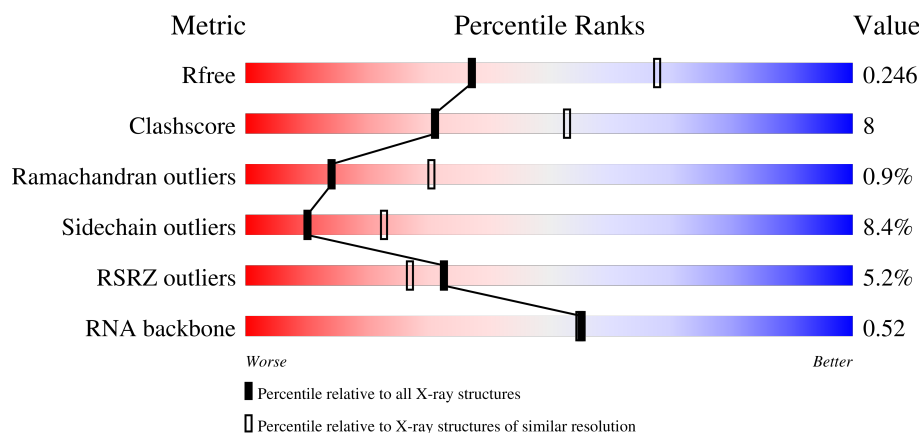
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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.



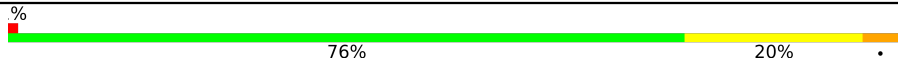
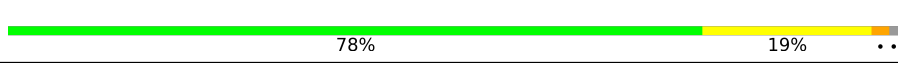
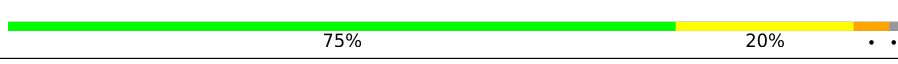
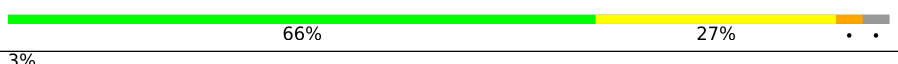
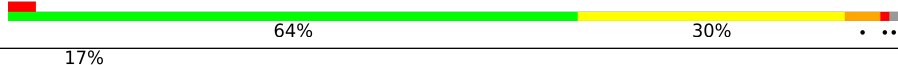
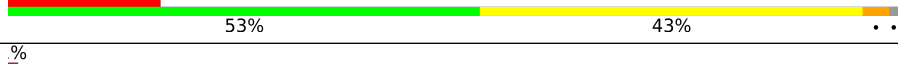
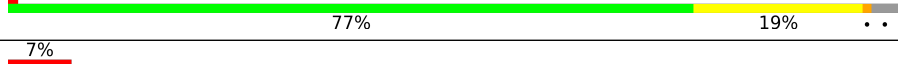
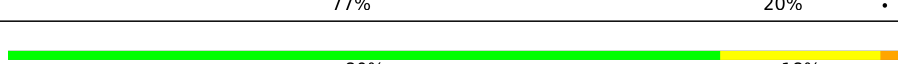
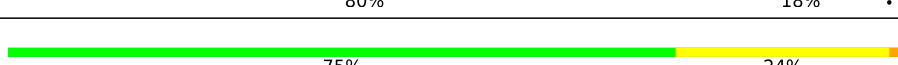
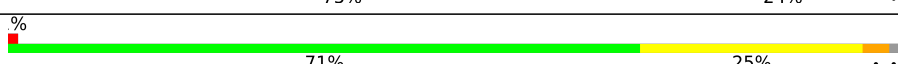
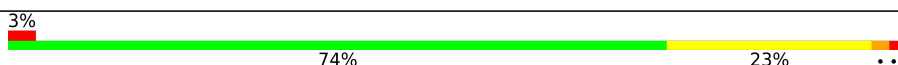
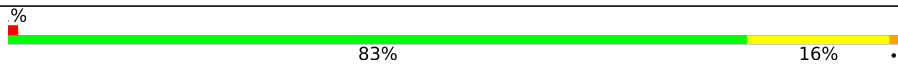
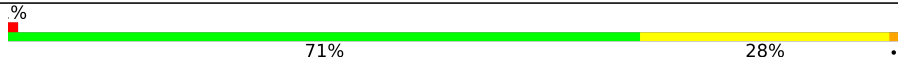
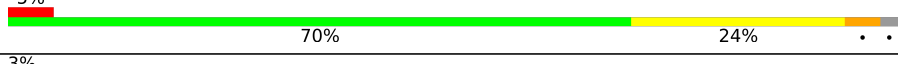
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	4008 (2.60-2.60)
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (2.60-2.60)
RNA backbone	3983	1014 (2.84-2.36)

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	5% 67% 26% 5%
1	2A	2915	6% 60% 31% 7%
2	1B	121	% 68% 28% ..
2	2B	121	% 61% 33% 5%

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

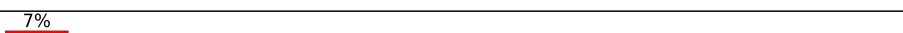
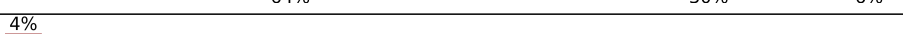
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Mol	Chain	Length	Quality of chain
15	2T	146	
16	1U	118	
16	2U	118	
17	1V	101	
17	2V	101	
18	1W	113	
18	2W	113	
19	1X	96	
19	2X	96	
20	1Y	110	
20	2Y	110	
21	1Z	206	
21	2Z	206	
22	10	85	
22	20	85	
23	11	98	
23	21	98	
24	12	72	
24	22	72	
25	13	60	
25	23	60	
26	14	71	
26	24	71	
27	15	60	
27	25	60	

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

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

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Mol	Chain	Length	Quality of chain
53	1y	113	
53	2y	113	

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
54	MG	1A	3591	-	-	-	X
54	MG	2A	3290	-	-	-	X

2 Entry composition

There are 61 unique types of molecules in this entry. The entry contains 297096 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	77	Total	C	N	O	S	0	0	0
			608	375	129	103	1			
22	20	77	Total	C	N	O	S	0	0	0
			608	375	129	103	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 MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
54	1A	1017	Total	Mg	0	0
			1017	1017		
54	1B	29	Total	Mg	0	0
			29	29		
54	1D	17	Total	Mg	0	0
			17	17		
54	1E	9	Total	Mg	0	0
			9	9		
54	1F	20	Total	Mg	0	0
			20	20		
54	1G	4	Total	Mg	0	0
			4	4		
54	1H	2	Total	Mg	0	0
			2	2		
54	1N	4	Total	Mg	0	0
			4	4		
54	1O	1	Total	Mg	0	0
			1	1		
54	1P	5	Total	Mg	0	0
			5	5		
54	1Q	5	Total	Mg	0	0
			5	5		
54	1R	6	Total	Mg	0	0
			6	6		
54	1T	4	Total	Mg	0	0
			4	4		
54	1U	9	Total	Mg	0	0
			9	9		
54	1V	7	Total	Mg	0	0
			7	7		
54	1W	4	Total	Mg	0	0
			4	4		
54	1X	2	Total	Mg	0	0
			2	2		
54	1Y	1	Total	Mg	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
54	1Z	1	Total 1	Mg 1	0	0
54	10	7	Total 7	Mg 7	0	0
54	11	5	Total 5	Mg 5	0	0
54	13	3	Total 3	Mg 3	0	0
54	14	1	Total 1	Mg 1	0	0
54	15	8	Total 8	Mg 8	0	0
54	17	6	Total 6	Mg 6	0	0
54	18	2	Total 2	Mg 2	0	0
54	19	2	Total 2	Mg 2	0	0
54	1a	276	Total 276	Mg 276	0	0
54	1b	1	Total 1	Mg 1	0	0
54	1d	6	Total 6	Mg 6	0	0
54	1e	2	Total 2	Mg 2	0	0
54	1f	2	Total 2	Mg 2	0	0
54	1g	3	Total 3	Mg 3	0	0
54	1h	2	Total 2	Mg 2	0	0
54	1i	1	Total 1	Mg 1	0	0
54	1k	1	Total 1	Mg 1	0	0
54	1l	2	Total 2	Mg 2	0	0
54	1m	1	Total 1	Mg 1	0	0
54	1n	2	Total 2	Mg 2	0	0

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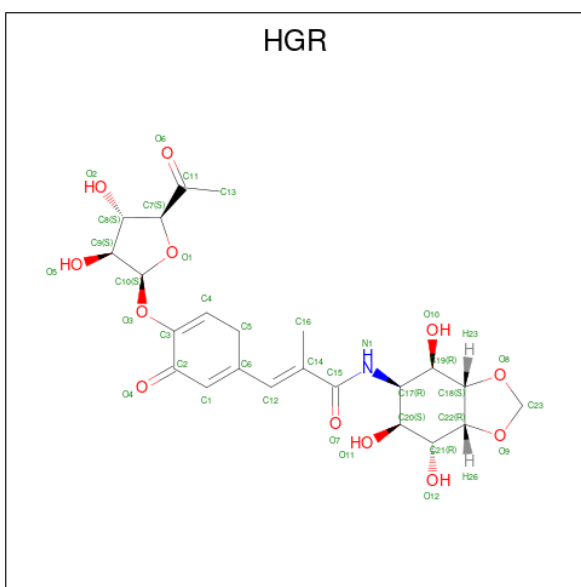
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
54	1o	1	Total 1	Mg 1	0	0
54	1t	1	Total 1	Mg 1	0	0
54	1y	4	Total 4	Mg 4	0	0
54	2A	737	Total 737	Mg 737	0	0
54	2B	19	Total 19	Mg 19	0	0
54	2D	11	Total 11	Mg 11	0	0
54	2E	6	Total 6	Mg 6	0	0
54	2F	4	Total 4	Mg 4	0	0
54	2G	3	Total 3	Mg 3	0	0
54	2I	1	Total 1	Mg 1	0	0
54	2N	1	Total 1	Mg 1	0	0
54	2O	2	Total 2	Mg 2	0	0
54	2P	4	Total 4	Mg 4	0	0
54	2Q	4	Total 4	Mg 4	0	0
54	2R	2	Total 2	Mg 2	0	0
54	2T	4	Total 4	Mg 4	0	0
54	2V	3	Total 3	Mg 3	0	0
54	2W	3	Total 3	Mg 3	0	0
54	2X	1	Total 1	Mg 1	0	0
54	20	2	Total 2	Mg 2	0	0
54	21	2	Total 2	Mg 2	0	0

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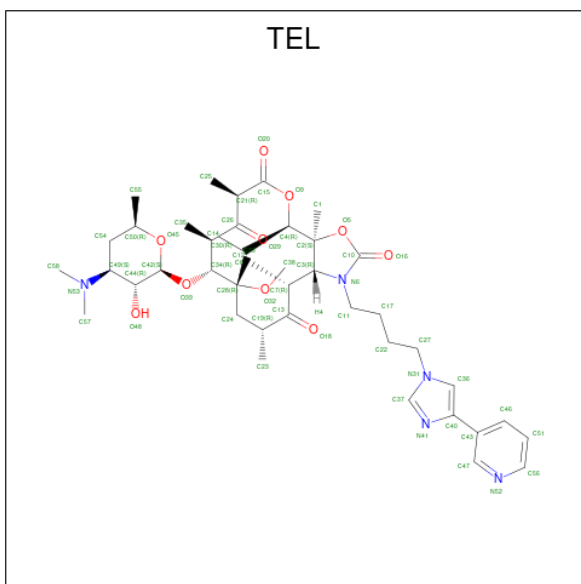
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
54	23	2	Total 2	Mg 2	0	0
54	25	4	Total 4	Mg 4	0	0
54	27	1	Total 1	Mg 1	0	0
54	28	2	Total 2	Mg 2	0	0
54	2a	184	Total 184	Mg 184	0	0
54	2e	2	Total 2	Mg 2	0	0
54	2f	1	Total 1	Mg 1	0	0
54	2j	1	Total 1	Mg 1	0	0
54	2k	1	Total 1	Mg 1	0	0
54	2l	1	Total 1	Mg 1	0	0
54	2n	1	Total 1	Mg 1	0	0
54	2t	1	Total 1	Mg 1	0	0
54	2y	1	Total 1	Mg 1	0	0

- Molecule 55 is Hygromycin A (CCD ID: HGR) (formula: $C_{23}H_{29}NO_{12}$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
55	1A	1	Total 36	C 23	N 1	O 12	0	0
55	2A	1	Total 36	C 23	N 1	O 12	0	0

- Molecule 56 is TELITHROMYCIN (CCD ID: TEL) (formula: $\text{C}_{43}\text{H}_{65}\text{N}_5\text{O}_{10}$) (labeled as "Ligand of Interest" by depositor).



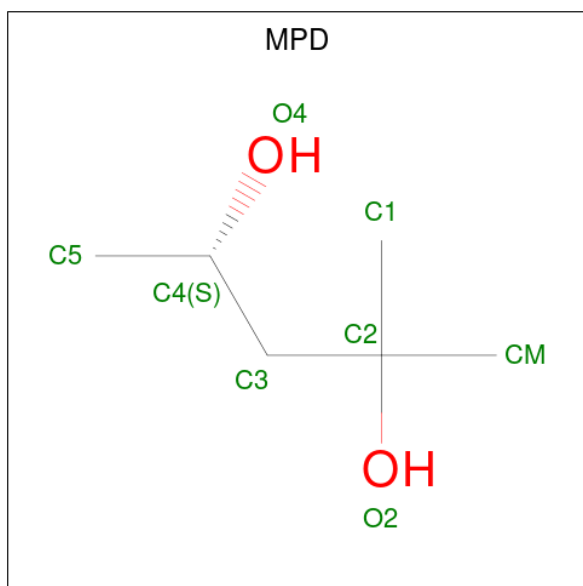
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
56	1A	1	Total	C	N	O	0	0
			58	43	5	10		

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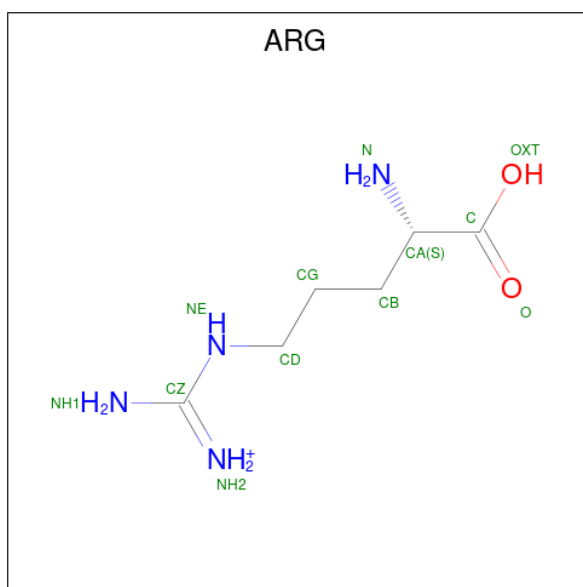
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
56	2A	1	Total	C	N	O	0	0
			58	43	5	10		

- Molecule 57 is (4S)-2-METHYL-2,4-PENTANEDIOL (CCD ID: MPD) (formula: $C_6H_{14}O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
57	1A	1	Total	C	O	0	0
			8	6	2		
57	1T	1	Total	C	O	0	0
			8	6	2		
57	18	1	Total	C	O	0	0
			8	6	2		
57	1a	1	Total	C	O	0	0
			8	6	2		
57	2A	1	Total	C	O	0	0
			8	6	2		
57	2A	1	Total	C	O	0	0
			8	6	2		
57	2B	1	Total	C	O	0	0
			8	6	2		

- Molecule 58 is ARGinine (CCD ID: ARG) (formula: $C_6H_{15}N_4O_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
58	1B	1	Total	C	N	O	0	0
			12	6	4	2		
58	1F	1	Total	C	N	O	0	0
			12	6	4	2		

- Molecule 59 is ZINC ION (CCD ID: ZN) (formula: Zn).

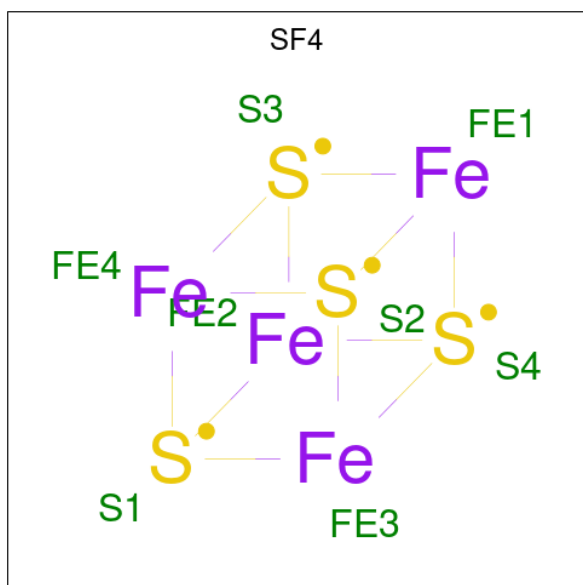
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
59	1Y	1	Total	Zn	0	0
			1	1		
59	14	1	Total	Zn	0	0
			1	1		
59	15	1	Total	Zn	0	0
			1	1		
59	16	1	Total	Zn	0	0
			1	1		
59	19	1	Total	Zn	0	0
			1	1		
59	1n	1	Total	Zn	0	0
			1	1		
59	2Y	1	Total	Zn	0	0
			1	1		
59	24	1	Total	Zn	0	0
			1	1		
59	25	1	Total	Zn	0	0
			1	1		
59	26	1	Total	Zn	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
59	29	1	Total	Zn	0	0
			1	1		
59	2n	1	Total	Zn	0	0
			1	1		

- Molecule 60 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe₄S₄).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
60	1d	1	Total	Fe	S	0	0
			8	4	4		
60	2d	1	Total	Fe	S	0	0
			8	4	4		

- Molecule 61 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
61	1A	3818	Total	O	0	0
			3818	3818		
61	1B	94	Total	O	0	0
			94	94		
61	1D	110	Total	O	0	0
			110	110		
61	1E	67	Total	O	0	0
			67	67		
61	1F	62	Total	O	0	0
			62	62		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
61	1G	15	Total	O	0	0
			15	15		
61	1H	17	Total	O	0	0
			17	17		
61	1I	7	Total	O	0	0
			7	7		
61	1N	45	Total	O	0	0
			45	45		
61	1O	24	Total	O	0	0
			24	24		
61	1P	57	Total	O	0	0
			57	57		
61	1Q	36	Total	O	0	0
			36	36		
61	1R	32	Total	O	0	0
			32	32		
61	1S	10	Total	O	0	0
			10	10		
61	1T	35	Total	O	0	0
			35	35		
61	1U	44	Total	O	0	0
			44	44		
61	1V	34	Total	O	0	0
			34	34		
61	1W	22	Total	O	0	0
			22	22		
61	1X	25	Total	O	0	0
			25	25		
61	1Y	13	Total	O	0	0
			13	13		
61	1Z	12	Total	O	0	0
			12	12		
61	10	25	Total	O	0	0
			25	25		
61	11	20	Total	O	0	0
			20	20		
61	12	15	Total	O	0	0
			15	15		
61	13	20	Total	O	0	0
			20	20		
61	14	4	Total	O	0	0
			4	4		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
61	15	25	Total 25	O 25	0	0
61	16	16	Total 16	O 16	0	0
61	17	15	Total 15	O 15	0	0
61	18	24	Total 24	O 24	0	0
61	19	2	Total 2	O 2	0	0
61	1a	406	Total 406	O 406	0	0
61	1d	7	Total 7	O 7	0	0
61	1e	5	Total 5	O 5	0	0
61	1f	2	Total 2	O 2	0	0
61	1h	1	Total 1	O 1	0	0
61	1i	1	Total 1	O 1	0	0
61	1j	1	Total 1	O 1	0	0
61	1k	1	Total 1	O 1	0	0
61	1l	4	Total 4	O 4	0	0
61	1o	3	Total 3	O 3	0	0
61	1p	2	Total 2	O 2	0	0
61	1q	2	Total 2	O 2	0	0
61	1u	1	Total 1	O 1	0	0
61	1y	2	Total 2	O 2	0	0
61	2A	2123	Total 2123	O 2123	0	0
61	2B	44	Total 44	O 44	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
61	2D	53	Total 53	O 53	0	0
61	2E	23	Total 23	O 23	0	0
61	2F	18	Total 18	O 18	0	0
61	2G	3	Total 3	O 3	0	0
61	2H	2	Total 2	O 2	0	0
61	2I	2	Total 2	O 2	0	0
61	2N	3	Total 3	O 3	0	0
61	2O	18	Total 18	O 18	0	0
61	2P	21	Total 21	O 21	0	0
61	2Q	17	Total 17	O 17	0	0
61	2R	18	Total 18	O 18	0	0
61	2S	2	Total 2	O 2	0	0
61	2T	8	Total 8	O 8	0	0
61	2U	13	Total 13	O 13	0	0
61	2V	6	Total 6	O 6	0	0
61	2W	18	Total 18	O 18	0	0
61	2X	8	Total 8	O 8	0	0
61	2Y	4	Total 4	O 4	0	0
61	2Z	8	Total 8	O 8	0	0
61	20	11	Total 11	O 11	0	0
61	21	16	Total 16	O 16	0	0

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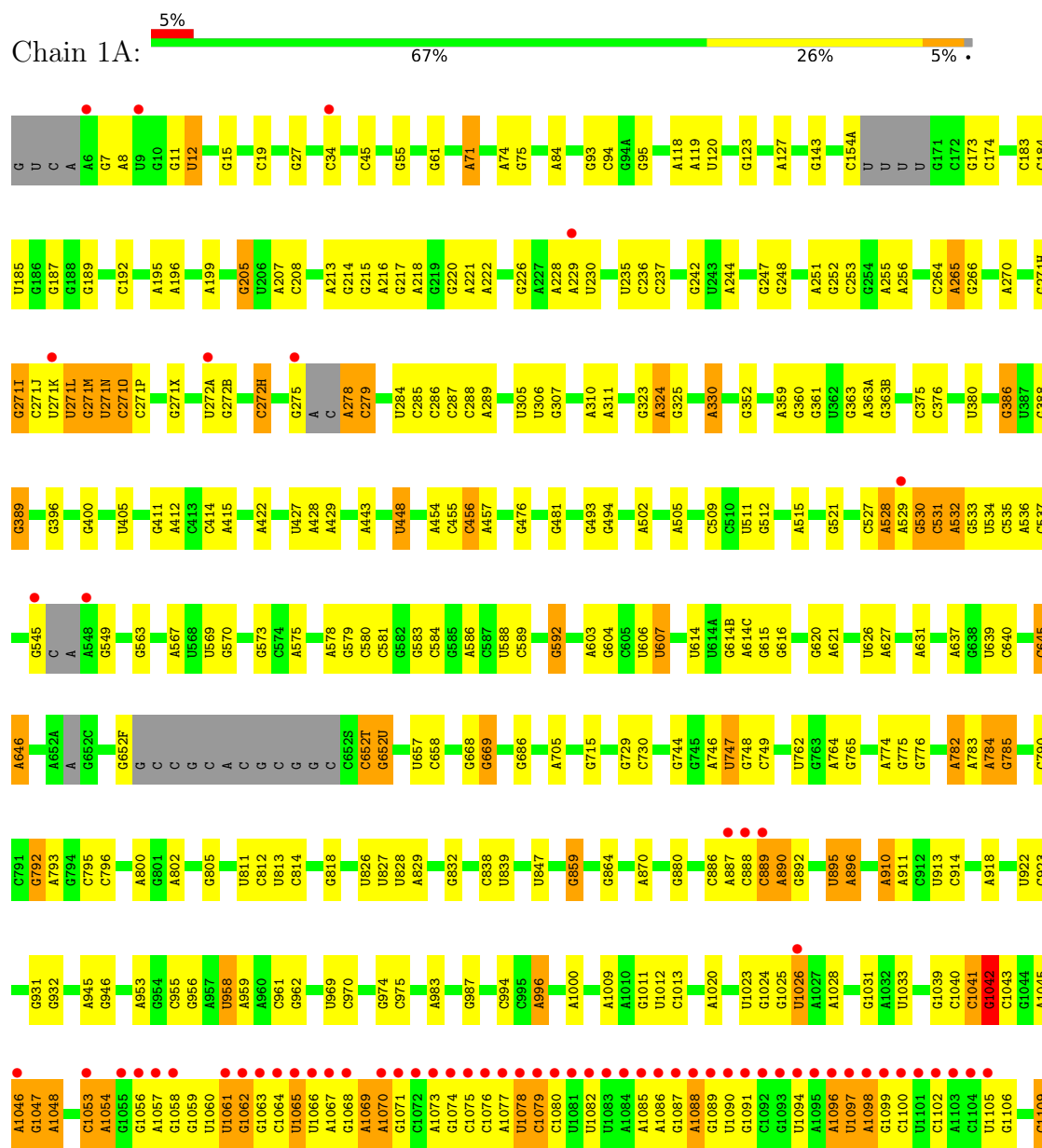
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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
61	22	1	Total O 1 1	0	0
61	23	3	Total O 3 3	0	0
61	24	1	Total O 1 1	0	0
61	25	10	Total O 10 10	0	0
61	26	5	Total O 5 5	0	0
61	27	6	Total O 6 6	0	0
61	28	10	Total O 10 10	0	0
61	29	1	Total O 1 1	0	0
61	2a	264	Total O 264 264	0	0
61	2d	2	Total O 2 2	0	0
61	2e	1	Total O 1 1	0	0
61	2f	3	Total O 3 3	0	0
61	2j	1	Total O 1 1	0	0
61	2l	2	Total O 2 2	0	0
61	2n	1	Total O 1 1	0	0
61	2o	2	Total O 2 2	0	0
61	2p	1	Total O 1 1	0	0
61	2q	1	Total O 1 1	0	0
61	2r	3	Total O 3 3	0	0
61	2t	1	Total O 1 1	0	0
61	2y	1	Total O 1 1	0	0

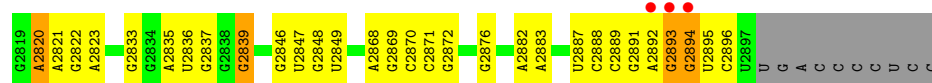
3 Residue-property plots

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.

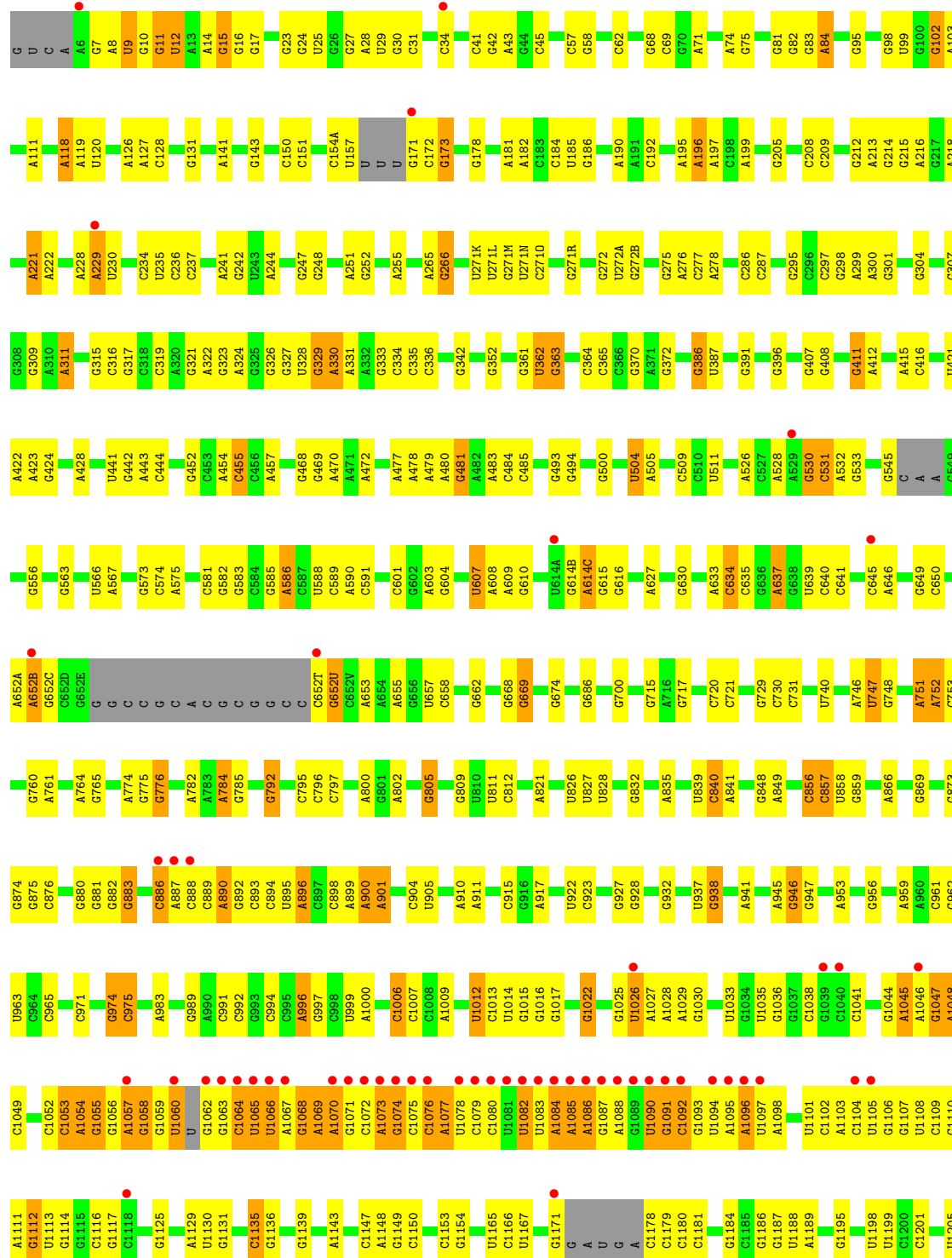
• Molecule 1: 23S Ribosomal RNA



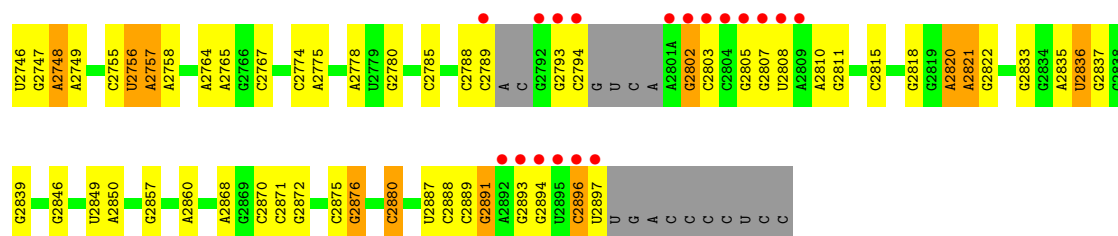
G2709	G2710	A2711	U2712	A2712A	A2713	G2714	G2718	G2722	G2723	U2726	G2732	A2733	G2747	G2751	A2752	A2753	U2754	G2755	A2758	G2759	A2764	A2765	G2766	G2777	A2778	A2781	G2784	A2790	G2791	G2792	G2793	G2794	G	U	C	A	G2802	G2803	G2804	G2805	G2807	A2810	G2811	G2818											
C2326	A2327	A2328	G2329	G2330	G2331	G2334	A2335	A2336	G2345	A2346	C2347	U2348	G2349	G2350	C2364	G2365	A2377	A2378	C2381	G2382	G2383	C2384	G2385	G2389	U2390	A2393	C2404	G2405	U2406	G2407	A2411	G2414	A2422	A2425	A2426	C2427	G2428	G2429	U2430	U2431	A2435	G2436	A2439	C2440	C2441										
G2442	G2443	G2444	G2445	G2446	G2447	A2448	G2458	C2464	G2468	A2469	G2470	C2474	G2475	A2476	G2477	A2478	G2486	U2491	G2494	C2498	G2502	A2503	U2504	G2505	U2506	A2518	G2529	G2535	G2536	U2537	G2538	G2548	U2552	G2553	U2554	G2548	U2562	U2563	A2564	A2565	A2566	G2567	A2572	G2573											
C2586	A2590	G2591	G2592	A2602	G2603	U2604	U2605	G2608	U2609	G2610	U2611	C2612	C2617	G2627	G2628	A2629	G2630	C2646	U2647	U2650	C2651	G2654	A2660	G2661	A2662	G2663	G2674	C2683	U2687	U2688	U2689	C2690	A2693	G2694	C2695	U2696	G2697	G2698	G2699	U2702	C2703	C2704	A2705												
C2138	C2139	C2140	G2141	C2142	C2143	U2144	C2145	C2146	G2147	G2148	G2149	U2150	G2151	G2152	G2153	G2154	G2155	G2156	G2157	A2158	G2159	G2160	C2161	G2162	C2163	C2164	G2165	G2166	U2167	G2168	A2169	G2170	C2171	C2172	A2173	C2174	C2175	A2176	G2182	C2183	G2184	C2185	G2186	G2187	C2188	U2189	G2190	G2191	G2192	A2198	C2201	G2206	G2207	A2208	U2218
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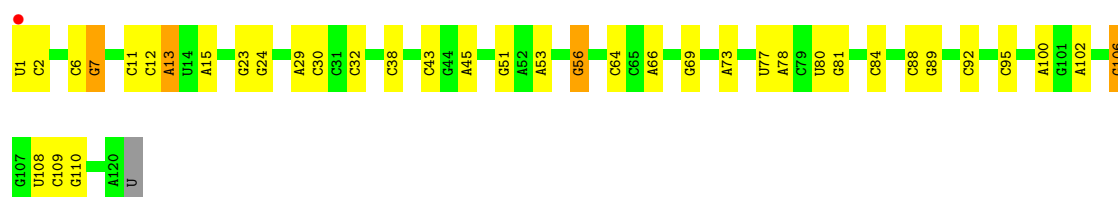
• Molecule 1: 23S Ribosomal RNA



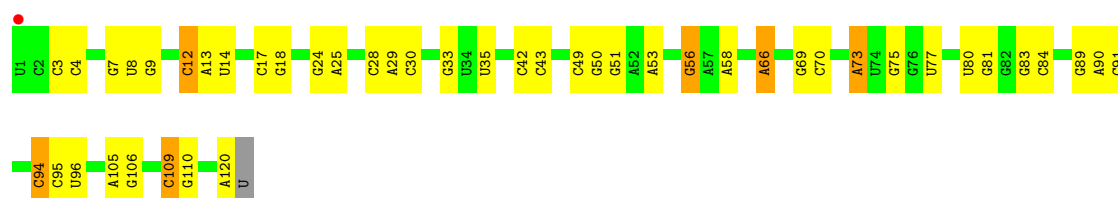
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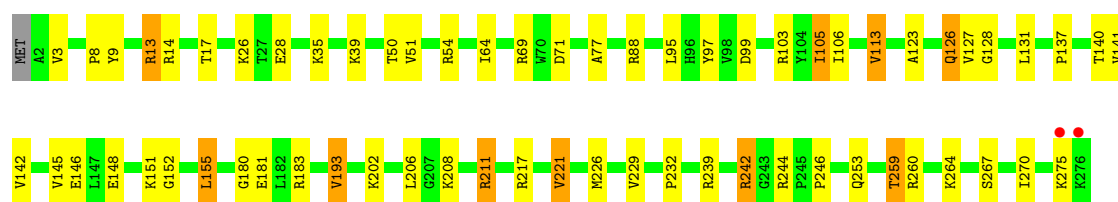
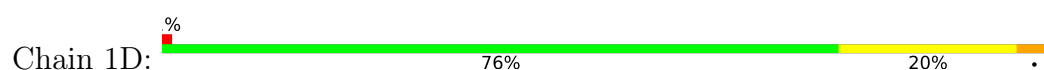
• Molecule 2: 5S Ribosomal RNA



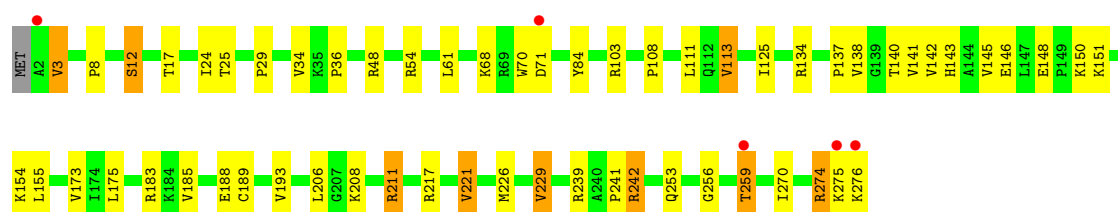
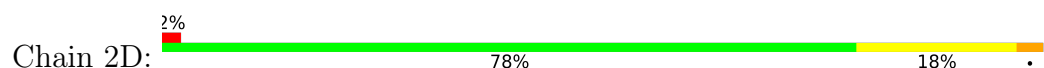
• Molecule 2: 5S Ribosomal RNA



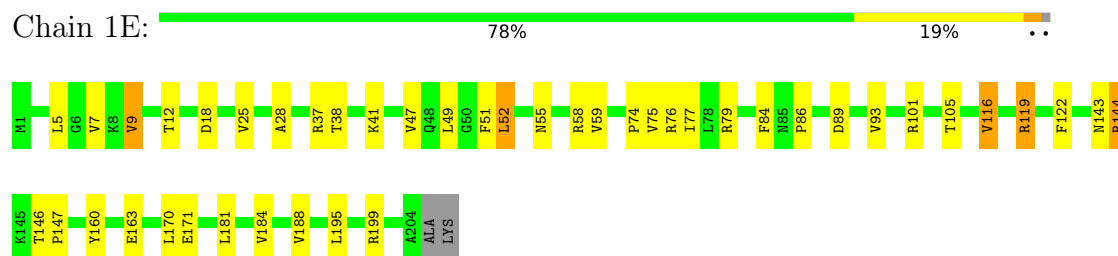
• Molecule 3: 50S ribosomal protein L2



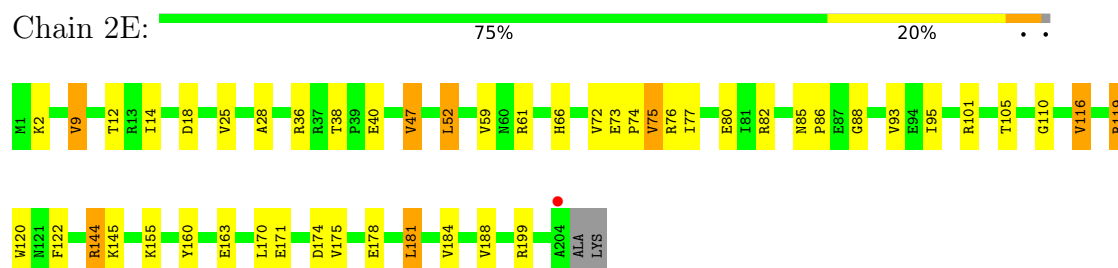
• Molecule 3: 50S ribosomal protein L2



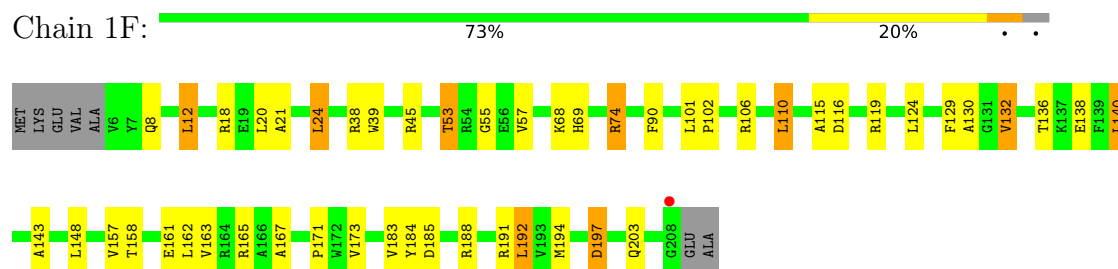
- Molecule 4: 50S ribosomal protein L3



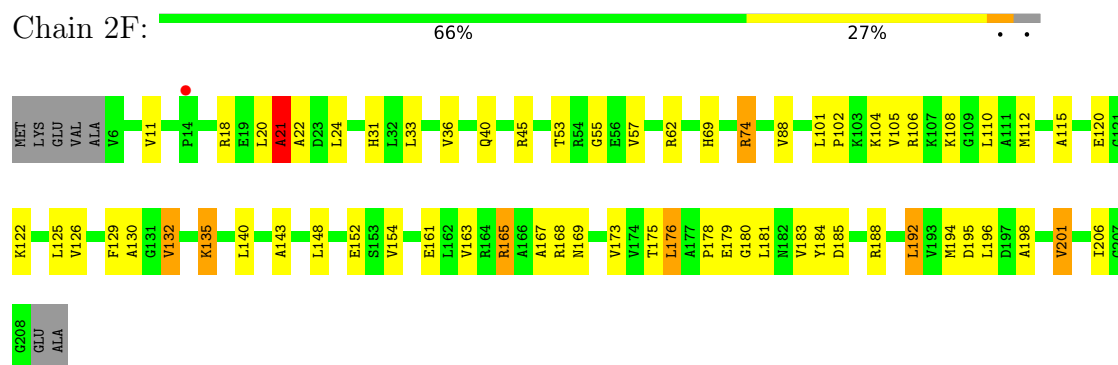
- Molecule 4: 50S ribosomal protein L3



- Molecule 5: 50S ribosomal protein L4

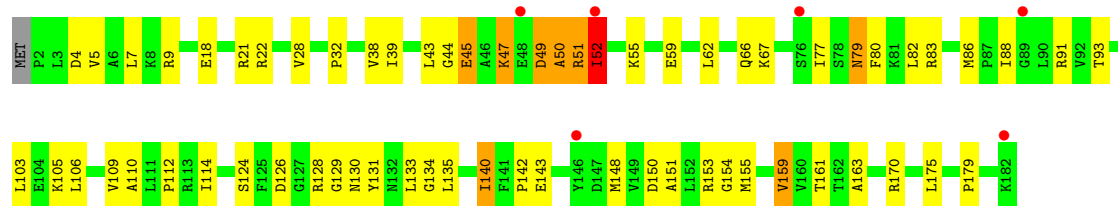


- Molecule 5: 50S ribosomal protein L4

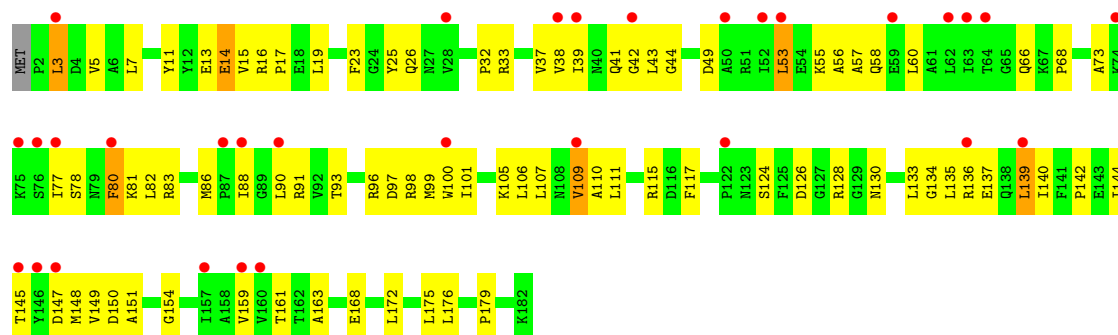


- Molecule 6: 50S ribosomal protein L5

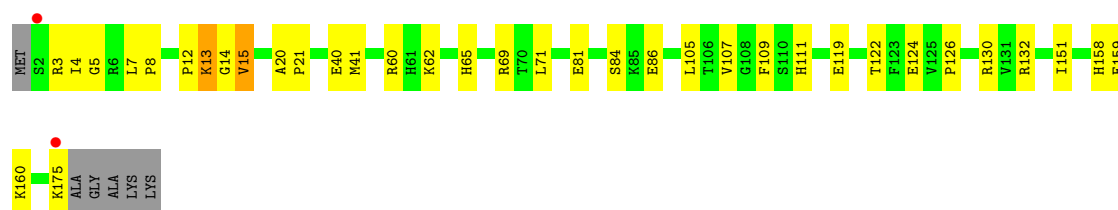
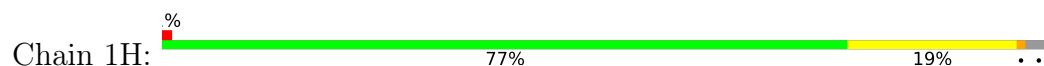




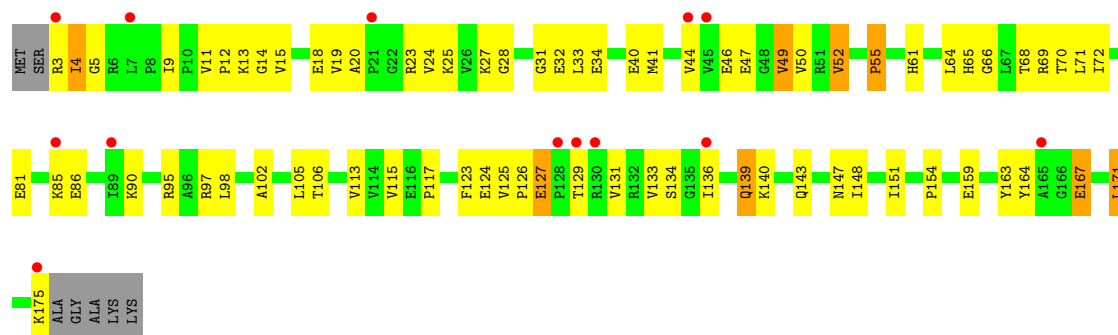
• Molecule 6: 50S ribosomal protein L5



• Molecule 7: 50S ribosomal protein L6

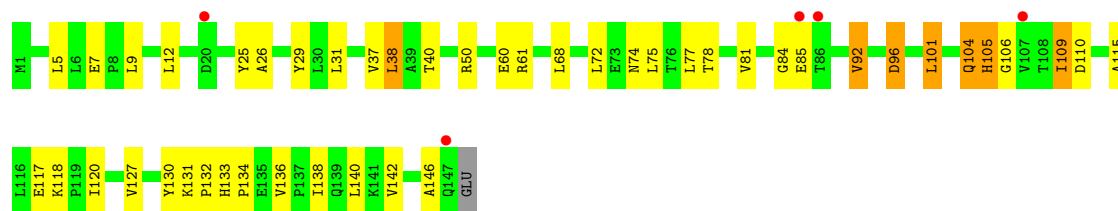


• Molecule 7: 50S ribosomal protein L6

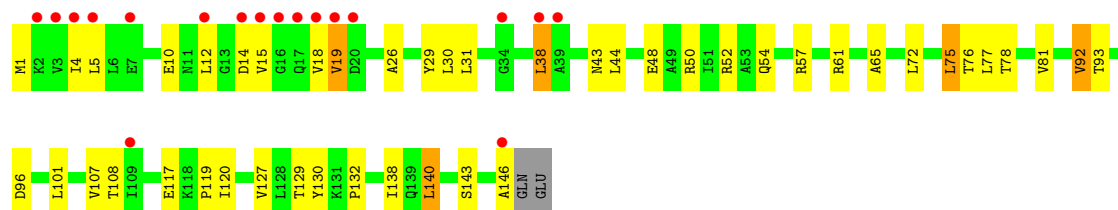


• Molecule 8: 50S ribosomal protein L9

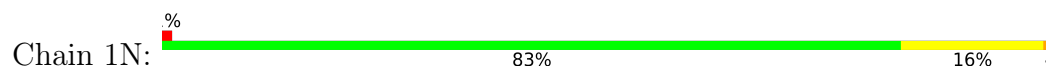




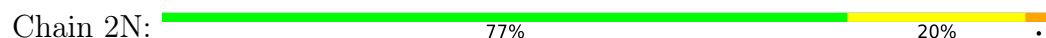
• Molecule 8: 50S ribosomal protein L9



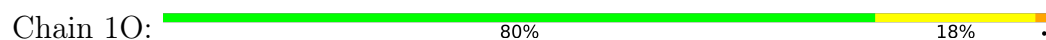
• Molecule 9: 50S ribosomal protein L13



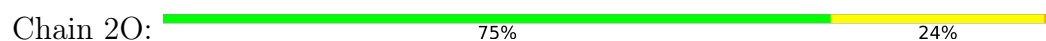
• Molecule 9: 50S ribosomal protein L13



• Molecule 10: 50S ribosomal protein L14

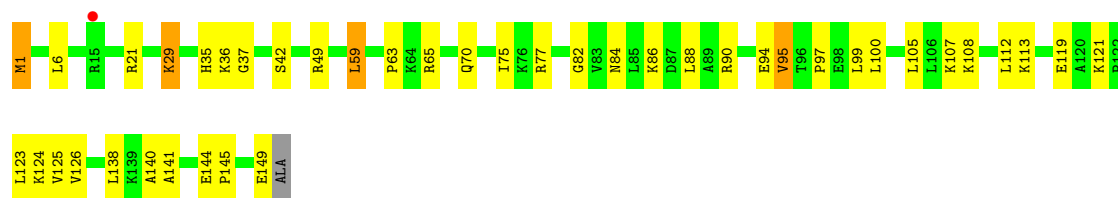


• Molecule 10: 50S ribosomal protein L14

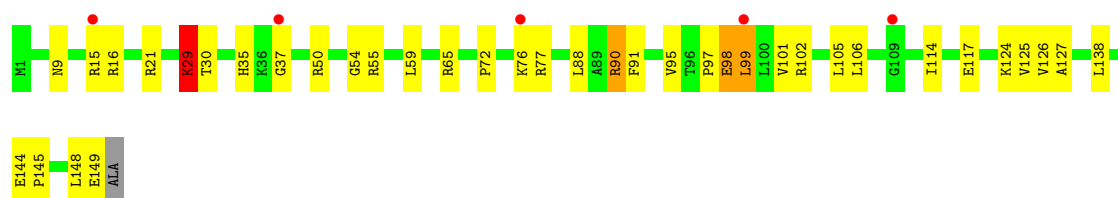
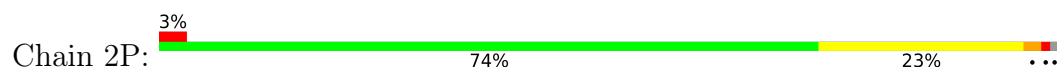


• Molecule 11: 50S ribosomal protein L15

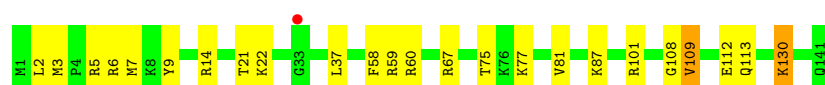
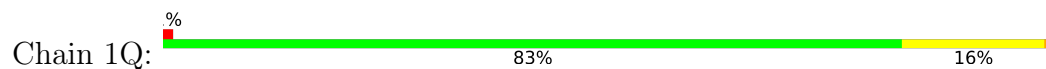




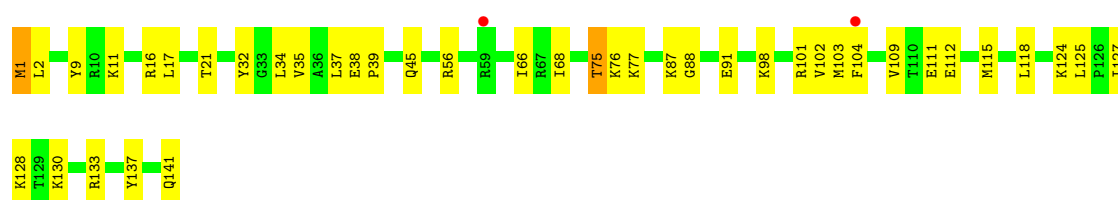
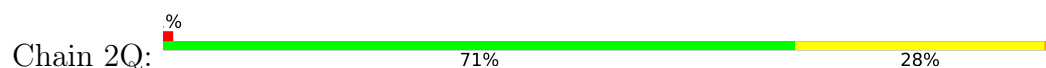
- Molecule 11: 50S ribosomal protein L15



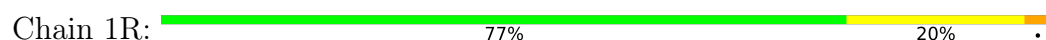
- Molecule 12: 50S ribosomal protein L16



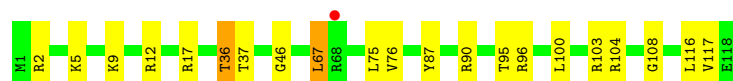
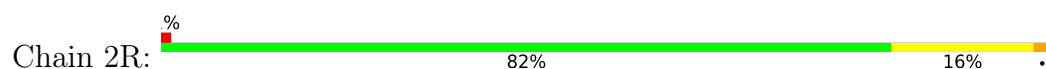
- Molecule 12: 50S ribosomal protein L16



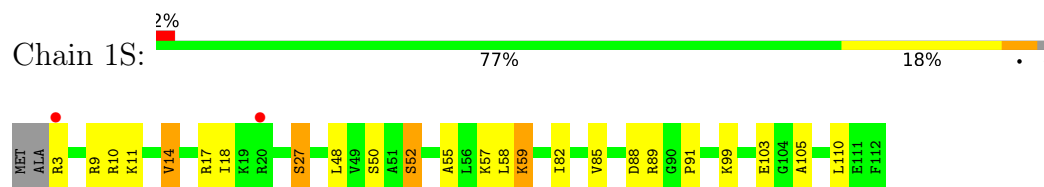
- Molecule 13: 50S ribosomal protein L17



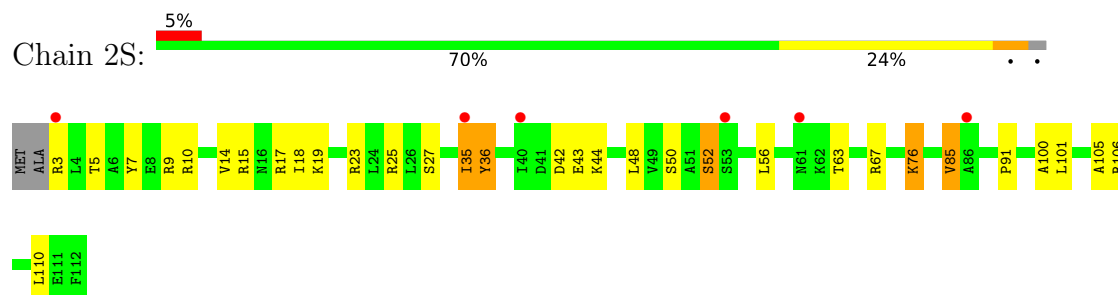
- Molecule 13: 50S ribosomal protein L17



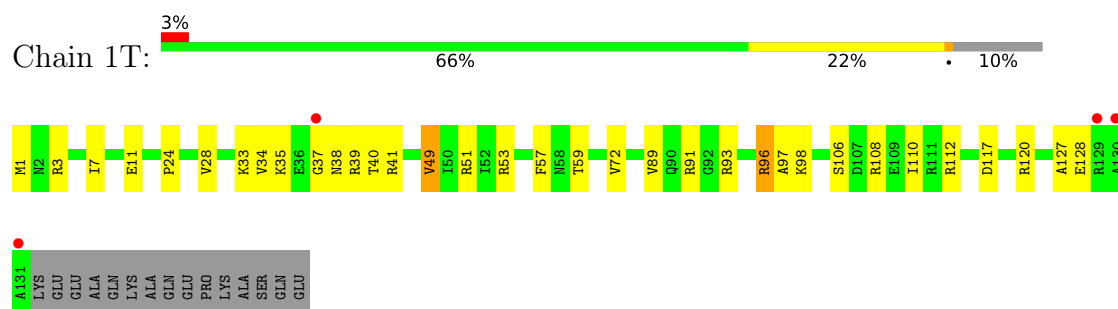
- Molecule 14: 50S ribosomal protein L18



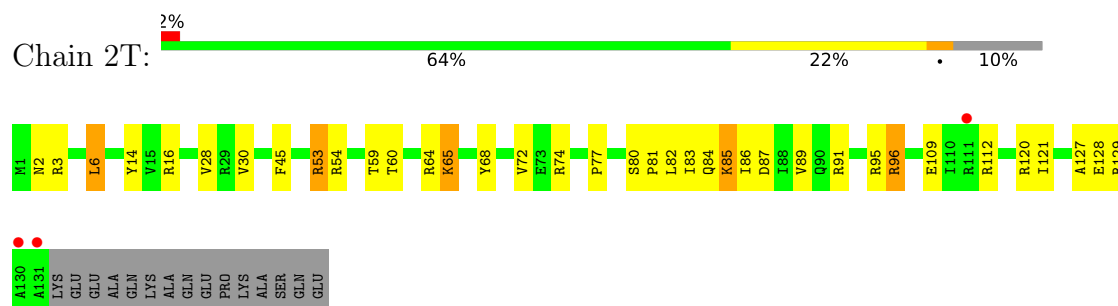
- Molecule 14: 50S ribosomal protein L18



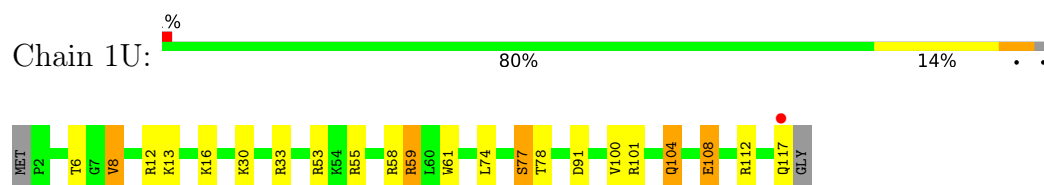
- Molecule 15: 50S ribosomal protein L19



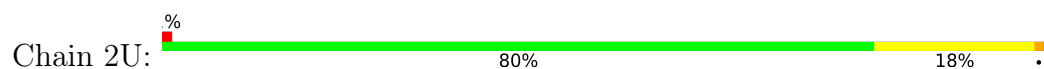
- Molecule 15: 50S ribosomal protein L19



- Molecule 16: 50S ribosomal protein L20



- Molecule 16: 50S ribosomal protein L20





- Molecule 17: 50S ribosomal protein L21

Chain 1V: 85% 14% .



- Molecule 17: 50S ribosomal protein L21

Chain 2V: 73% 24% ..



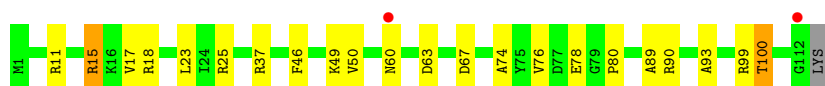
- Molecule 18: 50S ribosomal protein L22

Chain 1W: 88% 11% ..



- Molecule 18: 50S ribosomal protein L22

Chain 2W: 80% 18% ..



- Molecule 19: 50S ribosomal protein L23

Chain 1X: 84% 14% ..

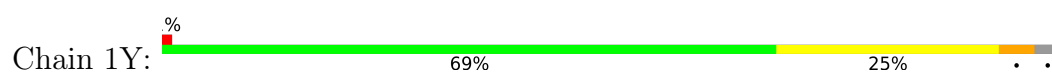


- Molecule 19: 50S ribosomal protein L23

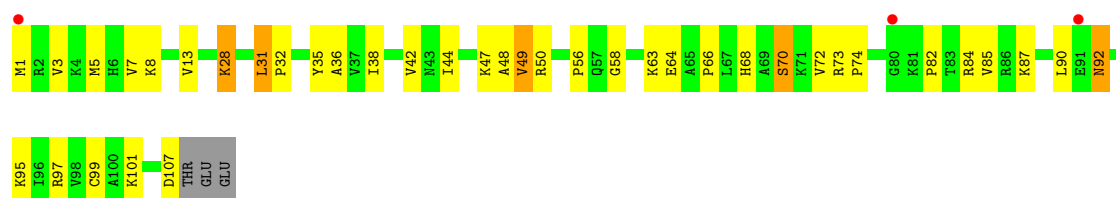
Chain 2X: 75% 24% .



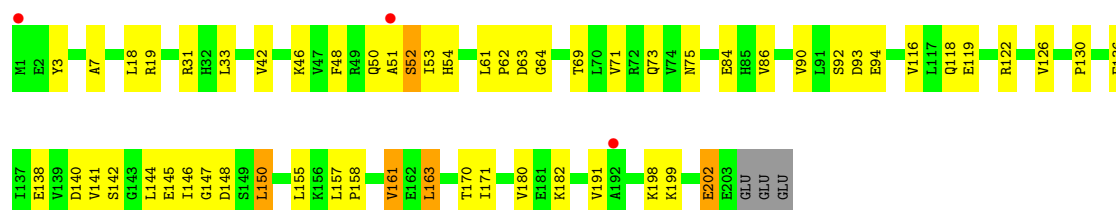
- Molecule 20: 50S ribosomal protein L24



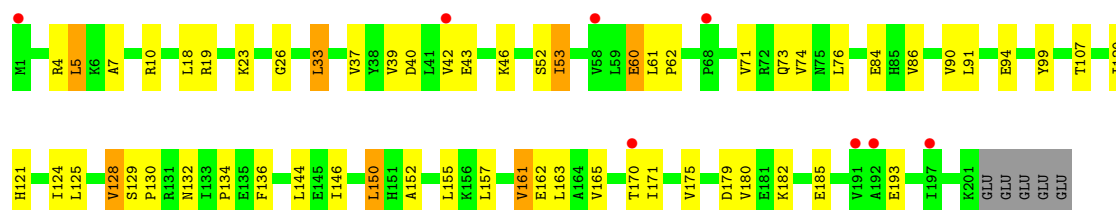
- Molecule 20: 50S ribosomal protein L24



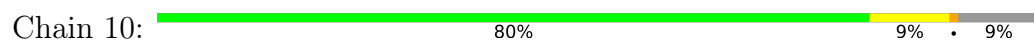
- Molecule 21: 50S ribosomal protein L25



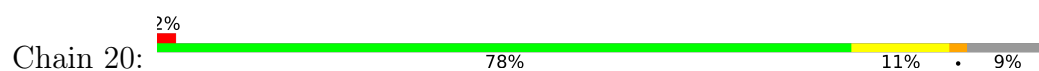
- Molecule 21: 50S ribosomal protein L25

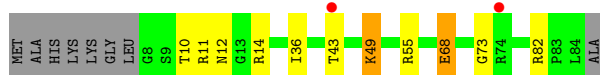


- Molecule 22: 50S ribosomal protein L27

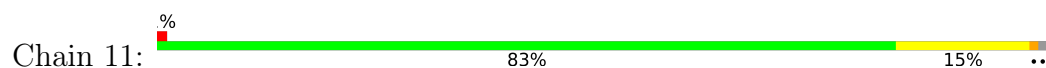


- Molecule 22: 50S ribosomal protein L27

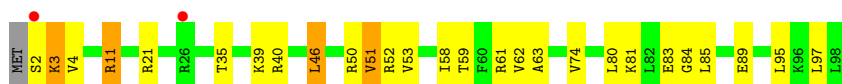




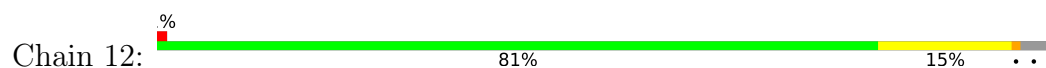
- Molecule 23: 50S ribosomal protein L28



- Molecule 23: 50S ribosomal protein L28



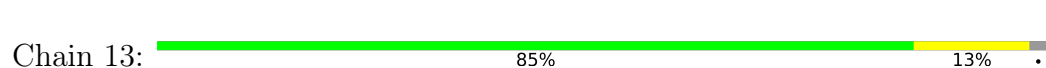
- Molecule 24: 50S ribosomal protein L29



- Molecule 24: 50S ribosomal protein L29



- Molecule 25: 50S ribosomal protein L30



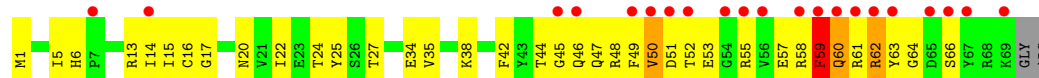
- Molecule 25: 50S ribosomal protein L30



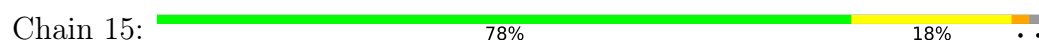
- Molecule 26: 50S ribosomal protein L31



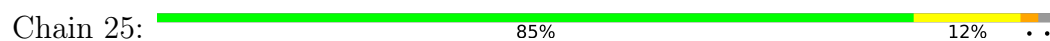
- Molecule 26: 50S ribosomal protein L31



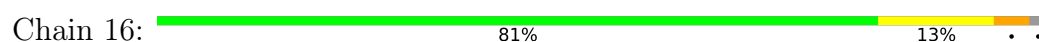
- Molecule 27: 50S ribosomal protein L32



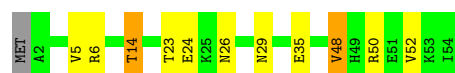
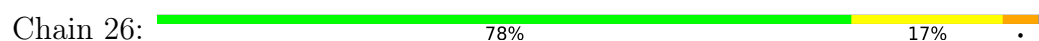
- Molecule 27: 50S ribosomal protein L32



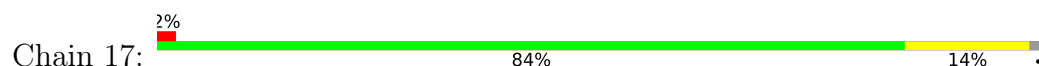
- Molecule 28: 50S ribosomal protein L33



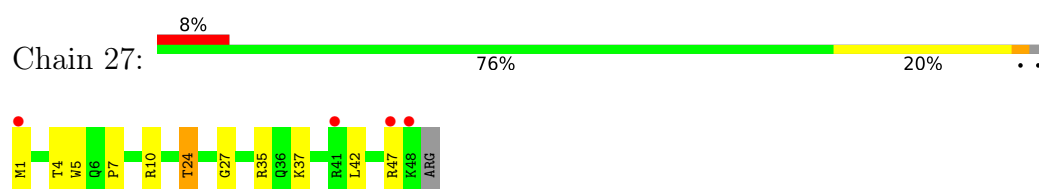
- Molecule 28: 50S ribosomal protein L33



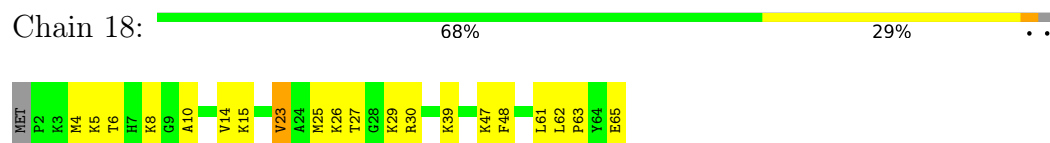
- Molecule 29: 50S ribosomal protein L34



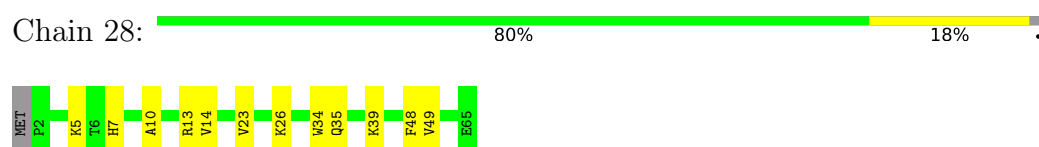
- Molecule 29: 50S ribosomal protein L34



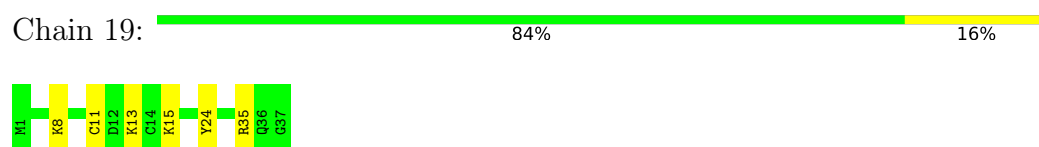
- Molecule 30: 50S ribosomal protein L35



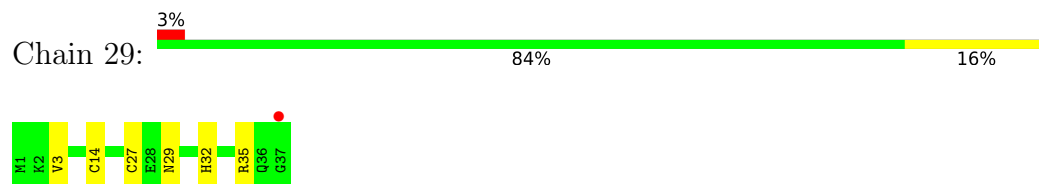
- Molecule 30: 50S ribosomal protein L35



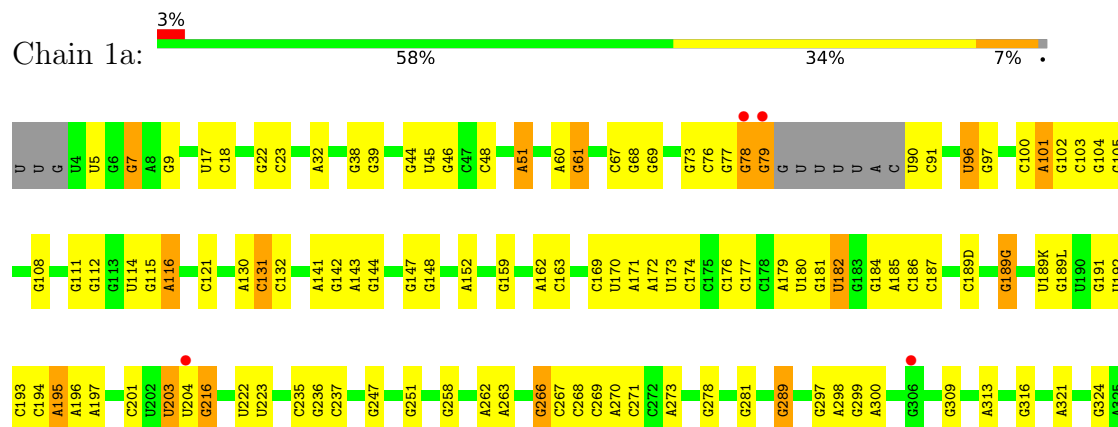
- Molecule 31: 50S ribosomal protein L36

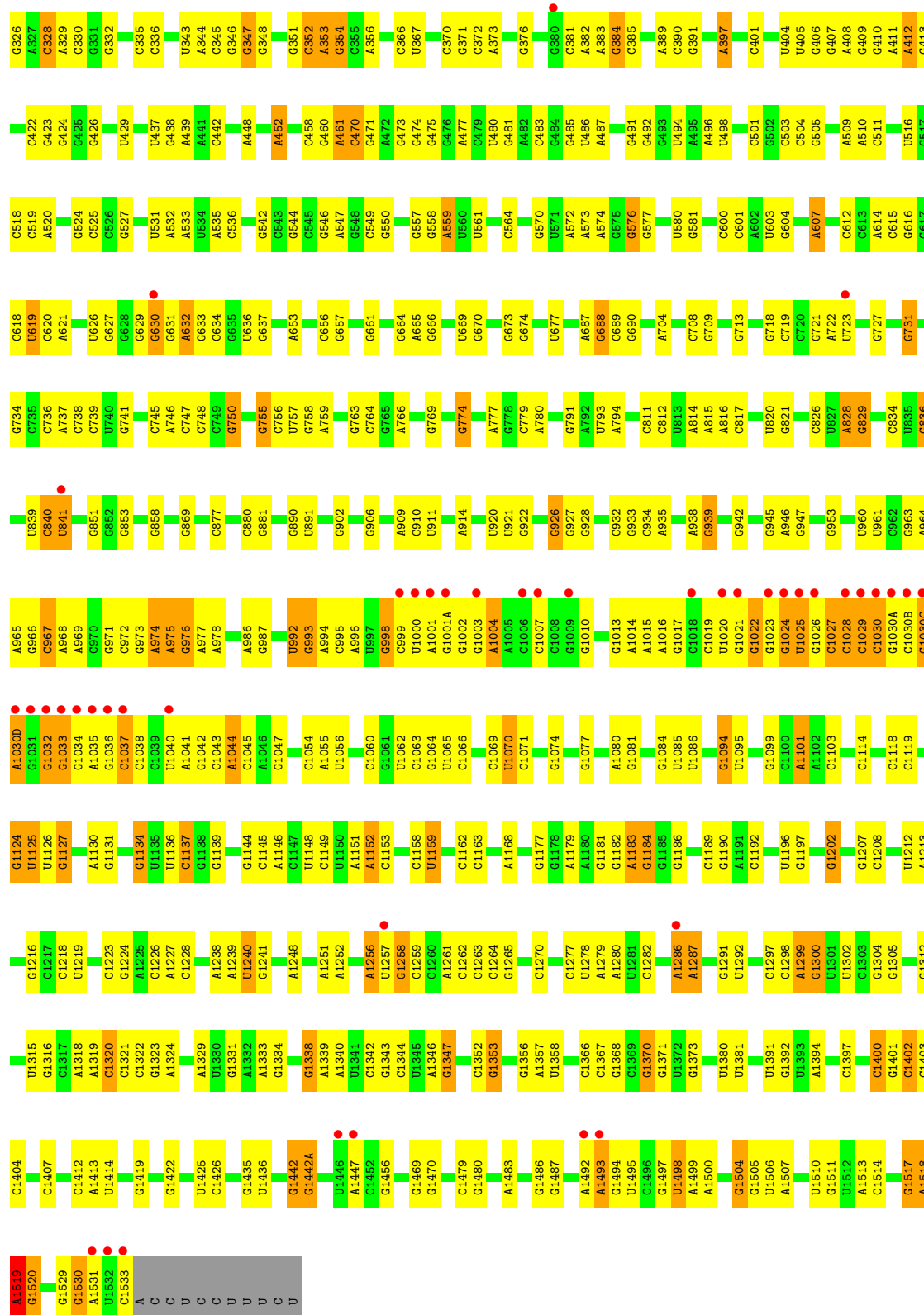


- Molecule 31: 50S ribosomal protein L36



- Molecule 32: 16S Ribosomal RNA

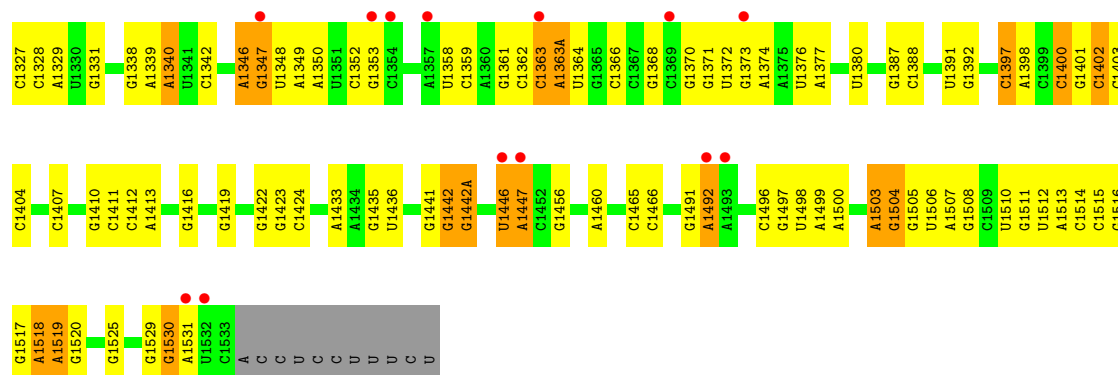




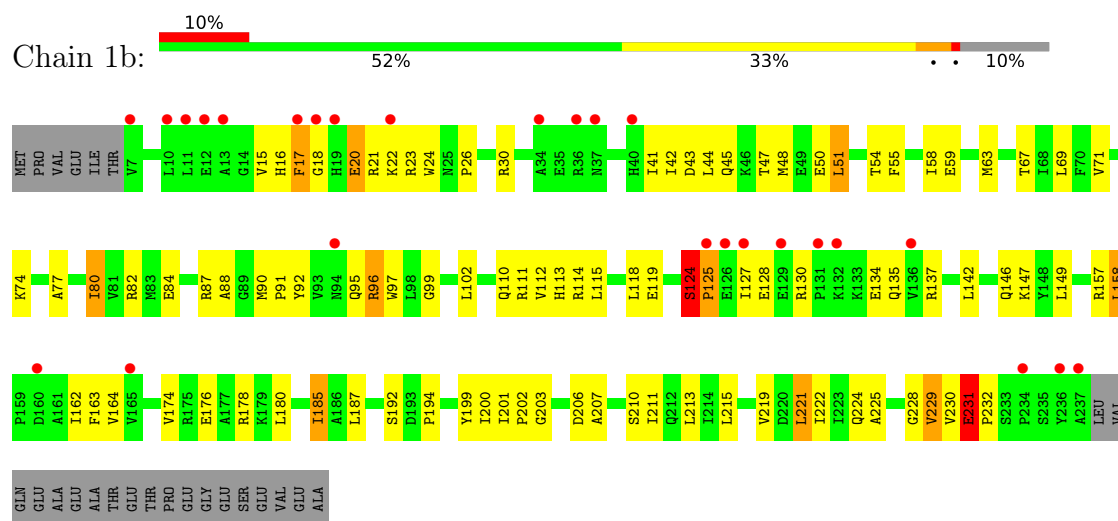
• Molecule 32: 16S Ribosomal RNA



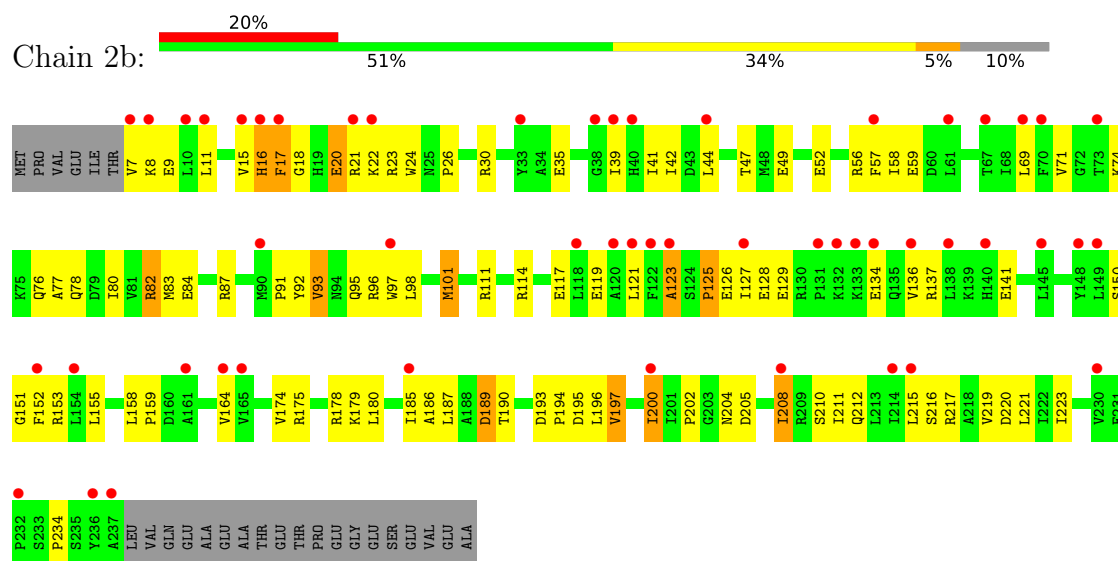
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C1259	G1181	A1101	G1026	A859	G750	C643	G537	G438	C328	U203	C110	G
C1260	A1182	C1102	C1027	C859	G751	C644	G538	A441	A329	U204	G111	U5
A1269	A1183	C1103	C1028	G869	A753	G645	G539	C442	G332	G216	G115	G6
G1270	G1184	G1106	C1029	C874	G754	U646	G540	C443	C335	C217	A116	G7
G1271	G1185	C1107	C1030	C875	G755	A653	G541	C444	C336	C218	G117	A8
G1272	G1186	G1108	G1030A	C876	G756	U647	G544	C445	A337	C221	G117	G9
G1273	A1190	C1109	G1030B	C877	G757	U648	G545	G446	A338	G222	C121	A10
G1274	A1191	C1110	G1030C	C878	G758	G660	G546	G447	A339	G223	C121	U17
G1275	C1192	C1111	G1030D	C879	G759	G661	A547	A448	A344	U223	A130	C18
C1277	C1193	C1112	G1031	G890	G760	G662	U551	A451	C345	G236	C131	C19
U1278	C1194	C1113	G1032	G902	A766	A663	U552	A452	C346	G237	A134	U20
U1279	U1196	C1114	G1033	G903	A767	G664	U553	A453	C347	G238	A135	G21
A1280	G1197	C1115	A1034	G904	A768	A665	G558	C458	C352	G239	A136	G22
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C1282	C1200	C1117	G1036	G906	G769	G667	U560	A461	G354	G241	G142	
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A1284	G1202	C1119	G1038	C910	A771	G669	U562	A463	A356	G251	G144	U30
A1285	G1203	C1120	U1039	C911	A772	G670	U563	A464	A357	U252	A149	G31
A1286	G1204	C1121	U1040	C912	A773	G671	U564	A465	C372	U253	C150	A32
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A1289	G1207	C1124	C1043	C915	A776	G674	U567	A468	A384	G256	G157	G40
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G1291	U1212	C1126	G1045	C917	A778	G676	U569	A470	A386	A263	G159	G42
G1292	A1213	C1127	U1046	C918	A779	G677	U570	A471	A387	G264	C163	G43
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G1296	G1217	C1131	C1054	C922	A783	G681	U574	A475	A391	A270	U173	U49
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G1301	G1222	C1136	C1063	C927	A788	G686	U579	A480	A396	G275	C187	G57
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C1303	G1224	C1138	G1065	C929	A790	G688	U581	A482	A398	A277	G189	A59
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G1305	C1226	C1140	C1067	C931	A792	G690	U583	A484	A401	G279	C191	G61
A1306	A1227	C1141	U1068	C932	A793	G691	U584	A485	A402	C280	C192	U64
A1307	C1228	C1142	G1075	C933	A794	G692	U585	A486	A403	G281	C193	G64
U1308	U1235	C1143	C1076	C934	A795	G693	U586	A487	A404	C282	C194	U65
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G1310	A1237	C1145	U1078	C936	A797	G695	U588	A489	A406	C284	C196	G67
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U1312	A1239	C1147	G1080	C938	A799	G697	U590	A491	A408	C286	C198	U69
U1313	U1240	C1148	U1081	C939	A800	G698	U591	A492	A409	C287	C199	G70
C1314	G1241	C1149	G1082	C940	A801	G699	U592	A493	A410	C288	C200	G80
C1317	C1242	C1150	U1083	C941	A802	G700	U593	A494	A411	C289	U189L	U
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C1326	C1254	C1159	A1016	C950	A811	G709	U602	A503	A420	C298		
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		C1184	U1041	C975	A836	G734	U627	A528	G539	A339		
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		C1191	U1048	C982	A843	G741	U634	A535	G546	A346		
		C1192	U1049	C983	A844	G742	U635	A536	G547	A347		
		C1193	U1050	C984	A845	G743	U636	A537	G548	A348		
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		C1198	U1055	C989	A850	G748	U641	A542	G553	A353		
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		C1201	U1058	C992	A853	G751	U644	A545	G556	A356		
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		C1211	U1068	C1002	A863	G761	U654	A555	G566	A366		
		C1212	U1069	C1003	A864	G762	U655	A556	G567	A367		
		C1213	U1070	C1004	A865	G763	U656	A557	G568	A368		
		C1214	U1071	C1005	A866	G764	U657	A558	G569	A369		
		C1215	U1072	C1006	A867	G765	U658	A559	G570	A370		
		C1216	U1073	C1007	A868	G766	U659	A560	G571	A371		
		C1217	U1074	C1008	A869	G767	U660	A561	G572	A372		
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• Molecule 33: 30S ribosomal protein S2

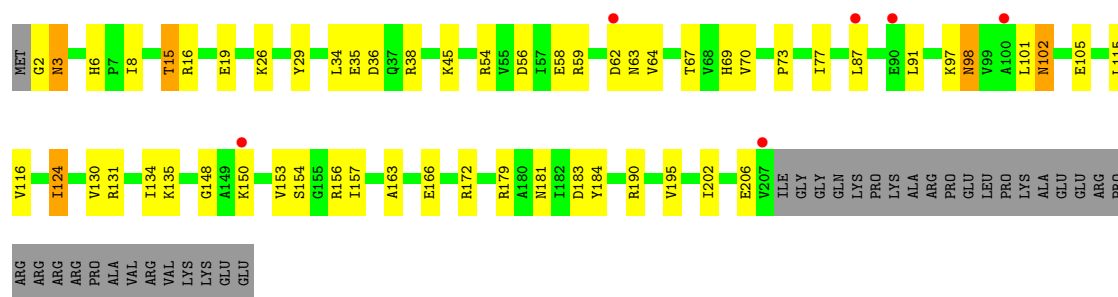


• Molecule 33: 30S ribosomal protein S2

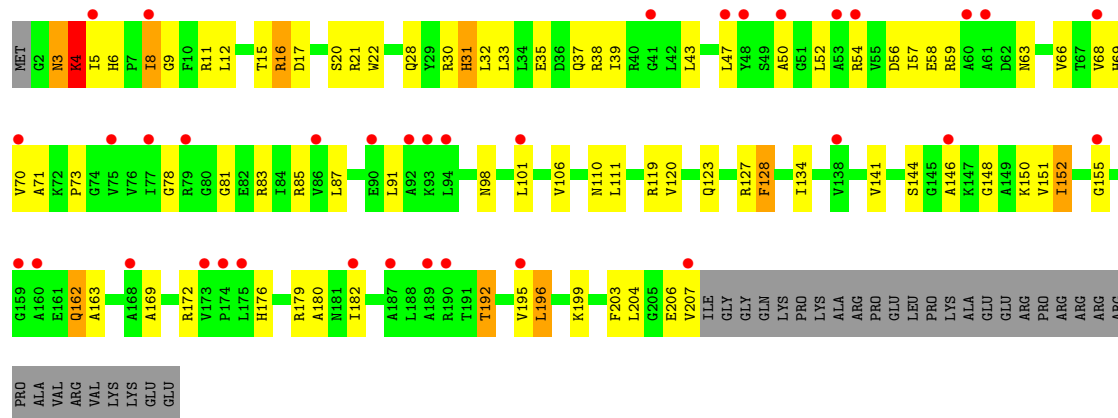


• Molecule 34: 30S ribosomal protein S3

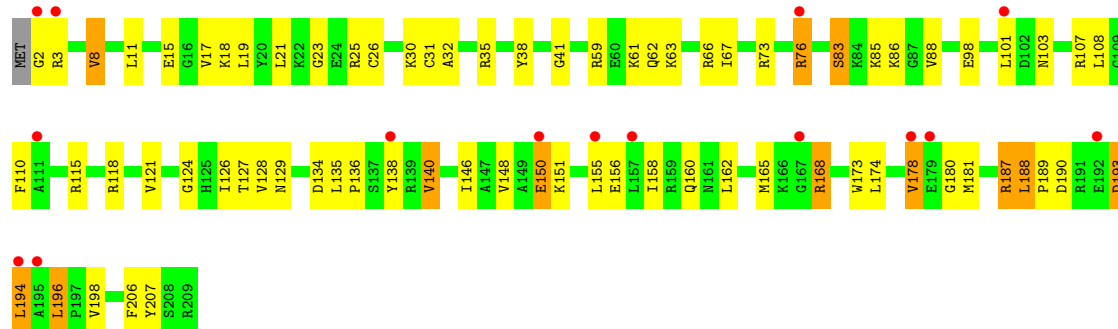




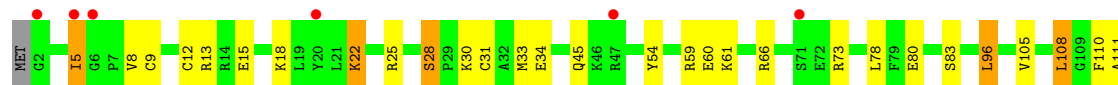
• Molecule 34: 30S ribosomal protein S3



• Molecule 35: 30S ribosomal protein S4

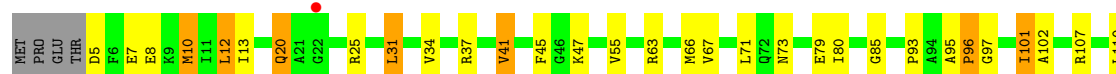


• Molecule 35: 30S ribosomal protein S4

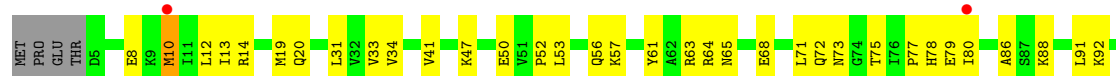




- Molecule 36: 30S ribosomal protein S5



- Molecule 36: 30S ribosomal protein S5



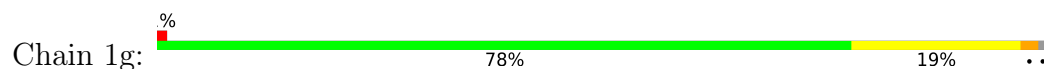
- Molecule 37: 30S ribosomal protein S6



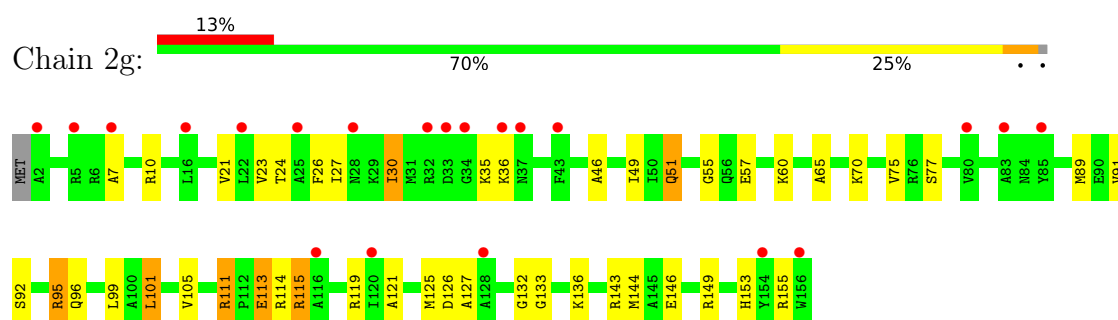
- Molecule 37: 30S ribosomal protein S6



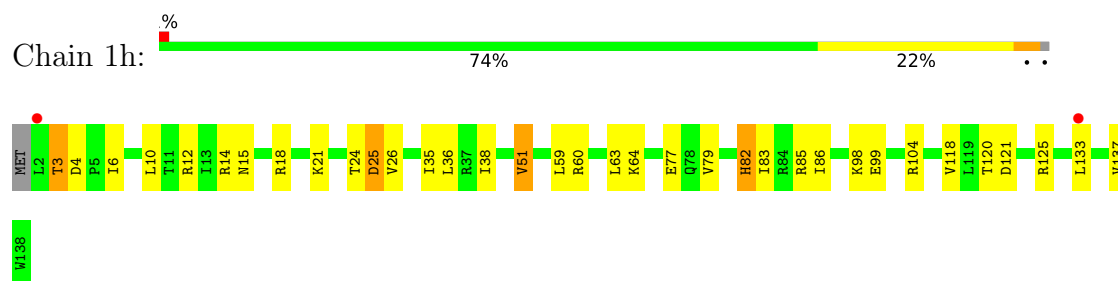
- Molecule 38: 30S ribosomal protein S7



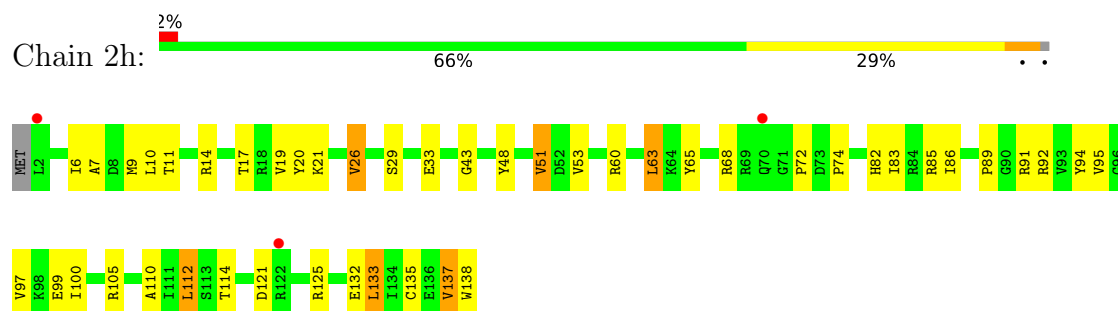
- Molecule 38: 30S ribosomal protein S7



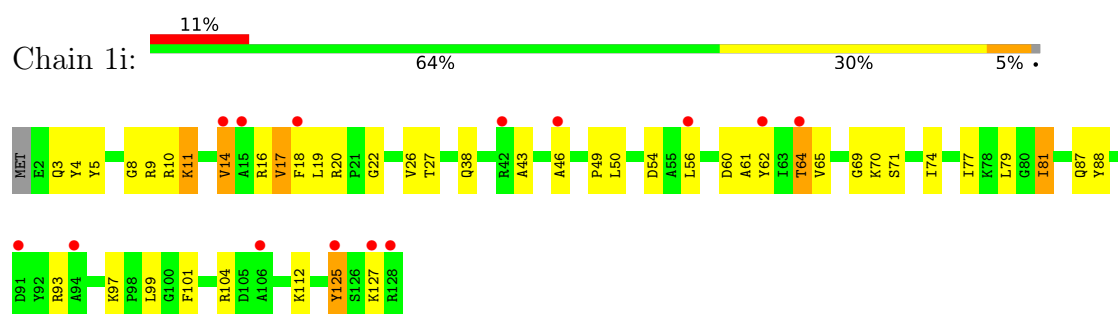
• Molecule 39: 30S ribosomal protein S8



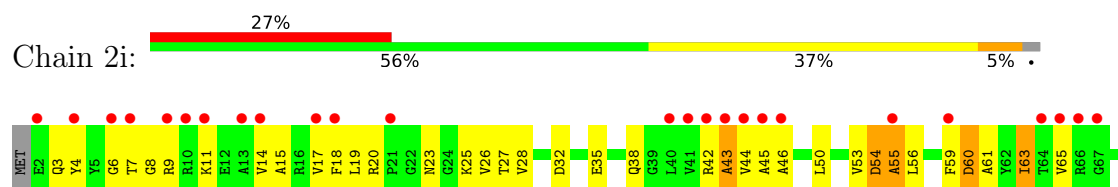
• Molecule 39: 30S ribosomal protein S8



• Molecule 40: 30S ribosomal protein S9

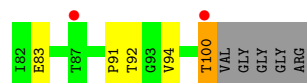
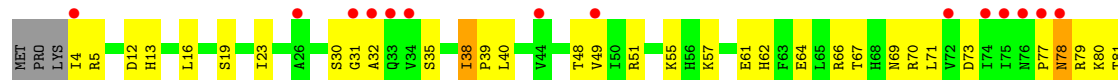


• Molecule 40: 30S ribosomal protein S9

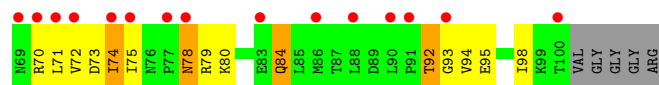
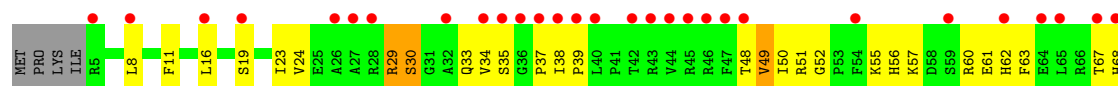
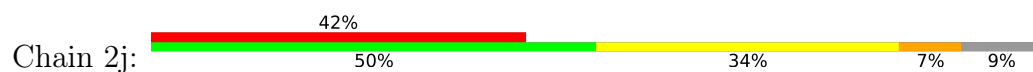




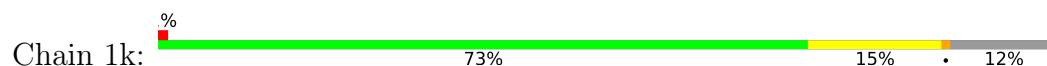
- Molecule 41: 30S ribosomal protein S10



- Molecule 41: 30S ribosomal protein S10



- Molecule 42: 30S ribosomal protein S11

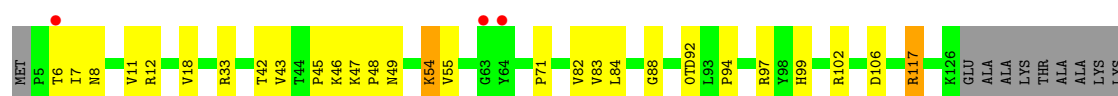


- Molecule 42: 30S ribosomal protein S11

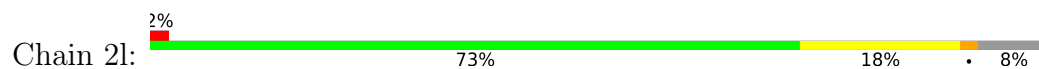


- Molecule 43: 30S ribosomal protein S12





- Molecule 43: 30S ribosomal protein S12



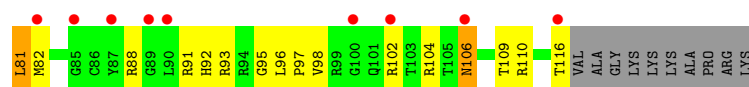
LYS

- Molecule 44: 30S ribosomal protein S13

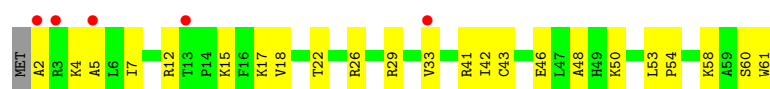


LYS
LYS
LYS
LYS
ALA
PRO
ARG
LYS

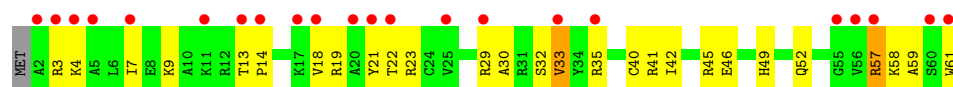
- Molecule 44: 30S ribosomal protein S13



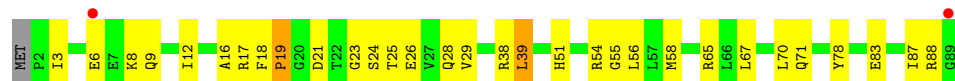
- Molecule 45: 30S ribosomal protein S14 type Z



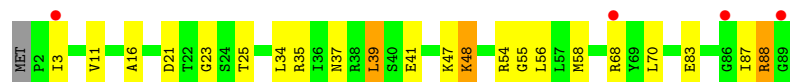
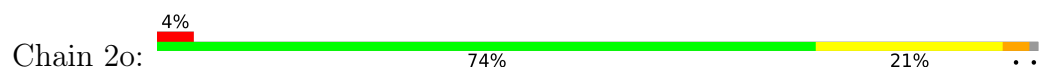
- Molecule 45: 30S ribosomal protein S14 type Z



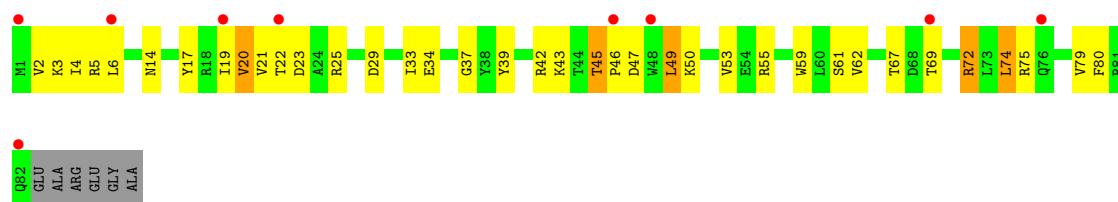
- Molecule 46: 30S ribosomal protein S15



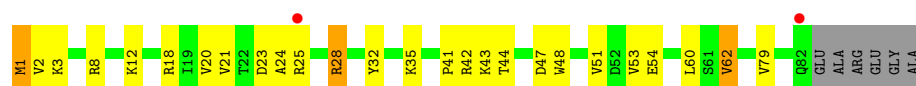
- Molecule 46: 30S ribosomal protein S15



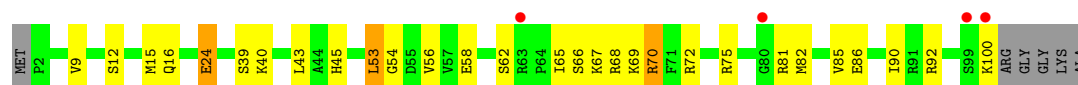
- Molecule 47: 30S ribosomal protein S16



- Molecule 47: 30S ribosomal protein S16



- Molecule 48: 30S ribosomal protein S17

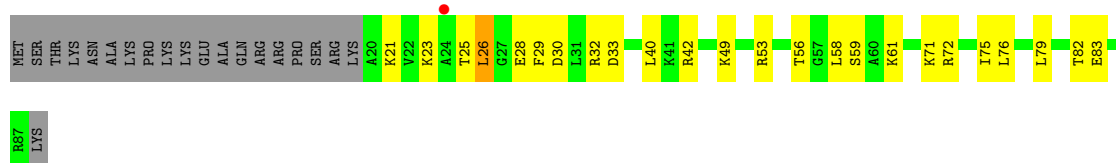


- Molecule 48: 30S ribosomal protein S17



- Molecule 49: 30S ribosomal protein S18

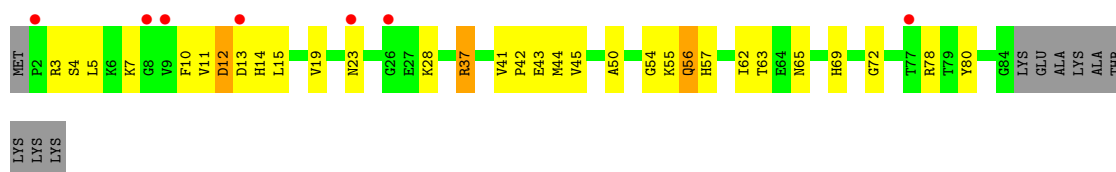




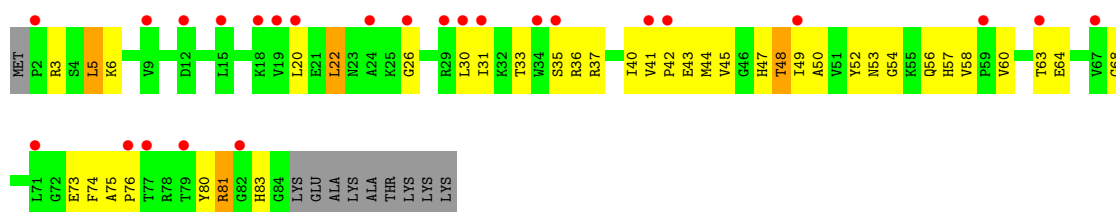
- Molecule 49: 30S ribosomal protein S18



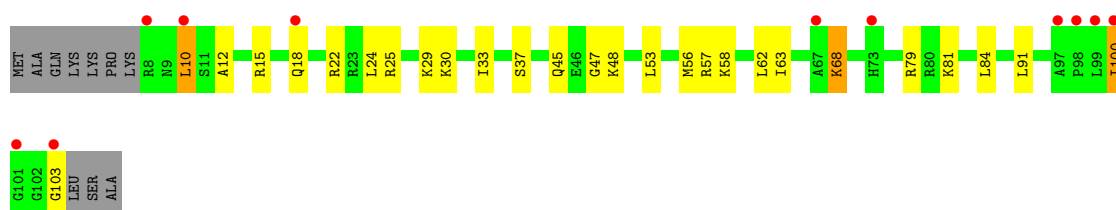
- Molecule 50: 30S ribosomal protein S19



- Molecule 50: 30S ribosomal protein S19



- Molecule 51: 30S ribosomal protein S20



- Molecule 51: 30S ribosomal protein S20

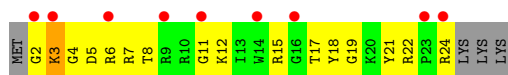




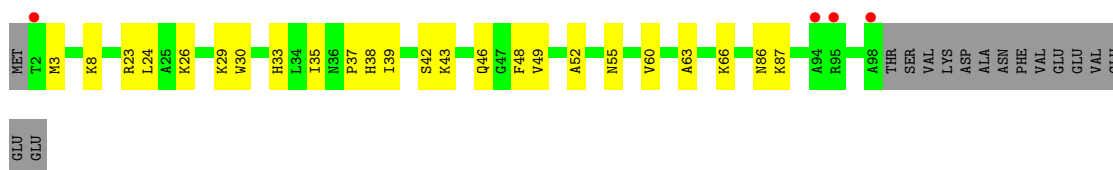
- Molecule 52: 30S ribosomal protein Thx



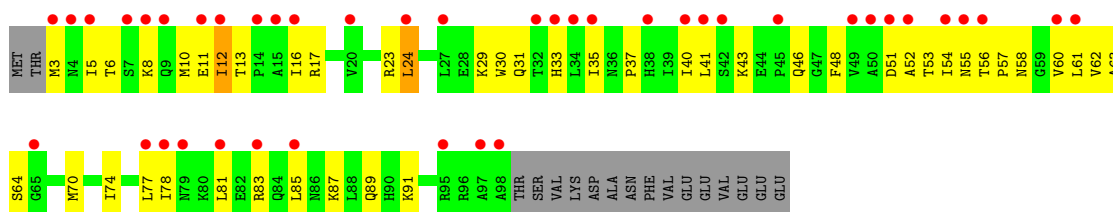
- Molecule 52: 30S ribosomal protein Thx



- Molecule 53: Ribosome-associated inhibitor A



- Molecule 53: Ribosome-associated inhibitor A



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	209.12Å 449.23Å 619.30Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	151.99 – 2.60 151.99 – 2.60	Depositor EDS
% Data completeness (in resolution range)	100.0 (151.99-2.60) 100.0 (151.99-2.60)	Depositor EDS
R_{merge}	0.24	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.26 (at 2.62Å)	Xtriage
Refinement program	PHENIX 1.8.2	Depositor
R, R_{free}	0.201 , 0.245 0.202 , 0.246	Depositor DCC
R_{free} test set	88487 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	50.4	Xtriage
Anisotropy	0.251	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 60.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.43$, $\langle L^2 \rangle = 0.26$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	297096	wwPDB-VP
Average B, all atoms (Å ²)	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.50% 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: TEL, 2MA, MA6, 4OC, HGR, 5MC, MPD, 2MU, OMC, PSU, ZN, 5MU, M2G, 0TD, UR3, OMG, G7M, MG, 2MG, SF4

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	0.30	0/69030	0.49	5/107750 (0.0%)
1	2A	0.24	0/68902	0.43	2/107548 (0.0%)
2	1B	0.24	0/2876	0.44	0/4486
2	2B	0.20	0/2878	0.37	0/4490
3	1D	0.28	0/2181	0.53	0/2940
3	2D	0.23	0/2186	0.51	0/2944
4	1E	0.27	0/1592	0.49	0/2149
4	2E	0.23	0/1592	0.46	0/2149
5	1F	0.27	0/1619	0.48	0/2193
5	2F	0.22	0/1615	0.48	2/2188 (0.1%)
6	1G	0.20	0/1451	0.43	0/1961
6	2G	0.21	0/1449	0.42	0/1957
7	1H	0.23	0/1356	0.44	0/1834
7	2H	0.19	0/1350	0.40	0/1826
8	1I	0.20	0/1109	0.42	0/1512
8	2I	0.19	0/1091	0.40	0/1490
9	1N	0.27	0/1148	0.47	0/1547
9	2N	0.21	0/1144	0.41	0/1543
10	1O	0.28	0/943	0.47	0/1269
10	2O	0.24	0/943	0.46	0/1269
11	1P	0.27	0/1152	0.50	0/1533
11	2P	0.21	0/1152	0.46	0/1533
12	1Q	0.26	0/1143	0.47	0/1527
12	2Q	0.21	0/1143	0.40	0/1527
13	1R	0.29	0/982	0.50	0/1312
13	2R	0.23	0/982	0.48	0/1312
14	1S	0.23	0/887	0.47	0/1180
14	2S	0.20	0/880	0.45	0/1172
15	1T	0.27	0/1105	0.53	0/1477
15	2T	0.23	0/1097	0.48	0/1468
16	1U	0.30	0/977	0.51	0/1301

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
16	2U	0.21	0/977	0.40	0/1301
17	1V	0.24	0/786	0.44	0/1053
17	2V	0.20	0/782	0.42	0/1049
18	1W	0.29	0/897	0.46	0/1205
18	2W	0.24	0/897	0.43	0/1205
19	1X	0.27	0/764	0.51	0/1025
19	2X	0.22	0/764	0.42	0/1025
20	1Y	0.26	0/823	0.52	0/1099
20	2Y	0.21	0/823	0.47	0/1100
21	1Z	0.22	0/1620	0.44	0/2200
21	2Z	0.20	0/1590	0.43	0/2162
22	10	0.27	0/616	0.48	0/821
22	20	0.21	0/616	0.43	0/821
23	11	0.24	0/761	0.45	0/1013
23	21	0.24	0/766	0.45	0/1018
24	12	0.24	0/590	0.46	0/781
24	22	0.19	0/594	0.37	0/785
25	13	0.26	0/474	0.46	0/635
25	23	0.19	0/469	0.42	0/630
26	14	0.23	0/559	0.64	0/754
26	24	0.28	0/549	0.63	2/741 (0.3%)
27	15	0.30	0/473	0.51	0/639
27	25	0.25	0/469	0.46	0/635
28	16	0.25	0/460	0.48	0/613
28	26	0.22	0/456	0.41	0/608
29	17	0.33	0/426	0.54	0/561
29	27	0.26	0/426	0.47	0/561
30	18	0.31	0/525	0.52	0/691
30	28	0.22	0/525	0.37	0/691
31	19	0.29	0/310	0.51	0/407
31	29	0.20	0/310	0.42	0/407
32	1a	0.21	0/35795	0.40	0/55864
32	2a	0.20	0/35890	0.39	2/56012 (0.0%)
33	1b	0.22	0/1876	0.48	1/2533 (0.0%)
33	2b	0.24	0/1860	0.47	0/2518
34	1c	0.21	0/1582	0.41	0/2137
34	2c	0.22	0/1566	0.44	0/2119
35	1d	0.20	0/1695	0.47	0/2274
35	2d	0.19	0/1698	0.43	0/2277
36	1e	0.21	0/1149	0.44	0/1548
36	2e	0.21	0/1149	0.42	0/1548
37	1f	0.21	0/827	0.38	0/1120
37	2f	0.19	0/829	0.39	0/1123

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
38	1g	0.19	0/1254	0.39	0/1683
38	2g	0.19	0/1248	0.39	0/1676
39	1h	0.20	0/1118	0.41	0/1506
39	2h	0.17	0/1108	0.42	0/1494
40	1i	0.21	0/1005	0.46	0/1351
40	2i	0.22	0/985	0.49	0/1329
41	1j	0.20	0/732	0.42	0/993
41	2j	0.23	0/723	0.46	0/984
42	1k	0.21	0/849	0.38	0/1150
42	2k	0.20	0/848	0.50	2/1149 (0.2%)
43	1l	0.20	0/937	0.45	0/1260
43	2l	0.19	0/937	0.43	0/1260
44	1m	0.20	0/924	0.46	0/1242
44	2m	0.21	0/905	0.46	0/1217
45	1n	0.19	0/501	0.42	0/664
45	2n	0.22	0/501	0.43	0/664
46	1o	0.20	0/739	0.39	0/985
46	2o	0.19	0/739	0.39	0/985
47	1p	0.20	0/697	0.48	0/939
47	2p	0.21	0/693	0.44	0/935
48	1q	0.20	0/836	0.43	0/1117
48	2q	0.21	0/836	0.49	1/1117 (0.1%)
49	1r	0.21	0/560	0.44	0/746
49	2r	0.20	0/560	0.37	0/746
50	1s	0.17	0/663	0.44	0/895
50	2s	0.20	0/660	0.38	0/893
51	1t	0.21	0/734	0.46	0/969
51	2t	0.19	0/736	0.44	0/976
52	1u	0.19	0/203	0.43	0/266
52	2u	0.20	0/203	0.46	0/266
53	1y	0.18	0/776	0.36	0/1048
53	2y	0.22	0/761	0.39	0/1030
All	All	0.24	0/309939	0.44	17/463231 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
11	1P	0	1
11	2P	0	1

Continued on next page...

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Mol	Chain	#Chirality outliers	#Planarity outliers
26	14	0	1
33	1b	0	1
33	2b	0	1
All	All	0	5

There are no bond length outliers.

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1A	1042	G	OP1-P-O3'	-9.76	78.73	108.00
48	2q	65	ILE	N-CA-C	-7.18	105.78	112.96
1	2A	1992	G	C2'-C3'-O3'	6.43	119.14	109.50
1	1A	1042	G	OP2-P-O3'	-6.17	89.49	108.00
1	1A	1653	G	C2'-C3'-O3'	5.85	118.27	109.50
42	2k	116	HIS	CA-C-N	5.84	132.21	121.70
42	2k	116	HIS	C-N-CA	5.84	132.21	121.70
26	24	59	PHE	CA-C-N	5.72	131.99	121.70
26	24	59	PHE	C-N-CA	5.72	131.99	121.70
32	2a	266	G	C2'-C3'-O3'	5.67	118.01	109.50
1	2A	752	A	C2'-C3'-O3'	5.61	117.92	109.50
33	1b	110	GLN	N-CA-C	-5.60	106.52	113.19
1	1A	1300	U	P-O3'-C3'	5.21	128.02	120.20
32	2a	266	G	P-O3'-C3'	5.20	128.00	120.20
5	2F	21	ALA	CA-C-N	5.09	130.86	121.70
5	2F	21	ALA	C-N-CA	5.09	130.86	121.70
1	1A	1300	U	C4'-C3'-O3'	5.04	116.96	109.40

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
26	14	67	TYR	Peptide
11	1P	35	HIS	Peptide
33	1b	231	GLU	Peptide
11	2P	35	HIS	Peptide
33	2b	126	GLU	Peptide

5.2 Too-close contacts ⓘ

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	544	0
1	2A	61758	0	31152	690	0
2	1B	2572	0	1305	24	0
2	2B	2573	0	1306	31	0
3	1D	2131	0	2207	47	0
3	2D	2136	0	2218	42	0
4	1E	1559	0	1618	25	0
4	2E	1559	0	1618	33	0
5	1F	1584	0	1625	38	0
5	2F	1580	0	1619	42	0
6	1G	1426	0	1445	41	0
6	2G	1424	0	1441	52	0
7	1H	1330	0	1407	22	0
7	2H	1324	0	1402	41	0
8	1I	1094	0	1127	32	0
8	2I	1076	0	1094	25	0
9	1N	1121	0	1195	13	0
9	2N	1117	0	1184	20	0
10	1O	933	0	996	16	0
10	2O	933	0	996	20	0
11	1P	1135	0	1212	33	0
11	2P	1135	0	1212	24	0
12	1Q	1122	0	1179	13	0
12	2Q	1122	0	1179	25	0
13	1R	968	0	1033	18	0
13	2R	968	0	1033	13	0
14	1S	877	0	938	16	0
14	2S	870	0	923	19	0
15	1T	1091	0	1151	27	0
15	2T	1083	0	1136	28	0
16	1U	959	0	1019	20	0
16	2U	959	0	1019	15	0
17	1V	775	0	841	9	0
17	2V	771	0	830	14	0
18	1W	886	0	940	6	0
18	2W	886	0	940	12	0
19	1X	750	0	814	11	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	2X	750	0	814	14	0
20	1Y	810	0	892	20	0
20	2Y	810	0	887	26	0
21	1Z	1587	0	1598	31	0
21	2Z	1557	0	1564	32	0
22	10	608	0	622	8	0
22	20	608	0	622	10	0
23	11	754	0	823	9	0
23	21	759	0	837	18	0
24	12	588	0	643	7	0
24	22	592	0	654	11	0
25	13	469	0	518	4	0
25	23	464	0	514	10	0
26	14	546	0	522	22	0
26	24	536	0	514	30	0
27	15	459	0	476	6	0
27	25	455	0	465	6	0
28	16	453	0	473	6	0
28	26	449	0	469	7	0
29	17	418	0	467	4	0
29	27	418	0	467	7	0
30	18	517	0	582	19	0
30	28	517	0	582	8	0
31	19	307	0	335	4	0
31	29	307	0	335	3	0
32	1a	32246	0	16294	407	0
32	2a	32331	0	16338	462	0
33	1b	1842	0	1862	50	0
33	2b	1825	0	1828	72	0
34	1c	1558	0	1557	38	0
34	2c	1542	0	1517	52	0
35	1d	1665	0	1687	62	0
35	2d	1668	0	1703	41	0
36	1e	1133	0	1191	33	0
36	2e	1133	0	1191	32	0
37	1f	814	0	808	15	0
37	2f	816	0	808	15	0
38	1g	1235	0	1249	24	0
38	2g	1229	0	1238	23	0
39	1h	1098	0	1143	22	0
39	2h	1088	0	1126	30	0
40	1i	986	0	990	39	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
40	2i	966	0	953	37	0
41	1j	719	0	672	23	0
41	2j	710	0	661	28	0
42	1k	834	0	838	11	0
42	2k	833	0	836	17	0
43	1l	932	0	981	17	0
43	2l	932	0	981	15	0
44	1m	914	0	954	27	0
44	2m	895	0	920	39	0
45	1n	492	0	529	17	0
45	2n	492	0	529	27	0
46	1o	728	0	760	22	0
46	2o	728	0	760	16	0
47	1p	681	0	697	23	0
47	2p	677	0	686	20	0
48	1q	823	0	891	17	0
48	2q	823	0	891	23	0
49	1r	555	0	618	13	0
49	2r	555	0	618	9	0
50	1s	648	0	658	23	0
50	2s	645	0	635	35	0
51	1t	732	0	809	16	0
51	2t	733	0	795	14	0
52	1u	199	0	208	3	0
52	2u	199	0	208	12	0
53	1y	764	0	786	15	0
53	2y	749	0	757	37	0
54	10	7	0	0	0	0
54	11	5	0	0	0	0
54	13	3	0	0	0	0
54	14	1	0	0	0	0
54	15	8	0	0	0	0
54	17	6	0	0	0	0
54	18	2	0	0	0	0
54	19	2	0	0	0	0
54	1A	1017	0	0	0	0
54	1B	29	0	0	0	0
54	1D	17	0	0	0	0
54	1E	9	0	0	0	0
54	1F	20	0	0	0	0
54	1G	4	0	0	0	0
54	1H	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
54	1N	4	0	0	0	0
54	1O	1	0	0	0	0
54	1P	5	0	0	0	0
54	1Q	5	0	0	0	0
54	1R	6	0	0	0	0
54	1T	4	0	0	0	0
54	1U	9	0	0	0	0
54	1V	7	0	0	0	0
54	1W	4	0	0	0	0
54	1X	2	0	0	0	0
54	1Y	1	0	0	0	0
54	1Z	1	0	0	0	0
54	1a	276	0	0	0	0
54	1b	1	0	0	0	0
54	1d	6	0	0	0	0
54	1e	2	0	0	0	0
54	1f	2	0	0	0	0
54	1g	3	0	0	0	0
54	1h	2	0	0	0	0
54	1i	1	0	0	0	0
54	1k	1	0	0	0	0
54	1l	2	0	0	0	0
54	1m	1	0	0	0	0
54	1n	2	0	0	0	0
54	1o	1	0	0	0	0
54	1t	1	0	0	0	0
54	1y	4	0	0	0	0
54	20	2	0	0	0	0
54	21	2	0	0	0	0
54	23	2	0	0	0	0
54	25	4	0	0	0	0
54	27	1	0	0	0	0
54	28	2	0	0	0	0
54	2A	737	0	0	0	0
54	2B	19	0	0	0	0
54	2D	11	0	0	0	0
54	2E	6	0	0	0	0
54	2F	4	0	0	0	0
54	2G	3	0	0	0	0
54	2I	1	0	0	0	0
54	2N	1	0	0	0	0
54	2O	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
54	2P	4	0	0	0	0
54	2Q	4	0	0	0	0
54	2R	2	0	0	0	0
54	2T	4	0	0	0	0
54	2V	3	0	0	0	0
54	2W	3	0	0	0	0
54	2X	1	0	0	0	0
54	2a	184	0	0	0	0
54	2e	2	0	0	0	0
54	2f	1	0	0	0	0
54	2j	1	0	0	0	0
54	2k	1	0	0	0	0
54	2l	1	0	0	0	0
54	2n	1	0	0	0	0
54	2t	1	0	0	0	0
54	2y	1	0	0	0	0
55	1A	36	0	29	2	0
55	2A	36	0	29	4	0
56	1A	58	0	65	2	0
56	2A	58	0	65	2	0
57	18	8	0	14	2	0
57	1A	8	0	14	1	0
57	1T	8	0	14	0	0
57	1a	8	0	12	3	0
57	2A	16	0	28	1	0
57	2B	8	0	14	0	0
58	1B	12	0	12	1	0
58	1F	12	0	12	1	0
59	14	1	0	0	0	0
59	15	1	0	0	0	0
59	16	1	0	0	0	0
59	19	1	0	0	0	0
59	1Y	1	0	0	0	0
59	1n	1	0	0	0	0
59	24	1	0	0	0	0
59	25	1	0	0	0	0
59	26	1	0	0	0	0
59	29	1	0	0	0	0
59	2Y	1	0	0	0	0
59	2n	1	0	0	0	0
60	1d	8	0	0	1	0
60	2d	8	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
61	10	25	0	0	0	0
61	11	20	0	0	0	0
61	12	15	0	0	1	0
61	13	20	0	0	0	0
61	14	4	0	0	0	0
61	15	25	0	0	1	0
61	16	16	0	0	1	0
61	17	15	0	0	1	0
61	18	24	0	0	1	0
61	19	2	0	0	0	0
61	1A	3818	0	0	88	0
61	1B	94	0	0	7	0
61	1D	110	0	0	5	0
61	1E	67	0	0	0	0
61	1F	62	0	0	3	0
61	1G	15	0	0	0	0
61	1H	17	0	0	0	0
61	1I	7	0	0	0	0
61	1N	45	0	0	0	0
61	1O	24	0	0	1	0
61	1P	57	0	0	4	0
61	1Q	36	0	0	1	0
61	1R	32	0	0	2	0
61	1S	10	0	0	0	0
61	1T	35	0	0	2	0
61	1U	44	0	0	3	0
61	1V	34	0	0	0	0
61	1W	22	0	0	0	0
61	1X	25	0	0	1	0
61	1Y	13	0	0	1	0
61	1Z	12	0	0	1	0
61	1a	406	0	0	24	0
61	1d	7	0	0	1	0
61	1e	5	0	0	2	0
61	1f	2	0	0	0	0
61	1h	1	0	0	0	0
61	1i	1	0	0	0	0
61	1j	1	0	0	0	0
61	1k	1	0	0	0	0
61	1l	4	0	0	0	0
61	1o	3	0	0	2	0
61	1p	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6l	1q	2	0	0	0	0
6l	1u	1	0	0	1	0
6l	1y	2	0	0	0	0
6l	20	11	0	0	0	0
6l	21	16	0	0	0	0
6l	22	1	0	0	1	0
6l	23	3	0	0	0	0
6l	24	1	0	0	0	0
6l	25	10	0	0	0	0
6l	26	5	0	0	0	0
6l	27	6	0	0	0	0
6l	28	10	0	0	1	0
6l	29	1	0	0	0	0
6l	2A	2123	0	0	94	0
6l	2B	44	0	0	6	0
6l	2D	53	0	0	1	0
6l	2E	23	0	0	0	0
6l	2F	18	0	0	0	0
6l	2G	3	0	0	0	0
6l	2H	2	0	0	0	0
6l	2I	2	0	0	0	0
6l	2N	3	0	0	1	0
6l	2O	18	0	0	0	0
6l	2P	21	0	0	2	0
6l	2Q	17	0	0	0	0
6l	2R	18	0	0	2	0
6l	2S	2	0	0	0	0
6l	2T	8	0	0	0	0
6l	2U	13	0	0	1	0
6l	2V	6	0	0	0	0
6l	2W	18	0	0	0	0
6l	2X	8	0	0	0	0
6l	2Y	4	0	0	1	0
6l	2Z	8	0	0	1	0
6l	2a	264	0	0	20	0
6l	2d	2	0	0	0	0
6l	2e	1	0	0	0	0
6l	2f	3	0	0	0	0
6l	2j	1	0	0	0	0
6l	2l	2	0	0	0	0
6l	2n	1	0	0	0	0
6l	2o	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
61	2p	1	0	0	0	0
61	2q	1	0	0	0	0
61	2r	3	0	0	0	0
61	2t	1	0	0	0	0
61	2y	1	0	0	0	0
All	All	297096	0	194704	3832	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 (3832) 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	1.41	1.16
1:2A:2139:C:N4	1:2A:2152:G:H1	1.52	1.07
32:2a:1003:G:H2'	32:2a:1004:A:H4'	1.47	0.96
1:1A:2137:C:N4	1:1A:2154:G:H1	1.64	0.95
1:1A:2319:G:H22	14:1S:3:ARG:HD3	1.30	0.94
3:1D:69:ARG:NH2	3:1D:128:GLY:O	2.02	0.93
32:1a:73:G:H1	32:1a:96:U:H3	1.17	0.92
22:10:10:THR:HG22	22:10:12:ASN:H	1.32	0.92
32:1a:1182:G:H4'	32:1a:1183:A:H5'	1.49	0.92
1:1A:1082:U:O4	1:1A:1086:A:N1	2.03	0.91
1:2A:1798:U:H5'	3:2D:259:THR:HG22	1.53	0.91
4:1E:47:VAL:HG21	4:1E:86:PRO:HD2	1.52	0.91
32:1a:559:A:OP1	36:1e:126:ARG:NH2	2.05	0.90
22:20:10:THR:HG22	22:20:12:ASN:H	1.35	0.90
32:1a:1086:U:H3	32:1a:1099:G:H22	1.19	0.89
1:2A:2427:C:OP1	61:2A:3802:HOH:O	1.89	0.89
20:1Y:92:ASN:HB2	20:1Y:94:LYS:H	1.37	0.89
1:2A:2602:A:H1'	1:2A:2603:G:H5''	1.54	0.88
6:1G:161:THR:HG22	6:1G:163:ALA:H	1.36	0.88
1:2A:2807:G:N2	1:2A:2893:G:O6	2.05	0.87
1:1A:1054:A:H61	1:1A:1105:U:H3	1.23	0.86
1:1A:1082:U:H3	1:1A:1086:A:H61	0.87	0.86
10:2O:48:PRO:HB3	32:2a:1422:G:H5''	1.55	0.86
32:2a:975:A:H4'	32:2a:976:G:H5''	1.57	0.86
1:1A:2102:U:O2	1:1A:2187:G:O6	1.93	0.86
1:2A:2131:G:H5''	1:2A:2132:U:H5'	1.58	0.85
4:2E:110:GLY:O	61:2R:301:HOH:O	1.94	0.85
1:2A:1647:G:OP1	61:2A:3803:HOH:O	1.94	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2099:U:H3	1:2A:2190:G:H1	1.22	0.85
1:2A:2102:U:O2	1:2A:2187:G:O6	1.96	0.84
36:2e:50:GLU:HB2	36:2e:53:LEU:HD13	1.59	0.84
1:2A:585:G:OP2	61:2A:3804:HOH:O	1.94	0.84
1:1A:279:C:H42	1:1A:361:G:H1	1.22	0.83
32:1a:201:C:H42	32:1a:216:G:H1	1.24	0.83
32:2a:1518:MA6:H93	32:2a:1519:MA6:H102	1.61	0.83
1:2A:881:G:H1	1:2A:895:U:H3	1.26	0.83
32:1a:992:U:H4'	32:1a:993:G:H5'	1.60	0.82
1:2A:2139:C:N3	1:2A:2152:G:N2	2.28	0.82
1:2A:1271:G:OP2	61:2A:3803:HOH:O	1.97	0.82
1:1A:2137:C:N3	1:1A:2154:G:N2	2.28	0.82
1:1A:2137:C:H42	1:1A:2154:G:H1	1.27	0.82
11:2P:29:LYS:HD3	11:2P:30:THR:HG23	1.62	0.82
41:1j:35:SER:HB3	41:1j:73:ASP:HB2	1.62	0.81
32:2a:718:G:H5'	42:2k:117:ASN:HD21	1.43	0.81
2:1B:102:A:N7	61:1B:301:HOH:O	2.14	0.81
1:2A:526:A:OP1	61:2A:3805:HOH:O	1.96	0.81
33:2b:178:ARG:HH22	39:2h:74:PRO:HB3	1.43	0.81
1:2A:1064:C:N4	1:2A:1074:G:O6	2.13	0.81
1:2A:2079:U:OP1	23:21:21:ARG:NH2	2.13	0.81
33:2b:16:HIS:HB2	33:2b:204:ASN:HB3	1.62	0.81
44:2m:5:ALA:HB2	44:2m:61:GLU:HG2	1.63	0.80
26:14:16:CYS:SG	26:14:17:GLY:N	2.55	0.80
53:2y:56:THR:HG22	53:2y:58:ASN:H	1.46	0.80
32:1a:544:G:OP1	35:1d:59:ARG:NH2	2.15	0.80
3:1D:242:ARG:HG3	3:1D:242:ARG:HH11	1.46	0.80
10:1O:48:PRO:HB3	32:1a:1422:G:H5''	1.64	0.80
1:2A:2296:U:OP2	14:2S:9:ARG:NH2	2.15	0.80
1:1A:1271:G:OP2	61:1A:4104:HOH:O	1.98	0.79
1:1A:1798:U:H5'	3:1D:259:THR:HG22	1.63	0.79
1:2A:1890:A:OP2	61:2A:3806:HOH:O	2.01	0.79
22:10:11:ARG:O	22:10:14:ARG:NH2	2.14	0.79
21:2Z:19:ARG:NH1	21:2Z:84:GLU:O	2.15	0.79
32:1a:1300:G:N7	61:1a:3307:HOH:O	2.16	0.79
1:1A:1670:C:OP2	61:1A:4105:HOH:O	2.00	0.79
16:1U:101:ARG:NH2	61:1U:301:HOH:O	2.16	0.79
1:1A:1669:A:OP2	61:1A:4105:HOH:O	2.00	0.78
38:2g:113:GLU:HG3	38:2g:119:ARG:HG2	1.65	0.78
32:1a:289:G:OP2	61:1a:3301:HOH:O	2.00	0.78
32:1a:366:C:N3	61:1a:3306:HOH:O	2.15	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:1j:49:VAL:HG23	45:1n:41:ARG:HB2	1.66	0.78
24:22:65:ASN:OD1	24:22:69:ARG:NH1	2.17	0.78
32:2a:1128:C:H1'	32:2a:1147:C:H42	1.49	0.78
33:2b:91:PRO:HG3	33:2b:155:LEU:HD13	1.64	0.78
32:1a:1151:A:HO2'	32:1a:1152:A:H8	1.31	0.78
32:1a:975:A:H4'	32:1a:976:G:H5''	1.65	0.78
46:1o:54:ARG:HG2	46:1o:58:MET:HE2	1.66	0.78
1:2A:1332:G:OP1	61:2A:3807:HOH:O	2.02	0.78
6:2G:161:THR:HG22	6:2G:163:ALA:H	1.47	0.78
32:1a:38:G:H22	32:1a:397:A:H5'	1.49	0.78
1:2A:1057:A:N6	1:2A:1087:G:OP1	2.17	0.78
33:2b:77:ALA:HB2	33:2b:211:ILE:HD13	1.64	0.77
1:1A:2427:C:OP1	61:1A:4106:HOH:O	2.02	0.77
32:1a:664:G:H22	32:1a:741:G:H1	1.30	0.77
1:1A:1359:A:H61	1:1A:1372:U:H3	1.28	0.77
1:2A:994:C:OP1	16:2U:53:ARG:NH2	2.17	0.77
1:1A:826:U:OP1	61:1A:4106:HOH:O	2.01	0.77
32:1a:116:A:OP1	61:1a:3301:HOH:O	2.03	0.77
32:2a:977:A:N6	32:2a:1224:G:OP1	2.16	0.77
37:2f:30:LEU:HD23	37:2f:75:LEU:HD11	1.67	0.77
23:11:50:ARG:HG2	23:11:59:THR:HG22	1.67	0.77
32:1a:612:C:O2	32:1a:629:G:N2	2.17	0.77
35:1d:15:GLU:OE2	35:1d:59:ARG:NH1	2.18	0.77
32:2a:1182:G:H4'	32:2a:1183:A:H3'	1.66	0.77
18:2W:18:ARG:NH1	18:2W:76:VAL:O	2.18	0.76
29:17:24:THR:HG23	29:17:27:GLY:H	1.51	0.76
1:2A:1530:C:O2'	1:2A:1531:C:O5'	2.03	0.76
32:2a:505:G:N7	61:2a:3210:HOH:O	2.17	0.76
50:2s:36:ARG:HH12	50:2s:75:ALA:HB3	1.49	0.76
1:2A:731:C:OP1	61:2A:3808:HOH:O	2.03	0.76
1:2A:242:G:OP1	61:2A:3809:HOH:O	2.04	0.76
32:2a:559:A:H4'	32:2a:560:U:H3'	1.68	0.76
1:1A:2242:G:OP1	61:1A:4107:HOH:O	2.03	0.76
47:1p:53:VAL:HG13	47:1p:79:VAL:HG12	1.66	0.76
8:1I:68:LEU:HD21	8:1I:109:ILE:HD11	1.68	0.76
1:2A:2306:C:H3'	1:2A:2307:G:H2'	1.66	0.76
35:2d:18:LYS:NZ	35:2d:31:CYS:SG	2.59	0.76
6:1G:83:ARG:H	6:1G:86:MET:HE2	1.50	0.76
1:2A:751:A:H5'	18:2W:90:ARG:HA	1.68	0.75
33:1b:82:ARG:NH1	33:1b:92:TYR:OH	2.20	0.75
8:2I:92:VAL:HG23	8:2I:120:ILE:HB	1.67	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:24:59:PHE:HA	26:24:61:ARG:N	2.01	0.75
1:2A:2748:A:H5'	7:2H:4:ILE:HD12	1.69	0.75
32:1a:1189:C:OP1	41:1j:51:ARG:NH2	2.20	0.75
1:2A:2123:G:O6	1:2A:2175:C:N3	2.20	0.74
5:2F:21:ALA:HB3	5:2F:22:ALA:HA	1.68	0.74
11:1P:42:SER:O	61:1P:301:HOH:O	2.03	0.74
32:1a:330:C:OP2	61:1a:3302:HOH:O	2.04	0.74
1:2A:674:G:OP2	61:2A:3811:HOH:O	2.05	0.74
1:2A:2110:G:OP1	1:2A:2118:U:N3	2.20	0.74
32:1a:1025:U:C2	32:1a:1036:G:O6	2.40	0.74
1:1A:11:G:H2'	1:1A:12:U:H5''	1.70	0.74
1:1A:1701:A:OP2	61:1A:4108:HOH:O	2.05	0.74
50:1s:55:LYS:HG2	50:1s:56:GLN:HG2	1.68	0.74
40:1i:3:GLN:HE21	40:1i:20:ARG:HE	1.34	0.74
1:2A:2610:C:O2'	61:2A:3810:HOH:O	2.05	0.74
51:2t:50:GLU:HB2	51:2t:99:LEU:HD23	1.68	0.74
23:11:21:ARG:HD3	23:11:35:THR:HG21	1.69	0.74
32:1a:945:G:OP1	61:1a:3303:HOH:O	2.04	0.74
38:1g:27:ILE:HD12	38:1g:40:ALA:HA	1.68	0.74
1:2A:826:U:OP1	61:2A:3802:HOH:O	2.05	0.73
1:2A:2141:G:O6	1:2A:2150:U:O2	2.06	0.73
40:2i:4:TYR:HB2	40:2i:19:LEU:HB2	1.69	0.73
32:2a:1129:C:H2'	32:2a:1139:G:N7	2.03	0.73
3:1D:71:ASP:HB3	3:1D:103:ARG:HH12	1.54	0.73
1:2A:991:C:OP2	61:2A:3812:HOH:O	2.07	0.73
1:2A:2134:A:O2'	1:2A:2159:G:N3	2.21	0.73
32:2a:201:C:H42	32:2a:216:G:H1	1.37	0.73
50:2s:50:ALA:HB1	50:2s:57:HIS:HB3	1.71	0.73
1:1A:2308:G:O2'	1:1A:2310:A:N7	2.21	0.73
1:1A:2822:G:OP2	61:1A:4109:HOH:O	2.05	0.73
36:2e:140:ARG:O	36:2e:143:ARG:NH2	2.22	0.73
32:2a:1285:A:H4'	32:2a:1286:A:H5'	1.70	0.73
1:1A:1062:G:H1'	1:1A:1088:A:H62	1.52	0.73
1:2A:2115:G:H22	1:2A:2119:A:H5'	1.54	0.73
32:2a:21:G:OP1	61:2a:3202:HOH:O	2.07	0.73
40:1i:50:LEU:HD13	40:1i:56:LEU:HA	1.69	0.72
1:2A:2822:G:OP2	61:2A:3813:HOH:O	2.07	0.72
11:2P:59:LEU:HD11	30:28:10:ALA:HB2	1.70	0.72
40:2i:46:ALA:HB2	40:2i:74:ILE:HG23	1.71	0.72
44:2m:58:GLU:O	44:2m:62:ASN:ND2	2.22	0.72
35:1d:59:ARG:HH12	35:1d:66:ARG:HH12	1.35	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:24:16:CYS:SG	26:24:17:GLY:N	2.62	0.72
32:2a:1030(A):G:H21	32:2a:1030(C):G:H3'	1.53	0.72
51:2t:57:ARG:HH22	51:2t:100:ILE:HD12	1.54	0.72
1:1A:511:U:OP2	61:1A:4110:HOH:O	2.07	0.72
1:1A:1173:G:H21	1:1A:1177:A:H2	1.38	0.72
8:1I:92:VAL:HG13	8:1I:120:ILE:HB	1.70	0.72
32:1a:1069:C:OP2	61:1a:3304:HOH:O	2.07	0.72
2:2B:75:G:OP1	61:2B:301:HOH:O	2.07	0.72
1:1A:1865:G:OP1	61:1A:4112:HOH:O	2.08	0.72
28:16:13:CYS:SG	28:16:47:THR:HG21	2.29	0.72
19:1X:35:THR:HG22	19:1X:38:GLU:H	1.53	0.72
32:1a:1025:U:O2	32:1a:1036:G:O6	2.07	0.72
1:2A:2168:G:HO2'	1:2A:2170:A:H62	1.36	0.72
32:2a:937:A:OP2	61:2a:3201:HOH:O	2.06	0.72
32:2a:1286:A:H8	32:2a:1287:A:H4'	1.54	0.72
1:1A:1634:A:OP2	61:1A:4111:HOH:O	2.07	0.72
27:25:16:ARG:NH1	27:25:17:ASP:OD1	2.23	0.72
32:2a:1005:A:OP2	32:2a:1024:G:N2	2.23	0.72
1:1A:1105:U:H2'	1:1A:1106:G:H8	1.55	0.71
1:1A:2464:C:O2'	61:1A:4118:HOH:O	2.08	0.71
37:1f:1:MET:HE3	37:1f:66:GLU:HG2	1.72	0.71
12:2Q:137:TYR:HB3	21:2Z:76:LEU:HD11	1.72	0.71
32:1a:501:C:OP1	43:1l:117:ARG:NH2	2.20	0.71
1:2A:1670:C:OP1	61:2A:3814:HOH:O	2.09	0.71
32:2a:407:G:OP1	35:2d:115:ARG:NH2	2.23	0.71
34:2c:47:LEU:HD13	34:2c:68:VAL:HG11	1.71	0.71
11:1P:59:LEU:HD11	30:18:10:ALA:HB2	1.73	0.71
32:1a:1077:G:N2	32:1a:1080:A:OP2	2.21	0.71
32:1a:1518:MA6:H93	32:1a:1519:MA6:H92	1.71	0.71
1:2A:1669:A:OP2	61:2A:3815:HOH:O	2.09	0.71
21:2Z:33:LEU:HD11	21:2Z:90:VAL:HG21	1.73	0.71
1:1A:220:G:O6	61:1A:4114:HOH:O	2.08	0.71
1:1A:1332:G:OP1	61:1A:4119:HOH:O	2.09	0.71
1:1A:2140:C:H2'	1:1A:2141:G:H8	1.55	0.71
1:2A:2104:G:N2	1:2A:2105:C:N3	2.38	0.71
1:2A:2805:G:H2'	1:2A:2807:G:C8	2.26	0.71
12:2Q:34:LEU:HB2	12:2Q:118:LEU:HD22	1.73	0.71
43:2l:32:PHE:HB3	43:2l:84:LEU:HD11	1.73	0.71
11:1P:141:ALA:HA	25:23:38:GLU:HG2	1.72	0.71
2:1B:81:G:N7	58:1B:230:ARG:NH2	2.38	0.70
32:2a:942:G:N2	40:2i:124:GLN:OE1	2.24	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:744:G:O6	61:1A:4113:HOH:O	2.08	0.70
1:2A:321:G:OP1	5:2F:135:LYS:NZ	2.23	0.70
1:1A:1970:A:OP1	61:1A:4120:HOH:O	2.09	0.70
32:2a:1004:A:H5''	32:2a:1025:U:C5	2.26	0.70
1:1A:2290:G:OP2	61:1A:4116:HOH:O	2.08	0.70
1:2A:2810:A:N6	1:2A:2891:G:O2'	2.24	0.70
46:2o:54:ARG:HG2	46:2o:58:MET:HE2	1.73	0.70
1:1A:1094:U:H1'	1:1A:1097:U:H5	1.56	0.70
44:1m:37:THR:O	44:1m:55:ARG:NH1	2.22	0.70
32:2a:1108:G:H5'	34:2c:176:HIS:HD2	1.57	0.70
1:2A:154(A):C:H42	1:2A:171:G:H1	1.38	0.70
1:1A:253:C:OP1	61:1A:4122:HOH:O	2.10	0.70
32:1a:1124:G:N2	32:1a:1125:U:O4	2.25	0.70
1:1A:521:G:O6	61:1A:4115:HOH:O	2.08	0.69
1:1A:2251:OMG:OP2	61:1A:4121:HOH:O	2.09	0.69
19:1X:76:ARG:NH1	61:1X:201:HOH:O	2.25	0.69
1:2A:326:G:N7	61:2A:3887:HOH:O	2.24	0.69
32:2a:17:U:H2'	32:2a:18:C:C6	2.27	0.69
35:1d:30:LYS:HA	35:1d:35:ARG:HE	1.57	0.69
1:2A:792:G:O6	61:2A:3816:HOH:O	2.09	0.69
1:2A:1101:U:H2'	1:2A:1102:C:H6	1.55	0.69
35:2d:175:SER:HB3	35:2d:186:LEU:HD21	1.75	0.69
1:1A:400:G:N7	61:1A:4171:HOH:O	2.24	0.69
1:2A:14:A:OP2	61:2A:3819:HOH:O	2.10	0.69
1:2A:2319:G:H22	14:2S:3:ARG:HD3	1.57	0.69
48:1q:66:SER:O	48:1q:70:ARG:NH1	2.25	0.69
1:2A:1648:C:OP1	61:2A:3803:HOH:O	2.09	0.69
1:1A:1185:C:OP2	61:1A:4123:HOH:O	2.10	0.69
1:2A:1030:G:OP2	12:2Q:128:LYS:NZ	2.25	0.69
1:2A:2469:A:H4'	12:2Q:56:ARG:HG2	1.74	0.69
32:2a:117:G:OP2	61:2a:3207:HOH:O	2.11	0.69
34:2c:58:GLU:HB3	41:2j:92:THR:HG21	1.73	0.69
32:2a:803:G:OP1	61:2a:3206:HOH:O	2.11	0.69
38:2g:114:ARG:H	38:2g:115:ARG:NH2	1.91	0.69
1:2A:452:G:OP2	61:2A:3820:HOH:O	2.10	0.69
1:2A:1771:C:OP1	61:2A:3821:HOH:O	2.11	0.69
1:1A:278:A:O2'	1:1A:279:C:OP1	2.10	0.69
1:1A:1047:G:H2'	1:1A:1110:G:H22	1.57	0.69
35:1d:18:LYS:NZ	35:1d:31:CYS:SG	2.66	0.69
1:1A:1054:A:N6	1:1A:1105:U:H3	1.91	0.69
1:2A:364:C:OP2	61:2A:3818:HOH:O	2.10	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:544:G:OP1	35:2d:59:ARG:NH2	2.21	0.69
34:2c:35:GLU:HA	34:2c:38:ARG:HD2	1.75	0.69
44:2m:15:VAL:HG11	44:2m:48:LEU:HD21	1.74	0.69
39:2h:110:ALA:HB1	39:2h:133:LEU:HD11	1.75	0.69
32:1a:1318:A:OP1	50:1s:3:ARG:NH2	2.26	0.68
40:2i:9:ARG:HB2	40:2i:104:ARG:HE	1.58	0.68
40:2i:9:ARG:HG2	40:2i:14:VAL:HG12	1.74	0.68
1:2A:963:U:OP2	61:2A:3823:HOH:O	2.11	0.68
32:2a:1416:G:OP2	61:2a:3205:HOH:O	2.10	0.68
1:2A:2104:G:O6	1:2A:2185:C:N3	2.27	0.68
1:2A:2206:G:H3'	1:2A:2207:G:C8	2.29	0.68
1:1A:1315:C:OP2	61:1A:4119:HOH:O	2.11	0.68
33:1b:63:MET:HG3	33:1b:225:ALA:HB1	1.76	0.68
1:2A:1507:A:O2'	1:2A:1508:A:O5'	2.12	0.68
1:2A:2046:G:OP1	61:2A:3824:HOH:O	2.11	0.68
40:2i:25:LYS:H	40:2i:60:ASP:HB3	1.58	0.68
35:1d:98:GLU:OE1	35:1d:103:ASN:ND2	2.23	0.68
1:2A:1266:G:O5'	18:2W:15:ARG:NH2	2.27	0.68
2:2B:49:C:OP1	61:2B:302:HOH:O	2.11	0.68
1:1A:2447:G:OP2	61:1A:4127:HOH:O	2.12	0.68
1:1A:1757:U:OP1	61:1A:4125:HOH:O	2.11	0.68
26:24:58:ARG:HH21	50:2s:68:GLY:H	1.42	0.68
32:2a:1500:A:OP2	61:2a:3204:HOH:O	2.10	0.68
1:1A:955:C:OP1	12:1Q:87:LYS:NZ	2.25	0.68
47:1p:45:THR:HG23	47:1p:47:ASP:H	1.59	0.68
40:2i:17:VAL:HA	40:2i:63:ILE:HG12	1.74	0.68
1:2A:15:G:OP2	61:2A:3819:HOH:O	2.10	0.68
1:1A:2126:A:H4'	1:1A:2127:G:O5'	1.93	0.67
1:1A:2133:G:H3'	1:1A:2157:G:H21	1.58	0.67
1:2A:309:G:N3	1:2A:329:G:O2'	2.27	0.67
1:2A:2425:A:N7	61:2A:3914:HOH:O	2.27	0.67
32:2a:1500:A:OP1	61:2a:3203:HOH:O	2.10	0.67
1:1A:631:A:OP1	11:1P:65:ARG:NH1	2.25	0.67
39:1h:10:LEU:HD22	39:1h:83:ILE:HD11	1.75	0.67
1:1A:1024:G:OP2	61:1A:4126:HOH:O	2.12	0.67
1:1A:1058:G:O6	1:1A:1080:C:N3	2.27	0.67
10:2O:35:VAL:HG21	10:2O:69:ILE:HD13	1.75	0.67
32:2a:1402:4OC:HM22	32:2a:1403:C:H5'	1.75	0.67
1:1A:256:A:OP2	61:1A:4124:HOH:O	2.11	0.67
1:2A:975:C:O2	61:2A:3817:HOH:O	2.09	0.67
1:2A:1063:G:H1	1:2A:1075:C:N4	1.92	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2431:U:OP1	61:2A:3825:HOH:O	2.12	0.67
5:2F:132:VAL:HG21	5:2F:163:VAL:HG22	1.75	0.67
32:2a:1305:G:N2	32:2a:1331:G:H1'	2.10	0.67
1:2A:1315:C:OP2	61:2A:3807:HOH:O	2.12	0.67
32:2a:1318:A:H1'	50:2s:37:ARG:HH11	1.58	0.67
1:2A:1184:G:OP1	25:23:30:ARG:NH1	2.27	0.67
8:1I:104:GLN:HB2	8:1I:105:HIS:HD2	1.59	0.67
1:2A:2139:C:H42	1:2A:2152:G:H1	0.76	0.67
1:2A:2379:G:O2'	14:2S:17:ARG:NH2	2.28	0.67
39:2h:51:VAL:HG11	39:2h:60:ARG:HH11	1.59	0.67
53:2y:53:THR:HG22	53:2y:62:VAL:HG22	1.77	0.67
1:1A:2683:C:OP1	15:1T:53:ARG:NH2	2.28	0.67
6:2G:101:ILE:HD13	26:24:25:TYR:HB2	1.77	0.67
29:27:24:THR:HG22	29:27:27:GLY:H	1.59	0.67
34:2c:155:GLY:HA3	34:2c:196:LEU:HD22	1.76	0.67
1:1A:784:A:H5'	1:1A:785:G:OP1	1.95	0.67
36:1e:8:GLU:HG2	36:1e:34:VAL:HG12	1.74	0.67
50:1s:50:ALA:HB1	50:1s:57:HIS:HB3	1.75	0.67
4:1E:105:THR:OG1	4:1E:199:ARG:NH2	2.27	0.67
7:2H:13:LYS:HD3	7:2H:14:GLY:HA2	1.76	0.67
34:2c:63:ASN:HB2	34:2c:98:ASN:HB2	1.76	0.67
3:2D:125:ILE:HB	37:2f:81:ILE:HD11	1.77	0.66
21:2Z:73:GLN:NE2	61:2Z:301:HOH:O	2.27	0.66
26:14:53:GLU:OE1	44:1m:65:LYS:NZ	2.28	0.66
1:1A:271(N):U:O2	61:1A:4117:HOH:O	2.08	0.66
6:1G:150:ASP:OD1	6:1G:151:ALA:N	2.27	0.66
1:2A:407:G:OP2	61:2A:3827:HOH:O	2.13	0.66
1:2A:2306:C:N4	6:2G:42:GLY:O	2.27	0.66
7:2H:46:GLU:HB2	7:2H:49:VAL:HG12	1.77	0.66
32:2a:1030(A):G:H2'	32:2a:1030(B):C:H5''	1.77	0.66
1:2A:1073:A:H2'	1:2A:1074:G:C8	2.31	0.66
1:2A:2126:A:H4'	1:2A:2127:G:O5'	1.95	0.66
17:2V:60:GLU:OE1	17:2V:97:LYS:NZ	2.29	0.66
33:2b:119:GLU:OE2	33:2b:153:ARG:NH1	2.29	0.66
53:2y:6:THR:HB	53:2y:40:ILE:HA	1.78	0.66
1:1A:1023:U:OP2	61:1A:4126:HOH:O	2.12	0.66
1:2A:1314:C:OP1	61:2A:3807:HOH:O	2.14	0.66
21:2Z:152:ALA:HA	21:2Z:155:LEU:HD13	1.76	0.66
32:1a:1047:G:H5''	45:1n:4:LYS:HD3	1.78	0.66
40:1i:46:ALA:HB2	40:1i:74:ILE:HG23	1.78	0.66
1:2A:7:G:H1	1:2A:2896:C:H42	1.44	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:2c:6:HIS:CD2	45:2n:49:HIS:HB3	2.31	0.66
1:1A:1359:A:N6	1:1A:1372:U:H3	1.94	0.66
1:2A:2353:G:N7	61:2A:3898:HOH:O	2.28	0.66
36:2e:122:GLU:O	36:2e:126:ARG:NH1	2.28	0.66
44:2m:3:ARG:HB2	44:2m:8:GLU:HA	1.78	0.66
1:1A:1648:C:OP1	61:1A:4104:HOH:O	2.12	0.66
3:2D:206:LEU:HD22	3:2D:211:ARG:HG2	1.76	0.66
7:2H:113:VAL:HG11	7:2H:151:ILE:HD13	1.78	0.66
32:2a:1143:G:H2'	32:2a:1144:G:C8	2.31	0.66
2:1B:106:G:H5'	21:1Z:31:ARG:HG2	1.77	0.65
32:1a:933:G:O6	38:1g:3:ARG:NH2	2.29	0.65
8:2I:4:ILE:HD11	8:2I:44:LEU:HD23	1.77	0.65
12:1Q:37:LEU:HD21	12:1Q:130:LYS:HE2	1.78	0.65
32:1a:1085:U:O2	61:1a:3305:HOH:O	2.11	0.65
1:2A:652(T):C:H2'	1:2A:652(U):G:C8	2.31	0.65
1:2A:1209:G:OP2	61:2A:3826:HOH:O	2.13	0.65
9:2N:46:VAL:HG23	9:2N:48:MET:HG2	1.78	0.65
1:1A:762:U:OP1	61:1A:4128:HOH:O	2.13	0.65
1:2A:805:G:OP1	61:2A:3832:HOH:O	2.15	0.65
1:2A:1840:G:OP2	61:2A:3828:HOH:O	2.14	0.65
1:2A:2267:A:OP2	61:2A:3830:HOH:O	2.15	0.65
32:2a:115:G:OP1	61:2a:3208:HOH:O	2.14	0.65
32:2a:976:G:H5'	32:2a:1358:U:O2'	1.95	0.65
35:1d:187:ARG:NH2	35:1d:193:ASP:OD2	2.30	0.65
1:2A:962:G:OP1	61:2A:3823:HOH:O	2.14	0.65
33:1b:231:GLU:HB3	33:1b:232:PRO:HD3	1.78	0.65
34:1c:63:ASN:HB3	34:1c:98:ASN:HD22	1.62	0.65
43:1l:6:THR:HG22	43:1l:8:ASN:H	1.61	0.65
2:1B:92:C:OP2	61:1B:302:HOH:O	2.14	0.65
5:1F:116:ASP:OD1	5:1F:119:ARG:NH2	2.29	0.65
12:2Q:11:LYS:HD3	12:2Q:87:LYS:HG2	1.78	0.65
38:2g:70:LYS:HG2	38:2g:96:GLN:HB3	1.79	0.65
1:1A:1671:U:O4	61:1A:4105:HOH:O	2.14	0.65
1:1A:2190:G:N7	61:1A:4212:HOH:O	2.28	0.65
32:2a:547:A:OP1	61:2a:3209:HOH:O	2.15	0.65
3:2D:134:ARG:NH1	3:2D:188:GLU:OE2	2.28	0.64
20:1Y:28:LYS:HG3	20:1Y:40:GLU:HG3	1.78	0.64
32:1a:376:G:H5''	47:1p:5:ARG:HD2	1.79	0.64
32:1a:1286:A:H2'	32:1a:1287:A:H4'	1.78	0.64
35:1d:140:VAL:HG11	35:1d:146:ILE:HD11	1.79	0.64
3:2D:12:SER:HB3	3:2D:208:LYS:HB3	1.78	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:2q:53:LEU:HD23	48:2q:82:MET:HE1	1.78	0.64
9:1N:46:VAL:HG23	9:1N:48:MET:HG2	1.77	0.64
36:1e:107:ARG:NH1	61:1e:303:HOH:O	2.31	0.64
46:1o:25:THR:HG21	46:1o:70:LEU:HB2	1.79	0.64
1:2A:1062:G:H2'	1:2A:1063:G:H8	1.62	0.64
1:2A:1063:G:H2'	1:2A:1065:U:H6	1.61	0.64
1:2A:1186:G:OP2	61:2A:3812:HOH:O	2.14	0.64
2:2B:58:A:OP2	61:2B:304:HOH:O	2.15	0.64
32:1a:922:G:H4'	36:1e:20:GLN:HA	1.78	0.64
1:2A:974:G:OP1	1:2A:1187:G:O2'	2.13	0.64
1:1A:1026:U:OP1	61:1A:4126:HOH:O	2.15	0.64
28:26:6:ARG:NH1	28:26:26:ASN:HB2	2.12	0.64
43:2l:60:LEU:HD21	43:2l:85:ILE:HD11	1.79	0.64
44:2m:13:LYS:HB2	44:2m:18:ALA:HB2	1.80	0.64
32:1a:1435:G:H2'	32:1a:1436:U:C6	2.33	0.64
43:2l:6:THR:HG22	43:2l:8:ASN:H	1.63	0.64
48:2q:45:HIS:HB2	48:2q:65:ILE:HD13	1.79	0.64
1:1A:2292:C:OP1	14:1S:17:ARG:NH2	2.31	0.64
26:14:61:ARG:HG3	26:14:62:ARG:H	1.62	0.64
1:2A:1912:A:OP1	61:2A:3831:HOH:O	2.15	0.64
3:2D:108:PRO:HD2	3:2D:111:LEU:HD22	1.78	0.64
32:2a:673:G:H2'	32:2a:674:G:C8	2.33	0.64
1:1A:2791:C:H5'	1:1A:2893:G:N2	2.13	0.64
33:1b:219:VAL:HA	33:1b:222:ILE:HD12	1.80	0.64
1:2A:387:U:OP1	61:2A:3833:HOH:O	2.15	0.64
1:2A:2122:U:H3	1:2A:2176:A:H61	1.44	0.64
34:2c:111:LEU:HD21	34:2c:146:ALA:HB2	1.79	0.64
21:1Z:136:PHE:HE1	21:1Z:138:GLU:HG3	1.63	0.64
40:1i:16:ARG:HD3	40:1i:64:THR:HG21	1.79	0.64
14:2S:50:SER:O	14:2S:76:LYS:NZ	2.25	0.64
32:2a:1286:A:C8	32:2a:1287:A:H4'	2.32	0.64
1:1A:123:G:OP2	61:1A:4131:HOH:O	2.15	0.63
11:1P:70:GLN:NE2	61:1P:303:HOH:O	2.31	0.63
1:2A:301:G:OP2	20:2Y:84:ARG:NH2	2.30	0.63
34:1c:3:ASN:OD1	34:1c:3:ASN:N	2.30	0.63
34:1c:6:HIS:HD2	34:1c:8:ILE:H	1.46	0.63
40:2i:53:VAL:O	40:2i:55:ALA:N	2.31	0.63
1:1A:1173:G:O2'	1:1A:1174:A:O5'	2.15	0.63
19:1X:31:HIS:HD2	19:1X:33:LYS:H	1.46	0.63
32:1a:460:G:N2	32:1a:471:G:N7	2.47	0.63
32:1a:1356:G:H2'	32:1a:1357:A:C8	2.33	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:1i:18:PHE:HB2	40:1i:62:TYR:HB3	1.81	0.63
1:2A:1017:G:O6	61:2A:3829:HOH:O	2.14	0.63
11:2P:90:ARG:HH21	11:2P:105:LEU:HD21	1.62	0.63
19:2X:43:VAL:HG21	19:2X:81:VAL:HG11	1.80	0.63
21:2Z:144:LEU:HD21	21:2Z:150:LEU:HD13	1.80	0.63
53:2y:12:ILE:HG23	53:2y:16:ILE:HG23	1.79	0.63
1:2A:2115:G:H21	1:2A:2171:A:H61	1.44	0.63
2:2B:58:A:OP2	61:2B:303:HOH:O	2.15	0.63
46:2o:25:THR:HG21	46:2o:70:LEU:HB2	1.80	0.63
1:1A:272(H):C:H42	1:1A:363(B):G:H1	1.46	0.63
38:1g:54:THR:O	38:1g:56:GLN:NE2	2.32	0.63
1:2A:641:C:O2'	1:2A:2350:C:OP1	2.11	0.63
7:2H:52:VAL:HG21	7:2H:69:ARG:HB2	1.81	0.63
1:1A:1783:A:H5'	1:1A:2608:G:H4'	1.81	0.63
1:2A:601:C:O2'	5:2F:104:LYS:NZ	2.32	0.63
6:2G:55:LYS:HZ1	6:2G:149:VAL:HA	1.64	0.63
20:2Y:82:PRO:O	20:2Y:101:LYS:NZ	2.26	0.63
32:1a:1015:A:H2'	32:1a:1016:A:C8	2.33	0.63
8:2I:78:THR:HG22	8:2I:143:SER:HB3	1.80	0.63
12:2Q:75:THR:HG21	12:2Q:87:LYS:HE3	1.79	0.63
1:2A:1796:U:H2'	1:2A:1797:C:C6	2.34	0.63
1:2A:2717:G:N7	61:2A:3944:HOH:O	2.31	0.63
32:2a:1005:A:O2'	32:2a:1036:G:N2	2.32	0.63
48:1q:67:LYS:O	48:1q:69:LYS:N	2.32	0.62
1:2A:1798:U:OP2	3:2D:274:ARG:NH2	2.23	0.62
1:2A:2206:G:H8	1:2A:2207:G:N7	1.97	0.62
1:2A:2857:G:N2	1:2A:2860:A:OP2	2.27	0.62
34:2c:6:HIS:CD2	34:2c:9:GLY:H	2.16	0.62
36:2e:102:ALA:HB1	36:2e:106:PRO:HG2	1.79	0.62
41:2j:51:ARG:O	45:2n:45:ARG:NH1	2.32	0.62
32:1a:677:U:H3	32:1a:713:G:H22	1.47	0.62
1:1A:1176:G:H1'	1:1A:1177:A:H5'	1.80	0.62
3:1D:17:THR:O	3:1D:211:ARG:NH2	2.29	0.62
32:1a:346:G:H5''	57:1a:3277:MPD:H4	1.81	0.62
15:2T:80:SER:HB3	15:2T:83:ILE:HD12	1.80	0.62
48:2q:66:SER:O	48:2q:70:ARG:NH1	2.31	0.62
1:1A:271(H):G:O2'	1:1A:271(I):G:OP2	2.18	0.62
10:1O:64:ARG:HG2	10:1O:83:ALA:HB3	1.81	0.62
10:2O:20:MET:HE3	10:2O:44:LYS:HE3	1.81	0.62
32:1a:890:G:O2'	32:1a:906:G:O6	2.16	0.62
34:1c:179:ARG:NH1	34:1c:206:GLU:OE1	2.32	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:1i:16:ARG:H	40:1i:64:THR:HG22	1.65	0.62
20:2Y:8:LYS:HG2	20:2Y:97:ARG:HH12	1.64	0.62
34:2c:11:ARG:HB3	34:2c:15:THR:HB	1.81	0.62
5:1F:12:LEU:HD22	5:1F:124:LEU:HD21	1.82	0.62
20:1Y:92:ASN:N	20:1Y:93:GLY:HA2	2.12	0.62
1:2A:1754:C:OP1	15:2T:96:ARG:NH1	2.32	0.62
26:24:48:ARG:HD2	26:24:52:THR:HA	1.80	0.62
40:1i:17:VAL:HG21	40:1i:81:ILE:HG22	1.82	0.62
46:1o:39:LEU:HD13	46:1o:56:LEU:HB2	1.82	0.62
32:2a:401:C:OP2	35:2d:73:ARG:NH2	2.32	0.62
32:2a:1119:C:H2'	32:2a:1120:G:H8	1.64	0.62
46:2o:39:LEU:HD13	46:2o:56:LEU:HB2	1.81	0.62
32:1a:269:C:H2'	32:1a:270:A:C8	2.35	0.62
32:1a:974:A:OP2	45:1n:29:ARG:NH2	2.32	0.62
52:1u:17:THR:O	52:1u:22:ARG:NH1	2.33	0.62
24:22:16:LEU:O	24:22:67:LYS:NZ	2.33	0.62
26:24:59:PHE:HA	26:24:60:GLN:C	2.25	0.62
32:2a:1352:C:OP1	52:2u:3:LYS:NZ	2.27	0.62
34:2c:150:LYS:HG3	34:2c:169:ALA:HB2	1.81	0.62
1:1A:1509(A):A:H2'	1:1A:1509(B):A:O4'	2.00	0.62
7:1H:84:SER:OG	7:1H:132:ARG:NH1	2.33	0.62
32:1a:411:A:OP2	35:1d:25:ARG:NH2	2.33	0.62
39:1h:12:ARG:NH1	39:1h:25:ASP:O	2.32	0.62
1:1A:1203:G:O6	61:1A:4129:HOH:O	2.14	0.61
32:1a:60:A:H4'	32:1a:61:G:H5'	1.82	0.61
33:1b:97:TRP:HH2	33:1b:176:GLU:CD	2.08	0.61
1:2A:1069:A:H2'	1:2A:1073:A:N7	2.15	0.61
26:24:50:VAL:HB	44:2m:65:LYS:HG2	1.81	0.61
32:2a:539:A:H2'	32:2a:540:G:C8	2.35	0.61
32:2a:1435:G:H2'	32:2a:1436:U:C6	2.35	0.61
33:2b:78:GLN:HE21	33:2b:95:GLN:HA	1.65	0.61
1:1A:286:C:H2'	1:1A:287:C:C6	2.35	0.61
51:1t:57:ARG:HH22	51:1t:100:ILE:HD12	1.64	0.61
33:2b:84:GLU:HB3	33:2b:219:VAL:HG21	1.81	0.61
1:1A:958:U:H5''	12:1Q:14:ARG:HD3	1.82	0.61
56:2A:3739:TEL:H381	56:2A:3739:TEL:H171	1.83	0.61
32:2a:662:G:H2'	32:2a:663:A:C8	2.35	0.61
32:2a:954:G:H21	32:2a:1227:A:H62	1.48	0.61
1:1A:1064:C:H3'	1:1A:1065:U:H5''	1.83	0.61
1:1A:1139:G:OP1	61:1A:4132:HOH:O	2.16	0.61
1:1A:2115:G:N3	1:1A:2117:A:N6	2.48	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2153:G:H2'	1:1A:2154:G:C8	2.34	0.61
1:2A:23:G:OP1	1:2A:504:U:N3	2.33	0.61
1:2A:2693:A:H2'	1:2A:2694:G:H8	1.64	0.61
7:2H:143:GLN:NE2	7:2H:147:ASN:OD1	2.33	0.61
28:26:35:GLU:OE2	28:26:50:ARG:NH1	2.32	0.61
32:1a:300:A:O2'	32:1a:564:C:N3	2.23	0.61
32:1a:965:A:OP2	53:1y:8:LYS:NZ	2.34	0.61
32:1a:1062:U:H2'	32:1a:1063:C:C6	2.36	0.61
1:2A:365:C:OP2	61:2A:3836:HOH:O	2.16	0.61
2:2B:14:U:OP2	2:2B:70:C:O2'	2.18	0.61
8:2I:48:GLU:HG3	8:2I:52:ARG:HH11	1.65	0.61
32:2a:1005:A:H1'	32:2a:1025:U:C2	2.36	0.61
1:1A:1069:A:H4'	1:1A:1070:A:H5''	1.83	0.61
32:1a:1442:G:H2'	32:1a:1442:G:N3	2.15	0.61
35:1d:88:VAL:HA	36:1e:97:GLY:HA3	1.82	0.61
1:2A:1803:A:O2'	3:2D:259:THR:HG21	1.99	0.61
1:1A:2305:A:H5''	6:1G:134:GLY:HA3	1.82	0.61
15:1T:51:ARG:NH1	61:1T:302:HOH:O	2.33	0.61
1:1A:994:C:OP1	16:1U:53:ARG:NH2	2.33	0.61
2:1B:77:U:OP1	21:1Z:19:ARG:NH2	2.34	0.61
8:1I:9:LEU:HD23	8:1I:12:LEU:HD22	1.83	0.61
50:1s:63:THR:OG1	50:1s:65:ASN:OD1	2.19	0.61
1:2A:1365:A:O2'	23:21:11:ARG:NH1	2.33	0.61
1:2A:2206:G:H3'	1:2A:2207:G:H8	1.66	0.61
6:2G:97:ASP:HA	6:2G:100:TRP:HD1	1.66	0.61
36:2e:88:LYS:HE2	36:2e:123:LEU:HD12	1.81	0.61
53:2y:51:ASP:OD1	53:2y:64:SER:OG	2.11	0.61
32:1a:1060:C:C5	34:1c:2:GLY:HA3	2.36	0.61
1:2A:1041:C:H42	1:2A:1114:G:H1	1.49	0.61
33:2b:155:LEU:HD21	33:2b:159:PRO:HG3	1.81	0.61
35:1d:173:TRP:CD1	35:1d:173:TRP:H	2.17	0.60
6:2G:145:THR:HG22	6:2G:148:MET:HG2	1.81	0.60
48:2q:67:LYS:O	48:2q:69:LYS:N	2.30	0.60
1:1A:1593:G:H2'	1:1A:1594:G:C8	2.36	0.60
4:1E:55:ASN:HB3	4:1E:58:ARG:HG3	1.83	0.60
6:1G:49:ASP:O	6:1G:51:ARG:N	2.34	0.60
36:1e:144:THR:H	36:1e:147:ASP:HB2	1.67	0.60
1:2A:2206:G:H5''	1:2A:2207:G:N7	2.16	0.60
2:1B:95:C:N4	61:1B:304:HOH:O	2.18	0.60
32:1a:911:U:OP2	43:1I:97:ARG:NH2	2.24	0.60
32:1a:1291:G:OP1	38:1g:37:ASN:ND2	2.35	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:2y:40:ILE:HB	53:2y:51:ASP:HB2	1.84	0.60
1:1A:1300:U:H4'	1:1A:1301:A:H5'	1.83	0.60
8:1I:109:ILE:HG13	8:1I:130:TYR:CZ	2.35	0.60
35:2d:122:ARG:NH1	35:2d:134:ASP:O	2.33	0.60
41:2j:55:LYS:O	41:2j:57:LYS:N	2.34	0.60
50:2s:20:LEU:HD21	50:2s:43:GLU:HG2	1.83	0.60
20:1Y:102:CYS:SG	20:1Y:103:GLY:N	2.74	0.60
1:2A:1378:A:OP1	29:27:10:ARG:NH2	2.34	0.60
2:2B:56:G:O2'	61:2B:305:HOH:O	2.16	0.60
6:2G:44:GLY:N	6:2G:88:ILE:O	2.33	0.60
1:1A:1771:C:OP1	61:1A:4134:HOH:O	2.16	0.60
1:1A:1796:U:H2'	1:1A:1797:C:C6	2.37	0.60
1:1A:1816:G:O6	3:1D:35:LYS:NZ	2.28	0.60
32:1a:972:C:OP1	61:1a:3308:HOH:O	2.16	0.60
1:2A:2118:U:O2'	1:2A:2119:A:H5''	2.02	0.60
32:2a:1025:U:O2'	32:2a:1026:G:N7	2.34	0.60
33:2b:178:ARG:HB3	39:2h:72:PRO:HA	1.82	0.60
36:2e:71:LEU:HD21	36:2e:115:VAL:HG22	1.82	0.60
1:1A:588:U:H2'	1:1A:589:C:C6	2.36	0.60
3:1D:242:ARG:NH1	61:1D:405:HOH:O	2.34	0.60
32:1a:222:U:H2'	32:1a:223:U:C6	2.36	0.60
32:1a:614:A:OP1	35:1d:85:LYS:NZ	2.34	0.60
15:1T:24:PRO:HA	15:1T:49:VAL:HG22	1.84	0.60
16:1U:101:ARG:NH1	61:1U:303:HOH:O	2.33	0.60
43:1I:71:PRO:O	43:1I:102:ARG:NH1	2.35	0.60
1:2A:2167:U:H2'	1:2A:2168:G:C4	2.36	0.60
6:2G:3:LEU:HD23	6:2G:3:LEU:H	1.66	0.60
19:2X:46:ALA:HB1	24:22:33:MET:HE1	1.83	0.60
21:2Z:40:ASP:HB3	21:2Z:43:GLU:HB2	1.84	0.60
32:2a:134:A:N6	47:2p:25:ARG:HH22	1.99	0.60
32:1a:1177:G:OP2	40:1i:97:LYS:NZ	2.27	0.60
1:2A:99:U:O4	20:2Y:8:LYS:NZ	2.35	0.60
32:1a:1010:G:N2	32:1a:1020:U:H1'	2.16	0.60
1:2A:468:G:O2'	5:2F:62:ARG:NH2	2.33	0.60
2:2B:66:A:H61	2:2B:109:C:H5'	1.66	0.60
32:2a:718:G:H5'	42:2k:117:ASN:ND2	2.15	0.60
1:1A:61:G:OP1	24:12:51:ARG:NH2	2.24	0.59
21:1Z:158:PRO:HG2	21:1Z:161:VAL:HG11	1.84	0.59
35:1d:83:SER:O	61:1d:401:HOH:O	2.15	0.59
35:1d:162:LEU:HD13	35:1d:181:MET:HG2	1.84	0.59
5:2F:24:LEU:HD23	5:2F:115:ALA:HA	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:2Z:179:ASP:O	21:2Z:182:LYS:HG2	2.02	0.59
1:1A:1385:G:O2'	1:1A:1396:U:O2	2.16	0.59
44:1m:15:VAL:HG11	44:1m:48:LEU:HD21	1.84	0.59
32:2a:1179:A:H2'	32:2a:1180:A:O4'	2.02	0.59
1:1A:2138:C:H42	1:1A:2153:G:H1	1.48	0.59
1:1A:2690:C:OP1	13:1R:17:ARG:NH2	2.35	0.59
6:1G:79:ASN:OD1	6:1G:79:ASN:N	2.32	0.59
21:1Z:145:GLU:H	21:1Z:148:ASP:HB2	1.67	0.59
46:1o:55:GLY:HA2	46:1o:58:MET:HE3	1.83	0.59
1:2A:652(T):C:H2'	1:2A:652(U):G:H8	1.65	0.59
4:2E:40:GLU:H	4:2E:40:GLU:CD	2.10	0.59
1:1A:2548:G:O6	61:1A:4133:HOH:O	2.16	0.59
32:1a:1305:G:N2	32:1a:1331:G:H1'	2.16	0.59
35:1d:148:VAL:HG11	35:1d:158:ILE:HD12	1.85	0.59
26:24:53:GLU:HG2	26:24:55:ARG:H	1.66	0.59
8:1I:77:LEU:HB3	8:1I:142:VAL:HG22	1.85	0.59
1:2A:2130:U:H2'	1:2A:2158:A:N1	2.17	0.59
15:1T:108:ARG:HH12	15:1T:112:ARG:HD3	1.68	0.59
39:1h:51:VAL:HG21	39:1h:60:ARG:HD2	1.84	0.59
1:2A:2127:G:O6	1:2A:2161:C:N3	2.36	0.59
32:2a:584:G:H5'	48:2q:91:ARG:HH22	1.67	0.59
1:1A:2876:G:OP1	61:1A:4135:HOH:O	2.16	0.59
48:1q:24:GLU:HG3	48:1q:39:SER:HB3	1.84	0.59
1:2A:2079:U:O3'	23:21:35:THR:OG1	2.20	0.59
2:1B:11:C:OP1	61:1B:303:HOH:O	2.17	0.59
32:1a:343:U:O2'	32:1a:346:G:O6	2.21	0.59
32:1a:461:A:O2'	32:1a:470:C:H5'	2.02	0.59
39:1h:86:ILE:HG13	39:1h:133:LEU:HD22	1.83	0.59
46:1o:87:ILE:HG22	46:1o:88:ARG:H	1.68	0.59
1:2A:1062:G:N7	1:2A:1070:A:H1'	2.17	0.59
1:2A:2218:U:O4'	23:21:52:ARG:NH2	2.35	0.59
6:2G:57:ALA:HB2	6:2G:90:LEU:HD13	1.84	0.59
10:2O:35:VAL:HG13	10:2O:65:THR:HG23	1.85	0.59
32:2a:164:U:H2'	32:2a:165:C:C6	2.38	0.59
32:2a:222:U:H2'	32:2a:223:U:C6	2.38	0.59
32:2a:537:G:OP1	43:2l:113:ARG:NH2	2.32	0.59
32:2a:1273:G:H3'	32:2a:1274:G:H8	1.68	0.59
32:2a:1401:G:O6	53:2y:83:ARG:NH2	2.36	0.59
32:2a:1504:G:OP1	32:2a:1507:A:H4'	2.03	0.59
38:2g:111:ARG:NH1	38:2g:113:GLU:OE2	2.34	0.59
1:1A:1300:U:H4'	1:1A:1301:A:C5'	2.33	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:79:G:C6	32:1a:90:U:N3	2.71	0.59
50:1s:12:ASP:O	50:1s:14:HIS:N	2.34	0.59
13:2R:67:LEU:HD13	13:2R:76:VAL:HG21	1.85	0.59
35:2d:25:ARG:HA	35:2d:28:SER:HB3	1.83	0.59
1:1A:1056:G:H5''	1:1A:1057:A:O4'	2.03	0.59
1:1A:1877:A:H5'	1:1A:1878:G:OP2	2.02	0.59
3:1D:206:LEU:HD22	3:1D:211:ARG:HG2	1.84	0.59
3:2D:71:ASP:HB3	3:2D:103:ARG:HH12	1.67	0.59
33:2b:189:ASP:OD1	33:2b:189:ASP:N	2.23	0.59
35:2d:60:GLU:HG3	35:2d:202:LEU:HD12	1.85	0.59
47:2p:43:LYS:HG2	47:2p:48:TRP:CD2	2.38	0.59
1:1A:2140:C:H2'	1:1A:2141:G:C8	2.36	0.58
4:1E:47:VAL:HG23	4:1E:84:PHE:O	2.03	0.58
32:1a:557:G:OP1	61:1a:3309:HOH:O	2.17	0.58
48:1q:53:LEU:HD23	48:1q:82:MET:HE1	1.83	0.58
1:2A:1915:5MU:H2'	1:2A:1916:A:O4'	2.02	0.58
5:2F:120:GLU:HB3	5:2F:122:LYS:HG2	1.85	0.58
11:2P:54:GLY:O	61:2P:301:HOH:O	2.17	0.58
23:21:50:ARG:HG2	23:21:59:THR:HG22	1.85	0.58
32:2a:501:C:OP1	43:2l:117:ARG:NH2	2.36	0.58
1:1A:531:C:H4'	1:1A:532:A:H5''	1.84	0.58
1:1A:1174:A:H1'	1:1A:1175:U:H5'	1.84	0.58
4:1E:116:VAL:HG13	4:1E:122:PHE:HB2	1.86	0.58
32:1a:1003:G:N2	32:1a:1004:A:N3	2.51	0.58
1:2A:82:G:N1	1:2A:103:A:OP2	2.30	0.58
1:2A:1278:A:OP1	13:2R:36:THR:HG23	2.03	0.58
1:2A:1830:C:OP2	61:2A:3838:HOH:O	2.17	0.58
1:2A:2849:U:OP2	15:2T:95:ARG:NH1	2.35	0.58
2:2B:75:G:H22	21:2Z:73:GLN:NE2	1.99	0.58
32:2a:238:G:OP1	48:2q:25:ARG:NH2	2.35	0.58
32:2a:662:G:O2'	32:2a:836:G:OP1	2.20	0.58
3:1D:239:ARG:NH1	61:1D:403:HOH:O	2.33	0.58
1:2A:1503:U:H2'	1:2A:1504:C:C6	2.37	0.58
1:2A:2602:A:H4'	1:2A:2603:G:OP1	2.01	0.58
6:2G:66:GLN:OE1	6:2G:98:ARG:NE	2.32	0.58
7:2H:9:ILE:HD11	7:2H:69:ARG:HG2	1.84	0.58
7:2H:18:GLU:HB3	7:2H:25:LYS:HB2	1.84	0.58
13:2R:103:ARG:NH1	13:2R:108:GLY:O	2.34	0.58
32:2a:965:A:O2'	53:2y:40:ILE:HG21	2.03	0.58
32:2a:1401:G:N7	53:2y:83:ARG:NH1	2.50	0.58
1:1A:286:C:H2'	1:1A:287:C:H6	1.67	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:1b:84:GLU:HB3	33:1b:219:VAL:HG21	1.86	0.58
1:2A:154(A):C:N4	1:2A:171:G:H1	2.01	0.58
1:2A:2128:C:H1'	1:2A:2173:A:H2	1.67	0.58
37:2f:35:ALA:HA	37:2f:67:MET:HB3	1.86	0.58
40:2i:43:ALA:O	40:2i:45:ALA:N	2.36	0.58
51:2t:42:GLN:O	51:2t:45:GLN:HB3	2.03	0.58
1:1A:271(M):G:H21	8:1I:50:ARG:HD3	1.67	0.58
1:1A:1803:A:O2'	3:1D:259:THR:HG21	2.03	0.58
32:1a:976:G:H5'	32:1a:1358:U:O2'	2.04	0.58
33:1b:71:VAL:HB	33:1b:164:VAL:HG22	1.85	0.58
1:2A:848:G:OP1	61:2A:3839:HOH:O	2.17	0.58
28:26:14:THR:OG1	28:26:48:VAL:O	2.20	0.58
14:1S:14:VAL:O	14:1S:18:ILE:HG12	2.03	0.58
30:18:23:VAL:HG11	30:18:47:LYS:HD3	1.84	0.58
33:1b:15:VAL:HG21	33:1b:213:LEU:HD12	1.85	0.58
1:2A:1007:C:OP1	9:2N:35:ARG:NH1	2.36	0.58
13:1R:67:LEU:HD13	13:1R:76:VAL:HG21	1.84	0.58
21:1Z:19:ARG:NH1	21:1Z:84:GLU:O	2.35	0.58
1:2A:1073:A:H2'	1:2A:1074:G:H8	1.67	0.58
1:2A:1654:A:OP1	61:2A:3834:HOH:O	2.16	0.58
32:2a:662:G:H2'	32:2a:663:A:H8	1.68	0.58
1:1A:2469:A:H5'	1:1A:2470:G:OP2	2.04	0.58
32:1a:673:G:H2'	32:1a:674:G:C8	2.38	0.58
1:2A:1068:G:H3'	1:2A:1096:A:OP2	2.04	0.58
1:2A:2376:A:N3	14:2S:106:ARG:NH2	2.46	0.58
1:2A:2839:G:H5'	13:2R:46:GLY:HA2	1.86	0.58
10:2O:115:VAL:HG13	10:2O:121:VAL:HG21	1.85	0.58
13:2R:12:ARG:O	13:2R:17:ARG:NH1	2.36	0.58
20:1Y:73:ARG:NH1	61:1Y:301:HOH:O	2.32	0.58
32:1a:1074:G:O2'	32:1a:1101:A:N1	2.35	0.58
1:2A:574:C:N3	4:2E:145:LYS:NZ	2.51	0.58
32:2a:335:C:O2'	32:2a:1433:A:N3	2.33	0.58
32:2a:1376:U:H2'	32:2a:1377:A:H8	1.69	0.58
1:1A:1647:G:OP1	61:1A:4104:HOH:O	2.17	0.58
14:1S:11:LYS:HG3	14:1S:91:PRO:HD3	1.85	0.58
27:15:40:LYS:NZ	27:15:44:THR:O	2.35	0.58
1:2A:62:C:OP1	61:2A:3842:HOH:O	2.17	0.58
1:2A:2150:U:H2'	1:2A:2151:G:C8	2.39	0.58
1:2A:2188:C:H2'	1:2A:2189:U:O4'	2.04	0.58
32:2a:1290:G:OP1	38:2g:35:LYS:NZ	2.36	0.58
1:1A:271(O):C:H2'	1:1A:271(P):C:C6	2.39	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1B:66:A:H61	2:1B:108:U:H2'	1.69	0.57
30:18:15:LYS:HB3	57:18:103:MPD:H52	1.85	0.57
6:2G:106:LEU:HA	6:2G:110:ALA:HB3	1.86	0.57
8:2I:93:THR:HG22	8:2I:119:PRO:HB3	1.85	0.57
32:2a:643:C:O2'	39:2h:132:GLU:OE1	2.16	0.57
7:1H:40:GLU:OE2	7:1H:60:ARG:NH1	2.37	0.57
32:1a:946:A:H2'	32:1a:947:G:C8	2.39	0.57
35:1d:15:GLU:OE2	35:1d:66:ARG:NH1	2.37	0.57
38:1g:113:GLU:HG2	38:1g:119:ARG:HG2	1.86	0.57
1:2A:2149:G:C2	1:2A:2150:U:H1'	2.39	0.57
1:2A:2206:G:H5''	1:2A:2207:G:C8	2.39	0.57
1:2A:2419:U:OP1	61:2A:3835:HOH:O	2.16	0.57
6:2G:11:TYR:HB2	6:2G:176:LEU:HD21	1.85	0.57
32:2a:390:C:O3'	47:2p:28:ARG:NH2	2.36	0.57
32:2a:1239:A:H62	32:2a:1299:A:H62	1.51	0.57
1:1A:2328:A:H2'	1:1A:2329:G:C8	2.39	0.57
6:1G:43:LEU:O	6:1G:45:GLU:N	2.35	0.57
39:1h:6:ILE:HB	39:1h:85:ARG:NH1	2.19	0.57
39:1h:14:ARG:O	39:1h:18:ARG:HG2	2.04	0.57
18:2W:78:GLU:OE2	18:2W:99:ARG:NH1	2.34	0.57
32:2a:425:G:O3'	35:2d:45:GLN:NE2	2.32	0.57
1:1A:889:C:O2'	1:1A:890:A:O5'	2.22	0.57
32:1a:407:G:H5''	35:1d:115:ARG:HG2	1.87	0.57
37:1f:38:GLU:HB2	37:1f:64:GLN:HG2	1.87	0.57
1:2A:2171:A:H4'	1:2A:2172:U:OP1	2.05	0.57
20:2Y:5:MET:HE2	20:2Y:32:PRO:HA	1.85	0.57
34:2c:50:ALA:HB1	34:2c:70:VAL:HG11	1.86	0.57
1:1A:1356:G:OP1	61:1A:4138:HOH:O	2.17	0.57
32:1a:626:U:H2'	32:1a:627:G:C8	2.39	0.57
35:1d:156:GLU:O	35:1d:160:GLN:HG2	2.04	0.57
1:2A:1688:U:O2	1:2A:1700:A:H5'	2.04	0.57
1:2A:2295:C:OP1	14:2S:10:ARG:NH1	2.36	0.57
32:2a:1181:G:O2'	32:2a:1182:G:N7	2.37	0.57
32:2a:1391:U:H2'	32:2a:1392:G:C8	2.40	0.57
1:2A:652(B):A:H61	1:2A:655:A:H1'	1.69	0.57
32:2a:992:U:H4'	32:2a:993:G:O5'	2.03	0.57
44:2m:3:ARG:HG3	44:2m:8:GLU:HG3	1.86	0.57
1:1A:1070:A:N7	1:1A:1097:U:H4'	2.19	0.57
17:1V:74:LYS:HB2	17:1V:83:ARG:HB2	1.86	0.57
46:1o:16:ALA:HB1	46:1o:21:ASP:HB3	1.85	0.57
1:2A:477:A:OP2	61:2A:3840:HOH:O	2.17	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1110:G:H1'	1:2A:1111:A:C8	2.39	0.57
1:2A:1250:G:H5''	61:2A:5584:HOH:O	2.04	0.57
5:2F:53:THR:HG23	5:2F:55:GLY:H	1.70	0.57
6:2G:60:LEU:HD23	6:2G:68:PRO:HG3	1.87	0.57
15:2T:85:LYS:NZ	15:2T:87:ASP:OD2	2.37	0.57
35:2d:78:LEU:HD22	35:2d:96:LEU:HB3	1.87	0.57
46:2o:16:ALA:HB1	46:2o:21:ASP:HB3	1.86	0.57
21:1Z:157:LEU:HD11	21:1Z:163:LEU:HD13	1.86	0.57
1:2A:1063:G:HO2'	1:2A:1064:C:H6	1.52	0.57
1:2A:2168:G:HO2'	1:2A:2170:A:N6	2.03	0.57
32:2a:1510:U:H2'	32:2a:1511:G:C8	2.38	0.57
1:1A:2820:A:OP2	13:1R:2:ARG:NH2	2.38	0.57
61:1A:4109:HOH:O	13:1R:3:HIS:NE2	2.33	0.57
33:1b:207:ALA:O	33:1b:211:ILE:HG13	2.05	0.57
1:2A:1920:OMC:HM22	1:2A:1921:G:H5'	1.86	0.57
15:2T:60:THR:HG22	15:2T:77:PRO:HA	1.87	0.57
32:2a:986:A:H1'	50:2s:54:GLY:O	2.05	0.57
1:1A:187:G:OP2	61:1A:4139:HOH:O	2.18	0.57
1:1A:749:C:OP2	61:1A:4141:HOH:O	2.18	0.57
1:1A:2049:G:N7	61:1A:4253:HOH:O	2.32	0.57
1:1A:2839:G:H5'	13:1R:46:GLY:HA2	1.87	0.57
1:2A:2152:G:H2'	1:2A:2153:G:C8	2.40	0.57
5:2F:192:LEU:HD13	5:2F:194:MET:HE2	1.86	0.57
5:2F:195:ASP:OD1	5:2F:196:LEU:N	2.38	0.57
8:2I:57:ARG:O	8:2I:61:ARG:HG2	2.05	0.57
33:2b:74:LYS:HD3	33:2b:76:GLN:HG3	1.86	0.57
10:1O:122:LEU:HD13	15:1T:72:VAL:HG11	1.87	0.56
36:1e:110:LEU:HD13	36:1e:118:ILE:HG21	1.86	0.56
8:2I:12:LEU:HD22	8:2I:19:VAL:HG21	1.86	0.56
31:29:14:CYS:HA	31:29:27:CYS:HB2	1.86	0.56
1:1A:1187:G:H5''	17:1V:81:TYR:CE1	2.41	0.56
1:1A:1378:A:OP1	29:17:10:ARG:NH2	2.37	0.56
32:1a:826:C:O2	39:1h:15:ASN:ND2	2.39	0.56
53:1y:24:LEU:HD11	53:1y:39:ILE:HD11	1.87	0.56
1:2A:335:C:H4'	20:2Y:73:ARG:HD2	1.87	0.56
61:2A:4053:HOH:O	5:2F:53:THR:HG21	2.04	0.56
32:2a:1226:C:OP2	44:2m:91:ARG:NH1	2.39	0.56
40:2i:3:GLN:NE2	40:2i:20:ARG:HH21	2.03	0.56
1:1A:607:U:OP1	5:1F:102:PRO:HA	2.05	0.56
1:1A:1113:U:H2'	1:1A:1114:G:C8	2.39	0.56
1:1A:1786:A:H1'	1:1A:1938:A:N6	2.21	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1939:5MU:OP1	1:1A:2604:U:O2'	2.20	0.56
1:1A:2029:G:N7	61:1A:4252:HOH:O	2.32	0.56
1:1A:2110:G:H5''	1:1A:2111:C:H5	1.69	0.56
1:1A:2327:A:H2'	1:1A:2328:A:C8	2.41	0.56
1:1A:2646:C:OP2	1:1A:2732:G:O2'	2.19	0.56
21:1Z:69:THR:HG22	21:1Z:90:VAL:HA	1.87	0.56
32:1a:999:C:H2'	32:1a:1000:U:O4'	2.06	0.56
36:1e:137:GLU:OE2	36:1e:141:GLN:NE2	2.35	0.56
44:1m:80:ARG:HH22	50:1s:69:HIS:HE1	1.51	0.56
50:1s:3:ARG:HH11	50:1s:10:PHE:HB2	1.69	0.56
1:2A:322:A:OP1	5:2F:168:ARG:NH1	2.39	0.56
3:2D:17:THR:O	3:2D:211:ARG:NH2	2.39	0.56
26:24:46:GLN:O	26:24:48:ARG:N	2.36	0.56
32:2a:632:A:H5'	32:2a:633:G:OP2	2.04	0.56
32:2a:922:G:H4'	36:2e:20:GLN:HA	1.86	0.56
1:1A:363(A):A:H2'	1:1A:363(B):G:C8	2.40	0.56
1:1A:1252:G:N3	16:1U:33:ARG:HG2	2.20	0.56
1:1A:2082:A:N1	61:1A:4256:HOH:O	2.33	0.56
6:1G:179:PRO:HB2	26:14:42:PHE:HE2	1.71	0.56
32:1a:176:C:H2'	32:1a:177:C:H6	1.69	0.56
33:1b:128:GLU:O	33:1b:135:GLN:NE2	2.37	0.56
1:2A:2314:C:H2'	1:2A:2315:G:C8	2.41	0.56
9:2N:58:ASP:OD1	9:2N:58:ASP:N	2.36	0.56
39:2h:121:ASP:HB2	39:2h:125:ARG:NH2	2.20	0.56
43:2l:28:LYS:NZ	43:2l:64:TYR:OH	2.38	0.56
1:1A:922:U:H2'	1:1A:923:C:C6	2.41	0.56
11:1P:59:LEU:HD21	30:18:10:ALA:HA	1.88	0.56
32:1a:1228:C:P	44:1m:108:ARG:HH22	2.28	0.56
32:1a:1391:U:H2'	32:1a:1392:G:C8	2.41	0.56
1:2A:800:A:H8	1:2A:800:A:OP1	1.88	0.56
1:2A:1359:A:N3	1:2A:1359:A:H5'	2.20	0.56
1:2A:1762:A:N1	61:2A:3950:HOH:O	2.32	0.56
2:2B:75:G:O3'	21:2Z:10:ARG:NH2	2.38	0.56
23:21:3:LYS:HB2	23:21:61:ARG:HH22	1.69	0.56
32:2a:1492:A:H5''	43:2l:47:LYS:HD3	1.86	0.56
33:2b:74:LYS:O	33:2b:78:GLN:N	2.39	0.56
1:1A:184:C:H2'	1:1A:185:U:C6	2.40	0.56
1:1A:1086:A:H3'	1:1A:1086:A:N3	2.21	0.56
2:2B:77:U:OP1	21:2Z:19:ARG:NH2	2.39	0.56
1:2A:1364:G:OP2	23:21:3:LYS:HG3	2.06	0.56
1:2A:2111:C:H42	1:2A:2147:G:H22	1.53	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:2c:22:TRP:HA	41:2j:93:GLY:HA2	1.88	0.56
1:1A:1250:G:H5''	61:1A:7316:HOH:O	2.06	0.56
1:1A:2849:U:H4'	1:1A:2868:A:C2	2.40	0.56
34:1c:67:THR:HA	34:1c:102:ASN:HB2	1.88	0.56
1:2A:2144:U:H1'	1:2A:2147:G:O6	2.06	0.56
2:2B:53:A:OP2	61:2B:306:HOH:O	2.18	0.56
18:2W:80:PRO:O	18:2W:100:THR:HB	2.05	0.56
32:2a:558:G:OP1	61:2a:3211:HOH:O	2.18	0.56
32:2a:1151:A:O2'	32:2a:1152:A:H8	1.89	0.56
33:2b:195:ASP:O	39:2h:68:ARG:NH2	2.38	0.56
33:2b:208:ILE:HA	33:2b:211:ILE:HD12	1.86	0.56
43:2l:5:PRO:HG2	43:2l:10:LEU:HD11	1.88	0.56
44:2m:54:VAL:HA	44:2m:57:ARG:HB3	1.86	0.56
1:1A:1011:G:OP1	16:1U:77:SER:OG	2.23	0.56
1:1A:2319:G:N1	14:1S:3:ARG:HA	2.21	0.56
21:1Z:52:SER:C	21:1Z:54:HIS:H	2.14	0.56
32:1a:973:G:H3'	32:1a:974:A:H5''	1.88	0.56
35:1d:128:VAL:HG12	35:1d:129:ASN:HD22	1.70	0.56
44:1m:11:ARG:C	44:1m:13:LYS:H	2.13	0.56
6:2G:107:LEU:HA	6:2G:111:LEU:HD12	1.87	0.56
32:2a:411:A:OP1	35:2d:30:LYS:NZ	2.38	0.56
4:1E:77:ILE:HD13	4:1E:195:LEU:HD13	1.88	0.56
32:1a:533:A:O2'	32:1a:535:A:OP2	2.21	0.56
32:1a:745:C:H2'	32:1a:746:A:C8	2.41	0.56
47:1p:14:ASN:OD1	47:1p:42:ARG:NH2	2.39	0.56
5:2F:122:LYS:NZ	5:2F:152:GLU:OE2	2.39	0.56
32:2a:1014:A:C2	32:2a:1219:U:H1'	2.41	0.56
47:2p:1:MET:HE3	47:2p:3:LYS:HD2	1.87	0.56
47:2p:43:LYS:HG2	47:2p:48:TRP:CE2	2.40	0.56
1:1A:2611:U:H5'	1:1A:2611:U:H6	1.71	0.55
15:1T:93:ARG:NH2	61:1T:304:HOH:O	2.38	0.55
32:1a:973:G:OP1	41:1j:57:LYS:NZ	2.38	0.55
33:1b:74:LYS:NZ	33:1b:206:ASP:OD1	2.39	0.55
38:1g:79:ARG:HA	38:1g:84:ASN:HA	1.87	0.55
1:2A:1063:G:H2'	1:2A:1065:U:C6	2.39	0.55
1:2A:1090:U:H2'	1:2A:1091:G:H8	1.70	0.55
2:2B:42:C:N3	6:2G:91:ARG:NH1	2.49	0.55
8:2I:29:TYR:HD2	8:2I:30:LEU:HD23	1.70	0.55
19:2X:40:LYS:HG3	19:2X:51:VAL:HB	1.88	0.55
32:2a:67:C:H2'	32:2a:68:G:C8	2.41	0.55
48:2q:40:LYS:HD3	48:2q:42:TYR:CZ	2.41	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2153:G:H2'	1:2A:2154:G:C8	2.41	0.55
6:2G:101:ILE:HG22	6:2G:105:LYS:HE2	1.87	0.55
32:2a:1190:G:O2'	34:2c:3:ASN:HB3	2.06	0.55
35:1d:165:MET:HA	35:1d:168:ARG:HB2	1.89	0.55
37:1f:95:GLU:O	49:1r:32:ARG:NH1	2.36	0.55
1:2A:796:C:H2'	1:2A:797:C:C6	2.41	0.55
1:2A:1084:A:H8	1:2A:1085:A:H4'	1.71	0.55
33:2b:71:VAL:HA	33:2b:93:VAL:HG22	1.89	0.55
33:2b:179:LYS:HA	39:2h:72:PRO:HG3	1.88	0.55
35:2d:15:GLU:OE2	35:2d:59:ARG:NH1	2.39	0.55
1:1A:2893:G:H4'	1:1A:2894:G:O5'	2.05	0.55
5:1F:185:ASP:HA	5:1F:188:ARG:HD3	1.89	0.55
8:1I:104:GLN:HE21	8:1I:105:HIS:CD2	2.24	0.55
32:1a:1256:A:OP2	34:1c:26:LYS:NZ	2.29	0.55
33:1b:114:ARG:O	33:1b:118:LEU:HG	2.07	0.55
1:1A:1165:U:H2'	1:1A:1166:C:C6	2.42	0.55
32:1a:390:C:H2'	32:1a:391:G:C8	2.42	0.55
51:1t:47:GLY:HA2	51:1t:48:LYS:HB2	1.89	0.55
1:2A:247:G:H4'	1:2A:386:G:C5	2.41	0.55
1:2A:2180:U:H2'	1:2A:2181:G:C8	2.42	0.55
6:2G:7:LEU:HD23	6:2G:100:TRP:HE3	1.70	0.55
25:23:7:LYS:HE3	25:23:32:GLN:HE21	1.71	0.55
32:2a:769:G:H4'	32:2a:1513:A:H4'	1.87	0.55
32:2a:976:G:P	45:2n:32:SER:H	2.29	0.55
34:2c:120:VAL:HA	34:2c:123:GLN:HB2	1.87	0.55
40:2i:54:ASP:O	40:2i:56:LEU:N	2.38	0.55
33:1b:134:GLU:HG3	33:1b:137:ARG:HH21	1.71	0.55
46:1o:9:GLN:HA	46:1o:12:ILE:HD12	1.89	0.55
51:1t:10:LEU:HB3	51:1t:12:ALA:H	1.70	0.55
1:2A:999:U:OP2	61:2A:3844:HOH:O	2.18	0.55
7:2H:164:TYR:HB2	7:2H:167:GLU:HB2	1.89	0.55
24:22:19:VAL:HG12	24:22:23:LYS:HE3	1.88	0.55
32:2a:1047:G:H5''	45:2n:4:LYS:HD3	1.89	0.55
34:2c:37:GLN:HE22	45:2n:52:GLN:HB3	1.70	0.55
1:1A:668:G:H5'	1:1A:669:G:OP2	2.06	0.55
1:1A:864:G:N7	12:1Q:22:LYS:NZ	2.46	0.55
1:1A:2245:U:O2'	1:1A:2436:G:OP2	2.21	0.55
2:1B:6:C:H2'	2:1B:7:G:H5''	1.88	0.55
7:2H:20:ALA:HB3	7:2H:23:ARG:HB2	1.89	0.55
26:24:34:GLU:HG2	26:24:35:VAL:HG12	1.88	0.55
32:2a:974:A:OP2	45:2n:29:ARG:NH2	2.40	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:2b:111:ARG:HH11	33:2b:111:ARG:HA	1.70	0.55
40:2i:42:ARG:NH1	40:2i:71:SER:O	2.40	0.55
53:2y:48:PHE:CD2	53:2y:70:MET:HB2	2.42	0.55
1:1A:71:A:N7	19:1X:31:HIS:HE1	2.04	0.55
26:14:46:GLN:O	26:14:48:ARG:N	2.38	0.55
1:2A:974:G:N2	61:2A:3872:HOH:O	2.22	0.55
1:2A:994:C:OP2	16:2U:54:LYS:NZ	2.38	0.55
1:2A:1045:A:H8	1:2A:1047:G:N3	2.05	0.55
1:2A:1786:A:H1'	1:2A:1938:A:N6	2.22	0.55
1:2A:1996:C:H4'	1:2A:1997:G:OP1	2.07	0.55
1:2A:2115:G:N2	1:2A:2119:A:H5'	2.20	0.55
1:2A:2706:G:N7	61:2A:3964:HOH:O	2.33	0.55
6:2G:53:LEU:HD12	6:2G:56:ALA:HB2	1.89	0.55
8:2I:130:TYR:HB3	8:2I:138:ILE:HB	1.88	0.55
17:2V:14:VAL:HB	17:2V:96:ILE:HG13	1.89	0.55
32:2a:501:C:H2'	32:2a:502:G:C8	2.42	0.55
32:2a:1202:G:H1'	45:2n:29:ARG:HD2	1.89	0.55
1:1A:911:A:H2'	12:1Q:9:TYR:OH	2.07	0.55
1:1A:1094:U:O2'	1:1A:1096:A:N7	2.38	0.55
6:1G:126:ASP:HB3	6:1G:128:ARG:H	1.71	0.55
32:1a:1240:U:OP2	38:1g:116:ALA:N	2.40	0.55
32:1a:1510:U:H2'	32:1a:1511:G:C8	2.41	0.55
1:2A:1064:C:H3'	1:2A:1065:U:C5'	2.35	0.55
1:2A:2316:C:O2'	6:2G:128:ARG:NH1	2.37	0.55
12:2Q:37:LEU:HD21	12:2Q:130:LYS:HE3	1.89	0.55
26:24:14:ILE:HB	26:24:22:ILE:HD13	1.89	0.55
32:2a:1318:A:H5''	50:2s:3:ARG:HH22	1.72	0.55
39:2h:121:ASP:N	39:2h:121:ASP:OD1	2.40	0.55
50:2s:22:LEU:O	50:2s:26:GLY:N	2.39	0.55
1:1A:1266:G:O5'	18:1W:15:ARG:NH2	2.40	0.55
4:1E:59:VAL:HG21	4:1E:74:PRO:HB3	1.88	0.55
5:1F:53:THR:CG2	5:1F:55:GLY:H	2.20	0.55
6:1G:126:ASP:N	6:1G:130:ASN:O	2.37	0.55
32:1a:108:G:C6	51:1t:15:ARG:HG2	2.41	0.55
1:2A:774:A:H2'	1:2A:774:A:N3	2.21	0.55
1:2A:811:U:H2'	11:2P:21:ARG:HA	1.90	0.55
26:24:46:GLN:OE1	26:24:48:ARG:NH2	2.38	0.55
32:2a:9:G:H2'	32:2a:10:A:C8	2.41	0.55
51:2t:18:GLN:O	51:2t:22:ARG:HG3	2.06	0.55
6:1G:143:GLU:OE2	26:14:26:SER:OG	2.21	0.54
10:1O:64:ARG:HB2	10:1O:79:PHE:CD2	2.42	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:1c:116:VAL:HG21	34:1c:202:ILE:HD11	1.89	0.54
44:1m:3:ARG:HG3	44:1m:4:ILE:H	1.72	0.54
1:2A:1066:U:O2'	1:2A:1068:G:OP2	2.23	0.54
1:2A:2144:U:H5''	1:2A:2145:C:C4	2.42	0.54
15:2T:91:ARG:HD2	15:2T:120:ARG:NH1	2.23	0.54
32:2a:108:G:C6	51:2t:15:ARG:HG2	2.42	0.54
32:2a:1131:G:H2'	32:2a:1132:C:H6	1.72	0.54
47:2p:53:VAL:HG22	47:2p:79:VAL:HG22	1.88	0.54
1:1A:429:A:OP2	61:1A:4140:HOH:O	2.18	0.54
5:1F:184:TYR:CE2	5:1F:188:ARG:HD2	2.42	0.54
12:1Q:67:ARG:O	12:1Q:101:ARG:NH2	2.34	0.54
17:1V:21:ARG:HD3	17:1V:91:TYR:CE1	2.42	0.54
25:13:7:LYS:HE3	25:13:32:GLN:NE2	2.22	0.54
32:1a:79:G:N1	32:1a:90:U:N3	2.54	0.54
35:1d:173:TRP:CD2	35:1d:189:PRO:HG3	2.41	0.54
1:2A:922:U:H2'	1:2A:923:C:C6	2.41	0.54
1:2A:1187:G:H5'	17:2V:81:TYR:CE1	2.42	0.54
1:2A:1495:A:H2'	1:2A:1496:A:C8	2.43	0.54
1:2A:2584:U:H2'	1:2A:2585:U:H2'	1.89	0.54
6:2G:80:PHE:O	6:2G:82:LEU:N	2.40	0.54
8:2I:4:ILE:HG12	8:2I:18:VAL:HG22	1.90	0.54
21:2Z:7:ALA:HB3	21:2Z:61:LEU:HD23	1.90	0.54
32:2a:9:G:H2'	32:2a:10:A:H8	1.72	0.54
32:2a:1503:A:H5'	32:2a:1531:A:H1'	1.88	0.54
34:2c:8:ILE:HD12	34:2c:16:ARG:HD2	1.87	0.54
32:1a:17:U:H2'	32:1a:18:C:C6	2.43	0.54
32:1a:1400:5MC:C2	53:1y:63:ALA:HA	2.43	0.54
15:2T:16:ARG:NH2	15:2T:83:ILE:O	2.39	0.54
32:2a:443:C:H2'	32:2a:444:C:H6	1.72	0.54
32:2a:1441:G:H5''	32:2a:1442:G:H5'	1.89	0.54
37:2f:67:MET:HE1	37:2f:75:LEU:HD22	1.89	0.54
38:2g:51:GLN:O	38:2g:55:GLY:HA2	2.07	0.54
40:2i:28:VAL:HG13	40:2i:63:ILE:HG22	1.89	0.54
50:2s:44:MET:HA	50:2s:47:HIS:CE1	2.42	0.54
1:1A:1178:C:H2'	1:1A:1179:C:C6	2.43	0.54
1:1A:2693:A:H2'	1:1A:2694:G:H8	1.72	0.54
7:1H:3:ARG:NH2	7:1H:65:HIS:HB3	2.23	0.54
32:1a:1498:UR3:H4'	32:1a:1519:MA6:H2	1.90	0.54
1:2A:588:U:H2'	1:2A:589:C:C6	2.42	0.54
1:2A:1796:U:H2'	1:2A:1797:C:H6	1.71	0.54
1:1A:279:C:N4	1:1A:361:G:H1	1.99	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1429:G:H2'	1:1A:1430:C:C6	2.42	0.54
1:1A:2506:U:OP1	4:1E:144:ARG:NH2	2.40	0.54
32:1a:1500:A:OP2	61:1a:3311:HOH:O	2.19	0.54
44:1m:40:ASN:HB3	44:1m:43:THR:HG23	1.88	0.54
52:1u:5:ASP:O	52:1u:11:GLY:HA3	2.07	0.54
1:2A:2321:G:O2'	1:2A:2322:A:OP1	2.22	0.54
3:2D:108:PRO:HG2	3:2D:111:LEU:HB2	1.90	0.54
52:2u:17:THR:O	52:2u:22:ARG:NH1	2.39	0.54
1:2A:8:A:H2'	1:2A:9:U:C6	2.42	0.54
1:2A:634:C:H2'	1:2A:635:C:C6	2.43	0.54
1:2A:1430:C:H2'	1:2A:1431:U:C6	2.43	0.54
1:2A:2074:U:H2'	1:2A:2075:U:C6	2.43	0.54
5:2F:184:TYR:CE2	5:2F:188:ARG:HD2	2.43	0.54
7:2H:15:VAL:HG12	7:2H:28:GLY:HA2	1.90	0.54
33:2b:121:LEU:HG	33:2b:127:ILE:HG23	1.89	0.54
41:2j:19:SER:O	41:2j:23:ILE:HG12	2.07	0.54
1:1A:305:U:H2'	1:1A:306:U:C6	2.42	0.54
1:1A:530:G:N1	1:1A:2023:G:OP1	2.32	0.54
32:1a:142:G:O2'	32:1a:196:A:N1	2.40	0.54
53:1y:49:VAL:HG22	53:1y:66:LYS:HG2	1.90	0.54
1:2A:1762:A:N6	61:2A:4026:HOH:O	2.40	0.54
1:2A:2103:C:H42	1:2A:2185:C:H42	1.54	0.54
1:2A:2123:G:N1	1:2A:2175:C:O2	2.32	0.54
21:2Z:23:LYS:HD3	21:2Z:40:ASP:HA	1.90	0.54
21:2Z:125:LEU:HB3	21:2Z:165:VAL:HG13	1.90	0.54
32:2a:978:A:O2'	32:2a:1322:C:N3	2.38	0.54
53:2y:35:ILE:HB	53:2y:55:ASN:HB3	1.89	0.54
1:1A:1486:A:H2'	1:1A:1487:G:C8	2.42	0.54
21:1Z:119:GLU:OE1	21:1Z:122:ARG:NH1	2.41	0.54
32:1a:111:G:OP2	61:1a:3310:HOH:O	2.18	0.54
32:1a:1412:C:H2'	32:1a:1413:A:C8	2.43	0.54
33:1b:112:VAL:HG12	33:1b:149:LEU:HD13	1.90	0.54
21:2Z:46:LYS:H	21:2Z:46:LYS:HD2	1.71	0.54
22:20:68:GLU:OE1	22:20:82:ARG:NE	2.25	0.54
32:2a:434:U:H2'	32:2a:435:C:C6	2.42	0.54
32:2a:1218:C:OP2	45:2n:9:LYS:NZ	2.35	0.54
32:2a:1271:G:H5'	32:2a:1314:C:H5''	1.89	0.54
34:2c:123:GLN:O	34:2c:128:PHE:HB2	2.08	0.54
35:2d:173:TRP:CD1	35:2d:189:PRO:HG3	2.42	0.54
41:2j:49:VAL:HG23	45:2n:41:ARG:HB2	1.89	0.54
1:1A:1096:A:H3'	1:1A:1097:U:H5''	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1721:G:H5'	1:1A:1722:A:OP2	2.08	0.54
1:1A:2142:C:C2	1:1A:2149:G:N1	2.75	0.54
32:1a:262:A:H2'	32:1a:263:A:C8	2.43	0.54
1:2A:212:G:H2'	1:2A:213:A:O4'	2.07	0.54
3:2D:108:PRO:HB3	3:2D:143:HIS:CE1	2.43	0.54
7:2H:3:ARG:NH1	7:2H:5:GLY:H	2.06	0.54
32:2a:420:U:H2'	32:2a:422:C:C5	2.43	0.54
32:2a:1080:A:H5'	36:2e:14:ARG:HH21	1.73	0.54
32:2a:1131:G:H2'	32:2a:1132:C:C6	2.43	0.54
32:2a:1273:G:H3'	32:2a:1274:G:C8	2.43	0.54
33:2b:158:LEU:HD21	33:2b:180:LEU:HD13	1.90	0.54
21:1Z:144:LEU:HD11	21:1Z:150:LEU:HD22	1.90	0.54
32:1a:1292:U:H5'	40:1i:38:GLN:OE1	2.08	0.54
41:1j:39:PRO:HA	41:1j:70:ARG:HD3	1.90	0.54
6:2G:41:GLN:NE2	6:2G:154:GLY:O	2.41	0.54
36:2e:110:LEU:HD13	36:2e:118:ILE:HG21	1.89	0.54
1:1A:2167:U:H2'	1:1A:2168:G:C8	2.43	0.53
5:1F:191:ARG:NH2	61:1F:404:HOH:O	2.40	0.53
32:1a:263:A:OP2	51:1t:79:ARG:NH1	2.42	0.53
32:1a:881:G:P	43:1l:12:ARG:HH22	2.30	0.53
32:1a:1034:G:H3'	32:1a:1035:A:C8	2.43	0.53
1:2A:586:A:N1	1:2A:809:G:O2'	2.36	0.53
1:2A:668:G:H5'	1:2A:669:G:OP2	2.08	0.53
1:2A:2564:A:C2	1:2A:2647:U:H4'	2.42	0.53
33:2b:24:TRP:CD1	33:2b:24:TRP:H	2.26	0.53
33:2b:71:VAL:HG23	33:2b:164:VAL:HA	1.89	0.53
35:2d:201:GLN:NE2	36:2e:116:THR:O	2.40	0.53
32:1a:877:C:HO2'	39:1h:3:THR:HG1	1.57	0.53
32:1a:1124:G:N7	32:1a:1145:C:O2'	2.41	0.53
42:1k:98:LEU:O	42:1k:101:SER:OG	2.18	0.53
1:2A:493:G:H2'	1:2A:494:G:O4'	2.08	0.53
1:2A:748:G:OP1	1:2A:2612:C:N4	2.41	0.53
1:2A:1877:A:H5'	1:2A:1878:G:OP2	2.08	0.53
19:2X:11:PRO:HB3	19:2X:92:LEU:HD11	1.90	0.53
1:1A:1486:A:H2'	1:1A:1487:G:H8	1.72	0.53
32:1a:769:G:H4'	32:1a:1513:A:H4'	1.90	0.53
33:1b:17:PHE:HB3	33:1b:44:LEU:HD11	1.89	0.53
33:1b:115:LEU:O	33:1b:119:GLU:HG2	2.08	0.53
1:2A:1047:G:H2'	1:2A:1110:G:H22	1.73	0.53
1:2A:1056:G:H5''	1:2A:1057:A:O4'	2.09	0.53
32:2a:337:C:H2'	32:2a:338:A:H8	1.73	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:2b:52:GLU:OE2	33:2b:56:ARG:NH2	2.41	0.53
34:2c:12:LEU:O	45:2n:57:ARG:NH1	2.41	0.53
34:2c:71:ALA:HA	34:2c:106:VAL:HB	1.89	0.53
53:2y:61:LEU:HB3	53:2y:81:LEU:HD22	1.90	0.53
1:1A:2023:G:H5'	1:1A:2617:C:H4'	1.90	0.53
1:1A:2345:G:N3	1:1A:2381:C:H2'	2.23	0.53
1:2A:1189:A:OP2	61:2A:3845:HOH:O	2.19	0.53
32:2a:1142:G:H2'	32:2a:1143:G:O4'	2.08	0.53
1:1A:1096:A:H5'	1:1A:1097:U:OP2	2.09	0.53
1:1A:2334:G:H5'	14:1S:9:ARG:HG2	1.90	0.53
1:1A:2693:A:H2'	1:1A:2694:G:C8	2.44	0.53
15:1T:127:ALA:O	15:1T:128:GLU:HB3	2.09	0.53
32:1a:131:C:O2'	32:1a:262:A:N3	2.35	0.53
32:1a:266:G:H5''	32:1a:268:C:H41	1.73	0.53
32:1a:1183:A:H3'	32:1a:1184:G:H5''	1.91	0.53
32:2a:1030:C:N4	32:2a:1032:G:O6	2.42	0.53
32:2a:1106:G:H5''	34:2c:172:ARG:HG2	1.89	0.53
32:1a:755:G:OP2	46:1o:65:ARG:HD2	2.09	0.53
53:1y:23:ARG:HH11	53:1y:26:LYS:HD2	1.72	0.53
1:2A:362:U:O2'	1:2A:363:G:H5'	2.09	0.53
1:2A:1631(A):A:N6	61:2A:3866:HOH:O	2.21	0.53
1:2A:2111:C:H42	1:2A:2147:G:N2	2.07	0.53
6:2G:179:PRO:HB2	26:24:42:PHE:HE2	1.74	0.53
11:2P:95:VAL:HA	11:2P:99:LEU:HD22	1.91	0.53
12:2Q:32:TYR:OH	12:2Q:111:GLU:OE2	2.22	0.53
17:2V:52:VAL:HG23	17:2V:55:ALA:HB3	1.91	0.53
32:2a:31:G:O2'	32:2a:48:C:N4	2.41	0.53
32:2a:1376:U:H2'	32:2a:1377:A:C8	2.44	0.53
32:2a:1387:G:H2'	32:2a:1388:C:C6	2.43	0.53
34:2c:21:ARG:HH22	34:2c:56:ASP:HB3	1.73	0.53
36:2e:8:GLU:HG2	36:2e:34:VAL:HG12	1.89	0.53
39:2h:112:LEU:HB3	39:2h:133:LEU:HA	1.90	0.53
1:1A:1143:A:OP1	9:1N:25:ARG:NH2	2.41	0.53
1:1A:2445:G:OP1	5:1F:74:ARG:NH2	2.37	0.53
21:1Z:199:LYS:NZ	61:1Z:402:HOH:O	2.41	0.53
32:1a:7:G:H5'	32:1a:298:A:O4'	2.07	0.53
32:1a:580:U:H2'	32:1a:581:G:O4'	2.09	0.53
50:1s:4:SER:HB2	50:1s:7:LYS:HG3	1.91	0.53
1:2A:657:U:H2'	1:2A:658:C:C6	2.44	0.53
1:2A:1012:U:C5	9:2N:28:THR:HG21	2.44	0.53
32:2a:1158:C:O2	32:2a:1158:C:H2'	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:2b:174:VAL:O	33:2b:178:ARG:HG2	2.09	0.53
37:2f:43:LEU:HD23	37:2f:46:ARG:HH22	1.72	0.53
53:2y:24:LEU:HD23	53:2y:78:ILE:HD12	1.91	0.53
1:1A:1628:G:H2'	1:1A:1629:U:C6	2.44	0.53
1:1A:2291:U:H2'	1:1A:2292:C:C6	2.44	0.53
28:16:6:ARG:NH1	28:16:26:ASN:HB2	2.24	0.53
32:1a:353:A:H5'	32:1a:353:A:H8	1.74	0.53
33:1b:102:LEU:HB3	33:1b:180:LEU:HD12	1.91	0.53
41:1j:30:SER:OG	41:1j:81:THR:HG22	2.09	0.53
1:2A:1053:C:H4'	1:2A:1054:A:OP1	2.09	0.53
5:2F:185:ASP:HA	5:2F:188:ARG:HD3	1.90	0.53
32:2a:890:G:O2'	32:2a:906:G:O6	2.21	0.53
32:2a:1251:A:H2'	32:2a:1252:A:C8	2.44	0.53
45:2n:29:ARG:HD3	45:2n:40:CYS:SG	2.48	0.53
1:1A:774:A:N3	1:1A:774:A:H2'	2.23	0.53
24:12:1:MET:HE3	24:12:6:VAL:HG22	1.90	0.53
1:2A:1566:A:OP1	3:2D:211:ARG:NH1	2.41	0.53
1:2A:2327:A:H2'	1:2A:2328:A:C8	2.43	0.53
14:2S:15:ARG:O	14:2S:19:LYS:HG2	2.09	0.53
15:2T:127:ALA:C	15:2T:129:ARG:H	2.16	0.53
32:2a:7:G:H5'	32:2a:298:A:O4'	2.09	0.53
32:2a:1003:G:H3'	32:2a:1003:G:N3	2.23	0.53
32:2a:1129:C:N4	32:2a:1143:G:H1	2.07	0.53
32:2a:1241:G:H2'	32:2a:1242:C:C6	2.43	0.53
32:2a:1513:A:H2'	32:2a:1514:C:C6	2.44	0.53
1:1A:2602:A:H4'	1:1A:2603:G:OP1	2.08	0.53
10:1O:98:VAL:HG22	10:1O:118:ALA:HA	1.91	0.53
20:1Y:53:PRO:O	20:1Y:56:PRO:HD3	2.09	0.53
39:1h:36:LEU:HD12	39:1h:59:LEU:HD13	1.90	0.53
40:1i:8:GLY:HA2	40:1i:79:LEU:HD23	1.89	0.53
1:2A:881:G:H2'	1:2A:882:G:C8	2.44	0.53
1:2A:2445:G:OP1	5:2F:74:ARG:NH2	2.33	0.53
26:24:58:ARG:NH2	50:2s:68:GLY:H	2.05	0.53
50:2s:30:LEU:HD11	50:2s:50:ALA:HB2	1.89	0.53
1:1A:1025:G:C4	1:1A:1135:C:H1'	2.44	0.52
1:1A:1098:A:H2'	1:1A:1099:G:O4'	2.09	0.52
1:1A:1105:U:H2'	1:1A:1106:G:C8	2.40	0.52
8:1I:115:ALA:HB2	8:1I:131:LYS:HE2	1.91	0.52
32:1a:45:U:H2'	32:1a:46:G:C8	2.44	0.52
32:1a:619:U:N3	35:1d:134:ASP:OD1	2.39	0.52
35:1d:15:GLU:HB3	35:1d:63:LYS:HE2	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:1p:22:THR:HA	47:1p:33:ILE:HG13	1.90	0.52
10:2O:16:ALA:HB2	10:2O:52:VAL:HG21	1.90	0.52
32:2a:353:A:H5'	32:2a:353:A:H8	1.74	0.52
32:2a:546:G:OP1	35:2d:73:ARG:HG2	2.09	0.52
32:2a:1289:A:N1	32:2a:1371:G:O2'	2.36	0.52
33:2b:127:ILE:C	33:2b:129:GLU:H	2.17	0.52
33:2b:197:VAL:HG12	33:2b:200:ILE:HG13	1.90	0.52
1:1A:1778:U:H2'	1:1A:1784:A:N6	2.24	0.52
1:1A:2660:A:N7	7:1H:175:LYS:NZ	2.56	0.52
7:1H:124:GLU:CG	7:1H:132:ARG:HB3	2.39	0.52
32:1a:524:G:H2'	32:1a:525:C:C6	2.44	0.52
32:1a:1414:U:H3	32:1a:1486:G:H1	1.56	0.52
1:2A:2602:A:H1'	1:2A:2603:G:C5'	2.34	0.52
10:2O:68:GLU:OE1	10:2O:78:ARG:NH1	2.41	0.52
13:2R:87:TYR:OH	13:2R:117:VAL:O	2.25	0.52
22:20:11:ARG:O	22:20:14:ARG:NH2	2.40	0.52
32:2a:1222:G:O6	61:2a:3212:HOH:O	2.19	0.52
36:2e:152:ARG:HB3	39:2h:43:GLY:HA3	1.91	0.52
47:2p:42:ARG:HB3	47:2p:44:THR:HG23	1.91	0.52
1:1A:870:A:OP1	12:1Q:6:ARG:NH1	2.37	0.52
1:1A:1518:U:H2'	1:1A:1519:G:O4'	2.09	0.52
1:1A:2753:A:N3	31:19:15:LYS:NZ	2.56	0.52
32:1a:603:U:H2'	32:1a:604:G:H8	1.73	0.52
32:1a:1186:G:N2	45:1n:61:TRP:O	2.36	0.52
41:1j:13:HIS:HA	41:1j:16:LEU:HB3	1.92	0.52
1:2A:511:U:OP2	61:2A:3846:HOH:O	2.19	0.52
10:2O:64:ARG:HB2	10:2O:79:PHE:CG	2.44	0.52
32:2a:1143:G:H2'	32:2a:1144:G:H8	1.70	0.52
1:1A:330:A:H2	1:1A:1210:A:H2'	1.75	0.52
1:1A:1588:C:H2'	1:1A:1589:C:C6	2.45	0.52
1:1A:2564:A:C2	1:1A:2647:U:H4'	2.44	0.52
3:1D:242:ARG:HD2	3:1D:246:PRO:HG3	1.92	0.52
30:18:62:LEU:HB3	30:18:65:GLU:CG	2.40	0.52
32:1a:1149:C:P	40:1i:9:ARG:HH21	2.33	0.52
46:1o:87:ILE:HG22	46:1o:88:ARG:N	2.24	0.52
1:2A:81:G:N7	61:2A:3967:HOH:O	2.34	0.52
1:2A:2105:C:H2'	1:2A:2106:G:C8	2.45	0.52
1:2A:2115:G:N1	1:2A:2119:A:OP2	2.42	0.52
17:2V:25:LEU:H	17:2V:92:THR:HG1	1.56	0.52
32:2a:130:A:O2'	32:2a:131:C:O5'	2.27	0.52
47:2p:18:ARG:NH1	47:2p:32:TYR:OH	2.41	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:2y:37:PRO:HB3	53:2y:54:ILE:HG23	1.92	0.52
6:1G:131:TYR:HB3	6:1G:159:VAL:HG13	1.91	0.52
32:1a:176:C:H2'	32:1a:177:C:C6	2.44	0.52
32:1a:600:C:H2'	32:1a:601:C:H6	1.74	0.52
1:2A:1014:U:H2'	1:2A:1015:G:H8	1.74	0.52
1:2A:2127:G:N1	1:2A:2161:C:O2	2.41	0.52
1:2A:2836:U:H2'	1:2A:2837:G:C8	2.45	0.52
8:2I:5:LEU:HD21	8:2I:12:LEU:HB3	1.90	0.52
21:2Z:10:ARG:HD3	21:2Z:37:VAL:O	2.09	0.52
32:2a:520:A:N1	32:2a:536:C:H1'	2.25	0.52
32:2a:1014:A:H2	32:2a:1219:U:H1'	1.74	0.52
32:2a:1318:A:H5''	50:2s:3:ARG:NH2	2.23	0.52
35:2d:22:LYS:HD2	60:2d:501:SF4:S3	2.50	0.52
32:1a:1400:5MC:N3	53:1y:63:ALA:HA	2.25	0.52
36:1e:8:GLU:OE2	36:1e:63:ARG:NH2	2.42	0.52
1:2A:1057:A:O2'	1:2A:1058:G:OP1	2.27	0.52
1:2A:1153:C:H2'	1:2A:1154:G:O4'	2.10	0.52
1:2A:1777:U:OP2	61:2A:3847:HOH:O	2.19	0.52
21:2Z:157:LEU:HB3	21:2Z:161:VAL:HG12	1.90	0.52
32:2a:1400:5MC:C2	53:2y:63:ALA:HA	2.45	0.52
34:2c:134:ILE:HG23	34:2c:151:VAL:HB	1.92	0.52
1:1A:1803:A:H4'	3:1D:259:THR:HG23	1.92	0.52
1:1A:2096:U:H2'	1:1A:2097:C:C6	2.45	0.52
21:1Z:145:GLU:O	21:1Z:148:ASP:N	2.43	0.52
35:1d:11:LEU:HG	35:1d:66:ARG:HD3	1.91	0.52
36:1e:37:ARG:HH12	36:1e:111:GLU:HG2	1.75	0.52
1:2A:1359:A:H61	1:2A:1372:U:H3	1.57	0.52
1:2A:2543:G:H2'	1:2A:2544:G:C8	2.44	0.52
12:2Q:38:GLU:HG3	12:2Q:127:ILE:HB	1.92	0.52
32:2a:580:U:H5''	46:2o:58:MET:HG2	1.90	0.52
32:2a:1069:C:O2'	32:2a:1192:C:O2	2.27	0.52
32:2a:1226:C:N4	44:2m:104:ARG:HD2	2.23	0.52
1:1A:2115:G:H2'	1:1A:2117:A:N6	2.25	0.52
40:1i:9:ARG:HB2	40:1i:104:ARG:HE	1.75	0.52
1:2A:607:U:OP1	5:2F:102:PRO:HA	2.10	0.52
1:2A:2104:G:N7	1:2A:2186:G:C2	2.77	0.52
2:2B:13:A:N1	2:2B:69:G:O2'	2.28	0.52
7:2H:11:VAL:HG13	7:2H:15:VAL:HG23	1.92	0.52
8:2I:1:MET:HE2	8:2I:38:LEU:HD21	1.91	0.52
1:1A:639:U:H2'	1:1A:640:C:C6	2.44	0.52
1:1A:1239:G:H2'	1:1A:1240:U:O4'	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1762:A:H2'	61:1A:7110:HOH:O	2.10	0.52
1:1A:2572:A:N7	4:1E:144:ARG:HD2	2.25	0.52
32:1a:186:C:H2'	32:1a:187:C:C6	2.45	0.52
32:1a:491:G:H2'	32:1a:492:G:O4'	2.10	0.52
32:1a:1118:C:H1'	32:1a:1179:A:C4	2.45	0.52
1:2A:1092:C:H2'	1:2A:1092:C:O2	2.10	0.52
1:2A:1371:G:HO2'	1:2A:1372:U:H5	1.56	0.52
20:2Y:90:LEU:HD12	20:2Y:92:ASN:HD22	1.74	0.52
32:2a:390:C:H2'	32:2a:391:G:C8	2.44	0.52
32:2a:920:U:H2'	32:2a:921:U:C6	2.44	0.52
32:2a:1031:G:H2'	32:2a:1032:G:C8	2.45	0.52
48:2q:3:LYS:HD3	48:2q:60:ILE:HD11	1.91	0.52
50:2s:41:VAL:HG12	50:2s:44:MET:HG2	1.92	0.52
53:2y:10:MET:HE1	53:2y:41:LEU:HB3	1.92	0.52
1:1A:626:U:O4	11:1P:107:LYS:HE2	2.10	0.52
1:1A:1651:G:OP1	13:1R:40:LYS:NZ	2.40	0.52
1:1A:2137:C:C2	1:1A:2154:G:N2	2.77	0.52
1:1A:2186:G:C2	1:1A:2187:G:C8	2.98	0.52
32:1a:747:C:OP2	32:1a:748:C:N4	2.37	0.52
32:1a:1218:C:H2'	32:1a:1219:U:C6	2.45	0.52
44:1m:11:ARG:O	44:1m:13:LYS:N	2.42	0.52
1:2A:1047:G:H21	1:2A:1111:A:H62	1.58	0.52
32:2a:926:G:N3	53:2y:91:LYS:HG2	2.25	0.52
39:2h:89:PRO:HA	39:2h:92:ARG:HE	1.75	0.52
1:1A:185:U:H4'	1:1A:218:A:H4'	1.92	0.51
32:1a:542:G:H5'	35:1d:41:GLY:HA3	1.91	0.51
36:1e:85:GLY:O	61:1e:302:HOH:O	2.19	0.51
48:1q:15:MET:HE1	48:1q:43:LEU:HD22	1.91	0.51
1:2A:1952:A:OP1	10:2O:42:SER:OG	2.26	0.51
1:2A:2645:G:N2	1:2A:2767:C:OP2	2.43	0.51
1:2A:2693:A:H2'	1:2A:2694:G:C8	2.44	0.51
34:2c:78:GLY:HA3	34:2c:83:ARG:H	1.75	0.51
41:2j:33:GLN:O	41:2j:74:ILE:HA	2.10	0.51
46:2o:37:ASN:O	46:2o:41:GLU:HG2	2.11	0.51
53:2y:74:ILE:O	53:2y:78:ILE:HG12	2.10	0.51
1:1A:1175:U:O3'	1:1A:1176:G:H4'	2.10	0.51
21:1Z:144:LEU:HD21	21:1Z:150:LEU:HD13	1.91	0.51
32:1a:1020:U:H2'	32:1a:1021:G:C8	2.45	0.51
39:1h:4:ASP:OD1	39:1h:85:ARG:NH1	2.43	0.51
1:2A:2319:G:N2	14:2S:3:ARG:HD3	2.24	0.51
61:2A:4455:HOH:O	5:2F:74:ARG:HD2	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:2G:11:TYR:HA	6:2G:15:VAL:HB	1.91	0.51
7:2H:55:PRO:HG2	7:2H:61:HIS:CE1	2.45	0.51
33:2b:164:VAL:HB	33:2b:186:ALA:HB2	1.91	0.51
41:2j:62:HIS:HB3	45:2n:59:ALA:HB3	1.92	0.51
1:1A:2047:U:O2'	1:1A:2823:A:N1	2.42	0.51
14:1S:105:ALA:HB1	14:1S:110:LEU:HD12	1.93	0.51
32:1a:503:C:H2'	32:1a:504:C:H6	1.76	0.51
32:1a:574:A:OP2	61:1a:3312:HOH:O	2.19	0.51
37:1f:42:GLU:OE2	37:1f:59:TYR:OH	2.23	0.51
47:1p:34:GLU:OE1	47:1p:55:ARG:NH2	2.43	0.51
1:2A:927:G:H2'	1:2A:928:G:O4'	2.10	0.51
1:2A:1769:G:O2'	1:2A:1958:C:OP1	2.27	0.51
1:2A:2704:C:H2'	1:2A:2705:A:O4'	2.11	0.51
4:2E:28:ALA:HB3	4:2E:93:VAL:HG12	1.93	0.51
15:2T:45:PHE:CE1	15:2T:74:ARG:HG3	2.44	0.51
33:2b:16:HIS:CG	33:2b:210:SER:HB3	2.46	0.51
1:1A:1359:A:N1	1:1A:1372:U:O4	2.43	0.51
19:1X:5:TYR:CZ	24:12:30:ARG:HB2	2.45	0.51
20:1Y:90:LEU:HB3	20:1Y:92:ASN:HD22	1.74	0.51
39:1h:6:ILE:O	39:1h:10:LEU:HG	2.09	0.51
1:2A:483:A:H5''	20:2Y:50:ARG:HD3	1.91	0.51
1:2A:1827:C:O2'	1:2A:1970:A:N3	2.37	0.51
1:2A:2115:G:N2	1:2A:2171:A:H61	2.06	0.51
1:2A:2756:U:H1'	1:2A:2757:A:H5''	1.92	0.51
6:2G:23:PHE:HB2	6:2G:25:TYR:CE2	2.46	0.51
32:2a:337:C:H2'	32:2a:338:A:C8	2.43	0.51
32:2a:559:A:OP1	36:2e:126:ARG:NH2	2.44	0.51
36:2e:10:MET:HG2	36:2e:13:ILE:HD11	1.92	0.51
40:2i:43:ALA:C	40:2i:45:ALA:H	2.18	0.51
40:2i:89:ASN:HB3	40:2i:92:TYR:CE2	2.44	0.51
41:2j:8:LEU:HB2	41:2j:70:ARG:HB2	1.93	0.51
1:1A:1817:G:OP1	3:1D:88:ARG:NH2	2.43	0.51
1:1A:1919:A:N1	32:1a:1495:U:O2'	2.41	0.51
6:1G:22:ARG:HH22	6:1G:175:LEU:HD21	1.75	0.51
6:1G:124:SER:HB2	6:1G:131:TYR:CE1	2.46	0.51
8:1I:31:LEU:HD21	8:1I:38:LEU:HD13	1.92	0.51
32:1a:159:G:N2	32:1a:162:A:OP2	2.26	0.51
32:1a:1292:U:OP2	38:1g:41:ARG:NH2	2.32	0.51
32:1a:1492:A:O5'	43:1l:47:LYS:HE3	2.10	0.51
37:1f:69:GLU:H	37:1f:69:GLU:CD	2.17	0.51
48:1q:45:HIS:HB2	48:1q:65:ILE:HD13	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:2D:29:PRO:HB2	3:2D:34:VAL:HG11	1.92	0.51
24:22:25:VAL:HG11	24:22:61:LEU:HD21	1.92	0.51
32:2a:1525:G:OP1	42:2k:120:ARG:NH2	2.43	0.51
34:2c:20:SER:OG	34:2c:22:TRP:NE1	2.43	0.51
41:2j:61:GLU:OE2	45:2n:58:LYS:NZ	2.43	0.51
44:2m:95:GLY:O	44:2m:110:ARG:HG3	2.10	0.51
1:1A:271(I):G:H2'	1:1A:271(J):C:C6	2.46	0.51
1:1A:987:G:O2'	1:1A:1000:A:N3	2.40	0.51
5:1F:192:LEU:HD13	5:1F:194:MET:HE2	1.92	0.51
38:1g:90:GLU:CD	38:1g:90:GLU:H	2.18	0.51
43:1l:46:LYS:HE3	43:1l:94:PRO:HG3	1.92	0.51
53:1y:33:HIS:CE1	53:1y:35:ILE:HG12	2.46	0.51
32:2a:660:G:H1	32:2a:745:C:H42	1.58	0.51
32:2a:1035:A:HO2'	32:2a:1036:G:H8	1.57	0.51
32:2a:1338:G:H2'	32:2a:1339:A:C8	2.46	0.51
1:1A:579:G:H2'	1:1A:580:C:C6	2.45	0.51
1:1A:1405:U:H2'	1:1A:1406:U:C6	2.45	0.51
32:1a:1492:A:H4'	32:1a:1493:A:C6	2.45	0.51
35:1d:178:VAL:C	35:1d:180:GLY:H	2.18	0.51
1:2A:2526:G:H5'	1:2A:2742:C:O2'	2.11	0.51
4:2E:9:VAL:HG13	4:2E:25:VAL:O	2.11	0.51
32:2a:944:G:H1'	32:2a:1339:A:H61	1.76	0.51
32:2a:1030(C):G:H2'	32:2a:1030(D):A:C8	2.45	0.51
32:2a:1129:C:H1'	32:2a:1130:A:N7	2.25	0.51
37:2f:2:ARG:NE	37:2f:69:GLU:HG2	2.25	0.51
44:2m:29:ARG:HA	44:2m:32:GLU:HB3	1.92	0.51
50:2s:50:ALA:HA	50:2s:58:VAL:O	2.11	0.51
1:1A:529:A:N1	61:1A:4259:HOH:O	2.33	0.51
1:1A:1583:A:H5'	1:1A:1584:C:OP1	2.11	0.51
1:1A:1968:G:OP2	61:1A:4144:HOH:O	2.19	0.51
10:1O:23:ARG:NH2	61:1O:303:HOH:O	2.43	0.51
11:1P:63:PRO:HD3	30:18:27:THR:HG22	1.92	0.51
32:1a:309:G:O2'	32:1a:607:A:N1	2.43	0.51
32:1a:618:C:H3'	32:1a:619:U:H5''	1.92	0.51
32:1a:1027:C:H2'	32:1a:1028:C:C5	2.45	0.51
5:2F:178:PRO:HB2	5:2F:201:VAL:HG21	1.92	0.51
12:2Q:68:ILE:HD13	12:2Q:103:MET:HG2	1.92	0.51
25:23:3:ARG:HB2	25:23:60:GLU:HA	1.92	0.51
32:2a:1005:A:H5''	32:2a:1006:C:C5	2.45	0.51
32:2a:1027:C:C5	32:2a:1034:G:O6	2.64	0.51
32:2a:1278:U:H5''	32:2a:1279:A:H5'	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:2b:83:MET:SD	33:2b:234:PRO:HB2	2.51	0.51
39:2h:11:THR:HG23	39:2h:14:ARG:HH21	1.76	0.51
53:2y:43:LYS:HA	53:2y:48:PHE:HA	1.93	0.51
53:2y:60:VAL:HG22	53:2y:62:VAL:HG23	1.92	0.51
1:1A:2377:A:H2'	1:1A:2378:A:C8	2.46	0.51
50:1s:3:ARG:NH1	50:1s:10:PHE:HB2	2.25	0.51
1:2A:30:G:H2'	1:2A:31:C:C6	2.46	0.51
1:2A:336:C:O2'	20:2Y:35:TYR:OH	2.28	0.51
1:2A:479:A:H4'	1:2A:480:A:OP1	2.11	0.51
1:2A:630:G:N2	1:2A:633:A:OP2	2.38	0.51
1:2A:637:A:H2'	11:2P:117:GLU:OE1	2.11	0.51
5:2F:11:VAL:HG22	5:2F:125:LEU:HB2	1.93	0.51
37:2f:89:MET:HE2	49:2r:76:LEU:HD22	1.93	0.51
41:2j:38:ILE:HD11	41:2j:71:LEU:HD23	1.92	0.51
1:1A:1045:A:H5'	1:1A:1046:A:H5'	1.93	0.51
1:1A:2022:U:O2'	1:1A:2617:C:H5'	2.11	0.51
3:1D:126:GLN:HG3	61:1D:419:HOH:O	2.11	0.51
6:1G:43:LEU:C	6:1G:45:GLU:H	2.19	0.51
11:1P:100:LEU:HD12	11:1P:112:LEU:HD21	1.92	0.51
15:1T:11:GLU:HG2	15:1T:57:PHE:CD2	2.46	0.51
20:1Y:92:ASN:HD22	20:1Y:92:ASN:H	1.59	0.51
23:11:52:ARG:NH2	23:11:55:GLY:O	2.42	0.51
26:14:7:PRO:HB2	26:14:27:THR:HG21	1.93	0.51
32:1a:1297:C:O2'	38:1g:114:ARG:NH1	2.41	0.51
41:1j:40:LEU:HB2	41:1j:69:ASN:HB2	1.92	0.51
42:1k:87:THR:O	42:1k:87:THR:OG1	2.24	0.51
1:2A:1062:G:C8	1:2A:1070:A:H1'	2.46	0.51
1:2A:1581:G:H2'	1:2A:1582:C:O4'	2.11	0.51
1:2A:2659:G:O2'	7:2H:175:LYS:HE2	2.11	0.51
32:2a:967:5MC:H2'	32:2a:968:A:N7	2.25	0.51
32:2a:1027:C:H5''	32:2a:1028:C:C5	2.46	0.51
32:2a:1116:C:H2'	32:2a:1117:G:H5''	1.93	0.51
32:2a:1151:A:O2'	32:2a:1152:A:O5'	2.29	0.51
32:2a:1412:C:H2'	32:2a:1413:A:C8	2.46	0.51
42:2k:69:ALA:O	42:2k:73:MET:HG3	2.11	0.51
53:2y:33:HIS:ND1	53:2y:35:ILE:HG12	2.26	0.51
1:1A:1340:U:OP1	19:1X:16:LYS:NZ	2.43	0.50
1:1A:1588:C:H2'	1:1A:1589:C:H6	1.76	0.50
1:1A:1947:C:HO2'	32:1a:1483:A:HO2'	1.54	0.50
1:1A:2611:U:C4	27:15:3:LYS:HG2	2.45	0.50
6:1G:82:LEU:HD21	6:1G:88:ILE:HD13	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:237:C:OP2	48:1q:40:LYS:NZ	2.43	0.50
32:1a:1394:A:N1	32:1a:1500:A:O2'	2.40	0.50
49:1r:53:ARG:HH21	49:1r:59:SER:HA	1.77	0.50
51:1t:57:ARG:HH12	51:1t:100:ILE:HD12	1.76	0.50
1:2A:956:G:H5''	12:2Q:77:LYS:HD2	1.93	0.50
1:2A:2572:A:C8	4:2E:144:ARG:HD2	2.46	0.50
32:2a:975:A:N1	41:2j:48:THR:HB	2.25	0.50
32:2a:1366:C:O2'	41:2j:60:ARG:NH2	2.37	0.50
1:1A:1203:G:OP2	1:1A:1204:A:O2'	2.14	0.50
1:1A:2712:U:H2'	1:1A:2714:G:H5''	1.93	0.50
5:1F:197:ASP:OD1	5:1F:197:ASP:N	2.36	0.50
32:1a:412:A:OP2	35:1d:35:ARG:NH2	2.44	0.50
35:1d:168:ARG:N	35:1d:168:ARG:HH11	2.10	0.50
1:2A:760:G:H2'	1:2A:761:A:O4'	2.12	0.50
4:2E:9:VAL:HB	15:2T:3:ARG:HG2	1.93	0.50
10:2O:77:ILE:HD12	15:2T:74:ARG:HD3	1.93	0.50
17:2V:10:LYS:NZ	17:2V:23:GLU:OE2	2.29	0.50
32:2a:673:G:H5''	37:2f:87:ARG:CZ	2.41	0.50
32:2a:750:G:N3	46:2o:23:GLY:HA3	2.26	0.50
32:2a:972:C:O3'	41:2j:57:LYS:HD2	2.11	0.50
32:2a:1387:G:H2'	32:2a:1388:C:H6	1.76	0.50
36:2e:34:VAL:HG21	36:2e:63:ARG:HG2	1.93	0.50
1:1A:247:G:H4'	1:1A:386:G:C5	2.46	0.50
1:1A:1178:C:H2'	1:1A:1179:C:H6	1.76	0.50
1:1A:2183:C:H2'	1:1A:2184:G:H8	1.77	0.50
1:1A:2790:A:H2'	1:1A:2790:A:N3	2.25	0.50
1:1A:2791:C:H2'	1:1A:2792:G:H8	1.75	0.50
23:11:3:LYS:O	23:11:12:PRO:HD3	2.12	0.50
32:1a:171:A:H2'	32:1a:172:A:C8	2.46	0.50
32:1a:636:U:H2'	32:1a:637:G:C8	2.47	0.50
32:1a:731:G:H5'	32:1a:766:A:H4'	1.93	0.50
32:1a:1003:G:C2'	32:1a:1004:A:H4'	2.41	0.50
33:1b:142:LEU:O	33:1b:146:GLN:HG3	2.11	0.50
43:1l:6:THR:HG22	43:1l:8:ASN:N	2.26	0.50
46:1o:29:VAL:HG11	46:1o:67:LEU:HD21	1.92	0.50
1:2A:455:C:N3	1:2A:472:A:H2'	2.27	0.50
1:2A:1593:G:H2'	1:2A:1594:G:C8	2.46	0.50
1:2A:2190:G:H2'	1:2A:2191:G:H8	1.76	0.50
20:2Y:107:ASP:OD2	61:2Y:601:HOH:O	2.19	0.50
26:24:24:THR:OG1	26:24:25:TYR:N	2.42	0.50
26:24:47:GLN:O	26:24:49:PHE:N	2.45	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:273:A:H1'	48:2q:16:GLN:HE21	1.75	0.50
32:2a:1312:G:H5'	50:2s:5:LEU:HD21	1.92	0.50
50:2s:31:ILE:HD12	50:2s:49:ILE:HD11	1.92	0.50
1:1A:2138:C:N4	1:1A:2153:G:H1	2.08	0.50
1:1A:2243:U:H2'	1:1A:2244:U:C6	2.47	0.50
1:1A:2443:C:OP1	5:1F:68:LYS:HD3	2.11	0.50
32:1a:933:G:OP2	38:1g:3:ARG:HB2	2.11	0.50
40:1i:22:GLY:HA3	40:1i:60:ASP:OD2	2.11	0.50
1:2A:234:C:H2'	1:2A:235:U:H6	1.77	0.50
1:2A:1028:A:H2'	1:2A:1029:A:C8	2.47	0.50
1:2A:1292:U:H2'	1:2A:1293:C:C6	2.47	0.50
1:2A:2001:A:H2'	1:2A:2002:G:C8	2.47	0.50
1:2A:2364:C:OP1	22:20:55:ARG:NH1	2.44	0.50
3:2D:24:ILE:HD13	3:2D:84:TYR:HB2	1.94	0.50
4:2E:75:VAL:HG13	4:2E:77:ILE:H	1.76	0.50
29:27:5:TRP:CD1	29:27:7:PRO:HD3	2.46	0.50
32:2a:1086:U:H3	32:2a:1099:G:H22	1.59	0.50
32:2a:1119:C:H2'	32:2a:1120:G:C8	2.46	0.50
38:2g:132:GLY:O	38:2g:136:LYS:HG2	2.11	0.50
40:2i:26:VAL:HG13	40:2i:61:ALA:HB3	1.91	0.50
44:2m:19:LEU:HD21	44:2m:56:LEU:HD21	1.93	0.50
1:1A:657:U:H2'	1:1A:658:C:C6	2.46	0.50
32:1a:603:U:H2'	32:1a:604:G:C8	2.47	0.50
32:1a:978:A:O2'	32:1a:1322:C:N3	2.41	0.50
32:2a:297:G:N2	32:2a:300:A:OP2	2.43	0.50
32:2a:1006:C:H2'	32:2a:1007:C:C6	2.47	0.50
33:2b:24:TRP:H	33:2b:24:TRP:HD1	1.60	0.50
1:1A:1227:G:OP2	16:1U:16:LYS:NZ	2.41	0.50
34:1c:62:ASP:O	34:1c:97:LYS:HB2	2.12	0.50
50:1s:23:ASN:HD21	50:1s:43:GLU:HB3	1.76	0.50
1:2A:1195:G:O2'	1:2A:1226:A:N1	2.42	0.50
3:2D:256:GLY:O	61:2D:401:HOH:O	2.20	0.50
7:2H:5:GLY:O	7:2H:65:HIS:NE2	2.45	0.50
7:2H:139:GLN:HG2	7:2H:140:LYS:N	2.27	0.50
36:2e:137:GLU:OE2	36:2e:141:GLN:NE2	2.42	0.50
1:1A:1815:A:OP2	3:1D:54:ARG:NH2	2.41	0.50
4:1E:28:ALA:HB3	4:1E:93:VAL:HG12	1.93	0.50
11:1P:90:ARG:HH21	11:1P:105:LEU:HD21	1.76	0.50
20:1Y:92:ASN:HB2	20:1Y:94:LYS:N	2.17	0.50
28:16:2:ALA:N	61:16:602:HOH:O	2.43	0.50
32:1a:669:U:H2'	32:1a:670:G:C8	2.47	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1030(C):G:H2'	32:1a:1030(D):A:H8	1.77	0.50
1:2A:234:C:H2'	1:2A:235:U:C6	2.47	0.50
1:2A:873:G:H1	1:2A:904:C:H42	1.59	0.50
1:2A:1292:U:H2'	1:2A:1293:C:H6	1.77	0.50
1:2A:1533:G:N2	1:2A:1536:C:N3	2.59	0.50
4:2E:36:ARG:NH1	4:2E:85:ASN:OD1	2.41	0.50
32:2a:1269:A:N1	32:2a:1312:G:O2'	2.38	0.50
36:2e:77:PRO:HG2	36:2e:78:HIS:HD2	1.76	0.50
44:2m:82:MET:HB3	44:2m:93:ARG:HD3	1.94	0.50
1:1A:226:G:H21	1:1A:228:A:H62	1.60	0.50
1:1A:1040:C:H2'	1:1A:1041:C:O4'	2.11	0.50
1:1A:2689:U:H4'	1:1A:2690:C:H5'	1.93	0.50
4:1E:7:VAL:HG23	4:1E:51:PHE:HE2	1.76	0.50
5:1F:8:GLN:HE22	5:1F:21:ALA:HB2	1.76	0.50
32:1a:967:5MC:H4'	40:1i:125:TYR:HE1	1.76	0.50
32:1a:1030:C:N4	32:1a:1032:G:O6	2.45	0.50
1:2A:251:A:C5	1:2A:252:G:H1'	2.47	0.50
1:2A:1889:A:N1	1:2A:2234:G:H1'	2.27	0.50
1:2A:2808:U:H5''	1:2A:2891:G:O6	2.12	0.50
32:2a:918:A:OP2	61:2a:3213:HOH:O	2.19	0.50
32:2a:1191:A:OP1	34:2c:4:LYS:HE2	2.12	0.50
32:2a:1326:C:OP1	52:2u:12:LYS:NZ	2.41	0.50
33:2b:16:HIS:CB	33:2b:210:SER:HB3	2.42	0.50
34:2c:28:GLN:NE2	34:2c:32:LEU:HD11	2.26	0.50
1:1A:578:A:H3'	61:1A:4680:HOH:O	2.12	0.50
1:1A:896:A:N1	12:1Q:60:ARG:NH1	2.60	0.50
8:1I:77:LEU:HD13	8:1I:101:LEU:HD23	1.94	0.50
32:1a:38:G:N2	32:1a:397:A:H5'	2.21	0.50
32:1a:79:G:C2	32:1a:90:U:O2	2.64	0.50
32:1a:546:G:OP1	35:1d:73:ARG:HG2	2.12	0.50
35:1d:107:ARG:HH21	35:1d:194:LEU:HD21	1.76	0.50
37:1f:78:GLU:O	37:1f:81:ILE:HG22	2.12	0.50
1:2A:27:G:O2'	1:2A:28:A:OP2	2.29	0.50
1:2A:2537:U:H2'	1:2A:2538:C:C6	2.47	0.50
1:2A:2810:A:H61	1:2A:2891:G:HO2'	1.57	0.50
6:2G:19:LEU:HD13	6:2G:32:PRO:HD2	1.94	0.50
11:2P:50:ARG:HD3	30:28:7:HIS:CD2	2.47	0.50
19:2X:60:ARG:NH2	29:27:47:ARG:HH22	2.10	0.50
32:2a:1126:U:O4'	32:2a:1281:U:H1'	2.12	0.50
40:2i:99:LEU:HB3	40:2i:101:PHE:CE1	2.47	0.50
41:2j:29:ARG:NH1	41:2j:30:SER:HB3	2.27	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1273:U:H2'	61:1A:6166:HOH:O	2.12	0.49
1:1A:1379:A:H4'	1:1A:1380:G:OP2	2.12	0.49
61:1A:5237:HOH:O	16:1U:59:ARG:HD2	2.10	0.49
7:1H:7:LEU:HD12	7:1H:8:PRO:HD2	1.94	0.49
8:1I:72:LEU:C	8:1I:74:ASN:H	2.20	0.49
34:1c:15:THR:HG21	34:1c:181:ASN:HA	1.93	0.49
34:1c:36:ASP:OD1	34:1c:59:ARG:NH2	2.42	0.49
44:1m:11:ARG:HA	44:1m:45:VAL:HB	1.94	0.49
48:1q:67:LYS:C	48:1q:69:LYS:H	2.20	0.49
1:2A:2154:G:H2'	1:2A:2155:G:C8	2.47	0.49
4:2E:174:ASP:OD1	4:2E:175:VAL:N	2.45	0.49
5:2F:31:HIS:HB2	11:2P:9:ASN:OD1	2.12	0.49
16:2U:8:VAL:HG13	16:2U:11:ARG:HH21	1.76	0.49
17:2V:43:GLU:OE1	17:2V:43:GLU:N	2.45	0.49
32:2a:573:A:OP2	61:2a:3214:HOH:O	2.20	0.49
42:2k:99:GLN:HG2	42:2k:105:VAL:HG21	1.94	0.49
49:2r:58:LEU:HD23	49:2r:62:GLU:HB3	1.94	0.49
3:1D:183:ARG:HG3	3:1D:270:ILE:HG12	1.94	0.49
7:1H:126:PRO:HB2	7:1H:130:ARG:HH21	1.75	0.49
12:1Q:109:VAL:HG22	12:1Q:113:GLN:CD	2.37	0.49
25:13:7:LYS:HE3	25:13:32:GLN:HE21	1.77	0.49
30:18:26:LYS:HD2	30:18:48:PHE:CD2	2.47	0.49
32:1a:410:G:OP1	35:1d:30:LYS:NZ	2.30	0.49
33:1b:185:ILE:HG22	33:1b:199:TYR:HD2	1.77	0.49
35:1d:8:VAL:HG22	35:1d:21:LEU:HD13	1.94	0.49
44:1m:77:ASN:HA	44:1m:80:ARG:HG2	1.94	0.49
1:2A:835:A:OP1	61:2A:3853:HOH:O	2.20	0.49
1:2A:856:C:H2'	1:2A:857:C:C6	2.47	0.49
1:2A:1025:G:C4	1:2A:1135:C:H1'	2.46	0.49
1:2A:1290:C:H2'	1:2A:1291:C:H6	1.77	0.49
1:2A:2320:A:N3	1:2A:2320:A:H2'	2.27	0.49
1:2A:2390:U:P	30:28:35:GLN:HE22	2.35	0.49
25:23:40:THR:HG22	25:23:42:ALA:H	1.77	0.49
32:2a:644:G:H5'	39:2h:92:ARG:HH12	1.76	0.49
32:2a:984:C:H2'	32:2a:985:C:H6	1.77	0.49
40:2i:92:TYR:O	40:2i:96:LEU:HB2	2.11	0.49
1:1A:1082:U:N3	1:1A:1086:A:N6	2.22	0.49
1:1A:2114:A:H3'	1:1A:2115:G:H8	1.77	0.49
2:1B:43:C:H5''	26:14:1:MET:HG2	1.94	0.49
32:1a:1148:U:O3'	40:1i:14:VAL:HG11	2.12	0.49
33:1b:20:GLU:HG2	33:1b:23:ARG:HH21	1.76	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:1c:131:ARG:HE	34:1c:135:LYS:HE3	1.77	0.49
34:1c:131:ARG:HD3	34:1c:166:GLU:OE2	2.12	0.49
1:2A:1839:G:C8	1:2A:1927:A:H1'	2.46	0.49
1:2A:2105:C:N4	1:2A:2106:G:O6	2.44	0.49
1:2A:2506:U:O2	55:2A:3738:HGR:H23	2.12	0.49
50:2s:50:ALA:CB	50:2s:57:HIS:HB3	2.40	0.49
6:1G:179:PRO:HG3	26:14:43:TYR:OH	2.12	0.49
7:1H:20:ALA:HB1	7:1H:21:PRO:HD2	1.95	0.49
11:1P:63:PRO:HG2	30:18:25:MET:HB2	1.95	0.49
32:1a:184:G:H2'	32:1a:185:A:H8	1.76	0.49
32:1a:194:C:H2'	32:1a:195:A:H5''	1.94	0.49
46:1o:51:HIS:ND1	61:1o:4602:HOH:O	2.34	0.49
51:1t:18:GLN:O	51:1t:22:ARG:HG3	2.12	0.49
53:1y:55:ASN:OD1	53:1y:60:VAL:HG12	2.13	0.49
1:2A:1086:A:OP1	1:2A:1104:C:O2'	2.31	0.49
1:2A:1104:C:H2'	1:2A:1105:U:H6	1.77	0.49
1:2A:1239:G:H2'	1:2A:1240:U:O4'	2.11	0.49
7:2H:12:PRO:O	7:2H:15:VAL:HG22	2.13	0.49
10:2O:120:GLU:HB2	15:2T:68:TYR:HE2	1.77	0.49
32:2a:1348:U:H4'	40:2i:120:ARG:HD2	1.94	0.49
33:2b:150:SER:OG	33:2b:151:GLY:N	2.45	0.49
16:1U:104:GLN:CD	16:1U:104:GLN:H	2.20	0.49
33:1b:59:GLU:HB2	33:1b:221:LEU:HD13	1.93	0.49
41:1j:39:PRO:HB3	41:1j:70:ARG:CZ	2.43	0.49
1:2A:111:A:N3	61:2A:3973:HOH:O	2.35	0.49
1:2A:1094:U:O5'	1:2A:1096:A:N6	2.45	0.49
13:2R:9:LYS:O	13:2R:17:ARG:HD3	2.12	0.49
15:2T:109:GLU:HG2	15:2T:112:ARG:HH12	1.78	0.49
32:2a:1465:C:H2'	32:2a:1466:C:O4'	2.12	0.49
33:2b:16:HIS:O	33:2b:16:HIS:ND1	2.45	0.49
52:2u:12:LYS:HE3	52:2u:19:GLY:HA3	1.95	0.49
53:2y:53:THR:HA	53:2y:61:LEU:O	2.12	0.49
1:1A:1078:U:C4	1:1A:1088:A:H5''	2.47	0.49
1:1A:2228:G:O6	61:1A:4143:HOH:O	2.19	0.49
32:1a:269:C:H2'	32:1a:270:A:H8	1.78	0.49
32:1a:1425:U:H2'	32:1a:1426:C:C6	2.47	0.49
32:1a:1504:G:OP1	32:1a:1507:A:H4'	2.13	0.49
40:1i:99:LEU:HD12	40:1i:99:LEU:H	1.78	0.49
1:2A:228:A:H2'	1:2A:229:A:H5'	1.93	0.49
1:2A:307:G:N7	61:2A:3977:HOH:O	2.35	0.49
1:2A:1053:C:H2'	1:2A:1054:A:C8	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1794:U:H2'	1:2A:1795:C:C6	2.48	0.49
3:2D:146:GLU:HB2	3:2D:189:CYS:HB3	1.93	0.49
18:2W:25:ARG:NH2	18:2W:74:ALA:O	2.44	0.49
32:2a:266:G:H3'	48:2q:67:LYS:HB2	1.93	0.49
32:2a:1096:C:H2'	32:2a:1097:C:H6	1.77	0.49
32:2a:1112:C:O2	34:2c:179:ARG:N	2.43	0.49
32:2a:1347:G:N2	32:2a:1373:G:H2'	2.26	0.49
35:2d:111:ALA:HB1	35:2d:116:GLN:HE21	1.77	0.49
1:1A:2107:C:N3	1:1A:2182:G:O6	2.46	0.49
1:1A:2271:G:OP1	22:10:18:ALA:HB1	2.13	0.49
32:1a:22:G:H2'	32:1a:23:C:C6	2.48	0.49
32:1a:791:G:N2	32:1a:1497:G:O3'	2.44	0.49
32:1a:998:G:H2'	32:1a:999:C:C6	2.48	0.49
32:1a:1094:G:OP1	61:1a:3314:HOH:O	2.20	0.49
32:1a:1338:G:H2'	32:1a:1339:A:C8	2.47	0.49
32:1a:1469:G:H2'	32:1a:1470:G:C8	2.47	0.49
35:1d:121:VAL:O	35:1d:134:ASP:HA	2.12	0.49
36:1e:10:MET:HG2	36:1e:13:ILE:HD11	1.95	0.49
42:1k:32:ILE:HG22	42:1k:77:MET:HE3	1.95	0.49
45:1n:4:LYS:O	45:1n:7:ILE:HG12	2.13	0.49
45:1n:26:ARG:HD3	45:1n:43:CYS:HB3	1.93	0.49
1:2A:583:G:OP2	16:2U:10:ARG:HD2	2.12	0.49
1:2A:874:G:O2'	21:2Z:120:ILE:HD11	2.12	0.49
1:2A:1622:G:OP2	61:2A:3843:HOH:O	2.18	0.49
8:2I:26:ALA:O	8:2I:31:LEU:HB2	2.12	0.49
11:2P:97:PRO:HD3	11:2P:126:VAL:O	2.13	0.49
32:2a:986:A:N3	50:2s:52:TYR:OH	2.38	0.49
32:2a:1305:G:H22	32:2a:1331:G:H1'	1.74	0.49
32:2a:1516:G:H2'	32:2a:1518:MA6:OP2	2.11	0.49
44:2m:17:VAL:O	44:2m:20:THR:OG1	2.30	0.49
1:1A:2059:A:O2'	5:1F:69:HIS:HD2	1.96	0.49
3:1D:145:VAL:HB	3:1D:155:LEU:HB2	1.93	0.49
4:1E:9:VAL:HG13	4:1E:25:VAL:O	2.13	0.49
10:1O:115:VAL:HG13	10:1O:121:VAL:HG21	1.94	0.49
14:1S:27:SER:HA	14:1S:88:ASP:HB3	1.95	0.49
32:1a:382:A:H2'	32:1a:383:A:C8	2.48	0.49
32:1a:407:G:OP1	35:1d:115:ARG:NH2	2.42	0.49
32:1a:626:U:H2'	32:1a:627:G:H8	1.76	0.49
32:1a:1183:A:H3'	32:1a:1184:G:C5'	2.41	0.49
41:1j:64:GLU:CD	41:1j:66:ARG:HD3	2.38	0.49
45:1n:42:ILE:O	45:1n:46:GLU:HG3	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:747:U:O2	1:2A:2014:A:H1'	2.13	0.49
1:2A:1082:U:H3	1:2A:1085:A:H2	1.60	0.49
1:2A:1405:U:H2'	1:2A:1406:U:C6	2.47	0.49
1:2A:2258:C:OP1	61:2A:3849:HOH:O	2.19	0.49
1:2A:2513:G:OP2	61:2A:3854:HOH:O	2.20	0.49
7:2H:154:PRO:HB3	7:2H:163:TYR:CE1	2.47	0.49
1:1A:1091:G:H1	1:1A:1100:C:N4	2.11	0.49
1:1A:2791:C:H2'	1:1A:2792:G:C8	2.48	0.49
2:1B:13:A:N1	2:1B:69:G:O2'	2.40	0.49
3:1D:148:GLU:HB2	3:1D:151:LYS:HD2	1.94	0.49
5:1F:102:PRO:O	5:1F:106:ARG:HG3	2.13	0.49
9:1N:73:THR:HG23	9:1N:82:LEU:HD11	1.95	0.49
11:1P:138:LEU:HD23	11:1P:145:PRO:HB3	1.94	0.49
21:1Z:3:TYR:HE1	21:1Z:50:GLN:NE2	2.10	0.49
31:19:24:TYR:CE1	31:19:35:ARG:HG3	2.48	0.49
32:1a:840:C:H5''	32:1a:841:U:C5	2.47	0.49
32:1a:1258:G:H2'	32:1a:1259:C:C6	2.48	0.49
32:1a:1333:A:H2'	32:1a:1334:G:O4'	2.13	0.49
41:1j:19:SER:O	41:1j:23:ILE:HG12	2.13	0.49
48:1q:58:GLU:OE2	48:1q:75:ARG:NH2	2.45	0.49
1:2A:1188:U:H4'	17:2V:79:VAL:HG22	1.93	0.49
1:2A:2815:C:H5'	27:25:29:THR:HG21	1.94	0.49
1:2A:2870:C:H2'	1:2A:2871:C:O4'	2.13	0.49
32:2a:666:G:H5'	32:2a:726:C:H1'	1.95	0.49
32:2a:1256:A:H61	32:2a:1278:U:H1'	1.78	0.49
42:2k:31:THR:HG23	42:2k:42:TRP:HB3	1.93	0.49
44:2m:19:LEU:HD21	44:2m:56:LEU:HD11	1.95	0.49
1:1A:859:G:O6	61:1A:4137:HOH:O	2.17	0.49
1:1A:2687:U:H2'	1:1A:2688:U:O4'	2.13	0.49
6:1G:77:ILE:HG21	6:1G:80:PHE:CD2	2.48	0.49
1:2A:2590:A:O3'	3:2D:239:ARG:NH2	2.45	0.49
3:2D:71:ASP:OD2	3:2D:103:ARG:NH2	2.32	0.49
32:2a:411:A:O2'	32:2a:413:G:H5'	2.13	0.49
32:2a:757:U:H2'	32:2a:758:G:O4'	2.12	0.49
38:2g:89:MET:HE1	38:2g:155:ARG:HA	1.95	0.49
39:2h:20:TYR:HA	39:2h:65:TYR:CZ	2.48	0.49
6:1G:22:ARG:NH2	6:1G:175:LEU:HD21	2.28	0.48
7:1H:124:GLU:HG2	7:1H:132:ARG:HB3	1.95	0.48
26:14:61:ARG:HH21	50:1s:42:PRO:HD3	1.77	0.48
32:1a:987:G:H1	32:1a:1218:C:H42	1.60	0.48
32:1a:1248:A:N3	40:1i:70:LYS:HE3	2.27	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:1d:101:LEU:HB2	35:1d:138:TYR:HB3	1.94	0.48
40:1i:5:TYR:H	40:1i:87:GLN:NE2	2.11	0.48
46:1o:6:GLU:OE1	46:1o:6:GLU:N	2.46	0.48
1:2A:784:A:C6	3:2D:229:VAL:HG11	2.47	0.48
1:2A:1379:A:H4'	1:2A:1380:G:OP2	2.13	0.48
1:2A:1470:G:N7	61:2A:3972:HOH:O	2.35	0.48
1:2A:1633:G:OP2	61:2A:3851:HOH:O	2.20	0.48
1:2A:2086:U:H2'	1:2A:2087:G:C8	2.48	0.48
1:2A:2887:U:H2'	1:2A:2888:C:H6	1.78	0.48
2:2B:43:C:H5''	26:24:1:MET:HG3	1.94	0.48
9:2N:31:ALA:HA	9:2N:34:LEU:HD12	1.95	0.48
32:2a:116:A:OP1	61:2a:3207:HOH:O	2.20	0.48
32:2a:848:C:H2'	32:2a:849:C:C6	2.48	0.48
32:2a:1358:U:OP1	45:2n:35:ARG:HG2	2.13	0.48
1:1A:956:G:H5''	12:1Q:77:LYS:HD2	1.95	0.48
1:1A:1582:C:H2'	1:1A:1583:A:O4'	2.14	0.48
1:1A:2116:G:P	1:1A:2166:G:H21	2.36	0.48
1:1A:2346:A:N1	61:1A:4281:HOH:O	2.35	0.48
1:1A:2611:U:C5	56:1A:4019:TEL:H352	2.47	0.48
1:1A:2747:G:O6	1:1A:2755:C:H5''	2.12	0.48
8:1I:38:LEU:HB3	8:1I:40:THR:HG23	1.95	0.48
8:1I:75:LEU:HD22	8:1I:105:HIS:ND1	2.29	0.48
44:1m:12:ASN:O	44:1m:44:ARG:NH1	2.43	0.48
1:2A:2637:U:OP1	4:2E:82:ARG:NH1	2.43	0.48
1:2A:2880:C:O3'	13:2R:90:ARG:NH1	2.46	0.48
5:2F:108:LYS:O	5:2F:112:MET:HG3	2.12	0.48
19:2X:12:VAL:HG22	19:2X:29:TRP:CE2	2.47	0.48
32:2a:582:U:OP1	46:2o:68:ARG:NH1	2.46	0.48
33:2b:18:GLY:HA3	33:2b:41:ILE:HD13	1.95	0.48
33:2b:137:ARG:O	33:2b:141:GLU:N	2.39	0.48
41:2j:50:ILE:HG22	41:2j:52:GLY:H	1.77	0.48
50:2s:41:VAL:HG13	50:2s:43:GLU:H	1.77	0.48
1:1A:363(A):A:H2'	1:1A:363(B):G:H8	1.78	0.48
1:1A:1578:U:H2'	1:1A:1579:A:H5'	1.94	0.48
1:1A:2805:G:H2'	1:1A:2807:G:C8	2.48	0.48
23:11:3:LYS:HG3	23:11:4:VAL:H	1.79	0.48
26:14:61:ARG:HH21	50:1s:42:PRO:CD	2.27	0.48
40:1i:77:ILE:O	40:1i:81:ILE:HG23	2.14	0.48
46:1o:18:PHE:HB2	46:1o:19:PRO:HD2	1.95	0.48
1:2A:1410:G:H2'	1:2A:1411:C:C6	2.47	0.48
1:2A:2104:G:N7	1:2A:2186:G:N2	2.60	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2104:G:N1	1:2A:2185:C:O2	2.46	0.48
1:2A:2483:C:N3	12:2Q:124:LYS:NZ	2.58	0.48
4:2E:119:ARG:HG2	4:2E:160:TYR:HB2	1.94	0.48
26:24:20:ASN:ND2	26:24:38:LYS:HG3	2.28	0.48
32:2a:742:G:P	46:2o:35:ARG:HH22	2.36	0.48
32:2a:1030(B):C:H41	32:2a:1030(C):G:H21	1.61	0.48
38:2g:26:PHE:O	38:2g:30:ILE:HG13	2.13	0.48
1:1A:2162:G:H4'	1:1A:2172:U:O2'	2.12	0.48
4:1E:101:ARG:NH2	4:1E:171:GLU:HB2	2.29	0.48
5:1F:161:GLU:O	5:1F:165:ARG:HG3	2.13	0.48
32:1a:405:U:O4	35:1d:2:GLY:N	2.46	0.48
32:1a:964:A:OP1	61:1a:3315:HOH:O	2.20	0.48
32:1a:1024:G:H2'	32:1a:1024:G:N3	2.28	0.48
32:1a:1125:U:H4'	41:1j:5:ARG:NH2	2.27	0.48
32:1a:1137:C:O5'	32:1a:1137:C:H6	1.96	0.48
32:1a:1479:C:H2'	32:1a:1480:G:H8	1.78	0.48
1:2A:2119:A:H61	1:2A:2168:G:N2	2.11	0.48
1:2A:2591:C:H2'	1:2A:2592:G:C8	2.48	0.48
3:2D:221:VAL:HG22	3:2D:226:MET:HE3	1.95	0.48
7:2H:90:LYS:HD3	7:2H:159:GLU:HG2	1.96	0.48
32:2a:1320:C:O4'	50:2s:73:GLU:HG2	2.13	0.48
44:2m:97:PRO:N	44:2m:110:ARG:HG2	2.28	0.48
1:1A:218:A:C2	1:1A:235:U:H4'	2.48	0.48
1:1A:265:A:N1	1:1A:427:U:O2'	2.43	0.48
21:1Z:140:ASP:OD1	21:1Z:142:SER:OG	2.29	0.48
32:1a:544:G:OP1	35:1d:62:GLN:NE2	2.35	0.48
35:1d:108:LEU:HD23	35:1d:110:PHE:CZ	2.49	0.48
46:1o:17:ARG:NH1	61:1o:4601:HOH:O	2.31	0.48
1:2A:322:A:OP2	5:2F:169:ASN:HB2	2.14	0.48
1:2A:911:A:H2'	12:2Q:9:TYR:OH	2.14	0.48
1:2A:2110:G:H4'	1:2A:2111:C:OP2	2.13	0.48
1:2A:2687:U:H2'	1:2A:2688:U:O4'	2.14	0.48
8:2I:72:LEU:HD12	8:2I:138:ILE:HG21	1.95	0.48
9:2N:38:HIS:CD2	9:2N:39:ARG:HG3	2.48	0.48
10:2O:49:ARG:NH1	32:2a:1422:G:O3'	2.46	0.48
23:21:51:VAL:N	23:21:58:ILE:O	2.47	0.48
32:2a:276:G:O3'	48:2q:68:ARG:NH1	2.46	0.48
32:2a:620:C:C2	35:2d:135:LEU:HG	2.48	0.48
32:2a:748:C:H4'	32:2a:749:C:O5'	2.14	0.48
32:2a:848:C:H2'	32:2a:849:C:H6	1.78	0.48
39:2h:10:LEU:HD23	39:2h:83:ILE:HG12	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1082:U:C4	1:1A:1086:A:N1	2.80	0.48
1:1A:1833:U:OP1	61:1A:4146:HOH:O	2.20	0.48
12:1Q:108:GLY:HA3	21:1Z:116:VAL:HG13	1.96	0.48
32:1a:1329:A:P	44:1m:28:ALA:HB3	2.53	0.48
34:1c:102:ASN:HD22	34:1c:102:ASN:N	2.12	0.48
44:1m:80:ARG:HH22	50:1s:69:HIS:CE1	2.29	0.48
1:2A:1637:A:H4'	1:2A:2711:A:O2'	2.14	0.48
9:2N:62:VAL:HG13	9:2N:66:LYS:HD2	1.95	0.48
17:2V:98:GLU:OE2	17:2V:100:ARG:HD3	2.13	0.48
21:2Z:53:ILE:HG22	21:2Z:71:VAL:HB	1.94	0.48
32:2a:17:U:H2'	32:2a:18:C:H6	1.77	0.48
32:2a:980:C:OP2	61:2a:3212:HOH:O	2.20	0.48
50:2s:52:TYR:HA	50:2s:56:GLN:O	2.13	0.48
1:1A:244:A:C2	1:1A:255:A:C4	3.02	0.48
1:1A:2286:A:H4'	1:1A:2287:A:O4'	2.14	0.48
30:18:47:LYS:HE2	57:18:103:MPD:H51	1.95	0.48
32:1a:757:U:H2'	32:1a:758:G:O4'	2.14	0.48
36:1e:71:LEU:HD11	36:1e:113:ALA:O	2.14	0.48
7:2H:117:PRO:HG3	7:2H:123:PHE:CD2	2.49	0.48
12:2Q:45:GLN:N	12:2Q:45:GLN:OE1	2.47	0.48
23:21:83:GLU:HA	23:21:84:GLY:HA2	1.58	0.48
32:2a:1186:G:H21	45:2n:61:TRP:C	2.22	0.48
34:2c:152:ILE:HG12	34:2c:199:LYS:HD2	1.95	0.48
41:2j:11:PHE:HE1	41:2j:67:THR:HG22	1.79	0.48
1:1A:271(L):U:P	8:1I:50:ARG:HH22	2.36	0.48
1:1A:1364:G:N7	23:11:3:LYS:HE2	2.29	0.48
1:1A:2110:G:H5''	1:1A:2111:C:C5	2.48	0.48
7:1H:41:MET:HE2	7:1H:65:HIS:HA	1.96	0.48
18:1W:18:ARG:NH1	18:1W:76:VAL:O	2.47	0.48
23:11:53:VAL:HG22	23:11:74:VAL:HG13	1.96	0.48
30:18:23:VAL:CG1	30:18:47:LYS:HD3	2.44	0.48
32:1a:928:G:O2'	32:1a:1533:C:OP1	2.32	0.48
44:1m:15:VAL:HG23	44:1m:41:PRO:HA	1.95	0.48
1:2A:483:A:O2'	20:2Y:49:VAL:O	2.28	0.48
1:2A:1815:A:OP2	3:2D:54:ARG:NH2	2.46	0.48
1:2A:2098:U:H2'	1:2A:2099:U:O4'	2.14	0.48
1:2A:2648:C:H2'	1:2A:2649:U:C6	2.48	0.48
4:2E:105:THR:OG1	4:2E:199:ARG:NH2	2.46	0.48
10:2O:80:ASP:OD2	15:2T:64:ARG:NH2	2.46	0.48
32:2a:1258:G:H2'	32:2a:1259:C:C6	2.49	0.48
32:2a:1291:G:O2'	40:2i:38:GLN:OE1	2.31	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:2d:111:ALA:HB2	35:2d:120:LEU:HD12	1.96	0.48
53:2y:52:ALA:HB1	53:2y:81:LEU:HD11	1.95	0.48
1:1A:207:A:H2'	1:1A:208:C:O4'	2.14	0.48
1:1A:1652:A:O2'	1:1A:1653:G:H5'	2.14	0.48
1:1A:2870:C:H2'	1:1A:2871:C:O4'	2.14	0.48
32:1a:1216:G:OP1	45:1n:2:ALA:HA	2.13	0.48
1:2A:1084:A:H3'	1:2A:1085:A:C4'	2.44	0.48
1:2A:1833:U:O2'	1:2A:1969:A:N1	2.32	0.48
2:2B:95:C:H2'	2:2B:96:U:C6	2.49	0.48
12:2Q:76:LYS:HB3	12:2Q:91:GLU:HG3	1.96	0.48
25:23:12:PRO:HB2	25:23:20:LYS:HG2	1.95	0.48
32:2a:60:A:H4'	32:2a:61:G:O5'	2.14	0.48
32:2a:598:U:H4'	39:2h:94:TYR:CD2	2.48	0.48
34:2c:162:GLN:NE2	34:2c:163:ALA:O	2.44	0.48
44:2m:20:THR:C	44:2m:22:ILE:H	2.21	0.48
1:1A:910:A:N1	1:1A:2277:G:H1'	2.29	0.48
61:1A:4202:HOH:O	29:17:19:ARG:NH1	2.47	0.48
6:1G:106:LEU:HA	6:1G:110:ALA:HB3	1.96	0.48
6:1G:126:ASP:HB2	6:1G:130:ASN:H	1.79	0.48
19:1X:31:HIS:CD2	19:1X:33:LYS:H	2.30	0.48
34:1c:8:ILE:HD12	34:1c:16:ARG:HD3	1.96	0.48
46:1o:8:LYS:O	46:1o:12:ILE:HG13	2.14	0.48
1:2A:1047:G:N2	1:2A:1111:A:H62	2.11	0.48
1:2A:1053:C:H2'	1:2A:1054:A:H8	1.79	0.48
1:2A:1359:A:N1	1:2A:1372:U:O4	2.47	0.48
1:2A:1803:A:H4'	3:2D:259:THR:HG23	1.96	0.48
1:2A:2059:A:O2'	5:2F:69:HIS:HD2	1.96	0.48
7:2H:18:GLU:HG2	7:2H:19:VAL:N	2.29	0.48
32:2a:737:A:H2'	32:2a:738:C:C6	2.49	0.48
32:2a:942:G:C2	32:2a:1342:C:C2	3.02	0.48
32:2a:1512:U:H2'	32:2a:1513:A:C8	2.49	0.48
39:2h:17:THR:HG22	39:2h:63:LEU:HG	1.95	0.48
47:2p:3:LYS:HG3	47:2p:24:ALA:HB2	1.96	0.48
50:2s:40:ILE:HA	50:2s:44:MET:SD	2.54	0.48
1:1A:380:U:OP1	61:1A:4147:HOH:O	2.20	0.47
1:1A:2722:G:H2'	1:1A:2723:C:C6	2.49	0.47
6:1G:129:GLY:O	6:1G:161:THR:HB	2.14	0.47
26:14:54:GLY:C	26:14:56:VAL:HA	2.39	0.47
26:14:57:GLU:HB2	26:14:58:ARG:HA	1.95	0.47
32:1a:347:G:C8	57:1a:3277:MPD:H53	2.49	0.47
32:1a:1442:G:O2'	32:1a:1442(A):G:H5'	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:1i:43:ALA:HA	40:1i:74:ILE:HD13	1.96	0.47
1:2A:143:G:H4'	19:2X:35:THR:HG21	1.94	0.47
1:2A:297:C:H2'	1:2A:298:G:O4'	2.14	0.47
1:2A:1514:U:H2'	1:2A:1515:G:H8	1.79	0.47
1:2A:2286:A:H4'	1:2A:2287:A:O4'	2.14	0.47
1:2A:2286:A:P	28:26:29:ASN:HD22	2.37	0.47
2:2B:24:G:H4'	2:2B:25:A:C8	2.49	0.47
16:2U:27:LEU:HA	16:2U:30:LYS:HB2	1.96	0.47
20:2Y:28:LYS:NZ	20:2Y:64:GLU:OE1	2.35	0.47
32:2a:849:C:H2'	32:2a:850:U:O4'	2.14	0.47
50:2s:53:ASN:ND2	50:2s:76:PRO:O	2.44	0.47
1:1A:1053:C:H2'	1:1A:1054:A:H8	1.79	0.47
1:1A:2038:G:H2'	1:1A:2039:C:O4'	2.14	0.47
1:1A:2805:G:H2'	1:1A:2807:G:H8	1.79	0.47
3:1D:26:LYS:HE2	3:1D:28:GLU:O	2.14	0.47
5:1F:38:ARG:NH2	61:1F:406:HOH:O	2.47	0.47
6:1G:18:GLU:OE2	6:1G:21:ARG:NH1	2.47	0.47
32:1a:335:C:H2'	32:1a:336:C:C6	2.49	0.47
32:1a:600:C:H2'	32:1a:601:C:C6	2.48	0.47
32:1a:1070:U:H2'	32:1a:1071:C:C6	2.50	0.47
50:1s:12:ASP:OD2	50:1s:37:ARG:HD2	2.14	0.47
1:2A:81:G:HO2'	1:2A:295:G:HO2'	1.60	0.47
1:2A:1826:G:H4'	3:2D:242:ARG:CZ	2.44	0.47
1:2A:2564:A:OP1	1:2A:2648:C:H4'	2.15	0.47
14:2S:14:VAL:O	14:2S:18:ILE:HG12	2.14	0.47
20:2Y:87:LYS:HB3	20:2Y:95:LYS:HD2	1.97	0.47
32:2a:593:G:H1	32:2a:646:U:H3	1.62	0.47
33:2b:193:ASP:OD2	33:2b:196:LEU:HB2	2.13	0.47
37:2f:91:VAL:HG11	49:2r:72:ARG:NH1	2.29	0.47
52:2u:2:GLY:C	52:2u:4:GLY:H	2.22	0.47
1:1A:1790:C:H5''	1:1A:1791:A:OP1	2.14	0.47
1:1A:2102:U:C2	1:1A:2187:G:O6	2.66	0.47
1:1A:2810:A:N6	1:1A:2891:G:O2'	2.39	0.47
5:1F:143:ALA:HB1	5:1F:148:LEU:HB2	1.96	0.47
10:1O:20:MET:HE3	10:1O:44:LYS:HE3	1.95	0.47
26:14:2:LYS:HB2	26:14:5:ILE:HD11	1.96	0.47
32:1a:840:C:H4'	32:1a:841:U:OP1	2.13	0.47
33:1b:128:GLU:HG2	33:1b:135:GLN:HE21	1.79	0.47
34:1c:8:ILE:HG12	34:1c:184:TYR:HB3	1.97	0.47
1:2A:2364:C:H2'	1:2A:2365:G:O4'	2.14	0.47
1:2A:2391:G:O6	1:2A:2425:A:H8	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:41:G:H2'	32:2a:42:G:C8	2.49	0.47
32:2a:1002:G:N3	32:2a:1003:G:C8	2.82	0.47
35:2d:141:ARG:N	35:2d:144:ASP:OD2	2.41	0.47
38:2g:113:GLU:H	38:2g:113:GLU:HG2	1.47	0.47
41:2j:63:PHE:HZ	45:2n:49:HIS:CE1	2.32	0.47
44:2m:59:TYR:CE1	44:2m:63:THR:HG21	2.50	0.47
1:1A:359:A:H2'	1:1A:360:G:O4'	2.14	0.47
1:1A:1810:A:H2'	1:1A:1811:G:O4'	2.13	0.47
1:1A:1899:G:N3	1:1A:1899:G:H2'	2.29	0.47
1:1A:2134:A:N6	1:1A:2157:G:H4'	2.29	0.47
3:1D:113:VAL:HG12	61:1D:448:HOH:O	2.15	0.47
8:1I:109:ILE:HD12	8:1I:109:ILE:HA	1.73	0.47
16:1U:78:THR:O	16:1U:117:GLN:NE2	2.47	0.47
32:1a:100:C:H2'	32:1a:101:A:C8	2.48	0.47
32:1a:278:G:OP2	48:1q:92:ARG:NH2	2.48	0.47
32:1a:501:C:H1'	32:1a:549:C:H1'	1.96	0.47
32:1a:632:A:H5'	32:1a:633:G:OP2	2.14	0.47
32:1a:1402:4OC:HM22	32:1a:1403:C:H5'	1.97	0.47
33:1b:88:ALA:HB2	33:1b:219:VAL:HG13	1.96	0.47
34:1c:29:TYR:OH	45:1n:54:PRO:O	2.30	0.47
39:1h:121:ASP:OD1	39:1h:121:ASP:N	2.46	0.47
47:1p:75:ARG:HG3	47:1p:80:PHE:HD2	1.79	0.47
1:2A:172:C:H2'	1:2A:173:G:H8	1.78	0.47
1:2A:2354:G:N7	61:2A:3976:HOH:O	2.35	0.47
1:2A:2504:U:OP2	61:2A:3850:HOH:O	2.20	0.47
32:2a:217:C:H2'	32:2a:218:C:C6	2.49	0.47
32:2a:790:A:H4'	53:2y:31:GLN:OE1	2.14	0.47
32:2a:955:U:O2'	50:2s:83:HIS:HD2	1.97	0.47
32:2a:1491:G:O2'	32:2a:1492:A:OP1	2.27	0.47
36:2e:72:GLN:HG3	36:2e:77:PRO:HB3	1.96	0.47
41:2j:80:LYS:O	41:2j:84:GLN:HB3	2.14	0.47
44:2m:10:PRO:HB2	44:2m:13:LYS:HG3	1.96	0.47
1:1A:288:C:H2'	1:1A:289:A:H8	1.79	0.47
1:1A:969:U:H2'	1:1A:970:C:C6	2.48	0.47
1:1A:1059:G:O6	1:1A:1079:C:N3	2.48	0.47
5:1F:132:VAL:HG22	5:1F:163:VAL:HG22	1.95	0.47
19:1X:5:TYR:CE1	24:12:30:ARG:HB2	2.50	0.47
20:1Y:86:ARG:HB2	20:1Y:98:VAL:HG23	1.97	0.47
29:17:21:ARG:NH1	61:17:202:HOH:O	2.39	0.47
32:1a:328:C:H4'	32:1a:329:A:H5'	1.97	0.47
32:1a:473:G:H2'	32:1a:474:G:H8	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1226:C:H2'	44:1m:103:THR:HB	1.96	0.47
1:2A:407:G:H2'	1:2A:408:G:H8	1.79	0.47
1:2A:886:C:H1'	1:2A:890:A:H61	1.79	0.47
1:2A:2136:C:H2'	1:2A:2137:C:H6	1.78	0.47
1:2A:2573:C:N4	55:2A:3738:HGR:O12	2.32	0.47
8:2I:101:LEU:HD11	8:2I:140:LEU:HD11	1.96	0.47
21:2Z:4:ARG:HH21	21:2Z:60:GLU:HG2	1.80	0.47
24:22:22:GLU:OE2	24:22:68:ARG:NH2	2.46	0.47
32:2a:443:C:H2'	32:2a:444:C:C6	2.49	0.47
32:2a:1090:U:H2'	32:2a:1091:U:H6	1.80	0.47
32:2a:1218:C:H2'	32:2a:1219:U:C6	2.50	0.47
43:2l:8:ASN:OD1	48:2q:34:LYS:NZ	2.23	0.47
53:2y:30:TRP:CD1	53:2y:89:GLN:HG3	2.48	0.47
1:1A:2759:G:N7	61:1A:4298:HOH:O	2.36	0.47
3:1D:180:GLY:HA3	3:1D:275:LYS:HG2	1.96	0.47
5:1F:167:ALA:HB1	5:1F:173:VAL:HG11	1.97	0.47
6:1G:32:PRO:HB3	6:1G:163:ALA:HB2	1.97	0.47
9:1N:75:TYR:CE2	9:1N:77:GLY:HA2	2.50	0.47
32:1a:104:G:C2	32:1a:105:G:C8	3.02	0.47
32:1a:964:A:OP1	61:1a:3316:HOH:O	2.20	0.47
32:1a:1291:G:OP1	38:1g:41:ARG:NH2	2.47	0.47
34:1c:73:PRO:O	34:1c:77:ILE:HG13	2.14	0.47
44:1m:17:VAL:O	44:1m:20:THR:OG1	2.24	0.47
47:1p:74:LEU:O	47:1p:79:VAL:HG22	2.14	0.47
1:2A:1065:U:H4'	1:2A:1066:U:H5'	1.96	0.47
1:2A:2573:C:H41	55:2A:3738:HGR:H29	1.58	0.47
1:2A:2745:C:H2'	1:2A:2746:U:O4'	2.14	0.47
1:2A:2820:A:O2'	1:2A:2821:A:OP1	2.32	0.47
4:2E:2:LYS:NZ	4:2E:95:ILE:O	2.40	0.47
32:2a:565:U:OP2	32:2a:566:G:O2'	2.31	0.47
32:2a:1227:A:OP1	50:2s:80:TYR:OH	2.22	0.47
1:1A:414:C:H2'	1:1A:415:A:C8	2.49	0.47
1:1A:448:U:O4	1:1A:583:G:H1'	2.15	0.47
1:1A:729:G:C6	3:1D:208:LYS:HB2	2.50	0.47
1:1A:962:G:OP1	61:1A:4145:HOH:O	2.20	0.47
1:1A:1919:A:O2'	32:1a:1517:G:N3	2.46	0.47
1:1A:1920:OMC:HM22	1:1A:1921:G:H5'	1.97	0.47
1:1A:2086:U:H2'	1:1A:2087:G:C8	2.49	0.47
1:1A:2102:U:O2	1:1A:2187:G:C6	2.66	0.47
2:1B:24:G:N7	2:1B:56:G:H2'	2.29	0.47
13:1R:97:VAL:HG22	13:1R:114:VAL:HG13	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:1S:10:ARG:O	14:1S:14:VAL:HG13	2.15	0.47
15:1T:39:ARG:HH21	32:1a:345:C:H5'	1.78	0.47
32:1a:620:C:H2'	32:1a:621:A:O4'	2.15	0.47
32:1a:1371:G:O3'	40:1i:69:GLY:HA3	2.14	0.47
32:1a:1499:A:OP2	61:1a:3311:HOH:O	2.20	0.47
45:1n:46:GLU:O	45:1n:50:LYS:HG3	2.15	0.47
50:1s:15:LEU:O	50:1s:19:VAL:HG23	2.15	0.47
1:2A:185:U:H2'	1:2A:186:G:C8	2.49	0.47
1:2A:904:C:H2'	1:2A:905:U:C6	2.50	0.47
1:2A:1316:U:H2'	1:2A:1317:A:C8	2.50	0.47
1:2A:2312:U:H5'	6:2G:88:ILE:HD11	1.97	0.47
1:2A:2365:G:O6	30:28:39:LYS:HE3	2.14	0.47
1:2A:2646:C:H2'	1:2A:2647:U:O4'	2.14	0.47
12:2Q:111:GLU:O	12:2Q:115:MET:HG2	2.14	0.47
20:2Y:73:ARG:HG2	20:2Y:73:ARG:HH11	1.78	0.47
32:2a:44:G:OP2	47:2p:12:LYS:NZ	2.35	0.47
32:2a:269:C:H2'	32:2a:270:A:C8	2.50	0.47
32:2a:972:C:O2'	41:2j:55:LYS:O	2.32	0.47
1:1A:1784:A:H4'	1:1A:1785:A:O5'	2.15	0.47
1:1A:1800:C:OP1	3:1D:264:LYS:NZ	2.45	0.47
6:1G:114:ILE:HG12	6:1G:140:ILE:HG12	1.97	0.47
21:1Z:3:TYR:CD2	21:1Z:51:ALA:HB2	2.50	0.47
32:1a:828:A:H2'	32:1a:829:G:O4'	2.14	0.47
3:2D:36:PRO:HA	3:2D:61:LEU:HD23	1.97	0.47
5:2F:143:ALA:HB1	5:2F:148:LEU:HB2	1.96	0.47
6:2G:83:ARG:H	6:2G:86:MET:HE1	1.80	0.47
7:2H:3:ARG:HH11	7:2H:4:ILE:H	1.63	0.47
18:2W:67:ASP:OD1	18:2W:67:ASP:N	2.48	0.47
32:2a:64:G:H4'	32:2a:65:U:H3'	1.96	0.47
32:2a:663:A:O3'	49:2r:64:ARG:NH2	2.43	0.47
32:2a:1106:G:H2'	32:2a:1107:C:H6	1.80	0.47
32:2a:1161:C:H2'	32:2a:1162:C:C6	2.50	0.47
32:2a:1295:G:O2'	44:2m:14:ARG:NH1	2.48	0.47
33:2b:16:HIS:HB2	33:2b:204:ASN:CB	2.40	0.47
40:2i:15:ALA:HB2	40:2i:65:VAL:HG23	1.96	0.47
1:1A:620:G:N3	1:1A:620:G:H5'	2.29	0.47
1:1A:996:A:H4'	16:1U:91:ASP:OD2	2.15	0.47
1:1A:1959:G:N7	61:1A:4294:HOH:O	2.35	0.47
1:1A:2390:U:OP2	61:1A:4149:HOH:O	2.21	0.47
1:1A:2889:C:H2'	1:1A:2891:G:O4'	2.14	0.47
17:1V:95:LEU:HD23	17:1V:97:LYS:HE3	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:14:16:CYS:HA	26:14:33:VAL:HG23	1.96	0.47
32:1a:576:G:O6	32:1a:880:C:O2'	2.28	0.47
33:1b:215:LEU:O	33:1b:219:VAL:HG23	2.15	0.47
36:1e:45:PHE:CD2	36:1e:47:LYS:HE3	2.50	0.47
40:1i:10:ARG:O	40:1i:11:LYS:C	2.57	0.47
1:2A:581:C:H2'	1:2A:582:G:C8	2.50	0.47
1:2A:1783:A:H5'	1:2A:2608:G:H4'	1.97	0.47
1:2A:2262:U:H4'	1:2A:2328:A:C2	2.50	0.47
3:2D:275:LYS:HE3	3:2D:276:LYS:HA	1.96	0.47
22:20:10:THR:HG22	22:20:12:ASN:N	2.17	0.47
32:2a:458:C:H2'	32:2a:460:G:O4'	2.14	0.47
32:2a:551:U:H2'	32:2a:552:U:C6	2.49	0.47
32:2a:1028:C:H2'	32:2a:1033:G:H22	1.79	0.47
32:2a:1068:G:H8	32:2a:1068:G:OP2	1.97	0.47
32:2a:1103:C:H5''	33:2b:98:LEU:HD22	1.97	0.47
32:2a:1220:G:O2'	50:2s:52:TYR:O	2.32	0.47
1:1A:652(T):C:H3'	1:1A:652(U):G:H5''	1.97	0.47
9:1N:36:GLY:HA3	9:1N:48:MET:HE2	1.97	0.47
11:1P:95:VAL:HG22	11:1P:125:VAL:HA	1.96	0.47
32:1a:967:5MC:H4'	40:1i:125:TYR:CE1	2.50	0.47
33:1b:163:PHE:HA	33:1b:185:ILE:HG12	1.96	0.47
37:1f:21:LEU:O	37:1f:25:ILE:HG12	2.15	0.47
38:1g:6:ARG:H	38:1g:6:ARG:HG3	1.46	0.47
39:1h:6:ILE:HD12	39:1h:35:ILE:HD12	1.96	0.47
1:2A:1641:A:H2'	1:2A:1642:G:O4'	2.15	0.47
1:2A:1849:G:H2'	1:2A:1850:G:H8	1.79	0.47
1:2A:2105:C:H2'	1:2A:2106:G:H8	1.79	0.47
2:2B:17:C:H2'	2:2B:18:G:O4'	2.15	0.47
7:2H:98:LEU:HD22	7:2H:125:VAL:HG23	1.97	0.47
10:2O:88:ASN:ND2	10:2O:90:GLN:H	2.13	0.47
32:2a:392:G:OP1	47:2p:8:ARG:NH2	2.47	0.47
32:2a:475:G:O2'	32:2a:476:G:H5'	2.15	0.47
32:2a:1036:G:H3'	32:2a:1037:C:C6	2.50	0.47
38:2g:23:VAL:O	38:2g:27:ILE:HG12	2.15	0.47
48:2q:83:ASP:O	48:2q:87:LYS:HG3	2.15	0.47
1:1A:747:U:O2	1:1A:2014:A:H1'	2.14	0.46
1:1A:813:U:H2'	1:1A:814:C:C6	2.50	0.46
1:1A:1754:C:OP1	15:1T:96:ARG:NH1	2.47	0.46
6:1G:135:LEU:O	6:1G:154:GLY:HA3	2.15	0.46
32:1a:191:G:N3	51:1t:103:GLY:HA3	2.30	0.46
47:1p:6:LEU:HB3	47:1p:17:TYR:CD1	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:1q:62:SER:HB3	48:1q:72:ARG:HD3	1.96	0.46
51:1t:53:LEU:HD23	51:1t:56:MET:HE2	1.97	0.46
1:2A:1091:G:H2'	1:2A:1091:G:N3	2.30	0.46
1:2A:1166:C:H2'	1:2A:1167:U:C6	2.51	0.46
1:2A:2032:G:OP2	1:2A:2454:G:O2'	2.24	0.46
7:2H:13:LYS:HA	7:2H:14:GLY:HA2	1.53	0.46
16:2U:78:THR:O	16:2U:117:GLN:NE2	2.47	0.46
21:2Z:128:VAL:HG22	21:2Z:129:SER:H	1.80	0.46
26:24:1:MET:HG2	26:24:6:HIS:NE2	2.30	0.46
32:2a:57:G:H2'	32:2a:58:C:C6	2.50	0.46
32:2a:519:C:OP2	43:2l:50:SER:OG	2.33	0.46
32:2a:731:G:H5'	32:2a:766:A:H4'	1.96	0.46
32:2a:738:C:OP1	37:2f:2:ARG:NH1	2.47	0.46
33:2b:114:ARG:NH1	33:2b:117:GLU:OE1	2.43	0.46
33:2b:217:ARG:HA	33:2b:220:ASP:HB2	1.97	0.46
35:2d:173:TRP:CD1	35:2d:174:LEU:HG	2.50	0.46
38:2g:92:SER:O	38:2g:96:GLN:HG3	2.15	0.46
1:1A:621:A:OP2	11:1P:108:LYS:NZ	2.48	0.46
1:1A:1028:A:N6	1:1A:1125:G:H2'	2.30	0.46
1:1A:2114:A:H3'	1:1A:2115:G:C8	2.50	0.46
1:1A:2137:C:N4	1:1A:2154:G:N1	2.39	0.46
1:1A:2277:G:OP2	22:10:10:THR:HG21	2.16	0.46
1:1A:2319:G:H1	14:1S:3:ARG:HA	1.80	0.46
19:1X:53:LYS:HB3	19:1X:82:GLN:HB3	1.97	0.46
21:1Z:146:ILE:HA	21:1Z:147:GLY:HA2	1.66	0.46
32:1a:1352:C:OP1	61:1u:101:HOH:O	2.21	0.46
32:1a:1499:A:H1'	32:1a:1520:G:H5'	1.97	0.46
46:1o:24:SER:O	46:1o:28:GLN:HG3	2.15	0.46
1:2A:300:A:H2'	1:2A:334:C:H1'	1.97	0.46
1:2A:1096:A:C8	1:2A:1097:U:H5	2.33	0.46
1:2A:1528:A:OP2	61:2A:3857:HOH:O	2.21	0.46
1:2A:2788:C:OP1	4:2E:61:ARG:NH2	2.48	0.46
11:2P:55:ARG:HA	61:2P:301:HOH:O	2.15	0.46
20:2Y:68:HIS:CE1	20:2Y:70:SER:HB3	2.50	0.46
32:2a:1053:G:N7	32:2a:1200:C:H5''	2.30	0.46
32:2a:1075:C:H5''	33:2b:179:LYS:HE2	1.97	0.46
39:2h:19:VAL:HG23	39:2h:21:LYS:HD3	1.98	0.46
40:2i:17:VAL:HG11	40:2i:80:GLY:C	2.39	0.46
44:2m:78:ILE:HA	44:2m:81:LEU:HD12	1.98	0.46
1:1A:330:A:H2	1:1A:1210:A:C2'	2.28	0.46
1:1A:330:A:H2	1:1A:1210:A:HO2'	1.60	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1140:C:O3'	9:1N:25:ARG:NH1	2.49	0.46
1:1A:1866:C:H2'	1:1A:1876:A:O4'	2.16	0.46
1:1A:2273:A:H2'	1:1A:2274:A:C8	2.51	0.46
5:1F:24:LEU:HB3	5:1F:115:ALA:HB2	1.97	0.46
32:1a:44:G:H2'	32:1a:45:U:O4'	2.16	0.46
32:1a:352:C:O2'	32:1a:354:G:OP1	2.28	0.46
41:1j:38:ILE:HG13	41:1j:71:LEU:HB3	1.97	0.46
42:1k:33:THR:HG22	42:1k:39:PRO:HA	1.98	0.46
1:2A:1147:C:H2'	1:2A:1148:A:H8	1.79	0.46
1:2A:1275:A:N1	1:2A:1295:C:O2'	2.42	0.46
1:2A:1530:C:O2'	1:2A:1531:C:H6	1.99	0.46
2:2B:8:U:H5'	14:2S:15:ARG:NH1	2.29	0.46
5:2F:21:ALA:CB	5:2F:22:ALA:HA	2.41	0.46
5:2F:148:LEU:HD22	5:2F:154:VAL:HG21	1.97	0.46
17:2V:76:LYS:HB2	17:2V:81:TYR:HB3	1.96	0.46
32:2a:474:G:H2'	32:2a:475:G:H8	1.79	0.46
32:2a:779:C:H2'	32:2a:780:A:O4'	2.15	0.46
32:2a:1359:C:O2'	32:2a:1361:G:N7	2.48	0.46
35:2d:112:VAL:H	35:2d:116:GLN:NE2	2.13	0.46
52:2u:2:GLY:O	52:2u:4:GLY:N	2.48	0.46
1:1A:1587:A:H2'	1:1A:1588:C:C6	2.50	0.46
1:1A:2506:U:O2	55:1A:4018:HGR:H23	2.14	0.46
5:1F:8:GLN:NE2	5:1F:21:ALA:HB2	2.30	0.46
6:1G:67:LYS:HD3	26:14:5:ILE:HB	1.97	0.46
8:1I:60:GLU:HG3	8:1I:61:ARG:NH1	2.30	0.46
11:1P:49:ARG:NH1	30:18:4:MET:HE1	2.31	0.46
15:1T:37:GLY:HA2	15:1T:38:ASN:HA	1.60	0.46
32:1a:192:U:H2'	32:1a:193:C:H6	1.80	0.46
32:1a:270:A:H2'	32:1a:271:C:C6	2.50	0.46
32:1a:382:A:H2'	32:1a:383:A:H8	1.79	0.46
32:1a:1479:C:H2'	32:1a:1480:G:C8	2.51	0.46
33:1b:67:THR:HA	33:1b:90:MET:HE2	1.97	0.46
34:1c:87:LEU:O	34:1c:91:LEU:N	2.42	0.46
41:1j:16:LEU:HD21	41:1j:70:ARG:HG2	1.96	0.46
41:1j:31:GLY:HA2	41:1j:32:ALA:HA	1.42	0.46
1:2A:11:G:H2'	1:2A:12:U:H5'	1.97	0.46
1:2A:184:C:H2'	1:2A:185:U:C6	2.51	0.46
1:2A:614(C):A:C4	5:2F:180:GLY:HA2	2.50	0.46
1:2A:1450:G:H2'	1:2A:1450(A):C:H6	1.80	0.46
1:2A:1539:G:H2'	1:2A:1540:U:H6	1.79	0.46
4:2E:101:ARG:CZ	4:2E:171:GLU:HB2	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:2G:124:SER:O	6:2G:124:SER:OG	2.30	0.46
32:2a:196:A:OP1	51:2t:68:LYS:NZ	2.37	0.46
32:2a:818:G:O2'	32:2a:819:A:H5'	2.15	0.46
32:2a:874:G:H2'	32:2a:875:C:H6	1.80	0.46
33:2b:80:ILE:HD11	33:2b:212:GLN:HA	1.98	0.46
33:2b:178:ARG:NH2	39:2h:74:PRO:HB3	2.20	0.46
35:2d:112:VAL:HG13	35:2d:116:GLN:HE22	1.80	0.46
1:1A:1386:C:H2'	1:1A:1387:C:C6	2.51	0.46
1:1A:2406:U:H2'	1:1A:2406:U:OP2	2.15	0.46
55:1A:4018:HGR:C16	55:1A:4018:HGR:H3	2.45	0.46
4:1E:5:LEU:HD11	4:1E:79:ARG:HB2	1.98	0.46
13:1R:71:GLN:NE2	61:1R:304:HOH:O	2.46	0.46
21:1Z:92:SER:O	21:1Z:130:PRO:HG2	2.16	0.46
30:18:62:LEU:HB3	30:18:65:GLU:HG3	1.97	0.46
32:1a:437:U:H5'	35:1d:155:LEU:HD11	1.96	0.46
32:1a:1151:A:O2'	32:1a:1152:A:H8	1.96	0.46
32:1a:1347:G:N2	32:1a:1373:G:H2'	2.30	0.46
35:1d:168:ARG:HD3	35:1d:168:ARG:HA	1.34	0.46
47:1p:4:ILE:HG22	47:1p:19:ILE:HD11	1.97	0.46
1:2A:7:G:H2'	1:2A:8:A:C8	2.50	0.46
1:2A:84:A:N1	1:2A:98:G:O2'	2.40	0.46
1:2A:424:G:N3	61:2A:3987:HOH:O	2.36	0.46
1:2A:652(A):A:H2'	1:2A:652(A):A:N3	2.30	0.46
1:2A:898:C:H2'	1:2A:899:A:O4'	2.16	0.46
1:2A:1049:C:O2	1:2A:1113:U:H4'	2.15	0.46
1:2A:1096:A:H2'	1:2A:1097:U:H6	1.80	0.46
1:2A:2439:A:H5'	1:2A:2439:A:C8	2.50	0.46
6:2G:150:ASP:OD1	6:2G:151:ALA:N	2.48	0.46
11:2P:98:GLU:HB3	11:2P:102:ARG:NH2	2.30	0.46
14:2S:35:ILE:HG12	14:2S:101:LEU:HD12	1.98	0.46
40:2i:8:GLY:HA2	40:2i:79:LEU:HD23	1.97	0.46
40:2i:32:ASP:HB3	40:2i:35:GLU:HB3	1.97	0.46
45:2n:23:ARG:NH1	45:2n:30:ALA:HB2	2.30	0.46
45:2n:42:ILE:O	45:2n:46:GLU:HG3	2.14	0.46
46:2o:55:GLY:HA2	46:2o:58:MET:HE3	1.97	0.46
47:2p:60:LEU:C	47:2p:62:VAL:H	2.23	0.46
1:1A:1721:G:H8	1:1A:1741:A:H62	1.62	0.46
56:1A:4019:TEL:H242	56:1A:4019:TEL:H30	1.81	0.46
61:1A:5044:HOH:O	5:1F:74:ARG:HG3	2.16	0.46
16:1U:108:GLU:O	16:1U:112:ARG:HG3	2.16	0.46
32:1a:1064:G:O2'	32:1a:1190:G:N2	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:1b:47:THR:HG22	33:1b:51:LEU:HD12	1.98	0.46
51:1t:33:ILE:O	51:1t:37:SER:OG	2.29	0.46
1:2A:221:A:O2'	1:2A:266:G:N7	2.48	0.46
1:2A:1647:G:H3'	1:2A:1647:G:OP2	2.15	0.46
1:2A:2119:A:H61	1:2A:2168:G:H21	1.63	0.46
1:2A:2802:G:H2'	1:2A:2803:C:O4'	2.14	0.46
5:2F:178:PRO:HB3	5:2F:198:ALA:HA	1.98	0.46
6:2G:126:ASP:HB2	6:2G:130:ASN:HB2	1.97	0.46
32:2a:110:C:H2'	32:2a:111:G:O4'	2.16	0.46
32:2a:273:A:H1'	48:2q:16:GLN:NE2	2.31	0.46
32:2a:611:A:H2	32:2a:630:G:H22	1.63	0.46
33:2b:87:ARG:O	33:2b:223:ILE:HD11	2.16	0.46
38:2g:46:ALA:HA	38:2g:49:ILE:HD12	1.97	0.46
1:1A:217:G:OP2	61:1A:4148:HOH:O	2.20	0.46
1:1A:1174:A:Cl'	1:1A:1175:U:H5'	2.44	0.46
1:1A:2023:G:H4'	1:1A:2617:C:O3'	2.16	0.46
32:1a:721:G:H4'	32:1a:722:A:O4'	2.15	0.46
35:1d:173:TRP:CE3	35:1d:174:LEU:HG	2.51	0.46
39:1h:82:HIS:C	39:1h:82:HIS:CD2	2.94	0.46
40:1i:93:ARG:HH21	40:1i:97:LYS:HD2	1.79	0.46
41:1j:35:SER:N	41:1j:73:ASP:O	2.44	0.46
43:1l:88:GLY:O	43:1l:99:HIS:HD2	1.97	0.46
1:2A:272:G:N7	1:2A:421:U:H2'	2.30	0.46
1:2A:2136:C:H2'	1:2A:2137:C:C6	2.50	0.46
1:2A:2820:A:OP1	13:2R:2:ARG:NH2	2.48	0.46
4:2E:18:ASP:HB3	15:2T:82:LEU:HD11	1.98	0.46
14:2S:36:TYR:HA	14:2S:52:SER:HA	1.97	0.46
19:2X:61:GLY:HA3	19:2X:73:ARG:O	2.16	0.46
32:2a:1004:A:N7	32:2a:1037:C:H2'	2.31	0.46
32:2a:1030(D):A:H3'	32:2a:1031:G:C8	2.50	0.46
38:2g:111:ARG:NH2	38:2g:126:ASP:OD2	2.49	0.46
1:1A:1068:G:O2'	1:1A:1096:A:O2'	2.30	0.46
1:1A:1289:C:H2'	1:1A:1290:C:C6	2.51	0.46
1:1A:1815:A:P	3:1D:54:ARG:HH22	2.39	0.46
1:1A:2336:A:H61	22:10:43:THR:HG22	1.81	0.46
32:1a:1003:G:C2	32:1a:1004:A:N3	2.84	0.46
32:1a:1131:G:OP1	40:1i:20:ARG:NH2	2.48	0.46
32:1a:1320:C:C2	50:1s:72:GLY:HA3	2.50	0.46
34:1c:148:GLY:HA3	34:1c:172:ARG:O	2.15	0.46
38:1g:111:ARG:NH2	38:1g:126:ASP:OD2	2.48	0.46
46:1o:3:ILE:HD11	46:1o:38:ARG:HG3	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:126:A:OP2	61:2A:3852:HOH:O	2.20	0.46
1:2A:241:A:H5''	61:2A:5588:HOH:O	2.16	0.46
1:2A:330:A:HO2'	1:2A:331:A:H8	1.60	0.46
1:2A:2540:C:H2'	1:2A:2541:A:O4'	2.15	0.46
8:2I:72:LEU:HD21	8:2I:107:VAL:HG11	1.98	0.46
13:2R:2:ARG:NH1	13:2R:5:LYS:O	2.49	0.46
32:2a:7:G:O2'	36:2e:120:THR:O	2.34	0.46
32:2a:157:G:H2'	32:2a:158:G:H8	1.80	0.46
32:2a:977:A:O2'	32:2a:981:U:N3	2.46	0.46
32:2a:979:C:O2	45:2n:19:ARG:NE	2.40	0.46
32:2a:1151:A:O4'	41:2j:39:PRO:HB2	2.16	0.46
32:2a:1310:G:OP2	44:2m:88:ARG:NH1	2.39	0.46
32:2a:1516:G:N1	32:2a:1519:MA6:OP2	2.48	0.46
34:2c:54:ARG:HB2	34:2c:69:HIS:HB2	1.97	0.46
40:2i:3:GLN:HE21	40:2i:20:ARG:HE	1.64	0.46
44:2m:20:THR:HA	44:2m:25:ILE:O	2.16	0.46
48:2q:81:ARG:HH21	48:2q:84:LEU:HD11	1.80	0.46
1:1A:251:A:C5	1:1A:252:G:H1'	2.50	0.46
1:1A:307:G:H21	1:1A:330:A:H62	1.63	0.46
1:1A:456:C:H4'	61:1A:4215:HOH:O	2.15	0.46
1:1A:493:G:H2'	1:1A:494:G:O4'	2.16	0.46
1:1A:2029:G:H2'	1:1A:2031:A:OP1	2.15	0.46
1:1A:2364:C:H2'	1:1A:2365:G:O4'	2.15	0.46
1:1A:2869:G:H2'	1:1A:2870:C:O4'	2.15	0.46
5:1F:101:LEU:HD12	5:1F:102:PRO:HD2	1.97	0.46
28:16:6:ARG:NE	28:16:24:GLU:OE2	2.35	0.46
32:1a:1239:A:H62	32:1a:1299:A:N6	2.13	0.46
32:1a:1261:A:H3'	32:1a:1262:C:C6	2.51	0.46
34:1c:134:ILE:HD11	34:1c:153:VAL:HB	1.97	0.46
44:1m:34:LEU:HD13	44:1m:41:PRO:HA	1.98	0.46
1:2A:1614:A:C2	18:2W:93:ALA:HB2	2.51	0.46
1:2A:1810:A:H2'	1:2A:1811:G:O4'	2.16	0.46
1:2A:2107:C:H42	1:2A:2182:G:H1	1.64	0.46
1:2A:2345:G:N3	1:2A:2381:C:H2'	2.31	0.46
9:2N:71:ILE:HG21	9:2N:84:LYS:HD3	1.97	0.46
11:2P:138:LEU:HD23	11:2P:145:PRO:HB3	1.97	0.46
33:2b:82:ARG:HB2	33:2b:92:TYR:CZ	2.51	0.46
61:1A:5720:HOH:O	4:1E:144:ARG:HD3	2.16	0.46
30:18:61:LEU:C	30:18:63:PRO:HD3	2.41	0.46
32:1a:1368:G:OP2	40:1i:112:LYS:HG3	2.16	0.46
36:1e:95:ALA:HB1	36:1e:96:PRO:HD2	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:1l:33:ARG:HD3	43:1l:33:ARG:HA	1.64	0.46
1:2A:609:A:H2'	1:2A:610:G:O4'	2.16	0.46
1:2A:2541:A:OP2	61:2A:3861:HOH:O	2.21	0.46
61:2A:4472:HOH:O	18:2W:18:ARG:HD3	2.16	0.46
6:2G:55:LYS:HA	6:2G:58:GLN:HB3	1.97	0.46
12:2Q:1:MET:HB3	12:2Q:1:MET:HE2	1.83	0.46
33:2b:211:ILE:O	33:2b:215:LEU:HB2	2.16	0.46
41:2j:11:PHE:CE1	41:2j:67:THR:HG22	2.51	0.46
42:2k:79:SER:HB2	42:2k:104:GLN:HB3	1.96	0.46
1:1A:895:U:H5'	1:1A:896:A:OP2	2.15	0.45
1:1A:1031:G:H5''	31:19:8:LYS:HE3	1.98	0.45
1:1A:1048:A:OP2	1:1A:1109:C:N4	2.49	0.45
1:1A:1173:G:O2'	1:1A:1174:A:O4'	2.31	0.45
1:1A:2096:U:H2'	1:1A:2097:C:H6	1.81	0.45
1:1A:2201:C:OP1	23:11:48:LYS:NZ	2.34	0.45
1:1A:2347:C:H2'	1:1A:2348:U:C6	2.51	0.45
1:1A:2704:C:H2'	1:1A:2705:A:O4'	2.16	0.45
21:1Z:198:LYS:HB3	21:1Z:202:GLU:O	2.15	0.45
32:1a:370:C:H2'	32:1a:371:G:C8	2.51	0.45
32:1a:995:C:H1'	45:1n:4:LYS:HE2	1.98	0.45
32:1a:1033:G:H2'	32:1a:1034:G:H8	1.81	0.45
36:1e:145:LYS:HE3	36:1e:149:GLU:OE2	2.16	0.45
37:1f:91:VAL:HG12	37:1f:92:LYS:O	2.16	0.45
47:1p:69:THR:HA	47:1p:72:ARG:HB3	1.99	0.45
1:2A:2199:A:N3	61:2A:3948:HOH:O	2.36	0.45
1:2A:2683:C:OP1	15:2T:53:ARG:NH2	2.48	0.45
1:2A:2746:U:OP1	7:2H:85:LYS:NZ	2.49	0.45
1:2A:2849:U:H4'	1:2A:2868:A:C2	2.51	0.45
5:2F:176:LEU:HD23	5:2F:176:LEU:HA	1.69	0.45
15:2T:6:LEU:HD12	15:2T:6:LEU:HA	1.77	0.45
26:24:64:GLY:C	26:24:66:SER:H	2.24	0.45
32:2a:325:A:H2'	32:2a:326:G:O4'	2.16	0.45
32:2a:938:A:C6	32:2a:939:G:C5	3.05	0.45
33:2b:30:ARG:HH22	33:2b:194:PRO:HB2	1.81	0.45
33:2b:35:GLU:HG3	33:2b:39:ILE:O	2.16	0.45
33:2b:47:THR:HA	33:2b:202:PRO:HG2	1.98	0.45
1:1A:1155:A:OP1	16:1U:55:ARG:HD3	2.15	0.45
1:1A:2718:G:O6	61:1A:4142:HOH:O	2.19	0.45
6:1G:66:GLN:NE2	6:1G:93:THR:O	2.49	0.45
32:1a:299:G:H2'	32:1a:300:A:C8	2.51	0.45
32:1a:814:A:H2'	32:1a:816:A:H5''	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:1b:42:ILE:HD12	33:1b:203:GLY:HA2	1.98	0.45
33:1b:124:SER:HA	33:1b:125:PRO:HA	1.63	0.45
40:1i:4:TYR:HA	40:1i:87:GLN:HE21	1.80	0.45
47:1p:79:VAL:HG23	47:1p:80:PHE:CD1	2.51	0.45
1:2A:236:C:H2'	1:2A:237:C:C6	2.51	0.45
1:2A:361:G:O2'	1:2A:362:U:H5'	2.16	0.45
1:2A:821:A:H2'	1:2A:946:G:H5''	1.97	0.45
1:2A:1340:U:OP1	19:2X:16:LYS:NZ	2.49	0.45
1:2A:2203:U:H2'	1:2A:2205:C:C6	2.51	0.45
1:2A:2629:A:H1'	1:2A:2630:G:H5''	1.99	0.45
6:2G:33:ARG:O	6:2G:161:THR:HG23	2.16	0.45
10:2O:36:GLY:HA3	10:2O:109:LYS:HD2	1.97	0.45
32:2a:23:C:OP2	32:2a:561:U:N3	2.40	0.45
32:2a:601:C:H2'	32:2a:602:A:C8	2.50	0.45
32:2a:685:G:C2	32:2a:686:U:C4	3.05	0.45
32:2a:921:U:O2	36:2e:19:MET:HB2	2.16	0.45
32:2a:1003:G:N7	32:2a:1004:A:H1'	2.30	0.45
32:2a:1277:C:O2'	32:2a:1279:A:C8	2.68	0.45
33:2b:175:ARG:HB3	33:2b:175:ARG:HH11	1.81	0.45
35:2d:150:GLU:HA	35:2d:153:ARG:HE	1.81	0.45
41:2j:78:ASN:O	41:2j:80:LYS:N	2.49	0.45
1:1A:284:U:H2'	1:1A:285:C:C6	2.51	0.45
1:1A:782:A:H5'	1:1A:783:A:N7	2.32	0.45
1:1A:2820:A:P	13:1R:2:ARG:HH22	2.39	0.45
7:1H:12:PRO:O	7:1H:15:VAL:HG13	2.16	0.45
32:1a:656:C:O2'	46:1o:28:GLN:NE2	2.49	0.45
32:1a:750:G:N3	46:1o:23:GLY:HA3	2.31	0.45
32:1a:1162:C:H2'	32:1a:1163:C:C6	2.51	0.45
33:1b:55:PHE:CD1	33:1b:58:ILE:HD12	2.51	0.45
41:1j:61:GLU:OE2	45:1n:58:LYS:NZ	2.42	0.45
42:1k:85:ARG:HD3	42:1k:113:PRO:HD3	1.97	0.45
49:1r:40:LEU:HB3	49:1r:79:LEU:HD11	1.99	0.45
1:2A:881:G:N2	1:2A:895:U:O2	2.39	0.45
1:2A:2305:A:H5''	6:2G:134:GLY:HA3	1.98	0.45
1:2A:2533:A:OP1	1:2A:2665:A:O2'	2.24	0.45
6:2G:19:LEU:HD11	6:2G:172:LEU:HB2	1.97	0.45
12:2Q:103:MET:HE1	12:2Q:125:LEU:HD13	1.97	0.45
23:21:53:VAL:HG22	23:21:74:VAL:HG13	1.97	0.45
34:2c:180:ALA:HB1	34:2c:203:PHE:CE1	2.51	0.45
36:2e:57:LYS:HG2	36:2e:61:TYR:HE2	1.81	0.45
39:2h:100:ILE:HD12	39:2h:125:ARG:HG3	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:2q:41:LYS:NZ	48:2q:92:ARG:HH21	2.15	0.45
1:1A:2116:G:OP2	1:1A:2166:G:N2	2.31	0.45
32:1a:114:U:H1'	32:1a:353:A:H1'	1.98	0.45
32:1a:1086:U:H3	32:1a:1099:G:N2	2.00	0.45
32:1a:1114:C:O2'	45:1n:60:SER:O	2.31	0.45
32:1a:1152:A:H2'	32:1a:1153:C:C6	2.51	0.45
32:1a:1298:C:H2'	38:1g:114:ARG:NH2	2.32	0.45
43:1l:45:PRO:HG2	43:1l:49:ASN:O	2.15	0.45
48:1q:86:GLU:O	48:1q:90:ILE:HG13	2.17	0.45
51:1t:58:LYS:HA	51:1t:58:LYS:HD2	1.72	0.45
1:2A:1028:A:N6	1:2A:1125:G:H2'	2.32	0.45
1:2A:1453:U:O2'	1:2A:1455:G:N7	2.44	0.45
6:2G:14:GLU:C	6:2G:17:PRO:HD2	2.41	0.45
6:2G:145:THR:HG22	6:2G:148:MET:HE3	1.97	0.45
17:2V:6:LYS:HB2	17:2V:38:LEU:HD11	1.98	0.45
32:2a:433:C:H2'	32:2a:434:U:H6	1.82	0.45
32:2a:501:C:H2'	32:2a:502:G:H8	1.81	0.45
33:2b:24:TRP:CZ3	33:2b:26:PRO:HA	2.52	0.45
35:2d:116:GLN:NE2	35:2d:157:LEU:HD21	2.31	0.45
1:1A:1268:A:H2'	1:1A:1269:A:O4'	2.16	0.45
1:1A:2143:C:N3	1:1A:2148:G:O6	2.49	0.45
61:1A:7587:HOH:O	58:1F:321:ARG:HB2	2.17	0.45
10:1O:110:GLY:HA2	10:1O:112:MET:HE1	1.99	0.45
27:15:15:ARG:NH1	61:15:201:HOH:O	2.30	0.45
32:1a:5:U:H1'	61:1a:3410:HOH:O	2.15	0.45
32:1a:812:C:N3	61:1a:3341:HOH:O	2.35	0.45
32:1a:1315:U:H2'	32:1a:1316:G:O4'	2.16	0.45
40:1i:16:ARG:O	40:1i:64:THR:N	2.43	0.45
1:2A:172:C:H2'	1:2A:173:G:C8	2.51	0.45
1:2A:1509(B):A:H2'	1:2A:1510:G:O4'	2.17	0.45
1:2A:2821:A:OP2	61:2R:301:HOH:O	2.21	0.45
32:2a:56:U:H2'	32:2a:57:G:H8	1.81	0.45
32:2a:664:G:H22	32:2a:741:G:H1	1.65	0.45
32:2a:737:A:H2'	32:2a:738:C:H6	1.82	0.45
42:2k:20:TYR:CZ	42:2k:83:ILE:HD13	2.51	0.45
42:2k:99:GLN:HG2	42:2k:105:VAL:HG11	1.98	0.45
44:2m:19:LEU:HD11	44:2m:56:LEU:HD21	1.98	0.45
47:2p:23:ASP:OD1	47:2p:25:ARG:HG2	2.16	0.45
1:1A:324:A:H2'	1:1A:325:G:O4'	2.17	0.45
1:1A:811:U:H2'	11:1P:21:ARG:HA	1.99	0.45
1:1A:1085:A:H2'	1:1A:1086:A:C8	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:1H:3:ARG:NH1	7:1H:5:GLY:H	2.15	0.45
8:1I:9:LEU:HD12	8:1I:9:LEU:HA	1.66	0.45
19:1X:54:VAL:HG22	19:1X:81:VAL:HG12	1.98	0.45
32:1a:266:G:C5'	32:1a:268:C:H41	2.30	0.45
32:1a:836:G:OP1	49:1r:61:LYS:NZ	2.49	0.45
32:1a:1352:C:OP1	52:1u:3:LYS:NZ	2.27	0.45
36:1e:102:ALA:O	36:1e:107:ARG:NH1	2.49	0.45
44:1m:108:ARG:HD3	44:1m:108:ARG:HA	1.71	0.45
1:2A:840:C:H2'	1:2A:841:A:C8	2.52	0.45
1:2A:1497:U:H5''	1:2A:1498:C:H5	1.82	0.45
1:2A:1557:C:H5''	1:2A:1558:A:OP2	2.17	0.45
1:2A:2749:A:OP1	7:2H:3:ARG:NH1	2.50	0.45
32:2a:109:A:C6	32:2a:326:G:C6	3.05	0.45
32:2a:261:U:OP2	51:2t:79:ARG:NH2	2.50	0.45
32:2a:409:G:H2'	32:2a:410:G:O4'	2.17	0.45
32:2a:881:G:P	43:2l:12:ARG:HH22	2.39	0.45
48:2q:67:LYS:C	48:2q:69:LYS:H	2.24	0.45
1:1A:534:U:H2'	1:1A:535:C:C6	2.52	0.45
1:1A:715:G:C2	46:1o:56:LEU:HD21	2.52	0.45
1:1A:1026:U:O2	1:1A:1026:U:H2'	2.16	0.45
1:1A:1060:U:H4'	1:1A:1061:U:H5'	1.99	0.45
1:1A:1065:U:O2'	1:1A:1066:U:O4'	2.27	0.45
1:1A:2206:G:H5''	1:1A:2207:G:C6	2.52	0.45
8:1I:84:GLY:O	8:1I:85:GLU:HB3	2.16	0.45
32:1a:384:G:H2'	32:1a:385:C:C6	2.52	0.45
32:1a:558:G:O6	61:1a:3313:HOH:O	2.20	0.45
34:1c:26:LYS:HB3	34:1c:26:LYS:HE2	1.79	0.45
35:1d:128:VAL:HG12	35:1d:129:ASN:ND2	2.30	0.45
42:1k:70:LYS:HE2	42:1k:70:LYS:HB2	1.74	0.45
44:1m:4:ILE:HA	44:1m:5:ALA:HA	1.64	0.45
1:2A:700:G:O2'	1:2A:1632:A:N3	2.33	0.45
1:2A:848:G:H2'	1:2A:849:A:C8	2.51	0.45
1:2A:2104:G:O6	1:2A:2185:C:C4	2.69	0.45
8:2I:77:LEU:HD22	8:2I:101:LEU:HG	1.98	0.45
12:2Q:35:VAL:HG22	12:2Q:102:VAL:HG22	1.98	0.45
16:2U:76:TYR:CZ	16:2U:80:ILE:HG13	2.52	0.45
17:2V:29:PRO:HA	17:2V:61:VAL:HG22	1.99	0.45
32:2a:991:U:H2'	32:2a:1212:U:C4	2.51	0.45
32:2a:1324:A:O4'	32:2a:1362:C:H4'	2.17	0.45
32:2a:1496:C:H2'	32:2a:1497:G:O4'	2.16	0.45
39:2h:9:MET:HG3	39:2h:26:VAL:HG11	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:55:G:O2'	1:1A:127:A:N1	2.47	0.45
1:1A:793:A:OP2	1:1A:2071:A:O2'	2.32	0.45
1:1A:800:A:H8	1:1A:800:A:OP1	2.00	0.45
3:1D:95:LEU:HD11	3:1D:105:ILE:HG12	1.99	0.45
3:1D:242:ARG:HG3	3:1D:242:ARG:NH1	2.25	0.45
18:1W:18:ARG:HG3	18:1W:76:VAL:HB	1.99	0.45
32:1a:1216:G:H5''	45:1n:5:ALA:HB2	1.98	0.45
33:1b:157:ARG:HG2	33:1b:158:LEU:H	1.82	0.45
47:1p:49:LEU:HG	47:1p:50:LYS:H	1.82	0.45
48:1q:54:GLY:O	48:1q:81:ARG:HB2	2.16	0.45
1:2A:2554:U:H2'	1:2A:2555:U:C6	2.52	0.45
55:2A:3738:HGR:C16	55:2A:3738:HGR:H3	2.47	0.45
6:2G:139:LEU:HA	6:2G:144:ILE:HB	1.98	0.45
14:2S:67:ARG:HB2	14:2S:100:ALA:HB1	1.99	0.45
19:2X:53:LYS:HB3	19:2X:82:GLN:HB3	1.98	0.45
32:2a:279:A:N6	48:2q:98:LEU:O	2.50	0.45
32:2a:1238:A:OP2	61:2a:3215:HOH:O	2.21	0.45
32:2a:1307:U:H2'	32:2a:1308:U:C6	2.52	0.45
34:2c:30:ARG:HD3	34:2c:31:HIS:CD2	2.52	0.45
50:2s:41:VAL:HG22	50:2s:42:PRO:HD2	1.99	0.45
1:1A:330:A:H2	1:1A:1210:A:O2'	1.99	0.45
1:1A:1024:G:C6	1:1A:1025:G:C6	3.05	0.45
1:1A:1427:A:H4'	1:1A:1428:C:O5'	2.16	0.45
1:1A:1549:C:H2'	1:1A:1550:C:H6	1.82	0.45
11:1P:88:LEU:HD21	11:1P:100:LEU:HD11	1.98	0.45
17:1V:21:ARG:HD3	17:1V:91:TYR:CD1	2.51	0.45
20:1Y:9:LYS:HA	20:1Y:10:GLY:HA2	1.60	0.45
32:1a:1016:A:H2'	32:1a:1017:G:O4'	2.16	0.45
32:1a:1020:U:H2'	32:1a:1021:G:H8	1.82	0.45
40:1i:18:PHE:HD2	40:1i:62:TYR:HD2	1.64	0.45
41:1j:48:THR:OG1	41:1j:62:HIS:ND1	2.47	0.45
1:2A:190:A:OP2	23:21:39:LYS:HE3	2.16	0.45
1:2A:242:G:C8	30:28:5:LYS:HG2	2.52	0.45
1:2A:443:A:H1'	1:2A:1201:C:O4'	2.17	0.45
1:2A:937:U:H2'	1:2A:938:G:O4'	2.16	0.45
1:2A:1790:C:H2'	1:2A:1791:A:C5	2.51	0.45
1:2A:2299:G:N1	1:2A:2318:G:N7	2.65	0.45
3:2D:150:LYS:HA	3:2D:150:LYS:HD3	1.85	0.45
7:2H:68:THR:HA	7:2H:71:LEU:HD12	1.99	0.45
9:2N:120:LEU:HG	9:2N:122:VAL:HG23	1.98	0.45
18:2W:37:ARG:NH1	27:25:48:GLU:OE2	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1323:G:H2'	32:2a:1324:A:C8	2.52	0.45
34:2c:57:ILE:HG12	34:2c:66:VAL:HG13	1.98	0.45
44:2m:15:VAL:HG12	44:2m:45:VAL:HG22	1.98	0.45
1:1A:1041:C:H5'	1:1A:1042:G:OP2	2.15	0.45
1:1A:1113:U:H2'	1:1A:1114:G:H8	1.81	0.45
1:1A:1131:G:H21	9:1N:73:THR:HG21	1.81	0.45
5:1F:53:THR:HG22	5:1F:55:GLY:H	1.82	0.45
13:1R:24:GLN:NE2	61:1R:307:HOH:O	2.51	0.45
15:1T:1:MET:HE2	15:1T:3:ARG:HG2	1.99	0.45
21:1Z:63:ASP:OD1	21:1Z:64:GLY:N	2.50	0.45
32:1a:115:G:H4'	32:1a:116:A:O5'	2.17	0.45
32:1a:963:G:H5'	61:1a:3511:HOH:O	2.16	0.45
33:1b:16:HIS:HB3	33:1b:210:SER:HB2	1.99	0.45
38:1g:26:PHE:O	38:1g:30:ILE:HG13	2.17	0.45
39:1h:83:ILE:HG13	39:1h:137:VAL:HG22	1.99	0.45
41:1j:4:ILE:N	41:1j:100:THR:HA	2.32	0.45
50:1s:41:VAL:HG22	50:1s:44:MET:SD	2.57	0.45
1:2A:185:U:H2'	1:2A:186:G:H8	1.81	0.45
1:2A:1721:G:H8	1:2A:1741:A:H62	1.63	0.45
1:2A:2417:C:OP1	11:2P:65:ARG:NH2	2.50	0.45
1:2A:2544:G:H1'	1:2A:2646:C:H4'	1.98	0.45
1:2A:2698:U:H2'	1:2A:2699:C:C6	2.52	0.45
56:2A:3739:TEL:H112	56:2A:3739:TEL:O18	2.17	0.45
2:2B:3:C:H2'	2:2B:4:C:C6	2.52	0.45
4:2E:178:GLU:CD	4:2E:178:GLU:H	2.25	0.45
11:2P:127:ALA:O	11:2P:148:LEU:HB2	2.16	0.45
17:2V:46:VAL:HG22	17:2V:52:VAL:HG11	1.99	0.45
32:2a:266:G:O2'	32:2a:267:C:OP2	2.21	0.45
32:2a:490:G:H2'	32:2a:491:G:C8	2.51	0.45
32:2a:910:C:H2'	32:2a:911:U:O4'	2.17	0.45
32:2a:1172:C:H2'	32:2a:1173:G:H8	1.81	0.45
38:2g:101:LEU:O	38:2g:105:VAL:HG23	2.17	0.45
1:1A:375:C:H2'	1:1A:376:C:C6	2.52	0.44
1:1A:1503:U:H2'	1:1A:1504:C:C6	2.51	0.44
1:1A:1693:U:H1'	3:1D:14:ARG:NH1	2.32	0.44
1:1A:1766:U:H2'	1:1A:1767:C:H6	1.82	0.44
1:1A:1799:G:H8	3:1D:181:GLU:OE1	2.00	0.44
1:1A:1937:A:H1'	1:1A:1939:5MU:H72	1.99	0.44
1:1A:2404:C:O3'	11:1P:77:ARG:NH2	2.50	0.44
7:1H:40:GLU:CD	7:1H:60:ARG:HH12	2.26	0.44
32:1a:1029:C:C2	32:1a:1032:G:N1	2.81	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:1h:21:LYS:O	39:1h:63:LEU:HD12	2.17	0.44
41:1j:78:ASN:O	41:1j:80:LYS:N	2.49	0.44
1:2A:900:A:H2'	1:2A:901:A:O4'	2.16	0.44
1:2A:1048:A:H2	1:2A:1112:G:N3	2.15	0.44
1:2A:1514:U:H2'	1:2A:1515:G:C8	2.53	0.44
1:2A:2336:A:H61	22:20:43:THR:CG2	2.29	0.44
2:2B:80:U:H2'	2:2B:81:G:C8	2.52	0.44
20:2Y:44:ILE:HA	20:2Y:63:LYS:O	2.17	0.44
32:2a:540:G:H2'	32:2a:541:G:O4'	2.17	0.44
1:1A:584:C:OP2	16:1U:6:THR:OG1	2.33	0.44
1:1A:2430:A:N3	1:1A:2430:A:H2'	2.32	0.44
2:1B:12:C:H2'	22:10:73:GLY:HA3	1.98	0.44
2:1B:23:G:O6	61:1B:305:HOH:O	2.18	0.44
32:1a:756:C:H2'	32:1a:757:U:O4'	2.17	0.44
32:1a:920:U:H2'	32:1a:921:U:C6	2.52	0.44
33:1b:185:ILE:HG22	33:1b:199:TYR:CD2	2.51	0.44
34:1c:190:ARG:HB2	34:1c:190:ARG:HH21	1.81	0.44
39:1h:85:ARG:HD2	39:1h:85:ARG:HA	1.72	0.44
50:1s:45:VAL:HA	50:1s:62:ILE:HG22	1.99	0.44
1:2A:1131:G:O6	1:2A:2040:C:H1'	2.17	0.44
1:2A:1180:C:H2'	1:2A:1181:C:C6	2.51	0.44
1:2A:2641:G:P	9:2N:74:ARG:HH21	2.40	0.44
2:2B:66:A:N6	2:2B:109:C:H5'	2.30	0.44
3:2D:25:THR:HG21	3:2D:113:VAL:HG11	1.99	0.44
4:2E:181:LEU:HD12	4:2E:181:LEU:HA	1.74	0.44
6:2G:83:ARG:H	6:2G:86:MET:CE	2.30	0.44
21:2Z:5:LEU:HD21	21:2Z:39:VAL:HB	1.98	0.44
21:2Z:99:TYR:HA	21:2Z:124:ILE:O	2.17	0.44
26:24:1:MET:HE2	26:24:6:HIS:CG	2.52	0.44
26:24:48:ARG:O	26:24:50:VAL:N	2.45	0.44
32:2a:664:G:P	49:2r:64:ARG:HH21	2.40	0.44
40:2i:53:VAL:C	40:2i:55:ALA:H	2.25	0.44
53:2y:52:ALA:HB2	53:2y:77:LEU:HD21	1.99	0.44
1:1A:515:A:H1'	1:1A:581:C:H1'	1.99	0.44
3:1D:146:GLU:HG2	3:1D:152:GLY:C	2.43	0.44
9:1N:96:GLU:H	9:1N:96:GLU:CD	2.26	0.44
32:1a:938:A:N6	32:1a:939:G:C6	2.85	0.44
32:1a:1010:G:H22	32:1a:1020:U:H1'	1.81	0.44
32:1a:1152:A:H5'	41:1j:13:HIS:CG	2.52	0.44
32:1a:1353:G:C2	32:1a:1370:G:C2	3.05	0.44
35:1d:124:GLY:C	35:1d:126:ILE:H	2.26	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:1p:39:TYR:HB2	47:1p:49:LEU:HD12	1.99	0.44
1:2A:493:G:OP2	61:2A:3860:HOH:O	2.21	0.44
1:2A:1045:A:H5'	1:2A:1047:G:O4'	2.18	0.44
1:2A:1178:C:H2'	1:2A:1179:C:H6	1.82	0.44
1:2A:2328:A:H2'	1:2A:2329:G:C8	2.53	0.44
2:2B:28:C:H2'	2:2B:29:A:O4'	2.17	0.44
7:2H:24:VAL:HG11	7:2H:72:ILE:HD11	1.99	0.44
13:2R:95:THR:HG22	13:2R:116:LEU:HD23	1.99	0.44
19:2X:31:HIS:CD2	19:2X:33:LYS:H	2.35	0.44
23:21:2:SER:HB3	23:21:46:LEU:HD12	2.00	0.44
26:24:59:PHE:CE2	50:2s:64:GLU:HB2	2.51	0.44
32:2a:8:A:H5'	36:2e:101:ILE:HG22	1.99	0.44
35:2d:22:LYS:O	35:2d:113:SER:HB3	2.16	0.44
46:2o:48:LYS:HA	46:2o:48:LYS:HD2	1.48	0.44
1:1A:748:G:C8	18:1W:89:ALA:HB1	2.52	0.44
1:1A:2074:U:H2'	1:1A:2075:U:C6	2.52	0.44
8:1I:110:ASP:N	8:1I:130:TYR:OH	2.41	0.44
15:1T:128:GLU:HG2	15:1T:128:GLU:O	2.18	0.44
32:1a:181:G:H4'	32:1a:182:U:H5'	2.00	0.44
32:1a:452:A:H4'	47:1p:72:ARG:NH1	2.32	0.44
32:1a:481:G:O2'	32:1a:483:C:N4	2.49	0.44
32:1a:727:G:OP2	61:1a:3318:HOH:O	2.21	0.44
32:1a:737:A:H2'	32:1a:738:C:C6	2.52	0.44
32:1a:1118:C:H2'	32:1a:1119:C:C6	2.53	0.44
32:1a:1134:G:N3	32:1a:1134:G:H2'	2.32	0.44
32:1a:1258:G:H2'	32:1a:1259:C:H6	1.83	0.44
1:2A:729:G:C6	3:2D:208:LYS:HB2	2.52	0.44
1:2A:1651:G:N7	61:2A:3979:HOH:O	2.35	0.44
1:2A:2506:U:OP1	4:2E:144:ARG:NH2	2.50	0.44
3:2D:276:LYS:HB2	3:2D:276:LYS:HE3	1.84	0.44
4:2E:47:VAL:HG21	4:2E:86:PRO:HD3	2.00	0.44
4:2E:52:LEU:HB2	4:2E:76:ARG:HB2	2.00	0.44
8:2I:72:LEU:HA	8:2I:75:LEU:HD22	2.00	0.44
18:2W:46:PHE:O	18:2W:50:VAL:HG23	2.18	0.44
32:2a:445:G:H2'	32:2a:446:G:O4'	2.17	0.44
33:2b:57:PHE:HE2	33:2b:185:ILE:HD11	1.82	0.44
40:2i:26:VAL:HG22	40:2i:61:ALA:HB3	1.99	0.44
40:2i:112:LYS:HE2	40:2i:117:HIS:O	2.17	0.44
1:1A:27:G:N2	1:1A:512:G:H1'	2.32	0.44
1:1A:1430:C:H2'	1:1A:1431:U:C6	2.52	0.44
3:1D:35:LYS:HD3	3:1D:64:ILE:HD11	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:1F:116:ASP:OD2	11:1P:1:MET:HB3	2.16	0.44
16:1U:8:VAL:HG11	16:1U:12:ARG:CZ	2.48	0.44
32:1a:96:U:H2'	32:1a:97:G:C8	2.53	0.44
32:1a:1056:U:H5'	34:1c:163:ALA:HB2	1.98	0.44
32:1a:1239:A:H4'	32:1a:1240:U:H5''	1.98	0.44
32:1a:1251:A:H2'	32:1a:1252:A:C8	2.53	0.44
35:1d:63:LYS:HE3	35:1d:63:LYS:HB2	1.76	0.44
1:2A:882:G:H1	1:2A:894:C:N4	2.15	0.44
1:2A:1449:A:N3	1:2A:1529:G:H1'	2.32	0.44
1:2A:1721:G:H2'	1:2A:1740:G:O6	2.17	0.44
1:2A:1843:C:H5'	3:2D:253:GLN:NE2	2.32	0.44
12:2Q:17:LEU:HD13	12:2Q:39:PRO:HB2	1.99	0.44
14:2S:23:ARG:NH1	14:2S:85:VAL:O	2.46	0.44
15:2T:16:ARG:HH21	15:2T:81:PRO:HA	1.83	0.44
20:2Y:56:PRO:C	20:2Y:58:GLY:H	2.25	0.44
32:2a:266:G:N3	32:2a:266:G:H5''	2.31	0.44
32:2a:328:C:H4'	32:2a:329:A:H5'	2.00	0.44
32:2a:1005:A:H5''	32:2a:1006:C:C6	2.53	0.44
32:2a:1077:G:N2	32:2a:1080:A:OP2	2.49	0.44
32:2a:1127:G:OP1	32:2a:1281:U:H4'	2.18	0.44
36:2e:92:LYS:HB3	36:2e:119:LEU:HB2	1.99	0.44
1:1A:1297:C:H5''	61:1A:4502:HOH:O	2.17	0.44
1:1A:2887:U:H2'	1:1A:2888:C:C6	2.52	0.44
3:1D:137:PRO:O	3:1D:140:THR:HG23	2.18	0.44
20:1Y:20:TYR:HB3	20:1Y:23:ARG:HG3	1.99	0.44
21:1Z:48:PHE:HE1	21:1Z:71:VAL:HG11	1.82	0.44
32:1a:1316:G:N1	32:1a:1319:A:OP2	2.50	0.44
32:1a:1402:4OC:CM2	32:1a:1403:C:H5'	2.47	0.44
40:1i:4:TYR:CZ	40:1i:88:TYR:HD1	2.35	0.44
42:1k:27:ASN:OD1	42:1k:28:THR:N	2.50	0.44
1:2A:1015:G:O2'	1:2A:1016:G:H5'	2.18	0.44
1:2A:1045:A:H8	1:2A:1047:G:C2	2.34	0.44
1:2A:2307:G:H8	1:2A:2307:G:OP1	2.00	0.44
2:2B:50:G:OP1	14:2S:63:THR:N	2.47	0.44
14:2S:43:GLU:OE2	22:20:49:LYS:NZ	2.51	0.44
15:2T:30:VAL:HG22	15:2T:86:ILE:HG12	2.00	0.44
19:2X:60:ARG:CZ	29:27:47:ARG:HH22	2.30	0.44
26:24:13:ARG:HA	26:24:22:ILE:O	2.18	0.44
32:2a:157:G:H2'	32:2a:158:G:C8	2.52	0.44
32:2a:1013:G:N2	32:2a:1016:A:OP2	2.51	0.44
32:2a:1117:G:H4'	40:2i:104:ARG:NH1	2.33	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1124:G:H4'	32:2a:1125:U:OP1	2.16	0.44
32:2a:1206:G:H4'	34:2c:192:THR:O	2.18	0.44
32:2a:1327:C:H2'	32:2a:1328:C:C6	2.52	0.44
32:2a:1371:G:C6	32:2a:1372:U:C4	3.06	0.44
32:2a:1397:C:H4'	32:2a:1398:A:OP2	2.18	0.44
34:2c:148:GLY:HA3	34:2c:172:ARG:O	2.18	0.44
36:2e:137:GLU:O	36:2e:141:GLN:HG3	2.17	0.44
38:2g:146:GLU:OE1	38:2g:149:ARG:NE	2.51	0.44
41:2j:57:LYS:O	41:2j:60:ARG:NE	2.46	0.44
42:2k:34:ASP:OD2	42:2k:38:ASN:HB2	2.18	0.44
52:2u:5:ASP:O	52:2u:11:GLY:HA3	2.18	0.44
1:1A:310:A:H2'	61:1A:5395:HOH:O	2.17	0.44
1:1A:527:C:H4'	1:1A:528:A:O5'	2.18	0.44
1:1A:567:A:OP2	11:1P:29:LYS:NZ	2.49	0.44
5:1F:110:LEU:HD23	5:1F:110:LEU:HA	1.84	0.44
6:1G:142:PRO:HB2	26:14:31:ILE:HG21	1.99	0.44
16:1U:58:ARG:HA	16:1U:61:TRP:CE3	2.53	0.44
32:1a:1202:G:H1'	45:1n:29:ARG:HD2	2.00	0.44
32:1a:1263:C:H2'	32:1a:1264:C:C6	2.53	0.44
35:1d:118:ARG:HG2	35:1d:136:PRO:HB3	2.00	0.44
37:1f:45:LEU:HD12	37:1f:59:TYR:HD1	1.83	0.44
37:1f:82:ARG:HB2	37:1f:85:VAL:HG23	1.99	0.44
40:1i:49:PRO:HA	40:1i:101:PHE:HD2	1.83	0.44
1:2A:407:G:H2'	1:2A:408:G:C8	2.53	0.44
1:2A:1104:C:H2'	1:2A:1105:U:C6	2.52	0.44
1:2A:1179:C:H2'	1:2A:1180:C:C6	2.53	0.44
1:2A:1359:A:H2'	1:2A:1360:A:H5'	1.99	0.44
1:2A:1540:U:H2'	1:2A:1541:G:O4'	2.18	0.44
1:2A:1991:U:H2'	1:2A:1992:G:H5''	2.00	0.44
1:2A:2022:U:O2'	1:2A:2617:C:H5'	2.18	0.44
1:2A:2336:A:H61	22:20:43:THR:HG22	1.83	0.44
1:2A:2774:C:H2'	1:2A:2775:A:O4'	2.17	0.44
1:2A:2815:C:C5'	27:25:29:THR:HG21	2.48	0.44
23:21:81:LYS:HE2	23:21:81:LYS:HB3	1.74	0.44
32:2a:1423:G:H2'	32:2a:1424:C:C6	2.53	0.44
32:2a:1508:G:OP1	61:2a:3203:HOH:O	2.21	0.44
33:2b:134:GLU:HA	33:2b:137:ARG:NH2	2.33	0.44
1:1A:1173:G:OP2	1:1A:1173:G:H2'	2.17	0.44
1:1A:1173:G:N2	1:1A:1177:A:H2	2.11	0.44
1:1A:2169:A:H8	1:1A:2169:A:OP1	2.01	0.44
1:1A:2646:C:H2'	1:1A:2647:U:O4'	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
61:1A:5160:HOH:O	16:1U:13:LYS:HE2	2.18	0.44
5:1F:90:PHE:HB2	61:1F:424:HOH:O	2.17	0.44
30:18:62:LEU:HB3	30:18:65:GLU:HG2	1.99	0.44
32:1a:7:G:H21	36:1e:121:LYS:HG2	1.83	0.44
32:1a:316:G:OP2	32:1a:351:G:O2'	2.32	0.44
32:1a:719:C:O2'	49:1r:49:LYS:HB3	2.17	0.44
32:1a:1004:A:C5	32:1a:1037:C:C2	3.06	0.44
32:1a:1492:A:H4'	32:1a:1493:A:C2	2.53	0.44
34:1c:58:GLU:HB3	41:1j:92:THR:HG21	1.99	0.44
35:1d:76:ARG:HD3	35:1d:207:TYR:CE1	2.53	0.44
1:2A:24:G:H2'	1:2A:25:U:O4'	2.17	0.44
1:2A:2647:U:H2'	1:2A:2648:C:C6	2.53	0.44
3:2D:145:VAL:HG12	3:2D:146:GLU:O	2.17	0.44
4:2E:59:VAL:HG21	4:2E:74:PRO:HB3	1.99	0.44
16:2U:104:GLN:CD	16:2U:104:GLN:H	2.25	0.44
32:2a:189(F):U:C4	48:2q:72:ARG:NH1	2.86	0.44
32:2a:191:G:C6	32:2a:192:U:C4	3.06	0.44
32:2a:689:C:H2'	32:2a:690:G:O4'	2.17	0.44
32:2a:828:A:N6	32:2a:858:G:O2'	2.51	0.44
33:2b:21:ARG:O	33:2b:23:ARG:N	2.45	0.44
34:2c:81:GLY:O	34:2c:85:ARG:NH1	2.51	0.44
36:2e:102:ALA:O	36:2e:107:ARG:NH1	2.50	0.44
51:2t:58:LYS:HE3	51:2t:62:LEU:HD21	1.99	0.44
1:1A:226:G:N2	1:1A:228:A:H62	2.16	0.44
1:1A:606:U:H4'	1:1A:658:C:H4'	1.99	0.44
1:1A:1794:U:H2'	1:1A:1795:C:C6	2.52	0.44
57:1A:4020:MPD:H4	57:1A:4020:MPD:HM2	1.77	0.44
2:1B:88:C:H2'	2:1B:89:G:O4'	2.17	0.44
3:1D:202:LYS:NZ	32:1a:774:G:OP1	2.46	0.44
8:1I:9:LEU:HB3	8:1I:12:LEU:HB3	1.99	0.44
8:1I:104:GLN:C	8:1I:106:GLY:H	2.26	0.44
12:1Q:3:MET:HE2	61:1Q:312:HOH:O	2.17	0.44
20:1Y:34:LYS:O	20:1Y:34:LYS:HD3	2.17	0.44
32:1a:344:A:H4'	32:1a:345:C:OP2	2.18	0.44
32:1a:1298:C:P	38:1g:114:ARG:HH22	2.39	0.44
33:1b:30:ARG:NH2	33:1b:194:PRO:HB2	2.33	0.44
34:1c:16:ARG:NH2	34:1c:54:ARG:HH21	2.16	0.44
47:1p:59:TRP:HA	47:1p:62:VAL:HG22	1.99	0.44
1:2A:218:A:C2	1:2A:235:U:H4'	2.53	0.44
1:2A:469:G:O6	29:27:37:LYS:NZ	2.45	0.44
1:2A:1366:A:H2'	1:2A:1367:A:O4'	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1772:G:O6	57:2A:3740:MPD:H32	2.18	0.44
4:2E:144:ARG:HB3	4:2E:145:LYS:H	1.54	0.44
5:2F:110:LEU:HD11	5:2F:181:LEU:HD23	2.00	0.44
8:2I:130:TYR:CE2	8:2I:132:PRO:HB3	2.53	0.44
32:2a:767:A:H2'	32:2a:768:A:O4'	2.18	0.44
32:2a:1012:U:H2'	32:2a:1013:G:O4'	2.17	0.44
42:2k:81:ASP:OD1	42:2k:106:LYS:HB2	2.17	0.44
50:2s:58:VAL:O	50:2s:60:VAL:HG23	2.18	0.44
1:1A:236:C:H2'	1:1A:237:C:C6	2.53	0.43
1:1A:454:A:H4'	1:1A:455:C:OP2	2.18	0.43
1:1A:832:G:OP1	61:1A:4151:HOH:O	2.21	0.43
1:1A:2698:U:H2'	1:1A:2699:C:C6	2.53	0.43
4:1E:18:ASP:OD2	15:1T:33:LYS:NZ	2.40	0.43
7:1H:13:LYS:HA	7:1H:14:GLY:HA2	1.55	0.43
8:1I:26:ALA:O	8:1I:31:LEU:HB2	2.17	0.43
10:1O:64:ARG:HB2	10:1O:79:PHE:CG	2.53	0.43
10:1O:64:ARG:NH2	10:1O:99:PHE:O	2.51	0.43
15:1T:39:ARG:HH11	15:1T:41:ARG:HB3	1.83	0.43
32:1a:79:G:N2	32:1a:90:U:O2	2.51	0.43
33:1b:84:GLU:OE1	33:1b:87:ARG:NH1	2.44	0.43
1:2A:875:G:H2'	1:2A:876:C:O4'	2.18	0.43
1:2A:1006:C:O2'	9:2N:106:MET:HB3	2.18	0.43
1:2A:1657:C:H2'	1:2A:1658:C:C6	2.53	0.43
1:2A:2785:C:O2'	4:2E:66:HIS:ND1	2.44	0.43
4:2E:116:VAL:HG13	4:2E:122:PHE:HB2	2.00	0.43
7:2H:115:VAL:HG11	7:2H:148:ILE:HD11	2.00	0.43
9:2N:1:MET:HE1	16:2U:94:ASN:ND2	2.33	0.43
20:2Y:31:LEU:HD12	20:2Y:36:ALA:HB3	2.00	0.43
32:2a:101:A:H5'	51:2t:10:LEU:HD21	1.99	0.43
32:2a:187:C:O2'	51:2t:89:ARG:HD3	2.18	0.43
32:2a:256:U:OP1	48:2q:17:LYS:NZ	2.31	0.43
32:2a:745:C:H5'	32:2a:851:G:H21	1.82	0.43
33:2b:16:HIS:CD2	33:2b:210:SER:HB3	2.53	0.43
50:2s:30:LEU:HD12	50:2s:48:THR:O	2.18	0.43
1:1A:1453:U:O2'	1:1A:1455:G:N7	2.51	0.43
1:1A:2127:G:H1	1:1A:2161:C:H42	1.66	0.43
1:1A:2784:C:H1'	4:1E:37:ARG:HH12	1.83	0.43
3:1D:8:PRO:HB3	3:1D:14:ARG:HG3	2.01	0.43
3:1D:142:VAL:HG23	3:1D:193:VAL:HA	2.00	0.43
5:1F:129:PHE:CD2	5:1F:163:VAL:HG21	2.53	0.43
40:1i:3:GLN:HE21	40:1i:20:ARG:NE	2.10	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:27:G:HO2'	1:2A:28:A:P	2.39	0.43
1:2A:422:A:H2'	1:2A:423:A:C8	2.53	0.43
1:2A:1055:G:H2'	1:2A:1056:G:O4'	2.18	0.43
1:2A:2118:U:H5	1:2A:2148:G:O2'	2.01	0.43
1:2A:2165:G:H2'	1:2A:2166:G:O4'	2.19	0.43
1:2A:2186:G:N1	1:2A:2187:G:C6	2.86	0.43
1:2A:2572:A:N7	4:2E:144:ARG:HD2	2.34	0.43
6:2G:139:LEU:H	6:2G:139:LEU:HG	1.59	0.43
32:2a:926:G:C6	32:2a:1505:G:C5	3.06	0.43
32:2a:1016:A:O5'	32:2a:1016:A:H8	2.01	0.43
32:2a:1292:U:C2	32:2a:1293:G:C8	3.07	0.43
37:2f:33:TYR:HB2	37:2f:75:LEU:HD12	1.99	0.43
39:2h:92:ARG:HD3	39:2h:92:ARG:HA	1.76	0.43
44:2m:74:VAL:O	44:2m:78:ILE:HG13	2.18	0.43
1:1A:143:G:O2'	19:1X:35:THR:HG21	2.18	0.43
1:1A:536:A:H2'	1:1A:537:C:C6	2.53	0.43
1:1A:818:G:H4'	1:1A:838:C:O3'	2.18	0.43
1:1A:1543:C:H5''	61:1A:6751:HOH:O	2.17	0.43
1:1A:2627:G:N2	1:1A:2777:G:OP2	2.51	0.43
61:1A:4151:HOH:O	11:1P:37:GLY:HA3	2.18	0.43
13:1R:59:ASP:OD1	13:1R:59:ASP:N	2.50	0.43
32:1a:203:U:H5'	32:1a:216:G:N2	2.33	0.43
36:1e:79:GLU:HG3	36:1e:93:PRO:HD2	1.99	0.43
1:2A:1035:U:H2'	1:2A:1036:G:C8	2.54	0.43
1:2A:1087:G:H22	1:2A:1102:C:H42	1.65	0.43
1:2A:1198:U:H2'	1:2A:1199:U:C6	2.54	0.43
1:2A:1450:G:H2'	1:2A:1450(A):C:C6	2.53	0.43
1:2A:2151:G:H2'	1:2A:2152:G:O4'	2.18	0.43
2:2B:3:C:H2'	2:2B:4:C:H6	1.83	0.43
2:2B:90:A:N7	2:2B:91:C:H1'	2.32	0.43
3:2D:175:LEU:HD12	3:2D:185:VAL:HG21	1.99	0.43
5:2F:120:GLU:CB	5:2F:122:LYS:HG2	2.48	0.43
11:2P:101:VAL:HA	11:2P:106:LEU:O	2.17	0.43
31:29:3:VAL:HA	31:29:35:ARG:O	2.18	0.43
32:2a:56:U:H2'	32:2a:57:G:C8	2.53	0.43
32:2a:737:A:H5''	37:2f:92:LYS:HG3	2.00	0.43
32:2a:1009:G:C2	32:2a:1010:G:C8	3.06	0.43
32:2a:1030(A):G:H1'	32:2a:1030(C):G:C5	2.52	0.43
32:2a:1376:U:O4	38:2g:10:ARG:NH1	2.51	0.43
34:2c:6:HIS:HD2	45:2n:49:HIS:HB3	1.82	0.43
40:2i:18:PHE:O	40:2i:61:ALA:HA	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:2k:20:TYR:CE1	42:2k:83:ILE:HD13	2.54	0.43
42:2k:21:ILE:HB	42:2k:84:VAL:HG22	2.00	0.43
1:1A:1045:A:H1'	1:1A:1047:G:N3	2.33	0.43
1:1A:2464:C:H1'	61:1A:7026:HOH:O	2.18	0.43
3:1D:106:ILE:HG12	61:1D:443:HOH:O	2.17	0.43
5:1F:12:LEU:HD13	5:1F:124:LEU:HD11	2.01	0.43
15:1T:96:ARG:HB3	15:1T:96:ARG:CZ	2.48	0.43
21:1Z:182:LYS:HE2	21:1Z:182:LYS:HB3	1.79	0.43
32:1a:67:C:O2'	32:1a:171:A:H1'	2.17	0.43
32:1a:73:G:H2'	32:1a:76:C:C6	2.53	0.43
39:1h:121:ASP:HB2	39:1h:125:ARG:NH2	2.32	0.43
48:1q:62:SER:CB	48:1q:72:ARG:HD3	2.48	0.43
53:1y:23:ARG:HD3	53:1y:23:ARG:HA	1.78	0.43
1:2A:16:G:H2'	1:2A:17:G:H8	1.83	0.43
1:2A:411:G:C5	11:2P:72:PRO:HB3	2.52	0.43
1:2A:1539:G:H2'	1:2A:1540:U:C6	2.54	0.43
1:2A:1580:A:H8	1:2A:1580:A:OP2	2.00	0.43
1:2A:1638:C:O3'	1:2A:2709:G:N2	2.51	0.43
1:2A:2224:G:H4'	1:2A:2226:C:C2	2.54	0.43
5:2F:192:LEU:HD23	5:2F:192:LEU:HA	1.82	0.43
21:2Z:152:ALA:HB1	21:2Z:163:LEU:HD21	2.00	0.43
32:2a:903:G:OP1	61:2a:3216:HOH:O	2.21	0.43
34:2c:68:VAL:HG12	34:2c:70:VAL:HG23	2.00	0.43
39:2h:6:ILE:HB	39:2h:85:ARG:NH1	2.33	0.43
40:2i:53:VAL:HG11	40:2i:92:TYR:CD1	2.53	0.43
1:1A:614:U:H5'	1:1A:614(C):A:N6	2.34	0.43
1:1A:1766:U:H2'	1:1A:1767:C:C6	2.52	0.43
3:1D:221:VAL:HG22	3:1D:226:MET:HE3	1.99	0.43
13:1R:73:VAL:O	13:1R:77:ARG:HB2	2.18	0.43
21:1Z:7:ALA:O	21:1Z:62:PRO:HD3	2.19	0.43
32:1a:152:A:N6	32:1a:170:U:C2	2.86	0.43
32:1a:266:G:H2'	32:1a:266:G:N3	2.33	0.43
32:1a:273:A:H1'	48:1q:16:GLN:NE2	2.33	0.43
32:1a:452:A:OP1	47:1p:43:LYS:NZ	2.50	0.43
32:1a:1007:C:N3	32:1a:1022:G:O6	2.52	0.43
32:1a:1043:C:H2'	32:1a:1044:A:O4'	2.18	0.43
32:1a:1144:G:O2'	32:1a:1145:C:H5'	2.18	0.43
32:1a:1486:G:H2'	32:1a:1487:G:O4'	2.18	0.43
42:1k:69:ALA:HB1	42:1k:103:LEU:HD12	2.00	0.43
1:2A:57:C:H2'	1:2A:58:G:O4'	2.18	0.43
1:2A:192:C:O2'	1:2A:802:A:N3	2.44	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:832:G:OP1	61:2A:3864:HOH:O	2.21	0.43
1:2A:2119:A:C2	1:2A:2170:A:H2'	2.53	0.43
2:2B:89:G:OP2	2:2B:89:G:H8	2.01	0.43
4:2E:14:ILE:HB	15:2T:14:TYR:CZ	2.54	0.43
8:2I:14:ASP:OD1	8:2I:15:VAL:N	2.51	0.43
14:2S:105:ALA:O	14:2S:110:LEU:HB2	2.18	0.43
32:2a:280:C:N3	48:2q:39:SER:OG	2.47	0.43
32:2a:448:A:P	32:2a:485:G:H22	2.41	0.43
34:2c:5:ILE:HD12	34:2c:6:HIS:H	1.83	0.43
35:2d:155:LEU:HD12	35:2d:156:GLU:H	1.83	0.43
53:2y:54:ILE:HB	53:2y:61:LEU:HD12	2.01	0.43
1:1A:1070:A:O2'	1:1A:1098:A:OP1	2.37	0.43
1:1A:1668:A:H4'	1:1A:1669:A:O5'	2.19	0.43
1:1A:2031:A:C6	1:1A:2498:C:H1'	2.54	0.43
1:1A:2155:G:H3'	1:1A:2156:G:C8	2.53	0.43
1:1A:2319:G:N2	14:1S:3:ARG:HD3	2.14	0.43
1:1A:2572:A:C8	4:1E:144:ARG:HD2	2.53	0.43
1:1A:2695:C:H2'	1:1A:2696:U:C6	2.53	0.43
1:1A:2712:U:O2'	1:1A:2713:A:H5'	2.19	0.43
2:1B:64:C:O2'	61:1B:306:HOH:O	2.21	0.43
7:1H:109:PHE:C	7:1H:111:HIS:H	2.27	0.43
15:1T:106:SER:O	15:1T:110:ILE:HG13	2.19	0.43
16:1U:74:LEU:HD12	16:1U:74:LEU:HA	1.87	0.43
17:1V:14:VAL:HB	17:1V:96:ILE:HG13	2.01	0.43
21:1Z:145:GLU:HB2	21:1Z:148:ASP:OD2	2.18	0.43
26:14:24:THR:OG1	26:14:25:TYR:N	2.52	0.43
32:1a:22:G:H2'	32:1a:23:C:H6	1.83	0.43
32:1a:235:C:H2'	32:1a:236:G:H8	1.84	0.43
32:1a:708:C:H2'	32:1a:709:G:H8	1.83	0.43
32:1a:1054:C:H4'	32:1a:1055:A:O5'	2.18	0.43
32:1a:1320:C:H2'	32:1a:1321:C:O4'	2.19	0.43
43:1l:42:THR:HG22	43:1l:54:LYS:HE3	2.00	0.43
1:2A:530:G:N1	1:2A:2023:G:OP1	2.46	0.43
1:2A:590:A:H2'	1:2A:591:C:C6	2.53	0.43
1:2A:1840:G:C6	1:2A:1841:U:C4	3.07	0.43
1:2A:2110:G:H5''	1:2A:2118:U:O2	2.19	0.43
21:2Z:91:LEU:HG	21:2Z:130:PRO:HG3	2.01	0.43
26:24:64:GLY:C	26:24:66:SER:N	2.77	0.43
32:2a:1122:U:C4	32:2a:1123:A:N7	2.86	0.43
1:1A:569:U:C4	1:1A:570:G:C6	3.07	0.43
1:1A:1702:G:H2'	1:1A:1703:G:O4'	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2069:G:O6	61:1A:4153:HOH:O	2.21	0.43
1:1A:2206:G:OP2	1:1A:2206:G:H4'	2.16	0.43
5:1F:53:THR:HG23	5:1F:55:GLY:H	1.83	0.43
5:1F:132:VAL:HA	5:1F:138:GLU:HB3	2.00	0.43
6:1G:109:VAL:C	6:1G:112:PRO:HD2	2.44	0.43
11:1P:6:LEU:HD23	11:1P:6:LEU:HA	1.87	0.43
32:1a:131:C:H2'	32:1a:132:C:C6	2.53	0.43
32:1a:458:C:H2'	32:1a:460:G:O4'	2.19	0.43
32:1a:657:G:O4'	46:1o:28:GLN:NE2	2.51	0.43
32:1a:669:U:H2'	32:1a:670:G:H8	1.84	0.43
32:1a:718:G:H5'	42:1k:117:ASN:HB2	2.01	0.43
32:1a:1032:G:H2'	32:1a:1033:G:O4'	2.19	0.43
33:1b:69:LEU:HD13	33:1b:91:PRO:HB2	2.00	0.43
33:1b:95:GLN:HG3	33:1b:147:LYS:O	2.19	0.43
36:1e:12:LEU:HB3	36:1e:31:LEU:HB2	1.99	0.43
44:1m:57:ARG:O	44:1m:61:GLU:HG3	2.18	0.43
53:1y:38:HIS:O	53:1y:52:ALA:HA	2.17	0.43
1:2A:1056:G:H21	1:2A:1103:A:H62	1.65	0.43
1:2A:1165:U:H2'	1:2A:1166:C:C6	2.54	0.43
1:2A:1695:G:H1'	3:2D:8:PRO:O	2.17	0.43
1:2A:2153:G:H2'	1:2A:2154:G:H8	1.82	0.43
5:2F:101:LEU:HD12	5:2F:102:PRO:HD2	2.01	0.43
20:2Y:13:VAL:HG12	20:2Y:74:PRO:HA	2.01	0.43
32:2a:41:G:H2'	32:2a:42:G:H8	1.83	0.43
32:2a:730:G:C5	32:2a:731:G:H1'	2.54	0.43
32:2a:1108:G:H5'	34:2c:176:HIS:CD2	2.46	0.43
32:2a:1346:A:N1	32:2a:1374:A:H5''	2.33	0.43
32:2a:1400:5MC:N3	53:2y:63:ALA:HA	2.34	0.43
34:2c:8:ILE:HD13	34:2c:8:ILE:HA	1.83	0.43
39:2h:86:ILE:HG12	39:2h:135:CYS:HA	2.00	0.43
44:2m:88:ARG:HG2	44:2m:98:VAL:HG13	2.00	0.43
1:1A:645:C:H5'	1:1A:646:A:OP2	2.18	0.43
1:1A:2627:G:O2'	1:1A:2781:A:N1	2.40	0.43
4:1E:146:THR:HA	4:1E:147:PRO:HA	1.84	0.43
6:1G:155:MET:HE2	6:1G:155:MET:HB3	1.91	0.43
20:1Y:107:ASP:OD1	20:1Y:107:ASP:N	2.52	0.43
32:1a:570:G:H1'	32:1a:820:U:C4	2.54	0.43
32:1a:1223:C:P	50:1s:78:ARG:HH21	2.42	0.43
33:1b:97:TRP:HZ3	33:1b:99:GLY:HA2	1.82	0.43
40:1i:54:ASP:O	40:1i:56:LEU:N	2.48	0.43
51:1t:45:GLN:HA	51:1t:91:LEU:HD22	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:441:U:H2'	1:2A:442:G:C8	2.54	0.43
1:2A:484:C:H2'	1:2A:485:C:C6	2.54	0.43
1:2A:1064:C:H3'	1:2A:1065:U:H5'	2.01	0.43
1:2A:1178:C:H2'	1:2A:1179:C:C6	2.54	0.43
1:2A:2286:A:OP1	28:26:29:ASN:ND2	2.51	0.43
1:2A:2643:G:H2'	1:2A:2644:G:O4'	2.19	0.43
1:2A:2846:G:P	15:2T:54:ARG:HB2	2.59	0.43
32:2a:175:C:H2'	32:2a:176:C:H6	1.83	0.43
32:2a:192:U:H2'	32:2a:193:C:H6	1.83	0.43
32:2a:684:A:O2'	42:2k:39:PRO:O	2.35	0.43
32:2a:1027:C:C4	32:2a:1034:G:O6	2.71	0.43
32:2a:1154:G:H2'	32:2a:1155:G:C8	2.54	0.43
32:2a:1183:A:H1'	32:2a:1184:G:OP1	2.19	0.43
34:2c:30:ARG:NH1	45:2n:35:ARG:O	2.52	0.43
1:1A:529:A:OP2	9:1N:114:ARG:NH2	2.41	0.43
1:1A:1354:A:H2'	1:1A:1355:G:O4'	2.19	0.43
1:1A:1865:G:O2'	1:1A:1876:A:N7	2.50	0.43
1:1A:2712:U:OP1	1:1A:2714:G:H4'	2.18	0.43
4:1E:119:ARG:HG2	4:1E:160:TYR:CG	2.54	0.43
7:1H:7:LEU:HG	7:1H:69:ARG:NH2	2.34	0.43
11:1P:97:PRO:HD3	11:1P:126:VAL:O	2.18	0.43
15:1T:39:ARG:H	15:1T:39:ARG:HG3	1.61	0.43
35:1d:146:ILE:H	35:1d:146:ILE:HD12	1.84	0.43
40:1i:26:VAL:HG13	40:1i:61:ALA:HB3	2.01	0.43
47:1p:3:LYS:HB3	47:1p:3:LYS:HE2	1.81	0.43
1:2A:328:U:H4'	20:2Y:68:HIS:CD2	2.54	0.43
1:2A:896:A:N1	21:2Z:146:ILE:HD13	2.33	0.43
1:2A:2887:U:H2'	1:2A:2888:C:C6	2.54	0.43
10:2O:68:GLU:HB3	10:2O:78:ARG:HB2	2.01	0.43
10:2O:120:GLU:HG2	10:2O:122:LEU:HG	2.01	0.43
32:2a:189:G:C5	32:2a:189(A):C:C4	3.07	0.43
32:2a:411:A:OP2	35:2d:25:ARG:NH2	2.45	0.43
32:2a:1320:C:H2'	32:2a:1321:C:O4'	2.18	0.43
33:2b:74:LYS:NZ	33:2b:205:ASP:O	2.51	0.43
34:2c:87:LEU:O	34:2c:91:LEU:N	2.47	0.43
35:2d:9:CYS:O	35:2d:13:ARG:HG3	2.19	0.43
49:2r:33:ASP:OD2	49:2r:36:ASN:HB2	2.19	0.43
1:1A:192:C:O2'	1:1A:802:A:N3	2.51	0.43
1:1A:1814:G:H4'	3:1D:51:VAL:HG21	2.01	0.43
1:1A:2439:A:H5'	1:1A:2439:A:C8	2.54	0.43
1:1A:2882:A:OP1	13:1R:96:ARG:HD3	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:1F:20:LEU:HG	5:1F:21:ALA:N	2.34	0.43
6:1G:179:PRO:HG3	26:14:43:TYR:CZ	2.54	0.43
13:1R:104:ARG:HD2	13:1R:107:ASP:OD1	2.19	0.43
32:1a:7:G:O2'	36:1e:120:THR:O	2.37	0.43
32:1a:235:C:H2'	32:1a:236:G:C8	2.54	0.43
32:1a:404:U:H2'	32:1a:405:U:C6	2.54	0.43
33:1b:21:ARG:O	33:1b:23:ARG:N	2.48	0.43
40:1i:9:ARG:HG2	40:1i:14:VAL:HG13	2.01	0.43
1:2A:1059:G:H2'	1:2A:1060:U:C5	2.54	0.43
1:2A:2028:U:H2'	1:2A:2029:G:O4'	2.18	0.43
1:2A:2115:G:H4'	1:2A:2166:G:O2'	2.19	0.43
1:2A:2163:C:H5''	1:2A:2164:C:OP2	2.19	0.43
1:2A:2182:G:H2'	1:2A:2183:C:C6	2.54	0.43
6:2G:145:THR:HG23	6:2G:147:ASP:H	1.84	0.43
8:2I:65:ALA:HB1	8:2I:132:PRO:HG2	2.00	0.43
9:2N:50:ASP:OD1	61:2N:301:HOH:O	2.21	0.43
21:2Z:150:LEU:HB3	21:2Z:171:ILE:HD11	2.01	0.43
32:2a:275:G:H5'	48:2q:14:LYS:HE3	1.99	0.43
32:2a:499:A:H4'	32:2a:500:G:OP1	2.18	0.43
32:2a:1202:G:N2	45:2n:46:GLU:OE2	2.52	0.43
32:2a:1442:G:H1'	32:2a:1442(A):G:OP1	2.19	0.43
32:2a:1530:G:H2'	32:2a:1531:A:C8	2.54	0.43
35:2d:105:VAL:HG13	35:2d:110:PHE:HB2	2.00	0.43
35:2d:118:ARG:O	35:2d:122:ARG:N	2.37	0.43
1:1A:1263:U:C4	1:1A:1264:G:C6	3.07	0.42
1:1A:2157:G:H5''	1:1A:2158:A:OP1	2.19	0.42
1:1A:2294:C:P	14:1S:89:ARG:HH22	2.41	0.42
1:1A:2406:U:H2'	1:1A:2406:U:H6	1.68	0.42
1:1A:2590:A:H2'	1:1A:2591:C:H6	1.84	0.42
1:1A:2784:C:H1'	4:1E:37:ARG:NH1	2.34	0.42
11:1P:94:GLU:HG3	11:1P:124:LYS:HD3	2.00	0.42
21:1Z:141:VAL:HB	21:1Z:144:LEU:HD12	2.01	0.42
32:1a:520:A:N1	32:1a:536:C:H1'	2.34	0.42
38:1g:38:LEU:O	38:1g:42:ILE:HG13	2.20	0.42
47:1p:4:ILE:HA	47:1p:20:VAL:O	2.19	0.42
1:2A:244:A:C2	1:2A:255:A:C4	3.07	0.42
1:2A:1012:U:H5	9:2N:28:THR:HG21	1.81	0.42
1:2A:1022:G:N7	9:2N:66:LYS:HE2	2.34	0.42
1:2A:1428:C:C5	1:2A:1569:A:H5''	2.54	0.42
1:2A:2298:A:N6	1:2A:2318:G:C8	2.87	0.42
1:2A:2321:G:HO2'	1:2A:2322:A:P	2.40	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2408:U:H2'	1:2A:2409:G:C8	2.54	0.42
61:2A:4940:HOH:O	3:2D:48:ARG:HD2	2.19	0.42
4:2E:47:VAL:O	4:2E:80:GLU:HA	2.19	0.42
29:27:35:ARG:HG3	29:27:42:LEU:HD11	2.00	0.42
32:2a:148:G:H2'	32:2a:149:A:C8	2.54	0.42
32:2a:560:U:H5'	32:2a:566:G:N2	2.33	0.42
32:2a:786:G:C2	32:2a:797:C:C2	3.07	0.42
32:2a:1035:A:O2'	32:2a:1036:G:H8	2.01	0.42
32:2a:1325:C:OP1	52:2u:15:ARG:HD3	2.19	0.42
32:2a:1368:G:H5''	40:2i:112:LYS:HB3	2.01	0.42
33:2b:18:GLY:HA2	33:2b:42:ILE:HD12	2.01	0.42
33:2b:187:LEU:H	33:2b:187:LEU:HD23	1.83	0.42
42:2k:73:MET:HG2	42:2k:103:LEU:HD21	2.00	0.42
1:1A:1064:C:C4	1:1A:1074:G:O6	2.72	0.42
1:1A:1174:A:H4'	1:1A:1175:U:OP1	2.19	0.42
1:1A:2101:G:H2'	1:1A:2102:U:O4'	2.19	0.42
1:1A:2562:U:O2'	10:1O:23:ARG:HD3	2.19	0.42
11:1P:100:LEU:HD22	11:1P:105:LEU:HD12	2.00	0.42
11:1P:121:LYS:HB3	11:1P:123:LEU:HG	2.02	0.42
13:1R:13:HIS:CE1	13:1R:16:HIS:HB2	2.54	0.42
21:1Z:3:TYR:CE2	21:1Z:51:ALA:HB2	2.54	0.42
30:18:4:MET:HE2	30:18:4:MET:HB3	1.81	0.42
43:1l:82:VAL:O	43:1l:106:ASP:HB2	2.19	0.42
45:1n:4:LYS:HG3	45:1n:7:ILE:HD11	2.00	0.42
51:1t:30:LYS:HB2	51:1t:30:LYS:HE3	1.61	0.42
1:2A:311:A:C6	1:2A:328:U:C4	3.06	0.42
6:2G:109:VAL:HG11	6:2G:142:PRO:HB3	2.01	0.42
7:2H:41:MET:HE3	7:2H:64:LEU:HB3	2.00	0.42
20:2Y:8:LYS:HG2	20:2Y:97:ARG:NH1	2.33	0.42
32:2a:1442:G:H2'	32:2a:1442:G:N3	2.33	0.42
40:2i:23:ASN:OD1	40:2i:23:ASN:N	2.50	0.42
1:1A:270:A:OP2	1:1A:271(X):G:N1	2.49	0.42
1:1A:1061:U:H3'	1:1A:1062:G:C5'	2.49	0.42
1:1A:1452:A:H5''	61:1A:5925:HOH:O	2.18	0.42
1:1A:1889:A:H2'	1:1A:1890:A:C8	2.55	0.42
1:1A:2537:U:H2'	1:1A:2538:C:C6	2.55	0.42
2:1B:32:C:C2	2:1B:51:G:N2	2.88	0.42
3:1D:123:ALA:HB3	3:1D:131:LEU:HG	2.02	0.42
7:1H:3:ARG:HH11	7:1H:4:ILE:H	1.67	0.42
15:1T:39:ARG:NH2	32:1a:345:C:H5''	2.34	0.42
21:1Z:136:PHE:CE1	21:1Z:138:GLU:HG3	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:12:56:GLN:O	24:12:60:LEU:HG	2.20	0.42
26:14:55:ARG:N	26:14:56:VAL:HA	2.34	0.42
32:1a:736:C:H2'	32:1a:737:A:C8	2.53	0.42
32:1a:814:A:N7	32:1a:816:A:C4	2.87	0.42
32:1a:1033:G:H2'	32:1a:1034:G:C8	2.55	0.42
32:1a:1342:C:H2'	32:1a:1343:G:H8	1.85	0.42
32:1a:1366:C:H2'	32:1a:1367:C:C6	2.54	0.42
33:1b:24:TRP:CZ3	33:1b:26:PRO:HA	2.54	0.42
33:1b:50:GLU:O	33:1b:54:THR:N	2.41	0.42
38:1g:75:VAL:HG11	38:1g:144:MET:HG3	2.00	0.42
43:1l:47:LYS:HA	43:1l:48:PRO:HA	1.79	0.42
53:1y:3:MET:HG3	53:1y:37:PRO:HG2	2.01	0.42
1:2A:42:G:H2'	1:2A:43:A:O4'	2.18	0.42
1:2A:483:A:O4'	20:2Y:48:ALA:HB1	2.19	0.42
1:2A:1588:C:H2'	1:2A:1589:C:C6	2.55	0.42
1:2A:1952:A:N3	10:2O:22:ILE:HD12	2.34	0.42
1:2A:2298:A:H2'	1:2A:2299:G:O4'	2.18	0.42
1:2A:2312:U:OP1	6:2G:73:ALA:HA	2.19	0.42
5:2F:167:ALA:HB1	5:2F:173:VAL:HG11	1.99	0.42
21:2Z:7:ALA:O	21:2Z:62:PRO:HD3	2.19	0.42
32:2a:344:A:O5'	32:2a:345:C:H5	2.02	0.42
32:2a:1446:U:O2'	32:2a:1447:A:C8	2.72	0.42
33:2b:59:GLU:HB2	33:2b:221:LEU:HD21	2.00	0.42
35:2d:61:LYS:HD2	35:2d:207:TYR:OH	2.19	0.42
43:2l:10:LEU:HD21	43:2l:15:ARG:NE	2.34	0.42
1:1A:1210:A:H5''	1:1A:1212:G:O4'	2.20	0.42
1:1A:1417:C:H2'	1:1A:1418:G:O4'	2.19	0.42
1:1A:2112:G:H8	1:1A:2112:G:OP2	2.02	0.42
1:1A:2206:G:H8	1:1A:2207:G:N2	2.17	0.42
1:1A:2591:C:H2'	1:1A:2592:G:C8	2.55	0.42
1:1A:2895:U:H2'	1:1A:2896:C:C6	2.54	0.42
3:1D:13:ARG:HA	3:1D:13:ARG:HD2	1.72	0.42
5:1F:136:THR:HG22	5:1F:140:LEU:HD22	2.01	0.42
9:1N:15:LEU:HB2	9:1N:135:PRO:HB2	2.01	0.42
15:1T:117:ASP:OD2	15:1T:120:ARG:NE	2.45	0.42
32:1a:448:A:C4	32:1a:487:A:C2	3.08	0.42
32:1a:953:G:N7	44:1m:104:ARG:NH2	2.55	0.42
32:1a:1264:C:H2'	32:1a:1265:G:C8	2.54	0.42
32:1a:1469:G:H2'	32:1a:1470:G:H8	1.83	0.42
34:1c:34:LEU:HG	34:1c:38:ARG:HD2	2.01	0.42
35:1d:194:LEU:HD13	35:1d:194:LEU:HA	1.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:1f:89:MET:HE1	49:1r:72:ARG:HB3	2.01	0.42
37:1f:99:ALA:HB1	49:1r:23:LYS:HE3	2.01	0.42
38:1g:101:LEU:O	38:1g:105:VAL:HG23	2.19	0.42
1:2A:484:C:H2'	1:2A:485:C:H6	1.85	0.42
1:2A:947:G:N2	1:2A:971:C:C2	2.88	0.42
1:2A:1139:G:O2'	1:2A:1143:A:N1	2.50	0.42
1:2A:1153:C:OP2	61:2A:3844:HOH:O	2.21	0.42
1:2A:1270:C:H5''	1:2A:1271:G:O5'	2.19	0.42
1:2A:1417:C:H2'	1:2A:1418:G:O4'	2.19	0.42
1:2A:1429:G:H2'	1:2A:1430:C:C6	2.54	0.42
3:2D:206:LEU:HD23	3:2D:206:LEU:HA	1.81	0.42
19:2X:3:THR:HG21	24:22:26:ARG:HG3	2.02	0.42
20:2Y:8:LYS:HD3	20:2Y:97:ARG:NH2	2.34	0.42
24:22:59:ARG:NH1	61:22:101:HOH:O	2.51	0.42
32:2a:624:C:H2'	32:2a:625:G:H8	1.84	0.42
32:2a:631:G:H2'	32:2a:632:A:O4'	2.20	0.42
32:2a:828:A:H2'	32:2a:829:G:O4'	2.19	0.42
32:2a:858:G:O6	32:2a:869:G:H3'	2.20	0.42
49:2r:56:THR:HB	49:2r:58:LEU:HD13	2.01	0.42
1:1A:7:G:H2'	1:1A:8:A:O4'	2.19	0.42
1:1A:1009:A:O4'	16:1U:59:ARG:HG2	2.19	0.42
1:1A:1188:U:H5'	17:1V:79:VAL:HG13	2.01	0.42
1:1A:1212:G:O6	61:1A:4152:HOH:O	2.21	0.42
1:1A:2405:G:O2'	1:1A:2411:A:N6	2.52	0.42
8:1I:72:LEU:HD12	8:1I:138:ILE:HG21	2.02	0.42
8:1I:101:LEU:HD23	8:1I:101:LEU:HA	1.93	0.42
32:1a:184:G:H2'	32:1a:185:A:C8	2.54	0.42
32:1a:473:G:H2'	32:1a:474:G:C8	2.55	0.42
32:1a:840:C:H5''	32:1a:841:U:C4	2.54	0.42
32:1a:946:A:O2'	32:1a:1333:A:N3	2.49	0.42
32:1a:986:A:H1'	50:1s:54:GLY:O	2.19	0.42
32:1a:1158:C:C5	32:1a:1181:G:N1	2.86	0.42
32:1a:1304:G:C6	32:1a:1305:G:N1	2.88	0.42
32:1a:1323:G:H2'	32:1a:1324:A:C8	2.53	0.42
34:1c:124:ILE:HG22	34:1c:130:VAL:HG22	2.00	0.42
36:1e:66:MET:HE3	36:1e:66:MET:HB3	1.82	0.42
1:2A:41:C:H2'	1:2A:42:G:H8	1.85	0.42
1:2A:1103:A:H2'	1:2A:1104:C:O4'	2.19	0.42
1:2A:2544:G:H2'	1:2A:2545:G:O4'	2.18	0.42
4:2E:72:VAL:HG12	4:2E:73:GLU:O	2.19	0.42
5:2F:178:PRO:HG2	5:2F:179:GLU:OE2	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:2G:96:ARG:N	6:2G:99:MET:HE2	2.35	0.42
12:2Q:87:LYS:HG3	12:2Q:88:GLY:N	2.34	0.42
15:2T:45:PHE:CE1	15:2T:65:LYS:HD3	2.54	0.42
23:21:50:ARG:HG2	23:21:59:THR:CG2	2.50	0.42
24:22:51:ARG:O	24:22:55:ARG:HG3	2.18	0.42
30:28:26:LYS:HD2	30:28:48:PHE:CD2	2.54	0.42
31:29:29:ASN:HB3	31:29:32:HIS:ND1	2.34	0.42
32:2a:130:A:H1'	32:2a:263:A:O2'	2.20	0.42
32:2a:130:A:H5'	48:2q:63:ARG:HE	1.84	0.42
32:2a:162:A:C5	32:2a:163:C:H1'	2.54	0.42
32:2a:685:G:N1	32:2a:686:U:O4	2.53	0.42
32:2a:841:U:OP1	32:2a:841:U:H6	2.03	0.42
32:2a:1090:U:H2'	32:2a:1091:U:C6	2.55	0.42
32:2a:1101:A:H4'	32:2a:1102:A:O5'	2.19	0.42
33:2b:158:LEU:HD12	33:2b:158:LEU:HA	1.87	0.42
34:2c:9:GLY:HA3	45:2n:49:HIS:HA	2.00	0.42
38:2g:57:GLU:HG3	38:2g:60:LYS:H	1.85	0.42
44:2m:96:LEU:C	44:2m:110:ARG:HG2	2.44	0.42
50:2s:22:LEU:HA	50:2s:22:LEU:HD13	1.78	0.42
1:1A:2336:A:H61	22:10:43:THR:CG2	2.32	0.42
1:1A:2751:G:H4'	7:1H:4:ILE:HD11	2.00	0.42
5:1F:74:ARG:HG3	5:1F:74:ARG:H	1.42	0.42
6:1G:39:ILE:O	6:1G:91:ARG:HA	2.20	0.42
6:1G:47:LYS:HB2	6:1G:86:MET:HE1	2.02	0.42
11:1P:119:GLU:HG3	25:23:3:ARG:HH21	1.85	0.42
13:1R:38:VAL:HG22	13:1R:112:ALA:HB2	2.02	0.42
15:1T:7:ILE:HG22	15:1T:11:GLU:OE1	2.20	0.42
20:1Y:7:VAL:HG21	20:1Y:72:VAL:HG12	2.01	0.42
32:1a:297:G:H4'	32:1a:557:G:H4'	2.01	0.42
32:1a:486:U:H2'	32:1a:487:A:C8	2.55	0.42
35:1d:23:GLY:N	35:1d:26:CYS:SG	2.90	0.42
35:1d:150:GLU:HG3	35:1d:151:LYS:N	2.35	0.42
35:1d:188:LEU:HA	35:1d:189:PRO:HD3	1.90	0.42
35:1d:196:LEU:O	35:1d:198:VAL:N	2.49	0.42
36:1e:45:PHE:CE2	36:1e:47:LYS:HE3	2.55	0.42
37:1f:99:ALA:O	49:1r:28:GLU:HA	2.19	0.42
41:1j:81:THR:C	41:1j:83:GLU:H	2.27	0.42
1:2A:1087:G:H22	1:2A:1102:C:N4	2.17	0.42
1:2A:1550:C:OP1	1:2A:1720:U:O2'	2.30	0.42
1:2A:2373:G:OP1	61:2A:3862:HOH:O	2.21	0.42
1:2A:2788:C:N3	1:2A:2789:C:N4	2.67	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:2E:36:ARG:NH2	4:2E:88:GLY:O	2.53	0.42
7:2H:3:ARG:HH22	7:2H:66:GLY:H	1.66	0.42
8:2I:93:THR:H	8:2I:96:ASP:HB2	1.84	0.42
32:2a:115:G:H4'	32:2a:116:A:O5'	2.19	0.42
32:2a:189:G:C6	32:2a:189(A):C:C4	3.08	0.42
35:2d:184:LYS:HG2	35:2d:186:LEU:HD23	2.01	0.42
37:2f:35:ALA:HB2	37:2f:67:MET:HE2	2.02	0.42
1:1A:93:G:H2'	1:1A:94:C:C6	2.55	0.42
1:1A:1020:A:N1	1:1A:1141:U:O2'	2.48	0.42
1:1A:1173:G:C2	1:1A:1175:U:H4'	2.55	0.42
1:1A:2183:C:H2'	1:1A:2184:G:C8	2.53	0.42
1:1A:2441:C:OP2	1:1A:2586:C:O2'	2.36	0.42
1:1A:2846:G:H2'	1:1A:2847:U:O4'	2.20	0.42
4:1E:143:ASN:HD22	4:1E:147:PRO:HD3	1.85	0.42
8:1I:81:VAL:O	8:1I:146:ALA:HA	2.20	0.42
32:1a:179:A:H2'	32:1a:180:U:C6	2.55	0.42
32:1a:858:G:O6	32:1a:869:G:H3'	2.20	0.42
32:1a:1084:G:C5	32:1a:1085:U:C4	3.08	0.42
32:1a:1343:G:H2'	32:1a:1344:C:C6	2.55	0.42
32:1a:1513:A:H2'	32:1a:1514:C:C6	2.54	0.42
35:1d:30:LYS:HA	35:1d:35:ARG:NE	2.31	0.42
35:1d:32:ALA:HB3	60:1d:307:SF4:S2	2.60	0.42
38:1g:50:ILE:HD11	38:1g:58:PRO:HB3	2.00	0.42
40:1i:18:PHE:N	40:1i:62:TYR:O	2.36	0.42
43:1l:102:ARG:HA	43:1l:102:ARG:HD2	1.79	0.42
1:2A:662:G:H5''	11:2P:16:ARG:HG3	2.02	0.42
1:2A:882:G:H2'	1:2A:883:G:O4'	2.19	0.42
1:2A:1518:U:H2'	1:2A:1519:G:O4'	2.20	0.42
1:2A:2126:A:N1	1:2A:2162:G:O2'	2.50	0.42
1:2A:2314:C:H2'	1:2A:2315:G:H8	1.84	0.42
1:2A:2441:C:OP2	1:2A:2586:C:O2'	2.30	0.42
6:2G:115:ARG:HD3	6:2G:136:ARG:NH2	2.35	0.42
9:2N:20:GLY:HA2	9:2N:61:ARG:HG3	2.00	0.42
32:2a:1039:C:H2'	32:2a:1040:U:O4'	2.20	0.42
32:2a:1301:U:O2'	32:2a:1302:U:H5'	2.20	0.42
44:2m:91:ARG:O	44:2m:96:LEU:N	2.48	0.42
46:2o:87:ILE:HG22	46:2o:88:ARG:N	2.35	0.42
47:2p:41:PRO:O	47:2p:43:LYS:HE2	2.20	0.42
53:2y:85:LEU:O	53:2y:89:GLN:HG2	2.20	0.42
1:1A:1843:C:H5'	3:1D:253:GLN:NE2	2.35	0.42
2:1B:29:A:H2'	2:1B:30:C:O4'	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:1P:100:LEU:HD23	11:1P:100:LEU:HA	1.85	0.42
11:1P:144:GLU:OE1	61:1P:302:HOH:O	2.22	0.42
61:1U:309:HOH:O	17:1V:13:ARG:HD2	2.19	0.42
32:1a:324:G:N2	32:1a:326:G:H3'	2.35	0.42
32:1a:632:A:OP1	39:1h:98:LYS:NZ	2.52	0.42
32:1a:633:G:H2'	32:1a:634:C:C6	2.55	0.42
32:1a:1277:C:H1'	32:1a:1282:C:O2	2.20	0.42
34:1c:19:GLU:HG2	34:1c:54:ARG:CZ	2.49	0.42
34:1c:45:LYS:HE3	34:1c:45:LYS:HB2	1.76	0.42
36:1e:31:LEU:HD23	36:1e:31:LEU:HA	1.83	0.42
48:1q:62:SER:HB3	48:1q:72:ARG:HH11	1.85	0.42
1:2A:415:A:H2'	1:2A:416:C:O4'	2.20	0.42
1:2A:478:A:N1	1:2A:500:G:H4'	2.34	0.42
1:2A:1076:C:H1'	1:2A:1077:A:H5'	2.02	0.42
1:2A:1469:A:H2'	1:2A:1470:G:O4'	2.20	0.42
1:2A:2243:U:H2'	1:2A:2244:U:C6	2.55	0.42
11:2P:114:ILE:HG13	11:2P:125:VAL:HG11	2.01	0.42
32:2a:29:G:O2'	32:2a:295:C:H4'	2.20	0.42
32:2a:221:C:H2'	32:2a:222:U:H6	1.85	0.42
32:2a:382:A:H2'	32:2a:383:A:C8	2.55	0.42
32:2a:1026:G:N3	32:2a:1026:G:H2'	2.34	0.42
32:2a:1340:A:OP1	53:2y:57:PRO:HB3	2.19	0.42
33:2b:16:HIS:ND1	33:2b:16:HIS:C	2.76	0.42
33:2b:30:ARG:NH2	33:2b:194:PRO:HB2	2.34	0.42
33:2b:93:VAL:HG21	33:2b:97:TRP:CD1	2.54	0.42
34:2c:35:GLU:O	34:2c:39:ILE:HG13	2.20	0.42
34:2c:152:ILE:HG12	34:2c:199:LYS:HB2	2.00	0.42
35:2d:15:GLU:OE2	35:2d:66:ARG:NH1	2.52	0.42
39:2h:33:GLU:HG2	39:2h:48:TYR:CE1	2.55	0.42
45:2n:21:TYR:HE1	45:2n:23:ARG:NE	2.17	0.42
1:1A:184:C:H2'	1:1A:185:U:H6	1.83	0.42
1:1A:323:G:C8	5:1F:171:PRO:HG3	2.55	0.42
1:1A:918:A:N3	2:1B:80:U:O2'	2.49	0.42
1:1A:1131:G:H21	9:1N:73:THR:CG2	2.33	0.42
1:1A:1472:A:H2'	1:1A:1473:G:O4'	2.20	0.42
1:1A:1914:C:H2'	1:1A:1915:5MU:O4'	2.20	0.42
1:1A:2443:C:O2'	1:1A:2444:G:H5'	2.19	0.42
21:1Z:75:ASN:O	21:1Z:84:GLU:HG2	2.20	0.42
24:12:3:LEU:HD23	24:12:3:LEU:HA	1.84	0.42
32:1a:90:U:H2'	32:1a:91:C:C6	2.55	0.42
32:1a:615:C:C2	32:1a:616:G:C8	3.08	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1014:A:H3'	32:1a:1015:A:C8	2.55	0.42
32:1a:1015:A:C6	32:1a:1016:A:C6	3.07	0.42
33:1b:18:GLY:HA3	33:1b:42:ILE:HG13	2.02	0.42
34:1c:101:LEU:C	34:1c:102:ASN:HD22	2.28	0.42
36:1e:41:VAL:HG23	36:1e:67:VAL:HG13	2.02	0.42
44:1m:4:ILE:HG22	44:1m:57:ARG:HG3	2.01	0.42
49:1r:56:THR:HB	49:1r:58:LEU:HD13	2.01	0.42
1:2A:275:G:H2'	1:2A:276:A:O4'	2.20	0.42
1:2A:286:C:H2'	1:2A:287:C:C6	2.54	0.42
1:2A:479:A:N3	1:2A:481:G:H5''	2.34	0.42
1:2A:784:A:C8	1:2A:792:G:C5	3.08	0.42
1:2A:1218:C:OP1	61:2A:3863:HOH:O	2.21	0.42
1:2A:1288:U:O2'	1:2A:1647:G:N2	2.53	0.42
1:2A:2262:U:H4'	1:2A:2328:A:H2	1.84	0.42
3:2D:68:LYS:O	3:2D:70:TRP:N	2.48	0.42
7:2H:154:PRO:HB3	7:2H:163:TYR:CZ	2.55	0.42
15:2T:91:ARG:HB2	15:2T:121:ILE:HG13	2.02	0.42
17:2V:52:VAL:CG2	17:2V:55:ALA:HB3	2.50	0.42
26:24:44:THR:O	26:24:46:GLN:N	2.53	0.42
32:2a:404:U:OP1	35:2d:118:ARG:NH2	2.52	0.42
32:2a:721:G:H4'	32:2a:722:A:O4'	2.19	0.42
32:2a:841:U:H6	32:2a:841:U:P	2.43	0.42
32:2a:918:A:H2'	32:2a:919:A:C8	2.54	0.42
32:2a:1328:C:OP1	52:2u:21:TYR:OH	2.36	0.42
32:2a:1349:A:C4	32:2a:1350:A:C8	3.08	0.42
38:2g:95:ARG:NH2	38:2g:99:LEU:HD21	2.35	0.42
39:2h:82:HIS:N	39:2h:138:TRP:O	2.51	0.42
1:1A:242:G:C8	30:18:5:LYS:HG2	2.55	0.42
1:1A:784:A:C8	1:1A:792:G:C5	3.08	0.42
1:1A:1045:A:H1'	1:1A:1047:G:C2	2.54	0.42
1:1A:2650:U:H2'	1:1A:2651:C:C6	2.54	0.42
2:1B:38:C:H5'	61:1B:360:HOH:O	2.20	0.42
4:1E:143:ASN:HD22	4:1E:147:PRO:CD	2.33	0.42
5:1F:185:ASP:OD1	5:1F:188:ARG:NH1	2.38	0.42
6:1G:106:LEU:HD12	6:1G:110:ALA:HB3	2.01	0.42
8:1I:132:PRO:HD2	8:1I:136:VAL:O	2.19	0.42
32:1a:112:G:H4'	32:1a:389:A:H4'	2.00	0.42
32:1a:1159:U:C2	32:1a:1182:G:C2	3.08	0.42
32:1a:1183:A:O2'	32:1a:1184:G:OP1	2.30	0.42
32:1a:1500:A:OP1	61:1a:3319:HOH:O	2.21	0.42
33:1b:187:LEU:HD12	33:1b:201:ILE:O	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:1b:224:GLN:HB2	33:1b:229:VAL:HG13	2.02	0.42
36:1e:7:GLU:O	36:1e:34:VAL:HA	2.20	0.42
36:1e:151:LEU:HD11	39:1h:77:GLU:CD	2.45	0.42
1:2A:299:A:N1	1:2A:322:A:O2'	2.36	0.42
1:2A:858:U:O2	1:2A:2268:A:H2'	2.20	0.42
1:2A:890:A:H2'	1:2A:892:G:O4'	2.18	0.42
1:2A:1106:G:H2'	1:2A:1107:G:H8	1.85	0.42
1:2A:1479:G:H5''	1:2A:1560:G:H4'	2.02	0.42
1:2A:1530:C:HO2'	1:2A:1531:C:P	2.42	0.42
1:2A:2037:G:H2'	1:2A:2038:G:C8	2.55	0.42
1:2A:2238:G:H2'	1:2A:2238:G:N3	2.35	0.42
1:2A:2889:C:H2'	1:2A:2891:G:O4'	2.19	0.42
61:2A:4265:HOH:O	11:2P:29:LYS:HG3	2.20	0.42
3:2D:137:PRO:O	3:2D:140:THR:HG23	2.20	0.42
8:2I:129:THR:HA	8:2I:138:ILE:O	2.20	0.42
9:2N:75:TYR:CE2	9:2N:77:GLY:HA2	2.55	0.42
32:2a:784:C:H2'	32:2a:785:G:O4'	2.20	0.42
32:2a:932:C:H2'	32:2a:933:G:C8	2.54	0.42
32:2a:1002:G:C2	32:2a:1003:G:C8	3.08	0.42
41:2j:37:PRO:HA	41:2j:72:VAL:HG12	2.02	0.42
43:2l:10:LEU:HD21	43:2l:15:ARG:HE	1.85	0.42
47:2p:51:VAL:O	47:2p:53:VAL:N	2.52	0.42
1:1A:388:G:O2'	1:1A:389:G:N7	2.50	0.41
1:1A:795:C:H2'	1:1A:796:C:C6	2.55	0.41
1:1A:829:A:N7	1:1A:2248:C:H5'	2.35	0.41
1:1A:2285:C:OP2	28:16:6:ARG:NH1	2.52	0.41
1:1A:2365:G:O6	30:18:39:LYS:HE3	2.20	0.41
3:1D:127:VAL:HA	3:1D:193:VAL:HG22	2.01	0.41
5:1F:39:TRP:CH2	5:1F:106:ARG:HD3	2.55	0.41
11:1P:82:GLY:HA2	11:1P:113:LYS:O	2.19	0.41
11:1P:84:ASN:HD22	11:1P:86:LYS:NZ	2.17	0.41
32:1a:189(G):G:H8	32:1a:189(G):G:OP1	2.03	0.41
32:1a:1004:A:O2'	32:1a:1038:C:O2	2.24	0.41
32:1a:1226:C:H4'	50:1s:80:TYR:OH	2.20	0.41
40:1i:71:SER:HA	40:1i:74:ILE:HD12	2.02	0.41
42:1k:18:ARG:HB2	42:1k:33:THR:OG1	2.20	0.41
47:1p:75:ARG:HG3	47:1p:80:PHE:CD2	2.55	0.41
1:2A:83:G:H1	1:2A:102:G:HO2'	1.63	0.41
1:2A:150:C:H2'	1:2A:151:C:C6	2.55	0.41
1:2A:315:G:H2'	1:2A:316:C:C6	2.54	0.41
1:2A:2123:G:C6	1:2A:2175:C:N3	2.88	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2279:G:O6	22:20:14:ARG:HD2	2.19	0.41
1:2A:2404:C:O3'	11:2P:77:ARG:NH2	2.53	0.41
1:2A:2420:C:OP1	30:28:34:TRP:HB3	2.19	0.41
61:2A:3864:HOH:O	11:2P:37:GLY:HA3	2.20	0.41
12:2Q:21:THR:HG21	12:2Q:101:ARG:HD3	2.02	0.41
32:2a:457:C:H2'	32:2a:458:C:H6	1.85	0.41
32:2a:620:C:H2'	32:2a:621:A:O4'	2.20	0.41
32:2a:741:G:H2'	32:2a:742:G:O4'	2.20	0.41
32:2a:939:G:H2'	32:2a:940:C:C6	2.55	0.41
32:2a:971:G:N2	32:2a:1363(A):A:OP2	2.48	0.41
32:2a:1411:C:H2'	32:2a:1412:C:H6	1.85	0.41
33:2b:216:SER:O	33:2b:220:ASP:N	2.33	0.41
1:1A:84:A:OP2	20:1Y:8:LYS:NZ	2.47	0.41
1:1A:2563:U:H4'	10:1O:28:SER:HA	2.03	0.41
7:1H:86:GLU:CD	7:1H:132:ARG:HH21	2.28	0.41
10:1O:68:GLU:HB3	10:1O:78:ARG:HB2	2.01	0.41
14:1S:48:LEU:HD23	14:1S:82:ILE:HD11	2.01	0.41
21:1Z:46:LYS:HE3	21:1Z:46:LYS:HB3	1.95	0.41
49:1r:26:LEU:HD23	49:1r:29:PHE:CE2	2.54	0.41
53:1y:30:TRP:CZ2	53:1y:86:ASN:HB2	2.55	0.41
1:2A:196:A:N3	1:2A:196:A:H2'	2.35	0.41
1:2A:566:U:H2'	1:2A:567:A:O4'	2.20	0.41
1:2A:965:C:OP2	61:2A:3867:HOH:O	2.21	0.41
1:2A:1009:A:OP2	9:2N:37:LYS:NZ	2.50	0.41
1:2A:1290:C:H2'	1:2A:1291:C:C6	2.55	0.41
1:2A:1668:A:H4'	1:2A:1669:A:O5'	2.20	0.41
1:2A:2119:A:C2	1:2A:2171:A:H5'	2.56	0.41
5:2F:36:VAL:O	5:2F:40:GLN:HG3	2.20	0.41
7:2H:24:VAL:HG21	7:2H:72:ILE:HG12	2.02	0.41
7:2H:127:GLU:C	7:2H:129:THR:H	2.27	0.41
20:2Y:1:MET:HE2	20:2Y:1:MET:HB3	1.93	0.41
20:2Y:38:ILE:HD11	20:2Y:66:PRO:HG3	2.02	0.41
32:2a:189(L):G:H2'	32:2a:190:U:H6	1.85	0.41
32:2a:685:G:O2'	32:2a:686:U:H5'	2.20	0.41
32:2a:853:G:C4	32:2a:854:G:C8	3.09	0.41
32:2a:1052:U:O2'	32:2a:1055:A:OP2	2.23	0.41
32:2a:1362:C:H2'	32:2a:1363:C:H5''	2.01	0.41
36:2e:78:HIS:HA	39:2h:105:ARG:HG3	2.02	0.41
47:2p:18:ARG:HD3	47:2p:35:LYS:HD2	2.01	0.41
50:2s:31:ILE:HB	50:2s:49:ILE:HG13	2.03	0.41
1:1A:1541:G:O6	61:1A:4154:HOH:O	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2143:C:H2'	1:1A:2144:U:H4'	2.02	0.41
1:1A:2590:A:H2'	1:1A:2591:C:C6	2.56	0.41
6:1G:103:LEU:HD23	6:1G:103:LEU:HA	1.88	0.41
32:1a:834:C:C2	32:1a:853:G:C2	3.09	0.41
34:1c:150:LYS:HE3	34:1c:150:LYS:HB2	1.77	0.41
36:1e:5:ASP:OD1	36:1e:5:ASP:N	2.53	0.41
51:1t:25:ARG:O	51:1t:29:LYS:HG3	2.20	0.41
1:2A:1448:G:H1'	1:2A:1528:A:N1	2.34	0.41
1:2A:1818:U:O2'	3:2D:154:LYS:O	2.36	0.41
1:2A:1903:G:OP1	3:2D:241:PRO:HB2	2.20	0.41
1:2A:2186:G:C2	1:2A:2187:G:C5	3.08	0.41
2:2B:90:A:C5	2:2B:91:C:H1'	2.56	0.41
7:2H:98:LEU:HD12	7:2H:102:ALA:O	2.21	0.41
15:2T:84:GLN:HG2	15:2T:85:LYS:HD3	2.01	0.41
16:2U:16:LYS:HE2	16:2U:16:LYS:HB3	1.76	0.41
19:2X:65:ARG:HE	19:2X:70:LEU:HD21	1.85	0.41
24:22:58:ALA:O	24:22:62:THR:OG1	2.35	0.41
32:2a:148:G:H2'	32:2a:149:A:H8	1.83	0.41
32:2a:451:A:N6	32:2a:480:U:H2'	2.36	0.41
32:2a:1411:C:H2'	32:2a:1412:C:C6	2.55	0.41
45:2n:22:THR:O	45:2n:33:VAL:HG21	2.20	0.41
47:2p:1:MET:HE2	47:2p:1:MET:N	2.36	0.41
1:1A:278:A:H2'	1:1A:279:C:C6	2.55	0.41
1:1A:1056:G:N1	1:1A:1102:C:OP2	2.49	0.41
1:1A:1064:C:N4	1:1A:1065:U:C2	2.88	0.41
1:1A:1798:U:H5'	3:1D:259:THR:CG2	2.41	0.41
1:1A:2130:U:O2'	1:1A:2133:G:O2'	2.36	0.41
2:1B:78:A:C2	2:1B:100:A:C4	3.08	0.41
32:1a:51:A:N7	32:1a:114:U:O2'	2.53	0.41
32:1a:130:A:H1'	32:1a:263:A:O2'	2.19	0.41
32:1a:189(K):U:H2'	32:1a:189(L):G:H8	1.85	0.41
32:1a:688:G:O2'	32:1a:704:A:N1	2.40	0.41
32:1a:779:C:H2'	32:1a:780:A:O4'	2.21	0.41
32:1a:1425:U:H2'	32:1a:1426:C:H6	1.85	0.41
44:1m:11:ARG:C	44:1m:13:LYS:N	2.78	0.41
1:2A:271(R):G:H5''	23:21:97:LEU:HD21	2.01	0.41
1:2A:304:G:O6	61:2A:3859:HOH:O	2.21	0.41
1:2A:1000:A:H62	1:2A:1154:G:H2'	1.85	0.41
1:2A:2875:C:O2'	15:2T:2:ASN:OD1	2.29	0.41
3:2D:148:GLU:HB2	3:2D:151:LYS:HD2	2.01	0.41
7:2H:117:PRO:HG3	7:2H:123:PHE:CE2	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:2T:53:ARG:HB3	15:2T:53:ARG:NH1	2.35	0.41
20:2Y:38:ILE:HD13	20:2Y:66:PRO:HA	2.02	0.41
21:2Z:132:ASN:O	21:2Z:134:PRO:HD3	2.21	0.41
26:24:57:GLU:HA	26:24:58:ARG:HA	1.62	0.41
32:2a:547:A:H5'	61:2a:3209:HOH:O	2.20	0.41
32:2a:792:A:H4'	32:2a:793:U:O5'	2.20	0.41
32:2a:967:5MC:H2'	32:2a:968:A:C8	2.56	0.41
33:2b:152:PHE:CE1	33:2b:155:LEU:HD23	2.55	0.41
34:2c:30:ARG:HH12	45:2n:35:ARG:HA	1.84	0.41
46:2o:11:VAL:HG21	46:2o:34:LEU:HD22	2.02	0.41
1:1A:864:G:N2	1:1A:913:U:C2	2.89	0.41
1:1A:2135:A:H62	1:1A:2156:G:H21	1.69	0.41
1:1A:2138:C:H2'	1:1A:2139:C:C6	2.56	0.41
6:1G:50:ALA:C	6:1G:52:ILE:H	2.27	0.41
7:1H:105:LEU:HD12	7:1H:151:ILE:HD12	2.03	0.41
15:1T:53:ARG:O	15:1T:59:THR:HA	2.21	0.41
20:1Y:30:VAL:HG13	20:1Y:37:VAL:HG12	2.02	0.41
26:14:7:PRO:HB2	26:14:27:THR:CG2	2.50	0.41
32:1a:77:G:C2'	32:1a:78:G:H5'	2.50	0.41
32:1a:141:A:H1'	32:1a:182:U:O2	2.21	0.41
32:1a:426:G:OP1	35:1d:38:TYR:OH	2.21	0.41
32:1a:689:C:H2'	32:1a:690:G:O4'	2.21	0.41
32:1a:909:A:H2'	32:1a:910:C:O4'	2.20	0.41
32:1a:926:G:O6	53:1y:87:LYS:HE2	2.21	0.41
32:1a:932:C:H5''	38:1g:4:ARG:CZ	2.51	0.41
32:1a:1070:U:OP1	36:1e:20:GLN:NE2	2.47	0.41
33:1b:41:ILE:HD13	33:1b:41:ILE:HA	1.94	0.41
1:2A:715:G:C2	46:2o:56:LEU:HD21	2.56	0.41
1:2A:720:C:H2'	1:2A:721:C:H6	1.86	0.41
1:2A:999:U:O2'	1:2A:1000:A:H5'	2.21	0.41
1:2A:1096:A:C4	1:2A:1097:U:H5	2.37	0.41
1:2A:1103:A:C6	1:2A:1104:C:C2	3.09	0.41
1:2A:1939:5MU:OP1	1:2A:2604:U:O2'	2.34	0.41
1:2A:2747:G:O6	1:2A:2755:C:H5''	2.20	0.41
6:2G:137:GLU:HB3	6:2G:139:LEU:HG	2.03	0.41
9:2N:62:VAL:CG1	9:2N:66:LYS:HB2	2.51	0.41
10:2O:64:ARG:HB2	10:2O:79:PHE:CD2	2.56	0.41
12:2Q:111:GLU:OE2	12:2Q:133:ARG:NH2	2.44	0.41
25:23:8:LEU:HG	25:23:31:LEU:HD22	2.02	0.41
28:26:35:GLU:HG3	28:26:50:ARG:HG2	2.03	0.41
32:2a:134:A:N1	47:2p:25:ARG:NH2	2.69	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:946:A:H2'	32:2a:947:G:C8	2.56	0.41
32:2a:1001:A:H2'	32:2a:1001(A):G:H8	1.86	0.41
32:2a:1247:U:H1'	32:2a:1291:G:N2	2.35	0.41
32:2a:1279:A:N3	32:2a:1279:A:H2'	2.36	0.41
33:2b:20:GLU:HB2	33:2b:190:THR:OG1	2.20	0.41
35:2d:201:GLN:HE22	36:2e:116:THR:HB	1.84	0.41
37:2f:8:ILE:HD11	37:2f:79:LEU:HD13	2.03	0.41
38:2g:133:GLY:HA2	38:2g:136:LYS:HB2	2.02	0.41
40:2i:6:GLY:O	40:2i:17:VAL:HG12	2.20	0.41
40:2i:42:ARG:HH12	40:2i:75:ASP:CG	2.28	0.41
41:2j:35:SER:HB3	41:2j:73:ASP:HB2	2.02	0.41
43:2l:46:LYS:HE2	43:2l:94:PRO:HG3	2.01	0.41
1:1A:1176:G:H4'	1:1A:1177:A:OP1	2.21	0.41
1:1A:1805:U:O2	3:1D:50:THR:HB	2.20	0.41
1:1A:1932:A:H2'	1:1A:1933:G:O4'	2.21	0.41
1:1A:2389:G:H5''	1:1A:2390:U:O4'	2.21	0.41
3:1D:77:ALA:HB2	3:1D:97:TYR:CD1	2.56	0.41
13:1R:2:ARG:HG2	13:1R:5:LYS:HB2	2.02	0.41
31:19:11:CYS:SG	31:19:13:LYS:HB2	2.60	0.41
32:1a:629:G:H2'	32:1a:630:G:O4'	2.21	0.41
32:1a:1060:C:C4	34:1c:2:GLY:HA3	2.55	0.41
49:1r:30:ASP:HB3	49:1r:33:ASP:HB2	2.02	0.41
51:1t:68:LYS:HB3	51:1t:68:LYS:HE2	1.95	0.41
1:2A:530:G:H4'	1:2A:531:C:OP1	2.20	0.41
1:2A:1112:G:H2'	1:2A:1113:U:O4'	2.20	0.41
1:2A:1354:A:H2'	1:2A:1355:G:O4'	2.20	0.41
1:2A:1357:U:H2'	1:2A:1358:G:O4'	2.21	0.41
4:2E:120:TRP:CD2	4:2E:155:LYS:HG2	2.55	0.41
6:2G:5:VAL:HG12	26:24:25:TYR:CE2	2.56	0.41
14:2S:7:TYR:CZ	14:2S:91:PRO:HG3	2.56	0.41
32:2a:436:C:H2'	32:2a:437:U:O4'	2.21	0.41
32:2a:782:A:O3'	32:2a:1515:C:H4'	2.20	0.41
32:2a:1003:G:C8	32:2a:1004:A:H1'	2.56	0.41
32:2a:1309:G:OP1	44:2m:88:ARG:HD3	2.21	0.41
33:2b:69:LEU:HD13	33:2b:155:LEU:HD22	2.03	0.41
33:2b:164:VAL:HB	33:2b:186:ALA:CB	2.51	0.41
34:2c:32:LEU:HB3	34:2c:59:ARG:NH1	2.36	0.41
35:2d:177:ASP:CG	35:2d:180:GLY:H	2.28	0.41
36:2e:71:LEU:HD11	36:2e:113:ALA:O	2.19	0.41
36:2e:80:ILE:HG22	36:2e:91:LEU:HB2	2.02	0.41
46:2o:39:LEU:HD23	46:2o:39:LEU:HA	1.92	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:264:C:O2'	1:1A:265:A:H2'	2.20	0.41
1:1A:1056:G:H5'	1:1A:1085:A:N1	2.36	0.41
1:1A:1301:A:C8	1:1A:1303:G:C8	3.08	0.41
1:1A:1698:A:N1	61:1A:4301:HOH:O	2.37	0.41
1:1A:2097:C:H2'	1:1A:2098:U:O4'	2.20	0.41
1:1A:2334:G:H4'	1:1A:2335:A:OP2	2.21	0.41
1:1A:2662:A:H5''	1:1A:2663:G:OP2	2.21	0.41
3:1D:260:ARG:NH1	3:1D:267:SER:OG	2.54	0.41
12:1Q:58:PHE:O	12:1Q:60:ARG:N	2.53	0.41
15:1T:91:ARG:HD2	15:1T:120:ARG:NH1	2.35	0.41
17:1V:71:LEU:HA	17:1V:71:LEU:HD23	1.68	0.41
18:1W:33:ARG:NH2	18:1W:52:GLU:OE1	2.41	0.41
32:1a:942:G:C2	32:1a:1342:C:C2	3.08	0.41
32:1a:1380:U:C4	38:1g:3:ARG:HG2	2.56	0.41
34:1c:130:VAL:HG21	34:1c:157:ILE:HG23	2.03	0.41
34:1c:183:ASP:N	34:1c:202:ILE:O	2.51	0.41
37:1f:100:ASN:C	49:1r:28:GLU:HG2	2.46	0.41
43:1l:7:ILE:O	43:1l:11:VAL:HG23	2.21	0.41
49:1r:71:LYS:O	49:1r:75:ILE:HG13	2.21	0.41
1:2A:29:U:H2'	1:2A:30:G:C8	2.56	0.41
1:2A:1149:G:H2'	1:2A:1150:C:C6	2.56	0.41
1:2A:1790:C:H5''	1:2A:1791:A:OP1	2.20	0.41
1:2A:1866:C:H2'	1:2A:1876:A:O4'	2.20	0.41
1:2A:2335:A:C8	1:2A:2337:G:C5	3.08	0.41
1:2A:2875:C:H2'	1:2A:2876:G:O4'	2.21	0.41
5:2F:102:PRO:HB2	5:2F:105:VAL:HG23	2.02	0.41
5:2F:161:GLU:O	5:2F:165:ARG:HG3	2.20	0.41
6:2G:145:THR:HG23	6:2G:147:ASP:N	2.35	0.41
7:2H:27:LYS:HA	7:2H:32:GLU:HA	2.03	0.41
10:2O:80:ASP:CG	15:2T:64:ARG:HH22	2.28	0.41
11:2P:88:LEU:O	11:2P:91:PHE:HD2	2.04	0.41
32:2a:190:U:C2	32:2a:191:G:C8	3.09	0.41
32:2a:719:C:O2'	49:2r:49:LYS:HB3	2.21	0.41
32:2a:947:G:O3'	44:2m:109:THR:OG1	2.39	0.41
32:2a:950:U:H2'	32:2a:951:G:C8	2.56	0.41
32:2a:1212:U:H4'	32:2a:1213:A:C8	2.56	0.41
33:2b:93:VAL:HG11	33:2b:101:MET:HE1	2.00	0.41
34:2c:43:LEU:HD23	34:2c:43:LEU:HA	1.87	0.41
35:2d:108:LEU:HD12	35:2d:108:LEU:HA	1.83	0.41
43:2l:83:VAL:HG21	43:2l:100:ILE:HD13	2.02	0.41
44:2m:92:HIS:CE1	44:2m:98:VAL:HG21	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:2s:40:ILE:HD11	50:2s:74:PHE:HE2	1.85	0.41
1:1A:1292:U:H2'	1:1A:1293:C:C6	2.56	0.41
1:1A:2168:G:C2	1:1A:2171:A:C8	3.09	0.41
1:1A:2187:G:N7	1:1A:2188:C:C4	2.88	0.41
2:1B:108:U:H2'	2:1B:109:C:H5''	2.03	0.41
9:1N:70:LYS:HD3	9:1N:87:LEU:HD22	2.02	0.41
14:1S:58:LEU:HD23	14:1S:58:LEU:HA	1.87	0.41
25:13:39:ASP:CG	25:13:44:ARG:HH21	2.28	0.41
28:16:11:LEU:HB2	28:16:21:TYR:HB2	2.02	0.41
30:18:6:THR:HB	30:18:8:LYS:HE2	2.03	0.41
32:1a:381:C:H2'	32:1a:382:A:O4'	2.21	0.41
32:1a:763:G:H2'	32:1a:764:C:H6	1.86	0.41
33:1b:47:THR:HA	33:1b:202:PRO:HG2	2.03	0.41
33:1b:174:VAL:O	33:1b:178:ARG:HG3	2.21	0.41
34:1c:190:ARG:HB2	34:1c:190:ARG:NH2	2.35	0.41
35:1d:85:LYS:HG3	35:1d:86:LYS:H	1.85	0.41
36:1e:101:ILE:HG13	36:1e:119:LEU:HD23	2.03	0.41
38:1g:28:ASN:HD21	38:1g:36:LYS:NZ	2.19	0.41
44:1m:80:ARG:O	44:1m:84:ILE:HG23	2.21	0.41
48:1q:56:VAL:HG23	48:1q:81:ARG:HG3	2.01	0.41
1:2A:992:C:OP1	16:2U:47:TYR:OH	2.30	0.41
1:2A:997:G:OP2	16:2U:58:ARG:NH1	2.53	0.41
1:2A:1316:U:H2'	1:2A:1317:A:H8	1.85	0.41
1:2A:1507:A:HO2'	1:2A:1508:A:P	2.42	0.41
1:2A:2119:A:O2'	1:2A:2120:G:H5'	2.21	0.41
1:2A:2122:U:H3	1:2A:2176:A:N6	2.13	0.41
1:2A:2128:C:N4	1:2A:2160:G:H1	2.18	0.41
6:2G:135:LEU:HD13	6:2G:140:ILE:HD11	2.01	0.41
13:2R:36:THR:HG22	13:2R:37:THR:H	1.86	0.41
32:2a:19:C:H5''	36:2e:86:ALA:HB3	2.03	0.41
32:2a:130:A:N3	32:2a:263:A:O2'	2.50	0.41
32:2a:671:G:H2'	32:2a:672:U:O4'	2.21	0.41
32:2a:1410:G:H2'	32:2a:1411:C:C6	2.56	0.41
33:2b:175:ARG:HB3	33:2b:175:ARG:NH1	2.35	0.41
35:2d:15:GLU:CD	35:2d:59:ARG:HH11	2.29	0.41
42:2k:78:GLN:O	42:2k:103:LEU:HA	2.21	0.41
44:2m:37:THR:HG21	44:2m:56:LEU:HA	2.02	0.41
44:2m:106:ASN:OD1	44:2m:106:ASN:N	2.53	0.41
53:2y:29:LYS:O	53:2y:31:GLN:HG3	2.21	0.41
1:1A:189:G:H2'	1:1A:205:G:N2	2.35	0.41
1:1A:847:U:OP2	61:1A:4155:HOH:O	2.22	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1153:C:H2'	1:1A:1154:G:O4'	2.21	0.41
1:1A:1264:G:OP1	27:15:19:ARG:NH2	2.29	0.41
1:1A:1676:A:H2'	1:1A:1677:A:O4'	2.21	0.41
1:1A:2134:A:O2'	1:1A:2159:G:N3	2.50	0.41
1:1A:2279:G:O6	22:10:14:ARG:HD2	2.21	0.41
7:1H:158:HIS:O	7:1H:160:LYS:N	2.54	0.41
8:1I:117:GLU:HG3	8:1I:118:LYS:H	1.86	0.41
9:1N:4:TYR:CD2	16:1U:100:VAL:HG11	2.56	0.41
14:1S:99:LYS:HE2	14:1S:103:GLU:OE2	2.20	0.41
15:1T:51:ARG:HG3	15:1T:98:LYS:HE3	2.01	0.41
15:1T:108:ARG:NH1	15:1T:112:ARG:HD3	2.33	0.41
20:1Y:38:ILE:HD11	20:1Y:66:PRO:HG3	2.03	0.41
24:12:36:ARG:HD3	61:12:110:HOH:O	2.21	0.41
32:1a:67:C:H2'	32:1a:68:G:C8	2.56	0.41
32:1a:102:G:H2'	32:1a:103:C:C6	2.55	0.41
32:1a:347:G:H8	57:1a:3277:MPD:H53	1.85	0.41
32:1a:406:G:O3'	35:1d:3:ARG:NH2	2.50	0.41
32:1a:1019:C:H2'	32:1a:1020:U:O4'	2.21	0.41
32:1a:1040:U:H2'	32:1a:1041:A:H8	1.85	0.41
32:1a:1152:A:H2'	32:1a:1153:C:H6	1.86	0.41
32:1a:1342:C:H2'	32:1a:1343:G:C8	2.56	0.41
32:1a:1530:G:H4'	32:1a:1530:G:OP1	2.20	0.41
34:1c:35:GLU:CD	34:1c:59:ARG:HH22	2.29	0.41
40:1i:3:GLN:HG3	40:1i:20:ARG:HG2	2.02	0.41
40:1i:16:ARG:HB2	40:1i:64:THR:HB	2.03	0.41
42:1k:62:GLN:O	42:1k:66:LEU:HG	2.21	0.41
45:1n:48:ALA:HB2	45:1n:53:LEU:HD12	2.03	0.41
47:1p:19:ILE:HG22	47:1p:37:GLY:C	2.46	0.41
47:1p:45:THR:OG1	47:1p:46:PRO:HD2	2.20	0.41
1:2A:323:G:O2'	1:2A:1205:U:N3	2.48	0.41
1:2A:900:A:O2'	1:2A:901:A:OP1	2.35	0.41
1:2A:1084:A:C8	1:2A:1085:A:H4'	2.53	0.41
1:2A:1529:G:O6	1:2A:1530:C:N4	2.53	0.41
1:2A:2424:C:O2	1:2A:2429:G:O2'	2.33	0.41
1:2A:2850:A:O2'	61:2A:3869:HOH:O	2.22	0.41
2:2B:12:C:H2'	22:20:73:GLY:HA3	2.03	0.41
2:2B:49:C:H2'	2:2B:50:G:C8	2.56	0.41
3:2D:3:VAL:HG13	3:2D:17:THR:HB	2.01	0.41
5:2F:129:PHE:CD2	5:2F:163:VAL:HG21	2.55	0.41
6:2G:11:TYR:CZ	6:2G:16:ARG:HD3	2.55	0.41
7:2H:124:GLU:O	7:2H:131:VAL:HA	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:2N:108:PRO:O	9:2N:113:GLY:HA3	2.21	0.41
12:2Q:137:TYR:O	12:2Q:141:GLN:HG2	2.21	0.41
14:2S:25:ARG:NH1	14:2S:42:ASP:OD1	2.54	0.41
16:2U:10:ARG:NH2	61:2U:202:HOH:O	2.54	0.41
16:2U:34:LYS:NZ	16:2U:37:GLU:OE1	2.52	0.41
27:25:48:GLU:O	27:25:60:VAL:HG11	2.20	0.41
32:2a:743:U:H2'	32:2a:744:C:C6	2.56	0.41
32:2a:857:C:H2'	32:2a:858:G:O4'	2.21	0.41
32:2a:965:A:C8	53:2y:8:LYS:HD2	2.56	0.41
32:2a:1099:G:C6	32:2a:1100:C:C4	3.08	0.41
32:2a:1118:C:H1'	32:2a:1179:A:C4	2.55	0.41
32:2a:1179:A:H5''	40:2i:102:LEU:HG	2.03	0.41
33:2b:17:PHE:CD2	33:2b:17:PHE:N	2.89	0.41
38:2g:65:ALA:HB1	38:2g:127:ALA:HB3	2.03	0.41
38:2g:91:VAL:O	38:2g:96:GLN:NE2	2.45	0.41
39:2h:7:ALA:O	39:2h:11:THR:OG1	2.30	0.41
39:2h:83:ILE:HG13	39:2h:137:VAL:HG13	2.02	0.41
44:2m:91:ARG:NE	44:2m:97:PRO:O	2.54	0.41
51:2t:10:LEU:HD12	51:2t:10:LEU:HA	1.84	0.41
51:2t:13:LEU:O	51:2t:17:ARG:HG3	2.21	0.41
52:2u:6:ARG:C	52:2u:8:THR:H	2.29	0.41
53:2y:24:LEU:HD23	53:2y:24:LEU:HA	1.72	0.41
1:1A:476:G:H4'	1:1A:502:A:N1	2.36	0.41
1:1A:1654:A:OP1	13:1R:1:MET:N	2.37	0.41
1:1A:2563:U:O2	1:1A:2565:A:H8	2.04	0.41
1:1A:2836:U:C4	1:1A:2883:A:N6	2.89	0.41
8:1I:133:HIS:ND1	8:1I:134:PRO:O	2.53	0.41
14:1S:52:SER:HB2	14:1S:55:ALA:H	1.86	0.41
25:13:31:LEU:HD23	25:13:31:LEU:HA	1.88	0.41
32:1a:116:A:H61	32:1a:313:A:H1'	1.86	0.41
32:1a:169:C:H2'	32:1a:170:U:H6	1.85	0.41
32:1a:401:C:OP2	35:1d:73:ARG:NH2	2.54	0.41
32:1a:1069:C:O2'	32:1a:1192:C:H1'	2.21	0.41
33:1b:192:SER:O	33:1b:194:PRO:HD3	2.21	0.41
35:1d:107:ARG:NH2	35:1d:194:LEU:HD21	2.36	0.41
51:1t:63:ILE:HG21	51:1t:81:LYS:HG3	2.03	0.41
1:2A:118:A:N3	1:2A:178:G:H1'	2.35	0.41
1:2A:127:A:H5''	1:2A:128:C:C6	2.56	0.41
1:2A:208:C:H2'	1:2A:209:C:C6	2.56	0.41
1:2A:300:A:H1'	1:2A:319:C:H1'	2.03	0.41
1:2A:1364:G:OP1	23:21:2:SER:HA	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2134:A:H1'	1:2A:2159:G:H1'	2.02	0.41
1:2A:2413:G:O6	61:2A:3856:HOH:O	2.21	0.41
8:2I:50:ARG:O	8:2I:54:GLN:HG2	2.21	0.41
16:2U:11:ARG:O	16:2U:15:LYS:HG3	2.20	0.41
32:2a:614:A:H2'	32:2a:615:C:C6	2.56	0.41
32:2a:689:C:OP1	42:2k:27:ASN:ND2	2.52	0.41
32:2a:742:G:OP2	46:2o:35:ARG:NH2	2.52	0.41
32:2a:941:G:H2'	32:2a:942:G:O4'	2.21	0.41
32:2a:1118:C:H1'	32:2a:1179:A:C5	2.55	0.41
34:2c:71:ALA:O	34:2c:73:PRO:HD3	2.21	0.41
1:1A:705:A:H1'	3:1D:9:TYR:CE2	2.56	0.40
1:1A:2152:G:H5''	1:1A:2153:G:OP2	2.21	0.40
1:1A:2266:A:H8	1:1A:2266:A:OP1	2.04	0.40
1:1A:2304:G:H22	1:1A:2312:U:H3	1.69	0.40
1:1A:2458:G:OP2	61:1A:4157:HOH:O	2.22	0.40
1:1A:2811:G:N2	1:1A:2891:G:H1'	2.36	0.40
6:1G:38:VAL:HG22	6:1G:93:THR:HG23	2.02	0.40
6:1G:105:LYS:HB2	6:1G:105:LYS:HE3	1.87	0.40
10:1O:2:ILE:HG13	10:1O:8:LEU:HD21	2.03	0.40
15:1T:35:LYS:HG2	15:1T:40:THR:HG22	2.02	0.40
20:1Y:20:TYR:CE2	20:1Y:43:ASN:HA	2.56	0.40
30:18:30:ARG:HD3	61:18:223:HOH:O	2.21	0.40
32:1a:408:A:H2'	32:1a:409:G:O4'	2.20	0.40
32:1a:996:A:N1	32:1a:1045:C:O2'	2.50	0.40
36:1e:12:LEU:HD22	36:1e:13:ILE:N	2.35	0.40
39:1h:64:LYS:HG2	39:1h:79:VAL:HG21	2.03	0.40
44:1m:12:ASN:O	44:1m:44:ARG:HD2	2.20	0.40
46:1o:71:GLN:HB2	46:1o:78:TYR:CG	2.56	0.40
47:1p:23:ASP:OD1	47:1p:25:ARG:HG3	2.21	0.40
53:1y:43:LYS:HD3	53:1y:48:PHE:CE1	2.55	0.40
1:2A:391:G:H1'	1:2A:411:G:O4'	2.21	0.40
1:2A:608:A:H2'	1:2A:609:A:C8	2.56	0.40
1:2A:2317:C:H2'	1:2A:2318:G:H5'	2.03	0.40
1:2A:2639:A:H2'	1:2A:2640:G:O4'	2.20	0.40
6:2G:37:VAL:HG23	6:2G:99:MET:HG3	2.03	0.40
11:2P:124:LYS:HA	11:2P:144:GLU:O	2.21	0.40
30:28:13:ARG:O	61:28:201:HOH:O	2.22	0.40
32:2a:141:A:H1'	32:2a:182:U:O2	2.22	0.40
32:2a:435:C:H2'	32:2a:436:C:H6	1.86	0.40
32:2a:1329:A:H5''	44:2m:26:GLY:H	1.86	0.40
33:2b:123:ALA:HB3	33:2b:125:PRO:HD2	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:2e:52:PRO:O	36:2e:56:GLN:HG2	2.21	0.40
38:2g:121:ALA:O	38:2g:125:MET:HG3	2.21	0.40
49:2r:45:SER:OG	49:2r:46:GLU:N	2.53	0.40
53:2y:13:THR:HB	53:2y:16:ILE:HG22	2.03	0.40
1:1A:592:G:O6	61:1A:4136:HOH:O	2.17	0.40
1:1A:1028:A:N3	1:1A:2486:G:O2'	2.51	0.40
1:1A:1638:C:O3'	1:1A:2709:G:N2	2.54	0.40
1:1A:1659:U:H2'	1:1A:1660:C:O4'	2.21	0.40
1:1A:2836:U:H2'	1:1A:2837:G:C8	2.55	0.40
1:1A:2848:G:C8	15:1T:97:ALA:HB2	2.56	0.40
4:1E:101:ARG:CZ	4:1E:171:GLU:HB2	2.51	0.40
18:1W:37:ARG:NH1	27:15:48:GLU:OE2	2.54	0.40
32:1a:195:A:C6	32:1a:196:A:N1	2.89	0.40
32:1a:438:G:O2'	32:1a:494:U:O4	2.31	0.40
32:1a:881:G:OP2	43:1l:12:ARG:NH2	2.50	0.40
37:1f:28:ARG:O	37:1f:32:ASN:N	2.46	0.40
39:1h:38:ILE:HD11	39:1h:118:VAL:O	2.22	0.40
53:1y:23:ARG:NH1	53:1y:26:LYS:HD2	2.37	0.40
1:2A:30:G:H2'	1:2A:31:C:H6	1.86	0.40
1:2A:657:U:H2'	1:2A:658:C:H6	1.86	0.40
1:2A:840:C:H2'	1:2A:841:A:H8	1.87	0.40
1:2A:994:C:O2'	1:2A:996:A:OP1	2.31	0.40
1:2A:1598:C:H2'	1:2A:1599:C:H6	1.85	0.40
1:2A:1761:C:H2'	1:2A:1762:A:H5''	2.02	0.40
1:2A:1880:C:O2'	1:2A:1881:C:H5'	2.21	0.40
1:2A:2144:U:H1'	1:2A:2147:G:C6	2.56	0.40
1:2A:2302:G:C2	1:2A:2303:G:C8	3.09	0.40
1:2A:2552:2MU:H6	1:2A:2552:2MU:O5'	2.22	0.40
1:2A:2793:G:H2'	1:2A:2794:C:O4'	2.21	0.40
2:2B:73:A:C4	2:2B:105:A:C2	3.10	0.40
6:2G:38:VAL:HG22	6:2G:93:THR:HG23	2.03	0.40
32:2a:110:C:O2'	47:2p:25:ARG:O	2.34	0.40
32:2a:189(A):C:H2'	32:2a:189(B):C:H6	1.86	0.40
32:2a:1062:U:H2'	32:2a:1063:C:C6	2.55	0.40
32:2a:1195:C:H5''	32:2a:1196:U:OP2	2.22	0.40
32:2a:1325:C:H5''	52:2u:17:THR:HG21	2.03	0.40
32:2a:1423:G:H2'	32:2a:1424:C:H6	1.85	0.40
32:2a:1504:G:H4'	32:2a:1505:G:C4	2.56	0.40
33:2b:78:GLN:NE2	33:2b:95:GLN:HA	2.32	0.40
35:2d:12:CYS:HB3	35:2d:33:MET:HG3	2.04	0.40
41:2j:63:PHE:HE1	45:2n:58:LYS:HG2	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:2m:70:LEU:O	44:2m:74:VAL:HG23	2.21	0.40
1:1A:228:A:H2'	1:1A:230:U:O4'	2.21	0.40
1:1A:1820:U:H4'	1:1A:1821:A:OP2	2.22	0.40
1:1A:2330:G:H2'	1:1A:2331:G:O4'	2.22	0.40
61:1A:4916:HOH:O	20:1Y:19:LYS:HD3	2.21	0.40
2:1B:1:U:O2	2:1B:1:U:H2'	2.20	0.40
2:1B:7:G:H5''	2:1B:7:G:H8	1.87	0.40
3:1D:232:PRO:HB3	3:1D:244:ARG:CZ	2.51	0.40
4:1E:52:LEU:O	4:1E:76:ARG:N	2.49	0.40
6:1G:4:ASP:CG	6:1G:9:ARG:HH21	2.29	0.40
7:1H:86:GLU:OE1	7:1H:130:ARG:HD2	2.21	0.40
8:1I:104:GLN:HB2	8:1I:105:HIS:CD2	2.47	0.40
27:15:8:LYS:O	27:15:9:LYS:HD2	2.21	0.40
32:1a:738:C:H2'	32:1a:739:C:C6	2.57	0.40
32:1a:1013:G:N2	32:1a:1016:A:OP2	2.53	0.40
32:1a:1125:U:C2	32:1a:1127:G:C8	3.10	0.40
34:1c:56:ASP:OD2	34:1c:69:HIS:HE1	2.03	0.40
35:1d:88:VAL:HG13	36:1e:97:GLY:HA2	2.03	0.40
1:2A:639:U:H2'	1:2A:640:C:C6	2.57	0.40
1:2A:776:G:P	61:2A:3921:HOH:O	2.79	0.40
1:2A:795:C:H2'	1:2A:796:C:C6	2.57	0.40
1:2A:974:G:C4	1:2A:989:G:C2	3.09	0.40
1:2A:1026:U:H4'	1:2A:1027:A:OP1	2.20	0.40
1:2A:1504:C:H2'	1:2A:1505:C:C6	2.57	0.40
1:2A:2061:G:H5''	1:2A:2503:2MA:C2	2.51	0.40
2:2B:83:G:H1	2:2B:94:C:H42	1.68	0.40
4:2E:28:ALA:HB3	4:2E:93:VAL:CG1	2.50	0.40
5:2F:184:TYR:O	5:2F:188:ARG:HG3	2.21	0.40
6:2G:15:VAL:HG13	6:2G:175:LEU:HB3	2.02	0.40
7:2H:171:LEU:H	7:2H:171:LEU:HD12	1.86	0.40
15:2T:54:ARG:HA	15:2T:59:THR:HG23	2.03	0.40
24:22:35:LEU:HD21	24:22:49:LYS:HE2	2.02	0.40
27:25:51:TYR:CE2	27:25:56:LYS:HD3	2.55	0.40
32:2a:109:A:H2'	32:2a:326:G:N2	2.36	0.40
32:2a:236:G:H2'	32:2a:237:C:O4'	2.20	0.40
32:2a:582:U:C2	32:2a:760:G:C6	3.09	0.40
32:2a:1326:C:H5''	52:2u:18:TYR:O	2.20	0.40
36:2e:12:LEU:HD11	36:2e:14:ARG:HD3	2.02	0.40
47:2p:47:ASP:OD1	47:2p:47:ASP:N	2.37	0.40
50:2s:42:PRO:O	50:2s:45:VAL:HG22	2.21	0.40
51:2t:57:ARG:NH2	51:2t:100:ILE:HD12	2.30	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:19:C:OP2	16:1U:30:LYS:NZ	2.55	0.40
1:1A:1478:G:O2'	1:1A:1558:A:N7	2.55	0.40
1:1A:1759:A:H1'	1:1A:2711:A:C2	2.57	0.40
1:1A:2629:A:H1'	1:1A:2630:G:H5''	2.02	0.40
6:1G:55:LYS:O	6:1G:59:GLU:HG3	2.21	0.40
8:1I:25:TYR:HE1	8:1I:29:TYR:CD2	2.40	0.40
8:1I:96:ASP:N	8:1I:96:ASP:OD1	2.55	0.40
11:1P:140:ALA:O	25:23:38:GLU:HG2	2.21	0.40
23:11:95:LEU:O	23:11:98:LEU:HB2	2.21	0.40
32:1a:147:G:H2'	32:1a:148:G:H8	1.87	0.40
32:1a:664:G:N2	32:1a:741:G:H1	2.07	0.40
32:1a:1103:C:OP1	33:1b:96:ARG:NH2	2.55	0.40
32:1a:1318:A:OP1	50:1s:7:LYS:NZ	2.43	0.40
32:1a:1401:G:C2	32:1a:1402:4OC:H1'	2.56	0.40
33:1b:77:ALA:HA	33:1b:80:ILE:HG23	2.03	0.40
35:1d:61:LYS:HD3	35:1d:206:PHE:CE2	2.56	0.40
50:1s:11:VAL:O	50:1s:13:ASP:N	2.53	0.40
1:2A:68:G:H2'	1:2A:69:C:O4'	2.22	0.40
1:2A:581:C:H2'	1:2A:582:G:H8	1.86	0.40
1:2A:748:G:C8	18:2W:89:ALA:HB1	2.56	0.40
1:2A:1876:A:H2'	1:2A:1877:A:C8	2.56	0.40
1:2A:2102:U:O2	1:2A:2187:G:C6	2.73	0.40
1:2A:2184:G:N1	1:2A:2185:C:O2	2.54	0.40
1:2A:2741:A:H2'	1:2A:2742:C:O4'	2.22	0.40
8:2I:81:VAL:O	8:2I:146:ALA:HA	2.21	0.40
21:2Z:10:ARG:NH1	21:2Z:26:GLY:H	2.20	0.40
23:21:3:LYS:HB3	23:21:4:VAL:H	1.66	0.40
23:21:62:VAL:HG22	23:21:63:ALA:O	2.21	0.40
25:23:10:LYS:HB3	25:23:53:LEU:HA	2.03	0.40
26:24:1:MET:HG2	26:24:6:HIS:CD2	2.56	0.40
28:26:23:THR:OG1	28:26:24:GLU:N	2.54	0.40
32:2a:116:A:H61	32:2a:313:A:H1'	1.86	0.40
32:2a:509:A:H5'	35:2d:54:TYR:HD2	1.87	0.40
32:2a:926:G:C6	53:2y:87:LYS:HG3	2.56	0.40
32:2a:1084:G:C5	32:2a:1085:U:C4	3.09	0.40
51:2t:99:LEU:HD12	51:2t:99:LEU:HA	1.88	0.40
1:1A:183:C:N4	1:1A:213:A:H61	2.20	0.40
1:1A:443:A:N7	5:1F:45:ARG:HG2	2.37	0.40
1:1A:2006:C:O5'	1:1A:2006:C:H6	2.05	0.40
1:1A:2151:G:H2'	1:1A:2152:G:O4'	2.22	0.40
1:1A:2674:G:H5''	10:1O:26:LYS:HE3	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:1P:36:LYS:NZ	61:1P:307:HOH:O	2.51	0.40
26:14:50:VAL:HG11	44:1m:65:LYS:HA	2.04	0.40
32:1a:763:G:H2'	32:1a:764:C:C6	2.57	0.40
32:1a:811:C:N4	61:1a:3341:HOH:O	2.54	0.40
32:1a:974:A:OP1	32:1a:974:A:H8	2.05	0.40
32:1a:1192:C:O2	36:1e:25:ARG:NH2	2.43	0.40
35:1d:59:ARG:NH2	35:1d:62:GLN:HG3	2.37	0.40
1:2A:41:C:H2'	1:2A:42:G:C8	2.57	0.40
1:2A:443:A:N7	5:2F:45:ARG:HG2	2.37	0.40
1:2A:649:G:H2'	1:2A:650:C:O4'	2.21	0.40
1:2A:839:U:H2'	1:2A:840:C:C6	2.55	0.40
1:2A:1287:A:O4'	13:2R:104:ARG:HD3	2.22	0.40
1:2A:1802:A:N1	1:2A:1822:G:H1'	2.37	0.40
1:2A:1900:A:N1	1:2A:1970:A:C6	2.89	0.40
1:2A:2018:G:H2'	1:2A:2019:A:O4'	2.21	0.40
1:2A:2350:C:H2'	1:2A:2351:G:O4'	2.22	0.40
7:2H:28:GLY:N	7:2H:31:GLY:O	2.55	0.40
12:2Q:66:ILE:HG12	12:2Q:104:PHE:CD1	2.57	0.40
21:2Z:91:LEU:HD12	21:2Z:91:LEU:HA	1.84	0.40
21:2Z:152:ALA:O	21:2Z:155:LEU:HB2	2.21	0.40
26:24:50:VAL:HG23	44:2m:65:LYS:HE3	2.04	0.40
32:2a:583:A:H2'	32:2a:584:G:O4'	2.21	0.40
32:2a:630:G:O2'	32:2a:631:G:H5'	2.22	0.40
32:2a:947:G:H2'	32:2a:948:C:O4'	2.21	0.40
32:2a:1346:A:OP1	40:2i:120:ARG:NH1	2.35	0.40
32:2a:1372:U:H2'	32:2a:1373:G:O4'	2.22	0.40
34:2c:110:ASN:O	34:2c:141:VAL:HG22	2.22	0.40
37:2f:37:VAL:HA	37:2f:65:VAL:HG12	2.04	0.40
41:2j:16:LEU:HD23	41:2j:94:VAL:HG22	2.04	0.40
50:2s:81:ARG:HB2	50:2s:81:ARG:NH1	2.37	0.40
53:2y:5:ILE:HD12	53:2y:17:ARG:HG2	2.04	0.40
53:2y:23:ARG:HG3	53:2y:78:ILE:HG13	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%)	257 (94%)	16 (6%)	0	100	100
3	2D	273/276 (99%)	256 (94%)	17 (6%)	0	100	100
4	1E	202/206 (98%)	193 (96%)	8 (4%)	1 (0%)	24	46
4	2E	202/206 (98%)	192 (95%)	9 (4%)	1 (0%)	24	46
5	1F	201/210 (96%)	195 (97%)	5 (2%)	1 (0%)	24	46
5	2F	201/210 (96%)	194 (96%)	5 (2%)	2 (1%)	12	28
6	1G	179/182 (98%)	164 (92%)	10 (6%)	5 (3%)	4	6
6	2G	179/182 (98%)	160 (89%)	16 (9%)	3 (2%)	7	15
7	1H	172/180 (96%)	163 (95%)	8 (5%)	1 (1%)	21	42
7	2H	171/180 (95%)	150 (88%)	18 (10%)	3 (2%)	6	14
8	1I	145/148 (98%)	128 (88%)	16 (11%)	1 (1%)	18	38
8	2I	144/148 (97%)	131 (91%)	11 (8%)	2 (1%)	9	19
9	1N	138/140 (99%)	135 (98%)	3 (2%)	0	100	100
9	2N	138/140 (99%)	133 (96%)	4 (3%)	1 (1%)	18	38
10	1O	120/122 (98%)	114 (95%)	6 (5%)	0	100	100
10	2O	120/122 (98%)	113 (94%)	6 (5%)	1 (1%)	16	34
11	1P	147/150 (98%)	137 (93%)	9 (6%)	1 (1%)	18	38
11	2P	147/150 (98%)	138 (94%)	8 (5%)	1 (1%)	18	38
12	1Q	139/141 (99%)	132 (95%)	6 (4%)	1 (1%)	18	38
12	2Q	139/141 (99%)	131 (94%)	8 (6%)	0	100	100
13	1R	116/118 (98%)	112 (97%)	4 (3%)	0	100	100
13	2R	116/118 (98%)	114 (98%)	2 (2%)	0	100	100
14	1S	108/112 (96%)	100 (93%)	7 (6%)	1 (1%)	14	30
14	2S	108/112 (96%)	104 (96%)	3 (3%)	1 (1%)	14	30
15	1T	129/146 (88%)	123 (95%)	6 (5%)	0	100	100
15	2T	129/146 (88%)	121 (94%)	7 (5%)	1 (1%)	16	34
16	1U	114/118 (97%)	113 (99%)	1 (1%)	0	100	100
16	2U	114/118 (97%)	111 (97%)	3 (3%)	0	100	100
17	1V	99/101 (98%)	92 (93%)	6 (6%)	1 (1%)	12	28

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	2V	99/101 (98%)	93 (94%)	5 (5%)	1 (1%)	12	28
18	1W	110/113 (97%)	107 (97%)	3 (3%)	0	100	100
18	2W	110/113 (97%)	110 (100%)	0	0	100	100
19	1X	93/96 (97%)	90 (97%)	2 (2%)	1 (1%)	11	25
19	2X	93/96 (97%)	90 (97%)	2 (2%)	1 (1%)	11	25
20	1Y	105/110 (96%)	94 (90%)	11 (10%)	0	100	100
20	2Y	105/110 (96%)	99 (94%)	6 (6%)	0	100	100
21	1Z	201/206 (98%)	191 (95%)	8 (4%)	2 (1%)	12	28
21	2Z	199/206 (97%)	179 (90%)	17 (8%)	3 (2%)	8	18
22	10	75/85 (88%)	71 (95%)	4 (5%)	0	100	100
22	20	75/85 (88%)	71 (95%)	4 (5%)	0	100	100
23	11	95/98 (97%)	93 (98%)	2 (2%)	0	100	100
23	21	95/98 (97%)	92 (97%)	2 (2%)	1 (1%)	11	25
24	12	68/72 (94%)	68 (100%)	0	0	100	100
24	22	68/72 (94%)	65 (96%)	3 (4%)	0	100	100
25	13	57/60 (95%)	56 (98%)	1 (2%)	0	100	100
25	23	57/60 (95%)	53 (93%)	4 (7%)	0	100	100
26	14	67/71 (94%)	55 (82%)	7 (10%)	5 (8%)	1	1
26	24	67/71 (94%)	47 (70%)	16 (24%)	4 (6%)	1	1
27	15	57/60 (95%)	55 (96%)	2 (4%)	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%)	50 (98%)	1 (2%)	0	100	100
29	17	46/49 (94%)	46 (100%)	0	0	100	100
29	27	46/49 (94%)	46 (100%)	0	0	100	100
30	18	62/65 (95%)	62 (100%)	0	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%)	195 (85%)	26 (11%)	8 (4%)	3	4
33	2b	229/256 (90%)	192 (84%)	31 (14%)	6 (3%)	4	7

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
34	1c	204/239 (85%)	192 (94%)	11 (5%)	1 (0%)	24	46
34	2c	204/239 (85%)	177 (87%)	24 (12%)	3 (2%)	8	18
35	1d	206/209 (99%)	196 (95%)	10 (5%)	0	100	100
35	2d	206/209 (99%)	190 (92%)	13 (6%)	3 (2%)	8	18
36	1e	146/162 (90%)	140 (96%)	5 (3%)	1 (1%)	18	38
36	2e	146/162 (90%)	135 (92%)	11 (8%)	0	100	100
37	1f	98/101 (97%)	95 (97%)	3 (3%)	0	100	100
37	2f	98/101 (97%)	94 (96%)	4 (4%)	0	100	100
38	1g	153/156 (98%)	143 (94%)	10 (6%)	0	100	100
38	2g	153/156 (98%)	141 (92%)	11 (7%)	1 (1%)	18	38
39	1h	135/138 (98%)	130 (96%)	5 (4%)	0	100	100
39	2h	135/138 (98%)	121 (90%)	12 (9%)	2 (2%)	8	18
40	1i	125/128 (98%)	113 (90%)	11 (9%)	1 (1%)	16	34
40	2i	124/128 (97%)	105 (85%)	13 (10%)	6 (5%)	2	2
41	1j	95/105 (90%)	80 (84%)	10 (10%)	5 (5%)	1	1
41	2j	94/105 (90%)	77 (82%)	12 (13%)	5 (5%)	1	1
42	1k	112/129 (87%)	102 (91%)	10 (9%)	0	100	100
42	2k	112/129 (87%)	100 (89%)	11 (10%)	1 (1%)	14	30
43	1l	119/132 (90%)	114 (96%)	5 (4%)	0	100	100
43	2l	119/132 (90%)	111 (93%)	8 (7%)	0	100	100
44	1m	114/126 (90%)	104 (91%)	8 (7%)	2 (2%)	6	14
44	2m	112/126 (89%)	98 (88%)	12 (11%)	2 (2%)	6	14
45	1n	58/61 (95%)	55 (95%)	3 (5%)	0	100	100
45	2n	58/61 (95%)	53 (91%)	4 (7%)	1 (2%)	7	15
46	1o	86/89 (97%)	81 (94%)	4 (5%)	1 (1%)	10	23
46	2o	86/89 (97%)	82 (95%)	3 (4%)	1 (1%)	10	23
47	1p	80/88 (91%)	72 (90%)	8 (10%)	0	100	100
47	2p	80/88 (91%)	65 (81%)	15 (19%)	0	100	100
48	1q	97/105 (92%)	88 (91%)	8 (8%)	1 (1%)	12	28
48	2q	97/105 (92%)	88 (91%)	8 (8%)	1 (1%)	12	28
49	1r	66/88 (75%)	64 (97%)	2 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
49	2r	66/88 (75%)	64 (97%)	2 (3%)	0	100	100
50	1s	81/93 (87%)	73 (90%)	7 (9%)	1 (1%)	10	23
50	2s	81/93 (87%)	72 (89%)	9 (11%)	0	100	100
51	1t	94/106 (89%)	86 (92%)	8 (8%)	0	100	100
51	2t	96/106 (91%)	88 (92%)	7 (7%)	1 (1%)	12	28
52	1u	21/27 (78%)	20 (95%)	1 (5%)	0	100	100
52	2u	21/27 (78%)	18 (86%)	1 (5%)	2 (10%)	0	0
53	1y	95/113 (84%)	94 (99%)	1 (1%)	0	100	100
53	2y	94/113 (83%)	91 (97%)	3 (3%)	0	100	100
All	All	11629/12354 (94%)	10823 (93%)	703 (6%)	103 (1%)	14	30

All (103) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	1F	130	ALA
6	1G	47	LYS
6	1G	50	ALA
26	14	55	ARG
33	1b	124	SER
33	1b	231	GLU
40	1i	11	LYS
44	1m	67	GLU
5	2F	130	ALA
26	24	45	GLY
35	2d	5	ILE
40	2i	43	ALA
41	2j	56	HIS
7	1H	159	GLU
19	1X	94	GLY
21	1Z	52	SER
26	14	47	GLN
26	14	57	GLU
41	1j	79	ARG
6	2G	78	SER
6	2G	81	LYS
7	2H	126	PRO
19	2X	94	GLY
33	2b	22	LYS
34	2c	4	LYS

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Mol	Chain	Res	Type
38	2g	7	ALA
40	2i	44	VAL
40	2i	54	ASP
40	2i	55	ALA
51	2t	100	ILE
52	2u	3	LYS
6	1G	44	GLY
14	1S	59	LYS
26	14	49	PHE
41	1j	55	LYS
41	1j	77	PRO
41	1j	78	ASN
46	1o	19	PRO
48	1q	68	ARG
50	1s	12	ASP
6	2G	117	PHE
8	2I	117	GLU
10	2O	5	GLN
11	2P	29	LYS
21	2Z	60	GLU
23	2l	3	LYS
26	24	62	ARG
33	2b	11	LEU
34	2c	144	SER
39	2h	133	LEU
41	2j	78	ASN
44	2m	67	GLU
4	1E	52	LEU
12	1Q	59	ARG
33	1b	17	PHE
33	1b	22	LYS
33	1b	228	GLY
34	1c	156	ARG
44	1m	12	ASN
4	2E	52	LEU
8	2I	10	GLU
26	24	51	ASP
33	2b	20	GLU
35	2d	156	GLU
40	2i	96	LEU
41	2j	79	ARG
17	1V	79	VAL

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Mol	Chain	Res	Type
33	1b	20	GLU
33	1b	127	ILE
5	2F	21	ALA
7	2H	47	GLU
9	2N	129	PRO
15	2T	128	GLU
21	2Z	52	SER
26	24	60	GLN
33	2b	125	PRO
35	2d	22	LYS
44	2m	21	TYR
46	2o	88	ARG
6	1G	51	ARG
8	1I	105	HIS
11	1P	29	LYS
26	14	61	ARG
14	2S	35	ILE
33	2b	17	PHE
33	2b	123	ALA
34	2c	204	LEU
40	2i	11	LYS
48	2q	68	ARG
52	2u	7	ARG
36	1e	96	PRO
17	2V	79	VAL
41	2j	24	VAL
41	2j	75	ILE
42	2k	105	VAL
41	1j	91	PRO
21	2Z	128	VAL
39	2h	51	VAL
6	1G	52	ILE
21	1Z	53	ILE
7	2H	55	PRO
45	2n	14	PRO
33	1b	125	PRO

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	1D	214/218 (98%)	198 (92%)	16 (8%)	12	28
3	2D	215/218 (99%)	197 (92%)	18 (8%)	10	23
4	1E	164/166 (99%)	149 (91%)	15 (9%)	9	19
4	2E	164/166 (99%)	151 (92%)	13 (8%)	11	26
5	1F	160/166 (96%)	144 (90%)	16 (10%)	7	16
5	2F	159/166 (96%)	141 (89%)	18 (11%)	5	12
6	1G	144/156 (92%)	130 (90%)	14 (10%)	8	17
6	2G	142/156 (91%)	127 (89%)	15 (11%)	6	14
7	1H	144/148 (97%)	136 (94%)	8 (6%)	19	40
7	2H	143/148 (97%)	121 (85%)	22 (15%)	2	5
8	1I	111/124 (90%)	99 (89%)	12 (11%)	6	13
8	2I	108/124 (87%)	99 (92%)	9 (8%)	10	23
9	1N	119/119 (100%)	108 (91%)	11 (9%)	8	19
9	2N	118/119 (99%)	109 (92%)	9 (8%)	12	27
10	1O	100/100 (100%)	95 (95%)	5 (5%)	22	46
10	2O	100/100 (100%)	95 (95%)	5 (5%)	22	46
11	1P	115/116 (99%)	109 (95%)	6 (5%)	21	44
11	2P	115/116 (99%)	108 (94%)	7 (6%)	17	37
12	1Q	111/111 (100%)	102 (92%)	9 (8%)	11	24
12	2Q	111/111 (100%)	104 (94%)	7 (6%)	16	36
13	1R	101/101 (100%)	94 (93%)	7 (7%)	14	32
13	2R	101/101 (100%)	96 (95%)	5 (5%)	22	46
14	1S	87/88 (99%)	80 (92%)	7 (8%)	11	25
14	2S	85/88 (97%)	76 (89%)	9 (11%)	6	14
15	1T	115/127 (91%)	110 (96%)	5 (4%)	26	51
15	2T	113/127 (89%)	105 (93%)	8 (7%)	13	31
16	1U	93/94 (99%)	88 (95%)	5 (5%)	20	42
16	2U	93/94 (99%)	89 (96%)	4 (4%)	26	51
17	1V	81/82 (99%)	77 (95%)	4 (5%)	22	47
17	2V	80/82 (98%)	71 (89%)	9 (11%)	5	12

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
18	1W	90/92 (98%)	83 (92%)	7 (8%)	11	26
18	2W	90/92 (98%)	82 (91%)	8 (9%)	9	20
19	1X	77/78 (99%)	74 (96%)	3 (4%)	28	55
19	2X	77/78 (99%)	76 (99%)	1 (1%)	61	82
20	1Y	86/91 (94%)	79 (92%)	7 (8%)	11	24
20	2Y	86/91 (94%)	74 (86%)	12 (14%)	3	6
21	1Z	169/179 (94%)	150 (89%)	19 (11%)	6	12
21	2Z	165/179 (92%)	146 (88%)	19 (12%)	5	11
22	10	61/67 (91%)	58 (95%)	3 (5%)	22	47
22	20	61/67 (91%)	58 (95%)	3 (5%)	22	47
23	11	79/83 (95%)	76 (96%)	3 (4%)	29	56
23	21	81/83 (98%)	73 (90%)	8 (10%)	7	16
24	12	65/67 (97%)	60 (92%)	5 (8%)	12	27
24	22	66/67 (98%)	62 (94%)	4 (6%)	17	37
25	13	51/52 (98%)	48 (94%)	3 (6%)	18	38
25	23	50/52 (96%)	46 (92%)	4 (8%)	11	25
26	14	58/63 (92%)	54 (93%)	4 (7%)	14	32
26	24	54/63 (86%)	47 (87%)	7 (13%)	4	8
27	15	51/52 (98%)	46 (90%)	5 (10%)	7	17
27	25	50/52 (96%)	48 (96%)	2 (4%)	28	55
28	16	51/52 (98%)	48 (94%)	3 (6%)	18	38
28	26	50/52 (96%)	46 (92%)	4 (8%)	11	25
29	17	41/42 (98%)	39 (95%)	2 (5%)	22	47
29	27	41/42 (98%)	38 (93%)	3 (7%)	13	29
30	18	54/55 (98%)	51 (94%)	3 (6%)	19	40
30	28	54/55 (98%)	51 (94%)	3 (6%)	19	40
31	19	34/34 (100%)	34 (100%)	0	100	100
31	29	34/34 (100%)	34 (100%)	0	100	100
33	1b	191/220 (87%)	174 (91%)	17 (9%)	9	20
33	2b	187/220 (85%)	169 (90%)	18 (10%)	8	17
34	1c	144/188 (77%)	133 (92%)	11 (8%)	12	27

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
34	2c	140/188 (74%)	120 (86%)	20 (14%)	3	6
35	1d	171/181 (94%)	153 (90%)	18 (10%)	6	14
35	2d	172/181 (95%)	155 (90%)	17 (10%)	7	16
36	1e	114/123 (93%)	104 (91%)	10 (9%)	9	21
36	2e	114/123 (93%)	101 (89%)	13 (11%)	5	11
37	1f	85/90 (94%)	79 (93%)	6 (7%)	13	31
37	2f	85/90 (94%)	73 (86%)	12 (14%)	3	6
38	1g	120/127 (94%)	114 (95%)	6 (5%)	22	46
38	2g	119/127 (94%)	104 (87%)	15 (13%)	4	9
39	1h	116/119 (98%)	107 (92%)	9 (8%)	11	26
39	2h	114/119 (96%)	103 (90%)	11 (10%)	8	17
40	1i	91/99 (92%)	82 (90%)	9 (10%)	7	16
40	2i	88/99 (89%)	79 (90%)	9 (10%)	7	15
41	1j	68/92 (74%)	63 (93%)	5 (7%)	13	29
41	2j	68/92 (74%)	58 (85%)	10 (15%)	3	6
42	1k	83/99 (84%)	80 (96%)	3 (4%)	31	58
42	2k	83/99 (84%)	78 (94%)	5 (6%)	17	37
43	1l	96/108 (89%)	89 (93%)	7 (7%)	13	29
43	2l	96/108 (89%)	89 (93%)	7 (7%)	13	29
44	1m	90/101 (89%)	86 (96%)	4 (4%)	25	50
44	2m	87/101 (86%)	79 (91%)	8 (9%)	8	19
45	1n	49/50 (98%)	43 (88%)	6 (12%)	5	10
45	2n	49/50 (98%)	43 (88%)	6 (12%)	5	10
46	1o	78/80 (98%)	75 (96%)	3 (4%)	29	56
46	2o	78/80 (98%)	73 (94%)	5 (6%)	16	35
47	1p	69/74 (93%)	59 (86%)	10 (14%)	3	6
47	2p	68/74 (92%)	61 (90%)	7 (10%)	7	15
48	1q	94/97 (97%)	87 (93%)	7 (7%)	13	29
48	2q	94/97 (97%)	88 (94%)	6 (6%)	16	35
49	1r	59/77 (77%)	52 (88%)	7 (12%)	5	10
49	2r	59/77 (77%)	51 (86%)	8 (14%)	3	7

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
50	1s	68/80 (85%)	64 (94%)	4 (6%)	18	38
50	2s	67/80 (84%)	59 (88%)	8 (12%)	5	10
51	1t	71/82 (87%)	65 (92%)	6 (8%)	10	22
51	2t	70/82 (85%)	59 (84%)	11 (16%)	2	4
52	1u	18/22 (82%)	18 (100%)	0	100	100
52	2u	18/22 (82%)	17 (94%)	1 (6%)	19	40
53	1y	82/98 (84%)	79 (96%)	3 (4%)	30	57
53	2y	79/98 (81%)	74 (94%)	5 (6%)	16	36
All	All	9524/10260 (93%)	8728 (92%)	796 (8%)	10	23

All (796) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	1D	3	VAL
3	1D	13	ARG
3	1D	39	LYS
3	1D	99	ASP
3	1D	105	ILE
3	1D	113	VAL
3	1D	126	GLN
3	1D	141	VAL
3	1D	155	LEU
3	1D	193	VAL
3	1D	211	ARG
3	1D	217	ARG
3	1D	221	VAL
3	1D	229	VAL
3	1D	242	ARG
3	1D	259	THR
4	1E	9	VAL
4	1E	12	THR
4	1E	38	THR
4	1E	41	LYS
4	1E	49	LEU
4	1E	75	VAL
4	1E	89	ASP
4	1E	116	VAL
4	1E	119	ARG
4	1E	144	ARG

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Mol	Chain	Res	Type
4	1E	163	GLU
4	1E	170	LEU
4	1E	181	LEU
4	1E	184	VAL
4	1E	188	VAL
5	1F	12	LEU
5	1F	18	ARG
5	1F	24	LEU
5	1F	53	THR
5	1F	57	VAL
5	1F	74	ARG
5	1F	110	LEU
5	1F	132	VAL
5	1F	140	LEU
5	1F	157	VAL
5	1F	158	THR
5	1F	162	LEU
5	1F	183	VAL
5	1F	192	LEU
5	1F	197	ASP
5	1F	203	GLN
6	1G	5	VAL
6	1G	7	LEU
6	1G	28	VAL
6	1G	45	GLU
6	1G	49	ASP
6	1G	52	ILE
6	1G	62	LEU
6	1G	79	ASN
6	1G	133	LEU
6	1G	140	ILE
6	1G	148	MET
6	1G	153	ARG
6	1G	159	VAL
6	1G	170	ARG
7	1H	13	LYS
7	1H	15	VAL
7	1H	62	LYS
7	1H	71	LEU
7	1H	81	GLU
7	1H	107	VAL
7	1H	119	GLU

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Mol	Chain	Res	Type
7	1H	122	THR
8	1I	5	LEU
8	1I	7	GLU
8	1I	37	VAL
8	1I	38	LEU
8	1I	78	THR
8	1I	92	VAL
8	1I	96	ASP
8	1I	101	LEU
8	1I	104	GLN
8	1I	109	ILE
8	1I	127	VAL
8	1I	140	LEU
9	1N	9	VAL
9	1N	14	VAL
9	1N	33	LEU
9	1N	48	MET
9	1N	59	LYS
9	1N	62	VAL
9	1N	67	LEU
9	1N	73	THR
9	1N	99	LEU
9	1N	119	ARG
9	1N	133	GLN
10	1O	23	ARG
10	1O	24	VAL
10	1O	70	LYS
10	1O	94	ARG
10	1O	98	VAL
11	1P	1	MET
11	1P	59	LEU
11	1P	75	ILE
11	1P	95	VAL
11	1P	99	LEU
11	1P	149	GLU
12	1Q	2	LEU
12	1Q	5	ARG
12	1Q	7	MET
12	1Q	21	THR
12	1Q	75	THR
12	1Q	81	VAL
12	1Q	109	VAL

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Mol	Chain	Res	Type
12	1Q	112	GLU
12	1Q	130	LYS
13	1R	8	ARG
13	1R	36	THR
13	1R	67	LEU
13	1R	75	LEU
13	1R	96	ARG
13	1R	100	LEU
13	1R	114	VAL
14	1S	14	VAL
14	1S	27	SER
14	1S	50	SER
14	1S	52	SER
14	1S	57	LYS
14	1S	59	LYS
14	1S	85	VAL
15	1T	28	VAL
15	1T	34	VAL
15	1T	49	VAL
15	1T	89	VAL
15	1T	96	ARG
16	1U	8	VAL
16	1U	59	ARG
16	1U	77	SER
16	1U	104	GLN
16	1U	108	GLU
17	1V	32	THR
17	1V	51	VAL
17	1V	61	VAL
17	1V	79	VAL
18	1W	11	ARG
18	1W	15	ARG
18	1W	17	VAL
18	1W	23	LEU
18	1W	49	LYS
18	1W	63	ASP
18	1W	100	THR
19	1X	35	THR
19	1X	52	VAL
19	1X	68	ARG
20	1Y	43	ASN
20	1Y	64	GLU

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Mol	Chain	Res	Type
20	1Y	67	LEU
20	1Y	72	VAL
20	1Y	73	ARG
20	1Y	99	CYS
20	1Y	107	ASP
21	1Z	18	LEU
21	1Z	33	LEU
21	1Z	42	VAL
21	1Z	61	LEU
21	1Z	73	GLN
21	1Z	86	VAL
21	1Z	93	ASP
21	1Z	94	GLU
21	1Z	118	GLN
21	1Z	126	VAL
21	1Z	150	LEU
21	1Z	155	LEU
21	1Z	161	VAL
21	1Z	163	LEU
21	1Z	170	THR
21	1Z	171	ILE
21	1Z	180	VAL
21	1Z	191	VAL
21	1Z	202	GLU
22	10	14	ARG
22	10	49	LYS
22	10	74	ARG
23	11	21	ARG
23	11	30	VAL
23	11	56	GLN
24	12	19	VAL
24	12	30	ARG
24	12	53	LEU
24	12	55	ARG
24	12	70	GLN
25	13	54	VAL
25	13	56	VAL
25	13	58	VAL
26	14	49	PHE
26	14	50	VAL
26	14	52	THR
26	14	60	GLN

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Mol	Chain	Res	Type
27	15	6	VAL
27	15	40	LYS
27	15	55	ARG
27	15	58	LEU
27	15	60	VAL
28	16	6	ARG
28	16	47	THR
28	16	52	VAL
29	17	1	MET
29	17	43	THR
30	18	14	VAL
30	18	23	VAL
30	18	29	LYS
33	1b	43	ASP
33	1b	45	GLN
33	1b	48	MET
33	1b	51	LEU
33	1b	80	ILE
33	1b	96	ARG
33	1b	111	ARG
33	1b	113	HIS
33	1b	124	SER
33	1b	130	ARG
33	1b	158	LEU
33	1b	162	ILE
33	1b	185	ILE
33	1b	200	ILE
33	1b	221	LEU
33	1b	229	VAL
33	1b	230	VAL
34	1c	3	ASN
34	1c	15	THR
34	1c	64	VAL
34	1c	70	VAL
34	1c	98	ASN
34	1c	102	ASN
34	1c	105	GLU
34	1c	115	LEU
34	1c	124	ILE
34	1c	154	SER
34	1c	195	VAL
35	1d	8	VAL

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Mol	Chain	Res	Type
35	1d	17	VAL
35	1d	19	LEU
35	1d	67	ILE
35	1d	76	ARG
35	1d	83	SER
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	188	LEU
35	1d	190	ASP
35	1d	193	ASP
35	1d	194	LEU
35	1d	196	LEU
36	1e	10	MET
36	1e	12	LEU
36	1e	20	GLN
36	1e	31	LEU
36	1e	41	VAL
36	1e	55	VAL
36	1e	73	ASN
36	1e	80	ILE
36	1e	101	ILE
36	1e	120	THR
37	1f	17	SER
37	1f	19	LEU
37	1f	57	GLN
37	1f	69	GLU
37	1f	78	GLU
37	1f	86	ARG
38	1g	6	ARG
38	1g	77	SER
38	1g	90	GLU
38	1g	91	VAL
38	1g	97	GLN
38	1g	113	GLU
39	1h	3	THR
39	1h	24	THR
39	1h	25	ASP

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Mol	Chain	Res	Type
39	1h	26	VAL
39	1h	51	VAL
39	1h	82	HIS
39	1h	99	GLU
39	1h	104	ARG
39	1h	120	THR
40	1i	14	VAL
40	1i	17	VAL
40	1i	19	LEU
40	1i	27	THR
40	1i	64	THR
40	1i	65	VAL
40	1i	81	ILE
40	1i	125	TYR
40	1i	127	LYS
41	1j	12	ASP
41	1j	38	ILE
41	1j	67	THR
41	1j	94	VAL
41	1j	100	THR
42	1k	16	SER
42	1k	30	VAL
42	1k	87	THR
43	1l	18	VAL
43	1l	43	VAL
43	1l	54	LYS
43	1l	55	VAL
43	1l	83	VAL
43	1l	84	LEU
43	1l	117	ARG
44	1m	14	ARG
44	1m	15	VAL
44	1m	56	LEU
44	1m	63	THR
45	1n	12	ARG
45	1n	15	LYS
45	1n	17	LYS
45	1n	18	VAL
45	1n	22	THR
45	1n	33	VAL
46	1o	26	GLU
46	1o	39	LEU

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Mol	Chain	Res	Type
46	1o	83	GLU
47	1p	2	VAL
47	1p	20	VAL
47	1p	21	VAL
47	1p	29	ASP
47	1p	45	THR
47	1p	49	LEU
47	1p	61	SER
47	1p	67	THR
47	1p	72	ARG
47	1p	74	LEU
48	1q	9	VAL
48	1q	12	SER
48	1q	24	GLU
48	1q	53	LEU
48	1q	70	ARG
48	1q	85	VAL
48	1q	100	LYS
49	1r	21	LYS
49	1r	25	THR
49	1r	26	LEU
49	1r	42	ARG
49	1r	76	LEU
49	1r	82	THR
49	1r	83	GLU
50	1s	5	LEU
50	1s	28	LYS
50	1s	37	ARG
50	1s	56	GLN
51	1t	10	LEU
51	1t	24	LEU
51	1t	62	LEU
51	1t	68	LYS
51	1t	84	LEU
51	1t	100	ILE
53	1y	29	LYS
53	1y	42	SER
53	1y	46	GLN
3	2D	3	VAL
3	2D	12	SER
3	2D	113	VAL
3	2D	138	VAL

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Mol	Chain	Res	Type
3	2D	141	VAL
3	2D	142	VAL
3	2D	155	LEU
3	2D	173	VAL
3	2D	183	ARG
3	2D	193	VAL
3	2D	211	ARG
3	2D	217	ARG
3	2D	221	VAL
3	2D	229	VAL
3	2D	242	ARG
3	2D	259	THR
3	2D	270	ILE
3	2D	274	ARG
4	2E	9	VAL
4	2E	12	THR
4	2E	38	THR
4	2E	47	VAL
4	2E	75	VAL
4	2E	116	VAL
4	2E	119	ARG
4	2E	144	ARG
4	2E	163	GLU
4	2E	170	LEU
4	2E	181	LEU
4	2E	184	VAL
4	2E	188	VAL
5	2F	18	ARG
5	2F	20	LEU
5	2F	33	LEU
5	2F	57	VAL
5	2F	74	ARG
5	2F	88	VAL
5	2F	106	ARG
5	2F	126	VAL
5	2F	132	VAL
5	2F	135	LYS
5	2F	140	LEU
5	2F	165	ARG
5	2F	175	THR
5	2F	176	LEU
5	2F	183	VAL

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Mol	Chain	Res	Type
5	2F	192	LEU
5	2F	201	VAL
5	2F	206	ILE
6	2G	3	LEU
6	2G	13	GLU
6	2G	14	GLU
6	2G	26	GLN
6	2G	39	ILE
6	2G	43	LEU
6	2G	49	ASP
6	2G	53	LEU
6	2G	77	ILE
6	2G	80	PHE
6	2G	109	VAL
6	2G	133	LEU
6	2G	139	LEU
6	2G	159	VAL
6	2G	168	GLU
7	2H	4	ILE
7	2H	33	LEU
7	2H	34	GLU
7	2H	40	GLU
7	2H	44	VAL
7	2H	49	VAL
7	2H	50	VAL
7	2H	52	VAL
7	2H	70	THR
7	2H	81	GLU
7	2H	86	GLU
7	2H	95	ARG
7	2H	97	ARG
7	2H	105	LEU
7	2H	106	THR
7	2H	127	GLU
7	2H	133	VAL
7	2H	134	SER
7	2H	136	ILE
7	2H	139	GLN
7	2H	167	GLU
7	2H	171	LEU
8	2I	19	VAL
8	2I	38	LEU

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Mol	Chain	Res	Type
8	2I	43	ASN
8	2I	75	LEU
8	2I	76	THR
8	2I	92	VAL
8	2I	108	THR
8	2I	127	VAL
8	2I	140	LEU
9	2N	28	THR
9	2N	32	THR
9	2N	48	MET
9	2N	58	ASP
9	2N	62	VAL
9	2N	67	LEU
9	2N	68	GLU
9	2N	87	LEU
9	2N	115	ARG
10	2O	20	MET
10	2O	24	VAL
10	2O	70	LYS
10	2O	92	GLU
10	2O	116	SER
11	2P	15	ARG
11	2P	29	LYS
11	2P	76	LYS
11	2P	90	ARG
11	2P	98	GLU
11	2P	99	LEU
11	2P	149	GLU
12	2Q	1	MET
12	2Q	2	LEU
12	2Q	16	ARG
12	2Q	75	THR
12	2Q	98	LYS
12	2Q	109	VAL
12	2Q	112	GLU
13	2R	36	THR
13	2R	67	LEU
13	2R	75	LEU
13	2R	96	ARG
13	2R	100	LEU
14	2S	5	THR
14	2S	27	SER

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Mol	Chain	Res	Type
14	2S	36	TYR
14	2S	44	LYS
14	2S	48	LEU
14	2S	52	SER
14	2S	56	LEU
14	2S	76	LYS
14	2S	85	VAL
15	2T	6	LEU
15	2T	28	VAL
15	2T	53	ARG
15	2T	65	LYS
15	2T	72	VAL
15	2T	85	LYS
15	2T	89	VAL
15	2T	96	ARG
16	2U	31	SER
16	2U	52	ARG
16	2U	104	GLN
16	2U	108	GLU
17	2V	18	LEU
17	2V	32	THR
17	2V	46	VAL
17	2V	51	VAL
17	2V	56	SER
17	2V	61	VAL
17	2V	62	LEU
17	2V	72	VAL
17	2V	79	VAL
18	2W	11	ARG
18	2W	15	ARG
18	2W	17	VAL
18	2W	23	LEU
18	2W	49	LYS
18	2W	60	ASN
18	2W	63	ASP
18	2W	100	THR
19	2X	49	VAL
20	2Y	3	VAL
20	2Y	7	VAL
20	2Y	28	LYS
20	2Y	31	LEU
20	2Y	42	VAL

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Mol	Chain	Res	Type
20	2Y	47	LYS
20	2Y	49	VAL
20	2Y	70	SER
20	2Y	72	VAL
20	2Y	85	VAL
20	2Y	92	ASN
20	2Y	99	CYS
21	2Z	5	LEU
21	2Z	18	LEU
21	2Z	33	LEU
21	2Z	42	VAL
21	2Z	53	ILE
21	2Z	74	VAL
21	2Z	86	VAL
21	2Z	94	GLU
21	2Z	107	THR
21	2Z	121	HIS
21	2Z	136	PHE
21	2Z	150	LEU
21	2Z	161	VAL
21	2Z	162	GLU
21	2Z	170	THR
21	2Z	175	VAL
21	2Z	180	VAL
21	2Z	185	GLU
21	2Z	193	GLU
22	20	36	ILE
22	20	49	LYS
22	20	68	GLU
23	21	11	ARG
23	21	40	ARG
23	21	46	LEU
23	21	51	VAL
23	21	80	LEU
23	21	85	LEU
23	21	89	GLU
23	21	95	LEU
24	22	32	LEU
24	22	41	ILE
24	22	52	ASP
24	22	53	LEU
25	23	23	LEU

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Mol	Chain	Res	Type
25	23	31	LEU
25	23	54	VAL
25	23	59	VAL
26	24	5	ILE
26	24	15	ILE
26	24	27	THR
26	24	50	VAL
26	24	59	PHE
26	24	62	ARG
26	24	63	TYR
27	25	6	VAL
27	25	29	THR
28	26	5	VAL
28	26	14	THR
28	26	48	VAL
28	26	52	VAL
29	27	1	MET
29	27	4	THR
29	27	24	THR
30	28	14	VAL
30	28	23	VAL
30	28	49	VAL
33	2b	7	VAL
33	2b	8	LYS
33	2b	9	GLU
33	2b	15	VAL
33	2b	16	HIS
33	2b	44	LEU
33	2b	49	GLU
33	2b	58	ILE
33	2b	82	ARG
33	2b	93	VAL
33	2b	96	ARG
33	2b	101	MET
33	2b	128	GLU
33	2b	136	VAL
33	2b	189	ASP
33	2b	197	VAL
33	2b	200	ILE
33	2b	208	ILE
34	2c	3	ASN
34	2c	4	LYS

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Mol	Chain	Res	Type
34	2c	8	ILE
34	2c	16	ARG
34	2c	17	ASP
34	2c	31	HIS
34	2c	33	LEU
34	2c	52	LEU
34	2c	101	LEU
34	2c	119	ARG
34	2c	127	ARG
34	2c	128	PHE
34	2c	152	ILE
34	2c	162	GLN
34	2c	182	ILE
34	2c	192	THR
34	2c	195	VAL
34	2c	196	LEU
34	2c	206	GLU
34	2c	207	VAL
35	2d	5	ILE
35	2d	8	VAL
35	2d	28	SER
35	2d	34	GLU
35	2d	80	GLU
35	2d	83	SER
35	2d	96	LEU
35	2d	108	LEU
35	2d	112	VAL
35	2d	122	ARG
35	2d	135	LEU
35	2d	150	GLU
35	2d	170	VAL
35	2d	175	SER
35	2d	184	LYS
35	2d	194	LEU
35	2d	209	ARG
36	2e	10	MET
36	2e	31	LEU
36	2e	33	VAL
36	2e	41	VAL
36	2e	47	LYS
36	2e	64	ARG
36	2e	65	ASN

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Mol	Chain	Res	Type
36	2e	68	GLU
36	2e	73	ASN
36	2e	75	THR
36	2e	79	GLU
36	2e	112	LEU
36	2e	135	THR
37	2f	19	LEU
37	2f	22	GLU
37	2f	37	VAL
37	2f	46	ARG
37	2f	61	LEU
37	2f	63	TYR
37	2f	69	GLU
37	2f	72	VAL
37	2f	73	ASN
37	2f	78	GLU
37	2f	81	ILE
37	2f	93	SER
38	2g	21	VAL
38	2g	24	THR
38	2g	30	ILE
38	2g	36	LYS
38	2g	51	GLN
38	2g	75	VAL
38	2g	77	SER
38	2g	95	ARG
38	2g	101	LEU
38	2g	111	ARG
38	2g	113	GLU
38	2g	115	ARG
38	2g	143	ARG
38	2g	144	MET
38	2g	153	HIS
39	2h	26	VAL
39	2h	29	SER
39	2h	53	VAL
39	2h	63	LEU
39	2h	91	ARG
39	2h	95	VAL
39	2h	97	VAL
39	2h	99	GLU
39	2h	112	LEU

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Mol	Chain	Res	Type
39	2h	114	THR
39	2h	137	VAL
40	2i	7	THR
40	2i	27	THR
40	2i	50	LEU
40	2i	59	PHE
40	2i	60	ASP
40	2i	63	ILE
40	2i	87	GLN
40	2i	117	HIS
40	2i	125	TYR
41	2j	29	ARG
41	2j	30	SER
41	2j	34	VAL
41	2j	49	VAL
41	2j	68	HIS
41	2j	74	ILE
41	2j	84	GLN
41	2j	92	THR
41	2j	95	GLU
41	2j	98	ILE
42	2k	48	ILE
42	2k	53	SER
42	2k	84	VAL
42	2k	109	VAL
42	2k	114	VAL
43	2l	10	LEU
43	2l	39	VAL
43	2l	41	ARG
43	2l	44	THR
43	2l	67	THR
43	2l	81	SER
43	2l	83	VAL
44	2m	8	GLU
44	2m	19	LEU
44	2m	27	LYS
44	2m	70	LEU
44	2m	81	LEU
44	2m	102	ARG
44	2m	106	ASN
44	2m	116	THR
45	2n	3	ARG

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Mol	Chain	Res	Type
45	2n	7	ILE
45	2n	13	THR
45	2n	18	VAL
45	2n	33	VAL
45	2n	57	ARG
46	2o	3	ILE
46	2o	39	LEU
46	2o	47	LYS
46	2o	48	LYS
46	2o	83	GLU
47	2p	1	MET
47	2p	2	VAL
47	2p	20	VAL
47	2p	21	VAL
47	2p	28	ARG
47	2p	54	GLU
47	2p	62	VAL
48	2q	53	LEU
48	2q	63	ARG
48	2q	70	ARG
48	2q	93	GLN
48	2q	96	GLU
48	2q	99	SER
49	2r	21	LYS
49	2r	25	THR
49	2r	26	LEU
49	2r	41	LYS
49	2r	42	ARG
49	2r	65	ILE
49	2r	69	THR
49	2r	76	LEU
50	2s	5	LEU
50	2s	6	LYS
50	2s	22	LEU
50	2s	33	THR
50	2s	35	SER
50	2s	48	THR
50	2s	63	THR
50	2s	81	ARG
51	2t	10	LEU
51	2t	20	LEU
51	2t	24	LEU

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Mol	Chain	Res	Type
51	2t	45	GLN
51	2t	46	GLU
51	2t	62	LEU
51	2t	71	THR
51	2t	84	LEU
51	2t	86	ARG
51	2t	99	LEU
51	2t	100	ILE
52	2u	24	ARG
53	2y	3	MET
53	2y	11	GLU
53	2y	12	ILE
53	2y	24	LEU
53	2y	46	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (155) such sidechains are listed below:

Mol	Chain	Res	Type
3	1D	87	ASN
3	1D	112	GLN
3	1D	253	GLN
4	1E	180	ASN
5	1F	8	GLN
5	1F	69	HIS
5	1F	203	GLN
6	1G	26	GLN
6	1G	108	ASN
6	1G	132	ASN
8	1I	104	GLN
9	1N	94	HIS
9	1N	133	GLN
11	1P	84	ASN
12	1Q	57	HIS
13	1R	50	HIS
13	1R	71	GLN
15	1T	123	GLN
16	1U	72	HIS
16	1U	81	HIS
16	1U	94	ASN
16	1U	104	GLN
19	1X	31	HIS
19	1X	82	GLN

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Mol	Chain	Res	Type
20	1Y	92	ASN
21	1Z	50	GLN
21	1Z	73	GLN
21	1Z	75	ASN
21	1Z	118	GLN
21	1Z	151	HIS
23	11	19	GLN
24	12	65	ASN
25	13	32	GLN
31	19	34	GLN
33	1b	19	HIS
33	1b	40	HIS
34	1c	6	HIS
34	1c	63	ASN
34	1c	69	HIS
34	1c	98	ASN
34	1c	102	ASN
34	1c	104	GLN
35	1d	123	HIS
35	1d	125	HIS
35	1d	129	ASN
36	1e	56	GLN
36	1e	73	ASN
37	1f	73	ASN
37	1f	100	ASN
38	1g	11	GLN
38	1g	28	ASN
38	1g	56	GLN
38	1g	64	GLN
38	1g	68	ASN
38	1g	122	HIS
39	1h	82	HIS
40	1i	3	GLN
40	1i	31	GLN
40	1i	87	GLN
41	1j	13	HIS
41	1j	69	ASN
41	1j	84	GLN
42	1k	22	HIS
42	1k	93	GLN
43	1l	99	HIS
44	1m	106	ASN

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Mol	Chain	Res	Type
46	1o	28	GLN
47	1p	16	HIS
48	1q	16	GLN
50	1s	23	ASN
50	1s	47	HIS
50	1s	57	HIS
50	1s	69	HIS
50	1s	83	HIS
53	1y	31	GLN
53	1y	38	HIS
3	2D	126	GLN
3	2D	253	GLN
5	2F	69	HIS
5	2F	133	ASN
5	2F	203	GLN
6	2G	26	GLN
6	2G	41	GLN
7	2H	139	GLN
8	2I	43	ASN
8	2I	104	GLN
9	2N	38	HIS
9	2N	56	ASN
10	2O	88	ASN
11	2P	27	HIS
12	2Q	141	GLN
13	2R	13	HIS
13	2R	31	HIS
13	2R	71	GLN
16	2U	94	ASN
17	2V	64	HIS
18	2W	60	ASN
19	2X	31	HIS
20	2Y	92	ASN
21	2Z	34	ASN
21	2Z	50	GLN
21	2Z	73	GLN
21	2Z	151	HIS
22	20	50	ASN
24	22	48	HIS
25	23	32	GLN
30	28	35	GLN
31	29	34	GLN

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Mol	Chain	Res	Type
33	2b	40	HIS
33	2b	78	GLN
33	2b	94	ASN
33	2b	135	GLN
33	2b	212	GLN
34	2c	6	HIS
34	2c	28	GLN
34	2c	31	HIS
34	2c	139	GLN
34	2c	170	GLN
34	2c	176	HIS
35	2d	43	HIS
35	2d	77	ASN
35	2d	116	GLN
35	2d	119	GLN
35	2d	123	HIS
35	2d	125	HIS
35	2d	161	ASN
35	2d	201	GLN
36	2e	20	GLN
36	2e	127	ASN
37	2f	94	GLN
38	2g	64	GLN
39	2h	81	HIS
39	2h	82	HIS
40	2i	3	GLN
41	2j	13	HIS
41	2j	21	GLN
41	2j	69	ASN
41	2j	84	GLN
42	2k	93	GLN
42	2k	99	GLN
42	2k	117	ASN
43	2l	99	HIS
44	2m	62	ASN
44	2m	92	HIS
46	2o	71	GLN
47	2p	16	HIS
48	2q	16	GLN
50	2s	14	HIS
50	2s	83	HIS
51	2t	90	GLN

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Mol	Chain	Res	Type
53	2y	9	GLN
53	2y	36	ASN
53	2y	46	GLN
53	2y	55	ASN
53	2y	79	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1A	2865/2915 (98%)	402 (14%)	32 (1%)
1	2A	2858/2915 (98%)	486 (17%)	35 (1%)
2	1B	119/121 (98%)	11 (9%)	0
2	2B	119/121 (98%)	16 (13%)	0
32	1a	1497/1521 (98%)	227 (15%)	0
32	2a	1501/1521 (98%)	254 (16%)	0
All	All	8959/9114 (98%)	1396 (15%)	67 (0%)

All (1396) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1A	12	U
1	1A	15	G
1	1A	34	C
1	1A	45	C
1	1A	71	A
1	1A	74	A
1	1A	75	G
1	1A	95	G
1	1A	118	A
1	1A	119	A
1	1A	120	U
1	1A	154(A)	C
1	1A	173	G
1	1A	174	C
1	1A	196	A
1	1A	199	A
1	1A	205	G
1	1A	214	G
1	1A	215	G
1	1A	216	A
1	1A	221	A

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Mol	Chain	Res	Type
1	1A	222	A
1	1A	229	A
1	1A	248	G
1	1A	265	A
1	1A	271(I)	G
1	1A	271(K)	U
1	1A	271(L)	U
1	1A	271(M)	G
1	1A	271(N)	U
1	1A	271(O)	C
1	1A	272(A)	U
1	1A	272(B)	G
1	1A	272(H)	C
1	1A	275	G
1	1A	279	C
1	1A	311	A
1	1A	324	A
1	1A	330	A
1	1A	352	G
1	1A	363	G
1	1A	386	G
1	1A	389	G
1	1A	396	G
1	1A	405	U
1	1A	411	G
1	1A	412	A
1	1A	422	A
1	1A	428	A
1	1A	448	U
1	1A	456	C
1	1A	457	A
1	1A	481	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

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Mol	Chain	Res	Type
1	1A	573	G
1	1A	575	A
1	1A	586	A
1	1A	592	G
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(F)	G
1	1A	652(T)	C
1	1A	652(U)	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	775	G
1	1A	776	G
1	1A	782	A
1	1A	784	A
1	1A	785	G
1	1A	790	C
1	1A	792	G
1	1A	805	G
1	1A	812	C
1	1A	827	U
1	1A	828	U
1	1A	859	G
1	1A	880	G
1	1A	886	C
1	1A	887	A
1	1A	888	C
1	1A	889	C
1	1A	890	A

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Mol	Chain	Res	Type
1	1A	892	G
1	1A	896	A
1	1A	910	A
1	1A	914	C
1	1A	931	G
1	1A	932	G
1	1A	945	A
1	1A	946	G
1	1A	953	A
1	1A	958	U
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	1041	C
1	1A	1042	G
1	1A	1043	C
1	1A	1046	A
1	1A	1047	G
1	1A	1048	A
1	1A	1053	C
1	1A	1054	A
1	1A	1061	U
1	1A	1062	G
1	1A	1063	G
1	1A	1065	U
1	1A	1067	A
1	1A	1069	A
1	1A	1070	A
1	1A	1071	G
1	1A	1073	A
1	1A	1075	C
1	1A	1076	C
1	1A	1077	A
1	1A	1078	U

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Mol	Chain	Res	Type
1	1A	1079	C
1	1A	1087	G
1	1A	1088	A
1	1A	1089	G
1	1A	1090	U
1	1A	1096	A
1	1A	1097	U
1	1A	1098	A
1	1A	1109	C
1	1A	1111	A
1	1A	1112	G
1	1A	1116	C
1	1A	1128	A
1	1A	1129	A
1	1A	1130	U
1	1A	1135	C
1	1A	1136	G
1	1A	1155	A
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
1	1A	1272	A
1	1A	1273	U
1	1A	1300	U
1	1A	1301	A
1	1A	1308	A
1	1A	1320	C
1	1A	1345	C
1	1A	1352	U
1	1A	1359	A
1	1A	1365	A
1	1A	1370	C

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Mol	Chain	Res	Type
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	1452	A
1	1A	1455	G
1	1A	1459	G
1	1A	1467	C
1	1A	1471	A
1	1A	1482	G
1	1A	1493	C
1	1A	1508	A
1	1A	1509	C
1	1A	1509(A)	A
1	1A	1525	G
1	1A	1542	A
1	1A	1543	C
1	1A	1554	A
1	1A	1558	A
1	1A	1569	A
1	1A	1578	U
1	1A	1579	A
1	1A	1581	G
1	1A	1584	C
1	1A	1586	A
1	1A	1608	A
1	1A	1609	A
1	1A	1610	A
1	1A	1648	C
1	1A	1654	A
1	1A	1664	A
1	1A	1674	G
1	1A	1696	G
1	1A	1700	A
1	1A	1701	A
1	1A	1722	A

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Mol	Chain	Res	Type
1	1A	1739	U
1	1A	1746	G
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	1816	G
1	1A	1817	G
1	1A	1839	G
1	1A	1847	A
1	1A	1877	A
1	1A	1878	G
1	1A	1900	A
1	1A	1906	G
1	1A	1913	A
1	1A	1929	G
1	1A	1930	G
1	1A	1937	A
1	1A	1938	A
1	1A	1955	U
1	1A	1963	U
1	1A	1965	C
1	1A	1967	C
1	1A	1970	A
1	1A	1971	A
1	1A	1972	A
1	1A	1993	U
1	1A	1997	G
1	1A	2020	A
1	1A	2023	G
1	1A	2031	A
1	1A	2032	G
1	1A	2033	A
1	1A	2043	C
1	1A	2055	C
1	1A	2056	G

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Mol	Chain	Res	Type
1	1A	2060	A
1	1A	2061	G
1	1A	2069	G
1	1A	2103	C
1	1A	2104	G
1	1A	2105	C
1	1A	2107	C
1	1A	2108	C
1	1A	2112	G
1	1A	2116	G
1	1A	2117	A
1	1A	2119	A
1	1A	2123	G
1	1A	2126	A
1	1A	2127	G
1	1A	2130	U
1	1A	2131	G
1	1A	2132	U
1	1A	2133	G
1	1A	2134	A
1	1A	2135	A
1	1A	2138	C
1	1A	2142	C
1	1A	2146	C
1	1A	2148	G
1	1A	2152	G
1	1A	2158	A
1	1A	2159	G
1	1A	2161	C
1	1A	2173	A
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	2225	A
1	1A	2235	G

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Mol	Chain	Res	Type
1	1A	2238	G
1	1A	2239	G
1	1A	2268	A
1	1A	2269	A
1	1A	2279	G
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	2325	G
1	1A	2326	C
1	1A	2334	G
1	1A	2336	A
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	2414	G
1	1A	2422	A
1	1A	2425	A
1	1A	2429	G
1	1A	2430	A
1	1A	2431	U
1	1A	2435	A
1	1A	2439	A
1	1A	2440	C
1	1A	2441	C
1	1A	2448	A
1	1A	2468	G
1	1A	2470	G
1	1A	2474	C
1	1A	2476	A
1	1A	2478	A
1	1A	2491	U
1	1A	2494	G
1	1A	2498	C

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Mol	Chain	Res	Type
1	1A	2502	G
1	1A	2505	G
1	1A	2506	U
1	1A	2518	A
1	1A	2529	G
1	1A	2535	G
1	1A	2554	U
1	1A	2566	A
1	1A	2567	G
1	1A	2573	C
1	1A	2602	A
1	1A	2603	G
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	2662	A
1	1A	2689	U
1	1A	2690	C
1	1A	2702	U
1	1A	2703	C
1	1A	2712(A)	A
1	1A	2713	A
1	1A	2714	G
1	1A	2726	U
1	1A	2733	A
1	1A	2758	A
1	1A	2764	A
1	1A	2765	A
1	1A	2766	G
1	1A	2778	A
1	1A	2790	A
1	1A	2791	C
1	1A	2802	G
1	1A	2818	G
1	1A	2820	A
1	1A	2821	A
1	1A	2833	G
1	1A	2835	A
1	1A	2839	G

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Mol	Chain	Res	Type
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	15	A
2	1B	45	A
2	1B	53	A
2	1B	56	G
2	1B	73	A
2	1B	84	C
2	1B	106	G
2	1B	110	G
32	1a	7	G
32	1a	9	G
32	1a	32	A
32	1a	39	G
32	1a	48	C
32	1a	51	A
32	1a	61	G
32	1a	69	G
32	1a	78	G
32	1a	79	G
32	1a	96	U
32	1a	101	A
32	1a	116	A
32	1a	121	C
32	1a	131	C
32	1a	143	A
32	1a	144	G
32	1a	163	C
32	1a	173	U
32	1a	174	C
32	1a	182	U
32	1a	189(D)	C
32	1a	189(G)	G
32	1a	195	A
32	1a	197	A
32	1a	203	U
32	1a	204	U
32	1a	216	G

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Mol	Chain	Res	Type
32	1a	247	G
32	1a	251	G
32	1a	258	G
32	1a	266	G
32	1a	267	C
32	1a	281	G
32	1a	289	G
32	1a	321	A
32	1a	328	C
32	1a	332	G
32	1a	347	G
32	1a	348	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	412	A
32	1a	413	G
32	1a	422	C
32	1a	423	G
32	1a	424	G
32	1a	429	U
32	1a	439	A
32	1a	442	C
32	1a	452	A
32	1a	461	A
32	1a	470	C
32	1a	475	G
32	1a	477	A
32	1a	480	U
32	1a	485	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

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Mol	Chain	Res	Type
32	1a	518	C
32	1a	519	C
32	1a	531	U
32	1a	532	A
32	1a	547	A
32	1a	550	G
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	607	A
32	1a	619	U
32	1a	630	G
32	1a	631	G
32	1a	632	A
32	1a	653	A
32	1a	661	G
32	1a	665	A
32	1a	666	G
32	1a	687	A
32	1a	688	G
32	1a	723	U
32	1a	731	G
32	1a	734	G
32	1a	750	G
32	1a	755	G
32	1a	759	A
32	1a	774	G
32	1a	777	A
32	1a	793	U
32	1a	794	A
32	1a	815	A
32	1a	817	C
32	1a	821	G
32	1a	828	A
32	1a	829	G
32	1a	836	G
32	1a	839	U
32	1a	840	C
32	1a	841	U

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Mol	Chain	Res	Type
32	1a	851	G
32	1a	891	U
32	1a	902	G
32	1a	914	A
32	1a	926	G
32	1a	927	G
32	1a	934	C
32	1a	935	A
32	1a	939	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	992	U
32	1a	993	G
32	1a	994	A
32	1a	998	G
32	1a	1001	A
32	1a	1001(A)	G
32	1a	1002	G
32	1a	1004	A
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
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	1033	G
32	1a	1037	C

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Mol	Chain	Res	Type
32	1a	1042	G
32	1a	1044	A
32	1a	1065	U
32	1a	1066	C
32	1a	1070	U
32	1a	1081	G
32	1a	1094	G
32	1a	1095	U
32	1a	1101	A
32	1a	1124	G
32	1a	1125	U
32	1a	1126	U
32	1a	1127	G
32	1a	1130	A
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	1168	A
32	1a	1183	A
32	1a	1184	G
32	1a	1196	U
32	1a	1197	G
32	1a	1202	G
32	1a	1208	C
32	1a	1212	U
32	1a	1213	A
32	1a	1224	G
32	1a	1227	A
32	1a	1238	A
32	1a	1240	U
32	1a	1241	G
32	1a	1256	A
32	1a	1257	U
32	1a	1258	G
32	1a	1270	C
32	1a	1278	U
32	1a	1279	A
32	1a	1280	A

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Mol	Chain	Res	Type
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	1338	G
32	1a	1340	A
32	1a	1346	A
32	1a	1347	G
32	1a	1353	G
32	1a	1370	G
32	1a	1381	U
32	1a	1397	C
32	1a	1419	G
32	1a	1442	G
32	1a	1442(A)	G
32	1a	1447	A
32	1a	1456	G
32	1a	1493	A
32	1a	1494	G
32	1a	1504	G
32	1a	1505	G
32	1a	1506	U
32	1a	1517	G
32	1a	1519	MA6
32	1a	1520	G
32	1a	1529	G
32	1a	1530	G
32	1a	1531	A
1	2A	10	G
1	2A	11	G
1	2A	12	U
1	2A	15	G
1	2A	34	C
1	2A	45	C
1	2A	71	A
1	2A	74	A
1	2A	75	G
1	2A	84	A
1	2A	95	G

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Mol	Chain	Res	Type
1	2A	102	G
1	2A	118	A
1	2A	119	A
1	2A	120	U
1	2A	131	G
1	2A	141	A
1	2A	157	U
1	2A	173	G
1	2A	181	A
1	2A	182	A
1	2A	196	A
1	2A	197	A
1	2A	199	A
1	2A	205	G
1	2A	214	G
1	2A	215	G
1	2A	216	A
1	2A	221	A
1	2A	222	A
1	2A	229	A
1	2A	230	U
1	2A	248	G
1	2A	265	A
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	311	A
1	2A	317	G
1	2A	324	A
1	2A	327	G
1	2A	329	G
1	2A	330	A
1	2A	333	G
1	2A	342	G
1	2A	352	G
1	2A	362	U

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Mol	Chain	Res	Type
1	2A	363	G
1	2A	370	G
1	2A	372	G
1	2A	386	G
1	2A	396	G
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	457	A
1	2A	470	A
1	2A	481	G
1	2A	504	U
1	2A	505	A
1	2A	509	C
1	2A	528	A
1	2A	530	G
1	2A	531	C
1	2A	532	A
1	2A	533	G
1	2A	545	G
1	2A	556	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	614(B)	G
1	2A	614(C)	A
1	2A	615	G
1	2A	616	G
1	2A	627	A
1	2A	634	C
1	2A	637	A
1	2A	645	C
1	2A	646	A
1	2A	652(B)	A
1	2A	652(C)	G

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Mol	Chain	Res	Type
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	740	U
1	2A	746	A
1	2A	747	U
1	2A	751	A
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	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	869	G
1	2A	880	G
1	2A	883	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	900	A
1	2A	901	A
1	2A	910	A
1	2A	915	C
1	2A	917	A

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Mol	Chain	Res	Type
1	2A	932	G
1	2A	938	G
1	2A	941	A
1	2A	945	A
1	2A	946	G
1	2A	953	A
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	1006	C
1	2A	1012	U
1	2A	1013	C
1	2A	1022	G
1	2A	1026	U
1	2A	1033	U
1	2A	1038	C
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	1053	C
1	2A	1054	A
1	2A	1055	G
1	2A	1058	G
1	2A	1060	U
1	2A	1064	C
1	2A	1065	U
1	2A	1066	U
1	2A	1067	A
1	2A	1068	G
1	2A	1069	A
1	2A	1070	A
1	2A	1071	G
1	2A	1072	C
1	2A	1073	A
1	2A	1074	G
1	2A	1076	C

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Mol	Chain	Res	Type
1	2A	1077	A
1	2A	1078	U
1	2A	1079	C
1	2A	1080	C
1	2A	1082	U
1	2A	1083	U
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	1098	A
1	2A	1108	U
1	2A	1109	C
1	2A	1112	G
1	2A	1116	C
1	2A	1117	G
1	2A	1129	A
1	2A	1130	U
1	2A	1135	C
1	2A	1136	G
1	2A	1171	G
1	2A	1211	U
1	2A	1212	G
1	2A	1220	A
1	2A	1229	G
1	2A	1236	G
1	2A	1244	G
1	2A	1253	A
1	2A	1256	G
1	2A	1271	G
1	2A	1272	A
1	2A	1276	A
1	2A	1287	A
1	2A	1300	U
1	2A	1301	A
1	2A	1303	G

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Mol	Chain	Res	Type
1	2A	1314	C
1	2A	1319	G
1	2A	1321	A
1	2A	1342	A
1	2A	1352	U
1	2A	1359	A
1	2A	1360	A
1	2A	1365	A
1	2A	1368	G
1	2A	1379	A
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	1427	A
1	2A	1428	C
1	2A	1445	A
1	2A	1450	G
1	2A	1455	G
1	2A	1458	C
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

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Mol	Chain	Res	Type
1	2A	1583	A
1	2A	1584	C
1	2A	1586	A
1	2A	1608	A
1	2A	1609	A
1	2A	1629	U
1	2A	1640	C
1	2A	1648	C
1	2A	1664	A
1	2A	1674	G
1	2A	1696	G
1	2A	1700	A
1	2A	1701	A
1	2A	1703	G
1	2A	1721	G
1	2A	1722	A
1	2A	1746	G
1	2A	1756	G
1	2A	1763	G
1	2A	1764	G
1	2A	1773	A
1	2A	1780	A
1	2A	1782	C
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	1839	G
1	2A	1847	A
1	2A	1848	A
1	2A	1860	G
1	2A	1877	A
1	2A	1878	G
1	2A	1889	A
1	2A	1900	A
1	2A	1906	G
1	2A	1914	C
1	2A	1927	A

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Mol	Chain	Res	Type
1	2A	1929	G
1	2A	1930	G
1	2A	1937	A
1	2A	1938	A
1	2A	1955	U
1	2A	1963	U
1	2A	1967	C
1	2A	1970	A
1	2A	1971	A
1	2A	1972	A
1	2A	1993	U
1	2A	1997	G
1	2A	2020	A
1	2A	2023	G
1	2A	2031	A
1	2A	2033	A
1	2A	2043	C
1	2A	2055	C
1	2A	2056	G
1	2A	2060	A
1	2A	2061	G
1	2A	2069	G
1	2A	2096	U
1	2A	2099	U
1	2A	2100	G
1	2A	2101	G
1	2A	2103	C
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	2116	G
1	2A	2117	A
1	2A	2118	U
1	2A	2121	G
1	2A	2123	G
1	2A	2126	A
1	2A	2127	G
1	2A	2129	C
1	2A	2131	G

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Mol	Chain	Res	Type
1	2A	2132	U
1	2A	2133	G
1	2A	2134	A
1	2A	2135	A
1	2A	2136	C
1	2A	2145	C
1	2A	2146	C
1	2A	2147	G
1	2A	2148	G
1	2A	2150	U
1	2A	2151	G
1	2A	2153	G
1	2A	2155	G
1	2A	2158	A
1	2A	2159	G
1	2A	2160	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	2171	A
1	2A	2172	U
1	2A	2173	A
1	2A	2176	A
1	2A	2178	C
1	2A	2180	U
1	2A	2182	G
1	2A	2183	C
1	2A	2184	G
1	2A	2186	G
1	2A	2188	C
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	2225	A

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Mol	Chain	Res	Type
1	2A	2238	G
1	2A	2239	G
1	2A	2269	A
1	2A	2274	A
1	2A	2275	C
1	2A	2279	G
1	2A	2280	G
1	2A	2283	C
1	2A	2287	A
1	2A	2289	G
1	2A	2293	C
1	2A	2305	A
1	2A	2308	G
1	2A	2311	A
1	2A	2320	A
1	2A	2321	G
1	2A	2322	A
1	2A	2325	G
1	2A	2335	A
1	2A	2336	A
1	2A	2347	C
1	2A	2350	C
1	2A	2354	G
1	2A	2366	A
1	2A	2379	G
1	2A	2383	G
1	2A	2385	C
1	2A	2406	U
1	2A	2407	G
1	2A	2419	U
1	2A	2422	A
1	2A	2423	U
1	2A	2425	A
1	2A	2429	G
1	2A	2430	A
1	2A	2435	A
1	2A	2439	A
1	2A	2441	C
1	2A	2448	A
1	2A	2474	C
1	2A	2476	A
1	2A	2478	A

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Mol	Chain	Res	Type
1	2A	2491	U
1	2A	2498	C
1	2A	2502	G
1	2A	2505	G
1	2A	2506	U
1	2A	2518	A
1	2A	2520	C
1	2A	2529	G
1	2A	2554	U
1	2A	2555	U
1	2A	2566	A
1	2A	2567	G
1	2A	2573	C
1	2A	2578	G
1	2A	2602	A
1	2A	2603	G
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	2703	C
1	2A	2712(A)	A
1	2A	2713	A
1	2A	2714	G
1	2A	2726	U
1	2A	2733	A
1	2A	2748	A
1	2A	2757	A
1	2A	2758	A
1	2A	2764	A
1	2A	2765	A
1	2A	2778	A
1	2A	2780	G
1	2A	2802	G
1	2A	2811	G

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Mol	Chain	Res	Type
1	2A	2818	G
1	2A	2820	A
1	2A	2821	A
1	2A	2833	G
1	2A	2835	A
1	2A	2836	U
1	2A	2872	G
1	2A	2876	G
1	2A	2880	C
1	2A	2891	G
1	2A	2894	G
1	2A	2896	C
1	2A	2897	U
2	2B	7	G
2	2B	9	G
2	2B	12	C
2	2B	30	C
2	2B	33	G
2	2B	35	U
2	2B	51	G
2	2B	56	G
2	2B	66	A
2	2B	73	A
2	2B	84	C
2	2B	94	C
2	2B	106	G
2	2B	109	C
2	2B	110	G
2	2B	120	A
32	2a	5	U
32	2a	7	G
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	52	G
32	2a	61	G
32	2a	66	G

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Mol	Chain	Res	Type
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	142	G
32	2a	151	A
32	2a	156	G
32	2a	163	C
32	2a	173	U
32	2a	174	C
32	2a	182	U
32	2a	189(C)	C
32	2a	189(D)	C
32	2a	195	A
32	2a	197	A
32	2a	201	C
32	2a	202	U
32	2a	203	U
32	2a	204	U
32	2a	216	G
32	2a	247	G
32	2a	250	A
32	2a	251	G
32	2a	258	G
32	2a	266	G
32	2a	267	C
32	2a	289	G
32	2a	298	A
32	2a	316	G
32	2a	321	A
32	2a	328	C
32	2a	332	G
32	2a	351	G
32	2a	352	C
32	2a	353	A
32	2a	354	G
32	2a	367	U
32	2a	372	C
32	2a	382	A
32	2a	384	G

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Mol	Chain	Res	Type
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	439	A
32	2a	442	C
32	2a	446	G
32	2a	452	A
32	2a	458	C
32	2a	461	A
32	2a	470	C
32	2a	471	G
32	2a	476	G
32	2a	482	A
32	2a	484	G
32	2a	485	G
32	2a	496	A
32	2a	498	U
32	2a	505	G
32	2a	509	A
32	2a	510	A
32	2a	511	C
32	2a	518	C
32	2a	521	G
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	592	G
32	2a	596	C
32	2a	630	G
32	2a	631	G
32	2a	632	A
32	2a	653	A

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Mol	Chain	Res	Type
32	2a	659	U
32	2a	665	A
32	2a	687	A
32	2a	688	G
32	2a	690	G
32	2a	693	G
32	2a	695	A
32	2a	702	A
32	2a	703	G
32	2a	723	U
32	2a	724	G
32	2a	731	G
32	2a	749	C
32	2a	753	A
32	2a	755	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	840	C
32	2a	841	U
32	2a	851	G
32	2a	854	G
32	2a	859	A
32	2a	902	G
32	2a	914	A
32	2a	916	G
32	2a	926	G
32	2a	927	G
32	2a	931	C
32	2a	934	C
32	2a	935	A
32	2a	942	G
32	2a	960	U
32	2a	961	U
32	2a	966	M2G
32	2a	968	A
32	2a	969	A
32	2a	971	G

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Mol	Chain	Res	Type
32	2a	972	C
32	2a	974	A
32	2a	975	A
32	2a	976	G
32	2a	977	A
32	2a	989	C
32	2a	992	U
32	2a	993	G
32	2a	994	A
32	2a	1004	A
32	2a	1005	A
32	2a	1006	C
32	2a	1007	C
32	2a	1009	G
32	2a	1020	U
32	2a	1022	G
32	2a	1023	G
32	2a	1025	U
32	2a	1026	G
32	2a	1027	C
32	2a	1028	C
32	2a	1029	C
32	2a	1030(A)	G
32	2a	1030(B)	C
32	2a	1032	G
32	2a	1033	G
32	2a	1041	A
32	2a	1043	C
32	2a	1047	G
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	1095	U
32	2a	1101	A
32	2a	1113	C
32	2a	1117	G
32	2a	1122	U

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Mol	Chain	Res	Type
32	2a	1125	U
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	1147	C
32	2a	1152	A
32	2a	1157	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	1211	U
32	2a	1212	U
32	2a	1214	C
32	2a	1216	G
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	1285	A
32	2a	1286	A
32	2a	1287	A
32	2a	1297	C

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Mol	Chain	Res	Type
32	2a	1300	G
32	2a	1302	U
32	2a	1303	C
32	2a	1317	C
32	2a	1320	C
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	1364	U
32	2a	1370	G
32	2a	1380	U
32	2a	1397	C
32	2a	1419	G
32	2a	1442	G
32	2a	1442(A)	G
32	2a	1446	U
32	2a	1447	A
32	2a	1456	G
32	2a	1460	A
32	2a	1492	A
32	2a	1499	A
32	2a	1503	A
32	2a	1504	G
32	2a	1506	U
32	2a	1517	G
32	2a	1520	G
32	2a	1529	G
32	2a	1530	G

All (67) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1A	195	A
1	1A	196	A
1	1A	266	G
1	1A	278	A
1	1A	746	A
1	1A	764	A
1	1A	839	U

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Mol	Chain	Res	Type
1	1A	888	C
1	1A	895	U
1	1A	958	U
1	1A	974	G
1	1A	1047	G
1	1A	1065	U
1	1A	1142(A)	A
1	1A	1175	U
1	1A	1176	G
1	1A	1210	A
1	1A	1300	U
1	1A	1301	A
1	1A	1442	G
1	1A	1608	A
1	1A	1653	G
1	1A	1997	G
1	1A	2111	C
1	1A	2126	A
1	1A	2406	U
1	1A	2430	A
1	1A	2439	A
1	1A	2602	A
1	1A	2611	U
1	1A	2689	U
1	1A	2893	G
1	2A	9	U
1	2A	195	A
1	2A	196	A
1	2A	266	G
1	2A	271(M)	G
1	2A	277	C
1	2A	746	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	1053	C
1	2A	1057	A
1	2A	1065	U
1	2A	1067	A

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Mol	Chain	Res	Type
1	2A	1073	A
1	2A	1076	C
1	2A	1210	A
1	2A	1275	A
1	2A	1420	U
1	2A	1442	G
1	2A	1491	G
1	2A	1992	G
1	2A	2126	A
1	2A	2171	A
1	2A	2172	U
1	2A	2321	G
1	2A	2406	U
1	2A	2439	A
1	2A	2601	C
1	2A	2602	A
1	2A	2689	U
1	2A	2756	U

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

48 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	5MU	2A	1939	1	19,22,23	1.41	4 (21%)	27,32,35	2.38	8 (29%)
1	5MC	2A	1942	1	19,22,23	1.66	3 (15%)	26,32,35	1.20	2 (7%)
1	OMC	1A	1920	1,54	19,22,23	0.82	0	25,31,34	0.91	1 (4%)
32	M2G	2a	966	32	24,27,28	1.26	3 (12%)	33,40,43	1.82	5 (15%)
43	0TD	1l	92	43	8,9,10	4.69	1 (12%)	6,11,13	5.25	3 (50%)
32	G7M	2a	527	32	23,26,27	2.41	5 (21%)	34,39,42	2.95	10 (29%)
32	MA6	2a	1518	32	23,26,27	0.37	0	33,38,41	2.00	9 (27%)
1	PSU	1A	2605	1,54	18,21,22	1.42	3 (16%)	21,30,33	2.16	4 (19%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
32	2MG	1a	1207	32	23,26,27	1.24	2 (8%)	33,38,41	2.44	9 (27%)
32	5MC	2a	1404	32	19,22,23	1.75	3 (15%)	26,32,35	1.18	2 (7%)
32	UR3	2a	1498	32	19,22,23	0.99	1 (5%)	26,32,35	1.69	3 (11%)
32	5MC	2a	1400	32	19,22,23	1.59	3 (15%)	26,32,35	1.14	2 (7%)
1	5MC	1A	1962	1	19,22,23	1.73	3 (15%)	26,32,35	1.15	2 (7%)
1	2MA	1A	2503	1,54	22,25,26	1.47	4 (18%)	32,37,40	2.38	9 (28%)
1	OMC	2A	1920	1	19,22,23	0.79	0	25,31,34	1.04	1 (4%)
1	PSU	1A	1917	1	18,21,22	1.34	2 (11%)	21,30,33	1.86	4 (19%)
1	OMG	1A	2251	1,54	23,26,27	1.23	3 (13%)	32,38,41	1.96	6 (18%)
1	PSU	1A	1911	1	18,21,22	1.33	2 (11%)	21,30,33	2.08	5 (23%)
32	PSU	2a	516	32,54	18,21,22	1.37	2 (11%)	21,30,33	2.06	5 (23%)
1	5MU	1A	1939	1,54	19,22,23	1.31	4 (21%)	27,32,35	2.36	6 (22%)
1	PSU	2A	2605	1	18,21,22	1.41	3 (16%)	21,30,33	2.09	5 (23%)
32	MA6	1a	1519	32	23,26,27	0.44	0	33,38,41	2.06	10 (30%)
1	PSU	2A	1917	1	18,21,22	1.39	2 (11%)	21,30,33	1.93	3 (14%)
1	5MC	2A	1962	1,54	19,22,23	1.74	3 (15%)	26,32,35	1.16	2 (7%)
1	2MU	2A	2552	1,54	19,22,24	1.28	3 (15%)	25,31,36	1.77	6 (24%)
32	M2G	1a	966	32	24,27,28	1.27	4 (16%)	33,40,43	1.83	6 (18%)
32	5MC	1a	1407	32	19,22,23	1.73	2 (10%)	26,32,35	1.10	3 (11%)
1	5MU	2A	1915	1	19,22,23	1.50	4 (21%)	27,32,35	2.17	9 (33%)
1	2MA	2A	2503	1,54	22,25,26	1.45	4 (18%)	32,37,40	2.36	8 (25%)
32	5MC	2a	967	32	19,22,23	1.80	3 (15%)	26,32,35	1.09	3 (11%)
32	PSU	1a	516	32,54	18,21,22	1.38	2 (11%)	21,30,33	1.99	4 (19%)
32	G7M	1a	527	32	23,26,27	2.34	5 (21%)	34,39,42	2.96	10 (29%)
32	UR3	1a	1498	32	19,22,23	0.99	2 (10%)	26,32,35	1.96	4 (15%)
32	5MC	1a	967	32	19,22,23	1.66	3 (15%)	26,32,35	1.05	2 (7%)
1	5MU	1A	1915	1	19,22,23	1.44	4 (21%)	27,32,35	2.23	10 (37%)
32	5MC	2a	1407	32	19,22,23	1.52	3 (15%)	26,32,35	1.15	3 (11%)
43	0TD	2l	92	43	8,9,10	4.39	1 (12%)	6,11,13	8.28	2 (33%)
32	MA6	1a	1518	32	23,26,27	0.39	0	33,38,41	1.96	9 (27%)
32	2MG	2a	1207	32	23,26,27	1.23	3 (13%)	33,38,41	2.13	8 (24%)
32	5MC	1a	1400	32	19,22,23	1.67	3 (15%)	26,32,35	1.18	2 (7%)
32	4OC	2a	1402	32	20,23,24	0.76	0	25,32,35	0.98	1 (4%)
32	5MC	1a	1404	32	19,22,23	1.76	2 (10%)	26,32,35	1.17	3 (11%)
32	4OC	1a	1402	32	20,23,24	0.74	0	25,32,35	1.12	1 (4%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	2MU	1A	2552	1,54	19,22,24	1.29	3 (15%)	25,31,36	1.91	6 (24%)
32	MA6	2a	1519	32	23,26,27	0.42	0	33,38,41	2.08	9 (27%)
1	OMG	2A	2251	1,54	23,26,27	1.22	3 (13%)	32,38,41	1.96	7 (21%)
1	5MC	1A	1942	1,54	19,22,23	1.61	3 (15%)	26,32,35	1.06	2 (7%)
1	PSU	2A	1911	1	18,21,22	1.39	2 (11%)	21,30,33	2.07	4 (19%)

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	5MU	2A	1939	1	-	0/7/25/26	0/2/2/2
1	5MC	2A	1942	1	-	0/7/25/26	0/2/2/2
1	OMC	1A	1920	1,54	-	1/9/27/28	0/2/2/2
32	M2G	2a	966	32	-	0/11/29/30	0/3/3/3
43	0TD	1l	92	43	-	2/7/12/14	-
32	G7M	2a	527	32	-	2/7/25/26	0/3/3/3
32	MA6	2a	1518	32	-	0/11/29/30	0/3/3/3
1	PSU	1A	2605	1,54	-	0/7/25/26	0/2/2/2
32	2MG	1a	1207	32	-	0/9/27/28	0/3/3/3
32	5MC	2a	1404	32	-	0/7/25/26	0/2/2/2
32	UR3	2a	1498	32	-	0/7/25/26	0/2/2/2
32	5MC	2a	1400	32	-	0/7/25/26	0/2/2/2
1	5MC	1A	1962	1	-	0/7/25/26	0/2/2/2
1	2MA	1A	2503	1,54	-	1/7/25/26	0/3/3/3
1	OMC	2A	1920	1	-	1/9/27/28	0/2/2/2
1	PSU	1A	1917	1	-	0/7/25/26	0/2/2/2
1	OMG	1A	2251	1,54	-	1/9/27/28	0/3/3/3
1	PSU	1A	1911	1	-	0/7/25/26	0/2/2/2
32	PSU	2a	516	32,54	-	0/7/25/26	0/2/2/2
1	5MU	1A	1939	1,54	-	0/7/25/26	0/2/2/2
1	PSU	2A	2605	1	-	0/7/25/26	0/2/2/2
32	MA6	1a	1519	32	-	2/11/29/30	0/3/3/3
1	PSU	2A	1917	1	-	0/7/25/26	0/2/2/2
1	5MC	2A	1962	1,54	-	0/7/25/26	0/2/2/2
1	2MU	2A	2552	1,54	-	0/9/27/28	0/2/2/2
32	M2G	1a	966	32	-	0/11/29/30	0/3/3/3
32	5MC	1a	1407	32	-	0/7/25/26	0/2/2/2
1	5MU	2A	1915	1	-	2/7/25/26	0/2/2/2
1	2MA	2A	2503	1,54	-	0/7/25/26	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
32	5MC	2a	967	32	-	0/7/25/26	0/2/2/2
32	PSU	1a	516	32,54	-	0/7/25/26	0/2/2/2
32	G7M	1a	527	32	-	2/7/25/26	0/3/3/3
32	UR3	1a	1498	32	-	0/7/25/26	0/2/2/2
32	5MC	1a	967	32	-	0/7/25/26	0/2/2/2
1	5MU	1A	1915	1	-	2/7/25/26	0/2/2/2
32	5MC	2a	1407	32	-	0/7/25/26	0/2/2/2
43	0TD	2l	92	43	-	3/7/12/14	-
32	MA6	1a	1518	32	-	0/11/29/30	0/3/3/3
32	2MG	2a	1207	32	-	0/9/27/28	0/3/3/3
32	5MC	1a	1400	32	-	2/7/25/26	0/2/2/2
32	4OC	2a	1402	32	-	0/9/29/30	0/2/2/2
32	5MC	1a	1404	32	-	0/7/25/26	0/2/2/2
32	4OC	1a	1402	32	-	1/9/29/30	0/2/2/2
1	2MU	1A	2552	1,54	-	0/9/27/28	0/2/2/2
32	MA6	2a	1519	32	-	3/11/29/30	0/3/3/3
1	OMG	2A	2251	1,54	-	0/9/27/28	0/3/3/3
1	5MC	1A	1942	1,54	-	0/7/25/26	0/2/2/2
1	PSU	2A	1911	1	-	0/7/25/26	0/2/2/2

All (115) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
43	1l	92	0TD	CB-SB	-12.82	1.69	1.82
43	2l	92	0TD	CB-SB	-12.04	1.70	1.82
32	2a	527	G7M	C8-N7	7.84	1.46	1.33
32	1a	527	G7M	C8-N7	7.51	1.45	1.33
32	2a	967	5MC	C5-C4	6.75	1.49	1.44
32	1a	1404	5MC	C5-C4	6.59	1.49	1.44
1	2A	1962	5MC	C5-C4	6.45	1.49	1.44
1	1A	1962	5MC	C5-C4	6.45	1.49	1.44
32	1a	1407	5MC	C5-C4	6.44	1.49	1.44
32	2a	1404	5MC	C5-C4	6.36	1.48	1.44
32	1a	967	5MC	C5-C4	5.97	1.48	1.44
1	2A	1942	5MC	C5-C4	5.96	1.48	1.44
32	1a	1400	5MC	C5-C4	5.92	1.48	1.44
1	1A	1942	5MC	C5-C4	5.80	1.48	1.44
32	2a	1400	5MC	C5-C4	5.69	1.48	1.44
32	2a	1407	5MC	C5-C4	5.39	1.48	1.44
32	2a	527	G7M	C5-N7	-4.70	1.33	1.39
32	1a	527	G7M	C5-N7	-4.61	1.33	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	2A	2503	2MA	C5-C4	4.32	1.46	1.39
32	1a	527	G7M	C8-N9	4.23	1.47	1.35
32	2a	527	G7M	C8-N9	4.22	1.47	1.35
1	1A	2503	2MA	C5-C4	4.03	1.46	1.39
32	2a	527	G7M	C5-C4	3.72	1.47	1.38
32	1a	527	G7M	C5-C4	3.68	1.47	1.38
32	1a	516	PSU	C6-C5	3.56	1.39	1.35
1	2A	1911	PSU	C6-C5	3.50	1.39	1.35
1	2A	2605	PSU	C6-C5	3.36	1.39	1.35
1	1A	1911	PSU	C6-C5	3.35	1.39	1.35
1	1A	1917	PSU	C6-C5	3.32	1.39	1.35
1	1A	2605	PSU	C6-C5	3.30	1.38	1.35
32	2a	516	PSU	C6-C5	3.28	1.38	1.35
32	2a	1207	2MG	C5-C4	3.26	1.47	1.38
1	2A	1917	PSU	C6-C5	3.25	1.38	1.35
32	1a	966	M2G	C5-C4	3.22	1.47	1.38
32	2a	966	M2G	C5-C4	3.21	1.47	1.38
1	2A	1915	5MU	C6-C5	3.20	1.39	1.34
1	1A	2251	OMG	C5-C4	3.15	1.47	1.38
1	2A	2251	OMG	C5-C4	3.10	1.47	1.38
1	1A	2503	2MA	C5-N7	-3.06	1.33	1.39
1	2A	1915	5MU	C2-N1	3.06	1.43	1.38
1	1A	1915	5MU	C2-N1	2.98	1.43	1.38
1	1A	2605	PSU	C4-N3	-2.96	1.33	1.38
32	1a	1207	2MG	C5-C4	2.92	1.46	1.38
32	2a	1404	5MC	C6-C5	2.92	1.39	1.34
1	2A	2552	2MU	C4-N3	-2.91	1.33	1.38
32	1a	967	5MC	C6-C5	2.89	1.39	1.34
1	2A	1939	5MU	C4-C5	2.87	1.49	1.44
32	1a	1404	5MC	C6-C5	2.84	1.39	1.34
1	1A	1915	5MU	C6-C5	2.83	1.39	1.34
1	2A	1939	5MU	C4-N3	-2.83	1.33	1.38
1	1A	1939	5MU	C6-C5	2.82	1.39	1.34
32	1a	1400	5MC	C6-C5	2.81	1.39	1.34
32	1a	1407	5MC	C6-C5	2.78	1.39	1.34
1	2A	2251	OMG	C6-N1	-2.78	1.33	1.38
32	2a	1400	5MC	C6-C5	2.77	1.39	1.34
1	2A	1962	5MC	C6-C5	2.77	1.39	1.34
1	2A	2605	PSU	C4-N3	-2.76	1.33	1.38
32	2a	967	5MC	C6-C5	2.74	1.39	1.34
1	1A	2552	2MU	C4-N3	-2.72	1.34	1.38
1	2A	1915	5MU	C4-N3	-2.71	1.33	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
32	2a	966	M2G	C2-N2	2.69	1.40	1.35
32	2a	1407	5MC	C6-C5	2.67	1.39	1.34
1	2A	1917	PSU	C4-N3	-2.66	1.33	1.38
1	1A	1942	5MC	C6-C5	2.64	1.38	1.34
1	2A	2503	2MA	C5-C6	2.62	1.48	1.41
1	1A	1939	5MU	C4-N3	-2.59	1.34	1.38
1	2A	1942	5MC	C6-C5	2.58	1.38	1.34
32	1a	1400	5MC	C6-N1	-2.57	1.33	1.38
32	1a	966	M2G	C6-N1	-2.56	1.34	1.38
1	2A	1939	5MU	C6-N1	-2.54	1.33	1.38
1	2A	1911	PSU	C4-N3	-2.53	1.34	1.38
1	1A	2251	OMG	C6-N1	-2.51	1.34	1.38
1	1A	1962	5MC	C6-N1	-2.49	1.33	1.38
32	1a	1207	2MG	C6-N1	-2.48	1.34	1.38
1	2A	2605	PSU	C2-N3	-2.48	1.33	1.37
1	2A	1939	5MU	C6-C5	2.48	1.38	1.34
1	1A	1911	PSU	C4-N3	-2.47	1.34	1.38
32	2a	516	PSU	C4-N3	-2.47	1.34	1.38
1	1A	1915	5MU	C4-N3	-2.45	1.34	1.38
32	2a	527	G7M	C6-N1	-2.43	1.34	1.38
1	1A	1939	5MU	C6-N1	-2.42	1.33	1.38
1	1A	1942	5MC	C6-N1	-2.40	1.33	1.38
32	1a	516	PSU	C4-N3	-2.39	1.34	1.38
1	1A	1962	5MC	C6-C5	2.39	1.38	1.34
1	1A	1915	5MU	C4-C5	2.39	1.48	1.44
32	1a	966	M2G	C2-N2	2.39	1.39	1.35
1	1A	2503	2MA	C4-N9	-2.38	1.32	1.37
1	1A	1917	PSU	C4-N3	-2.38	1.34	1.38
1	2A	1915	5MU	C4-C5	2.35	1.48	1.44
1	2A	1942	5MC	C6-N1	-2.34	1.34	1.38
32	2a	1400	5MC	C6-N1	-2.31	1.34	1.38
1	2A	2251	OMG	C5-N7	-2.30	1.34	1.39
1	2A	1962	5MC	C6-N1	-2.30	1.34	1.38
1	1A	2552	2MU	C5-C4	2.27	1.48	1.43
32	2a	1404	5MC	C6-N1	-2.26	1.34	1.38
32	2a	1498	UR3	C6-C5	2.21	1.40	1.35
1	2A	2503	2MA	C5-N7	-2.19	1.35	1.39
1	2A	2503	2MA	C8-N7	2.18	1.35	1.31
1	1A	2503	2MA	C5-C6	2.18	1.47	1.41
32	1a	527	G7M	C6-N1	-2.17	1.34	1.38
32	2a	966	M2G	C6-N1	-2.17	1.34	1.38
1	1A	2251	OMG	C5-N7	-2.17	1.34	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1A	2552	2MU	C2-N3	-2.15	1.34	1.38
32	2a	1407	5MC	C6-N1	-2.14	1.34	1.38
32	1a	967	5MC	C6-N1	-2.13	1.34	1.38
1	2A	2552	2MU	C2-N3	-2.10	1.34	1.38
32	1a	966	M2G	C5-N7	-2.10	1.34	1.39
32	2a	967	5MC	C6-N1	-2.10	1.34	1.38
1	1A	2605	PSU	C2-N3	-2.10	1.34	1.37
32	2a	1207	2MG	C6-N1	-2.07	1.35	1.38
1	1A	1939	5MU	C4-C5	2.07	1.48	1.44
32	1a	1498	UR3	C2-N1	2.05	1.41	1.38
32	1a	1498	UR3	C6-C5	2.04	1.39	1.35
1	2A	2552	2MU	C5-C4	2.03	1.48	1.43
32	2a	1207	2MG	C4-N9	-2.01	1.33	1.38

All (238) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
43	2l	92	0TD	CSB-SB-CB	-19.94	66.52	102.36
43	1l	92	0TD	CSB-SB-CB	-11.97	80.85	102.36
1	2A	2503	2MA	C5-C4-N3	-8.27	118.47	127.18
1	1A	2503	2MA	C5-C4-N3	-8.20	118.55	127.18
32	1a	527	G7M	CN7-N7-C8	-8.12	112.50	124.79
32	2a	527	G7M	CN7-N7-C8	-8.04	112.62	124.79
32	1a	1498	UR3	C4-N3-C2	-7.82	118.29	124.58
32	1a	1207	2MG	C2-N3-C4	7.34	121.18	112.00
32	2a	1498	UR3	C4-N3-C2	-6.94	119.00	124.58
32	1a	527	G7M	N9-C8-N7	-6.91	95.70	112.48
32	2a	527	G7M	N9-C8-N7	-6.85	95.86	112.48
1	1A	2605	PSU	N1-C2-N3	6.83	122.37	115.17
1	2A	2503	2MA	N3-C4-N9	6.79	135.60	126.99
1	2A	1911	PSU	N1-C2-N3	6.59	122.12	115.17
1	1A	2503	2MA	N3-C4-N9	6.59	135.35	126.99
32	1a	527	G7M	C8-N7-C5	6.57	116.00	107.78
1	2A	2605	PSU	N1-C2-N3	6.54	122.07	115.17
32	2a	527	G7M	C8-N7-C5	6.51	115.93	107.78
32	2a	1207	2MG	C2-N3-C4	6.49	120.12	112.00
1	1A	1911	PSU	N1-C2-N3	6.47	121.99	115.17
32	2a	516	PSU	N1-C2-N3	6.33	121.85	115.17
1	2A	2251	OMG	C5-C4-N3	-6.18	118.55	128.39
32	1a	966	M2G	C5-C4-N3	-6.04	118.77	128.39
1	2A	1917	PSU	N1-C2-N3	5.98	121.48	115.17
32	2a	527	G7M	N9-C4-N3	5.98	137.91	125.95

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	1a	516	PSU	N1-C2-N3	5.98	121.47	115.17
1	1A	2251	OMG	C5-C4-N3	-5.97	118.88	128.39
1	2A	1939	5MU	C4-N3-C2	-5.89	119.61	127.34
32	1a	1207	2MG	C5-C4-N3	-5.87	119.05	128.39
32	1a	527	G7M	N9-C4-N3	5.79	137.52	125.95
32	2a	966	M2G	C5-C4-N3	-5.74	119.25	128.39
1	1A	1939	5MU	C4-N3-C2	-5.72	119.84	127.34
1	2A	1939	5MU	N3-C2-N1	5.61	122.19	114.89
1	1A	1917	PSU	N1-C2-N3	5.56	121.03	115.17
32	2a	1207	2MG	C5-C4-N3	-5.54	119.57	128.39
1	2A	1915	5MU	N3-C2-N1	5.42	121.95	114.89
1	1A	1939	5MU	N3-C2-N1	5.41	121.94	114.89
32	2a	527	G7M	C5-C4-N3	-5.15	118.41	128.15
1	1A	2552	2MU	N3-C2-N1	5.11	121.55	114.89
1	2A	2251	OMG	C2-N3-C4	5.04	120.98	112.30
1	1A	2251	OMG	C2-N3-C4	4.95	120.83	112.30
1	1A	1915	5MU	N3-C2-N1	4.92	121.30	114.89
32	1a	527	G7M	C5-C4-N3	-4.87	118.95	128.15
1	1A	2503	2MA	N6-C6-N1	4.85	123.57	117.03
32	1a	1519	MA6	N1-C2-N3	-4.82	121.29	128.58
32	1a	1519	MA6	C5-C4-N3	-4.80	120.10	126.72
32	2a	1518	MA6	N1-C2-N3	-4.77	121.36	128.58
1	1A	1939	5MU	O4-C4-C5	-4.74	119.49	124.92
32	2a	1519	MA6	N1-C2-N3	-4.71	121.45	128.58
1	2A	1915	5MU	C4-N3-C2	-4.70	121.18	127.34
1	1A	1939	5MU	C5-C4-N3	4.69	119.40	115.32
1	2A	2552	2MU	N3-C2-N1	4.67	120.97	114.89
32	1a	1518	MA6	N1-C2-N3	-4.60	121.62	128.58
1	1A	2251	OMG	N9-C4-N3	4.56	135.07	125.95
1	2A	2251	OMG	N9-C4-N3	4.55	135.06	125.95
32	2a	1519	MA6	C5-C4-N3	-4.55	120.45	126.72
1	2A	1939	5MU	C5-C4-N3	4.53	119.26	115.32
1	2A	2552	2MU	C4-N3-C2	-4.52	121.01	126.61
1	1A	1915	5MU	C1'-N1-C2	4.51	125.69	117.59
32	2a	966	M2G	C2-N3-C4	4.47	120.78	112.51
32	1a	527	G7M	C8-N9-C4	4.42	118.03	107.09
1	1A	2552	2MU	C4-N3-C2	-4.42	121.13	126.61
1	1A	1915	5MU	C4-N3-C2	-4.41	121.55	127.34
1	2A	2605	PSU	C4-N3-C2	-4.40	120.31	126.37
32	1a	966	M2G	N9-C4-N3	4.35	134.65	125.95
32	1a	1518	MA6	C5-C4-N3	-4.30	120.80	126.72
32	2a	527	G7M	C8-N9-C4	4.29	117.72	107.09

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1A	2605	PSU	C4-N3-C2	-4.29	120.46	126.37
1	2A	1939	5MU	C5-C6-N1	-4.26	118.69	123.31
32	1a	527	G7M	C2-N3-C4	4.20	119.54	112.30
32	1a	966	M2G	C2-N3-C4	4.18	120.23	112.51
1	1A	1939	5MU	O2-C2-N1	-4.17	117.37	122.80
1	1A	1911	PSU	C4-N3-C2	-4.17	120.63	126.37
32	2a	516	PSU	C4-N3-C2	-4.15	120.65	126.37
1	2A	1911	PSU	C4-N3-C2	-4.14	120.67	126.37
32	2a	1518	MA6	C5-C4-N3	-4.14	121.02	126.72
32	2a	527	G7M	C2-N3-C4	4.11	119.38	112.30
32	1a	1404	5MC	C5-C6-N1	-4.04	118.93	123.31
32	1a	1519	MA6	C2-N1-C6	4.02	121.64	111.83
1	1A	1939	5MU	C5-C6-N1	-4.01	118.95	123.31
1	2A	1915	5MU	C5-C4-N3	4.01	118.81	115.32
32	2a	1518	MA6	C2-N1-C6	3.98	121.55	111.83
32	2a	1519	MA6	C4-C5-N7	-3.97	106.04	110.58
32	2a	516	PSU	O2-C2-N1	-3.95	118.71	122.79
32	2a	966	M2G	N9-C4-N3	3.95	133.85	125.95
32	2a	1519	MA6	C5-N7-C8	3.94	109.65	103.45
1	1A	1911	PSU	O2-C2-N1	-3.93	118.74	122.79
1	1A	1915	5MU	C5-C4-N3	3.92	118.73	115.32
32	1a	1207	2MG	C6-C5-N7	3.91	137.41	130.29
1	2A	1917	PSU	O2-C2-N1	-3.90	118.76	122.79
32	1a	1518	MA6	C2-N1-C6	3.86	121.26	111.83
32	1a	516	PSU	C4-N3-C2	-3.85	121.07	126.37
32	1a	516	PSU	O2-C2-N1	-3.85	118.82	122.79
32	2a	1518	MA6	C5-N7-C8	3.84	109.49	103.45
32	1a	1519	MA6	C4-C5-N7	-3.84	106.20	110.58
1	2A	1939	5MU	O2-C2-N1	-3.83	117.82	122.80
32	1a	1400	5MC	C5-C6-N1	-3.81	119.17	123.31
32	2a	1519	MA6	C2-N1-C6	3.81	121.12	111.83
32	1a	527	G7M	CN7-N7-C5	3.77	131.50	126.80
32	1a	1207	2MG	N9-C4-N3	3.77	133.48	125.95
32	2a	1207	2MG	N9-C4-N3	3.76	133.48	125.95
32	2a	527	G7M	CN7-N7-C5	3.74	131.46	126.80
1	1A	1915	5MU	O4-C4-C5	-3.72	120.67	124.92
32	2a	1518	MA6	C4-C5-N7	-3.70	106.36	110.58
1	1A	2552	2MU	C2'-C1'-N1	-3.70	107.22	114.24
1	1A	2605	PSU	O2-C2-N1	-3.66	119.01	122.79
1	1A	1915	5MU	C1'-N1-C6	-3.66	115.12	121.15
32	1a	1518	MA6	C5-N7-C8	3.64	109.17	103.45
32	2a	1400	5MC	C5-C6-N1	-3.63	119.38	123.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1A	1917	PSU	C4-N3-C2	-3.61	121.40	126.37
43	1l	92	0TD	OD2-CG-CB	3.61	120.94	113.15
1	2A	1911	PSU	O2-C2-N1	-3.58	119.09	122.79
32	2a	966	M2G	C6-C5-N7	3.55	136.75	130.29
1	2A	1917	PSU	C4-N3-C2	-3.55	121.48	126.37
32	1a	1207	2MG	N1-C2-N2	3.55	120.18	116.56
1	2A	1962	5MC	C5-C6-N1	-3.52	119.49	123.31
1	1A	1917	PSU	O2-C2-N1	-3.51	119.17	122.79
32	1a	1519	MA6	C5-N7-C8	3.50	108.95	103.45
32	2a	1404	5MC	C5-C4-N3	-3.49	118.17	121.75
32	2a	527	G7M	C1'-N9-C8	-3.49	114.95	126.74
32	1a	1519	MA6	C2-N3-C4	3.49	120.36	111.83
32	2a	1519	MA6	N9-C8-N7	-3.46	109.02	113.94
1	1A	1962	5MC	C5-C6-N1	-3.46	119.55	123.31
32	2a	1519	MA6	C2-N3-C4	3.45	120.25	111.83
32	1a	967	5MC	C5-C6-N1	-3.45	119.57	123.31
32	2a	1518	MA6	N9-C8-N7	-3.44	109.05	113.94
32	2a	967	5MC	C5-C6-N1	-3.43	119.58	123.31
32	2a	1207	2MG	C6-C5-N7	3.41	136.50	130.29
1	2A	1939	5MU	O4-C4-C5	-3.41	121.02	124.92
32	1a	1498	UR3	C5-C4-N3	3.38	119.50	115.04
32	1a	1518	MA6	C4-C5-N7	-3.37	106.73	110.58
1	1A	1942	5MC	C5-C6-N1	-3.36	119.66	123.31
1	2A	1915	5MU	C1'-N1-C2	3.35	123.61	117.59
1	1A	2251	OMG	C6-C5-N7	3.35	136.38	130.29
1	2A	1915	5MU	O4-C4-C5	-3.33	121.11	124.92
1	2A	2503	2MA	C4-C5-N7	-3.32	106.78	110.58
32	1a	1518	MA6	N9-C8-N7	-3.31	109.24	113.94
32	1a	527	G7M	C1'-N9-C8	-3.30	115.61	126.74
32	2a	1518	MA6	C2-N3-C4	3.30	119.88	111.83
32	2a	1207	2MG	N1-C2-N2	3.29	119.92	116.56
32	2a	1404	5MC	C5-C6-N1	-3.28	119.75	123.31
1	2A	2503	2MA	N6-C6-N1	3.27	121.44	117.03
32	1a	1518	MA6	C2-N3-C4	3.25	119.78	111.83
32	1a	1498	UR3	C3U-N3-C2	3.22	122.94	117.33
1	2A	2251	OMG	C6-C5-N7	3.20	136.10	130.29
1	2A	2503	2MA	C4-N9-C8	3.18	109.08	105.74
1	2A	1942	5MC	C5-C6-N1	-3.12	119.92	123.31
32	1a	966	M2G	C6-C5-N7	3.09	135.92	130.29
32	2a	1498	UR3	C5-C4-N3	3.05	119.05	115.04
1	2A	1942	5MC	C5-C4-N3	-3.04	118.64	121.75
32	2a	1207	2MG	N2-C2-N3	-3.04	116.64	120.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	1a	1400	5MC	C5-C4-N3	-3.02	118.66	121.75
1	2A	2552	2MU	C5-C4-N3	2.99	118.98	114.80
32	1a	1207	2MG	C4-C5-N7	-2.98	105.94	110.67
1	1A	2552	2MU	O2-C2-N1	-2.96	118.94	122.80
32	1a	1519	MA6	C4-C5-C6	2.91	118.92	115.91
1	1A	2503	2MA	C4-C5-N7	-2.88	107.28	110.58
32	2a	1207	2MG	C4-C5-N7	-2.85	106.15	110.67
43	2l	92	0TD	OD2-CG-CB	2.84	119.29	113.15
32	1a	1518	MA6	N3-C4-N9	2.84	132.00	127.17
32	2a	1407	5MC	C5-C6-N1	-2.82	120.25	123.31
32	1a	1402	4OC	C6-C5-C4	2.81	120.39	117.00
1	2A	1920	OMC	O2-C2-N3	-2.81	117.90	122.33
32	2a	1407	5MC	C5-C4-N3	-2.81	118.88	121.75
1	2A	1939	5MU	C5M-C5-C4	2.78	121.75	118.78
32	1a	1407	5MC	C5-C4-N3	-2.77	118.91	121.75
1	2A	1915	5MU	C5-C6-N1	-2.77	120.30	123.31
32	1a	1519	MA6	N9-C8-N7	-2.74	110.05	113.94
32	2a	966	M2G	C4-C5-N7	-2.72	106.35	110.67
1	2A	2605	PSU	O2-C2-N1	-2.72	119.98	122.79
32	1a	1207	2MG	N2-C2-N3	-2.70	117.07	120.51
32	2a	1519	MA6	N3-C4-N9	2.70	131.75	127.17
1	1A	2552	2MU	C5-C4-N3	2.68	118.55	114.80
1	2A	2503	2MA	C5-N7-C8	2.67	107.65	103.45
1	2A	1939	5MU	C5M-C5-C6	-2.65	119.27	122.85
1	2A	1915	5MU	O2-C2-N3	-2.64	116.63	121.49
32	1a	1407	5MC	C5-C6-N1	-2.63	120.46	123.31
1	2A	2552	2MU	O4-C4-C5	-2.61	120.66	125.16
32	1a	1519	MA6	N3-C4-N9	2.61	131.60	127.17
32	1a	966	M2G	C4-C5-N7	-2.60	106.55	110.67
1	1A	1942	5MC	C5-C4-N3	-2.59	119.10	121.75
1	1A	2552	2MU	O4-C4-C5	-2.58	120.71	125.16
1	1A	2251	OMG	C4-C5-N7	-2.58	106.58	110.67
32	2a	1518	MA6	N3-C4-N9	2.57	131.55	127.17
32	1a	1207	2MG	CM2-N2-C2	-2.56	118.14	123.65
1	1A	1915	5MU	O2-C2-N3	-2.56	116.77	121.49
32	1a	1498	UR3	C6-N1-C2	-2.55	119.71	121.80
32	1a	967	5MC	C5-C4-N3	-2.51	119.19	121.75
1	2A	2605	PSU	C5-C6-N1	-2.51	118.66	122.14
1	1A	2503	2MA	C4-N9-C8	2.50	108.37	105.74
32	2a	1407	5MC	O2-C2-N3	-2.49	118.41	122.33
1	2A	2552	2MU	O2-C2-N1	-2.49	119.56	122.80
32	1a	527	G7M	O6-C6-C5	-2.46	122.53	128.01

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1A	1962	5MC	CM5-C5-C6	-2.45	119.53	122.85
32	2a	1400	5MC	C5-C4-N3	-2.40	119.29	121.75
1	2A	2503	2MA	N9-C8-N7	-2.39	110.55	113.94
1	2A	2251	OMG	C4-C5-N7	-2.37	106.92	110.67
32	1a	1207	2MG	O3'-C3'-C2'	2.35	119.35	111.82
1	2A	1915	5MU	C1'-N1-C6	-2.34	117.29	121.15
32	1a	1518	MA6	C4-C5-C6	2.34	118.33	115.91
1	2A	1962	5MC	C5-C4-N3	-2.33	119.36	121.75
32	2a	967	5MC	C5-C4-N3	-2.31	119.39	121.75
32	2a	1402	4OC	C6-C5-C4	2.30	119.77	117.00
32	1a	1404	5MC	C5-C4-N3	-2.30	119.40	121.75
32	1a	1407	5MC	CM5-C5-C6	-2.29	119.75	122.85
32	2a	527	G7M	O6-C6-C5	-2.28	122.92	128.01
32	1a	1519	MA6	C5-C4-N9	2.28	108.29	105.81
1	2A	1915	5MU	C6-N1-C2	-2.26	119.06	121.30
32	2a	1519	MA6	C4-C5-C6	2.26	118.24	115.91
1	1A	2503	2MA	C5-N7-C8	2.23	106.96	103.45
43	1l	92	0TD	OD1-CG-CB	-2.22	117.78	122.44
1	2A	1911	PSU	C5-C6-N1	-2.22	119.05	122.14
32	1a	1404	5MC	CM5-C5-C6	-2.22	119.84	122.85
1	2A	2251	OMG	O6-C6-C5	-2.21	120.69	126.53
1	1A	2503	2MA	C2-N1-C6	2.21	121.49	118.10
1	2A	2605	PSU	O2-C2-N3	-2.20	117.95	121.86
1	2A	2503	2MA	C2-N1-C6	2.20	121.49	118.10
1	2A	2552	2MU	C2'-C1'-N1	-2.20	110.07	114.24
32	2a	516	PSU	C5-C6-N1	-2.16	119.15	122.14
1	1A	1917	PSU	C6-C5-C4	-2.15	116.72	118.17
1	1A	1911	PSU	O4'-C1'-C2'	2.14	108.11	105.15
32	2a	516	PSU	O4'-C1'-C2'	2.14	108.11	105.15
1	1A	1915	5MU	C6-N1-C2	-2.13	119.18	121.30
32	1a	966	M2G	O6-C6-C5	-2.13	120.91	126.53
1	1A	1911	PSU	C5-C6-N1	-2.13	119.19	122.14
1	1A	2251	OMG	O6-C6-C5	-2.11	120.97	126.53
32	1a	516	PSU	C6-C5-C4	-2.11	116.75	118.17
32	2a	1207	2MG	CM2-N2-C2	-2.11	119.12	123.65
1	1A	2503	2MA	CM2-C2-N1	2.10	120.27	117.13
1	1A	1915	5MU	C5M-C5-C4	2.09	121.02	118.78
1	1A	2605	PSU	C5-C6-N1	-2.08	119.25	122.14
32	2a	1498	UR3	C3U-N3-C2	2.07	120.93	117.33
1	1A	1920	OMC	O2-C2-N3	-2.04	119.12	122.33
1	1A	1915	5MU	C5-C6-N1	-2.03	121.11	123.31
1	1A	2503	2MA	C5-C6-N6	-2.03	118.26	123.29

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	2A	2251	OMG	C5-C6-N1	2.03	118.42	113.25
32	2a	1518	MA6	C4-C5-C6	2.03	118.00	115.91
32	2a	967	5MC	CM5-C5-C6	-2.00	120.14	122.85

There are no chirality outliers.

All (25) 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
32	1a	1519	MA6	O4'-C4'-C5'-O5'
43	1l	92	0TD	CG-CB-SB-CSB
1	2A	1915	5MU	O4'-C1'-N1-C2
1	2A	1915	5MU	O4'-C1'-N1-C6
43	2l	92	0TD	O-C-CA-CB
32	2a	1519	MA6	O4'-C4'-C5'-O5'
32	1a	1519	MA6	C3'-C4'-C5'-O5'
32	2a	527	G7M	C3'-C4'-C5'-O5'
32	2a	1519	MA6	C3'-C4'-C5'-O5'
32	1a	1400	5MC	O4'-C4'-C5'-O5'
32	2a	527	G7M	O4'-C4'-C5'-O5'
32	1a	1402	4OC	O4'-C4'-C5'-O5'
43	2l	92	0TD	SB-CB-CG-OD1
32	2a	1519	MA6	C4'-C5'-O5'-P
1	1A	2503	2MA	C4'-C5'-O5'-P
32	1a	527	G7M	C3'-C4'-C5'-O5'
43	1l	92	0TD	CA-CB-SB-CSB
1	1A	2251	OMG	C4'-C5'-O5'-P
43	2l	92	0TD	CG-CB-SB-CSB
32	1a	527	G7M	C4'-C5'-O5'-P
32	1a	1400	5MC	C3'-C4'-C5'-O5'
1	2A	1920	OMC	C2'-C1'-N1-C2
1	1A	1920	OMC	C2'-C1'-N1-C2

There are no ring outliers.

20 monomers are involved in 27 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	2A	1939	5MU	1	0
1	1A	1920	OMC	1	0
32	2a	1518	MA6	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
32	2a	1400	5MC	2	0
1	2A	1920	OMC	1	0
1	1A	2251	OMG	1	0
1	1A	1939	5MU	2	0
32	1a	1519	MA6	2	0
1	2A	2552	2MU	1	0
1	2A	1915	5MU	1	0
1	2A	2503	2MA	1	0
32	2a	967	5MC	2	0
32	1a	1498	UR3	1	0
32	1a	967	5MC	2	0
1	1A	1915	5MU	1	0
32	1a	1518	MA6	1	0
32	1a	1400	5MC	2	0
32	2a	1402	4OC	1	0
32	1a	1402	4OC	3	0
32	2a	1519	MA6	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2524 ligands modelled in this entry, 2509 are monoatomic - leaving 15 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
57	MPD	2B	220	-	7,7,7	0.32	0	9,10,10	0.15	0
57	MPD	1a	3277	32	7,7,7	0.39	0	9,10,10	0.71	0
56	TEL	1A	4019	-	60,62,62	1.34	6 (10%)	78,92,92	1.75	18 (23%)
57	MPD	1A	4020	-	7,7,7	0.38	0	9,10,10	0.45	0
60	SF4	2d	501	35	0,12,12	-	-	-	-	-
58	ARG	1B	230	54	10,11,11	0.75	1 (10%)	9,13,13	1.05	1 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
56	TEL	2A	3739	-	60,62,62	1.35	7 (11%)	78,92,92	1.94	17 (21%)
57	MPD	1T	205	-	7,7,7	0.37	0	9,10,10	0.36	0
55	HGR	2A	3738	-	39,39,39	2.41	10 (25%)	48,58,58	1.56	8 (16%)
57	MPD	2A	3741	-	7,7,7	0.31	0	9,10,10	0.25	0
57	MPD	18	103	-	7,7,7	0.25	0	9,10,10	0.45	0
58	ARG	1F	321	-	10,11,11	0.70	0	9,13,13	0.97	1 (11%)
55	HGR	1A	4018	-	39,39,39	2.42	9 (23%)	48,58,58	1.68	14 (29%)
60	SF4	1d	307	35	0,12,12	-	-	-	-	-
57	MPD	2A	3740	-	7,7,7	0.35	0	9,10,10	0.23	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
57	MPD	2B	220	-	-	4/5/5/5	-
57	MPD	1a	3277	32	-	4/5/5/5	-
56	TEL	1A	4019	-	-	3/73/108/108	0/4/5/5
57	MPD	1A	4020	-	-	2/5/5/5	-
60	SF4	2d	501	35	-	-	0/6/5/5
58	ARG	1B	230	54	-	4/11/11/11	-
56	TEL	2A	3739	-	-	6/73/108/108	0/4/5/5
57	MPD	1T	205	-	-	2/5/5/5	-
55	HGR	2A	3738	-	-	9/20/79/79	0/4/4/4
57	MPD	2A	3741	-	-	3/5/5/5	-
57	MPD	18	103	-	-	2/5/5/5	-
58	ARG	1F	321	-	-	2/11/11/11	-
55	HGR	1A	4018	-	-	7/20/79/79	0/4/4/4
60	SF4	1d	307	35	-	-	0/6/5/5
57	MPD	2A	3740	-	-	0/5/5/5	-

All (33) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
55	1A	4018	HGR	C12-C14	8.77	1.54	1.33
55	2A	3738	HGR	C12-C14	8.64	1.54	1.33
55	2A	3738	HGR	C5-C4	-5.48	1.39	1.49
55	1A	4018	HGR	C5-C4	-5.44	1.39	1.49

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
55	1A	4018	HGR	C5-C6	-5.38	1.39	1.50
55	2A	3738	HGR	C5-C6	-5.26	1.39	1.50
56	1A	4019	TEL	O5-C10	5.21	1.44	1.35
56	2A	3739	TEL	O5-C10	5.17	1.44	1.35
56	2A	3739	TEL	O9-C15	4.92	1.45	1.34
55	2A	3738	HGR	C3-C2	-4.87	1.39	1.48
55	1A	4018	HGR	C3-C2	-4.65	1.39	1.48
55	1A	4018	HGR	O4-C2	4.56	1.36	1.24
56	1A	4019	TEL	O9-C15	4.55	1.44	1.34
55	2A	3738	HGR	O4-C2	4.34	1.36	1.24
56	2A	3739	TEL	C40-N41	-3.60	1.34	1.38
56	1A	4019	TEL	C40-N41	-3.32	1.35	1.38
56	1A	4019	TEL	O9-C4	-3.10	1.41	1.46
56	2A	3739	TEL	O5-C2	-3.08	1.43	1.47
56	1A	4019	TEL	O5-C2	-3.05	1.43	1.47
56	1A	4019	TEL	C36-N31	-2.82	1.33	1.37
55	1A	4018	HGR	O8-C23	2.62	1.45	1.41
55	2A	3738	HGR	O9-C23	2.57	1.45	1.41
56	2A	3739	TEL	O9-C4	-2.56	1.42	1.46
56	2A	3739	TEL	C21-C26	-2.51	1.49	1.52
55	2A	3738	HGR	O8-C23	2.50	1.45	1.41
55	2A	3738	HGR	O1-C10	2.48	1.46	1.41
55	1A	4018	HGR	O1-C10	2.47	1.46	1.41
55	2A	3738	HGR	C17-N1	2.24	1.49	1.45
55	1A	4018	HGR	C8-C7	-2.21	1.50	1.53
58	1B	230	ARG	OXT-C	-2.21	1.23	1.30
55	2A	3738	HGR	C1-C2	-2.18	1.39	1.44
56	2A	3739	TEL	C30-C26	-2.10	1.49	1.52
55	1A	4018	HGR	C1-C2	-2.07	1.39	1.44

All (59) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
56	2A	3739	TEL	O9-C15-C21	7.51	118.35	110.93
56	1A	4019	TEL	C17-C11-N6	-7.32	102.15	113.25
56	2A	3739	TEL	C17-C11-N6	-7.24	102.28	113.25
56	1A	4019	TEL	O9-C15-C21	5.52	116.38	110.93
56	2A	3739	TEL	C4-O9-C15	-4.74	109.92	118.20
55	1A	4018	HGR	C4-C5-C6	4.25	121.42	112.35
55	2A	3738	HGR	C4-C5-C6	4.20	121.32	112.35
55	2A	3738	HGR	C12-C6-C1	-4.08	114.80	119.35
56	2A	3739	TEL	N31-C37-N41	-4.05	109.12	112.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
56	1A	4019	TEL	N31-C37-N41	-3.98	109.18	112.35
56	1A	4019	TEL	C36-N31-C37	3.94	108.65	106.71
55	1A	4018	HGR	C23-O9-C22	-3.72	100.64	106.31
55	2A	3738	HGR	O8-C18-C22	-3.54	98.54	106.03
56	2A	3739	TEL	O5-C2-C1	3.54	113.04	106.80
55	1A	4018	HGR	C4-C3-C2	-3.51	118.78	121.81
56	2A	3739	TEL	C36-N31-C37	3.26	108.31	106.71
56	2A	3739	TEL	C8-C4-C2	-3.25	110.75	115.23
56	2A	3739	TEL	C28-C24-C19	-3.19	110.89	116.10
56	1A	4019	TEL	C38-O32-C28	3.09	123.80	117.51
58	1B	230	ARG	OXT-C-O	-3.01	117.25	124.08
55	1A	4018	HGR	O3-C10-C9	2.99	111.55	106.69
58	1F	321	ARG	OXT-C-O	-2.83	117.66	124.08
56	2A	3739	TEL	O18-C13-C19	-2.81	116.21	121.30
55	1A	4018	HGR	O9-C22-C18	-2.81	100.08	106.03
56	1A	4019	TEL	C43-C40-N41	2.78	126.31	122.45
56	1A	4019	TEL	C4-O9-C15	-2.73	113.43	118.20
55	1A	4018	HGR	C12-C6-C1	-2.72	116.31	119.35
55	2A	3738	HGR	O4-C2-C3	-2.69	117.24	121.28
55	1A	4018	HGR	O3-C3-C2	2.66	117.35	112.51
55	2A	3738	HGR	O9-C22-C18	-2.63	100.47	106.03
55	2A	3738	HGR	C1-C2-C3	2.57	120.90	116.06
56	1A	4019	TEL	O39-C34-C28	2.56	112.39	106.44
56	2A	3739	TEL	C19-C13-C7	2.56	123.46	119.13
55	1A	4018	HGR	C1-C2-C3	2.55	120.86	116.06
56	1A	4019	TEL	C33-C28-C34	2.51	113.49	109.79
56	1A	4019	TEL	C8-C4-C2	-2.44	111.86	115.23
56	2A	3739	TEL	C47-C43-C40	-2.40	119.12	121.02
55	2A	3738	HGR	C4-C3-C2	-2.40	119.74	121.81
55	1A	4018	HGR	O8-C18-C22	-2.39	100.98	106.03
55	1A	4018	HGR	O4-C2-C3	-2.38	117.70	121.28
56	2A	3739	TEL	C37-N41-C40	2.38	107.85	105.94
55	1A	4018	HGR	C10-C9-C8	-2.32	99.40	102.29
56	2A	3739	TEL	C38-O32-C28	2.30	122.19	117.51
56	2A	3739	TEL	O9-C15-O20	-2.30	119.80	123.95
55	1A	4018	HGR	C9-C8-C7	-2.29	98.98	101.69
55	1A	4018	HGR	O1-C10-C9	-2.28	102.08	104.98
56	1A	4019	TEL	C43-C40-C36	-2.26	126.19	129.65
56	2A	3739	TEL	O5-C2-C3	2.22	105.54	103.28
55	2A	3738	HGR	C23-O9-C22	-2.22	102.93	106.31
56	1A	4019	TEL	C56-N52-C47	2.17	120.66	116.85
56	2A	3739	TEL	O20-C15-C21	-2.16	121.85	124.65

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
56	2A	3739	TEL	C56-N52-C47	2.14	120.60	116.85
56	1A	4019	TEL	C2-O5-C10	-2.12	107.38	109.23
56	1A	4019	TEL	C19-C13-C7	2.11	122.70	119.13
55	1A	4018	HGR	C20-C17-C19	-2.09	106.74	110.89
56	1A	4019	TEL	O9-C15-O20	-2.08	120.20	123.95
56	1A	4019	TEL	O5-C2-C1	2.08	110.46	106.80
56	1A	4019	TEL	C46-C43-C47	2.05	119.90	117.61
56	1A	4019	TEL	O18-C13-C19	-2.05	117.60	121.30

There are no chirality outliers.

All (48) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
55	1A	4018	HGR	C14-C12-C6-C1
55	2A	3738	HGR	C2-C3-O3-C10
55	2A	3738	HGR	C14-C12-C6-C1
56	2A	3739	TEL	C24-C28-O32-C38
57	1a	3277	MPD	C2-C3-C4-O4
57	1a	3277	MPD	C2-C3-C4-C5
57	2B	220	MPD	C2-C3-C4-C5
58	1F	321	ARG	C-CA-CB-CG
58	1B	230	ARG	NE-CD-CG-CB
56	2A	3739	TEL	N6-C11-C17-C22
58	1B	230	ARG	CA-CB-CG-CD
56	1A	4019	TEL	C33-C28-O32-C38
56	2A	3739	TEL	C33-C28-O32-C38
55	1A	4018	HGR	C12-C14-C15-O7
55	1A	4018	HGR	C12-C14-C15-N1
55	2A	3738	HGR	C12-C14-C15-O7
55	2A	3738	HGR	C12-C14-C15-N1
56	1A	4019	TEL	C34-C28-O32-C38
56	2A	3739	TEL	C34-C28-O32-C38
57	1A	4020	MPD	O2-C2-C3-C4
57	1T	205	MPD	O2-C2-C3-C4
55	1A	4018	HGR	C2-C3-O3-C10
55	2A	3738	HGR	O6-C11-C7-O1
57	18	103	MPD	C2-C3-C4-O4
57	1a	3277	MPD	C1-C2-C3-C4
57	2A	3741	MPD	C1-C2-C3-C4
57	18	103	MPD	C2-C3-C4-C5
55	1A	4018	HGR	C16-C14-C15-O7
55	2A	3738	HGR	C16-C14-C15-O7

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Mol	Chain	Res	Type	Atoms
56	1A	4019	TEL	C24-C28-O32-C38
56	2A	3739	TEL	O5-C2-C4-C8
55	1A	4018	HGR	C16-C14-C15-N1
55	2A	3738	HGR	C16-C14-C15-N1
55	2A	3738	HGR	C14-C12-C6-C5
55	2A	3738	HGR	C19-C17-N1-C15
57	1A	4020	MPD	C2-C3-C4-O4
57	1T	205	MPD	C2-C3-C4-O4
57	2A	3741	MPD	C2-C3-C4-O4
57	2B	220	MPD	C2-C3-C4-O4
57	1a	3277	MPD	CM-C2-C3-C4
57	2A	3741	MPD	CM-C2-C3-C4
57	2B	220	MPD	C1-C2-C3-C4
57	2B	220	MPD	CM-C2-C3-C4
58	1B	230	ARG	OXT-C-CA-N
55	1A	4018	HGR	C19-C17-N1-C15
56	2A	3739	TEL	C1-C2-C4-C8
58	1B	230	ARG	O-C-CA-N
58	1F	321	ARG	OXT-C-CA-N

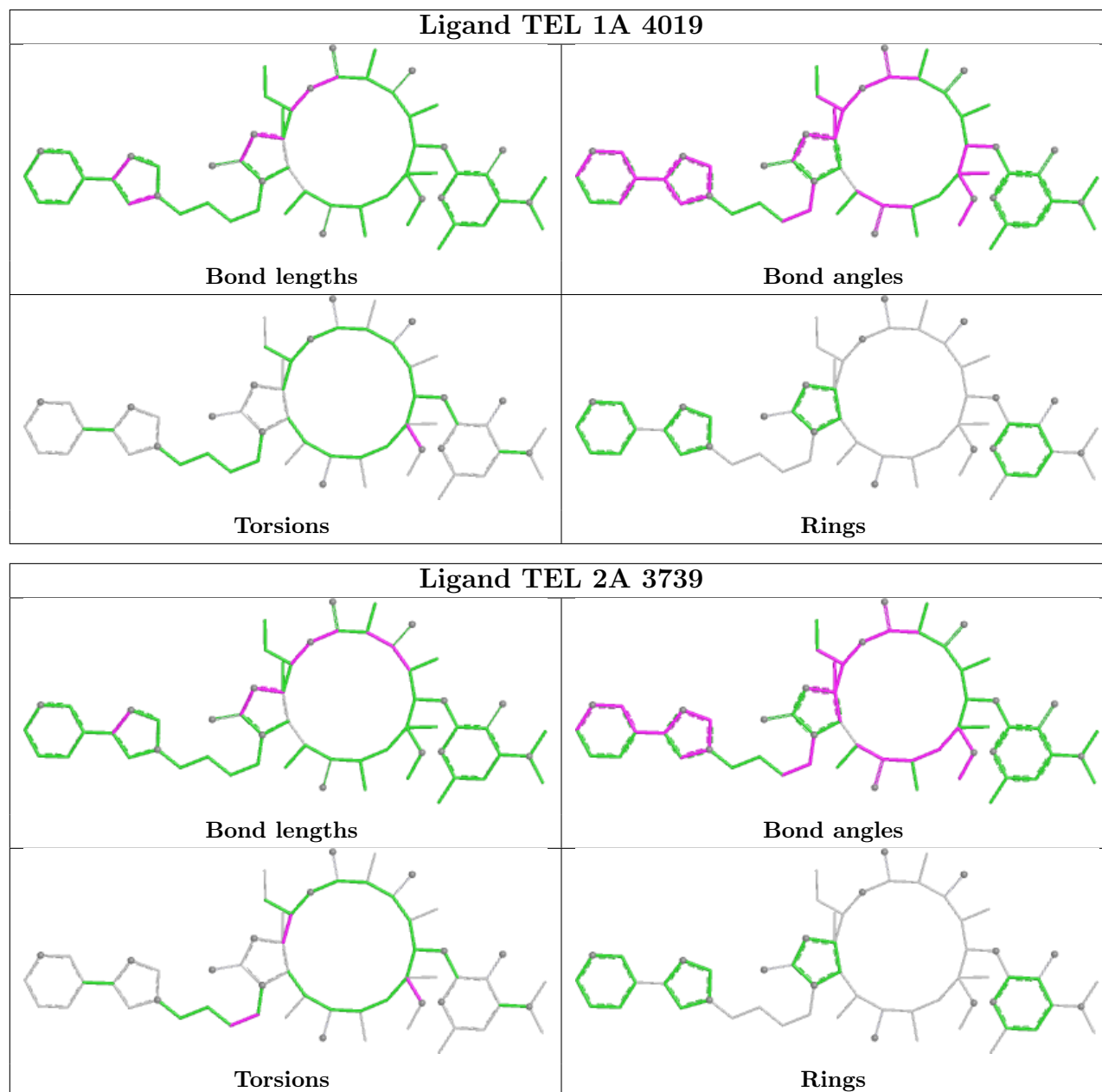
There are no ring outliers.

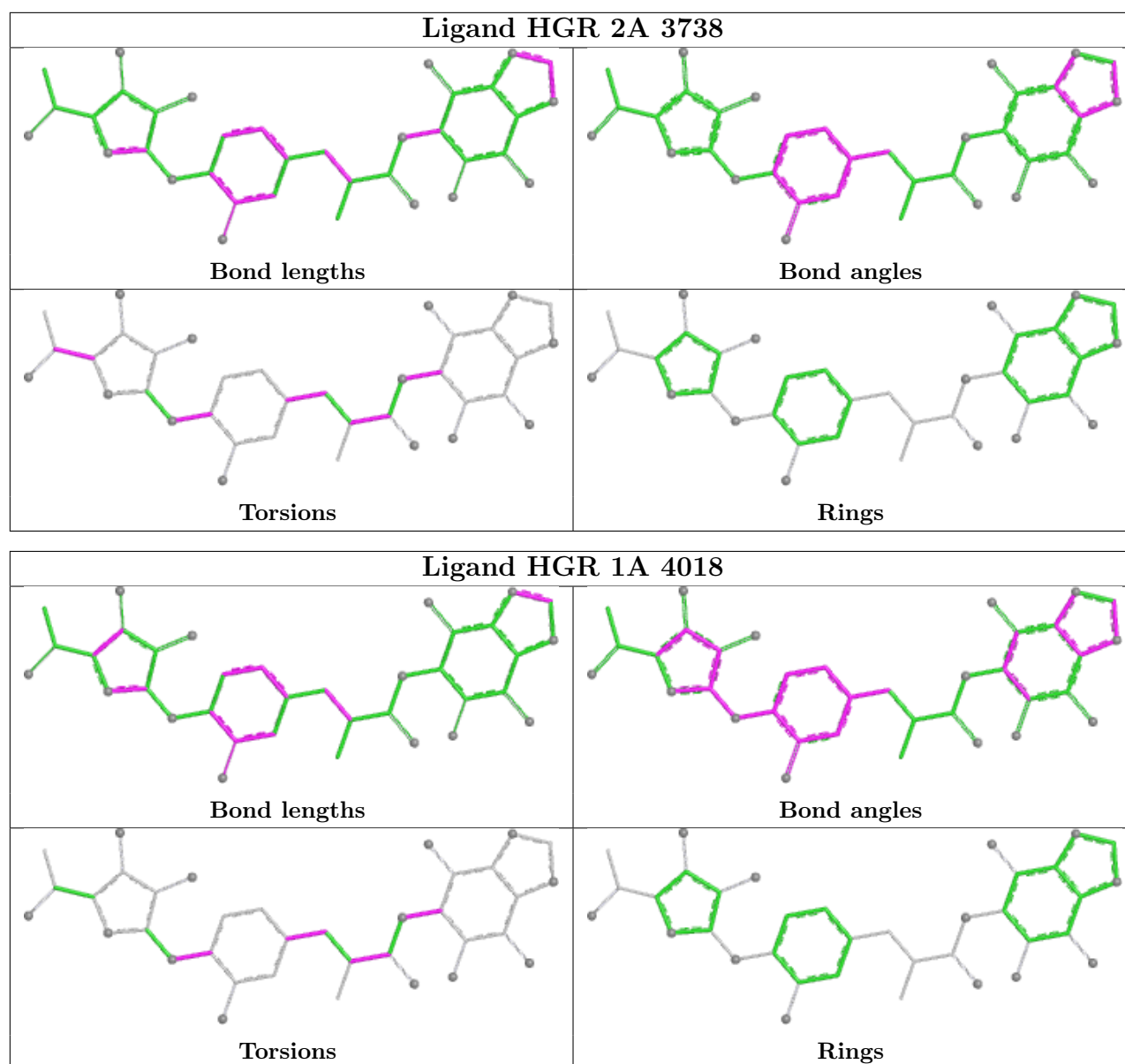
12 monomers are involved in 21 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
57	1a	3277	MPD	3	0
56	1A	4019	TEL	2	0
57	1A	4020	MPD	1	0
60	2d	501	SF4	1	0
58	1B	230	ARG	1	0
56	2A	3739	TEL	2	0
55	2A	3738	HGR	4	0
57	18	103	MPD	2	0
58	1F	321	ARG	1	0
55	1A	4018	HGR	2	0
60	1d	307	SF4	1	0
57	2A	3740	MPD	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier.

Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





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%)	-0.61	135 (4%)	36	30	18, 33, 89, 102	0
1	2A	2856/2915 (97%)	-0.13	165 (5%)	29	23	27, 51, 91, 101	0
2	1B	120/121 (99%)	-0.50	1 (0%)	82	80	27, 46, 60, 78	0
2	2B	120/121 (99%)	0.46	1 (0%)	82	80	55, 72, 80, 86	0
3	1D	275/276 (99%)	-0.35	2 (0%)	84	82	20, 34, 48, 71	0
3	2D	275/276 (99%)	0.00	5 (1%)	67	63	26, 46, 58, 73	0
4	1E	204/206 (99%)	-0.32	0	100	100	17, 36, 57, 67	0
4	2E	204/206 (99%)	0.04	1 (0%)	87	85	29, 50, 64, 81	0
5	1F	203/210 (96%)	-0.23	1 (0%)	87	85	17, 37, 63, 79	0
5	2F	203/210 (96%)	0.32	1 (0%)	87	85	30, 60, 74, 79	0
6	1G	181/182 (99%)	0.47	6 (3%)	49	43	43, 59, 72, 84	0
6	2G	181/182 (99%)	1.30	31 (17%)	4	3	68, 76, 82, 85	0
7	1H	174/180 (96%)	0.04	2 (1%)	78	74	34, 49, 61, 68	0
7	2H	173/180 (96%)	0.99	13 (7%)	20	16	62, 73, 79, 86	0
8	1I	147/148 (99%)	0.70	5 (3%)	48	42	40, 65, 75, 80	0
8	2I	146/148 (98%)	1.12	18 (12%)	8	6	50, 68, 77, 82	0
9	1N	140/140 (100%)	-0.32	1 (0%)	84	82	23, 35, 56, 69	0
9	2N	140/140 (100%)	0.23	0	100	100	40, 56, 68, 74	0
10	1O	122/122 (100%)	-0.34	0	100	100	27, 36, 52, 59	0
10	2O	122/122 (100%)	0.05	0	100	100	37, 48, 63, 69	0
11	1P	149/150 (99%)	-0.09	1 (0%)	84	82	19, 42, 63, 76	0
11	2P	149/150 (99%)	0.39	5 (3%)	48	42	32, 60, 74, 79	0
12	1Q	141/141 (100%)	-0.32	1 (0%)	84	82	26, 36, 48, 60	0
12	2Q	141/141 (100%)	0.42	2 (1%)	73	69	38, 57, 68, 73	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
13	1R	118/118 (100%)	-0.46	0 100 100	23, 31, 43, 56	0
13	2R	118/118 (100%)	-0.05	1 (0%) 82 80	33, 46, 55, 63	0
14	1S	110/112 (98%)	0.02	2 (1%) 67 63	35, 45, 57, 64	0
14	2S	110/112 (98%)	0.97	6 (5%) 30 25	60, 68, 74, 77	0
15	1T	131/146 (89%)	-0.13	4 (3%) 51 45	29, 41, 62, 76	0
15	2T	131/146 (89%)	0.22	3 (2%) 61 55	43, 52, 70, 77	0
16	1U	116/118 (98%)	-0.49	1 (0%) 81 78	19, 27, 40, 59	0
16	2U	116/118 (98%)	0.25	1 (0%) 81 78	36, 52, 65, 73	0
17	1V	101/101 (100%)	-0.33	0 100 100	20, 36, 53, 63	0
17	2V	101/101 (100%)	0.43	1 (0%) 79 76	37, 62, 69, 77	0
18	1W	112/113 (99%)	-0.43	2 (1%) 67 63	21, 28, 48, 79	0
18	2W	112/113 (99%)	-0.04	2 (1%) 67 63	34, 43, 60, 84	0
19	1X	95/96 (98%)	-0.17	2 (2%) 63 58	24, 34, 54, 68	0
19	2X	95/96 (98%)	0.67	2 (2%) 63 58	39, 55, 68, 75	0
20	1Y	107/110 (97%)	0.03	1 (0%) 81 78	31, 43, 61, 70	0
20	2Y	107/110 (97%)	0.71	3 (2%) 55 49	51, 63, 73, 78	0
21	1Z	203/206 (98%)	0.20	3 (1%) 72 68	35, 53, 69, 76	0
21	2Z	201/206 (97%)	0.92	8 (3%) 42 37	59, 71, 78, 82	0
22	10	77/85 (90%)	-0.33	0 100 100	25, 34, 48, 55	0
22	20	77/85 (90%)	0.58	2 (2%) 57 51	45, 57, 68, 71	0
23	11	97/98 (98%)	0.01	1 (1%) 79 76	25, 40, 61, 69	0
23	21	97/98 (98%)	0.27	2 (2%) 63 58	38, 50, 67, 73	0
24	12	70/72 (97%)	0.06	1 (1%) 73 69	32, 44, 56, 73	0
24	22	70/72 (97%)	0.51	1 (1%) 73 69	55, 64, 70, 74	0
25	13	59/60 (98%)	-0.34	0 100 100	23, 32, 58, 67	0
25	23	59/60 (98%)	0.38	2 (3%) 48 42	46, 57, 72, 78	0
26	14	69/71 (97%)	1.20	14 (20%) 3 2	52, 72, 84, 89	0
26	24	69/71 (97%)	1.77	21 (30%) 1 1	72, 82, 87, 91	0
27	15	59/60 (98%)	-0.59	0 100 100	19, 30, 44, 56	0
27	25	59/60 (98%)	-0.21	0 100 100	32, 45, 56, 65	0
28	16	53/54 (98%)	-0.35	0 100 100	30, 38, 52, 57	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
28	26	53/54 (98%)	0.23	0 100 100	45, 54, 62, 67	0
29	17	48/49 (97%)	-0.33	1 (2%) 63 58	19, 25, 50, 57	0
29	27	48/49 (97%)	-0.05	4 (8%) 17 13	29, 37, 57, 66	0
30	18	64/65 (98%)	-0.39	0 100 100	24, 30, 39, 47	0
30	28	64/65 (98%)	0.18	0 100 100	39, 48, 56, 60	0
31	19	37/37 (100%)	-0.18	0 100 100	28, 37, 52, 54	0
31	29	37/37 (100%)	0.65	1 (2%) 56 50	53, 59, 67, 69	0
32	1a	1488/1521 (97%)	0.18	47 (3%) 50 44	34, 63, 86, 99	0
32	2a	1492/1521 (98%)	0.44	66 (4%) 39 33	42, 71, 89, 99	0
33	1b	231/256 (90%)	1.08	26 (11%) 10 8	61, 72, 81, 85	0
33	2b	231/256 (90%)	1.46	52 (22%) 2 2	67, 78, 85, 88	0
34	1c	206/239 (86%)	0.69	6 (2%) 53 48	56, 68, 77, 81	0
34	2c	206/239 (86%)	1.39	36 (17%) 4 3	70, 78, 83, 86	0
35	1d	208/209 (99%)	0.71	15 (7%) 21 17	52, 66, 74, 79	0
35	2d	208/209 (99%)	0.94	9 (4%) 40 34	59, 67, 74, 77	0
36	1e	148/162 (91%)	0.35	1 (0%) 84 82	45, 61, 69, 81	0
36	2e	148/162 (91%)	0.72	3 (2%) 65 60	56, 67, 74, 79	0
37	1f	100/101 (99%)	0.31	0 100 100	49, 60, 69, 72	0
37	2f	100/101 (99%)	0.41	0 100 100	54, 63, 71, 77	0
38	1g	155/156 (99%)	0.66	1 (0%) 85 83	57, 67, 74, 80	0
38	2g	155/156 (99%)	1.17	21 (13%) 7 5	66, 75, 81, 85	0
39	1h	137/138 (99%)	0.48	2 (1%) 72 68	52, 62, 70, 75	0
39	2h	137/138 (99%)	0.64	3 (2%) 62 57	57, 68, 73, 78	0
40	1i	127/128 (99%)	1.08	14 (11%) 10 8	57, 71, 79, 82	0
40	2i	126/128 (98%)	1.69	34 (26%) 1 1	70, 79, 84, 86	0
41	1j	97/105 (92%)	1.16	16 (16%) 4 3	55, 73, 82, 84	0
41	2j	96/105 (91%)	2.04	44 (45%) 0 0	70, 80, 85, 87	0
42	1k	114/129 (88%)	0.31	1 (0%) 81 78	42, 59, 70, 74	0
42	2k	114/129 (88%)	0.73	7 (6%) 27 22	51, 67, 74, 79	0
43	1l	121/132 (91%)	0.41	3 (2%) 58 52	46, 54, 67, 72	0
43	2l	121/132 (91%)	0.35	2 (1%) 69 64	46, 60, 68, 73	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
44	1m	116/126 (92%)	0.78	8 (6%) 23 18	56, 69, 75, 77	0
44	2m	114/126 (90%)	1.46	24 (21%) 2 2	71, 78, 82, 84	0
45	1n	60/61 (98%)	0.80	5 (8%) 17 13	59, 65, 74, 75	0
45	2n	60/61 (98%)	1.91	22 (36%) 1 0	69, 78, 83, 86	0
46	1o	88/89 (98%)	0.50	2 (2%) 61 55	44, 59, 71, 77	0
46	2o	88/89 (98%)	0.70	4 (4%) 38 32	55, 66, 74, 82	0
47	1p	82/88 (93%)	1.28	9 (10%) 10 8	58, 66, 75, 79	0
47	2p	82/88 (93%)	0.86	2 (2%) 59 54	55, 63, 73, 78	0
48	1q	99/105 (94%)	0.71	4 (4%) 42 37	51, 63, 72, 75	0
48	2q	99/105 (94%)	0.54	2 (2%) 65 60	51, 64, 73, 78	0
49	1r	68/88 (77%)	0.29	1 (1%) 72 68	52, 60, 74, 75	0
49	2r	68/88 (77%)	0.59	2 (2%) 53 48	58, 65, 75, 79	0
50	1s	83/93 (89%)	0.90	7 (8%) 17 13	60, 70, 76, 80	0
50	2s	83/93 (89%)	1.75	25 (30%) 1 1	71, 81, 85, 87	0
51	1t	96/106 (90%)	0.88	11 (11%) 9 7	55, 66, 75, 77	0
51	2t	98/106 (92%)	0.66	6 (6%) 27 22	52, 64, 76, 78	0
52	1u	23/27 (85%)	1.26	2 (8%) 16 12	64, 66, 71, 72	0
52	2u	23/27 (85%)	2.16	9 (39%) 1 0	73, 75, 79, 80	0
53	1y	97/113 (85%)	0.52	4 (4%) 41 36	51, 60, 70, 74	0
53	2y	96/113 (84%)	1.87	42 (43%) 0 0	66, 76, 81, 83	0
All	All	20766/21468 (96%)	0.21	1089 (5%) 33 27	17, 58, 82, 102	0

All (1089) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	1A	1087	G	10.0
1	1A	1076	C	7.9
1	1A	1090	U	7.6
45	2n	2	ALA	7.6
1	1A	1077	A	7.5
1	1A	1078	U	6.7
23	21	2	SER	6.7
1	1A	1089	G	6.6
1	1A	1064	C	6.2
1	1A	1072	C	6.0

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Mol	Chain	Res	Type	RSRZ
51	1t	103	GLY	6.0
1	1A	1091	G	6.0
41	2j	34	VAL	5.9
26	14	49	PHE	5.8
1	2A	2147	G	5.8
1	1A	1088	A	5.7
1	1A	1103	A	5.6
1	1A	1079	C	5.5
1	1A	1080	C	5.5
41	2j	37	PRO	5.5
1	2A	2805	G	5.4
1	1A	1065	U	5.3
1	1A	2804	C	5.3
32	2a	1030(A)	G	5.3
1	2A	2804	C	5.1
23	11	2	SER	5.1
1	1A	2803	C	5.0
26	24	56	VAL	5.0
1	1A	1075	C	5.0
1	1A	1066	U	5.0
1	1A	2793	G	5.0
1	1A	1102	C	5.0
1	2A	2793	G	4.9
1	2A	1085	A	4.9
1	1A	1071	G	4.9
1	2A	1536	C	4.8
1	2A	2803	C	4.8
1	2A	2124	G	4.8
32	2a	1030(B)	C	4.8
1	1A	2805	G	4.8
8	2I	146	ALA	4.8
1	2A	2146	C	4.8
1	1A	1104	C	4.7
35	1d	2	GLY	4.7
1	2A	2125	G	4.7
1	2A	2153	G	4.7
1	1A	1074	G	4.6
1	2A	2154	G	4.6
1	1A	2602	A	4.6
8	2I	3	VAL	4.6
1	2A	2155	G	4.6
1	1A	2794	C	4.5

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Mol	Chain	Res	Type	RSRZ
53	2y	98	ALA	4.5
8	2I	20	ASP	4.5
32	1a	1001	A	4.5
32	1a	1036	G	4.5
32	2a	1030	C	4.4
53	1y	98	ALA	4.4
51	2t	103	GLY	4.4
1	1A	1081	U	4.4
32	1a	1030(A)	G	4.4
1	2A	2139	C	4.4
1	2A	2145	C	4.4
1	1A	1086	A	4.3
32	2a	1003	G	4.3
44	1m	2	ALA	4.3
26	14	59	PHE	4.3
1	1A	2168	G	4.3
32	2a	1036	G	4.3
40	2i	2	GLU	4.3
1	2A	2893	G	4.3
44	2m	102	ARG	4.2
45	1n	2	ALA	4.2
1	1A	1063	G	4.2
26	14	50	VAL	4.2
1	1A	2117	A	4.2
7	1H	2	SER	4.2
15	1T	37	GLY	4.2
41	1j	4	ILE	4.2
38	2g	5	ARG	4.2
1	2A	2130	U	4.2
1	2A	2172	U	4.2
1	1A	1067	A	4.2
1	2A	1076	C	4.2
1	1A	888	C	4.1
32	2a	1034	G	4.1
26	14	46	GLN	4.1
1	2A	6	A	4.1
1	2A	2174	C	4.1
5	1F	208	GLY	4.1
1	2A	2808	U	4.1
26	14	56	VAL	4.1
50	2s	35	SER	4.1
32	2a	1373	G	4.0

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Mol	Chain	Res	Type	RSRZ
1	2A	2602	A	4.0
1	2A	2142	C	4.0
1	2A	2807	G	4.0
40	2i	102	LEU	4.0
40	2i	126	SER	4.0
1	2A	1067	A	4.0
1	2A	2144	U	4.0
1	2A	2168	G	4.0
2	1B	1	U	4.0
8	2I	5	LEU	3.9
1	2A	1064	C	3.9
32	1a	1257	U	3.9
32	2a	1257	U	3.9
51	2t	6	PRO	3.9
1	2A	2111	C	3.9
1	2A	2133	G	3.9
1	2A	2135	A	3.9
32	2a	1035	A	3.9
26	24	49	PHE	3.9
35	1d	179	GLU	3.8
1	2A	2127	G	3.8
1	2A	2162	G	3.8
1	2A	2892	A	3.8
44	2m	100	GLY	3.8
1	2A	2143	C	3.8
12	1Q	33	GLY	3.8
1	2A	1046	A	3.8
45	2n	18	VAL	3.8
1	2A	1083	U	3.8
32	2a	1028	C	3.8
45	2n	3	ARG	3.8
1	1A	1082	U	3.8
1	1A	2145	C	3.8
1	2A	2138	C	3.8
1	2A	1082	U	3.7
32	2a	1025	U	3.7
1	2A	2140	C	3.7
32	1a	1030(B)	C	3.7
32	2a	1038	C	3.7
1	1A	1092	C	3.7
45	2n	13	THR	3.7
1	2A	2173	A	3.7

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Mol	Chain	Res	Type	RSRZ
1	1A	1094	U	3.7
1	2A	2118	U	3.7
1	2A	2152	G	3.7
1	2A	2894	G	3.7
1	2A	2107	C	3.7
1	2A	2896	C	3.7
50	2s	2	PRO	3.7
1	1A	34	C	3.6
1	2A	2136	C	3.6
32	1a	1030	C	3.6
32	2a	1027	C	3.6
50	2s	15	LEU	3.6
1	1A	2167	U	3.6
1	2A	1084	A	3.6
1	1A	1176	G	3.6
41	2j	91	PRO	3.6
41	2j	75	ILE	3.6
42	1k	25	TYR	3.6
12	2Q	104	PHE	3.6
1	2A	2165	G	3.6
34	2c	77	ILE	3.6
50	1s	13	ASP	3.6
1	1A	2132	U	3.6
1	1A	1073	A	3.6
1	2A	652(B)	A	3.6
32	2a	1033	G	3.5
6	1G	48	GLU	3.5
1	2A	2169	A	3.5
46	2o	3	ILE	3.5
53	2y	40	ILE	3.5
32	2a	1037	C	3.5
1	1A	1093	G	3.5
1	1A	2115	G	3.5
8	1I	147	GLN	3.5
19	1X	95	LEU	3.5
26	24	63	TYR	3.4
1	1A	2129	C	3.4
29	27	48	LYS	3.4
1	2A	1091	G	3.4
32	1a	1286	A	3.4
33	2b	136	VAL	3.4
40	2i	10	ARG	3.4

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Mol	Chain	Res	Type	RSRZ
48	1q	63	ARG	3.4
52	2u	14	TRP	3.4
1	2A	2129	C	3.4
1	2A	2175	C	3.4
36	1e	22	GLY	3.4
33	2b	44	LEU	3.4
1	1A	1058	G	3.4
1	1A	1062	G	3.4
1	1A	1099	G	3.4
6	2G	146	TYR	3.4
1	2A	2113	U	3.4
1	2A	229	A	3.4
33	1b	7	VAL	3.4
41	2j	38	ILE	3.3
1	2A	2109	U	3.3
1	2A	2179	C	3.3
1	1A	2166	G	3.3
1	2A	2792	G	3.3
32	1a	1023	G	3.3
44	2m	87	TYR	3.3
41	2j	46	ARG	3.3
52	2u	24	ARG	3.3
18	1W	111	HIS	3.3
1	1A	1057	A	3.3
26	14	63	TYR	3.3
38	2g	32	ARG	3.3
33	2b	118	LEU	3.3
33	2b	237	ALA	3.3
53	1y	94	ALA	3.3
8	2I	18	VAL	3.3
41	2j	44	VAL	3.3
41	1j	75	ILE	3.3
1	1A	548	A	3.3
1	1A	2119	A	3.3
1	2A	2114	A	3.3
1	2A	171	G	3.3
32	2a	1031	G	3.3
40	2i	6	GLY	3.3
21	1Z	51	ALA	3.3
26	24	55	ARG	3.2
41	2j	71	LEU	3.2
53	2y	97	ALA	3.2

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Mol	Chain	Res	Type	RSRZ
1	2A	2131	G	3.2
1	2A	2802	G	3.2
32	1a	1001(A)	G	3.2
32	1a	1024	G	3.2
14	2S	35	ILE	3.2
44	2m	106	ASN	3.2
41	2j	100	THR	3.2
53	2y	38	HIS	3.2
50	1s	8	GLY	3.2
38	2g	80	VAL	3.2
50	2s	9	VAL	3.2
1	2A	2112	G	3.2
12	2Q	59	ARG	3.2
53	2y	27	LEU	3.2
52	2u	23	PRO	3.2
15	1T	131	ALA	3.2
34	1c	207	VAL	3.2
1	2A	2126	A	3.2
32	2a	1286	A	3.2
41	2j	90	LEU	3.2
1	1A	2112	G	3.2
1	2A	1090	U	3.2
1	2A	2106	G	3.2
33	2b	97	TRP	3.2
40	2i	7	THR	3.2
50	2s	63	THR	3.2
41	2j	72	VAL	3.2
1	2A	645	C	3.1
6	2G	136	ARG	3.1
32	2a	1030(D)	A	3.1
26	14	52	THR	3.1
32	1a	1000	U	3.1
1	2A	1533	G	3.1
32	1a	1031	G	3.1
33	1b	236	TYR	3.1
33	2b	236	TYR	3.1
32	1a	1533	C	3.1
33	1b	131	PRO	3.1
47	1p	82	GLN	3.1
1	1A	2170	A	3.1
1	2A	2117	A	3.1
40	2i	43	ALA	3.1

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Mol	Chain	Res	Type	RSRZ
1	2A	2132	U	3.1
19	2X	95	LEU	3.1
1	2A	2116	G	3.1
1	2A	2123	G	3.1
34	1c	90	GLU	3.1
33	1b	127	ILE	3.1
32	2a	1531	A	3.1
1	2A	1097	U	3.1
45	2n	14	PRO	3.1
1	2A	2148	G	3.1
1	2A	2207	G	3.1
44	2m	89	GLY	3.1
40	2i	14	VAL	3.1
44	2m	60	VAL	3.1
1	1A	229	A	3.0
35	1d	194	LEU	3.0
24	12	70	GLN	3.0
26	14	54	GLY	3.0
35	2d	5	ILE	3.0
19	1X	68	ARG	3.0
45	2n	33	VAL	3.0
26	24	66	SER	3.0
32	2a	630	G	3.0
1	1A	1053	C	3.0
32	1a	1006	C	3.0
41	2j	69	ASN	3.0
1	1A	2171	A	3.0
1	1A	1083	U	3.0
1	2A	2167	U	3.0
47	1p	19	ILE	3.0
26	24	50	VAL	3.0
33	2b	15	VAL	3.0
50	2s	41	VAL	3.0
39	2h	2	LEU	3.0
1	2A	1089	G	3.0
1	2A	2149	G	3.0
1	2A	1070	A	3.0
1	2A	2119	A	3.0
1	2A	2171	A	3.0
6	2G	77	ILE	3.0
33	2b	208	ILE	3.0
33	1b	237	ALA	3.0

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Mol	Chain	Res	Type	RSRZ
41	1j	32	ALA	3.0
34	2c	207	VAL	3.0
44	1m	117	VAL	3.0
51	1t	10	LEU	3.0
1	1A	2147	G	3.0
1	1A	2893	G	3.0
1	2A	2105	C	3.0
1	1A	1070	A	3.0
1	1A	1085	A	3.0
1	1A	2173	A	3.0
1	1A	2790	A	3.0
6	1G	182	LYS	2.9
47	2p	82	GLN	2.9
33	2b	214	ILE	2.9
33	2b	38	GLY	2.9
26	24	52	THR	2.9
15	2T	131	ALA	2.9
53	2y	52	ALA	2.9
41	2j	47	PHE	2.9
1	2A	1092	C	2.9
1	1A	1095	A	2.9
1	1A	2158	A	2.9
1	2A	1073	A	2.9
1	2A	1096	A	2.9
32	1a	1032	G	2.9
32	2a	1032	G	2.9
53	2y	7	SER	2.9
41	1j	74	ILE	2.9
45	2n	7	ILE	2.9
52	2u	16	GLY	2.9
41	2j	42	THR	2.9
7	2H	165	ALA	2.9
38	2g	83	ALA	2.9
40	2i	109	VAL	2.9
44	2m	54	VAL	2.9
19	2X	92	LEU	2.9
50	2s	76	PRO	2.9
1	1A	2142	C	2.9
1	2A	1075	C	2.9
1	2A	2176	A	2.9
32	1a	1447	A	2.9
1	2A	2110	G	2.9

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Mol	Chain	Res	Type	RSRZ
1	2A	2121	G	2.9
1	2A	2141	G	2.9
1	2A	2150	U	2.9
1	2A	2159	G	2.9
32	2a	1026	G	2.9
41	1j	76	ASN	2.9
8	1I	20	ASP	2.9
43	1l	63	GLY	2.9
45	2n	55	GLY	2.9
41	2j	27	ALA	2.9
41	2j	39	PRO	2.9
52	1u	24	ARG	2.9
52	2u	6	ARG	2.9
1	2A	1072	C	2.9
1	2A	1081	U	2.9
1	2A	2163	C	2.9
2	2B	1	U	2.9
26	24	54	GLY	2.9
41	1j	87	THR	2.9
1	1A	2116	G	2.9
1	1A	2792	G	2.9
1	1A	2894	G	2.9
6	2G	90	LEU	2.9
32	2a	1030(C)	G	2.9
33	2b	22	LYS	2.9
34	2c	187	ALA	2.9
38	2g	16	LEU	2.9
41	2j	40	LEU	2.9
41	2j	65	LEU	2.9
39	2h	122	ARG	2.8
6	2G	76	SER	2.8
41	1j	78	ASN	2.8
40	2i	127	LYS	2.8
6	2G	3	LEU	2.8
15	1T	130	ALA	2.8
15	2T	130	ALA	2.8
38	2g	128	ALA	2.8
41	2j	8	LEU	2.8
1	2A	2122	U	2.8
33	2b	164	VAL	2.8
32	2a	1004	A	2.8
32	1a	1033	G	2.8

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Mol	Chain	Res	Type	RSRZ
8	2I	4	ILE	2.8
48	1q	99	SER	2.8
17	2V	42	GLY	2.8
44	2m	6	GLY	2.8
39	1h	2	LEU	2.8
40	1i	46	ALA	2.8
40	2i	4	TYR	2.8
8	2I	19	VAL	2.8
33	2b	122	PHE	2.8
26	14	48	ARG	2.8
32	2a	1249	C	2.8
1	1A	1056	G	2.8
1	1A	2125	G	2.8
1	2A	1171	G	2.8
26	14	45	GLY	2.8
26	24	51	ASP	2.8
6	2G	109	VAL	2.8
21	1Z	192	ALA	2.8
34	2c	48	TYR	2.8
45	2n	20	ALA	2.8
53	2y	49	VAL	2.8
1	2A	1095	A	2.8
1	2A	2134	A	2.8
32	2a	1447	A	2.8
1	2A	1079	C	2.8
1	2A	2128	C	2.8
1	2A	2161	C	2.8
35	1d	157	LEU	2.8
44	1m	56	LEU	2.8
53	2y	85	LEU	2.8
7	2H	129	THR	2.8
33	2b	230	VAL	2.8
42	2k	89	ALA	2.8
1	1A	2159	G	2.8
1	2A	2187	G	2.8
32	1a	1026	G	2.8
32	2a	1002	G	2.8
26	24	46	GLN	2.7
40	2i	78	LYS	2.7
32	1a	1532	U	2.7
6	2G	42	GLY	2.7
52	2u	11	GLY	2.7

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Mol	Chain	Res	Type	RSRZ
33	2b	16	HIS	2.7
26	24	65	ASP	2.7
1	2A	34	C	2.7
1	2A	2137	C	2.7
34	2c	92	ALA	2.7
40	1i	106	ALA	2.7
44	2m	116	THR	2.7
7	2H	21	PRO	2.7
1	1A	2133	G	2.7
1	1A	2155	G	2.7
1	2A	2206	G	2.7
53	2y	16	ILE	2.7
21	2Z	1	MET	2.7
33	1b	94	ASN	2.7
53	2y	3	MET	2.7
1	1A	2144	U	2.7
33	1b	129	GLU	2.7
34	2c	90	GLU	2.7
33	1b	17	PHE	2.7
47	1p	22	THR	2.7
32	1a	1030(D)	A	2.7
33	2b	232	PRO	2.7
26	24	67	TYR	2.7
33	2b	133	LYS	2.7
40	1i	127	LYS	2.7
42	2k	25	TYR	2.7
1	1A	1100	C	2.7
1	2A	1509	C	2.7
8	2I	12	LEU	2.7
8	2I	38	LEU	2.7
34	2c	94	LEU	2.7
1	1A	1068	G	2.7
1	1A	2127	G	2.7
1	2A	1087	G	2.7
32	1a	630	G	2.7
41	2j	5	ARG	2.7
6	2G	145	THR	2.7
41	2j	26	ALA	2.7
50	2s	79	THR	2.7
53	1y	2	THR	2.7
1	1A	1098	A	2.7
1	2A	1088	A	2.7

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Mol	Chain	Res	Type	RSRZ
1	2A	2801(A)	A	2.7
32	1a	1492	A	2.7
1	1A	2143	C	2.7
53	2y	41	LEU	2.7
44	2m	58	GLU	2.7
33	2b	120	ALA	2.7
40	2i	101	PHE	2.7
41	2j	67	THR	2.7
53	2y	8	LYS	2.7
53	2y	50	ALA	2.7
1	1A	2165	G	2.6
1	2A	2166	G	2.6
1	1A	2130	U	2.6
1	2A	2180	U	2.6
38	2g	154	TYR	2.6
6	1G	52	ILE	2.6
48	2q	98	LEU	2.6
11	1P	15	ARG	2.6
50	2s	82	GLY	2.6
1	1A	2146	C	2.6
1	2A	888	C	2.6
53	2y	4	ASN	2.6
33	2b	7	VAL	2.6
33	2b	165	VAL	2.6
38	2g	25	ALA	2.6
50	2s	19	VAL	2.6
22	20	43	THR	2.6
6	2G	147	ASP	2.6
38	2g	33	ASP	2.6
38	2g	85	TYR	2.6
44	1m	4	ILE	2.6
1	1A	2113	U	2.6
1	2A	1026	U	2.6
1	2A	1071	G	2.6
32	2a	1001(A)	G	2.6
32	2a	1532	U	2.6
26	14	55	ARG	2.6
34	2c	79	ARG	2.6
8	2I	16	GLY	2.6
11	2P	76	LYS	2.6
26	24	45	GLY	2.6
34	2c	41	GLY	2.6

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Mol	Chain	Res	Type	RSRZ
52	1u	2	GLY	2.6
1	1A	2114	A	2.6
40	2i	21	PRO	2.6
40	2i	123	PRO	2.6
43	2l	5	PRO	2.6
1	1A	1532	C	2.6
1	2A	2108	C	2.6
1	2A	2789	C	2.6
32	2a	1029	C	2.6
44	2m	82	MET	2.6
11	2P	99	LEU	2.6
53	2y	61	LEU	2.6
14	2S	3	ARG	2.6
41	2j	70	ARG	2.6
45	2n	17	LYS	2.6
25	23	60	GLU	2.6
35	2d	156	GLU	2.6
1	2A	2186	G	2.6
4	2E	204	ALA	2.6
34	2c	146	ALA	2.6
50	2s	42	PRO	2.6
6	1G	76	SER	2.6
21	2Z	170	THR	2.6
1	1A	2169	A	2.6
50	2s	31	ILE	2.6
1	2A	1104	C	2.6
1	2A	2188	C	2.6
1	2A	2794	C	2.6
40	1i	56	LEU	2.6
41	2j	88	LEU	2.6
40	2i	66	ARG	2.6
41	2j	43	ARG	2.6
26	14	69	LYS	2.6
1	1A	2118	U	2.6
1	2A	2897	U	2.6
6	2G	122	PRO	2.6
45	2n	5	ALA	2.6
53	2y	60	VAL	2.6
40	1i	64	THR	2.5
53	2y	9	GLN	2.6
1	2A	1062	G	2.5
6	2G	157	ILE	2.5

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Mol	Chain	Res	Type	RSRZ
34	2c	8	ILE	2.5
1	2A	529	A	2.5
32	1a	1035	A	2.5
33	2b	121	LEU	2.5
15	1T	129	ARG	2.5
51	1t	8	ARG	2.5
45	2n	21	TYR	2.5
1	1A	2161	C	2.5
32	1a	1029	C	2.5
6	2G	87	PRO	2.5
1	2A	614(A)	U	2.5
1	2A	1066	U	2.5
45	2n	60	SER	2.5
3	2D	71	ASP	2.5
14	1S	20	ARG	2.5
33	2b	215	LEU	2.5
51	1t	99	LEU	2.5
53	2y	33	HIS	2.5
1	1A	2123	G	2.5
1	1A	2153	G	2.5
32	1a	1034	G	2.5
6	1G	146	TYR	2.5
38	1g	85	TYR	2.5
46	1o	89	GLY	2.5
25	23	2	PRO	2.5
33	1b	165	VAL	2.5
40	2i	65	VAL	2.5
45	1n	33	VAL	2.5
33	2b	152	PHE	2.5
1	1A	889	C	2.5
1	1A	2107	C	2.5
1	2A	1118	C	2.5
20	2Y	1	MET	2.5
32	2a	1277	C	2.5
40	2i	64	THR	2.5
41	2j	48	THR	2.5
53	2y	42	SER	2.5
51	2t	7	LYS	2.5
14	1S	3	ARG	2.5
41	2j	45	ARG	2.5
45	1n	3	ARG	2.5
53	2y	54	ILE	2.5

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Mol	Chain	Res	Type	RSRZ
32	2a	1000	U	2.5
32	2a	1020	U	2.5
50	2s	71	LEU	2.5
26	14	64	GLY	2.5
1	2A	1057	A	2.5
1	2A	1086	A	2.5
1	2A	2120	G	2.5
1	2A	2170	A	2.5
8	1I	107	VAL	2.5
32	1a	1030(C)	G	2.5
32	2a	1248	A	2.5
40	2i	41	VAL	2.5
50	1s	9	VAL	2.5
41	1j	26	ALA	2.5
50	1s	77	THR	2.5
53	2y	79	ASN	2.5
8	2I	109	ILE	2.5
45	2n	35	ARG	2.5
32	1a	1007	C	2.5
32	1a	1037	C	2.5
33	1b	234	PRO	2.5
35	1d	138	TYR	2.5
38	2g	34	GLY	2.5
40	2i	125	TYR	2.5
35	1d	178	VAL	2.5
40	2i	44	VAL	2.5
45	2n	25	VAL	2.5
38	2g	7	ALA	2.5
34	2c	93	LYS	2.4
41	1j	100	THR	2.4
50	2s	77	THR	2.4
1	1A	2892	A	2.4
18	2W	60	ASN	2.4
32	2a	1005	A	2.4
32	2a	1183	A	2.4
6	2G	39	ILE	2.4
6	2G	53	LEU	2.4
6	2G	88	ILE	2.4
33	2b	39	ILE	2.4
41	2j	74	ILE	2.4
50	2s	20	LEU	2.4
53	2y	5	ILE	2.4

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Mol	Chain	Res	Type	RSRZ
1	2A	1074	G	2.4
32	2a	1024	G	2.4
35	1d	192	GLU	2.4
1	1A	2175	C	2.4
46	2o	86	GLY	2.4
43	1l	64	TYR	2.4
33	2b	132	LYS	2.4
38	2g	36	LYS	2.4
34	2c	53	ALA	2.4
34	2c	189	ALA	2.4
40	2i	55	ALA	2.4
40	2i	9	ARG	2.4
47	2p	25	ARG	2.4
53	2y	32	THR	2.4
6	2G	62	LEU	2.4
14	2S	40	ILE	2.4
39	1h	133	LEU	2.4
50	2s	30	LEU	2.4
1	1A	1096	A	2.4
1	1A	2176	A	2.4
1	2A	2809	A	2.4
32	2a	965	A	2.4
1	2A	2104	G	2.4
32	1a	1003	G	2.4
53	2y	65	GLY	2.4
26	24	69	LYS	2.4
1	1A	1116	C	2.4
1	1A	2139	C	2.4
8	2I	15	VAL	2.4
34	2c	75	VAL	2.4
1	1A	2109	U	2.4
32	1a	204	U	2.4
42	2k	75	TYR	2.4
45	2n	29	ARG	2.4
52	2u	9	ARG	2.4
33	2b	69	LEU	2.4
33	2b	149	LEU	2.4
53	2y	12	ILE	2.4
53	2y	55	ASN	2.4
41	2j	62	HIS	2.4
33	1b	126	GLU	2.4
3	2D	275	LYS	2.4

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Mol	Chain	Res	Type	RSRZ
32	1a	1531	A	2.4
32	2a	532	A	2.4
32	2a	1256	A	2.4
33	1b	22	LYS	2.4
33	1b	132	LYS	2.4
40	2i	11	LYS	2.4
11	2P	109	GLY	2.4
41	2j	93	GLY	2.4
47	1p	46	PRO	2.4
41	1j	33	GLN	2.4
40	2i	86	VAL	2.4
44	2m	15	VAL	2.4
1	1A	2124	G	2.4
29	27	47	ARG	2.4
32	2a	1124	G	2.4
33	2b	123	ALA	2.4
34	2c	190	ARG	2.4
40	2i	45	ALA	2.4
41	2j	16	LEU	2.4
53	2y	81	LEU	2.4
1	1A	1026	U	2.4
1	1A	2172	U	2.4
1	2A	2164	C	2.4
35	2d	154	ASN	2.4
41	2j	68	HIS	2.4
14	2S	53	SER	2.4
41	2j	35	SER	2.4
47	1p	1	MET	2.4
6	2G	74	LYS	2.4
33	2b	8	LYS	2.4
43	2l	17	LYS	2.4
48	1q	80	GLY	2.4
34	2c	195	VAL	2.4
1	1A	1084	A	2.4
1	2A	887	A	2.4
33	2b	161	ALA	2.4
38	2g	2	ALA	2.4
33	2b	11	LEU	2.3
33	2b	33	TYR	2.3
34	1c	87	LEU	2.3
35	2d	20	TYR	2.3
1	1A	1061	U	2.3

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Mol	Chain	Res	Type	RSRZ
1	1A	1105	U	2.3
1	1A	1117	G	2.3
1	1A	2150	U	2.3
1	2A	2156	G	2.3
1	2A	2160	G	2.3
32	1a	1021	G	2.3
32	2a	999	C	2.3
51	1t	98	PRO	2.3
40	2i	42	ARG	2.3
26	24	59	PHE	2.3
34	2c	101	LEU	2.3
35	1d	111	ALA	2.3
44	2m	59	TYR	2.3
1	1A	2126	A	2.3
33	1b	40	HIS	2.3
38	2g	37	ASN	2.3
1	1A	1101	U	2.3
32	1a	841	U	2.3
1	2A	2157	G	2.3
32	1a	1009	G	2.3
32	2a	1202	G	2.3
32	2a	1347	G	2.3
33	1b	125	PRO	2.3
1	1A	1584	C	2.3
1	2A	1040	C	2.3
13	2R	68	ARG	2.3
16	1U	117	GLN	2.3
26	24	60	GLN	2.3
32	2a	1006	C	2.3
32	2a	1019	C	2.3
42	2k	13	GLN	2.3
46	2o	89	GLY	2.3
47	1p	76	GLN	2.3
3	2D	2	ALA	2.3
7	2H	7	LEU	2.3
33	1b	34	ALA	2.3
33	2b	138	LEU	2.3
34	2c	47	LEU	2.3
41	2j	32	ALA	2.3
51	1t	67	ALA	2.3
53	2y	24	LEU	2.3
34	2c	182	ILE	2.3

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Mol	Chain	Res	Type	RSRZ
53	2y	35	ILE	2.3
1	1A	887	A	2.3
7	2H	3	ARG	2.3
26	24	58	ARG	2.3
11	2P	37	GLY	2.3
33	1b	18	GLY	2.3
1	1A	1175	U	2.3
9	1N	9	VAL	2.3
21	2Z	191	VAL	2.3
33	1b	136	VAL	2.3
34	2c	86	VAL	2.3
44	2m	90	LEU	2.3
1	1A	545	G	2.3
1	1A	1055	G	2.3
1	1A	2164	C	2.3
1	2A	2103	C	2.3
1	2A	2191	G	2.3
32	1a	78	G	2.3
44	2m	9	ILE	2.3
33	1b	19	HIS	2.3
33	2b	140	HIS	2.3
8	1I	86	THR	2.3
29	17	48	LYS	2.3
29	27	1	MET	2.3
33	2b	90	MET	2.3
45	2n	11	LYS	2.3
48	1q	100	LYS	2.3
40	1i	125	TYR	2.3
33	2b	134	GLU	2.3
14	2S	61	ASN	2.3
5	2F	14	PRO	2.3
7	2H	130	ARG	2.3
35	2d	71	SER	2.3
41	2j	19	SER	2.3
50	2s	12	ASP	2.3
1	1A	6	A	2.3
1	1A	529	A	2.3
1	1A	1046	A	2.3
48	2q	93	GLN	2.3
51	1t	18	GLN	2.3
41	2j	36	GLY	2.3
44	2m	56	LEU	2.3

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Mol	Chain	Res	Type	RSRZ
44	2m	66	LEU	2.3
1	2A	1065	U	2.2
32	1a	1446	U	2.2
34	2c	160	ALA	2.2
53	2y	15	ALA	2.2
51	1t	73	HIS	2.2
41	2j	64	GLU	2.2
46	1o	6	GLU	2.2
32	2a	1363	C	2.2
1	1A	1537	G	2.2
1	2A	2319	G	2.2
40	1i	42	ARG	2.2
40	1i	128	ARG	2.2
49	2r	87	ARG	2.2
53	2y	83	ARG	2.2
41	2j	77	PRO	2.2
31	29	37	GLY	2.2
47	1p	48	TRP	2.2
21	2Z	58	VAL	2.2
34	2c	138	VAL	2.2
1	1A	2135	A	2.2
3	1D	275	LYS	2.2
3	1D	276	LYS	2.2
6	2G	75	LYS	2.2
7	2H	175	LYS	2.2
33	2b	40	HIS	2.2
40	1i	94	ALA	2.2
40	2i	46	ALA	2.2
44	2m	27	LYS	2.2
41	2j	86	MET	2.2
1	2A	1060	U	2.2
32	1a	1020	U	2.2
32	2a	1125	U	2.2
32	2a	1281	U	2.2
33	1b	12	GLU	2.2
15	2T	111	ARG	2.2
22	20	74	ARG	2.2
38	2g	28	ASN	2.2
44	1m	102	ARG	2.2
53	1y	95	ARG	2.2
1	2A	2185	C	2.2
8	2I	14	ASP	2.2

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Mol	Chain	Res	Type	RSRZ
1	2A	2151	G	2.2
18	1W	112	GLY	2.2
20	2Y	80	GLY	2.2
34	1c	62	ASP	2.2
32	2a	1190	G	2.2
47	1p	6	LEU	2.2
6	2G	38	VAL	2.2
6	2G	63	ILE	2.2
33	2b	57	PHE	2.2
6	2G	50	ALA	2.2
35	1d	150	GLU	2.2
1	2A	2158	A	2.2
43	1l	6	THR	2.2
1	1A	9	U	2.2
32	1a	723	U	2.2
45	2n	57	ARG	2.2
33	2b	148	TYR	2.2
53	2y	14	PRO	2.2
35	1d	101	LEU	2.2
21	1Z	1	MET	2.2
36	2e	10	MET	2.2
1	2A	886	C	2.2
7	2H	136	ILE	2.2
32	2a	1007	C	2.2
32	2a	1354	C	2.2
45	2n	61	TRP	2.2
34	1c	100	ALA	2.2
40	1i	15	ALA	2.2
1	1A	275	G	2.2
1	1A	1173	G	2.2
1	1A	2206	G	2.2
32	2a	1353	G	2.2
11	2P	15	ARG	2.2
35	1d	3	ARG	2.2
41	2j	28	ARG	2.2
21	2Z	68	PRO	2.2
32	2a	1123	A	2.2
32	2a	1493	A	2.2
41	2j	78	ASN	2.2
44	1m	115	LYS	2.2
45	2n	4	LYS	2.2
52	2u	3	LYS	2.2

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Mol	Chain	Res	Type	RSRZ
50	2s	26	GLY	2.2
16	2U	56	ASP	2.2
40	1i	91	ASP	2.2
6	2G	28	VAL	2.2
36	2e	109	ILE	2.2
42	2k	109	VAL	2.2
38	2g	43	PHE	2.2
34	2c	60	ALA	2.1
34	2c	61	ALA	2.1
50	2s	34	TRP	2.1
20	2Y	91	GLU	2.1
1	1A	2174	C	2.1
1	2A	2177	C	2.1
23	2l	26	ARG	2.1
33	2b	21	ARG	2.1
33	2b	67	THR	2.1
1	2A	1039	G	2.1
32	1a	306	G	2.1
32	2a	1224	G	2.1
3	2D	276	LYS	2.1
33	1b	10	LEU	2.1
33	2b	145	LEU	2.1
35	1d	155	LEU	2.1
32	2a	1492	A	2.1
34	2c	159	GLY	2.1
35	2d	6	GLY	2.1
40	2i	67	GLY	2.1
51	2t	96	GLY	2.1
1	1A	271(K)	U	2.1
1	2A	2189	U	2.1
1	2A	2895	U	2.1
6	2G	52	ILE	2.1
6	2G	160	VAL	2.1
7	2H	45	VAL	2.1
34	2c	173	VAL	2.1
40	2i	17	VAL	2.1
41	1j	44	VAL	2.1
49	2r	86	VAL	2.1
53	2y	78	ILE	2.1
33	2b	17	PHE	2.1
33	1b	13	ALA	2.1
38	2g	116	ALA	2.1

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Mol	Chain	Res	Type	RSRZ
49	1r	24	ALA	2.1
8	1I	85	GLU	2.1
8	2I	7	GLU	2.1
41	2j	83	GLU	2.1
6	2G	64	THR	2.1
33	2b	73	THR	2.1
45	2n	22	THR	2.1
7	2H	85	LYS	2.1
44	2m	31	LYS	2.1
50	1s	2	PRO	2.1
53	2y	45	PRO	2.1
1	2A	1080	C	2.1
33	2b	154	LEU	2.1
40	1i	62	TYR	2.1
8	2I	34	GLY	2.1
18	2W	112	GLY	2.1
35	2d	2	GLY	2.1
6	2G	159	VAL	2.1
33	2b	185	ILE	2.1
34	2c	5	ILE	2.1
41	1j	34	VAL	2.1
41	1j	49	VAL	2.1
45	2n	56	VAL	2.1
53	2y	51	ASP	2.1
40	2i	18	PHE	2.1
40	2i	59	PHE	2.1
41	2j	59	SER	2.1
1	2A	1078	U	2.1
6	2G	59	GLU	2.1
32	1a	1040	U	2.1
34	2c	50	ALA	2.1
34	2c	168	ALA	2.1
35	1d	195	ALA	2.1
44	2m	51	ALA	2.1
51	1t	97	ALA	2.1
33	1b	36	ARG	2.1
53	2y	95	ARG	2.1
3	2D	259	THR	2.1
44	1m	116	THR	2.1
45	1n	13	THR	2.1
50	2s	59	PRO	2.1
8	2I	17	GLN	2.1

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Mol	Chain	Res	Type	RSRZ
33	2b	61	LEU	2.1
34	2c	155	GLY	2.1
35	1d	167	GLY	2.1
52	2u	2	GLY	2.1
1	1A	2138	C	2.1
7	2H	89	ILE	2.1
32	1a	1028	C	2.1
33	2b	127	ILE	2.1
34	2c	68	VAL	2.1
40	1i	14	VAL	2.1
41	1j	72	VAL	2.1
44	2m	78	ILE	2.1
33	1b	160	ASP	2.1
33	2b	70	PHE	2.1
21	2Z	192	ALA	2.1
26	14	68	ARG	2.1
34	2c	54	ARG	2.1
44	2m	18	ALA	2.1
45	1n	5	ALA	2.1
46	2o	68	ARG	2.1
50	2s	24	ALA	2.1
1	1A	2157	G	2.1
1	2A	2115	G	2.1
6	2G	100	TRP	2.1
32	2a	963	G	2.1
1	1A	1177	A	2.1
1	2A	1105	U	2.1
32	1a	1493	A	2.1
32	2a	956	U	2.1
32	2a	1001	A	2.1
32	2a	1280	A	2.1
32	2a	1446	U	2.1
42	2k	31	THR	2.1
24	22	70	GLN	2.1
6	2G	139	LEU	2.1
33	1b	11	LEU	2.1
38	2g	22	LEU	2.1
40	2i	40	LEU	2.1
53	2y	34	LEU	2.1
41	1j	31	GLY	2.1
44	2m	85	GLY	2.1
51	2t	102	GLY	2.1

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Mol	Chain	Res	Type	RSRZ
7	2H	44	VAL	2.1
21	2Z	42	VAL	2.1
53	2y	20	VAL	2.1
6	2G	80	PHE	2.1
50	2s	29	ARG	2.0
14	2S	86	ALA	2.0
1	1A	2111	C	2.0
1	2A	1584	C	2.0
7	1H	175	LYS	2.0
8	2I	2	LYS	2.0
32	1a	999	C	2.0
32	2a	1369	C	2.0
50	2s	18	LYS	2.0
47	1p	69	THR	2.0
7	2H	128	PRO	2.0
26	24	7	PRO	2.0
33	2b	131	PRO	2.0
34	2c	174	PRO	2.0
41	1j	77	PRO	2.0
1	1A	1097	U	2.0
1	2A	1094	U	2.0
32	2a	1235	U	2.0
34	2c	175	LEU	2.0
39	2h	70	GLN	2.0
1	1A	2162	G	2.0
1	2A	1063	G	2.0
1	2A	1460	A	2.0
32	1a	79	G	2.0
32	1a	380	G	2.0
32	2a	1357	A	2.0
20	1Y	92	ASN	2.0
50	1s	23	ASN	2.0
6	1G	89	GLY	2.0
21	2Z	197	ILE	2.0
36	2e	80	ILE	2.0
26	24	61	ARG	2.0
26	24	62	ARG	2.0
35	1d	76	ARG	2.0
35	2d	47	ARG	2.0
40	1i	18	PHE	2.0
41	2j	54	PHE	2.0
53	2y	11	GLU	2.0

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Mol	Chain	Res	Type	RSRZ
8	2I	39	ALA	2.0
34	1c	150	LYS	2.0
40	2i	13	ALA	2.0
38	2g	156	TRP	2.0
53	2y	56	THR	2.0
1	2A	652(T)	C	2.0
32	1a	1018	C	2.0
32	2a	1260	C	2.0
33	2b	10	LEU	2.0
35	2d	162	LEU	2.0
53	2y	77	LEU	2.0
1	1A	272(A)	U	2.0
32	1a	1025	U	2.0
26	24	14	ILE	2.0
33	1b	37	ASN	2.0
33	2b	200	ILE	2.0
38	2g	120	ILE	2.0
42	2k	90	GLY	2.0
50	1s	26	GLY	2.0
50	2s	49	ILE	2.0
51	1t	100	ILE	2.0
51	1t	101	GLY	2.0
51	2t	9	ASN	2.0
1	2A	2320	A	2.0
29	27	41	ARG	2.0
34	2c	70	VAL	2.0
44	1m	3	ARG	2.0
44	2m	7	VAL	2.0
50	2s	67	VAL	2.0

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

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	0.79	0.12	76,82,86,102	0
32	2MG	2a	1207	24/25	0.86	0.12	76,82,86,94	0
32	M2G	2a	966	25/26	0.89	0.14	59,66,81,90	0
1	PSU	2A	1917	20/21	0.89	0.10	67,75,82,84	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
43	0TD	2l	92	10/11	0.89	0.12	59,62,65,79	0
1	5MU	1A	1915	21/22	0.90	0.11	61,70,75,79	0
32	2MG	1a	1207	24/25	0.91	0.10	56,69,72,72	0
43	0TD	1l	92	10/11	0.91	0.10	48,52,56,68	0
1	PSU	2A	1911	20/21	0.91	0.08	62,67,73,79	0
1	PSU	1A	1917	20/21	0.91	0.10	58,66,80,83	0
32	5MC	2a	967	21/22	0.92	0.14	64,69,72,79	0
32	4OC	2a	1402	22/23	0.93	0.10	52,62,67,70	0
32	5MC	1a	967	21/22	0.93	0.10	55,63,70,75	0
32	G7M	2a	527	24/25	0.94	0.10	54,62,67,72	0
1	OMC	2A	1920	21/22	0.94	0.10	60,65,69,71	0
32	5MC	2a	1407	21/22	0.94	0.10	53,63,67,68	0
32	PSU	2a	516	20/21	0.94	0.08	67,73,76,77	0
1	PSU	1A	1911	20/21	0.95	0.08	54,62,65,67	0
32	5MC	2a	1404	21/22	0.95	0.09	47,55,61,63	0
32	5MC	1a	1407	21/22	0.95	0.10	39,51,54,55	0
32	5MC	2a	1400	21/22	0.95	0.12	62,67,72,74	0
32	MA6	1a	1518	24/25	0.96	0.10	41,46,51,54	0
32	PSU	1a	516	20/21	0.96	0.07	54,59,62,62	0
32	G7M	1a	527	24/25	0.96	0.08	42,50,55,57	0
32	5MC	1a	1400	21/22	0.96	0.09	41,50,55,58	0
32	4OC	1a	1402	22/23	0.96	0.08	46,49,52,55	0
32	5MC	1a	1404	21/22	0.96	0.09	40,44,50,54	0
32	M2G	1a	966	25/26	0.96	0.08	50,56,61,63	0
32	UR3	2a	1498	21/22	0.96	0.08	52,55,59,63	0
32	MA6	2a	1518	24/25	0.96	0.10	52,60,65,66	0
32	MA6	2a	1519	24/25	0.96	0.10	53,60,64,64	0
32	UR3	1a	1498	21/22	0.96	0.08	40,43,49,58	0
1	5MC	2A	1962	21/22	0.97	0.09	38,44,51,56	0
1	OMG	2A	2251	24/25	0.97	0.08	31,35,40,41	0
1	2MA	2A	2503	23/24	0.97	0.08	26,30,33,37	0
32	MA6	1a	1519	24/25	0.97	0.09	38,46,50,51	0
1	PSU	1A	2605	20/21	0.97	0.08	24,27,29,32	0
1	5MC	1A	1942	21/22	0.97	0.07	27,32,39,46	0
1	5MU	2A	1939	21/22	0.97	0.07	30,35,39,42	0
1	5MC	2A	1942	21/22	0.97	0.07	40,48,52,55	0
1	2MA	1A	2503	23/24	0.98	0.06	16,20,25,26	0
1	2MU	2A	2552	21/23	0.98	0.07	32,36,41,42	0
1	PSU	2A	2605	20/21	0.98	0.06	27,31,36,40	0
1	2MU	1A	2552	21/23	0.98	0.06	22,28,30,33	0
1	5MU	1A	1939	21/22	0.98	0.08	19,25,31,33	0
1	OMC	1A	1920	21/22	0.98	0.07	41,52,57,57	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
1	5MC	1A	1962	21/22	0.98	0.07	27,31,37,38	0
1	OMG	1A	2251	24/25	0.98	0.05	20,23,27,31	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
54	MG	1A	4001	1/1	0.33	0.36	88,88,88,88	0
54	MG	1A	3653	1/1	0.44	0.25	60,60,60,60	0
54	MG	2A	3729	1/1	0.46	0.30	76,76,76,76	0
54	MG	2B	212	1/1	0.58	0.32	70,70,70,70	0
54	MG	2A	3422	1/1	0.59	0.31	80,80,80,80	0
54	MG	1A	3694	1/1	0.59	0.18	69,69,69,69	0
54	MG	1A	3334	1/1	0.59	0.31	74,74,74,74	0
54	MG	2A	3401	1/1	0.60	0.21	49,49,49,49	0
54	MG	1a	3188	1/1	0.61	0.26	85,85,85,85	0
54	MG	2A	3196	1/1	0.61	0.38	74,74,74,74	0
54	MG	1A	3646	1/1	0.62	0.34	40,40,40,40	0
54	MG	2O	202	1/1	0.63	0.22	79,79,79,79	0
54	MG	1A	3265	1/1	0.64	0.24	68,68,68,68	0
54	MG	1A	3749	1/1	0.64	0.16	63,63,63,63	0
54	MG	2A	3385	1/1	0.65	0.22	81,81,81,81	0
54	MG	1A	3889	1/1	0.65	0.21	58,58,58,58	0
54	MG	1A	3273	1/1	0.67	0.28	72,72,72,72	0
54	MG	2A	3513	1/1	0.68	0.22	68,68,68,68	0
54	MG	1A	3992	1/1	0.68	0.23	59,59,59,59	0
54	MG	1a	3203	1/1	0.68	0.23	73,73,73,73	0
54	MG	1B	226	1/1	0.68	0.17	68,68,68,68	0
54	MG	2A	3708	1/1	0.69	0.15	67,67,67,67	0
54	MG	1A	3982	1/1	0.69	0.14	31,31,31,31	0
54	MG	2A	3290	1/1	0.69	0.42	80,80,80,80	0
54	MG	1A	3591	1/1	0.69	0.42	43,43,43,43	0
54	MG	2A	3436	1/1	0.70	0.18	75,75,75,75	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	2A	3735	1/1	0.70	0.22	70,70,70,70	0
54	MG	2A	3125	1/1	0.70	0.13	61,61,61,61	0
54	MG	2A	3094	1/1	0.70	0.26	74,74,74,74	0
58	ARG	1F	321	12/12	0.70	0.21	52,67,79,82	0
54	MG	2A	3459	1/1	0.71	0.18	58,58,58,58	0
54	MG	1A	3869	1/1	0.71	0.17	65,65,65,65	0
54	MG	1A	4009	1/1	0.72	0.29	48,48,48,48	0
54	MG	1A	3427	1/1	0.72	0.21	57,57,57,57	0
54	MG	2A	3443	1/1	0.72	0.19	69,69,69,69	0
54	MG	2a	3058	1/1	0.72	0.33	67,67,67,67	0
54	MG	2A	3454	1/1	0.72	0.17	55,55,55,55	0
54	MG	1E	307	1/1	0.73	0.13	50,50,50,50	0
54	MG	1a	3267	1/1	0.73	0.20	76,76,76,76	0
54	MG	2A	3659	1/1	0.73	0.16	78,78,78,78	0
54	MG	2a	3038	1/1	0.73	0.23	69,69,69,69	0
54	MG	1a	3187	1/1	0.73	0.15	79,79,79,79	0
54	MG	2j	201	1/1	0.73	0.20	71,71,71,71	0
54	MG	1A	3962	1/1	0.73	0.19	63,63,63,63	0
54	MG	2B	204	1/1	0.74	0.26	77,77,77,77	0
54	MG	1A	3580	1/1	0.74	0.12	68,68,68,68	0
54	MG	1a	3226	1/1	0.74	0.19	78,78,78,78	0
54	MG	2A	3167	1/1	0.74	0.24	82,82,82,82	0
54	MG	1A	3702	1/1	0.74	0.20	47,47,47,47	0
54	MG	2A	3229	1/1	0.74	0.14	65,65,65,65	0
54	MG	1b	301	1/1	0.74	0.22	76,76,76,76	0
54	MG	1A	3239	1/1	0.75	0.18	65,65,65,65	0
54	MG	2a	3010	1/1	0.75	0.25	71,71,71,71	0
54	MG	2A	3272	1/1	0.75	0.26	68,68,68,68	0
54	MG	2A	3522	1/1	0.75	0.17	71,71,71,71	0
54	MG	2A	3626	1/1	0.75	0.16	73,73,73,73	0
57	MPD	2B	220	8/8	0.75	0.26	59,68,69,75	0
54	MG	1a	3237	1/1	0.75	0.16	69,69,69,69	0
54	MG	2B	209	1/1	0.76	0.26	73,73,73,73	0
54	MG	2A	3412	1/1	0.76	0.26	66,66,66,66	0
54	MG	2A	3586	1/1	0.76	0.17	67,67,67,67	0
54	MG	1a	3074	1/1	0.76	0.24	67,67,67,67	0
54	MG	1A	3789	1/1	0.76	0.16	47,47,47,47	0
54	MG	14	101	1/1	0.76	0.12	74,74,74,74	0
54	MG	2A	3298	1/1	0.76	0.24	56,56,56,56	0
54	MG	2A	3176	1/1	0.76	0.14	71,71,71,71	0
54	MG	1a	3067	1/1	0.76	0.22	70,70,70,70	0
54	MG	1A	3849	1/1	0.77	0.14	39,39,39,39	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	2A	3537	1/1	0.77	0.11	58,58,58,58	0
54	MG	1A	3857	1/1	0.77	0.12	58,58,58,58	0
54	MG	1a	3201	1/1	0.77	0.15	77,77,77,77	0
54	MG	1A	3448	1/1	0.77	0.14	42,42,42,42	0
54	MG	1A	3881	1/1	0.77	0.19	68,68,68,68	0
54	MG	1A	3689	1/1	0.77	0.17	62,62,62,62	0
54	MG	2A	3330	1/1	0.77	0.18	62,62,62,62	0
54	MG	2A	3375	1/1	0.77	0.27	77,77,77,77	0
54	MG	1a	3238	1/1	0.77	0.21	72,72,72,72	0
54	MG	1a	3252	1/1	0.77	0.17	60,60,60,60	0
54	MG	2B	214	1/1	0.77	0.14	64,64,64,64	0
54	MG	1T	201	1/1	0.77	0.24	70,70,70,70	0
54	MG	1a	3271	1/1	0.77	0.12	67,67,67,67	0
54	MG	1a	3276	1/1	0.77	0.27	65,65,65,65	0
54	MG	1A	3810	1/1	0.77	0.26	37,37,37,37	0
54	MG	2a	3147	1/1	0.77	0.14	52,52,52,52	0
54	MG	1A	3980	1/1	0.77	0.20	75,75,75,75	0
54	MG	1A	3832	1/1	0.77	0.15	50,50,50,50	0
54	MG	1a	3084	1/1	0.77	0.26	68,68,68,68	0
54	MG	2A	3506	1/1	0.78	0.22	66,66,66,66	0
54	MG	2I	3801	1/1	0.78	0.25	77,77,77,77	0
54	MG	2A	3090	1/1	0.78	0.25	70,70,70,70	0
54	MG	2A	3321	1/1	0.78	0.21	60,60,60,60	0
54	MG	1A	3778	1/1	0.78	0.12	21,21,21,21	0
54	MG	2a	3122	1/1	0.78	0.20	73,73,73,73	0
54	MG	1a	3079	1/1	0.78	0.27	74,74,74,74	0
54	MG	2a	3156	1/1	0.78	0.24	65,65,65,65	0
54	MG	2A	3128	1/1	0.78	0.18	66,66,66,66	0
54	MG	2y	201	1/1	0.78	0.25	60,60,60,60	0
57	MPD	1T	205	8/8	0.78	0.20	51,61,67,77	0
54	MG	1A	3375	1/1	0.78	0.17	62,62,62,62	0
54	MG	2G	203	1/1	0.78	0.19	69,69,69,69	0
54	MG	1E	305	1/1	0.79	0.20	48,48,48,48	0
54	MG	1A	3809	1/1	0.79	0.23	67,67,67,67	0
54	MG	1A	3433	1/1	0.79	0.17	68,68,68,68	0
54	MG	1A	3144	1/1	0.79	0.34	73,73,73,73	0
54	MG	1a	3232	1/1	0.79	0.20	74,74,74,74	0
54	MG	1a	3236	1/1	0.79	0.17	45,45,45,45	0
54	MG	1A	3704	1/1	0.79	0.18	38,38,38,38	0
54	MG	2A	3183	1/1	0.79	0.16	64,64,64,64	0
54	MG	1A	3217	1/1	0.79	0.16	71,71,71,71	0
54	MG	2a	3016	1/1	0.79	0.19	72,72,72,72	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	2A	3225	1/1	0.79	0.20	66,66,66,66	0
54	MG	1a	3241	1/1	0.79	0.19	70,70,70,70	0
54	MG	2a	3061	1/1	0.79	0.27	80,80,80,80	0
54	MG	2a	3098	1/1	0.79	0.26	63,63,63,63	0
54	MG	2a	3102	1/1	0.79	0.18	41,41,41,41	0
54	MG	2a	3103	1/1	0.79	0.15	70,70,70,70	0
54	MG	2A	3235	1/1	0.79	0.28	73,73,73,73	0
54	MG	1a	3246	1/1	0.79	0.13	66,66,66,66	0
54	MG	1A	3587	1/1	0.79	0.12	33,33,33,33	0
54	MG	2A	3605	1/1	0.79	0.23	64,64,64,64	0
54	MG	2A	3292	1/1	0.79	0.33	66,66,66,66	0
54	MG	1A	3873	1/1	0.79	0.10	24,24,24,24	0
54	MG	1a	3141	1/1	0.79	0.13	71,71,71,71	0
54	MG	1A	3690	1/1	0.79	0.21	78,78,78,78	0
54	MG	1a	3036	1/1	0.80	0.20	68,68,68,68	0
54	MG	2A	3429	1/1	0.80	0.15	59,59,59,59	0
54	MG	1A	3545	1/1	0.80	0.24	55,55,55,55	0
54	MG	2A	3166	1/1	0.80	0.20	67,67,67,67	0
54	MG	1A	3323	1/1	0.80	0.27	70,70,70,70	0
54	MG	1A	3274	1/1	0.80	0.17	62,62,62,62	0
54	MG	2B	206	1/1	0.80	0.12	67,67,67,67	0
54	MG	1P	203	1/1	0.80	0.23	38,38,38,38	0
54	MG	2A	3363	1/1	0.80	0.13	78,78,78,78	0
54	MG	2A	3521	1/1	0.80	0.15	67,67,67,67	0
54	MG	2a	3174	1/1	0.80	0.23	73,73,73,73	0
54	MG	2e	201	1/1	0.80	0.36	79,79,79,79	0
54	MG	1A	3530	1/1	0.80	0.13	55,55,55,55	0
54	MG	2k	201	1/1	0.80	0.23	71,71,71,71	0
54	MG	2A	3024	1/1	0.80	0.12	54,54,54,54	0
54	MG	1A	3595	1/1	0.80	0.14	61,61,61,61	0
54	MG	2a	3006	1/1	0.80	0.14	65,65,65,65	0
54	MG	1a	3015	1/1	0.80	0.14	56,56,56,56	0
54	MG	1a	3121	1/1	0.81	0.16	57,57,57,57	0
54	MG	2A	3514	1/1	0.81	0.20	69,69,69,69	0
54	MG	2A	3519	1/1	0.81	0.12	74,74,74,74	0
54	MG	1A	3498	1/1	0.81	0.12	22,22,22,22	0
54	MG	2a	3013	1/1	0.81	0.24	70,70,70,70	0
54	MG	1a	3146	1/1	0.81	0.15	67,67,67,67	0
54	MG	1d	301	1/1	0.81	0.22	69,69,69,69	0
54	MG	2a	3057	1/1	0.81	0.25	73,73,73,73	0
54	MG	2A	3213	1/1	0.81	0.36	58,58,58,58	0
54	MG	1a	3152	1/1	0.81	0.14	70,70,70,70	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	2a	3082	1/1	0.81	0.21	62,62,62,62	0
54	MG	1A	3446	1/1	0.81	0.12	29,29,29,29	0
54	MG	2A	3642	1/1	0.81	0.17	81,81,81,81	0
54	MG	1a	3092	1/1	0.81	0.16	66,66,66,66	0
54	MG	2A	3428	1/1	0.81	0.18	65,65,65,65	0
54	MG	2a	3126	1/1	0.81	0.28	77,77,77,77	0
54	MG	2A	3727	1/1	0.81	0.21	64,64,64,64	0
54	MG	2A	3111	1/1	0.81	0.14	60,60,60,60	0
54	MG	2a	3161	1/1	0.81	0.14	85,85,85,85	0
54	MG	2A	3285	1/1	0.81	0.12	52,52,52,52	0
54	MG	1a	3196	1/1	0.81	0.13	69,69,69,69	0
54	MG	1a	3095	1/1	0.81	0.20	68,68,68,68	0
54	MG	1a	3105	1/1	0.81	0.26	67,67,67,67	0
54	MG	2A	3480	1/1	0.81	0.14	64,64,64,64	0
54	MG	2A	3483	1/1	0.81	0.25	64,64,64,64	0
54	MG	2B	215	1/1	0.81	0.10	72,72,72,72	0
54	MG	2A	3299	1/1	0.81	0.18	73,73,73,73	0
54	MG	1A	3904	1/1	0.82	0.16	51,51,51,51	0
54	MG	1A	3667	1/1	0.82	0.10	41,41,41,41	0
54	MG	1A	3975	1/1	0.82	0.13	55,55,55,55	0
54	MG	2B	207	1/1	0.82	0.24	73,73,73,73	0
54	MG	1A	3034	1/1	0.82	0.16	56,56,56,56	0
54	MG	1a	3157	1/1	0.82	0.26	60,60,60,60	0
54	MG	2A	3439	1/1	0.82	0.10	79,79,79,79	0
54	MG	1A	3193	1/1	0.82	0.13	63,63,63,63	0
54	MG	2A	3448	1/1	0.82	0.18	59,59,59,59	0
54	MG	2I	201	1/1	0.82	0.21	71,71,71,71	0
54	MG	1A	3990	1/1	0.82	0.18	52,52,52,52	0
54	MG	1A	3597	1/1	0.82	0.12	37,37,37,37	0
54	MG	2A	3242	1/1	0.82	0.27	66,66,66,66	0
54	MG	1d	303	1/1	0.82	0.16	64,64,64,64	0
54	MG	2A	3492	1/1	0.82	0.14	48,48,48,48	0
54	MG	1n	101	1/1	0.82	0.13	59,59,59,59	0
54	MG	2A	3289	1/1	0.82	0.34	62,62,62,62	0
54	MG	1y	201	1/1	0.82	0.13	63,63,63,63	0
54	MG	2A	3517	1/1	0.82	0.08	68,68,68,68	0
54	MG	1A	3087	1/1	0.82	0.09	52,52,52,52	0
54	MG	1A	3650	1/1	0.82	0.18	33,33,33,33	0
54	MG	2a	3084	1/1	0.82	0.17	60,60,60,60	0
54	MG	1a	3089	1/1	0.82	0.28	60,60,60,60	0
54	MG	2A	3526	1/1	0.82	0.16	35,35,35,35	0
54	MG	2A	3103	1/1	0.82	0.28	60,60,60,60	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	2A	3544	1/1	0.82	0.18	55,55,55,55	0
54	MG	2A	3556	1/1	0.82	0.13	63,63,63,63	0
54	MG	2A	3563	1/1	0.82	0.25	62,62,62,62	0
54	MG	1A	3652	1/1	0.82	0.27	62,62,62,62	0
54	MG	2A	3337	1/1	0.82	0.15	46,46,46,46	0
54	MG	2A	3611	1/1	0.82	0.14	61,61,61,61	0
54	MG	2A	3620	1/1	0.82	0.21	53,53,53,53	0
54	MG	2A	3120	1/1	0.82	0.18	73,73,73,73	0
54	MG	1A	3516	1/1	0.82	0.10	44,44,44,44	0
54	MG	1A	3655	1/1	0.82	0.14	58,58,58,58	0
54	MG	2A	3400	1/1	0.82	0.16	43,43,43,43	0
54	MG	1a	3106	1/1	0.82	0.21	65,65,65,65	0
54	MG	2A	3402	1/1	0.82	0.17	46,46,46,46	0
54	MG	1A	3633	1/1	0.83	0.17	61,61,61,61	0
54	MG	1A	3909	1/1	0.83	0.10	25,25,25,25	0
54	MG	2G	202	1/1	0.83	0.17	77,77,77,77	0
54	MG	1A	3939	1/1	0.83	0.12	55,55,55,55	0
54	MG	1A	3948	1/1	0.83	0.13	75,75,75,75	0
54	MG	1a	3116	1/1	0.83	0.25	73,73,73,73	0
54	MG	1a	3247	1/1	0.83	0.19	67,67,67,67	0
54	MG	1A	3824	1/1	0.83	0.17	69,69,69,69	0
54	MG	1T	203	1/1	0.83	0.17	61,61,61,61	0
54	MG	2A	3188	1/1	0.83	0.15	60,60,60,60	0
54	MG	1A	3212	1/1	0.83	0.26	62,62,62,62	0
54	MG	2A	3205	1/1	0.83	0.09	55,55,55,55	0
54	MG	2a	3052	1/1	0.83	0.25	65,65,65,65	0
54	MG	2A	3577	1/1	0.83	0.18	39,39,39,39	0
54	MG	1A	3682	1/1	0.83	0.16	54,54,54,54	0
54	MG	1a	3027	1/1	0.83	0.18	56,56,56,56	0
54	MG	1A	3760	1/1	0.83	0.23	66,66,66,66	0
54	MG	2A	3432	1/1	0.83	0.23	66,66,66,66	0
54	MG	1A	3985	1/1	0.83	0.14	46,46,46,46	0
54	MG	2A	3628	1/1	0.83	0.18	44,44,44,44	0
54	MG	2A	3630	1/1	0.83	0.12	79,79,79,79	0
54	MG	1a	3071	1/1	0.83	0.31	61,61,61,61	0
54	MG	2A	3254	1/1	0.83	0.23	61,61,61,61	0
54	MG	2a	3129	1/1	0.83	0.17	68,68,68,68	0
54	MG	2A	3673	1/1	0.83	0.19	69,69,69,69	0
54	MG	1A	3528	1/1	0.83	0.12	60,60,60,60	0
54	MG	2A	3714	1/1	0.83	0.30	73,73,73,73	0
54	MG	1y	202	1/1	0.83	0.13	61,61,61,61	0
54	MG	1A	3781	1/1	0.83	0.14	24,24,24,24	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1a	3207	1/1	0.83	0.16	65,65,65,65	0
54	MG	1A	3079	1/1	0.83	0.17	55,55,55,55	0
54	MG	2A	3295	1/1	0.83	0.20	57,57,57,57	0
54	MG	2A	3499	1/1	0.83	0.14	52,52,52,52	0
57	MPD	1a	3277	8/8	0.83	0.15	49,62,67,72	0
54	MG	2A	3500	1/1	0.83	0.11	62,62,62,62	0
54	MG	1A	3617	1/1	0.83	0.12	65,65,65,65	0
54	MG	2B	201	1/1	0.84	0.23	75,75,75,75	0
54	MG	2B	202	1/1	0.84	0.19	72,72,72,72	0
54	MG	2A	3481	1/1	0.84	0.17	56,56,56,56	0
54	MG	1A	3608	1/1	0.84	0.11	41,41,41,41	0
54	MG	1A	3676	1/1	0.84	0.10	51,51,51,51	0
54	MG	1A	3568	1/1	0.84	0.11	57,57,57,57	0
54	MG	2A	3042	1/1	0.84	0.20	66,66,66,66	0
54	MG	2A	3047	1/1	0.84	0.11	63,63,63,63	0
54	MG	2A	3508	1/1	0.84	0.15	59,59,59,59	0
54	MG	2A	3058	1/1	0.84	0.13	57,57,57,57	0
54	MG	1a	3077	1/1	0.84	0.19	71,71,71,71	0
54	MG	1A	4014	1/1	0.84	0.19	73,73,73,73	0
54	MG	1B	203	1/1	0.84	0.20	62,62,62,62	0
54	MG	2R	202	1/1	0.84	0.15	46,46,46,46	0
54	MG	2T	204	1/1	0.84	0.12	47,47,47,47	0
54	MG	2A	3104	1/1	0.84	0.17	53,53,53,53	0
54	MG	2A	3322	1/1	0.84	0.13	61,61,61,61	0
54	MG	1A	3570	1/1	0.84	0.14	59,59,59,59	0
54	MG	1A	3941	1/1	0.84	0.11	41,41,41,41	0
54	MG	1A	3636	1/1	0.84	0.14	57,57,57,57	0
54	MG	2a	3026	1/1	0.84	0.19	70,70,70,70	0
54	MG	2a	3036	1/1	0.84	0.12	74,74,74,74	0
54	MG	2A	3545	1/1	0.84	0.13	54,54,54,54	0
54	MG	1G	202	1/1	0.84	0.13	57,57,57,57	0
54	MG	2A	3558	1/1	0.84	0.14	65,65,65,65	0
54	MG	1A	3027	1/1	0.84	0.13	66,66,66,66	0
54	MG	1a	3113	1/1	0.84	0.14	74,74,74,74	0
54	MG	2a	3063	1/1	0.84	0.22	70,70,70,70	0
54	MG	1A	3647	1/1	0.84	0.17	57,57,57,57	0
54	MG	1a	3250	1/1	0.84	0.12	61,61,61,61	0
54	MG	1a	3117	1/1	0.84	0.26	66,66,66,66	0
54	MG	2A	3420	1/1	0.84	0.21	71,71,71,71	0
54	MG	1A	3463	1/1	0.84	0.09	43,43,43,43	0
54	MG	2a	3114	1/1	0.84	0.25	69,69,69,69	0
54	MG	2A	3198	1/1	0.84	0.16	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1A	3464	1/1	0.84	0.10	49,49,49,49	0
54	MG	2A	3637	1/1	0.84	0.15	63,63,63,63	0
54	MG	2A	3639	1/1	0.84	0.11	67,67,67,67	0
54	MG	1A	3539	1/1	0.84	0.15	50,50,50,50	0
54	MG	2A	3218	1/1	0.84	0.38	74,74,74,74	0
54	MG	2a	3167	1/1	0.84	0.27	62,62,62,62	0
54	MG	2a	3173	1/1	0.84	0.23	69,69,69,69	0
54	MG	1A	3987	1/1	0.84	0.09	21,21,21,21	0
54	MG	1A	3285	1/1	0.84	0.14	72,72,72,72	0
54	MG	1a	3164	1/1	0.84	0.16	59,59,59,59	0
54	MG	2A	3241	1/1	0.84	0.17	62,62,62,62	0
54	MG	2A	3728	1/1	0.84	0.12	57,57,57,57	0
54	MG	1a	3053	1/1	0.84	0.12	60,60,60,60	0
54	MG	2A	3731	1/1	0.84	0.17	58,58,58,58	0
54	MG	2A	3249	1/1	0.84	0.14	64,64,64,64	0
54	MG	2A	3736	1/1	0.84	0.21	61,61,61,61	0
54	MG	1a	3108	1/1	0.85	0.31	67,67,67,67	0
54	MG	2Q	202	1/1	0.85	0.22	50,50,50,50	0
54	MG	2A	3581	1/1	0.85	0.19	55,55,55,55	0
54	MG	2A	3061	1/1	0.85	0.30	66,66,66,66	0
54	MG	2A	3087	1/1	0.85	0.15	67,67,67,67	0
54	MG	1A	3998	1/1	0.85	0.16	59,59,59,59	0
54	MG	1A	3842	1/1	0.85	0.21	59,59,59,59	0
54	MG	2A	3287	1/1	0.85	0.28	62,62,62,62	0
54	MG	2a	3015	1/1	0.85	0.14	60,60,60,60	0
54	MG	1A	3041	1/1	0.85	0.13	50,50,50,50	0
54	MG	2a	3025	1/1	0.85	0.28	64,64,64,64	0
54	MG	1A	3391	1/1	0.85	0.13	64,64,64,64	0
54	MG	1a	3242	1/1	0.85	0.12	56,56,56,56	0
54	MG	2A	3638	1/1	0.85	0.21	49,49,49,49	0
54	MG	2a	3045	1/1	0.85	0.19	64,64,64,64	0
54	MG	1B	201	1/1	0.85	0.18	58,58,58,58	0
54	MG	2A	3487	1/1	0.85	0.20	67,67,67,67	0
54	MG	1A	3861	1/1	0.85	0.13	48,48,48,48	0
54	MG	1A	3972	1/1	0.85	0.20	59,59,59,59	0
54	MG	2A	3683	1/1	0.85	0.15	58,58,58,58	0
54	MG	2A	3686	1/1	0.85	0.13	51,51,51,51	0
54	MG	2A	3689	1/1	0.85	0.17	69,69,69,69	0
54	MG	2a	3093	1/1	0.85	0.31	60,60,60,60	0
54	MG	2A	3143	1/1	0.85	0.17	55,55,55,55	0
54	MG	2A	3501	1/1	0.85	0.11	51,51,51,51	0
54	MG	2A	3503	1/1	0.85	0.15	71,71,71,71	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	2a	3109	1/1	0.85	0.20	72,72,72,72	0
54	MG	2a	3111	1/1	0.85	0.14	58,58,58,58	0
54	MG	1A	3629	1/1	0.85	0.13	21,21,21,21	0
54	MG	1a	3078	1/1	0.85	0.42	72,72,72,72	0
54	MG	2A	3511	1/1	0.85	0.17	67,67,67,67	0
54	MG	1a	3268	1/1	0.85	0.21	63,63,63,63	0
54	MG	1a	3183	1/1	0.85	0.15	70,70,70,70	0
54	MG	2a	3148	1/1	0.85	0.16	48,48,48,48	0
54	MG	1A	3659	1/1	0.85	0.18	61,61,61,61	0
54	MG	2a	3158	1/1	0.85	0.12	58,58,58,58	0
54	MG	1A	3767	1/1	0.85	0.14	59,59,59,59	0
54	MG	2A	3389	1/1	0.85	0.17	58,58,58,58	0
54	MG	1A	3288	1/1	0.85	0.20	70,70,70,70	0
54	MG	1A	3836	1/1	0.85	0.13	27,27,27,27	0
54	MG	2a	3183	1/1	0.85	0.30	54,54,54,54	0
54	MG	2A	3534	1/1	0.85	0.16	72,72,72,72	0
54	MG	1A	3905	1/1	0.85	0.11	22,22,22,22	0
54	MG	1l	104	1/1	0.85	0.15	57,57,57,57	0
54	MG	1a	3213	1/1	0.85	0.33	77,77,77,77	0
54	MG	2D	308	1/1	0.85	0.22	36,36,36,36	0
54	MG	1a	3218	1/1	0.85	0.26	65,65,65,65	0
54	MG	1a	3220	1/1	0.85	0.11	56,56,56,56	0
54	MG	1A	3837	1/1	0.85	0.11	53,53,53,53	0
54	MG	1a	3205	1/1	0.86	0.12	72,72,72,72	0
54	MG	1A	3713	1/1	0.86	0.12	53,53,53,53	0
54	MG	1A	3718	1/1	0.86	0.21	46,46,46,46	0
54	MG	2A	3373	1/1	0.86	0.18	56,56,56,56	0
54	MG	1A	3735	1/1	0.86	0.13	58,58,58,58	0
54	MG	1A	3600	1/1	0.86	0.20	63,63,63,63	0
54	MG	1A	3875	1/1	0.86	0.15	31,31,31,31	0
54	MG	2A	3561	1/1	0.86	0.22	53,53,53,53	0
54	MG	2a	3005	1/1	0.86	0.33	69,69,69,69	0
54	MG	1A	4003	1/1	0.86	0.34	41,41,41,41	0
54	MG	2A	3575	1/1	0.86	0.13	37,37,37,37	0
54	MG	1a	3233	1/1	0.86	0.20	69,69,69,69	0
54	MG	2A	3580	1/1	0.86	0.12	59,59,59,59	0
54	MG	2A	3139	1/1	0.86	0.20	64,64,64,64	0
54	MG	1A	3756	1/1	0.86	0.21	55,55,55,55	0
54	MG	2A	3416	1/1	0.86	0.10	54,54,54,54	0
54	MG	1a	3091	1/1	0.86	0.10	49,49,49,49	0
54	MG	2A	3614	1/1	0.86	0.16	43,43,43,43	0
54	MG	1A	3888	1/1	0.86	0.12	38,38,38,38	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1A	3331	1/1	0.86	0.12	58,58,58,58	0
54	MG	1A	3611	1/1	0.86	0.13	42,42,42,42	0
54	MG	1A	3503	1/1	0.86	0.10	69,69,69,69	0
54	MG	2A	3634	1/1	0.86	0.17	72,72,72,72	0
54	MG	2a	3062	1/1	0.86	0.17	76,76,76,76	0
54	MG	1B	228	1/1	0.86	0.10	58,58,58,58	0
54	MG	1a	3112	1/1	0.86	0.10	60,60,60,60	0
54	MG	1A	3906	1/1	0.86	0.12	23,23,23,23	0
54	MG	2a	3087	1/1	0.86	0.33	73,73,73,73	0
54	MG	1a	3266	1/1	0.86	0.22	59,59,59,59	0
54	MG	2A	3643	1/1	0.86	0.16	67,67,67,67	0
54	MG	2A	3215	1/1	0.86	0.24	64,64,64,64	0
54	MG	1A	3083	1/1	0.86	0.12	42,42,42,42	0
54	MG	2A	3471	1/1	0.86	0.18	72,72,72,72	0
54	MG	1A	3920	1/1	0.86	0.13	28,28,28,28	0
54	MG	1H	201	1/1	0.86	0.13	58,58,58,58	0
54	MG	2A	3704	1/1	0.86	0.12	49,49,49,49	0
54	MG	1A	3585	1/1	0.86	0.11	54,54,54,54	0
54	MG	2A	3710	1/1	0.86	0.17	68,68,68,68	0
54	MG	2a	3144	1/1	0.86	0.13	53,53,53,53	0
54	MG	1A	3687	1/1	0.86	0.11	47,47,47,47	0
54	MG	2A	3491	1/1	0.86	0.15	59,59,59,59	0
54	MG	1A	3343	1/1	0.86	0.14	55,55,55,55	0
54	MG	2A	3494	1/1	0.86	0.15	64,64,64,64	0
54	MG	1a	3155	1/1	0.86	0.11	54,54,54,54	0
54	MG	1e	201	1/1	0.86	0.20	56,56,56,56	0
54	MG	1g	202	1/1	0.86	0.17	70,70,70,70	0
54	MG	10	105	1/1	0.86	0.13	50,50,50,50	0
54	MG	1A	3958	1/1	0.86	0.15	70,70,70,70	0
54	MG	1a	3174	1/1	0.86	0.09	45,45,45,45	0
54	MG	1A	3363	1/1	0.86	0.11	48,48,48,48	0
54	MG	1A	3593	1/1	0.86	0.11	44,44,44,44	0
54	MG	1A	3699	1/1	0.86	0.15	60,60,60,60	0
54	MG	1A	3700	1/1	0.86	0.11	47,47,47,47	0
54	MG	1A	3302	1/1	0.86	0.10	43,43,43,43	0
54	MG	2A	3085	1/1	0.86	0.55	52,52,52,52	0
54	MG	1A	3149	1/1	0.86	0.16	63,63,63,63	0
54	MG	1a	3197	1/1	0.87	0.17	52,52,52,52	0
54	MG	1A	3474	1/1	0.87	0.10	37,37,37,37	0
54	MG	1A	3573	1/1	0.87	0.10	62,62,62,62	0
54	MG	2D	309	1/1	0.87	0.11	35,35,35,35	0
54	MG	2A	3069	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
54	MG	2A	3080	1/1	0.87	0.14	60,60,60,60	0
54	MG	1A	3306	1/1	0.87	0.17	48,48,48,48	0
54	MG	2A	3323	1/1	0.87	0.16	48,48,48,48	0
54	MG	1A	3307	1/1	0.87	0.18	42,42,42,42	0
54	MG	2A	3334	1/1	0.87	0.23	67,67,67,67	0
54	MG	1A	3506	1/1	0.87	0.14	29,29,29,29	0
54	MG	1A	3642	1/1	0.87	0.10	34,34,34,34	0
54	MG	2A	3097	1/1	0.87	0.12	59,59,59,59	0
54	MG	2A	3098	1/1	0.87	0.12	53,53,53,53	0
54	MG	1a	3088	1/1	0.87	0.19	59,59,59,59	0
54	MG	1A	3790	1/1	0.87	0.14	53,53,53,53	0
54	MG	2A	3110	1/1	0.87	0.12	47,47,47,47	0
54	MG	2A	3587	1/1	0.87	0.09	45,45,45,45	0
54	MG	2a	3024	1/1	0.87	0.28	70,70,70,70	0
54	MG	2A	3593	1/1	0.87	0.13	46,46,46,46	0
54	MG	1A	3791	1/1	0.87	0.12	26,26,26,26	0
54	MG	1B	216	1/1	0.87	0.12	44,44,44,44	0
54	MG	1A	3792	1/1	0.87	0.14	56,56,56,56	0
54	MG	2a	3043	1/1	0.87	0.20	77,77,77,77	0
54	MG	2A	3616	1/1	0.87	0.11	32,32,32,32	0
54	MG	2a	3048	1/1	0.87	0.28	65,65,65,65	0
54	MG	1A	3695	1/1	0.87	0.12	36,36,36,36	0
54	MG	2a	3053	1/1	0.87	0.26	65,65,65,65	0
54	MG	2A	3622	1/1	0.87	0.16	42,42,42,42	0
54	MG	1D	316	1/1	0.87	0.12	46,46,46,46	0
54	MG	2A	3627	1/1	0.87	0.14	33,33,33,33	0
54	MG	1A	3928	1/1	0.87	0.15	61,61,61,61	0
54	MG	2A	3147	1/1	0.87	0.13	61,61,61,61	0
54	MG	2A	3633	1/1	0.87	0.14	55,55,55,55	0
54	MG	2A	3165	1/1	0.87	0.21	63,63,63,63	0
54	MG	1A	3438	1/1	0.87	0.15	42,42,42,42	0
54	MG	2a	3091	1/1	0.87	0.39	73,73,73,73	0
54	MG	1A	3439	1/1	0.87	0.13	33,33,33,33	0
54	MG	2a	3097	1/1	0.87	0.35	61,61,61,61	0
54	MG	1A	3355	1/1	0.87	0.11	40,40,40,40	0
54	MG	1A	3834	1/1	0.87	0.11	46,46,46,46	0
54	MG	1A	3960	1/1	0.87	0.15	60,60,60,60	0
54	MG	1a	3138	1/1	0.87	0.14	59,59,59,59	0
54	MG	2a	3110	1/1	0.87	0.18	74,74,74,74	0
54	MG	1A	3315	1/1	0.87	0.09	36,36,36,36	0
54	MG	2a	3112	1/1	0.87	0.10	65,65,65,65	0
54	MG	2A	3678	1/1	0.87	0.12	61,61,61,61	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	2A	3682	1/1	0.87	0.13	65,65,65,65	0
54	MG	1a	3145	1/1	0.87	0.15	63,63,63,63	0
54	MG	1A	3965	1/1	0.87	0.14	67,67,67,67	0
54	MG	1a	3273	1/1	0.87	0.23	63,63,63,63	0
54	MG	2a	3146	1/1	0.87	0.14	69,69,69,69	0
54	MG	1A	3707	1/1	0.87	0.22	40,40,40,40	0
54	MG	2A	3220	1/1	0.87	0.09	59,59,59,59	0
54	MG	2a	3153	1/1	0.87	0.11	63,63,63,63	0
54	MG	1A	3275	1/1	0.87	0.12	40,40,40,40	0
54	MG	1a	3156	1/1	0.87	0.21	70,70,70,70	0
54	MG	1A	3843	1/1	0.87	0.20	56,56,56,56	0
54	MG	2A	3497	1/1	0.87	0.18	67,67,67,67	0
54	MG	2a	3171	1/1	0.87	0.11	65,65,65,65	0
54	MG	1d	306	1/1	0.87	0.09	81,81,81,81	0
54	MG	1A	3604	1/1	0.87	0.14	62,62,62,62	0
54	MG	2a	3181	1/1	0.87	0.34	55,55,55,55	0
54	MG	1a	3168	1/1	0.87	0.15	67,67,67,67	0
54	MG	1A	3607	1/1	0.87	0.11	51,51,51,51	0
54	MG	2A	3255	1/1	0.87	0.14	57,57,57,57	0
54	MG	2A	3258	1/1	0.87	0.09	65,65,65,65	0
54	MG	1a	3040	1/1	0.87	0.14	60,60,60,60	0
54	MG	1a	3048	1/1	0.87	0.37	70,70,70,70	0
54	MG	1A	3270	1/1	0.87	0.34	59,59,59,59	0
57	MPD	2A	3740	8/8	0.87	0.24	42,45,51,55	0
54	MG	2A	3031	1/1	0.87	0.19	69,69,69,69	0
54	MG	1A	3754	1/1	0.87	0.27	41,41,41,41	0
54	MG	2A	3012	1/1	0.88	0.19	54,54,54,54	0
54	MG	1A	3684	1/1	0.88	0.08	54,54,54,54	0
54	MG	1A	3637	1/1	0.88	0.11	42,42,42,42	0
54	MG	1F	319	1/1	0.88	0.13	54,54,54,54	0
54	MG	1A	3390	1/1	0.88	0.12	39,39,39,39	0
54	MG	1A	3890	1/1	0.88	0.13	51,51,51,51	0
54	MG	1A	3892	1/1	0.88	0.27	33,33,33,33	0
54	MG	1a	3097	1/1	0.88	0.15	57,57,57,57	0
54	MG	2A	3074	1/1	0.88	0.32	69,69,69,69	0
54	MG	1a	3101	1/1	0.88	0.13	51,51,51,51	0
54	MG	1Q	204	1/1	0.88	0.13	43,43,43,43	0
54	MG	1A	3452	1/1	0.88	0.23	68,68,68,68	0
54	MG	2A	3524	1/1	0.88	0.17	58,58,58,58	0
54	MG	1a	3230	1/1	0.88	0.10	62,62,62,62	0
54	MG	2A	3532	1/1	0.88	0.15	63,63,63,63	0
54	MG	2A	3300	1/1	0.88	0.12	35,35,35,35	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	2A	3312	1/1	0.88	0.11	50,50,50,50	0
54	MG	1A	3989	1/1	0.88	0.16	39,39,39,39	0
54	MG	2A	3095	1/1	0.88	0.18	51,51,51,51	0
54	MG	2A	3554	1/1	0.88	0.09	63,63,63,63	0
54	MG	1a	3111	1/1	0.88	0.27	61,61,61,61	0
54	MG	2A	3557	1/1	0.88	0.08	55,55,55,55	0
54	MG	1A	3455	1/1	0.88	0.12	48,48,48,48	0
54	MG	1A	3165	1/1	0.88	0.18	46,46,46,46	0
54	MG	2a	3030	1/1	0.88	0.17	68,68,68,68	0
54	MG	2a	3033	1/1	0.88	0.32	65,65,65,65	0
54	MG	1A	3993	1/1	0.88	0.09	52,52,52,52	0
54	MG	2a	3037	1/1	0.88	0.10	81,81,81,81	0
54	MG	2A	3353	1/1	0.88	0.12	54,54,54,54	0
54	MG	2a	3041	1/1	0.88	0.22	55,55,55,55	0
54	MG	2A	3359	1/1	0.88	0.14	37,37,37,37	0
54	MG	1a	3239	1/1	0.88	0.15	68,68,68,68	0
54	MG	2A	3364	1/1	0.88	0.08	30,30,30,30	0
54	MG	1A	3392	1/1	0.88	0.13	57,57,57,57	0
54	MG	2A	3112	1/1	0.88	0.17	69,69,69,69	0
54	MG	1A	3425	1/1	0.88	0.20	49,49,49,49	0
54	MG	2A	3387	1/1	0.88	0.11	30,30,30,30	0
54	MG	2a	3060	1/1	0.88	0.24	65,65,65,65	0
54	MG	2A	3607	1/1	0.88	0.10	46,46,46,46	0
54	MG	2A	3388	1/1	0.88	0.16	54,54,54,54	0
54	MG	1a	3244	1/1	0.88	0.15	55,55,55,55	0
54	MG	2A	3398	1/1	0.88	0.14	50,50,50,50	0
54	MG	1a	3137	1/1	0.88	0.12	58,58,58,58	0
54	MG	2A	3131	1/1	0.88	0.15	60,60,60,60	0
54	MG	1A	3785	1/1	0.88	0.17	33,33,33,33	0
54	MG	2A	3407	1/1	0.88	0.13	43,43,43,43	0
54	MG	2A	3408	1/1	0.88	0.15	72,72,72,72	0
54	MG	1A	3930	1/1	0.88	0.09	56,56,56,56	0
54	MG	2A	3632	1/1	0.88	0.10	44,44,44,44	0
54	MG	1A	3344	1/1	0.88	0.09	24,24,24,24	0
54	MG	2a	3108	1/1	0.88	0.19	61,61,61,61	0
54	MG	1a	3261	1/1	0.88	0.13	64,64,64,64	0
54	MG	1a	3049	1/1	0.88	0.22	60,60,60,60	0
54	MG	1A	3346	1/1	0.88	0.11	41,41,41,41	0
54	MG	1a	3060	1/1	0.88	0.15	62,62,62,62	0
54	MG	1a	3061	1/1	0.88	0.18	68,68,68,68	0
54	MG	2A	3186	1/1	0.88	0.22	69,69,69,69	0
54	MG	2a	3123	1/1	0.88	0.12	66,66,66,66	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	2A	3438	1/1	0.88	0.12	45,45,45,45	0
54	MG	1A	3310	1/1	0.88	0.54	43,43,43,43	0
54	MG	2a	3130	1/1	0.88	0.18	68,68,68,68	0
54	MG	2A	3192	1/1	0.88	0.27	47,47,47,47	0
54	MG	1B	207	1/1	0.88	0.18	57,57,57,57	0
54	MG	2A	3453	1/1	0.88	0.16	67,67,67,67	0
54	MG	1a	3167	1/1	0.88	0.13	60,60,60,60	0
54	MG	1A	3872	1/1	0.88	0.14	49,49,49,49	0
54	MG	2A	3463	1/1	0.88	0.12	49,49,49,49	0
54	MG	2A	3706	1/1	0.88	0.11	48,48,48,48	0
54	MG	2A	3466	1/1	0.88	0.21	61,61,61,61	0
54	MG	2a	3164	1/1	0.88	0.18	59,59,59,59	0
54	MG	2A	3470	1/1	0.88	0.17	75,75,75,75	0
54	MG	1A	3229	1/1	0.88	0.13	49,49,49,49	0
54	MG	2A	3722	1/1	0.88	0.10	46,46,46,46	0
54	MG	2A	3723	1/1	0.88	0.17	59,59,59,59	0
54	MG	2A	3479	1/1	0.88	0.17	57,57,57,57	0
54	MG	1A	3341	1/1	0.88	0.12	63,63,63,63	0
54	MG	2a	3184	1/1	0.88	0.26	57,57,57,57	0
54	MG	1A	3877	1/1	0.88	0.10	47,47,47,47	0
54	MG	1a	3081	1/1	0.88	0.09	62,62,62,62	0
54	MG	2A	3222	1/1	0.88	0.13	59,59,59,59	0
54	MG	2n	101	1/1	0.88	0.26	65,65,65,65	0
54	MG	1l	202	1/1	0.88	0.12	70,70,70,70	0
55	HGR	2A	3738	36/36	0.88	0.15	32,45,55,69	0
54	MG	1a	3191	1/1	0.88	0.29	68,68,68,68	0
54	MG	1a	3192	1/1	0.88	0.13	73,73,73,73	0
54	MG	1a	3194	1/1	0.88	0.26	54,54,54,54	0
54	MG	2B	205	1/1	0.88	0.10	55,55,55,55	0
54	MG	1y	203	1/1	0.88	0.14	60,60,60,60	0
54	MG	2A	3154	1/1	0.89	0.28	58,58,58,58	0
54	MG	2A	3450	1/1	0.89	0.17	38,38,38,38	0
54	MG	2A	3730	1/1	0.89	0.21	47,47,47,47	0
54	MG	1A	3574	1/1	0.89	0.15	46,46,46,46	0
54	MG	1A	3940	1/1	0.89	0.09	55,55,55,55	0
54	MG	1a	3093	1/1	0.89	0.16	60,60,60,60	0
54	MG	1A	3759	1/1	0.89	0.09	35,35,35,35	0
54	MG	2A	3182	1/1	0.89	0.20	63,63,63,63	0
54	MG	2A	3468	1/1	0.89	0.11	51,51,51,51	0
54	MG	1A	3494	1/1	0.89	0.10	36,36,36,36	0
54	MG	2A	3184	1/1	0.89	0.10	50,50,50,50	0
54	MG	2A	3474	1/1	0.89	0.08	55,55,55,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	2A	3476	1/1	0.89	0.09	72,72,72,72	0
54	MG	1A	3851	1/1	0.89	0.15	50,50,50,50	0
54	MG	1A	3445	1/1	0.89	0.16	53,53,53,53	0
54	MG	1A	3771	1/1	0.89	0.12	51,51,51,51	0
54	MG	2A	3482	1/1	0.89	0.12	58,58,58,58	0
54	MG	1A	3867	1/1	0.89	0.08	29,29,29,29	0
54	MG	1N	203	1/1	0.89	0.11	54,54,54,54	0
54	MG	1A	3971	1/1	0.89	0.15	49,49,49,49	0
54	MG	1A	3400	1/1	0.89	0.09	18,18,18,18	0
54	MG	1R	203	1/1	0.89	0.23	39,39,39,39	0
54	MG	1A	3403	1/1	0.89	0.16	34,34,34,34	0
54	MG	1a	3118	1/1	0.89	0.10	51,51,51,51	0
54	MG	2T	202	1/1	0.89	0.15	61,61,61,61	0
54	MG	1A	3782	1/1	0.89	0.24	43,43,43,43	0
54	MG	2A	3223	1/1	0.89	0.11	62,62,62,62	0
54	MG	2a	3004	1/1	0.89	0.17	62,62,62,62	0
54	MG	1a	3124	1/1	0.89	0.24	64,64,64,64	0
54	MG	1a	3132	1/1	0.89	0.13	68,68,68,68	0
54	MG	1A	3515	1/1	0.89	0.13	45,45,45,45	0
54	MG	10	106	1/1	0.89	0.11	42,42,42,42	0
54	MG	1A	3788	1/1	0.89	0.12	33,33,33,33	0
54	MG	1A	3258	1/1	0.89	0.13	71,71,71,71	0
54	MG	1d	305	1/1	0.89	0.09	63,63,63,63	0
54	MG	1a	3001	1/1	0.89	0.14	71,71,71,71	0
54	MG	1a	3005	1/1	0.89	0.09	59,59,59,59	0
54	MG	2A	3262	1/1	0.89	0.17	55,55,55,55	0
54	MG	2A	3270	1/1	0.89	0.37	55,55,55,55	0
54	MG	1a	3006	1/1	0.89	0.12	57,57,57,57	0
54	MG	2A	3528	1/1	0.89	0.15	63,63,63,63	0
54	MG	2A	3278	1/1	0.89	0.11	58,58,58,58	0
54	MG	2a	3039	1/1	0.89	0.19	71,71,71,71	0
54	MG	2A	3284	1/1	0.89	0.14	62,62,62,62	0
54	MG	1i	201	1/1	0.89	0.18	61,61,61,61	0
54	MG	2A	3539	1/1	0.89	0.15	59,59,59,59	0
54	MG	2a	3047	1/1	0.89	0.16	65,65,65,65	0
54	MG	1a	3009	1/1	0.89	0.26	60,60,60,60	0
54	MG	1a	3010	1/1	0.89	0.14	74,74,74,74	0
54	MG	2A	3551	1/1	0.89	0.15	59,59,59,59	0
54	MG	1a	3160	1/1	0.89	0.24	66,66,66,66	0
54	MG	1a	3161	1/1	0.89	0.12	52,52,52,52	0
54	MG	1A	3988	1/1	0.89	0.26	42,42,42,42	0
54	MG	1A	3883	1/1	0.89	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
54	MG	2A	3019	1/1	0.89	0.37	46,46,46,46	0
54	MG	1A	3191	1/1	0.89	0.08	52,52,52,52	0
54	MG	2a	3066	1/1	0.89	0.19	63,63,63,63	0
54	MG	2a	3068	1/1	0.89	0.39	63,63,63,63	0
54	MG	2a	3078	1/1	0.89	0.29	64,64,64,64	0
54	MG	2a	3079	1/1	0.89	0.32	61,61,61,61	0
54	MG	2a	3080	1/1	0.89	0.20	70,70,70,70	0
54	MG	2A	3574	1/1	0.89	0.14	37,37,37,37	0
54	MG	1a	3039	1/1	0.89	0.12	66,66,66,66	0
54	MG	2A	3035	1/1	0.89	0.17	57,57,57,57	0
54	MG	1a	3175	1/1	0.89	0.13	63,63,63,63	0
54	MG	1a	3179	1/1	0.89	0.17	66,66,66,66	0
54	MG	1a	3181	1/1	0.89	0.16	50,50,50,50	0
54	MG	2A	3331	1/1	0.89	0.12	53,53,53,53	0
54	MG	1A	3991	1/1	0.89	0.13	54,54,54,54	0
54	MG	2A	3595	1/1	0.89	0.09	45,45,45,45	0
54	MG	2a	3104	1/1	0.89	0.12	58,58,58,58	0
54	MG	2a	3107	1/1	0.89	0.10	52,52,52,52	0
54	MG	2A	3602	1/1	0.89	0.11	62,62,62,62	0
54	MG	1a	3042	1/1	0.89	0.21	53,53,53,53	0
54	MG	1A	3461	1/1	0.89	0.19	62,62,62,62	0
54	MG	1A	3534	1/1	0.89	0.11	25,25,25,25	0
54	MG	2A	3360	1/1	0.89	0.13	70,70,70,70	0
54	MG	1A	3799	1/1	0.89	0.15	59,59,59,59	0
54	MG	2a	3116	1/1	0.89	0.12	60,60,60,60	0
54	MG	2A	3086	1/1	0.89	0.11	40,40,40,40	0
54	MG	2A	3366	1/1	0.89	0.12	43,43,43,43	0
54	MG	2a	3124	1/1	0.89	0.16	62,62,62,62	0
54	MG	1A	3903	1/1	0.89	0.10	46,46,46,46	0
54	MG	2a	3128	1/1	0.89	0.20	48,48,48,48	0
54	MG	1A	3327	1/1	0.89	0.16	48,48,48,48	0
54	MG	2A	3384	1/1	0.89	0.24	58,58,58,58	0
54	MG	2a	3134	1/1	0.89	0.08	58,58,58,58	0
54	MG	2a	3138	1/1	0.89	0.15	73,73,73,73	0
54	MG	2A	3093	1/1	0.89	0.25	62,62,62,62	0
54	MG	1A	3097	1/1	0.89	0.10	52,52,52,52	0
54	MG	1A	3730	1/1	0.89	0.12	63,63,63,63	0
54	MG	1A	4015	1/1	0.89	0.15	51,51,51,51	0
54	MG	2a	3150	1/1	0.89	0.12	69,69,69,69	0
54	MG	2A	3392	1/1	0.89	0.14	60,60,60,60	0
54	MG	1a	3204	1/1	0.89	0.18	64,64,64,64	0
54	MG	1A	4016	1/1	0.89	0.19	61,61,61,61	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1A	3469	1/1	0.89	0.12	45,45,45,45	0
54	MG	1a	3211	1/1	0.89	0.20	68,68,68,68	0
54	MG	1A	3747	1/1	0.89	0.09	71,71,71,71	0
54	MG	1a	3214	1/1	0.89	0.11	69,69,69,69	0
54	MG	2A	3674	1/1	0.89	0.12	63,63,63,63	0
54	MG	1a	3217	1/1	0.89	0.24	56,56,56,56	0
54	MG	2a	3178	1/1	0.89	0.21	61,61,61,61	0
54	MG	1A	3035	1/1	0.89	0.12	44,44,44,44	0
54	MG	1a	3082	1/1	0.89	0.16	59,59,59,59	0
54	MG	2A	3130	1/1	0.89	0.25	56,56,56,56	0
54	MG	2A	3427	1/1	0.89	0.11	41,41,41,41	0
54	MG	2A	3693	1/1	0.89	0.10	49,49,49,49	0
54	MG	1A	3485	1/1	0.89	0.11	42,42,42,42	0
54	MG	2A	3135	1/1	0.89	0.17	58,58,58,58	0
54	MG	1B	218	1/1	0.89	0.10	52,52,52,52	0
54	MG	2A	3434	1/1	0.89	0.12	49,49,49,49	0
54	MG	2A	3712	1/1	0.89	0.41	51,51,51,51	0
54	MG	1a	3231	1/1	0.89	0.11	71,71,71,71	0
54	MG	2A	3146	1/1	0.89	0.15	67,67,67,67	0
57	MPD	2A	3741	8/8	0.89	0.21	57,59,64,67	0
54	MG	1B	221	1/1	0.89	0.12	37,37,37,37	0
54	MG	2A	3153	1/1	0.89	0.11	49,49,49,49	0
54	MG	2A	3275	1/1	0.90	0.15	53,53,53,53	0
54	MG	1B	229	1/1	0.90	0.09	64,64,64,64	0
54	MG	2D	307	1/1	0.90	0.24	46,46,46,46	0
54	MG	2A	3049	1/1	0.90	0.16	52,52,52,52	0
54	MG	2A	3052	1/1	0.90	0.11	47,47,47,47	0
54	MG	1A	3961	1/1	0.90	0.16	61,61,61,61	0
54	MG	1A	3590	1/1	0.90	0.19	52,52,52,52	0
54	MG	2A	3064	1/1	0.90	0.10	48,48,48,48	0
54	MG	2A	3065	1/1	0.90	0.08	42,42,42,42	0
54	MG	1E	306	1/1	0.90	0.09	22,22,22,22	0
54	MG	2A	3073	1/1	0.90	0.15	47,47,47,47	0
54	MG	1A	3643	1/1	0.90	0.18	49,49,49,49	0
54	MG	1A	3970	1/1	0.90	0.14	53,53,53,53	0
54	MG	2A	3309	1/1	0.90	0.23	61,61,61,61	0
54	MG	2I	3802	1/1	0.90	0.22	56,56,56,56	0
54	MG	1A	3102	1/1	0.90	0.11	55,55,55,55	0
54	MG	2A	3314	1/1	0.90	0.14	58,58,58,58	0
54	MG	2A	3316	1/1	0.90	0.08	28,28,28,28	0
54	MG	2A	3530	1/1	0.90	0.18	51,51,51,51	0
54	MG	2A	3318	1/1	0.90	0.12	32,32,32,32	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1A	3303	1/1	0.90	0.22	57,57,57,57	0
54	MG	1A	3319	1/1	0.90	0.12	51,51,51,51	0
54	MG	2a	3019	1/1	0.90	0.14	72,72,72,72	0
54	MG	1N	204	1/1	0.90	0.16	45,45,45,45	0
54	MG	2A	3543	1/1	0.90	0.16	74,74,74,74	0
54	MG	2A	3326	1/1	0.90	0.19	64,64,64,64	0
54	MG	2a	3027	1/1	0.90	0.11	58,58,58,58	0
54	MG	1A	3979	1/1	0.90	0.11	51,51,51,51	0
54	MG	2a	3032	1/1	0.90	0.26	54,54,54,54	0
54	MG	2A	3547	1/1	0.90	0.07	29,29,29,29	0
54	MG	2A	3550	1/1	0.90	0.14	28,28,28,28	0
54	MG	1a	3219	1/1	0.90	0.24	69,69,69,69	0
54	MG	2A	3552	1/1	0.90	0.09	44,44,44,44	0
54	MG	1P	204	1/1	0.90	0.10	61,61,61,61	0
54	MG	1A	3651	1/1	0.90	0.08	64,64,64,64	0
54	MG	2A	3348	1/1	0.90	0.09	39,39,39,39	0
54	MG	2a	3044	1/1	0.90	0.24	59,59,59,59	0
54	MG	1a	3227	1/1	0.90	0.10	54,54,54,54	0
54	MG	2a	3046	1/1	0.90	0.27	54,54,54,54	0
54	MG	2A	3560	1/1	0.90	0.16	72,72,72,72	0
54	MG	2A	3102	1/1	0.90	0.15	49,49,49,49	0
54	MG	2a	3051	1/1	0.90	0.15	55,55,55,55	0
54	MG	1a	3228	1/1	0.90	0.14	60,60,60,60	0
54	MG	2A	3571	1/1	0.90	0.10	63,63,63,63	0
54	MG	2a	3054	1/1	0.90	0.13	58,58,58,58	0
54	MG	1A	3486	1/1	0.90	0.14	55,55,55,55	0
54	MG	1A	3984	1/1	0.90	0.08	64,64,64,64	0
54	MG	1A	3366	1/1	0.90	0.10	41,41,41,41	0
54	MG	1U	207	1/1	0.90	0.26	40,40,40,40	0
54	MG	1V	207	1/1	0.90	0.13	72,72,72,72	0
54	MG	2A	3380	1/1	0.90	0.10	57,57,57,57	0
54	MG	1a	3115	1/1	0.90	0.27	66,66,66,66	0
54	MG	2a	3067	1/1	0.90	0.11	66,66,66,66	0
54	MG	10	102	1/1	0.90	0.29	41,41,41,41	0
54	MG	2a	3076	1/1	0.90	0.20	61,61,61,61	0
54	MG	1A	3370	1/1	0.90	0.09	33,33,33,33	0
54	MG	2A	3598	1/1	0.90	0.09	53,53,53,53	0
54	MG	1A	3831	1/1	0.90	0.13	49,49,49,49	0
54	MG	2A	3132	1/1	0.90	0.21	63,63,63,63	0
54	MG	2A	3391	1/1	0.90	0.19	61,61,61,61	0
54	MG	11	102	1/1	0.90	0.20	55,55,55,55	0
54	MG	1A	3080	1/1	0.90	0.34	42,42,42,42	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	2a	3092	1/1	0.90	0.31	55,55,55,55	0
54	MG	1a	3127	1/1	0.90	0.11	55,55,55,55	0
54	MG	2a	3096	1/1	0.90	0.45	58,58,58,58	0
54	MG	1A	3387	1/1	0.90	0.09	48,48,48,48	0
54	MG	1A	3835	1/1	0.90	0.10	63,63,63,63	0
54	MG	2a	3101	1/1	0.90	0.11	67,67,67,67	0
54	MG	1A	3675	1/1	0.90	0.24	30,30,30,30	0
54	MG	1A	3507	1/1	0.90	0.10	53,53,53,53	0
54	MG	1a	3264	1/1	0.90	0.08	39,39,39,39	0
54	MG	2a	3106	1/1	0.90	0.10	51,51,51,51	0
54	MG	1A	3995	1/1	0.90	0.11	67,67,67,67	0
54	MG	2A	3418	1/1	0.90	0.13	62,62,62,62	0
54	MG	1A	3912	1/1	0.90	0.17	46,46,46,46	0
54	MG	2A	3172	1/1	0.90	0.17	51,51,51,51	0
54	MG	2A	3636	1/1	0.90	0.12	59,59,59,59	0
54	MG	2A	3426	1/1	0.90	0.16	59,59,59,59	0
54	MG	1A	3914	1/1	0.90	0.11	48,48,48,48	0
54	MG	1a	3016	1/1	0.90	0.11	54,54,54,54	0
54	MG	1a	3272	1/1	0.90	0.23	61,61,61,61	0
54	MG	1A	3678	1/1	0.90	0.09	59,59,59,59	0
54	MG	2A	3658	1/1	0.90	0.08	64,64,64,64	0
54	MG	1a	3034	1/1	0.90	0.19	53,53,53,53	0
54	MG	1A	3926	1/1	0.90	0.19	47,47,47,47	0
54	MG	2A	3189	1/1	0.90	0.11	58,58,58,58	0
54	MG	2A	3190	1/1	0.90	0.22	60,60,60,60	0
54	MG	2a	3131	1/1	0.90	0.27	60,60,60,60	0
54	MG	1A	3435	1/1	0.90	0.08	57,57,57,57	0
54	MG	2a	3136	1/1	0.90	0.14	72,72,72,72	0
54	MG	2A	3444	1/1	0.90	0.17	63,63,63,63	0
54	MG	2a	3139	1/1	0.90	0.17	61,61,61,61	0
54	MG	1A	3581	1/1	0.90	0.12	39,39,39,39	0
54	MG	1A	3935	1/1	0.90	0.10	55,55,55,55	0
54	MG	1A	3632	1/1	0.90	0.10	21,21,21,21	0
54	MG	1A	3582	1/1	0.90	0.13	39,39,39,39	0
54	MG	2A	3455	1/1	0.90	0.15	65,65,65,65	0
54	MG	1f	202	1/1	0.90	0.12	45,45,45,45	0
54	MG	2A	3461	1/1	0.90	0.11	61,61,61,61	0
54	MG	1a	3052	1/1	0.90	0.22	57,57,57,57	0
54	MG	2A	3713	1/1	0.90	0.12	65,65,65,65	0
54	MG	1A	3635	1/1	0.90	0.10	18,18,18,18	0
54	MG	2A	3718	1/1	0.90	0.16	59,59,59,59	0
54	MG	1a	3058	1/1	0.90	0.17	58,58,58,58	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1a	3182	1/1	0.90	0.15	64,64,64,64	0
54	MG	1B	210	1/1	0.90	0.11	52,52,52,52	0
54	MG	2A	3472	1/1	0.90	0.12	38,38,38,38	0
54	MG	2a	3180	1/1	0.90	0.14	50,50,50,50	0
54	MG	1a	3186	1/1	0.90	0.15	62,62,62,62	0
54	MG	1A	3943	1/1	0.90	0.10	41,41,41,41	0
54	MG	1A	3946	1/1	0.90	0.15	51,51,51,51	0
54	MG	2A	3733	1/1	0.90	0.22	64,64,64,64	0
54	MG	2f	201	1/1	0.90	0.12	52,52,52,52	0
54	MG	2A	3016	1/1	0.90	0.24	56,56,56,56	0
54	MG	1a	3190	1/1	0.90	0.16	69,69,69,69	0
54	MG	2A	3253	1/1	0.90	0.22	59,59,59,59	0
54	MG	1A	3059	1/1	0.90	0.08	43,43,43,43	0
54	MG	2B	203	1/1	0.90	0.18	68,68,68,68	0
54	MG	1B	222	1/1	0.90	0.23	68,68,68,68	0
54	MG	2A	3490	1/1	0.90	0.13	57,57,57,57	0
54	MG	2A	3034	1/1	0.90	0.21	71,71,71,71	0
54	MG	1A	3518	1/1	0.90	0.10	65,65,65,65	0
54	MG	1A	3870	1/1	0.90	0.09	37,37,37,37	0
54	MG	2A	3045	1/1	0.90	0.15	54,54,54,54	0
54	MG	1A	3130	1/1	0.91	0.08	43,43,43,43	0
54	MG	2A	3187	1/1	0.91	0.17	54,54,54,54	0
54	MG	1A	3361	1/1	0.91	0.10	48,48,48,48	0
54	MG	1A	3167	1/1	0.91	0.11	54,54,54,54	0
54	MG	2A	3473	1/1	0.91	0.11	52,52,52,52	0
54	MG	2B	210	1/1	0.91	0.28	58,58,58,58	0
54	MG	1a	3248	1/1	0.91	0.12	57,57,57,57	0
54	MG	1A	3524	1/1	0.91	0.08	19,19,19,19	0
54	MG	1D	312	1/1	0.91	0.28	47,47,47,47	0
54	MG	1a	3104	1/1	0.91	0.12	61,61,61,61	0
54	MG	1a	3263	1/1	0.91	0.21	66,66,66,66	0
54	MG	2A	3212	1/1	0.91	0.16	51,51,51,51	0
54	MG	2D	311	1/1	0.91	0.13	68,68,68,68	0
54	MG	2E	303	1/1	0.91	0.12	31,31,31,31	0
54	MG	2F	303	1/1	0.91	0.19	54,54,54,54	0
54	MG	1A	3641	1/1	0.91	0.17	64,64,64,64	0
54	MG	1A	3177	1/1	0.91	0.11	51,51,51,51	0
54	MG	1A	3529	1/1	0.91	0.07	51,51,51,51	0
54	MG	1A	3367	1/1	0.91	0.10	49,49,49,49	0
54	MG	1F	318	1/1	0.91	0.18	39,39,39,39	0
54	MG	1A	3187	1/1	0.91	0.09	60,60,60,60	0
54	MG	1a	3114	1/1	0.91	0.08	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1A	3449	1/1	0.91	0.23	58,58,58,58	0
54	MG	2V	201	1/1	0.91	0.14	65,65,65,65	0
54	MG	1A	3544	1/1	0.91	0.13	29,29,29,29	0
54	MG	1A	3188	1/1	0.91	0.23	31,31,31,31	0
54	MG	23	101	1/1	0.91	0.21	57,57,57,57	0
54	MG	25	103	1/1	0.91	0.12	53,53,53,53	0
54	MG	2a	3003	1/1	0.91	0.11	59,59,59,59	0
54	MG	1A	3563	1/1	0.91	0.07	33,33,33,33	0
54	MG	1A	3798	1/1	0.91	0.14	55,55,55,55	0
54	MG	1A	3565	1/1	0.91	0.19	48,48,48,48	0
54	MG	1A	3454	1/1	0.91	0.18	50,50,50,50	0
54	MG	1a	3128	1/1	0.91	0.14	66,66,66,66	0
54	MG	2A	3256	1/1	0.91	0.31	66,66,66,66	0
54	MG	1A	3376	1/1	0.91	0.09	39,39,39,39	0
54	MG	2a	3018	1/1	0.91	0.28	56,56,56,56	0
54	MG	1R	205	1/1	0.91	0.13	42,42,42,42	0
54	MG	2a	3021	1/1	0.91	0.19	60,60,60,60	0
54	MG	2a	3023	1/1	0.91	0.29	64,64,64,64	0
54	MG	2A	3267	1/1	0.91	0.12	53,53,53,53	0
54	MG	1A	3671	1/1	0.91	0.13	46,46,46,46	0
54	MG	1a	3139	1/1	0.91	0.11	55,55,55,55	0
54	MG	1T	202	1/1	0.91	0.08	51,51,51,51	0
54	MG	2A	3277	1/1	0.91	0.17	56,56,56,56	0
54	MG	2a	3031	1/1	0.91	0.16	66,66,66,66	0
54	MG	1A	3830	1/1	0.91	0.12	53,53,53,53	0
54	MG	1A	3672	1/1	0.91	0.11	23,23,23,23	0
54	MG	1y	204	1/1	0.91	0.15	74,74,74,74	0
54	MG	2A	3003	1/1	0.91	0.17	51,51,51,51	0
54	MG	2A	3538	1/1	0.91	0.13	64,64,64,64	0
54	MG	2A	3288	1/1	0.91	0.31	49,49,49,49	0
54	MG	2A	3542	1/1	0.91	0.18	63,63,63,63	0
54	MG	1A	3572	1/1	0.91	0.10	56,56,56,56	0
54	MG	1A	3381	1/1	0.91	0.21	65,65,65,65	0
54	MG	1A	3136	1/1	0.91	0.10	46,46,46,46	0
54	MG	1A	3577	1/1	0.91	0.09	46,46,46,46	0
54	MG	1a	3158	1/1	0.91	0.09	47,47,47,47	0
54	MG	2A	3032	1/1	0.91	0.30	60,60,60,60	0
54	MG	2A	3033	1/1	0.91	0.16	47,47,47,47	0
54	MG	1A	3388	1/1	0.91	0.14	41,41,41,41	0
54	MG	1A	3840	1/1	0.91	0.09	39,39,39,39	0
54	MG	2A	3036	1/1	0.91	0.25	66,66,66,66	0
54	MG	1l	105	1/1	0.91	0.07	35,35,35,35	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	13	102	1/1	0.91	0.10	60,60,60,60	0
54	MG	2A	3320	1/1	0.91	0.12	59,59,59,59	0
54	MG	1A	3686	1/1	0.91	0.13	58,58,58,58	0
54	MG	19	101	1/1	0.91	0.15	54,54,54,54	0
54	MG	1A	3983	1/1	0.91	0.09	39,39,39,39	0
54	MG	2a	3065	1/1	0.91	0.13	59,59,59,59	0
54	MG	2A	3053	1/1	0.91	0.28	59,59,59,59	0
54	MG	1a	3002	1/1	0.91	0.09	56,56,56,56	0
54	MG	2A	3578	1/1	0.91	0.10	50,50,50,50	0
54	MG	2a	3072	1/1	0.91	0.22	63,63,63,63	0
54	MG	2a	3073	1/1	0.91	0.09	70,70,70,70	0
54	MG	2a	3074	1/1	0.91	0.13	63,63,63,63	0
54	MG	1a	3180	1/1	0.91	0.12	58,58,58,58	0
54	MG	1a	3003	1/1	0.91	0.08	51,51,51,51	0
54	MG	1A	3468	1/1	0.91	0.10	43,43,43,43	0
54	MG	2A	3339	1/1	0.91	0.11	39,39,39,39	0
54	MG	2A	3066	1/1	0.91	0.08	55,55,55,55	0
54	MG	1A	3846	1/1	0.91	0.13	56,56,56,56	0
54	MG	1A	3062	1/1	0.91	0.07	30,30,30,30	0
54	MG	1A	3473	1/1	0.91	0.07	19,19,19,19	0
54	MG	1A	3283	1/1	0.91	0.13	48,48,48,48	0
54	MG	1A	3859	1/1	0.91	0.13	41,41,41,41	0
54	MG	1a	3020	1/1	0.91	0.12	52,52,52,52	0
54	MG	2A	3370	1/1	0.91	0.13	45,45,45,45	0
54	MG	1A	3475	1/1	0.91	0.17	61,61,61,61	0
54	MG	1A	3862	1/1	0.91	0.08	50,50,50,50	0
54	MG	1A	3478	1/1	0.91	0.10	47,47,47,47	0
54	MG	2A	3624	1/1	0.91	0.11	69,69,69,69	0
54	MG	1a	3037	1/1	0.91	0.26	68,68,68,68	0
54	MG	1A	3484	1/1	0.91	0.12	52,52,52,52	0
54	MG	1A	3201	1/1	0.91	0.14	49,49,49,49	0
54	MG	1A	4000	1/1	0.91	0.12	46,46,46,46	0
54	MG	1a	3045	1/1	0.91	0.23	62,62,62,62	0
54	MG	1A	3335	1/1	0.91	0.16	50,50,50,50	0
54	MG	1A	3598	1/1	0.91	0.12	53,53,53,53	0
54	MG	2A	3395	1/1	0.91	0.08	60,60,60,60	0
54	MG	2A	3396	1/1	0.91	0.07	30,30,30,30	0
54	MG	1A	4007	1/1	0.91	0.26	38,38,38,38	0
54	MG	1A	3489	1/1	0.91	0.08	16,16,16,16	0
54	MG	1a	3215	1/1	0.91	0.10	53,53,53,53	0
54	MG	2A	3118	1/1	0.91	0.14	56,56,56,56	0
54	MG	2A	3652	1/1	0.91	0.11	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	2A	3656	1/1	0.91	0.15	54,54,54,54	0
54	MG	2A	3657	1/1	0.91	0.12	47,47,47,47	0
54	MG	2A	3404	1/1	0.91	0.14	36,36,36,36	0
54	MG	2A	3405	1/1	0.91	0.08	48,48,48,48	0
54	MG	2A	3406	1/1	0.91	0.12	51,51,51,51	0
54	MG	1a	3216	1/1	0.91	0.14	70,70,70,70	0
54	MG	1A	4012	1/1	0.91	0.16	43,43,43,43	0
54	MG	1a	3059	1/1	0.91	0.18	66,66,66,66	0
54	MG	2a	3143	1/1	0.91	0.15	50,50,50,50	0
54	MG	2A	3413	1/1	0.91	0.14	51,51,51,51	0
54	MG	2A	3684	1/1	0.91	0.07	42,42,42,42	0
54	MG	2A	3685	1/1	0.91	0.12	73,73,73,73	0
54	MG	2A	3129	1/1	0.91	0.20	54,54,54,54	0
54	MG	1A	3401	1/1	0.91	0.07	16,16,16,16	0
54	MG	1A	3721	1/1	0.91	0.17	37,37,37,37	0
54	MG	2A	3700	1/1	0.91	0.15	45,45,45,45	0
54	MG	2A	3701	1/1	0.91	0.21	61,61,61,61	0
54	MG	1a	3222	1/1	0.91	0.09	67,67,67,67	0
54	MG	1a	3223	1/1	0.91	0.14	59,59,59,59	0
54	MG	2A	3707	1/1	0.91	0.12	51,51,51,51	0
54	MG	2a	3168	1/1	0.91	0.17	70,70,70,70	0
54	MG	2a	3169	1/1	0.91	0.14	54,54,54,54	0
54	MG	1a	3224	1/1	0.91	0.10	64,64,64,64	0
54	MG	1A	3123	1/1	0.91	0.23	53,53,53,53	0
54	MG	1A	3501	1/1	0.91	0.08	21,21,21,21	0
54	MG	1B	202	1/1	0.91	0.10	54,54,54,54	0
54	MG	2A	3150	1/1	0.91	0.17	55,55,55,55	0
54	MG	2A	3152	1/1	0.91	0.15	68,68,68,68	0
54	MG	1A	3738	1/1	0.91	0.09	48,48,48,48	0
54	MG	1B	206	1/1	0.91	0.08	45,45,45,45	0
54	MG	2A	3724	1/1	0.91	0.14	63,63,63,63	0
54	MG	2e	202	1/1	0.91	0.26	67,67,67,67	0
54	MG	1A	3292	1/1	0.91	0.20	42,42,42,42	0
54	MG	1a	3080	1/1	0.91	0.20	64,64,64,64	0
54	MG	1B	208	1/1	0.91	0.23	50,50,50,50	0
54	MG	2l	201	1/1	0.91	0.31	61,61,61,61	0
54	MG	1A	3153	1/1	0.91	0.18	54,54,54,54	0
54	MG	2A	3175	1/1	0.91	0.11	52,52,52,52	0
54	MG	2A	3732	1/1	0.91	0.21	49,49,49,49	0
57	MPD	1A	4020	8/8	0.91	0.17	42,47,52,52	0
54	MG	1B	211	1/1	0.91	0.28	68,68,68,68	0
54	MG	2A	3179	1/1	0.91	0.11	50,50,50,50	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	2A	3180	1/1	0.91	0.10	57,57,57,57	0
54	MG	1A	3162	1/1	0.91	0.22	58,58,58,58	0
54	MG	1A	3514	1/1	0.91	0.11	44,44,44,44	0
54	MG	1A	3757	1/1	0.91	0.13	41,41,41,41	0
54	MG	2B	218	1/1	0.92	0.08	59,59,59,59	0
54	MG	2D	303	1/1	0.92	0.36	50,50,50,50	0
54	MG	2A	3489	1/1	0.92	0.09	72,72,72,72	0
54	MG	1A	3126	1/1	0.92	0.10	45,45,45,45	0
54	MG	1a	3136	1/1	0.92	0.10	56,56,56,56	0
54	MG	1A	3547	1/1	0.92	0.11	51,51,51,51	0
54	MG	1f	201	1/1	0.92	0.26	66,66,66,66	0
54	MG	2A	3495	1/1	0.92	0.14	27,27,27,27	0
54	MG	2A	3496	1/1	0.92	0.11	36,36,36,36	0
54	MG	1A	3720	1/1	0.92	0.17	30,30,30,30	0
54	MG	2A	3236	1/1	0.92	0.18	54,54,54,54	0
54	MG	10	107	1/1	0.92	0.09	55,55,55,55	0
54	MG	1A	3559	1/1	0.92	0.19	47,47,47,47	0
54	MG	1A	3194	1/1	0.92	0.20	55,55,55,55	0
54	MG	1A	3030	1/1	0.92	0.10	30,30,30,30	0
54	MG	2T	203	1/1	0.92	0.10	59,59,59,59	0
54	MG	1n	102	1/1	0.92	0.14	60,60,60,60	0
54	MG	2A	3510	1/1	0.92	0.10	50,50,50,50	0
54	MG	1A	3639	1/1	0.92	0.08	23,23,23,23	0
54	MG	1a	3153	1/1	0.92	0.19	44,44,44,44	0
54	MG	1A	3746	1/1	0.92	0.18	50,50,50,50	0
54	MG	25	102	1/1	0.92	0.15	33,33,33,33	0
54	MG	15	103	1/1	0.92	0.23	32,32,32,32	0
54	MG	2A	3518	1/1	0.92	0.12	56,56,56,56	0
54	MG	2A	3001	1/1	0.92	0.29	58,58,58,58	0
54	MG	15	106	1/1	0.92	0.14	39,39,39,39	0
54	MG	1A	3567	1/1	0.92	0.08	36,36,36,36	0
54	MG	2a	3007	1/1	0.92	0.09	48,48,48,48	0
54	MG	2A	3523	1/1	0.92	0.10	49,49,49,49	0
54	MG	2A	3274	1/1	0.92	0.10	49,49,49,49	0
54	MG	1A	3996	1/1	0.92	0.08	55,55,55,55	0
54	MG	2A	3017	1/1	0.92	0.12	54,54,54,54	0
54	MG	1A	3487	1/1	0.92	0.09	18,18,18,18	0
54	MG	1A	3569	1/1	0.92	0.23	55,55,55,55	0
54	MG	2A	3025	1/1	0.92	0.12	43,43,43,43	0
54	MG	2A	3028	1/1	0.92	0.13	47,47,47,47	0
54	MG	1A	3317	1/1	0.92	0.15	43,43,43,43	0
54	MG	1A	3492	1/1	0.92	0.12	21,21,21,21	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1a	3171	1/1	0.92	0.12	63,63,63,63	0
54	MG	1A	3443	1/1	0.92	0.07	13,13,13,13	0
54	MG	1A	3206	1/1	0.92	0.22	51,51,51,51	0
54	MG	1a	3176	1/1	0.92	0.20	59,59,59,59	0
54	MG	1a	3178	1/1	0.92	0.14	58,58,58,58	0
54	MG	2A	3044	1/1	0.92	0.16	55,55,55,55	0
54	MG	1A	3210	1/1	0.92	0.24	38,38,38,38	0
54	MG	1A	3891	1/1	0.92	0.14	32,32,32,32	0
54	MG	1a	3018	1/1	0.92	0.13	55,55,55,55	0
54	MG	1A	3378	1/1	0.92	0.07	45,45,45,45	0
54	MG	1A	3897	1/1	0.92	0.09	53,53,53,53	0
54	MG	1a	3029	1/1	0.92	0.25	60,60,60,60	0
54	MG	1a	3030	1/1	0.92	0.17	57,57,57,57	0
54	MG	1A	3902	1/1	0.92	0.08	59,59,59,59	0
54	MG	2A	3562	1/1	0.92	0.12	57,57,57,57	0
54	MG	1a	3189	1/1	0.92	0.15	64,64,64,64	0
54	MG	1A	3131	1/1	0.92	0.21	31,31,31,31	0
54	MG	2a	3049	1/1	0.92	0.27	49,49,49,49	0
54	MG	2A	3327	1/1	0.92	0.08	61,61,61,61	0
54	MG	1A	3656	1/1	0.92	0.10	37,37,37,37	0
54	MG	1A	3658	1/1	0.92	0.08	56,56,56,56	0
54	MG	1a	3193	1/1	0.92	0.10	63,63,63,63	0
54	MG	2A	3079	1/1	0.92	0.14	52,52,52,52	0
54	MG	1A	3386	1/1	0.92	0.13	65,65,65,65	0
54	MG	2a	3059	1/1	0.92	0.24	72,72,72,72	0
54	MG	2A	3585	1/1	0.92	0.12	53,53,53,53	0
54	MG	1A	3661	1/1	0.92	0.14	51,51,51,51	0
54	MG	1A	3508	1/1	0.92	0.17	50,50,50,50	0
54	MG	1a	3198	1/1	0.92	0.14	69,69,69,69	0
54	MG	1A	3586	1/1	0.92	0.11	18,18,18,18	0
54	MG	2A	3361	1/1	0.92	0.14	37,37,37,37	0
54	MG	2A	3600	1/1	0.92	0.13	63,63,63,63	0
54	MG	1B	215	1/1	0.92	0.08	43,43,43,43	0
54	MG	1a	3051	1/1	0.92	0.18	56,56,56,56	0
54	MG	1A	3513	1/1	0.92	0.12	54,54,54,54	0
54	MG	1A	3100	1/1	0.92	0.24	30,30,30,30	0
54	MG	2A	3371	1/1	0.92	0.14	68,68,68,68	0
54	MG	1a	3210	1/1	0.92	0.10	55,55,55,55	0
54	MG	1A	3795	1/1	0.92	0.11	48,48,48,48	0
54	MG	1A	3796	1/1	0.92	0.15	53,53,53,53	0
54	MG	1A	3286	1/1	0.92	0.18	67,67,67,67	0
54	MG	2A	3107	1/1	0.92	0.15	64,64,64,64	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	2a	3085	1/1	0.92	0.10	64,64,64,64	0
54	MG	1A	3287	1/1	0.92	0.08	32,32,32,32	0
54	MG	1a	3063	1/1	0.92	0.10	64,64,64,64	0
54	MG	1A	3807	1/1	0.92	0.07	46,46,46,46	0
54	MG	2A	3115	1/1	0.92	0.21	49,49,49,49	0
54	MG	1A	3084	1/1	0.92	0.35	47,47,47,47	0
54	MG	2A	3393	1/1	0.92	0.12	56,56,56,56	0
54	MG	1D	313	1/1	0.92	0.11	59,59,59,59	0
54	MG	2A	3124	1/1	0.92	0.15	53,53,53,53	0
54	MG	2A	3397	1/1	0.92	0.08	34,34,34,34	0
54	MG	1A	3289	1/1	0.92	0.17	58,58,58,58	0
54	MG	2A	3399	1/1	0.92	0.10	59,59,59,59	0
54	MG	1D	317	1/1	0.92	0.18	57,57,57,57	0
54	MG	1E	303	1/1	0.92	0.12	22,22,22,22	0
54	MG	1A	3526	1/1	0.92	0.07	54,54,54,54	0
54	MG	1A	3829	1/1	0.92	0.08	46,46,46,46	0
54	MG	1A	3954	1/1	0.92	0.10	47,47,47,47	0
54	MG	1F	317	1/1	0.92	0.12	59,59,59,59	0
54	MG	2A	3669	1/1	0.92	0.08	20,20,20,20	0
54	MG	2a	3113	1/1	0.92	0.08	53,53,53,53	0
54	MG	1a	3087	1/1	0.92	0.10	52,52,52,52	0
54	MG	2a	3115	1/1	0.92	0.15	70,70,70,70	0
54	MG	2A	3140	1/1	0.92	0.13	44,44,44,44	0
54	MG	2a	3118	1/1	0.92	0.09	72,72,72,72	0
54	MG	2A	3677	1/1	0.92	0.11	60,60,60,60	0
54	MG	2A	3142	1/1	0.92	0.10	40,40,40,40	0
54	MG	2A	3679	1/1	0.92	0.08	53,53,53,53	0
54	MG	1A	3955	1/1	0.92	0.12	42,42,42,42	0
54	MG	1A	3072	1/1	0.92	0.09	45,45,45,45	0
54	MG	1G	201	1/1	0.92	0.11	62,62,62,62	0
54	MG	1a	3234	1/1	0.92	0.14	74,74,74,74	0
54	MG	1A	3240	1/1	0.92	0.28	64,64,64,64	0
54	MG	2A	3425	1/1	0.92	0.07	29,29,29,29	0
54	MG	2A	3692	1/1	0.92	0.14	63,63,63,63	0
54	MG	1G	203	1/1	0.92	0.09	47,47,47,47	0
54	MG	1A	3253	1/1	0.92	0.09	52,52,52,52	0
54	MG	2a	3142	1/1	0.92	0.14	42,42,42,42	0
54	MG	2A	3163	1/1	0.92	0.19	44,44,44,44	0
54	MG	2A	3702	1/1	0.92	0.07	40,40,40,40	0
54	MG	1H	202	1/1	0.92	0.07	44,44,44,44	0
54	MG	1a	3098	1/1	0.92	0.23	54,54,54,54	0
54	MG	1a	3100	1/1	0.92	0.30	60,60,60,60	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1A	3692	1/1	0.92	0.10	36,36,36,36	0
54	MG	2a	3152	1/1	0.92	0.09	62,62,62,62	0
54	MG	1A	3360	1/1	0.92	0.14	48,48,48,48	0
54	MG	2a	3155	1/1	0.92	0.20	59,59,59,59	0
54	MG	1A	3609	1/1	0.92	0.24	41,41,41,41	0
54	MG	2A	3440	1/1	0.92	0.12	50,50,50,50	0
54	MG	2a	3160	1/1	0.92	0.17	50,50,50,50	0
54	MG	1A	3124	1/1	0.92	0.21	51,51,51,51	0
54	MG	1A	3615	1/1	0.92	0.10	26,26,26,26	0
54	MG	1a	3251	1/1	0.92	0.21	75,75,75,75	0
54	MG	1a	3109	1/1	0.92	0.33	60,60,60,60	0
54	MG	1a	3259	1/1	0.92	0.23	61,61,61,61	0
54	MG	1A	3542	1/1	0.92	0.08	40,40,40,40	0
54	MG	1R	204	1/1	0.92	0.15	35,35,35,35	0
54	MG	1A	3624	1/1	0.92	0.20	30,30,30,30	0
54	MG	2a	3175	1/1	0.92	0.10	81,81,81,81	0
54	MG	2A	3460	1/1	0.92	0.12	57,57,57,57	0
54	MG	1R	206	1/1	0.92	0.13	40,40,40,40	0
54	MG	1A	3430	1/1	0.92	0.07	24,24,24,24	0
54	MG	2A	3464	1/1	0.92	0.12	56,56,56,56	0
54	MG	2A	3734	1/1	0.92	0.24	65,65,65,65	0
54	MG	2A	3191	1/1	0.92	0.22	67,67,67,67	0
54	MG	1A	3981	1/1	0.92	0.07	52,52,52,52	0
54	MG	2A	3194	1/1	0.92	0.17	40,40,40,40	0
54	MG	1A	3710	1/1	0.92	0.18	53,53,53,53	0
54	MG	1U	201	1/1	0.92	0.25	36,36,36,36	0
54	MG	2A	3201	1/1	0.92	0.29	62,62,62,62	0
54	MG	1A	3711	1/1	0.92	0.08	47,47,47,47	0
54	MG	2A	3211	1/1	0.92	0.14	57,57,57,57	0
54	MG	1a	3275	1/1	0.92	0.23	46,46,46,46	0
54	MG	1U	209	1/1	0.92	0.17	64,64,64,64	0
54	MG	1a	3125	1/1	0.92	0.21	53,53,53,53	0
54	MG	2B	211	1/1	0.92	0.12	69,69,69,69	0
54	MG	2A	3216	1/1	0.92	0.19	53,53,53,53	0
54	MG	1A	3856	1/1	0.92	0.12	30,30,30,30	0
54	MG	1Z	301	1/1	0.92	0.10	55,55,55,55	0
54	MG	2B	216	1/1	0.92	0.18	58,58,58,58	0
54	MG	1A	3640	1/1	0.93	0.10	24,24,24,24	0
54	MG	1a	3102	1/1	0.93	0.33	51,51,51,51	0
54	MG	1a	3103	1/1	0.93	0.12	59,59,59,59	0
54	MG	1A	3768	1/1	0.93	0.10	39,39,39,39	0
54	MG	1A	3769	1/1	0.93	0.07	31,31,31,31	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1A	3546	1/1	0.93	0.11	48,48,48,48	0
54	MG	1O	201	1/1	0.93	0.11	53,53,53,53	0
54	MG	1A	3379	1/1	0.93	0.08	19,19,19,19	0
54	MG	2A	3467	1/1	0.93	0.07	40,40,40,40	0
54	MG	1A	3552	1/1	0.93	0.08	27,27,27,27	0
54	MG	1A	3556	1/1	0.93	0.14	40,40,40,40	0
54	MG	2A	3197	1/1	0.93	0.25	56,56,56,56	0
54	MG	1A	3010	1/1	0.93	0.11	46,46,46,46	0
54	MG	1A	3786	1/1	0.93	0.08	36,36,36,36	0
54	MG	2A	3202	1/1	0.93	0.11	53,53,53,53	0
54	MG	1A	3562	1/1	0.93	0.18	37,37,37,37	0
54	MG	2A	3477	1/1	0.93	0.16	55,55,55,55	0
54	MG	2A	3206	1/1	0.93	0.30	48,48,48,48	0
54	MG	1A	3383	1/1	0.93	0.07	30,30,30,30	0
54	MG	1A	3021	1/1	0.93	0.16	36,36,36,36	0
54	MG	1A	3566	1/1	0.93	0.09	45,45,45,45	0
54	MG	1a	3120	1/1	0.93	0.17	58,58,58,58	0
54	MG	2G	201	1/1	0.93	0.12	76,76,76,76	0
54	MG	1A	3654	1/1	0.93	0.20	30,30,30,30	0
54	MG	2A	3488	1/1	0.93	0.11	61,61,61,61	0
54	MG	2A	3217	1/1	0.93	0.28	56,56,56,56	0
54	MG	1a	3122	1/1	0.93	0.18	61,61,61,61	0
54	MG	2P	202	1/1	0.93	0.13	56,56,56,56	0
54	MG	1A	3963	1/1	0.93	0.10	45,45,45,45	0
54	MG	2A	3221	1/1	0.93	0.09	44,44,44,44	0
54	MG	2A	3493	1/1	0.93	0.12	58,58,58,58	0
54	MG	1U	202	1/1	0.93	0.09	35,35,35,35	0
54	MG	1A	3328	1/1	0.93	0.14	53,53,53,53	0
54	MG	1A	3968	1/1	0.93	0.14	41,41,41,41	0
54	MG	1h	201	1/1	0.93	0.16	44,44,44,44	0
54	MG	1h	202	1/1	0.93	0.12	57,57,57,57	0
54	MG	1a	3129	1/1	0.93	0.08	42,42,42,42	0
54	MG	25	101	1/1	0.93	0.44	43,43,43,43	0
54	MG	2A	3240	1/1	0.93	0.22	59,59,59,59	0
54	MG	1k	201	1/1	0.93	0.10	49,49,49,49	0
54	MG	2a	3001	1/1	0.93	0.09	41,41,41,41	0
54	MG	2A	3505	1/1	0.93	0.07	57,57,57,57	0
54	MG	1V	205	1/1	0.93	0.14	52,52,52,52	0
54	MG	1A	3169	1/1	0.93	0.13	40,40,40,40	0
54	MG	2A	3252	1/1	0.93	0.12	49,49,49,49	0
54	MG	1A	3797	1/1	0.93	0.15	58,58,58,58	0
54	MG	2A	3512	1/1	0.93	0.09	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	2a	3012	1/1	0.93	0.12	51,51,51,51	0
54	MG	1A	3333	1/1	0.93	0.14	44,44,44,44	0
54	MG	1A	3176	1/1	0.93	0.19	33,33,33,33	0
54	MG	2A	3516	1/1	0.93	0.09	57,57,57,57	0
54	MG	1A	3480	1/1	0.93	0.07	49,49,49,49	0
54	MG	1A	3663	1/1	0.93	0.10	41,41,41,41	0
54	MG	1A	3223	1/1	0.93	0.29	39,39,39,39	0
54	MG	1A	3819	1/1	0.93	0.08	27,27,27,27	0
54	MG	2A	3269	1/1	0.93	0.17	58,58,58,58	0
54	MG	2A	3005	1/1	0.93	0.10	55,55,55,55	0
54	MG	1A	3397	1/1	0.93	0.21	52,52,52,52	0
54	MG	1A	3826	1/1	0.93	0.12	31,31,31,31	0
54	MG	2A	3527	1/1	0.93	0.06	46,46,46,46	0
54	MG	1A	3576	1/1	0.93	0.17	48,48,48,48	0
54	MG	1A	3025	1/1	0.93	0.30	40,40,40,40	0
54	MG	1A	3186	1/1	0.93	0.08	46,46,46,46	0
54	MG	2a	3035	1/1	0.93	0.11	61,61,61,61	0
54	MG	2A	3279	1/1	0.93	0.23	51,51,51,51	0
54	MG	15	108	1/1	0.93	0.14	60,60,60,60	0
54	MG	1A	3004	1/1	0.93	0.11	48,48,48,48	0
54	MG	1a	3163	1/1	0.93	0.12	50,50,50,50	0
54	MG	2a	3040	1/1	0.93	0.25	59,59,59,59	0
54	MG	1A	3404	1/1	0.93	0.10	38,38,38,38	0
54	MG	1a	3165	1/1	0.93	0.17	56,56,56,56	0
54	MG	1A	3410	1/1	0.93	0.07	34,34,34,34	0
54	MG	1A	3685	1/1	0.93	0.13	45,45,45,45	0
54	MG	2A	3293	1/1	0.93	0.10	58,58,58,58	0
54	MG	1a	3169	1/1	0.93	0.13	54,54,54,54	0
54	MG	2A	3296	1/1	0.93	0.14	60,60,60,60	0
54	MG	2A	3297	1/1	0.93	0.09	36,36,36,36	0
54	MG	2A	3553	1/1	0.93	0.07	63,63,63,63	0
54	MG	2A	3038	1/1	0.93	0.17	52,52,52,52	0
54	MG	1A	3495	1/1	0.93	0.08	26,26,26,26	0
54	MG	1A	3417	1/1	0.93	0.07	23,23,23,23	0
54	MG	2a	3056	1/1	0.93	0.17	65,65,65,65	0
54	MG	2A	3303	1/1	0.93	0.08	43,43,43,43	0
54	MG	2A	3304	1/1	0.93	0.11	20,20,20,20	0
54	MG	1A	3688	1/1	0.93	0.09	61,61,61,61	0
54	MG	1A	3345	1/1	0.93	0.10	23,23,23,23	0
54	MG	2A	3048	1/1	0.93	0.09	55,55,55,55	0
54	MG	2A	3565	1/1	0.93	0.17	50,50,50,50	0
54	MG	1A	3999	1/1	0.93	0.11	55,55,55,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	2a	3064	1/1	0.93	0.12	72,72,72,72	0
54	MG	1A	3251	1/1	0.93	0.13	36,36,36,36	0
54	MG	1A	3592	1/1	0.93	0.22	50,50,50,50	0
54	MG	2A	3576	1/1	0.93	0.11	39,39,39,39	0
54	MG	2A	3055	1/1	0.93	0.23	57,57,57,57	0
54	MG	2a	3070	1/1	0.93	0.23	56,56,56,56	0
54	MG	1A	3348	1/1	0.93	0.07	20,20,20,20	0
54	MG	1a	3021	1/1	0.93	0.15	48,48,48,48	0
54	MG	2A	3324	1/1	0.93	0.12	35,35,35,35	0
54	MG	2A	3584	1/1	0.93	0.13	51,51,51,51	0
54	MG	1a	3025	1/1	0.93	0.11	69,69,69,69	0
54	MG	1a	3185	1/1	0.93	0.06	59,59,59,59	0
54	MG	1A	4004	1/1	0.93	0.27	54,54,54,54	0
54	MG	1A	3353	1/1	0.93	0.09	52,52,52,52	0
54	MG	1A	3434	1/1	0.93	0.06	23,23,23,23	0
54	MG	1A	3052	1/1	0.93	0.20	39,39,39,39	0
54	MG	1A	4013	1/1	0.93	0.21	45,45,45,45	0
54	MG	2A	3347	1/1	0.93	0.07	30,30,30,30	0
54	MG	1A	3860	1/1	0.93	0.07	48,48,48,48	0
54	MG	2A	3606	1/1	0.93	0.11	29,29,29,29	0
54	MG	2A	3350	1/1	0.93	0.07	26,26,26,26	0
54	MG	2A	3352	1/1	0.93	0.12	50,50,50,50	0
54	MG	1a	3038	1/1	0.93	0.24	60,60,60,60	0
54	MG	1A	3436	1/1	0.93	0.10	25,25,25,25	0
54	MG	1A	3703	1/1	0.93	0.24	43,43,43,43	0
54	MG	2A	3088	1/1	0.93	0.08	37,37,37,37	0
54	MG	2A	3623	1/1	0.93	0.11	58,58,58,58	0
54	MG	2A	3362	1/1	0.93	0.09	35,35,35,35	0
54	MG	2A	3089	1/1	0.93	0.11	59,59,59,59	0
54	MG	1A	3437	1/1	0.93	0.10	27,27,27,27	0
54	MG	2A	3365	1/1	0.93	0.14	67,67,67,67	0
54	MG	1A	3606	1/1	0.93	0.09	34,34,34,34	0
54	MG	2A	3367	1/1	0.93	0.12	40,40,40,40	0
54	MG	1A	3254	1/1	0.93	0.20	61,61,61,61	0
54	MG	1A	3517	1/1	0.93	0.07	25,25,25,25	0
54	MG	2A	3096	1/1	0.93	0.22	51,51,51,51	0
54	MG	1A	3257	1/1	0.93	0.07	37,37,37,37	0
54	MG	1A	3610	1/1	0.93	0.09	34,34,34,34	0
54	MG	2A	3381	1/1	0.93	0.12	52,52,52,52	0
54	MG	2a	3120	1/1	0.93	0.15	66,66,66,66	0
54	MG	2A	3382	1/1	0.93	0.17	57,57,57,57	0
54	MG	1A	3523	1/1	0.93	0.10	19,19,19,19	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	2A	3645	1/1	0.93	0.10	50,50,50,50	0
54	MG	2A	3648	1/1	0.93	0.08	50,50,50,50	0
54	MG	2a	3127	1/1	0.93	0.16	56,56,56,56	0
54	MG	1a	3206	1/1	0.93	0.26	61,61,61,61	0
54	MG	2A	3386	1/1	0.93	0.17	62,62,62,62	0
54	MG	1a	3054	1/1	0.93	0.12	61,61,61,61	0
54	MG	1a	3209	1/1	0.93	0.10	55,55,55,55	0
54	MG	1a	3057	1/1	0.93	0.20	59,59,59,59	0
54	MG	2A	3668	1/1	0.93	0.06	35,35,35,35	0
54	MG	1A	3106	1/1	0.93	0.14	34,34,34,34	0
54	MG	2A	3672	1/1	0.93	0.07	59,59,59,59	0
54	MG	1A	3723	1/1	0.93	0.11	44,44,44,44	0
54	MG	1A	3884	1/1	0.93	0.07	54,54,54,54	0
54	MG	1A	3886	1/1	0.93	0.10	42,42,42,42	0
54	MG	1A	3729	1/1	0.93	0.12	38,38,38,38	0
54	MG	1a	3064	1/1	0.93	0.21	64,64,64,64	0
54	MG	1a	3066	1/1	0.93	0.17	57,57,57,57	0
54	MG	1A	3364	1/1	0.93	0.10	46,46,46,46	0
54	MG	1a	3068	1/1	0.93	0.11	59,59,59,59	0
54	MG	1a	3221	1/1	0.93	0.12	57,57,57,57	0
54	MG	1a	3069	1/1	0.93	0.27	57,57,57,57	0
54	MG	1A	3732	1/1	0.93	0.10	64,64,64,64	0
54	MG	1A	3121	1/1	0.93	0.12	37,37,37,37	0
54	MG	1A	3625	1/1	0.93	0.16	40,40,40,40	0
54	MG	2A	3697	1/1	0.93	0.10	52,52,52,52	0
54	MG	1A	3739	1/1	0.93	0.12	50,50,50,50	0
54	MG	1A	3901	1/1	0.93	0.11	57,57,57,57	0
54	MG	1A	3740	1/1	0.93	0.11	31,31,31,31	0
54	MG	1A	3627	1/1	0.93	0.13	58,58,58,58	0
54	MG	1A	3314	1/1	0.93	0.07	32,32,32,32	0
54	MG	1A	3268	1/1	0.93	0.24	32,32,32,32	0
54	MG	1A	3371	1/1	0.93	0.09	19,19,19,19	0
54	MG	1A	3755	1/1	0.93	0.14	62,62,62,62	0
54	MG	2A	3711	1/1	0.93	0.14	64,64,64,64	0
54	MG	2a	3179	1/1	0.93	0.25	54,54,54,54	0
54	MG	1F	314	1/1	0.93	0.10	29,29,29,29	0
54	MG	2A	3158	1/1	0.93	0.11	53,53,53,53	0
54	MG	2A	3160	1/1	0.93	0.17	65,65,65,65	0
54	MG	2A	3715	1/1	0.93	0.07	74,74,74,74	0
54	MG	2A	3716	1/1	0.93	0.14	73,73,73,73	0
54	MG	1a	3090	1/1	0.93	0.32	63,63,63,63	0
54	MG	2A	3720	1/1	0.93	0.17	59,59,59,59	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1F	316	1/1	0.93	0.10	45,45,45,45	0
54	MG	2A	3431	1/1	0.93	0.17	61,61,61,61	0
54	MG	1a	3240	1/1	0.93	0.13	71,71,71,71	0
54	MG	1A	3122	1/1	0.93	0.10	30,30,30,30	0
54	MG	2A	3171	1/1	0.93	0.11	56,56,56,56	0
54	MG	1A	3318	1/1	0.93	0.16	61,61,61,61	0
54	MG	2A	3173	1/1	0.93	0.12	50,50,50,50	0
54	MG	1a	3243	1/1	0.93	0.18	57,57,57,57	0
54	MG	1a	3094	1/1	0.93	0.31	68,68,68,68	0
54	MG	1A	3459	1/1	0.93	0.08	32,32,32,32	0
54	MG	1A	3924	1/1	0.93	0.12	60,60,60,60	0
54	MG	1A	3058	1/1	0.93	0.10	21,21,21,21	0
58	ARG	1B	230	12/12	0.93	0.10	27,40,55,59	0
54	MG	1A	3765	1/1	0.93	0.12	41,41,41,41	0
54	MG	1A	3002	1/1	0.94	0.09	39,39,39,39	0
54	MG	1A	3218	1/1	0.94	0.09	54,54,54,54	0
54	MG	1A	3793	1/1	0.94	0.07	28,28,28,28	0
54	MG	1A	3947	1/1	0.94	0.09	56,56,56,56	0
54	MG	2A	3437	1/1	0.94	0.06	42,42,42,42	0
54	MG	1A	3500	1/1	0.94	0.11	23,23,23,23	0
54	MG	1A	3952	1/1	0.94	0.09	26,26,26,26	0
54	MG	2A	3181	1/1	0.94	0.28	65,65,65,65	0
54	MG	1A	3953	1/1	0.94	0.10	50,50,50,50	0
54	MG	1a	3257	1/1	0.94	0.12	64,64,64,64	0
54	MG	2A	3446	1/1	0.94	0.07	38,38,38,38	0
54	MG	1a	3258	1/1	0.94	0.17	49,49,49,49	0
54	MG	1A	3352	1/1	0.94	0.09	28,28,28,28	0
54	MG	2A	3451	1/1	0.94	0.07	56,56,56,56	0
54	MG	1a	3107	1/1	0.94	0.27	58,58,58,58	0
54	MG	1A	3219	1/1	0.94	0.18	33,33,33,33	0
54	MG	1A	3681	1/1	0.94	0.07	35,35,35,35	0
54	MG	2A	3457	1/1	0.94	0.06	53,53,53,53	0
54	MG	2A	3458	1/1	0.94	0.10	56,56,56,56	0
54	MG	1A	3220	1/1	0.94	0.18	37,37,37,37	0
54	MG	1A	3800	1/1	0.94	0.06	41,41,41,41	0
54	MG	1A	3802	1/1	0.94	0.17	48,48,48,48	0
54	MG	2A	3462	1/1	0.94	0.08	49,49,49,49	0
54	MG	1a	3269	1/1	0.94	0.09	61,61,61,61	0
54	MG	2A	3195	1/1	0.94	0.23	62,62,62,62	0
54	MG	1A	3805	1/1	0.94	0.10	56,56,56,56	0
54	MG	1A	3011	1/1	0.94	0.10	38,38,38,38	0
54	MG	1A	3967	1/1	0.94	0.13	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1A	3055	1/1	0.94	0.09	39,39,39,39	0
54	MG	1A	3510	1/1	0.94	0.06	45,45,45,45	0
54	MG	2D	306	1/1	0.94	0.22	47,47,47,47	0
54	MG	2A	3203	1/1	0.94	0.10	47,47,47,47	0
54	MG	1a	3119	1/1	0.94	0.15	51,51,51,51	0
54	MG	1A	3814	1/1	0.94	0.09	39,39,39,39	0
54	MG	2D	310	1/1	0.94	0.14	51,51,51,51	0
54	MG	2A	3475	1/1	0.94	0.14	54,54,54,54	0
54	MG	2E	301	1/1	0.94	0.16	37,37,37,37	0
54	MG	2A	3207	1/1	0.94	0.10	46,46,46,46	0
54	MG	2F	301	1/1	0.94	0.40	47,47,47,47	0
54	MG	2A	3209	1/1	0.94	0.31	65,65,65,65	0
54	MG	2A	3210	1/1	0.94	0.20	57,57,57,57	0
54	MG	1d	302	1/1	0.94	0.14	59,59,59,59	0
54	MG	1W	201	1/1	0.94	0.17	43,43,43,43	0
54	MG	1W	204	1/1	0.94	0.09	54,54,54,54	0
54	MG	1a	3123	1/1	0.94	0.12	55,55,55,55	0
54	MG	2A	3485	1/1	0.94	0.07	52,52,52,52	0
54	MG	1X	101	1/1	0.94	0.07	52,52,52,52	0
54	MG	2Q	204	1/1	0.94	0.31	57,57,57,57	0
54	MG	1A	3817	1/1	0.94	0.10	46,46,46,46	0
54	MG	1a	3126	1/1	0.94	0.10	54,54,54,54	0
54	MG	1A	3512	1/1	0.94	0.09	48,48,48,48	0
54	MG	10	103	1/1	0.94	0.08	45,45,45,45	0
54	MG	1A	3976	1/1	0.94	0.09	52,52,52,52	0
54	MG	2V	203	1/1	0.94	0.09	62,62,62,62	0
54	MG	1A	3014	1/1	0.94	0.17	51,51,51,51	0
54	MG	1a	3135	1/1	0.94	0.13	66,66,66,66	0
54	MG	1l	201	1/1	0.94	0.16	55,55,55,55	0
54	MG	1A	3594	1/1	0.94	0.08	44,44,44,44	0
54	MG	1m	201	1/1	0.94	0.07	66,66,66,66	0
54	MG	2A	3237	1/1	0.94	0.30	61,61,61,61	0
54	MG	28	102	1/1	0.94	0.19	48,48,48,48	0
54	MG	1A	3086	1/1	0.94	0.36	38,38,38,38	0
54	MG	1A	3246	1/1	0.94	0.12	46,46,46,46	0
54	MG	2A	3502	1/1	0.94	0.06	30,30,30,30	0
54	MG	1t	201	1/1	0.94	0.09	58,58,58,58	0
54	MG	1A	3008	1/1	0.94	0.06	33,33,33,33	0
54	MG	1A	3440	1/1	0.94	0.09	19,19,19,19	0
54	MG	2a	3008	1/1	0.94	0.14	61,61,61,61	0
54	MG	2a	3009	1/1	0.94	0.26	59,59,59,59	0
54	MG	1A	3833	1/1	0.94	0.07	46,46,46,46	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	2a	3011	1/1	0.94	0.20	55,55,55,55	0
54	MG	1A	3696	1/1	0.94	0.07	47,47,47,47	0
54	MG	1a	3147	1/1	0.94	0.13	60,60,60,60	0
54	MG	1a	3149	1/1	0.94	0.07	49,49,49,49	0
54	MG	2A	3257	1/1	0.94	0.09	56,56,56,56	0
54	MG	1a	3150	1/1	0.94	0.10	51,51,51,51	0
54	MG	2A	3515	1/1	0.94	0.13	37,37,37,37	0
54	MG	2A	3260	1/1	0.94	0.12	45,45,45,45	0
54	MG	2A	3010	1/1	0.94	0.11	57,57,57,57	0
54	MG	2A	3264	1/1	0.94	0.18	40,40,40,40	0
54	MG	2A	3265	1/1	0.94	0.13	49,49,49,49	0
54	MG	2A	3520	1/1	0.94	0.09	62,62,62,62	0
54	MG	1A	3022	1/1	0.94	0.08	39,39,39,39	0
54	MG	2a	3029	1/1	0.94	0.17	54,54,54,54	0
54	MG	1A	3098	1/1	0.94	0.12	26,26,26,26	0
54	MG	17	101	1/1	0.94	0.08	31,31,31,31	0
54	MG	2A	3271	1/1	0.94	0.08	50,50,50,50	0
54	MG	17	104	1/1	0.94	0.14	31,31,31,31	0
54	MG	2A	3273	1/1	0.94	0.16	58,58,58,58	0
54	MG	18	102	1/1	0.94	0.14	37,37,37,37	0
54	MG	1A	3372	1/1	0.94	0.10	24,24,24,24	0
54	MG	19	102	1/1	0.94	0.10	58,58,58,58	0
54	MG	1A	3065	1/1	0.94	0.10	55,55,55,55	0
54	MG	1A	3066	1/1	0.94	0.09	44,44,44,44	0
54	MG	2A	3280	1/1	0.94	0.20	54,54,54,54	0
54	MG	1A	3450	1/1	0.94	0.14	58,58,58,58	0
54	MG	2A	3541	1/1	0.94	0.16	51,51,51,51	0
54	MG	1a	3004	1/1	0.94	0.15	52,52,52,52	0
54	MG	2A	3286	1/1	0.94	0.09	60,60,60,60	0
54	MG	1a	3166	1/1	0.94	0.08	58,58,58,58	0
54	MG	1A	3259	1/1	0.94	0.11	45,45,45,45	0
54	MG	1A	3848	1/1	0.94	0.05	36,36,36,36	0
54	MG	2a	3050	1/1	0.94	0.17	53,53,53,53	0
54	MG	2A	3549	1/1	0.94	0.09	32,32,32,32	0
54	MG	2A	3039	1/1	0.94	0.17	53,53,53,53	0
54	MG	1A	3613	1/1	0.94	0.08	40,40,40,40	0
54	MG	2A	3043	1/1	0.94	0.16	43,43,43,43	0
54	MG	1a	3170	1/1	0.94	0.10	54,54,54,54	0
54	MG	1A	3850	1/1	0.94	0.12	39,39,39,39	0
54	MG	2A	3555	1/1	0.94	0.08	56,56,56,56	0
54	MG	1A	3531	1/1	0.94	0.06	17,17,17,17	0
54	MG	1A	3714	1/1	0.94	0.09	36,36,36,36	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1A	3532	1/1	0.94	0.16	42,42,42,42	0
54	MG	2A	3051	1/1	0.94	0.06	36,36,36,36	0
54	MG	1a	3177	1/1	0.94	0.14	56,56,56,56	0
54	MG	1A	3719	1/1	0.94	0.09	57,57,57,57	0
54	MG	2A	3054	1/1	0.94	0.20	65,65,65,65	0
54	MG	1A	3533	1/1	0.94	0.12	57,57,57,57	0
54	MG	2A	3570	1/1	0.94	0.15	57,57,57,57	0
54	MG	1a	3023	1/1	0.94	0.07	59,59,59,59	0
54	MG	2a	3069	1/1	0.94	0.23	46,46,46,46	0
54	MG	2A	3572	1/1	0.94	0.14	56,56,56,56	0
54	MG	1A	3263	1/1	0.94	0.07	35,35,35,35	0
54	MG	1a	3026	1/1	0.94	0.22	60,60,60,60	0
54	MG	2A	3319	1/1	0.94	0.08	33,33,33,33	0
54	MG	1A	4011	1/1	0.94	0.10	38,38,38,38	0
54	MG	2a	3077	1/1	0.94	0.37	60,60,60,60	0
54	MG	1a	3184	1/1	0.94	0.11	66,66,66,66	0
54	MG	2A	3067	1/1	0.94	0.10	45,45,45,45	0
54	MG	1a	3028	1/1	0.94	0.10	40,40,40,40	0
54	MG	1A	3538	1/1	0.94	0.29	29,29,29,29	0
54	MG	1A	3380	1/1	0.94	0.08	13,13,13,13	0
54	MG	2A	3075	1/1	0.94	0.28	47,47,47,47	0
54	MG	2A	3329	1/1	0.94	0.10	35,35,35,35	0
54	MG	2A	3588	1/1	0.94	0.07	44,44,44,44	0
54	MG	2A	3589	1/1	0.94	0.09	39,39,39,39	0
54	MG	2A	3591	1/1	0.94	0.12	50,50,50,50	0
54	MG	2a	3095	1/1	0.94	0.38	57,57,57,57	0
54	MG	1A	3325	1/1	0.94	0.15	24,24,24,24	0
54	MG	1A	3382	1/1	0.94	0.07	39,39,39,39	0
54	MG	2A	3332	1/1	0.94	0.20	61,61,61,61	0
54	MG	2a	3099	1/1	0.94	0.32	53,53,53,53	0
54	MG	2a	3100	1/1	0.94	0.11	67,67,67,67	0
54	MG	1A	3462	1/1	0.94	0.12	52,52,52,52	0
54	MG	2A	3335	1/1	0.94	0.10	48,48,48,48	0
54	MG	2A	3604	1/1	0.94	0.06	32,32,32,32	0
54	MG	1A	3326	1/1	0.94	0.16	37,37,37,37	0
54	MG	2a	3105	1/1	0.94	0.11	51,51,51,51	0
54	MG	1A	3199	1/1	0.94	0.07	41,41,41,41	0
54	MG	1A	3549	1/1	0.94	0.12	58,58,58,58	0
54	MG	2A	3609	1/1	0.94	0.06	60,60,60,60	0
54	MG	1A	3200	1/1	0.94	0.28	54,54,54,54	0
54	MG	1A	3553	1/1	0.94	0.08	27,27,27,27	0
54	MG	2A	3091	1/1	0.94	0.13	41,41,41,41	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	2A	3619	1/1	0.94	0.06	23,23,23,23	0
54	MG	1A	3555	1/1	0.94	0.07	27,27,27,27	0
54	MG	2A	3357	1/1	0.94	0.19	61,61,61,61	0
54	MG	1A	3753	1/1	0.94	0.08	21,21,21,21	0
54	MG	1a	3199	1/1	0.94	0.17	61,61,61,61	0
54	MG	2A	3625	1/1	0.94	0.10	52,52,52,52	0
54	MG	1a	3200	1/1	0.94	0.12	54,54,54,54	0
54	MG	1A	3329	1/1	0.94	0.37	46,46,46,46	0
54	MG	1B	212	1/1	0.94	0.06	45,45,45,45	0
54	MG	1A	3645	1/1	0.94	0.20	53,53,53,53	0
54	MG	1A	3472	1/1	0.94	0.09	35,35,35,35	0
54	MG	1a	3056	1/1	0.94	0.24	60,60,60,60	0
54	MG	1A	3330	1/1	0.94	0.17	30,30,30,30	0
54	MG	2A	3108	1/1	0.94	0.10	47,47,47,47	0
54	MG	1B	219	1/1	0.94	0.10	42,42,42,42	0
54	MG	1A	3269	1/1	0.94	0.10	51,51,51,51	0
54	MG	1A	3038	1/1	0.94	0.08	45,45,45,45	0
54	MG	2a	3135	1/1	0.94	0.16	55,55,55,55	0
54	MG	2A	3377	1/1	0.94	0.09	45,45,45,45	0
54	MG	1B	224	1/1	0.94	0.12	56,56,56,56	0
54	MG	2A	3116	1/1	0.94	0.21	52,52,52,52	0
54	MG	2a	3141	1/1	0.94	0.07	39,39,39,39	0
54	MG	2A	3117	1/1	0.94	0.21	58,58,58,58	0
54	MG	1a	3062	1/1	0.94	0.13	58,58,58,58	0
54	MG	2A	3654	1/1	0.94	0.06	49,49,49,49	0
54	MG	2a	3145	1/1	0.94	0.11	63,63,63,63	0
54	MG	2A	3655	1/1	0.94	0.08	54,54,54,54	0
54	MG	2A	3119	1/1	0.94	0.31	54,54,54,54	0
54	MG	1B	225	1/1	0.94	0.07	39,39,39,39	0
54	MG	1A	3764	1/1	0.94	0.13	48,48,48,48	0
54	MG	1B	227	1/1	0.94	0.14	62,62,62,62	0
54	MG	2A	3665	1/1	0.94	0.10	29,29,29,29	0
54	MG	1A	3394	1/1	0.94	0.12	46,46,46,46	0
54	MG	1A	3395	1/1	0.94	0.07	43,43,43,43	0
54	MG	1A	3156	1/1	0.94	0.08	41,41,41,41	0
54	MG	2a	3159	1/1	0.94	0.09	63,63,63,63	0
54	MG	1A	3209	1/1	0.94	0.09	40,40,40,40	0
54	MG	1A	3770	1/1	0.94	0.15	51,51,51,51	0
54	MG	2a	3162	1/1	0.94	0.09	60,60,60,60	0
54	MG	2A	3133	1/1	0.94	0.19	54,54,54,54	0
54	MG	2a	3165	1/1	0.94	0.07	65,65,65,65	0
54	MG	1A	3112	1/1	0.94	0.11	47,47,47,47	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1A	3910	1/1	0.94	0.08	34,34,34,34	0
54	MG	1A	3911	1/1	0.94	0.05	13,13,13,13	0
54	MG	2A	3141	1/1	0.94	0.12	58,58,58,58	0
54	MG	1A	3775	1/1	0.94	0.07	31,31,31,31	0
54	MG	1A	3571	1/1	0.94	0.07	33,33,33,33	0
54	MG	1F	309	1/1	0.94	0.24	27,27,27,27	0
54	MG	2A	3687	1/1	0.94	0.08	35,35,35,35	0
54	MG	1a	3083	1/1	0.94	0.17	59,59,59,59	0
54	MG	2A	3690	1/1	0.94	0.09	35,35,35,35	0
54	MG	2A	3148	1/1	0.94	0.14	42,42,42,42	0
54	MG	1A	3278	1/1	0.94	0.17	47,47,47,47	0
54	MG	2A	3694	1/1	0.94	0.13	58,58,58,58	0
54	MG	1A	3921	1/1	0.94	0.10	40,40,40,40	0
54	MG	1A	3115	1/1	0.94	0.15	33,33,33,33	0
54	MG	1A	3783	1/1	0.94	0.12	38,38,38,38	0
54	MG	2A	3414	1/1	0.94	0.07	30,30,30,30	0
54	MG	2A	3703	1/1	0.94	0.10	54,54,54,54	0
54	MG	1A	3214	1/1	0.94	0.12	42,42,42,42	0
54	MG	2A	3159	1/1	0.94	0.15	59,59,59,59	0
54	MG	2t	201	1/1	0.94	0.14	40,40,40,40	0
54	MG	2A	3419	1/1	0.94	0.08	44,44,44,44	0
54	MG	1A	3664	1/1	0.94	0.12	53,53,53,53	0
54	MG	2A	3421	1/1	0.94	0.06	29,29,29,29	0
54	MG	1A	3665	1/1	0.94	0.29	48,48,48,48	0
54	MG	2A	3424	1/1	0.94	0.08	35,35,35,35	0
54	MG	1A	3936	1/1	0.94	0.12	49,49,49,49	0
54	MG	1G	204	1/1	0.94	0.07	46,46,46,46	0
54	MG	1A	3411	1/1	0.94	0.07	35,35,35,35	0
54	MG	2A	3168	1/1	0.94	0.10	58,58,58,58	0
54	MG	1A	3670	1/1	0.94	0.05	17,17,17,17	0
54	MG	1a	3096	1/1	0.95	0.19	57,57,57,57	0
54	MG	1A	3579	1/1	0.95	0.12	20,20,20,20	0
54	MG	1a	3265	1/1	0.95	0.08	43,43,43,43	0
54	MG	1A	3929	1/1	0.95	0.08	36,36,36,36	0
54	MG	1a	3099	1/1	0.95	0.21	50,50,50,50	0
54	MG	1A	3674	1/1	0.95	0.11	55,55,55,55	0
54	MG	2A	3193	1/1	0.95	0.15	57,57,57,57	0
54	MG	1A	3931	1/1	0.95	0.09	51,51,51,51	0
54	MG	1A	3414	1/1	0.95	0.06	17,17,17,17	0
54	MG	1A	3075	1/1	0.95	0.05	42,42,42,42	0
54	MG	2A	3737	1/1	0.95	0.07	54,54,54,54	0
54	MG	1A	3419	1/1	0.95	0.15	50,50,50,50	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1a	3274	1/1	0.95	0.08	61,61,61,61	0
54	MG	2A	3200	1/1	0.95	0.08	42,42,42,42	0
54	MG	1A	3584	1/1	0.95	0.11	57,57,57,57	0
54	MG	1A	3504	1/1	0.95	0.09	26,26,26,26	0
54	MG	1A	3155	1/1	0.95	0.43	42,42,42,42	0
54	MG	2A	3204	1/1	0.95	0.15	59,59,59,59	0
54	MG	1Q	205	1/1	0.95	0.14	42,42,42,42	0
54	MG	1A	3049	1/1	0.95	0.16	35,35,35,35	0
54	MG	1A	3211	1/1	0.95	0.19	37,37,37,37	0
54	MG	2A	3469	1/1	0.95	0.11	42,42,42,42	0
54	MG	2B	213	1/1	0.95	0.07	64,64,64,64	0
54	MG	2A	3208	1/1	0.95	0.12	52,52,52,52	0
54	MG	1A	3431	1/1	0.95	0.12	21,21,21,21	0
54	MG	1A	3949	1/1	0.95	0.05	26,26,26,26	0
54	MG	1A	3950	1/1	0.95	0.07	26,26,26,26	0
54	MG	1e	202	1/1	0.95	0.10	55,55,55,55	0
54	MG	2D	304	1/1	0.95	0.24	35,35,35,35	0
54	MG	1A	3951	1/1	0.95	0.15	23,23,23,23	0
54	MG	2A	3214	1/1	0.95	0.19	49,49,49,49	0
54	MG	1A	3803	1/1	0.95	0.07	32,32,32,32	0
54	MG	1g	201	1/1	0.95	0.34	59,59,59,59	0
54	MG	1A	3804	1/1	0.95	0.28	41,41,41,41	0
54	MG	1A	3511	1/1	0.95	0.06	38,38,38,38	0
54	MG	1U	204	1/1	0.95	0.23	57,57,57,57	0
54	MG	1A	3113	1/1	0.95	0.17	32,32,32,32	0
54	MG	2E	304	1/1	0.95	0.08	43,43,43,43	0
54	MG	1A	3957	1/1	0.95	0.06	51,51,51,51	0
54	MG	2F	302	1/1	0.95	0.07	36,36,36,36	0
54	MG	2A	3486	1/1	0.95	0.09	28,28,28,28	0
54	MG	1V	204	1/1	0.95	0.09	52,52,52,52	0
54	MG	1A	3163	1/1	0.95	0.13	48,48,48,48	0
54	MG	1A	3050	1/1	0.95	0.28	41,41,41,41	0
54	MG	2A	3234	1/1	0.95	0.24	44,44,44,44	0
54	MG	1A	3166	1/1	0.95	0.06	31,31,31,31	0
54	MG	1A	3296	1/1	0.95	0.08	30,30,30,30	0
54	MG	2P	203	1/1	0.95	0.10	62,62,62,62	0
54	MG	1o	101	1/1	0.95	0.16	49,49,49,49	0
54	MG	2A	3238	1/1	0.95	0.10	44,44,44,44	0
54	MG	1A	3818	1/1	0.95	0.08	59,59,59,59	0
54	MG	2T	201	1/1	0.95	0.22	54,54,54,54	0
54	MG	1A	3297	1/1	0.95	0.07	37,37,37,37	0
54	MG	1A	3966	1/1	0.95	0.19	39,39,39,39	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	2A	3243	1/1	0.95	0.07	52,52,52,52	0
54	MG	2A	3247	1/1	0.95	0.19	58,58,58,58	0
54	MG	2V	202	1/1	0.95	0.21	41,41,41,41	0
54	MG	1A	3820	1/1	0.95	0.13	34,34,34,34	0
54	MG	2W	201	1/1	0.95	0.34	47,47,47,47	0
54	MG	2X	101	1/1	0.95	0.09	50,50,50,50	0
54	MG	20	101	1/1	0.95	0.10	53,53,53,53	0
54	MG	2A	3250	1/1	0.95	0.15	56,56,56,56	0
54	MG	2A	3251	1/1	0.95	0.27	47,47,47,47	0
54	MG	1a	3133	1/1	0.95	0.14	51,51,51,51	0
54	MG	1A	3116	1/1	0.95	0.29	36,36,36,36	0
54	MG	2A	3002	1/1	0.95	0.07	42,42,42,42	0
54	MG	2A	3509	1/1	0.95	0.13	41,41,41,41	0
54	MG	1A	3825	1/1	0.95	0.12	19,19,19,19	0
54	MG	1A	3521	1/1	0.95	0.06	20,20,20,20	0
54	MG	2A	3006	1/1	0.95	0.10	47,47,47,47	0
54	MG	2A	3009	1/1	0.95	0.07	39,39,39,39	0
54	MG	11	101	1/1	0.95	0.20	42,42,42,42	0
54	MG	1A	3828	1/1	0.95	0.06	22,22,22,22	0
54	MG	1a	3140	1/1	0.95	0.17	60,60,60,60	0
54	MG	1A	3701	1/1	0.95	0.20	27,27,27,27	0
54	MG	1a	3143	1/1	0.95	0.12	66,66,66,66	0
54	MG	1A	3060	1/1	0.95	0.08	47,47,47,47	0
54	MG	1A	3304	1/1	0.95	0.07	47,47,47,47	0
54	MG	1A	3444	1/1	0.95	0.08	27,27,27,27	0
54	MG	1A	3051	1/1	0.95	0.17	39,39,39,39	0
54	MG	2a	3014	1/1	0.95	0.18	60,60,60,60	0
54	MG	1A	3709	1/1	0.95	0.21	42,42,42,42	0
54	MG	15	107	1/1	0.95	0.06	42,42,42,42	0
54	MG	1A	3063	1/1	0.95	0.08	41,41,41,41	0
54	MG	1a	3154	1/1	0.95	0.10	47,47,47,47	0
54	MG	1A	3374	1/1	0.95	0.10	46,46,46,46	0
54	MG	2A	3529	1/1	0.95	0.08	30,30,30,30	0
54	MG	1A	3712	1/1	0.95	0.13	38,38,38,38	0
54	MG	2A	3531	1/1	0.95	0.26	42,42,42,42	0
54	MG	17	105	1/1	0.95	0.12	52,52,52,52	0
54	MG	2A	3283	1/1	0.95	0.15	51,51,51,51	0
54	MG	2a	3028	1/1	0.95	0.20	59,59,59,59	0
54	MG	2A	3040	1/1	0.95	0.15	42,42,42,42	0
54	MG	17	106	1/1	0.95	0.09	47,47,47,47	0
54	MG	1A	3986	1/1	0.95	0.06	47,47,47,47	0
54	MG	1A	3839	1/1	0.95	0.05	30,30,30,30	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1A	3236	1/1	0.95	0.17	33,33,33,33	0
54	MG	2A	3046	1/1	0.95	0.10	54,54,54,54	0
54	MG	1A	3616	1/1	0.95	0.26	29,29,29,29	0
54	MG	1A	3311	1/1	0.95	0.28	38,38,38,38	0
54	MG	1A	3845	1/1	0.95	0.10	42,42,42,42	0
54	MG	1A	3618	1/1	0.95	0.11	56,56,56,56	0
54	MG	1A	3619	1/1	0.95	0.19	32,32,32,32	0
54	MG	1A	3994	1/1	0.95	0.11	33,33,33,33	0
54	MG	2a	3042	1/1	0.95	0.14	65,65,65,65	0
54	MG	1a	3007	1/1	0.95	0.06	54,54,54,54	0
54	MG	1a	3008	1/1	0.95	0.16	51,51,51,51	0
54	MG	1A	3182	1/1	0.95	0.24	53,53,53,53	0
54	MG	1A	3184	1/1	0.95	0.17	35,35,35,35	0
54	MG	2A	3063	1/1	0.95	0.19	47,47,47,47	0
54	MG	1a	3013	1/1	0.95	0.06	56,56,56,56	0
54	MG	1a	3014	1/1	0.95	0.07	58,58,58,58	0
54	MG	2A	3559	1/1	0.95	0.17	61,61,61,61	0
54	MG	1A	3997	1/1	0.95	0.12	51,51,51,51	0
54	MG	2A	3315	1/1	0.95	0.05	33,33,33,33	0
54	MG	1A	3724	1/1	0.95	0.06	28,28,28,28	0
54	MG	1A	3852	1/1	0.95	0.08	37,37,37,37	0
54	MG	1A	3853	1/1	0.95	0.06	44,44,44,44	0
54	MG	2A	3568	1/1	0.95	0.10	47,47,47,47	0
54	MG	1A	3855	1/1	0.95	0.11	38,38,38,38	0
54	MG	1A	3535	1/1	0.95	0.08	54,54,54,54	0
54	MG	1a	3024	1/1	0.95	0.09	47,47,47,47	0
54	MG	2A	3573	1/1	0.95	0.12	55,55,55,55	0
54	MG	1A	3316	1/1	0.95	0.06	33,33,33,33	0
54	MG	1A	3019	1/1	0.95	0.29	30,30,30,30	0
54	MG	1A	3460	1/1	0.95	0.11	46,46,46,46	0
54	MG	1A	3736	1/1	0.95	0.08	44,44,44,44	0
54	MG	1A	3543	1/1	0.95	0.08	53,53,53,53	0
54	MG	1A	3863	1/1	0.95	0.10	34,34,34,34	0
54	MG	1a	3031	1/1	0.95	0.08	34,34,34,34	0
54	MG	2A	3582	1/1	0.95	0.06	45,45,45,45	0
54	MG	1a	3033	1/1	0.95	0.26	57,57,57,57	0
54	MG	2a	3071	1/1	0.95	0.08	63,63,63,63	0
54	MG	1A	3089	1/1	0.95	0.10	41,41,41,41	0
54	MG	1a	3035	1/1	0.95	0.14	43,43,43,43	0
54	MG	1A	3090	1/1	0.95	0.20	35,35,35,35	0
54	MG	2a	3075	1/1	0.95	0.08	50,50,50,50	0
54	MG	1A	3384	1/1	0.95	0.05	22,22,22,22	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	2A	3340	1/1	0.95	0.08	37,37,37,37	0
54	MG	2A	3342	1/1	0.95	0.07	38,38,38,38	0
54	MG	1A	3189	1/1	0.95	0.19	41,41,41,41	0
54	MG	2A	3594	1/1	0.95	0.11	42,42,42,42	0
54	MG	2a	3081	1/1	0.95	0.08	59,59,59,59	0
54	MG	1A	3255	1/1	0.95	0.12	44,44,44,44	0
54	MG	2a	3083	1/1	0.95	0.15	53,53,53,53	0
54	MG	2A	3349	1/1	0.95	0.08	42,42,42,42	0
54	MG	1A	3750	1/1	0.95	0.09	45,45,45,45	0
54	MG	2A	3601	1/1	0.95	0.09	50,50,50,50	0
54	MG	2a	3089	1/1	0.95	0.26	47,47,47,47	0
54	MG	2a	3090	1/1	0.95	0.08	57,57,57,57	0
54	MG	1a	3041	1/1	0.95	0.14	48,48,48,48	0
54	MG	1A	3036	1/1	0.95	0.08	38,38,38,38	0
54	MG	2A	3354	1/1	0.95	0.09	31,31,31,31	0
54	MG	1a	3044	1/1	0.95	0.23	54,54,54,54	0
54	MG	1A	3471	1/1	0.95	0.09	46,46,46,46	0
54	MG	1A	3554	1/1	0.95	0.08	36,36,36,36	0
54	MG	1A	3192	1/1	0.95	0.20	51,51,51,51	0
54	MG	2A	3613	1/1	0.95	0.07	36,36,36,36	0
54	MG	1a	3208	1/1	0.95	0.11	56,56,56,56	0
54	MG	2A	3615	1/1	0.95	0.06	49,49,49,49	0
54	MG	2A	3113	1/1	0.95	0.10	63,63,63,63	0
54	MG	2A	3618	1/1	0.95	0.07	42,42,42,42	0
54	MG	1A	3885	1/1	0.95	0.06	26,26,26,26	0
54	MG	1A	3133	1/1	0.95	0.11	43,43,43,43	0
54	MG	1A	3887	1/1	0.95	0.07	44,44,44,44	0
54	MG	1A	3758	1/1	0.95	0.06	43,43,43,43	0
54	MG	2A	3368	1/1	0.95	0.04	30,30,30,30	0
54	MG	2A	3369	1/1	0.95	0.06	32,32,32,32	0
54	MG	1a	3055	1/1	0.95	0.23	42,42,42,42	0
54	MG	1B	217	1/1	0.95	0.13	60,60,60,60	0
54	MG	2A	3372	1/1	0.95	0.13	49,49,49,49	0
54	MG	2A	3121	1/1	0.95	0.10	47,47,47,47	0
54	MG	2A	3631	1/1	0.95	0.11	55,55,55,55	0
54	MG	2A	3122	1/1	0.95	0.11	40,40,40,40	0
54	MG	1A	3262	1/1	0.95	0.22	38,38,38,38	0
54	MG	1A	3069	1/1	0.95	0.31	40,40,40,40	0
54	MG	2a	3119	1/1	0.95	0.11	57,57,57,57	0
54	MG	1A	3195	1/1	0.95	0.14	33,33,33,33	0
54	MG	1A	3564	1/1	0.95	0.08	54,54,54,54	0
54	MG	1A	3893	1/1	0.95	0.08	38,38,38,38	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1A	3894	1/1	0.95	0.08	32,32,32,32	0
54	MG	2a	3125	1/1	0.95	0.16	68,68,68,68	0
54	MG	1A	3895	1/1	0.95	0.07	41,41,41,41	0
54	MG	1A	3396	1/1	0.95	0.11	43,43,43,43	0
54	MG	1a	3065	1/1	0.95	0.32	53,53,53,53	0
54	MG	2A	3646	1/1	0.95	0.08	42,42,42,42	0
54	MG	2A	3136	1/1	0.95	0.18	59,59,59,59	0
54	MG	2A	3390	1/1	0.95	0.13	38,38,38,38	0
54	MG	2a	3133	1/1	0.95	0.13	62,62,62,62	0
54	MG	2A	3653	1/1	0.95	0.07	48,48,48,48	0
54	MG	1A	3197	1/1	0.95	0.17	50,50,50,50	0
54	MG	1A	3071	1/1	0.95	0.15	26,26,26,26	0
54	MG	1D	304	1/1	0.95	0.10	32,32,32,32	0
54	MG	2A	3394	1/1	0.95	0.07	61,61,61,61	0
54	MG	1a	3229	1/1	0.95	0.10	61,61,61,61	0
54	MG	1D	310	1/1	0.95	0.22	32,32,32,32	0
54	MG	2A	3663	1/1	0.95	0.09	48,48,48,48	0
54	MG	1D	311	1/1	0.95	0.08	47,47,47,47	0
54	MG	1a	3072	1/1	0.95	0.17	64,64,64,64	0
54	MG	1a	3073	1/1	0.95	0.29	50,50,50,50	0
54	MG	1A	3147	1/1	0.95	0.07	42,42,42,42	0
54	MG	2A	3151	1/1	0.95	0.08	38,38,38,38	0
54	MG	2a	3149	1/1	0.95	0.12	45,45,45,45	0
54	MG	1a	3075	1/1	0.95	0.08	48,48,48,48	0
54	MG	2A	3675	1/1	0.95	0.10	49,49,49,49	0
54	MG	1A	3402	1/1	0.95	0.06	25,25,25,25	0
54	MG	1A	3660	1/1	0.95	0.07	37,37,37,37	0
54	MG	2A	3157	1/1	0.95	0.28	49,49,49,49	0
54	MG	2a	3157	1/1	0.95	0.10	46,46,46,46	0
54	MG	2A	3680	1/1	0.95	0.10	36,36,36,36	0
54	MG	2A	3681	1/1	0.95	0.12	35,35,35,35	0
54	MG	1A	3339	1/1	0.95	0.11	35,35,35,35	0
54	MG	1A	3779	1/1	0.95	0.08	43,43,43,43	0
54	MG	2A	3409	1/1	0.95	0.25	62,62,62,62	0
54	MG	1A	3490	1/1	0.95	0.08	25,25,25,25	0
54	MG	2A	3162	1/1	0.95	0.17	47,47,47,47	0
54	MG	2a	3166	1/1	0.95	0.12	51,51,51,51	0
54	MG	1A	3057	1/1	0.95	0.12	46,46,46,46	0
54	MG	2A	3688	1/1	0.95	0.08	64,64,64,64	0
54	MG	2A	3415	1/1	0.95	0.09	51,51,51,51	0
54	MG	2A	3164	1/1	0.95	0.16	54,54,54,54	0
54	MG	1A	3409	1/1	0.95	0.07	26,26,26,26	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1F	306	1/1	0.95	0.24	31,31,31,31	0
54	MG	1a	3086	1/1	0.95	0.14	50,50,50,50	0
54	MG	2A	3695	1/1	0.95	0.13	51,51,51,51	0
54	MG	2A	3696	1/1	0.95	0.11	45,45,45,45	0
54	MG	1A	3913	1/1	0.95	0.15	24,24,24,24	0
54	MG	2A	3169	1/1	0.95	0.10	46,46,46,46	0
54	MG	2A	3423	1/1	0.95	0.07	48,48,48,48	0
54	MG	2A	3170	1/1	0.95	0.18	45,45,45,45	0
54	MG	1A	3784	1/1	0.95	0.07	39,39,39,39	0
54	MG	1a	3249	1/1	0.95	0.10	44,44,44,44	0
54	MG	2A	3705	1/1	0.95	0.06	55,55,55,55	0
54	MG	1F	315	1/1	0.95	0.34	37,37,37,37	0
54	MG	1A	3204	1/1	0.95	0.19	31,31,31,31	0
54	MG	1A	3668	1/1	0.95	0.07	22,22,22,22	0
54	MG	2A	3430	1/1	0.95	0.08	53,53,53,53	0
54	MG	2A	3177	1/1	0.95	0.08	46,46,46,46	0
54	MG	1a	3255	1/1	0.95	0.05	47,47,47,47	0
55	HGR	1A	4018	36/36	0.95	0.10	22,26,37,38	0
54	MG	1a	3256	1/1	0.95	0.08	62,62,62,62	0
54	MG	2A	3435	1/1	0.95	0.25	47,47,47,47	0
54	MG	1A	3922	1/1	0.95	0.08	54,54,54,54	0
57	MPD	18	103	8/8	0.95	0.12	24,31,35,44	0
54	MG	1A	3205	1/1	0.95	0.08	45,45,45,45	0
54	MG	1A	3925	1/1	0.95	0.10	38,38,38,38	0
54	MG	1A	3499	1/1	0.95	0.05	58,58,58,58	0
54	MG	1a	3262	1/1	0.95	0.08	58,58,58,58	0
54	MG	2A	3441	1/1	0.95	0.08	33,33,33,33	0
54	MG	2A	3442	1/1	0.95	0.12	50,50,50,50	0
54	MG	2A	3226	1/1	0.96	0.08	61,61,61,61	0
54	MG	2A	3478	1/1	0.96	0.18	55,55,55,55	0
54	MG	1A	3561	1/1	0.96	0.20	51,51,51,51	0
54	MG	2A	3230	1/1	0.96	0.12	47,47,47,47	0
54	MG	2A	3231	1/1	0.96	0.16	35,35,35,35	0
54	MG	2A	3233	1/1	0.96	0.27	40,40,40,40	0
54	MG	1A	3225	1/1	0.96	0.18	37,37,37,37	0
54	MG	2A	3484	1/1	0.96	0.13	50,50,50,50	0
54	MG	2B	217	1/1	0.96	0.07	65,65,65,65	0
54	MG	1A	3673	1/1	0.96	0.05	39,39,39,39	0
54	MG	2B	219	1/1	0.96	0.12	60,60,60,60	0
54	MG	1A	3298	1/1	0.96	0.19	43,43,43,43	0
54	MG	1A	3806	1/1	0.96	0.09	48,48,48,48	0
54	MG	2D	305	1/1	0.96	0.06	36,36,36,36	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1a	3130	1/1	0.96	0.07	31,31,31,31	0
54	MG	1A	3959	1/1	0.96	0.06	38,38,38,38	0
54	MG	1A	3227	1/1	0.96	0.09	31,31,31,31	0
54	MG	1A	3808	1/1	0.96	0.24	45,45,45,45	0
54	MG	1A	3185	1/1	0.96	0.07	51,51,51,51	0
54	MG	2A	3245	1/1	0.96	0.21	39,39,39,39	0
54	MG	2A	3246	1/1	0.96	0.20	58,58,58,58	0
54	MG	1A	3467	1/1	0.96	0.07	53,53,53,53	0
54	MG	2A	3014	1/1	0.96	0.08	48,48,48,48	0
54	MG	2E	305	1/1	0.96	0.09	28,28,28,28	0
54	MG	2E	306	1/1	0.96	0.21	57,57,57,57	0
54	MG	1A	3811	1/1	0.96	0.14	41,41,41,41	0
54	MG	1A	3812	1/1	0.96	0.13	30,30,30,30	0
54	MG	1A	3813	1/1	0.96	0.08	47,47,47,47	0
54	MG	2F	304	1/1	0.96	0.30	43,43,43,43	0
54	MG	1A	3230	1/1	0.96	0.14	30,30,30,30	0
54	MG	1A	3969	1/1	0.96	0.08	28,28,28,28	0
54	MG	13	101	1/1	0.96	0.14	30,30,30,30	0
54	MG	1A	3235	1/1	0.96	0.12	36,36,36,36	0
54	MG	2N	201	1/1	0.96	0.07	62,62,62,62	0
54	MG	2O	201	1/1	0.96	0.10	49,49,49,49	0
54	MG	1A	3683	1/1	0.96	0.17	31,31,31,31	0
54	MG	2P	201	1/1	0.96	0.08	52,52,52,52	0
54	MG	15	101	1/1	0.96	0.10	38,38,38,38	0
54	MG	1A	3046	1/1	0.96	0.24	47,47,47,47	0
54	MG	2P	204	1/1	0.96	0.06	58,58,58,58	0
54	MG	2A	3261	1/1	0.96	0.37	40,40,40,40	0
54	MG	2Q	203	1/1	0.96	0.26	51,51,51,51	0
54	MG	1a	3151	1/1	0.96	0.10	58,58,58,58	0
54	MG	15	104	1/1	0.96	0.19	27,27,27,27	0
54	MG	15	105	1/1	0.96	0.16	26,26,26,26	0
54	MG	1A	3103	1/1	0.96	0.26	29,29,29,29	0
54	MG	1A	3821	1/1	0.96	0.10	31,31,31,31	0
54	MG	1A	3977	1/1	0.96	0.09	46,46,46,46	0
54	MG	1A	3978	1/1	0.96	0.14	44,44,44,44	0
54	MG	17	102	1/1	0.96	0.08	38,38,38,38	0
54	MG	1a	3159	1/1	0.96	0.10	44,44,44,44	0
54	MG	17	103	1/1	0.96	0.12	33,33,33,33	0
54	MG	2W	202	1/1	0.96	0.18	43,43,43,43	0
54	MG	2W	203	1/1	0.96	0.08	50,50,50,50	0
54	MG	1A	3067	1/1	0.96	0.16	37,37,37,37	0
54	MG	1a	3162	1/1	0.96	0.04	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	20	102	1/1	0.96	0.14	50,50,50,50	0
54	MG	1A	3241	1/1	0.96	0.23	50,50,50,50	0
54	MG	1A	3244	1/1	0.96	0.08	53,53,53,53	0
54	MG	18	101	1/1	0.96	0.08	36,36,36,36	0
54	MG	2A	3282	1/1	0.96	0.06	43,43,43,43	0
54	MG	1A	3476	1/1	0.96	0.07	39,39,39,39	0
54	MG	1A	3141	1/1	0.96	0.08	35,35,35,35	0
54	MG	25	104	1/1	0.96	0.07	55,55,55,55	0
54	MG	27	101	1/1	0.96	0.24	46,46,46,46	0
54	MG	28	101	1/1	0.96	0.07	60,60,60,60	0
54	MG	1A	3248	1/1	0.96	0.13	32,32,32,32	0
54	MG	2A	3056	1/1	0.96	0.20	54,54,54,54	0
54	MG	2a	3002	1/1	0.96	0.26	58,58,58,58	0
54	MG	1A	3481	1/1	0.96	0.06	41,41,41,41	0
54	MG	2A	3533	1/1	0.96	0.09	58,58,58,58	0
54	MG	2A	3060	1/1	0.96	0.07	56,56,56,56	0
54	MG	2A	3536	1/1	0.96	0.11	57,57,57,57	0
54	MG	1A	3250	1/1	0.96	0.12	35,35,35,35	0
54	MG	1A	3393	1/1	0.96	0.09	30,30,30,30	0
54	MG	1A	3143	1/1	0.96	0.16	28,28,28,28	0
54	MG	1A	3583	1/1	0.96	0.10	41,41,41,41	0
54	MG	1A	3109	1/1	0.96	0.08	48,48,48,48	0
54	MG	1A	3145	1/1	0.96	0.08	32,32,32,32	0
54	MG	2A	3068	1/1	0.96	0.27	51,51,51,51	0
54	MG	1A	3110	1/1	0.96	0.13	25,25,25,25	0
54	MG	2A	3546	1/1	0.96	0.10	46,46,46,46	0
54	MG	1A	3111	1/1	0.96	0.28	26,26,26,26	0
54	MG	2a	3017	1/1	0.96	0.07	45,45,45,45	0
54	MG	1A	3493	1/1	0.96	0.08	26,26,26,26	0
54	MG	1a	3011	1/1	0.96	0.11	28,28,28,28	0
54	MG	2a	3020	1/1	0.96	0.08	48,48,48,48	0
54	MG	2A	3076	1/1	0.96	0.09	52,52,52,52	0
54	MG	2a	3022	1/1	0.96	0.09	45,45,45,45	0
54	MG	2A	3307	1/1	0.96	0.06	39,39,39,39	0
54	MG	2A	3077	1/1	0.96	0.09	52,52,52,52	0
54	MG	2A	3078	1/1	0.96	0.06	50,50,50,50	0
54	MG	1a	3012	1/1	0.96	0.11	56,56,56,56	0
54	MG	1A	3708	1/1	0.96	0.05	30,30,30,30	0
54	MG	2A	3081	1/1	0.96	0.05	43,43,43,43	0
54	MG	2A	3084	1/1	0.96	0.08	46,46,46,46	0
54	MG	1A	3151	1/1	0.96	0.27	37,37,37,37	0
54	MG	1A	3048	1/1	0.96	0.13	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1A	3497	1/1	0.96	0.07	28,28,28,28	0
54	MG	1a	3017	1/1	0.96	0.05	61,61,61,61	0
54	MG	1A	3260	1/1	0.96	0.11	40,40,40,40	0
54	MG	2A	3564	1/1	0.96	0.06	36,36,36,36	0
54	MG	1A	3070	1/1	0.96	0.26	28,28,28,28	0
54	MG	2A	3567	1/1	0.96	0.11	46,46,46,46	0
54	MG	1A	3405	1/1	0.96	0.07	28,28,28,28	0
54	MG	2A	3569	1/1	0.96	0.08	65,65,65,65	0
54	MG	2A	3092	1/1	0.96	0.27	49,49,49,49	0
54	MG	2A	3328	1/1	0.96	0.13	46,46,46,46	0
54	MG	1A	4002	1/1	0.96	0.06	54,54,54,54	0
54	MG	1A	3716	1/1	0.96	0.10	23,23,23,23	0
54	MG	1A	3406	1/1	0.96	0.08	26,26,26,26	0
54	MG	1A	4006	1/1	0.96	0.06	39,39,39,39	0
54	MG	1A	3599	1/1	0.96	0.10	58,58,58,58	0
54	MG	1A	4008	1/1	0.96	0.10	47,47,47,47	0
54	MG	2A	3336	1/1	0.96	0.06	23,23,23,23	0
54	MG	2A	3101	1/1	0.96	0.15	54,54,54,54	0
54	MG	2A	3338	1/1	0.96	0.12	46,46,46,46	0
54	MG	1A	3408	1/1	0.96	0.09	17,17,17,17	0
54	MG	1A	4010	1/1	0.96	0.11	39,39,39,39	0
54	MG	2A	3341	1/1	0.96	0.09	52,52,52,52	0
54	MG	1A	3053	1/1	0.96	0.26	28,28,28,28	0
54	MG	2A	3344	1/1	0.96	0.09	27,27,27,27	0
54	MG	2A	3105	1/1	0.96	0.08	45,45,45,45	0
54	MG	1a	3032	1/1	0.96	0.14	45,45,45,45	0
54	MG	2A	3590	1/1	0.96	0.07	56,56,56,56	0
54	MG	1a	3202	1/1	0.96	0.07	61,61,61,61	0
54	MG	1A	3858	1/1	0.96	0.06	31,31,31,31	0
54	MG	2A	3351	1/1	0.96	0.12	34,34,34,34	0
54	MG	1A	3505	1/1	0.96	0.08	23,23,23,23	0
54	MG	1A	3202	1/1	0.96	0.19	43,43,43,43	0
54	MG	1A	3727	1/1	0.96	0.06	26,26,26,26	0
54	MG	1A	3728	1/1	0.96	0.07	46,46,46,46	0
54	MG	1A	3266	1/1	0.96	0.20	41,41,41,41	0
54	MG	1A	3864	1/1	0.96	0.09	33,33,33,33	0
54	MG	1A	3865	1/1	0.96	0.06	60,60,60,60	0
54	MG	1A	3412	1/1	0.96	0.12	21,21,21,21	0
54	MG	1A	3868	1/1	0.96	0.10	40,40,40,40	0
54	MG	1a	3043	1/1	0.96	0.15	48,48,48,48	0
54	MG	2A	3610	1/1	0.96	0.15	62,62,62,62	0
54	MG	1A	3731	1/1	0.96	0.10	26,26,26,26	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	2A	3612	1/1	0.96	0.07	45,45,45,45	0
54	MG	2A	3123	1/1	0.96	0.08	34,34,34,34	0
54	MG	1A	3509	1/1	0.96	0.07	19,19,19,19	0
54	MG	1a	3046	1/1	0.96	0.16	37,37,37,37	0
54	MG	1A	3871	1/1	0.96	0.05	33,33,33,33	0
54	MG	1A	3733	1/1	0.96	0.05	26,26,26,26	0
54	MG	1A	3338	1/1	0.96	0.08	30,30,30,30	0
54	MG	1A	3415	1/1	0.96	0.10	17,17,17,17	0
54	MG	2A	3621	1/1	0.96	0.05	58,58,58,58	0
54	MG	1A	3614	1/1	0.96	0.09	57,57,57,57	0
54	MG	1A	3878	1/1	0.96	0.05	40,40,40,40	0
54	MG	2a	3088	1/1	0.96	0.39	56,56,56,56	0
54	MG	2A	3376	1/1	0.96	0.10	43,43,43,43	0
54	MG	1A	3416	1/1	0.96	0.07	19,19,19,19	0
54	MG	1a	3225	1/1	0.96	0.22	64,64,64,64	0
54	MG	2A	3137	1/1	0.96	0.09	51,51,51,51	0
54	MG	1A	3203	1/1	0.96	0.11	45,45,45,45	0
54	MG	2A	3629	1/1	0.96	0.11	47,47,47,47	0
54	MG	2A	3383	1/1	0.96	0.11	51,51,51,51	0
54	MG	1A	3742	1/1	0.96	0.12	24,24,24,24	0
54	MG	1A	3743	1/1	0.96	0.07	42,42,42,42	0
54	MG	1A	3745	1/1	0.96	0.08	44,44,44,44	0
54	MG	1A	3340	1/1	0.96	0.08	37,37,37,37	0
54	MG	2A	3145	1/1	0.96	0.11	48,48,48,48	0
54	MG	1A	3420	1/1	0.96	0.07	42,42,42,42	0
54	MG	1A	3748	1/1	0.96	0.07	57,57,57,57	0
54	MG	1A	3422	1/1	0.96	0.15	59,59,59,59	0
54	MG	2A	3149	1/1	0.96	0.08	39,39,39,39	0
54	MG	1D	301	1/1	0.96	0.18	27,27,27,27	0
54	MG	2A	3644	1/1	0.96	0.08	56,56,56,56	0
54	MG	1D	302	1/1	0.96	0.20	41,41,41,41	0
54	MG	1A	3623	1/1	0.96	0.10	30,30,30,30	0
54	MG	1A	3157	1/1	0.96	0.17	29,29,29,29	0
54	MG	1A	3160	1/1	0.96	0.15	40,40,40,40	0
54	MG	2A	3155	1/1	0.96	0.07	38,38,38,38	0
54	MG	1A	3626	1/1	0.96	0.17	32,32,32,32	0
54	MG	1a	3070	1/1	0.96	0.23	54,54,54,54	0
54	MG	1A	3520	1/1	0.96	0.07	48,48,48,48	0
54	MG	1A	3428	1/1	0.96	0.10	27,27,27,27	0
54	MG	2a	3117	1/1	0.96	0.14	54,54,54,54	0
54	MG	2A	3403	1/1	0.96	0.11	47,47,47,47	0
54	MG	2A	3161	1/1	0.96	0.23	40,40,40,40	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	2A	3662	1/1	0.96	0.12	50,50,50,50	0
54	MG	1A	3272	1/1	0.96	0.11	30,30,30,30	0
54	MG	2A	3664	1/1	0.96	0.08	40,40,40,40	0
54	MG	1a	3245	1/1	0.96	0.14	53,53,53,53	0
54	MG	1A	3054	1/1	0.96	0.33	33,33,33,33	0
54	MG	1A	3525	1/1	0.96	0.04	36,36,36,36	0
54	MG	1a	3076	1/1	0.96	0.13	50,50,50,50	0
54	MG	2A	3411	1/1	0.96	0.08	32,32,32,32	0
54	MG	1A	3763	1/1	0.96	0.10	56,56,56,56	0
54	MG	1A	3432	1/1	0.96	0.12	21,21,21,21	0
54	MG	1E	308	1/1	0.96	0.09	28,28,28,28	0
54	MG	1F	302	1/1	0.96	0.05	30,30,30,30	0
54	MG	1a	3253	1/1	0.96	0.06	50,50,50,50	0
54	MG	2A	3417	1/1	0.96	0.09	28,28,28,28	0
54	MG	1a	3254	1/1	0.96	0.08	53,53,53,53	0
54	MG	2a	3137	1/1	0.96	0.07	61,61,61,61	0
54	MG	1F	303	1/1	0.96	0.28	31,31,31,31	0
54	MG	1A	3527	1/1	0.96	0.07	14,14,14,14	0
54	MG	1A	3074	1/1	0.96	0.07	30,30,30,30	0
54	MG	1F	313	1/1	0.96	0.41	47,47,47,47	0
54	MG	2A	3178	1/1	0.96	0.14	42,42,42,42	0
54	MG	1a	3085	1/1	0.96	0.08	56,56,56,56	0
54	MG	1A	3091	1/1	0.96	0.12	46,46,46,46	0
54	MG	1A	3276	1/1	0.96	0.20	38,38,38,38	0
54	MG	1A	3277	1/1	0.96	0.10	41,41,41,41	0
54	MG	1A	3354	1/1	0.96	0.08	29,29,29,29	0
54	MG	1A	3772	1/1	0.96	0.06	28,28,28,28	0
54	MG	2A	3185	1/1	0.96	0.09	43,43,43,43	0
54	MG	1A	3012	1/1	0.96	0.12	35,35,35,35	0
54	MG	1A	3356	1/1	0.96	0.09	34,34,34,34	0
54	MG	2a	3154	1/1	0.96	0.06	55,55,55,55	0
54	MG	2A	3433	1/1	0.96	0.16	38,38,38,38	0
54	MG	2A	3699	1/1	0.96	0.13	42,42,42,42	0
54	MG	1A	3357	1/1	0.96	0.06	31,31,31,31	0
54	MG	1A	3923	1/1	0.96	0.05	51,51,51,51	0
54	MG	1a	3270	1/1	0.96	0.06	53,53,53,53	0
54	MG	1A	3780	1/1	0.96	0.14	37,37,37,37	0
54	MG	1A	3649	1/1	0.96	0.07	38,38,38,38	0
54	MG	1A	3442	1/1	0.96	0.09	23,23,23,23	0
54	MG	1N	201	1/1	0.96	0.12	40,40,40,40	0
54	MG	1N	202	1/1	0.96	0.22	37,37,37,37	0
54	MG	1A	3359	1/1	0.96	0.07	35,35,35,35	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	2A	3709	1/1	0.96	0.11	62,62,62,62	0
54	MG	1A	3540	1/1	0.96	0.07	34,34,34,34	0
54	MG	1A	3076	1/1	0.96	0.31	41,41,41,41	0
54	MG	2a	3170	1/1	0.96	0.12	60,60,60,60	0
54	MG	2A	3445	1/1	0.96	0.18	57,57,57,57	0
54	MG	2A	3199	1/1	0.96	0.06	46,46,46,46	0
54	MG	1A	3125	1/1	0.96	0.17	38,38,38,38	0
54	MG	1A	3099	1/1	0.96	0.13	40,40,40,40	0
54	MG	2a	3176	1/1	0.96	0.10	77,77,77,77	0
54	MG	2a	3177	1/1	0.96	0.24	43,43,43,43	0
54	MG	1d	304	1/1	0.96	0.15	57,57,57,57	0
54	MG	1Q	201	1/1	0.96	0.07	37,37,37,37	0
54	MG	2A	3719	1/1	0.96	0.06	35,35,35,35	0
54	MG	1Q	203	1/1	0.96	0.18	48,48,48,48	0
54	MG	1A	3127	1/1	0.96	0.10	62,62,62,62	0
54	MG	1A	3937	1/1	0.96	0.05	33,33,33,33	0
54	MG	1A	3181	1/1	0.96	0.30	40,40,40,40	0
54	MG	2A	3726	1/1	0.96	0.06	43,43,43,43	0
54	MG	1a	3110	1/1	0.96	0.30	49,49,49,49	0
54	MG	1A	3129	1/1	0.96	0.18	31,31,31,31	0
54	MG	1A	3451	1/1	0.96	0.06	55,55,55,55	0
54	MG	1g	203	1/1	0.96	0.09	52,52,52,52	0
54	MG	1A	3942	1/1	0.96	0.06	20,20,20,20	0
54	MG	1A	3551	1/1	0.96	0.05	19,19,19,19	0
54	MG	2A	3465	1/1	0.96	0.14	63,63,63,63	0
54	MG	1A	3945	1/1	0.96	0.08	44,44,44,44	0
54	MG	1A	3794	1/1	0.96	0.08	60,60,60,60	0
54	MG	1A	3222	1/1	0.96	0.06	39,39,39,39	0
54	MG	1A	3293	1/1	0.96	0.29	29,29,29,29	0
54	MG	1A	3294	1/1	0.96	0.08	42,42,42,42	0
54	MG	2A	3219	1/1	0.96	0.09	53,53,53,53	0
54	MG	1U	205	1/1	0.96	0.21	40,40,40,40	0
54	MG	1A	3457	1/1	0.96	0.07	48,48,48,48	0
54	MG	1A	3295	1/1	0.96	0.12	39,39,39,39	0
54	MG	1V	203	1/1	0.96	0.14	37,37,37,37	0
54	MG	1A	3020	1/1	0.96	0.32	41,41,41,41	0
59	ZN	14	102	1/1	0.96	0.07	110,110,110,110	0
59	ZN	24	501	1/1	0.96	0.11	124,124,124,124	0
54	MG	1A	3001	1/1	0.97	0.04	33,33,33,33	0
54	MG	1W	203	1/1	0.97	0.11	31,31,31,31	0
54	MG	1A	3061	1/1	0.97	0.13	31,31,31,31	0
54	MG	1A	3715	1/1	0.97	0.09	40,40,40,40	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1A	3164	1/1	0.97	0.06	29,29,29,29	0
54	MG	1A	3717	1/1	0.97	0.07	46,46,46,46	0
54	MG	1A	3349	1/1	0.97	0.04	29,29,29,29	0
54	MG	10	104	1/1	0.97	0.06	51,51,51,51	0
54	MG	1A	3841	1/1	0.97	0.08	40,40,40,40	0
54	MG	1A	3612	1/1	0.97	0.13	36,36,36,36	0
54	MG	2A	3579	1/1	0.97	0.07	30,30,30,30	0
54	MG	23	102	1/1	0.97	0.07	42,42,42,42	0
54	MG	1A	3350	1/1	0.97	0.12	11,11,11,11	0
54	MG	1A	3016	1/1	0.97	0.23	28,28,28,28	0
54	MG	1A	3213	1/1	0.97	0.23	34,34,34,34	0
54	MG	1A	3101	1/1	0.97	0.18	29,29,29,29	0
54	MG	1A	3726	1/1	0.97	0.08	69,69,69,69	0
54	MG	1A	3215	1/1	0.97	0.12	28,28,28,28	0
54	MG	1A	3128	1/1	0.97	0.05	27,27,27,27	0
54	MG	1a	3131	1/1	0.97	0.08	37,37,37,37	0
54	MG	13	103	1/1	0.97	0.07	37,37,37,37	0
54	MG	1A	3281	1/1	0.97	0.27	33,33,33,33	0
54	MG	1A	3620	1/1	0.97	0.15	28,28,28,28	0
54	MG	1A	3854	1/1	0.97	0.05	51,51,51,51	0
54	MG	1A	3621	1/1	0.97	0.20	33,33,33,33	0
54	MG	1A	3622	1/1	0.97	0.25	25,25,25,25	0
54	MG	2A	3596	1/1	0.97	0.07	49,49,49,49	0
54	MG	1A	3358	1/1	0.97	0.09	36,36,36,36	0
54	MG	1A	3734	1/1	0.97	0.05	33,33,33,33	0
54	MG	1A	3282	1/1	0.97	0.20	36,36,36,36	0
54	MG	1A	3441	1/1	0.97	0.09	23,23,23,23	0
54	MG	1A	3017	1/1	0.97	0.23	31,31,31,31	0
54	MG	1A	3170	1/1	0.97	0.23	50,50,50,50	0
54	MG	1A	3628	1/1	0.97	0.07	40,40,40,40	0
54	MG	1a	3148	1/1	0.97	0.08	45,45,45,45	0
54	MG	1A	3741	1/1	0.97	0.06	50,50,50,50	0
54	MG	1A	3362	1/1	0.97	0.06	19,19,19,19	0
54	MG	1A	3630	1/1	0.97	0.06	19,19,19,19	0
54	MG	1A	4005	1/1	0.97	0.04	37,37,37,37	0
54	MG	1A	3172	1/1	0.97	0.08	29,29,29,29	0
54	MG	1A	3221	1/1	0.97	0.20	41,41,41,41	0
54	MG	1A	3173	1/1	0.97	0.09	44,44,44,44	0
54	MG	1A	3175	1/1	0.97	0.19	51,51,51,51	0
54	MG	1A	3368	1/1	0.97	0.04	29,29,29,29	0
54	MG	2A	3011	1/1	0.97	0.05	30,30,30,30	0
54	MG	1A	3638	1/1	0.97	0.06	25,25,25,25	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1A	3874	1/1	0.97	0.04	36,36,36,36	0
54	MG	2A	3015	1/1	0.97	0.15	26,26,26,26	0
54	MG	1A	3751	1/1	0.97	0.06	26,26,26,26	0
54	MG	1A	3752	1/1	0.97	0.08	26,26,26,26	0
54	MG	2A	3018	1/1	0.97	0.20	43,43,43,43	0
54	MG	1A	3369	1/1	0.97	0.05	19,19,19,19	0
54	MG	2a	3034	1/1	0.97	0.07	37,37,37,37	0
54	MG	2A	3020	1/1	0.97	0.20	40,40,40,40	0
54	MG	2A	3023	1/1	0.97	0.16	53,53,53,53	0
54	MG	1A	3879	1/1	0.97	0.08	27,27,27,27	0
54	MG	1A	3880	1/1	0.97	0.06	22,22,22,22	0
54	MG	2A	3026	1/1	0.97	0.06	43,43,43,43	0
54	MG	2A	3027	1/1	0.97	0.08	28,28,28,28	0
54	MG	1A	3064	1/1	0.97	0.05	27,27,27,27	0
54	MG	2A	3030	1/1	0.97	0.10	36,36,36,36	0
54	MG	1A	3882	1/1	0.97	0.05	37,37,37,37	0
54	MG	1B	204	1/1	0.97	0.05	45,45,45,45	0
54	MG	1B	205	1/1	0.97	0.20	37,37,37,37	0
54	MG	1A	3104	1/1	0.97	0.26	28,28,28,28	0
54	MG	2A	3640	1/1	0.97	0.07	54,54,54,54	0
54	MG	1A	3180	1/1	0.97	0.09	30,30,30,30	0
54	MG	1A	3373	1/1	0.97	0.05	21,21,21,21	0
54	MG	2A	3037	1/1	0.97	0.14	44,44,44,44	0
54	MG	1a	3172	1/1	0.97	0.16	51,51,51,51	0
54	MG	1a	3173	1/1	0.97	0.07	60,60,60,60	0
54	MG	2A	3647	1/1	0.97	0.06	56,56,56,56	0
54	MG	1B	209	1/1	0.97	0.04	34,34,34,34	0
54	MG	2a	3055	1/1	0.97	0.09	50,50,50,50	0
54	MG	2A	3649	1/1	0.97	0.04	50,50,50,50	0
54	MG	2A	3227	1/1	0.97	0.06	46,46,46,46	0
54	MG	2A	3228	1/1	0.97	0.07	46,46,46,46	0
54	MG	1A	3644	1/1	0.97	0.06	38,38,38,38	0
54	MG	1A	3081	1/1	0.97	0.09	34,34,34,34	0
54	MG	1a	3022	1/1	0.97	0.09	53,53,53,53	0
54	MG	1A	3548	1/1	0.97	0.08	49,49,49,49	0
54	MG	1A	3761	1/1	0.97	0.11	36,36,36,36	0
54	MG	1A	3232	1/1	0.97	0.15	33,33,33,33	0
54	MG	1A	3234	1/1	0.97	0.26	40,40,40,40	0
54	MG	1A	3107	1/1	0.97	0.07	35,35,35,35	0
54	MG	2A	3050	1/1	0.97	0.12	47,47,47,47	0
54	MG	2A	3239	1/1	0.97	0.08	58,58,58,58	0
54	MG	2A	3667	1/1	0.97	0.05	30,30,30,30	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1A	3766	1/1	0.97	0.06	23,23,23,23	0
54	MG	2A	3447	1/1	0.97	0.08	53,53,53,53	0
54	MG	2A	3670	1/1	0.97	0.05	66,66,66,66	0
54	MG	2A	3671	1/1	0.97	0.06	49,49,49,49	0
54	MG	1B	220	1/1	0.97	0.05	25,25,25,25	0
54	MG	2A	3449	1/1	0.97	0.09	33,33,33,33	0
54	MG	1A	3183	1/1	0.97	0.14	35,35,35,35	0
54	MG	1A	3237	1/1	0.97	0.26	33,33,33,33	0
54	MG	2A	3452	1/1	0.97	0.05	47,47,47,47	0
54	MG	2A	3244	1/1	0.97	0.33	40,40,40,40	0
54	MG	1A	3238	1/1	0.97	0.18	24,24,24,24	0
54	MG	1A	3898	1/1	0.97	0.07	41,41,41,41	0
54	MG	1A	3305	1/1	0.97	0.07	37,37,37,37	0
54	MG	2A	3248	1/1	0.97	0.14	32,32,32,32	0
54	MG	2A	3059	1/1	0.97	0.08	51,51,51,51	0
54	MG	1A	3557	1/1	0.97	0.06	29,29,29,29	0
54	MG	1A	3138	1/1	0.97	0.16	39,39,39,39	0
54	MG	1A	3657	1/1	0.97	0.09	29,29,29,29	0
54	MG	1A	3777	1/1	0.97	0.05	34,34,34,34	0
54	MG	1A	3560	1/1	0.97	0.04	46,46,46,46	0
54	MG	1a	3195	1/1	0.97	0.08	66,66,66,66	0
54	MG	1D	303	1/1	0.97	0.10	45,45,45,45	0
54	MG	1A	3908	1/1	0.97	0.04	39,39,39,39	0
54	MG	2a	3094	1/1	0.97	0.31	53,53,53,53	0
54	MG	1D	306	1/1	0.97	0.23	38,38,38,38	0
54	MG	2A	3259	1/1	0.97	0.14	38,38,38,38	0
54	MG	1A	3139	1/1	0.97	0.10	35,35,35,35	0
54	MG	1A	3385	1/1	0.97	0.07	29,29,29,29	0
54	MG	1A	3308	1/1	0.97	0.04	24,24,24,24	0
54	MG	2A	3698	1/1	0.97	0.10	49,49,49,49	0
54	MG	1A	3309	1/1	0.97	0.11	27,27,27,27	0
54	MG	1D	314	1/1	0.97	0.06	56,56,56,56	0
54	MG	2A	3266	1/1	0.97	0.08	23,23,23,23	0
54	MG	1A	3140	1/1	0.97	0.09	18,18,18,18	0
54	MG	2A	3268	1/1	0.97	0.25	44,44,44,44	0
54	MG	1a	3050	1/1	0.97	0.07	45,45,45,45	0
54	MG	1A	3243	1/1	0.97	0.18	33,33,33,33	0
54	MG	1E	302	1/1	0.97	0.18	29,29,29,29	0
54	MG	1A	3918	1/1	0.97	0.05	48,48,48,48	0
54	MG	1A	3919	1/1	0.97	0.06	47,47,47,47	0
54	MG	1A	3312	1/1	0.97	0.08	50,50,50,50	0
54	MG	1A	3313	1/1	0.97	0.23	43,43,43,43	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1A	3669	1/1	0.97	0.07	55,55,55,55	0
54	MG	1A	3037	1/1	0.97	0.07	46,46,46,46	0
54	MG	1A	3483	1/1	0.97	0.04	27,27,27,27	0
54	MG	1A	3245	1/1	0.97	0.17	31,31,31,31	0
54	MG	2A	3281	1/1	0.97	0.18	44,44,44,44	0
54	MG	1F	307	1/1	0.97	0.22	31,31,31,31	0
54	MG	2A	3717	1/1	0.97	0.10	70,70,70,70	0
54	MG	1F	308	1/1	0.97	0.10	33,33,33,33	0
54	MG	2a	3121	1/1	0.97	0.06	65,65,65,65	0
54	MG	1A	3142	1/1	0.97	0.05	31,31,31,31	0
54	MG	1F	310	1/1	0.97	0.15	34,34,34,34	0
54	MG	2A	3721	1/1	0.97	0.07	38,38,38,38	0
54	MG	1F	312	1/1	0.97	0.06	35,35,35,35	0
54	MG	1A	3247	1/1	0.97	0.24	41,41,41,41	0
54	MG	1A	3007	1/1	0.97	0.09	30,30,30,30	0
54	MG	2A	3725	1/1	0.97	0.09	43,43,43,43	0
54	MG	1A	3398	1/1	0.97	0.12	33,33,33,33	0
54	MG	1A	3399	1/1	0.97	0.06	28,28,28,28	0
54	MG	2A	3291	1/1	0.97	0.34	49,49,49,49	0
54	MG	1A	3932	1/1	0.97	0.11	32,32,32,32	0
54	MG	1A	3934	1/1	0.97	0.08	50,50,50,50	0
54	MG	1A	3679	1/1	0.97	0.13	43,43,43,43	0
54	MG	2A	3504	1/1	0.97	0.06	44,44,44,44	0
54	MG	1A	3680	1/1	0.97	0.12	41,41,41,41	0
54	MG	1A	3578	1/1	0.97	0.15	37,37,37,37	0
54	MG	2A	3109	1/1	0.97	0.09	44,44,44,44	0
54	MG	2a	3140	1/1	0.97	0.09	64,64,64,64	0
54	MG	1A	3039	1/1	0.97	0.12	50,50,50,50	0
54	MG	1A	3801	1/1	0.97	0.07	28,28,28,28	0
54	MG	2A	3301	1/1	0.97	0.17	52,52,52,52	0
54	MG	1A	3321	1/1	0.97	0.24	59,59,59,59	0
54	MG	1A	3322	1/1	0.97	0.07	19,19,19,19	0
54	MG	2A	3306	1/1	0.97	0.08	30,30,30,30	0
54	MG	2A	3114	1/1	0.97	0.22	49,49,49,49	0
54	MG	2A	3308	1/1	0.97	0.08	39,39,39,39	0
54	MG	1a	3235	1/1	0.97	0.08	51,51,51,51	0
54	MG	2B	208	1/1	0.97	0.09	65,65,65,65	0
54	MG	2A	3311	1/1	0.97	0.20	57,57,57,57	0
54	MG	1A	3068	1/1	0.97	0.07	36,36,36,36	0
54	MG	2A	3313	1/1	0.97	0.08	52,52,52,52	0
54	MG	1A	3496	1/1	0.97	0.07	27,27,27,27	0
54	MG	1A	3146	1/1	0.97	0.28	28,28,28,28	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1A	3088	1/1	0.97	0.06	38,38,38,38	0
54	MG	2A	3317	1/1	0.97	0.05	37,37,37,37	0
54	MG	2A	3525	1/1	0.97	0.07	53,53,53,53	0
54	MG	1A	3148	1/1	0.97	0.06	39,39,39,39	0
54	MG	1P	202	1/1	0.97	0.21	30,30,30,30	0
54	MG	1A	3256	1/1	0.97	0.15	31,31,31,31	0
54	MG	2a	3163	1/1	0.97	0.15	53,53,53,53	0
54	MG	2D	301	1/1	0.97	0.11	39,39,39,39	0
54	MG	2D	302	1/1	0.97	0.17	45,45,45,45	0
54	MG	1A	3691	1/1	0.97	0.06	40,40,40,40	0
54	MG	1A	3589	1/1	0.97	0.11	31,31,31,31	0
54	MG	1Q	202	1/1	0.97	0.12	28,28,28,28	0
54	MG	2A	3126	1/1	0.97	0.38	42,42,42,42	0
54	MG	2A	3127	1/1	0.97	0.19	39,39,39,39	0
54	MG	1A	3040	1/1	0.97	0.11	39,39,39,39	0
54	MG	2a	3172	1/1	0.97	0.07	56,56,56,56	0
54	MG	2A	3535	1/1	0.97	0.17	68,68,68,68	0
54	MG	1A	3150	1/1	0.97	0.12	43,43,43,43	0
54	MG	1A	3003	1/1	0.97	0.04	20,20,20,20	0
54	MG	1R	202	1/1	0.97	0.16	36,36,36,36	0
54	MG	1A	3816	1/1	0.97	0.05	39,39,39,39	0
54	MG	2A	3540	1/1	0.97	0.07	56,56,56,56	0
54	MG	1A	3956	1/1	0.97	0.06	54,54,54,54	0
54	MG	2A	3134	1/1	0.97	0.16	28,28,28,28	0
54	MG	1A	3117	1/1	0.97	0.12	28,28,28,28	0
54	MG	2a	3182	1/1	0.97	0.15	54,54,54,54	0
54	MG	1A	3261	1/1	0.97	0.26	35,35,35,35	0
54	MG	1A	3120	1/1	0.97	0.10	28,28,28,28	0
54	MG	1A	3596	1/1	0.97	0.07	46,46,46,46	0
54	MG	1A	3031	1/1	0.97	0.08	16,16,16,16	0
54	MG	1T	204	1/1	0.97	0.08	42,42,42,42	0
54	MG	1A	3822	1/1	0.97	0.21	38,38,38,38	0
54	MG	1A	3264	1/1	0.97	0.06	43,43,43,43	0
54	MG	2A	3343	1/1	0.97	0.07	40,40,40,40	0
54	MG	2A	3144	1/1	0.97	0.08	33,33,33,33	0
54	MG	1a	3260	1/1	0.97	0.10	51,51,51,51	0
54	MG	1U	203	1/1	0.97	0.11	30,30,30,30	0
54	MG	1A	3705	1/1	0.97	0.21	35,35,35,35	0
54	MG	1A	3706	1/1	0.97	0.13	50,50,50,50	0
56	TEL	1A	4019	58/58	0.97	0.07	12,21,26,26	0
56	TEL	2A	3739	58/58	0.97	0.07	24,30,39,43	0
54	MG	1A	3092	1/1	0.97	0.18	32,32,32,32	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	2Q	201	1/1	0.97	0.05	50,50,50,50	0
54	MG	1A	3159	1/1	0.97	0.18	29,29,29,29	0
54	MG	1V	201	1/1	0.97	0.23	26,26,26,26	0
54	MG	1A	3033	1/1	0.97	0.10	40,40,40,40	0
54	MG	2A	3355	1/1	0.97	0.06	29,29,29,29	0
54	MG	1A	3605	1/1	0.97	0.08	40,40,40,40	0
54	MG	1A	3423	1/1	0.97	0.06	19,19,19,19	0
54	MG	1V	206	1/1	0.97	0.09	54,54,54,54	0
54	MG	2A	3156	1/1	0.97	0.09	48,48,48,48	0
59	ZN	2Y	501	1/1	0.97	0.05	86,86,86,86	0
54	MG	1A	3208	1/1	0.97	0.10	38,38,38,38	0
54	MG	1A	3168	1/1	0.98	0.19	31,31,31,31	0
54	MG	1V	202	1/1	0.98	0.19	28,28,28,28	0
54	MG	1A	3291	1/1	0.98	0.07	13,13,13,13	0
54	MG	1A	3114	1/1	0.98	0.15	27,27,27,27	0
54	MG	1A	3550	1/1	0.98	0.23	31,31,31,31	0
54	MG	2A	3356	1/1	0.98	0.04	42,42,42,42	0
54	MG	2A	3691	1/1	0.98	0.06	43,43,43,43	0
54	MG	1A	3005	1/1	0.98	0.08	18,18,18,18	0
54	MG	1A	3407	1/1	0.98	0.07	19,19,19,19	0
54	MG	1A	3477	1/1	0.98	0.05	34,34,34,34	0
54	MG	1W	202	1/1	0.98	0.13	42,42,42,42	0
54	MG	1A	3029	1/1	0.98	0.10	37,37,37,37	0
54	MG	1A	3351	1/1	0.98	0.05	36,36,36,36	0
54	MG	1A	4017	1/1	0.98	0.07	48,48,48,48	0
54	MG	1Y	201	1/1	0.98	0.05	52,52,52,52	0
54	MG	1A	3093	1/1	0.98	0.19	24,24,24,24	0
54	MG	10	101	1/1	0.98	0.06	39,39,39,39	0
54	MG	1A	3634	1/1	0.98	0.13	50,50,50,50	0
54	MG	1A	3207	1/1	0.98	0.12	39,39,39,39	0
54	MG	1A	3558	1/1	0.98	0.05	32,32,32,32	0
54	MG	1A	3249	1/1	0.98	0.20	41,41,41,41	0
54	MG	1A	3916	1/1	0.98	0.04	31,31,31,31	0
54	MG	1A	3917	1/1	0.98	0.18	27,27,27,27	0
54	MG	2A	3070	1/1	0.98	0.18	30,30,30,30	0
54	MG	2A	3071	1/1	0.98	0.08	47,47,47,47	0
54	MG	2A	3072	1/1	0.98	0.03	23,23,23,23	0
54	MG	2A	3378	1/1	0.98	0.03	26,26,26,26	0
54	MG	1A	3413	1/1	0.98	0.08	18,18,18,18	0
54	MG	1A	3722	1/1	0.98	0.03	21,21,21,21	0
54	MG	1A	3815	1/1	0.98	0.04	30,30,30,30	0
54	MG	1A	3174	1/1	0.98	0.15	30,30,30,30	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1A	3299	1/1	0.98	0.04	43,43,43,43	0
54	MG	1B	213	1/1	0.98	0.04	35,35,35,35	0
54	MG	1B	214	1/1	0.98	0.04	41,41,41,41	0
54	MG	1A	3488	1/1	0.98	0.10	38,38,38,38	0
54	MG	1A	3300	1/1	0.98	0.15	33,33,33,33	0
54	MG	2A	3082	1/1	0.98	0.12	50,50,50,50	0
54	MG	2A	3548	1/1	0.98	0.07	35,35,35,35	0
54	MG	2A	3083	1/1	0.98	0.07	46,46,46,46	0
54	MG	15	102	1/1	0.98	0.22	27,27,27,27	0
54	MG	1A	3301	1/1	0.98	0.13	30,30,30,30	0
54	MG	2A	3232	1/1	0.98	0.18	52,52,52,52	0
54	MG	1A	3491	1/1	0.98	0.04	22,22,22,22	0
54	MG	1A	3118	1/1	0.98	0.20	31,31,31,31	0
54	MG	1A	3823	1/1	0.98	0.20	26,26,26,26	0
54	MG	1A	3252	1/1	0.98	0.07	38,38,38,38	0
54	MG	1A	3421	1/1	0.98	0.08	22,22,22,22	0
54	MG	1A	3648	1/1	0.98	0.21	26,26,26,26	0
54	MG	1A	3933	1/1	0.98	0.12	40,40,40,40	0
54	MG	2a	3086	1/1	0.98	0.22	46,46,46,46	0
54	MG	1A	3827	1/1	0.98	0.05	20,20,20,20	0
54	MG	1A	3119	1/1	0.98	0.06	15,15,15,15	0
54	MG	1A	3013	1/1	0.98	0.03	20,20,20,20	0
54	MG	1A	3424	1/1	0.98	0.05	36,36,36,36	0
54	MG	1A	3938	1/1	0.98	0.07	55,55,55,55	0
54	MG	1A	3737	1/1	0.98	0.12	33,33,33,33	0
54	MG	2A	3566	1/1	0.98	0.05	24,24,24,24	0
54	MG	2A	3099	1/1	0.98	0.04	44,44,44,44	0
54	MG	2A	3100	1/1	0.98	0.10	41,41,41,41	0
54	MG	1A	3178	1/1	0.98	0.11	37,37,37,37	0
54	MG	2A	3410	1/1	0.98	0.08	26,26,26,26	0
54	MG	1A	3179	1/1	0.98	0.14	32,32,32,32	0
54	MG	1D	305	1/1	0.98	0.05	37,37,37,37	0
54	MG	1A	3575	1/1	0.98	0.08	35,35,35,35	0
54	MG	1D	308	1/1	0.98	0.07	47,47,47,47	0
54	MG	2A	3106	1/1	0.98	0.06	30,30,30,30	0
54	MG	1D	309	1/1	0.98	0.10	27,27,27,27	0
54	MG	1A	3365	1/1	0.98	0.06	21,21,21,21	0
54	MG	1a	3134	1/1	0.98	0.06	36,36,36,36	0
54	MG	1A	3944	1/1	0.98	0.09	40,40,40,40	0
54	MG	1A	3429	1/1	0.98	0.03	27,27,27,27	0
54	MG	1A	3502	1/1	0.98	0.05	32,32,32,32	0
54	MG	1A	3838	1/1	0.98	0.10	42,42,42,42	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	2A	3583	1/1	0.98	0.04	42,42,42,42	0
54	MG	1D	315	1/1	0.98	0.10	53,53,53,53	0
54	MG	1A	3744	1/1	0.98	0.08	40,40,40,40	0
54	MG	2A	3263	1/1	0.98	0.14	19,19,19,19	0
54	MG	1A	3077	1/1	0.98	0.24	33,33,33,33	0
54	MG	1a	3142	1/1	0.98	0.04	38,38,38,38	0
54	MG	1E	301	1/1	0.98	0.17	36,36,36,36	0
54	MG	1A	3078	1/1	0.98	0.10	33,33,33,33	0
54	MG	1A	3018	1/1	0.98	0.11	25,25,25,25	0
54	MG	1A	3032	1/1	0.98	0.10	48,48,48,48	0
54	MG	1A	3662	1/1	0.98	0.10	45,45,45,45	0
54	MG	1A	3023	1/1	0.98	0.16	27,27,27,27	0
54	MG	2E	302	1/1	0.98	0.07	42,42,42,42	0
54	MG	1a	3019	1/1	0.98	0.03	43,43,43,43	0
54	MG	1A	3847	1/1	0.98	0.04	37,37,37,37	0
54	MG	2A	3599	1/1	0.98	0.04	65,65,65,65	0
54	MG	1E	309	1/1	0.98	0.05	49,49,49,49	0
54	MG	1F	301	1/1	0.98	0.11	26,26,26,26	0
54	MG	2A	3276	1/1	0.98	0.10	47,47,47,47	0
54	MG	2A	3603	1/1	0.98	0.04	49,49,49,49	0
54	MG	1A	3152	1/1	0.98	0.09	30,30,30,30	0
54	MG	1A	3082	1/1	0.98	0.17	28,28,28,28	0
54	MG	2a	3132	1/1	0.98	0.12	58,58,58,58	0
54	MG	1F	305	1/1	0.98	0.20	35,35,35,35	0
54	MG	1A	3666	1/1	0.98	0.06	32,32,32,32	0
54	MG	2A	3608	1/1	0.98	0.05	31,31,31,31	0
54	MG	1A	3154	1/1	0.98	0.17	40,40,40,40	0
54	MG	1A	3043	1/1	0.98	0.09	16,16,16,16	0
54	MG	1A	3224	1/1	0.98	0.06	36,36,36,36	0
54	MG	1A	3267	1/1	0.98	0.20	30,30,30,30	0
54	MG	1F	311	1/1	0.98	0.11	39,39,39,39	0
54	MG	1A	3056	1/1	0.98	0.06	40,40,40,40	0
54	MG	2A	3138	1/1	0.98	0.05	42,42,42,42	0
54	MG	1A	3964	1/1	0.98	0.06	42,42,42,42	0
54	MG	1A	3320	1/1	0.98	0.15	41,41,41,41	0
54	MG	1A	3226	1/1	0.98	0.23	36,36,36,36	0
54	MG	1A	3190	1/1	0.98	0.11	33,33,33,33	0
54	MG	2R	201	1/1	0.98	0.17	41,41,41,41	0
54	MG	1A	3762	1/1	0.98	0.19	30,30,30,30	0
54	MG	1A	3271	1/1	0.98	0.18	42,42,42,42	0
54	MG	2A	3294	1/1	0.98	0.05	57,57,57,57	0
54	MG	2a	3151	1/1	0.98	0.10	51,51,51,51	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1A	3324	1/1	0.98	0.05	35,35,35,35	0
54	MG	1F	320	1/1	0.98	0.04	35,35,35,35	0
54	MG	1A	3677	1/1	0.98	0.04	49,49,49,49	0
54	MG	1A	3447	1/1	0.98	0.05	31,31,31,31	0
54	MG	1A	3085	1/1	0.98	0.24	35,35,35,35	0
54	MG	1A	3108	1/1	0.98	0.15	31,31,31,31	0
54	MG	1A	3866	1/1	0.98	0.05	26,26,26,26	0
54	MG	1A	3231	1/1	0.98	0.22	30,30,30,30	0
54	MG	1a	3047	1/1	0.98	0.14	49,49,49,49	0
54	MG	1A	3601	1/1	0.98	0.05	41,41,41,41	0
54	MG	2A	3008	1/1	0.98	0.07	37,37,37,37	0
54	MG	2A	3635	1/1	0.98	0.04	45,45,45,45	0
54	MG	1A	3602	1/1	0.98	0.06	20,20,20,20	0
54	MG	1A	3603	1/1	0.98	0.07	45,45,45,45	0
54	MG	2A	3310	1/1	0.98	0.08	33,33,33,33	0
54	MG	1A	3774	1/1	0.98	0.05	41,41,41,41	0
54	MG	1A	3044	1/1	0.98	0.14	22,22,22,22	0
54	MG	2A	3013	1/1	0.98	0.05	21,21,21,21	0
54	MG	1P	201	1/1	0.98	0.38	32,32,32,32	0
54	MG	1A	3776	1/1	0.98	0.05	36,36,36,36	0
54	MG	1A	3233	1/1	0.98	0.11	28,28,28,28	0
54	MG	1A	3132	1/1	0.98	0.18	34,34,34,34	0
54	MG	1P	205	1/1	0.98	0.03	25,25,25,25	0
54	MG	1A	3006	1/1	0.98	0.04	21,21,21,21	0
54	MG	1A	3456	1/1	0.98	0.05	48,48,48,48	0
54	MG	2A	3650	1/1	0.98	0.04	33,33,33,33	0
54	MG	2A	3021	1/1	0.98	0.07	39,39,39,39	0
54	MG	2A	3022	1/1	0.98	0.20	43,43,43,43	0
54	MG	1A	3332	1/1	0.98	0.04	24,24,24,24	0
54	MG	1A	3279	1/1	0.98	0.08	20,20,20,20	0
54	MG	1A	3196	1/1	0.98	0.18	39,39,39,39	0
54	MG	1R	201	1/1	0.98	0.14	34,34,34,34	0
54	MG	2A	3174	1/1	0.98	0.04	46,46,46,46	0
54	MG	1A	3693	1/1	0.98	0.03	38,38,38,38	0
54	MG	2A	3660	1/1	0.98	0.06	45,45,45,45	0
54	MG	2A	3661	1/1	0.98	0.08	52,52,52,52	0
54	MG	1A	3047	1/1	0.98	0.07	15,15,15,15	0
54	MG	1A	3198	1/1	0.98	0.04	47,47,47,47	0
54	MG	1A	3787	1/1	0.98	0.06	43,43,43,43	0
54	MG	2A	3333	1/1	0.98	0.05	43,43,43,43	0
54	MG	2A	3666	1/1	0.98	0.08	26,26,26,26	0
54	MG	1A	3537	1/1	0.98	0.03	19,19,19,19	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1A	3697	1/1	0.98	0.04	44,44,44,44	0
54	MG	1A	3698	1/1	0.98	0.14	37,37,37,37	0
54	MG	1A	3284	1/1	0.98	0.05	39,39,39,39	0
54	MG	1A	3137	1/1	0.98	0.04	39,39,39,39	0
54	MG	1A	3466	1/1	0.98	0.04	19,19,19,19	0
54	MG	1A	3026	1/1	0.98	0.18	29,29,29,29	0
54	MG	1A	3342	1/1	0.98	0.10	18,18,18,18	0
54	MG	1A	3073	1/1	0.98	0.05	32,32,32,32	0
54	MG	2A	3041	1/1	0.98	0.05	25,25,25,25	0
54	MG	1A	3470	1/1	0.98	0.07	37,37,37,37	0
54	MG	2A	3345	1/1	0.98	0.08	28,28,28,28	0
54	MG	2A	3507	1/1	0.98	0.04	27,27,27,27	0
54	MG	1U	206	1/1	0.98	0.27	26,26,26,26	0
59	ZN	1Y	202	1/1	0.98	0.04	51,51,51,51	0
54	MG	1A	3896	1/1	0.98	0.10	38,38,38,38	0
54	MG	1U	208	1/1	0.98	0.16	35,35,35,35	0
54	MG	1A	3242	1/1	0.98	0.30	34,34,34,34	0
59	ZN	29	501	1/1	0.98	0.03	60,60,60,60	0
60	SF4	1d	307	8/8	0.98	0.05	58,61,69,69	0
60	SF4	2d	501	8/8	0.98	0.04	65,70,82,82	0
54	MG	1A	3216	1/1	0.99	0.10	24,24,24,24	0
54	MG	2A	3325	1/1	0.99	0.07	27,27,27,27	0
54	MG	1A	3171	1/1	0.99	0.05	36,36,36,36	0
54	MG	1A	3876	1/1	0.99	0.07	29,29,29,29	0
54	MG	1D	307	1/1	0.99	0.06	9,9,9,9	0
54	MG	1A	3336	1/1	0.99	0.10	9,9,9,9	0
54	MG	1A	3377	1/1	0.99	0.03	9,9,9,9	0
54	MG	1A	3631	1/1	0.99	0.06	25,25,25,25	0
54	MG	1A	3337	1/1	0.99	0.06	25,25,25,25	0
54	MG	2A	3676	1/1	0.99	0.02	31,31,31,31	0
54	MG	1I	103	1/1	0.99	0.04	46,46,46,46	0
54	MG	1A	3094	1/1	0.99	0.04	37,37,37,37	0
54	MG	1A	3844	1/1	0.99	0.05	18,18,18,18	0
54	MG	1A	3158	1/1	0.99	0.12	31,31,31,31	0
54	MG	1A	3773	1/1	0.99	0.07	38,38,38,38	0
54	MG	1A	3927	1/1	0.99	0.04	37,37,37,37	0
54	MG	1A	3536	1/1	0.99	0.03	41,41,41,41	0
54	MG	1A	3426	1/1	0.99	0.03	19,19,19,19	0
54	MG	1A	3973	1/1	0.99	0.06	17,17,17,17	0
54	MG	1A	3974	1/1	0.99	0.04	27,27,27,27	0
54	MG	1E	304	1/1	0.99	0.06	38,38,38,38	0
54	MG	1A	3134	1/1	0.99	0.24	27,27,27,27	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	2A	3224	1/1	0.99	0.04	43,43,43,43	0
54	MG	2A	3617	1/1	0.99	0.06	37,37,37,37	0
54	MG	2A	3346	1/1	0.99	0.10	26,26,26,26	0
54	MG	1A	3479	1/1	0.99	0.05	40,40,40,40	0
54	MG	1A	3135	1/1	0.99	0.19	25,25,25,25	0
54	MG	1A	3541	1/1	0.99	0.03	18,18,18,18	0
54	MG	1a	3144	1/1	0.99	0.06	34,34,34,34	0
54	MG	1A	3453	1/1	0.99	0.05	12,12,12,12	0
54	MG	1A	3161	1/1	0.99	0.10	30,30,30,30	0
54	MG	1A	3095	1/1	0.99	0.10	26,26,26,26	0
54	MG	2A	3057	1/1	0.99	0.07	32,32,32,32	0
54	MG	1A	3105	1/1	0.99	0.17	30,30,30,30	0
54	MG	1F	304	1/1	0.99	0.14	33,33,33,33	0
54	MG	1A	3096	1/1	0.99	0.04	15,15,15,15	0
54	MG	2A	3358	1/1	0.99	0.06	35,35,35,35	0
54	MG	2A	3004	1/1	0.99	0.04	34,34,34,34	0
54	MG	2A	3062	1/1	0.99	0.05	32,32,32,32	0
54	MG	1A	3458	1/1	0.99	0.03	23,23,23,23	0
54	MG	1A	3028	1/1	0.99	0.18	25,25,25,25	0
54	MG	2A	3007	1/1	0.99	0.08	40,40,40,40	0
54	MG	1A	3347	1/1	0.99	0.04	18,18,18,18	0
54	MG	2A	3498	1/1	0.99	0.04	42,42,42,42	0
54	MG	1A	3899	1/1	0.99	0.03	29,29,29,29	0
54	MG	2A	3302	1/1	0.99	0.04	26,26,26,26	0
54	MG	1A	3900	1/1	0.99	0.04	34,34,34,34	0
54	MG	2A	3641	1/1	0.99	0.07	60,60,60,60	0
54	MG	1A	3389	1/1	0.99	0.03	19,19,19,19	0
54	MG	2A	3305	1/1	0.99	0.07	47,47,47,47	0
54	MG	1A	3519	1/1	0.99	0.05	49,49,49,49	0
54	MG	1A	3009	1/1	0.99	0.04	25,25,25,25	0
54	MG	1A	3042	1/1	0.99	0.09	20,20,20,20	0
54	MG	1a	3212	1/1	0.99	0.07	55,55,55,55	0
54	MG	2A	3374	1/1	0.99	0.04	36,36,36,36	0
54	MG	1A	3522	1/1	0.99	0.06	18,18,18,18	0
54	MG	1A	3015	1/1	0.99	0.08	27,27,27,27	0
54	MG	2A	3651	1/1	0.99	0.05	26,26,26,26	0
54	MG	1B	223	1/1	0.99	0.07	49,49,49,49	0
54	MG	1A	3907	1/1	0.99	0.02	21,21,21,21	0
54	MG	2A	3379	1/1	0.99	0.05	32,32,32,32	0
54	MG	1A	3588	1/1	0.99	0.08	22,22,22,22	0
54	MG	1A	3465	1/1	0.99	0.05	20,20,20,20	0
54	MG	1A	3725	1/1	0.99	0.02	36,36,36,36	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1A	3024	1/1	0.99	0.05	14,14,14,14	0
54	MG	1A	3280	1/1	0.99	0.05	31,31,31,31	0
54	MG	1X	102	1/1	0.99	0.08	30,30,30,30	0
54	MG	1A	3045	1/1	0.99	0.02	8,8,8,8	0
59	ZN	15	109	1/1	0.99	0.02	32,32,32,32	0
59	ZN	16	501	1/1	0.99	0.07	41,41,41,41	0
59	ZN	19	103	1/1	0.99	0.05	40,40,40,40	0
59	ZN	1n	103	1/1	0.99	0.03	66,66,66,66	0
54	MG	1A	3418	1/1	0.99	0.06	22,22,22,22	0
54	MG	1A	3915	1/1	0.99	0.04	11,11,11,11	0
59	ZN	25	105	1/1	0.99	0.03	48,48,48,48	0
59	ZN	26	501	1/1	0.99	0.03	56,56,56,56	0
54	MG	2A	3029	1/1	0.99	0.06	39,39,39,39	0
59	ZN	2n	102	1/1	0.99	0.04	86,86,86,86	0
54	MG	2A	3592	1/1	0.99	0.04	54,54,54,54	0
54	MG	2A	3456	1/1	0.99	0.04	49,49,49,49	0
54	MG	1A	3482	1/1	1.00	0.03	24,24,24,24	0
54	MG	1A	3290	1/1	1.00	0.11	17,17,17,17	0
54	MG	2A	3597	1/1	1.00	0.07	28,28,28,28	0
54	MG	1A	3228	1/1	1.00	0.12	30,30,30,30	0

6.5 Other polymers

There are no such residues in this entry.