



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 1, 2026 – 03:14 AM UTC

PDB ID : 9MTS / pdb_00009mts
Title : Crystal structure of the wild-type *Thermus thermophilus* 70S ribosome in complex with mRNA, A-site Q230-unmodified Release Factor 1, and P-site fMEA AAKC-peptidyl-tRNAcys at 2.70Å resolution
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Deposited on : 2025-01-12
Resolution : 2.70 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

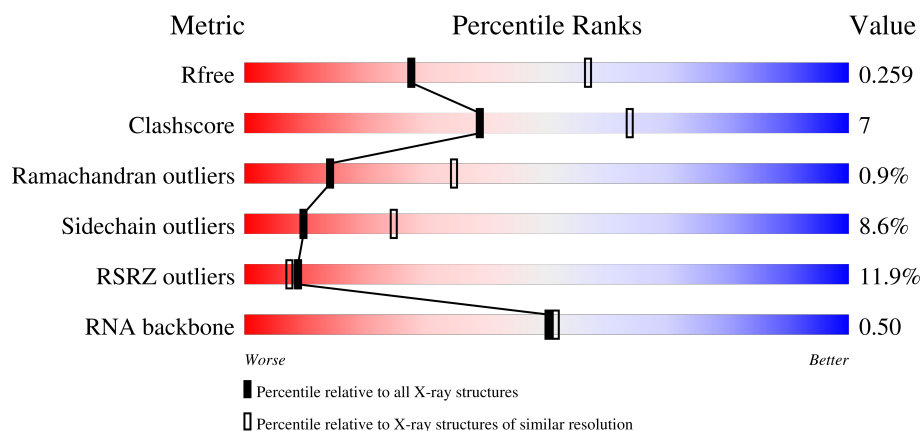
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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	3538 (2.70-2.70)
Clashscore	190562	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)
RSRZ outliers	180081	3538 (2.70-2.70)
RNA backbone	3983	1044 (2.90-2.50)

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	7% 70% 23% 5%
1	2A	2915	6% 64% 26% 6%
2	1B	121	80% 17%

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Mol	Chain	Length	Quality of chain
2	2B	121	
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	

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Mol	Chain	Length	Quality of chain
15	1T	146	
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	

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Mol	Chain	Length	Quality of chain
27	25	60	
28	16	54	
28	26	54	
29	17	49	
29	27	49	
30	18	65	
30	28	65	
31	19	37	
31	29	37	
32	1a	1521	
32	2a	1521	
33	1b	256	
33	2b	256	
34	1c	239	
34	2c	239	
35	1d	209	
35	2d	209	
36	1e	162	
36	2e	162	
37	1f	101	
37	2f	101	
38	1g	156	
38	2g	156	
39	1h	138	
39	2h	138	

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

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Mol	Chain	Length	Quality of chain
52	2u	27	
53	1v	24	
53	2v	24	
54	1w	354	
54	2w	354	
55	1x	74	
55	2x	74	
56	1z	7	
56	2z	7	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
57	MG	2A	3239	-	-	-	X

2 Entry composition

There are 61 unique types of molecules in this entry. The entry contains 296409 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	2871	Total	C	N	O	P	0	0	0
			61852	27531	11572	19878	2871			
1	2A	2800	Total	C	N	O	P	0	0	0
			60322	26848	11284	19390	2800			

- 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
			2577	1146	476	835	120			
2	2B	120	Total	C	N	O	P	0	0	0
			2575	1146	476	833	120			

- 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
			2136	1349	423	361	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
			1423	913	253	253	4			
6	2G	181	Total	C	N	O	S	0	0	0
			1428	913	258	253	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	174	Total	C	N	O	S	0	0	0
			1330	845	248	236	1			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	1I	146	Total	C	N	O	S	0	0	0
			1097	701	191	204	1			
8	2I	146	Total	C	N	O	S	0	0	0
			1064	681	186	196	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
			1117	719	207	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
			873	550	174	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
			771	495	140	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
			806	517	152	131	6			
20	2Y	107	Total	C	N	O	S	0	0	0
			806	517	152	131	6			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
21	1Z	154	Total	C	N	O	S	0	0	0
			1240	795	222	220	3			
21	2Z	160	Total	C	N	O	S	0	0	0
			1271	814	228	227	2			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	10	76	Total	C	N	O	S	0	0	0
			604	373	128	102	1			
22	20	76	Total	C	N	O	S	0	0	0
			604	373	128	102	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
			755	475	148	131	1			
23	21	97	Total	C	N	O	S	0	0	0
			755	475	148	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
			588	365	118	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
			552	349	99	99	5			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	24	69	Total	C	N	O	S	0	0	0
			532	339	97	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
			455	285	89	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	1503	Total	C	N	O	P	0	0	0
			32327	14396	5990	10438	1503			

- 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
			1846	1179	331	331	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
			1548	973	301	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
			1655	1038	326	284	7			
35	2d	208	Total	C	N	O	S	0	0	0
			1674	1050	333	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
			1129	714	213	198	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
			810	514	144	149	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
			1231	766	243	216	6			
38	2g	155	Total	C	N	O	S	0	0	0
			1235	769	244	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
			1088	689	206	191	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
			983	623	193	167			
40	2i	127	Total	C	N	O	0	0	0
			978	619	190	169			

- 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
			709	440	138	131			
41	2j	96	Total	C	N	O	0	0	0
			714	445	138	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
			829	516	155	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	118	Total	C	N	O	S	0	0	0
			919	566	190	161	2			
44	2m	116	Total	C	N	O	S	0	0	0
			907	558	188	159	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
			652	417	120	113	2			
50	2s	83	Total	C	N	O	S	0	0	0
			646	412	119	113	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
			728	446	156	124	2			
51	2t	96	Total	C	N	O	S	0	0	0
			727	446	155	124	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 RNA chain called CYS-Stop mRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
53	1v	13	Total	C	N	O	P	0	0	0
			277	125	51	88	13			
53	2v	9	Total	C	N	O	P	0	0	0
			190	86	34	61	9			

- Molecule 54 is a protein called Peptide chain release factor 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
54	1w	249	Total	C	N	O	S	0	0	0
			1938	1198	360	371	9			
54	2w	253	Total	C	N	O	S	0	0	0
			1956	1209	361	377	9			

- Molecule 55 is a RNA chain called P-site Peptidyl-tRNA fMEAAAKC-tRNA_{cys} RNA-part.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
55	1x	74	Total	C	N	O	P	S	0	0	0
			1577	704	281	517	74	1			
55	2x	74	Total	C	N	O	P	S	0	0	0
			1577	704	281	517	74	1			

- Molecule 56 is a protein called P-site Peptidyl-tRNA fMEAAAKC-tRNA_{cys} Peptide-part.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
56	1z	5	Total	C	N	O	S	0	0	0
			30	18	6	5	1			
56	2z	5	Total	C	N	O	S	0	0	0
			30	18	6	5	1			

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
57	1A	1046	Total	Mg	0	0
			1046	1046		
57	1B	38	Total	Mg	0	0
			38	38		
57	1D	13	Total	Mg	0	0
			13	13		
57	1E	12	Total	Mg	0	0
			12	12		
57	1F	13	Total	Mg	0	0
			13	13		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
57	1G	5	Total 5	Mg 5	0	0
57	1I	1	Total 1	Mg 1	0	0
57	1N	6	Total 6	Mg 6	0	0
57	1O	5	Total 5	Mg 5	0	0
57	1P	3	Total 3	Mg 3	0	0
57	1Q	7	Total 7	Mg 7	0	0
57	1R	7	Total 7	Mg 7	0	0
57	1S	3	Total 3	Mg 3	0	0
57	1T	2	Total 2	Mg 2	0	0
57	1U	10	Total 10	Mg 10	0	0
57	1V	6	Total 6	Mg 6	0	0
57	1W	9	Total 9	Mg 9	0	0
57	1X	5	Total 5	Mg 5	0	0
57	1Y	3	Total 3	Mg 3	0	0
57	1Z	2	Total 2	Mg 2	0	0
57	10	8	Total 8	Mg 8	0	0
57	11	5	Total 5	Mg 5	0	0
57	12	2	Total 2	Mg 2	0	0
57	13	4	Total 4	Mg 4	0	0
57	15	7	Total 7	Mg 7	0	0
57	16	1	Total 1	Mg 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
57	17	4	Total 4	Mg 4	0	0
57	18	3	Total 3	Mg 3	0	0
57	19	1	Total 1	Mg 1	0	0
57	1a	205	Total 205	Mg 205	0	0
57	1b	2	Total 2	Mg 2	0	0
57	1d	1	Total 1	Mg 1	0	0
57	1e	2	Total 2	Mg 2	0	0
57	1f	1	Total 1	Mg 1	0	0
57	1k	1	Total 1	Mg 1	0	0
57	1l	2	Total 2	Mg 2	0	0
57	1m	1	Total 1	Mg 1	0	0
57	1n	2	Total 2	Mg 2	0	0
57	1p	1	Total 1	Mg 1	0	0
57	1r	1	Total 1	Mg 1	0	0
57	1t	1	Total 1	Mg 1	0	0
57	1v	2	Total 2	Mg 2	0	0
57	1w	1	Total 1	Mg 1	0	0
57	1x	11	Total 11	Mg 11	0	0
57	2A	846	Total 846	Mg 846	0	0
57	2B	19	Total 19	Mg 19	0	0
57	2D	10	Total 10	Mg 10	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
57	2E	7	Total 7	Mg 7	0	0
57	2F	7	Total 7	Mg 7	0	0
57	2G	1	Total 1	Mg 1	0	0
57	2N	1	Total 1	Mg 1	0	0
57	2O	2	Total 2	Mg 2	0	0
57	2P	3	Total 3	Mg 3	0	0
57	2Q	4	Total 4	Mg 4	0	0
57	2R	2	Total 2	Mg 2	0	0
57	2T	5	Total 5	Mg 5	0	0
57	2U	1	Total 1	Mg 1	0	0
57	2V	3	Total 3	Mg 3	0	0
57	2W	2	Total 2	Mg 2	0	0
57	2X	1	Total 1	Mg 1	0	0
57	2Y	1	Total 1	Mg 1	0	0
57	2Z	1	Total 1	Mg 1	0	0
57	20	1	Total 1	Mg 1	0	0
57	21	1	Total 1	Mg 1	0	0
57	23	1	Total 1	Mg 1	0	0
57	25	6	Total 6	Mg 6	0	0
57	26	1	Total 1	Mg 1	0	0
57	27	1	Total 1	Mg 1	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
57	28	3	Total Mg 3 3	0	0
57	2a	171	Total Mg 171 171	0	0
57	2d	2	Total Mg 2 2	0	0
57	2e	1	Total Mg 1 1	0	0
57	2f	1	Total Mg 1 1	0	0
57	2i	1	Total Mg 1 1	0	0
57	2j	1	Total Mg 1 1	0	0
57	2k	1	Total Mg 1 1	0	0
57	2l	3	Total Mg 3 3	0	0
57	2n	1	Total Mg 1 1	0	0
57	2q	1	Total Mg 1 1	0	0
57	2t	2	Total Mg 2 2	0	0
57	2v	2	Total Mg 2 2	0	0
57	2x	7	Total Mg 7 7	0	0

- Molecule 58 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
58	1A	1	Total K 1 1	0	0

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

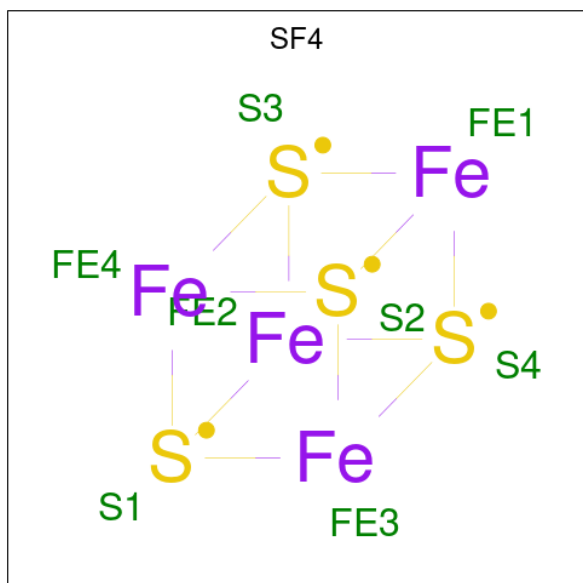
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
59	1Y	1	Total Zn 1 1	0	0
59	14	1	Total Zn 1 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
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		
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: Fe_4S_4).



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

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

- Molecule 61 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
61	1A	1729	Total	O	0	0
			1729	1729		
61	1B	58	Total	O	0	0
			58	58		
61	1D	23	Total	O	0	0
			23	23		
61	1E	27	Total	O	0	0
			27	27		
61	1F	15	Total	O	0	0
			15	15		
61	1G	5	Total	O	0	0
			5	5		
61	1H	2	Total	O	0	0
			2	2		
61	1I	1	Total	O	0	0
			1	1		
61	1N	7	Total	O	0	0
			7	7		
61	1O	7	Total	O	0	0
			7	7		
61	1P	20	Total	O	0	0
			20	20		
61	1Q	8	Total	O	0	0
			8	8		
61	1R	10	Total	O	0	0
			10	10		
61	1S	3	Total	O	0	0
			3	3		
61	1T	6	Total	O	0	0
			6	6		
61	1U	13	Total	O	0	0
			13	13		
61	1V	8	Total	O	0	0
			8	8		
61	1W	12	Total	O	0	0
			12	12		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
61	1X	4	Total 4	O 4	0	0
61	1Y	1	Total 1	O 1	0	0
61	1Z	1	Total 1	O 1	0	0
61	10	11	Total 11	O 11	0	0
61	11	8	Total 8	O 8	0	0
61	12	3	Total 3	O 3	0	0
61	13	6	Total 6	O 6	0	0
61	14	1	Total 1	O 1	0	0
61	15	6	Total 6	O 6	0	0
61	17	7	Total 7	O 7	0	0
61	18	9	Total 9	O 9	0	0
61	1a	211	Total 211	O 211	0	0
61	1b	1	Total 1	O 1	0	0
61	1i	1	Total 1	O 1	0	0
61	1l	2	Total 2	O 2	0	0
61	1q	3	Total 3	O 3	0	0
61	1v	4	Total 4	O 4	0	0
61	1w	2	Total 2	O 2	0	0
61	1x	19	Total 19	O 19	0	0
61	1z	1	Total 1	O 1	0	0
61	2A	974	Total 974	O 974	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
61	2B	20	Total	O	0	0
			20	20		
61	2D	18	Total	O	0	0
			18	18		
61	2E	15	Total	O	0	0
			15	15		
61	2F	10	Total	O	0	0
			10	10		
61	2I	1	Total	O	0	0
			1	1		
61	2N	1	Total	O	0	0
			1	1		
61	2O	2	Total	O	0	0
			2	2		
61	2P	14	Total	O	0	0
			14	14		
61	2Q	1	Total	O	0	0
			1	1		
61	2R	2	Total	O	0	0
			2	2		
61	2T	5	Total	O	0	0
			5	5		
61	2U	3	Total	O	0	0
			3	3		
61	2V	1	Total	O	0	0
			1	1		
61	2W	2	Total	O	0	0
			2	2		
61	2X	4	Total	O	0	0
			4	4		
61	2Z	2	Total	O	0	0
			2	2		
61	20	3	Total	O	0	0
			3	3		
61	21	9	Total	O	0	0
			9	9		
61	22	1	Total	O	0	0
			1	1		
61	23	2	Total	O	0	0
			2	2		
61	25	2	Total	O	0	0
			2	2		

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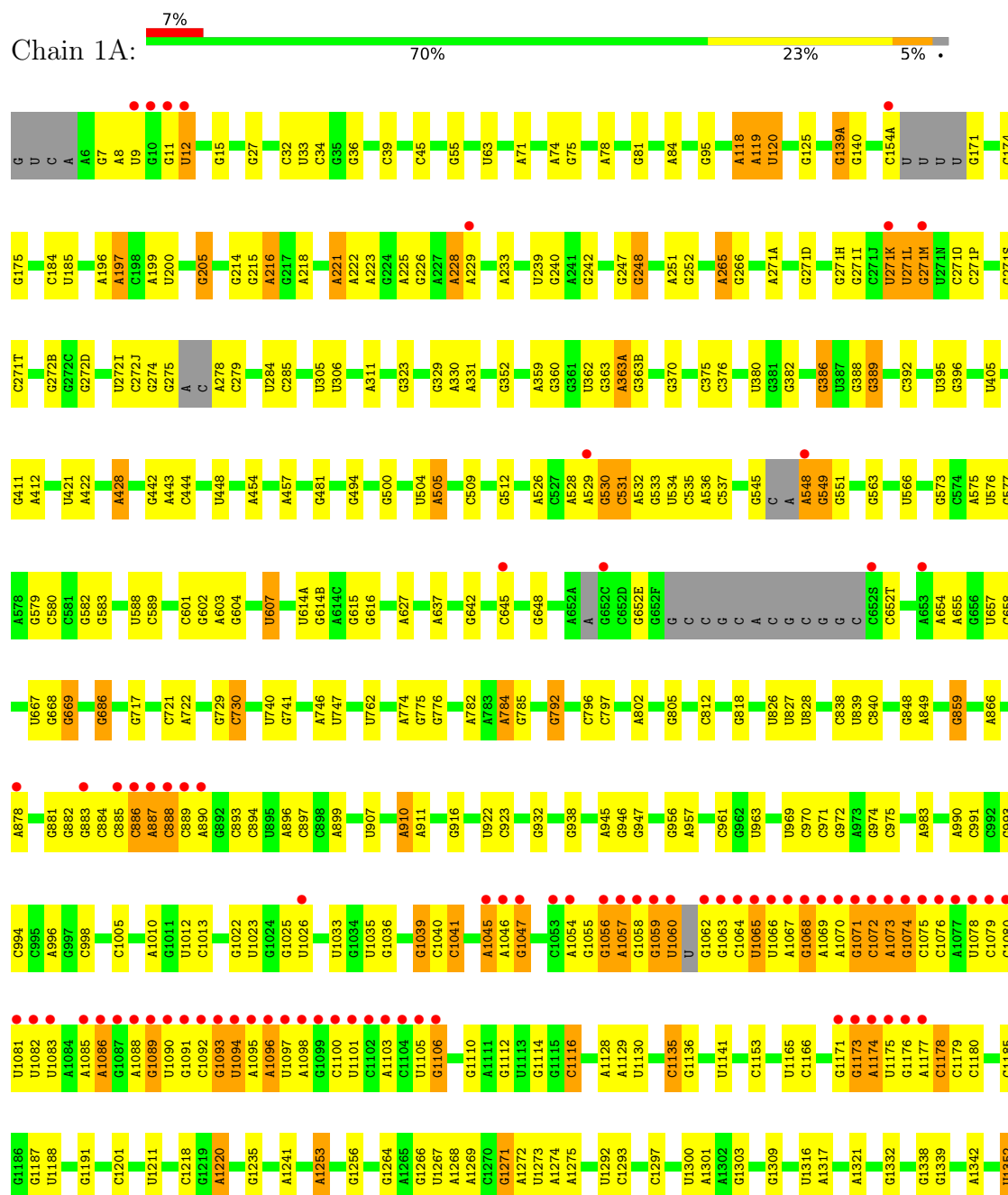
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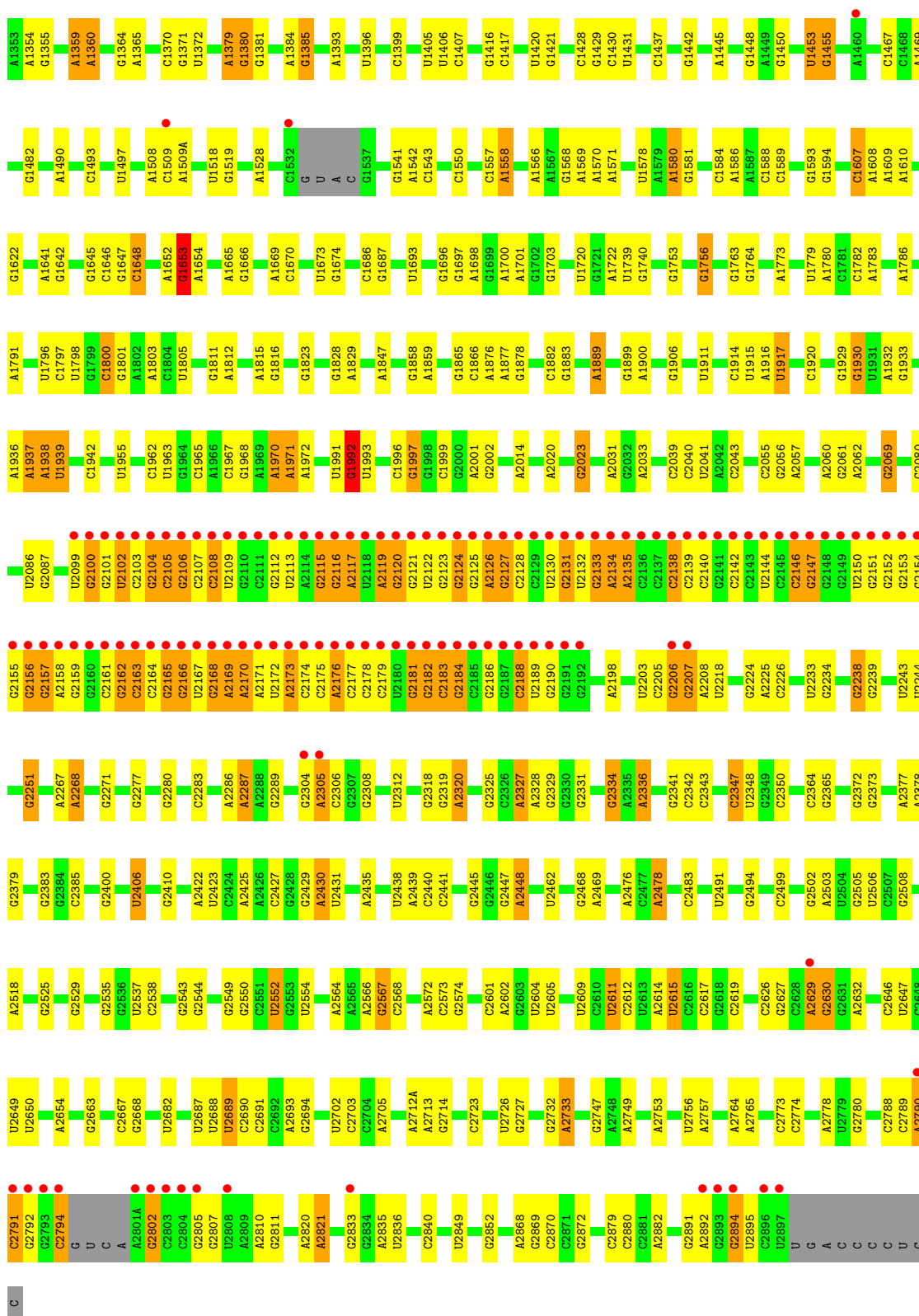
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
61	27	1	Total 1	O 1	0	0
61	28	5	Total 5	O 5	0	0
61	29	1	Total 1	O 1	0	0
61	2a	120	Total 120	O 120	0	0
61	2d	2	Total 2	O 2	0	0
61	2e	1	Total 1	O 1	0	0
61	2j	4	Total 4	O 4	0	0
61	2l	4	Total 4	O 4	0	0
61	2n	1	Total 1	O 1	0	0
61	2q	2	Total 2	O 2	0	0
61	2w	1	Total 1	O 1	0	0
61	2x	12	Total 12	O 12	0	0

3 Residue-property plots

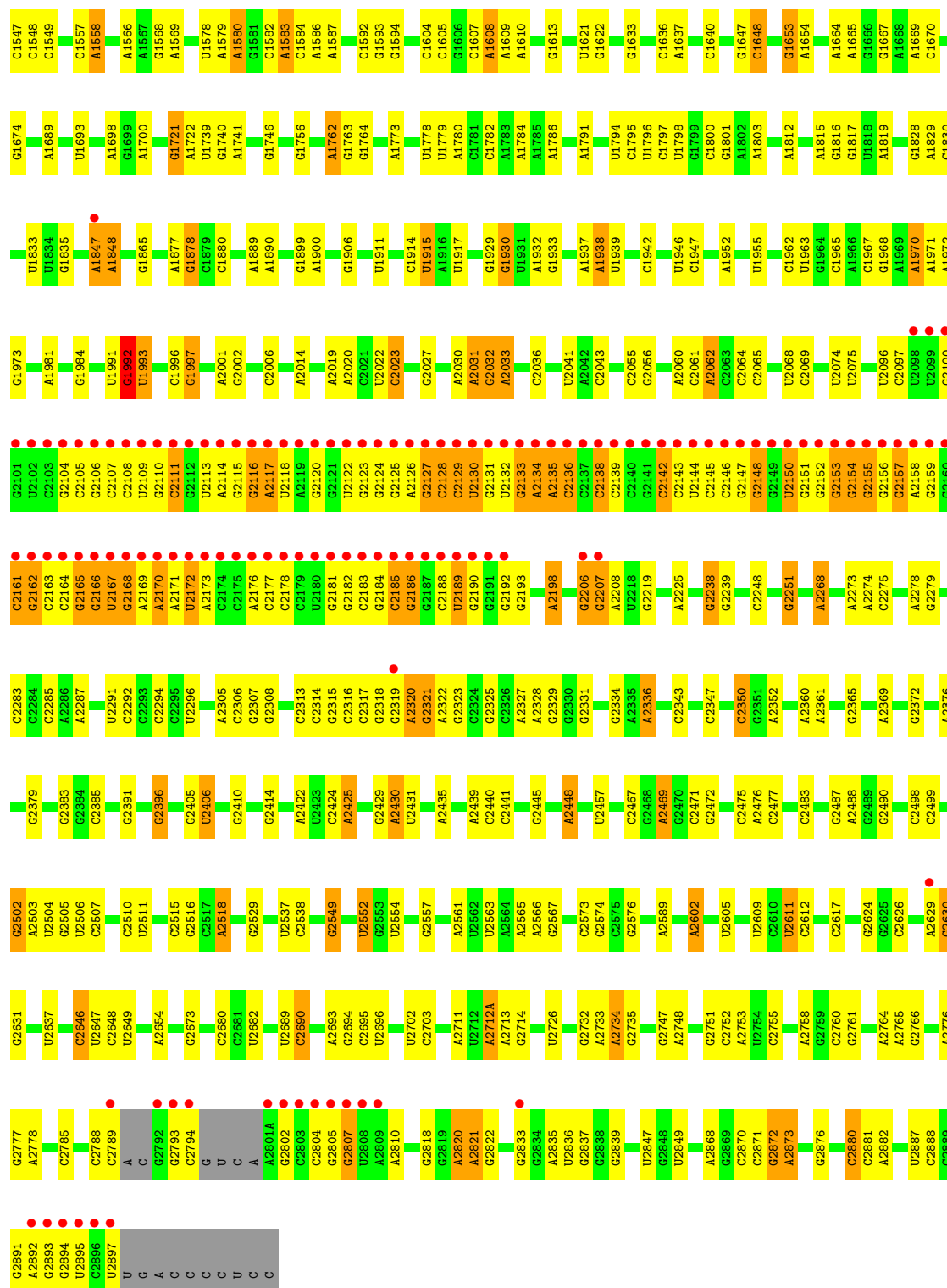
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

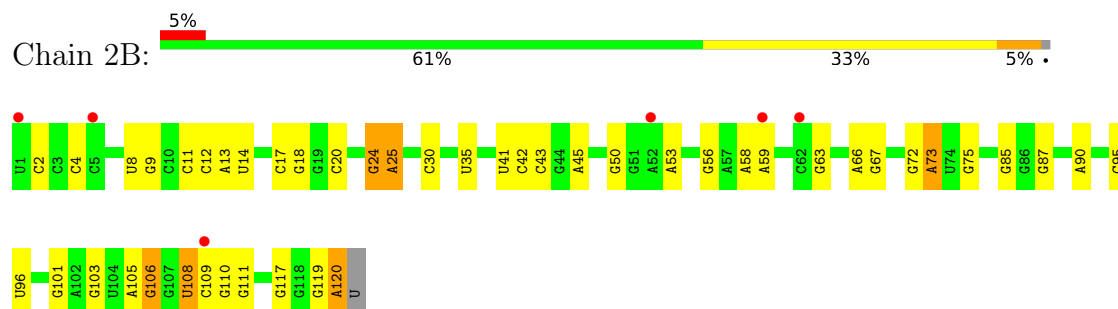




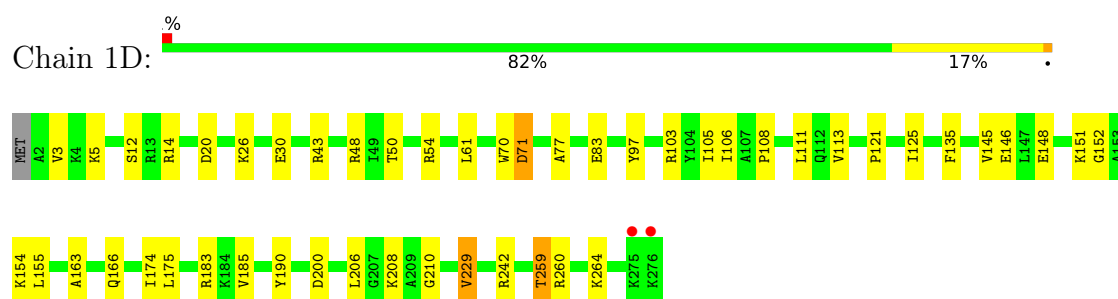




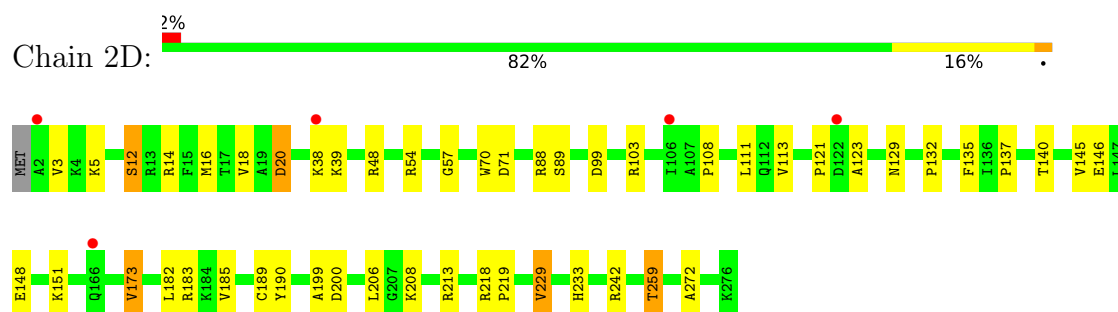
- Molecule 2: 5S Ribosomal RNA



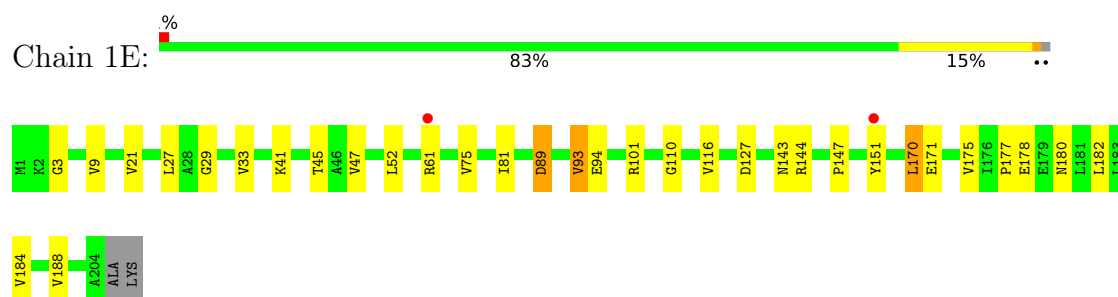
- Molecule 3: 50S ribosomal protein L2



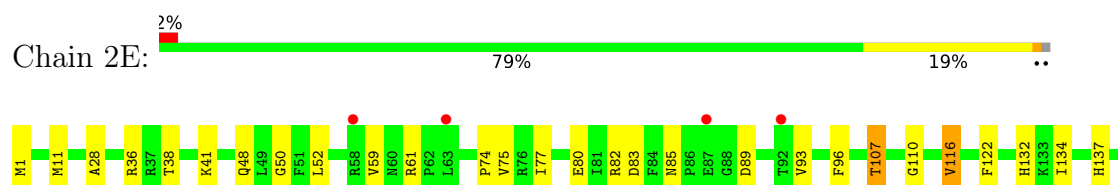
- Molecule 3: 50S ribosomal protein L2



- Molecule 4: 50S ribosomal protein L3



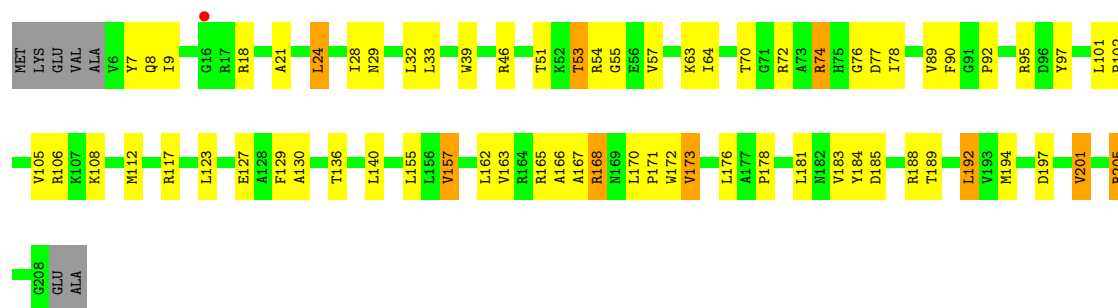
- Molecule 4: 50S ribosomal protein L3





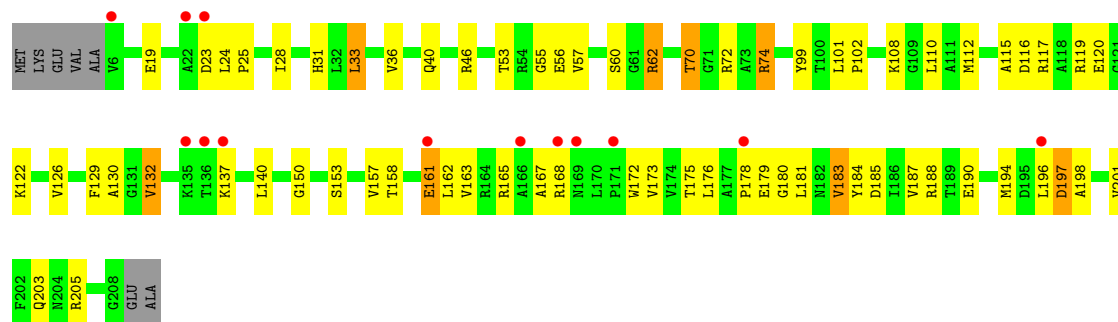
- Molecule 5: 50S ribosomal protein L4

Chain 1F: 64% 28%



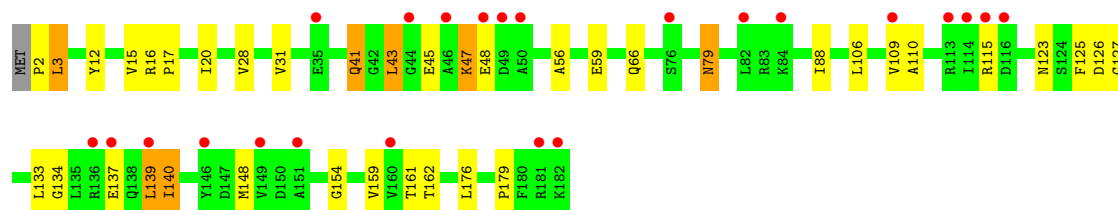
- Molecule 5: 50S ribosomal protein L4

Chain 2F: 6% 64% 29%



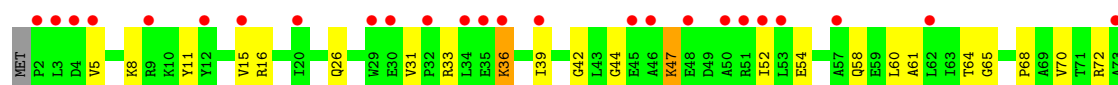
- Molecule 6: 50S ribosomal protein L5

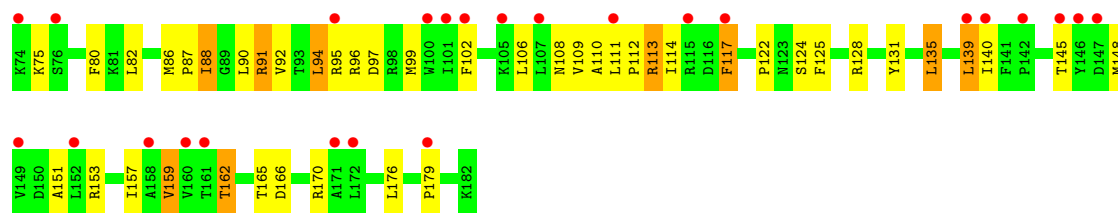
Chain 1G: 13% 78% 18%



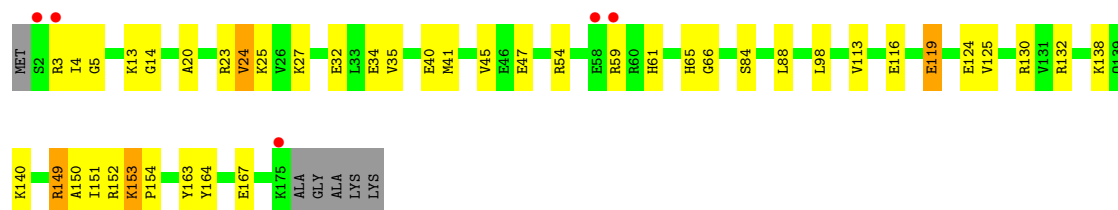
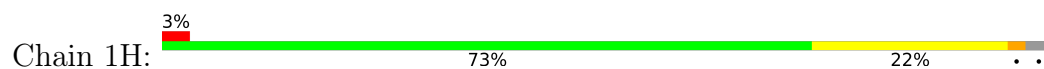
- Molecule 6: 50S ribosomal protein L5

Chain 2G: 27% 63% 31% 6%

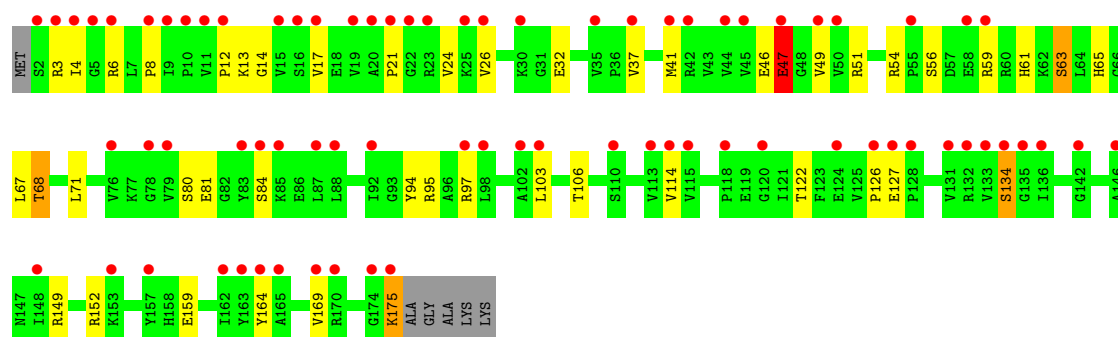
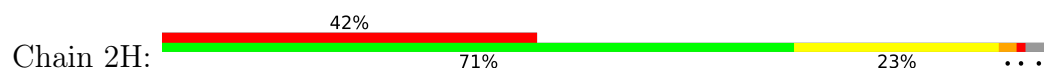




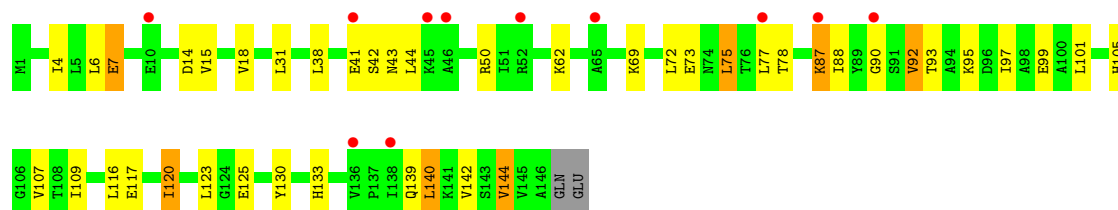
• Molecule 7: 50S ribosomal protein L6



• Molecule 7: 50S ribosomal protein L6

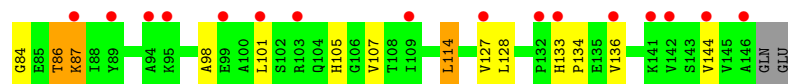


• Molecule 8: 50S ribosomal protein L9

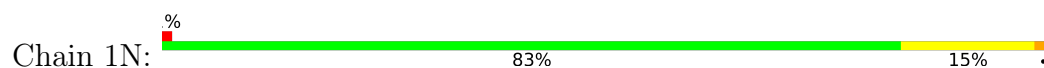


• Molecule 8: 50S ribosomal protein L9

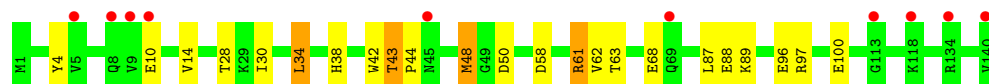
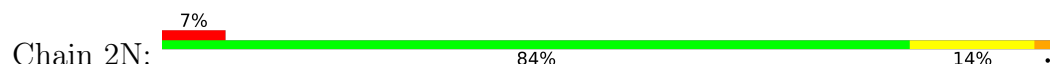




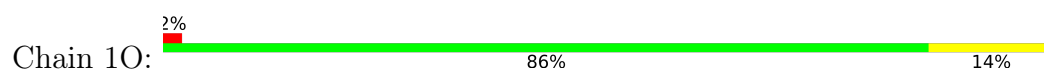
- Molecule 9: 50S ribosomal protein L13



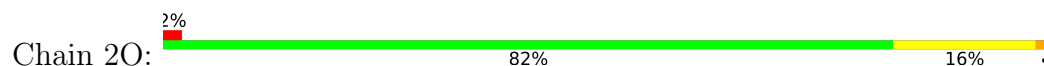
- Molecule 9: 50S ribosomal protein L13



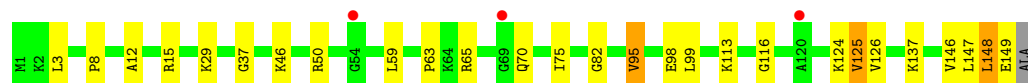
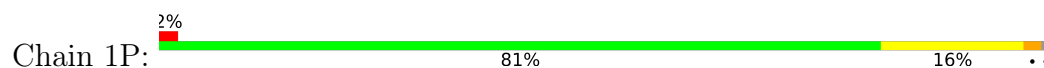
- Molecule 10: 50S ribosomal protein L14



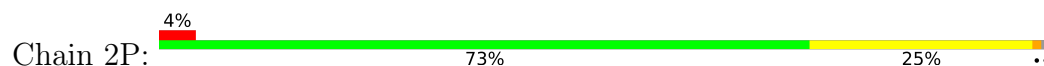
- Molecule 10: 50S ribosomal protein L14

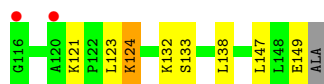


- Molecule 11: 50S ribosomal protein L15

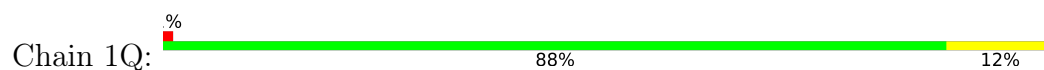


- Molecule 11: 50S ribosomal protein L15

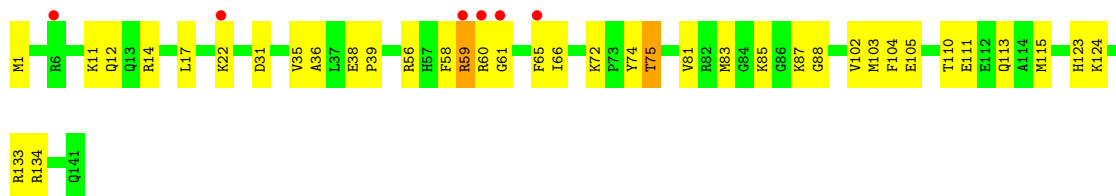
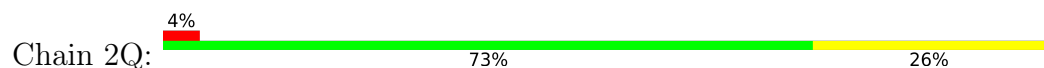




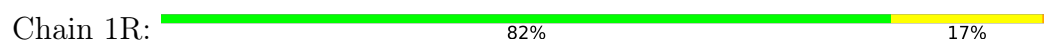
- Molecule 12: 50S ribosomal protein L16



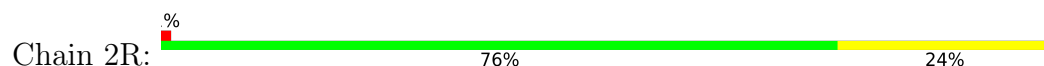
- Molecule 12: 50S ribosomal protein L16



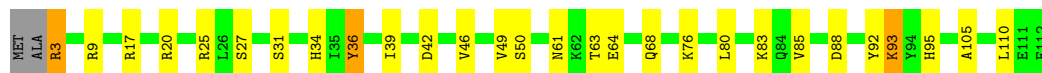
- Molecule 13: 50S ribosomal protein L17



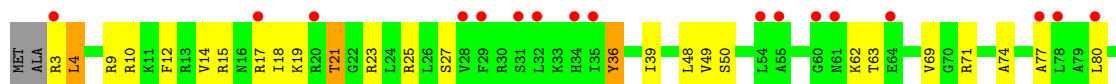
- Molecule 13: 50S ribosomal protein L17

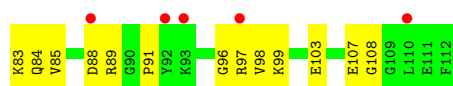


- Molecule 14: 50S ribosomal protein L18

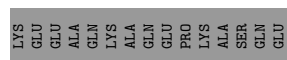
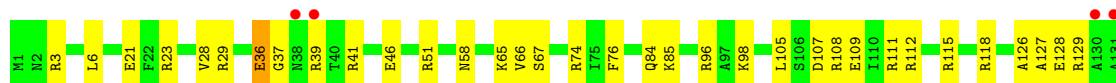


- Molecule 14: 50S ribosomal protein L18

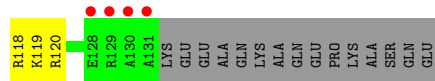
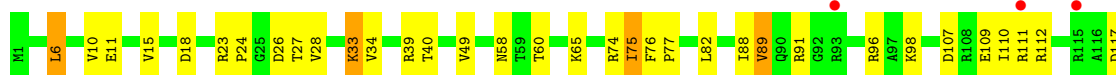




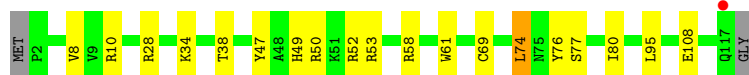
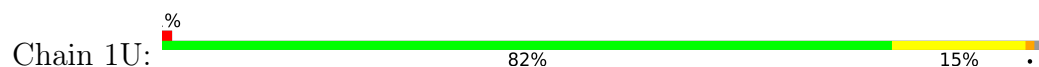
- Molecule 15: 50S ribosomal protein L19



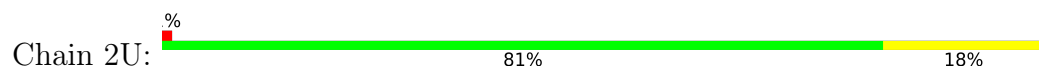
- Molecule 15: 50S ribosomal protein L19



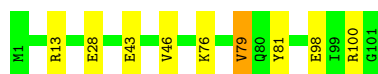
- Molecule 16: 50S ribosomal protein L20



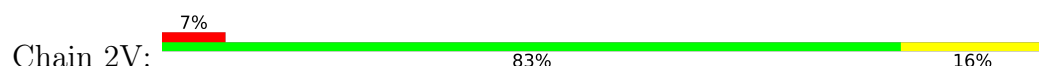
- Molecule 16: 50S ribosomal protein L20

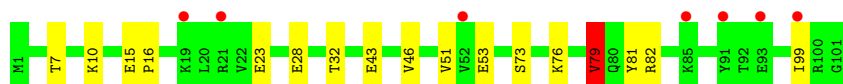


- Molecule 17: 50S ribosomal protein L21



- Molecule 17: 50S ribosomal protein L21





- Molecule 18: 50S ribosomal protein L22

Chain 1W: 90% 8% ..



- Molecule 18: 50S ribosomal protein L22

Chain 2W: 78% 19% ..



- Molecule 19: 50S ribosomal protein L23

Chain 1X: 76% 21% ..



- Molecule 19: 50S ribosomal protein L23

Chain 2X: 77% 20% ..



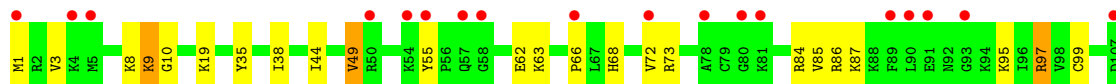
- Molecule 20: 50S ribosomal protein L24

Chain 1Y: 80% 15% ..



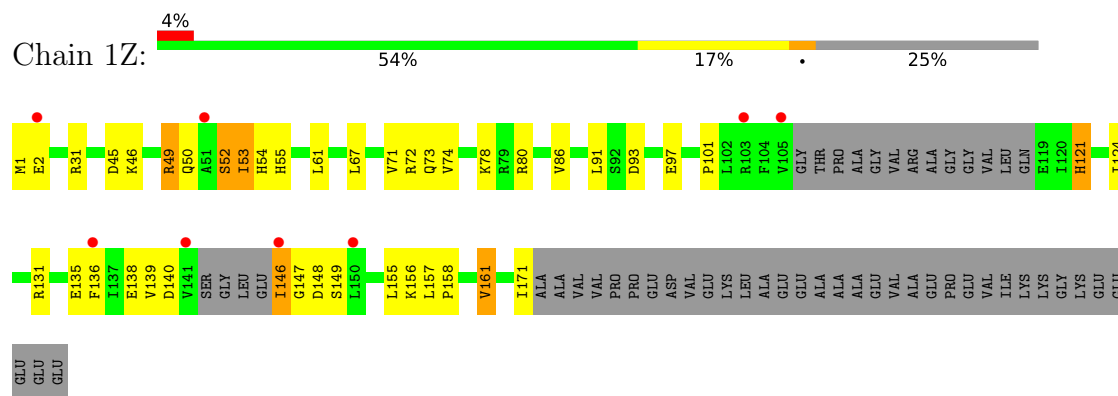
- Molecule 20: 50S ribosomal protein L24

Chain 2Y: 75% 19% ..

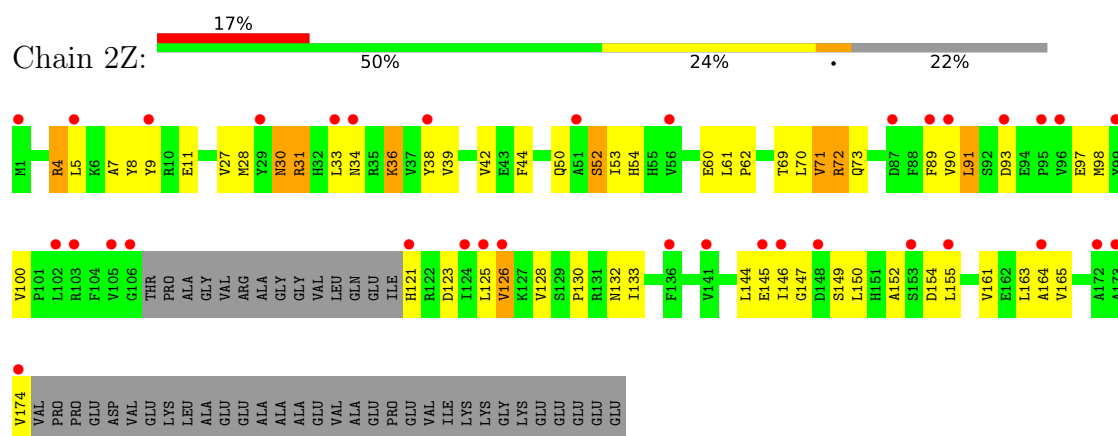


THR
GLU
GLU

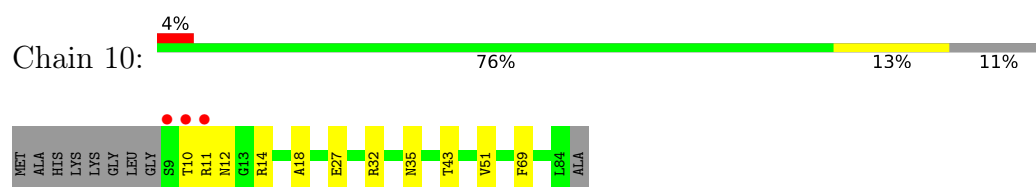
- Molecule 21: 50S ribosomal protein L25



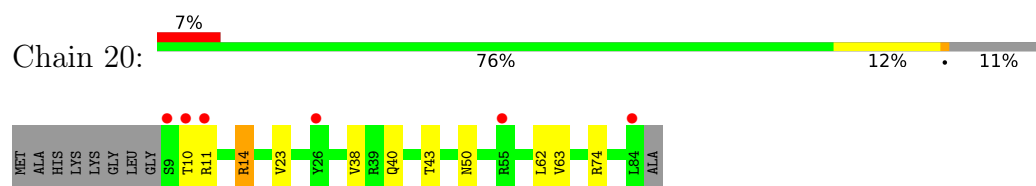
- Molecule 21: 50S ribosomal protein L25



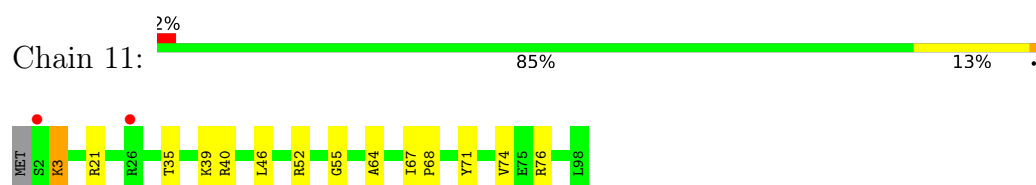
- Molecule 22: 50S ribosomal protein L27



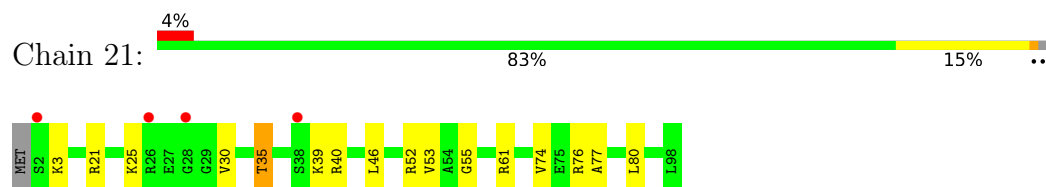
- Molecule 22: 50S ribosomal protein L27



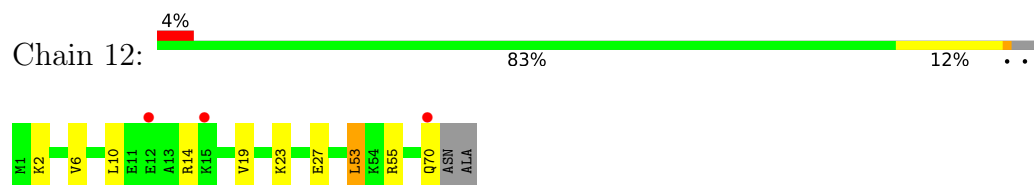
- Molecule 23: 50S ribosomal protein L28



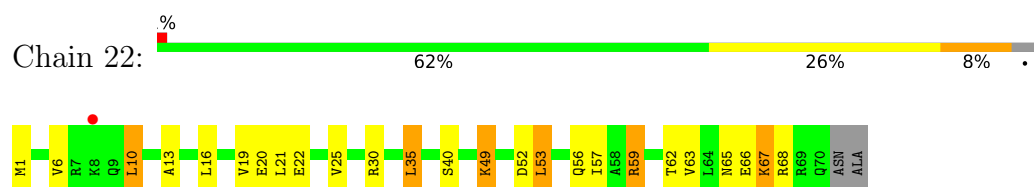
- Molecule 23: 50S ribosomal protein L28



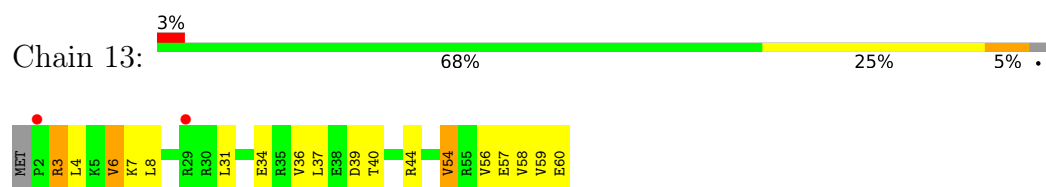
- Molecule 24: 50S ribosomal protein L29



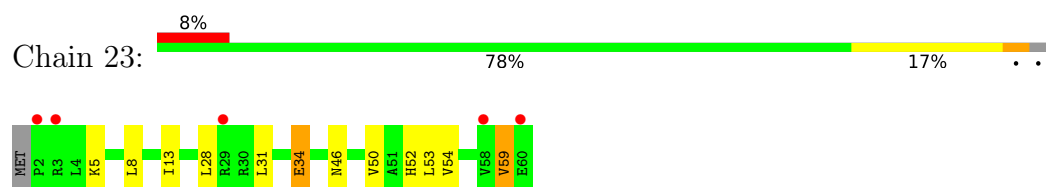
- Molecule 24: 50S ribosomal protein L29



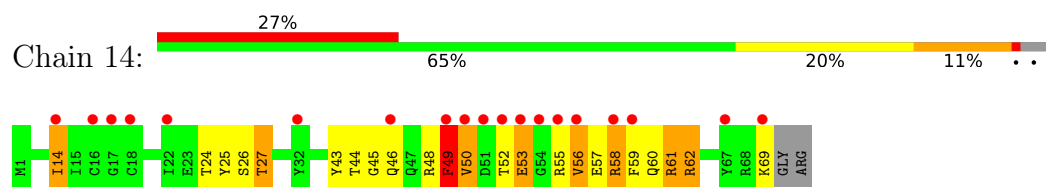
- Molecule 25: 50S ribosomal protein L30



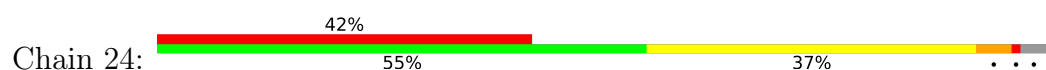
- Molecule 25: 50S ribosomal protein L30

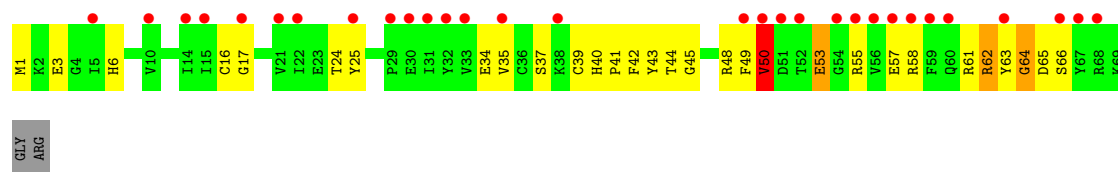


- Molecule 26: 50S ribosomal protein L31



- Molecule 26: 50S ribosomal protein L31

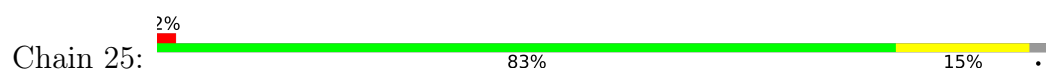




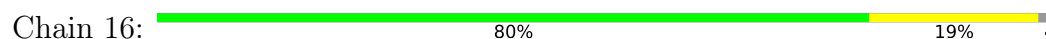
- Molecule 27: 50S ribosomal protein L32



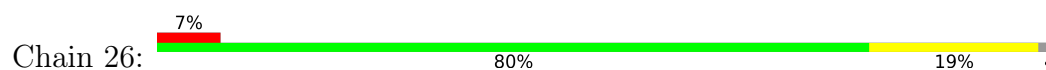
- Molecule 27: 50S ribosomal protein L32



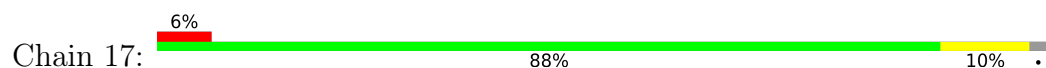
- Molecule 28: 50S ribosomal protein L33



- Molecule 28: 50S ribosomal protein L33



- Molecule 29: 50S ribosomal protein L34

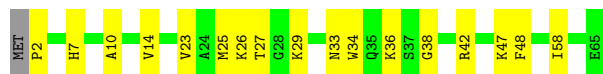


- Molecule 29: 50S ribosomal protein L34



- Molecule 30: 50S ribosomal protein L35

Chain 18:  72% 26% .



- Molecule 30: 50S ribosomal protein L35

Chain 28:  77% 20% . .



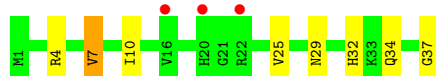
- Molecule 31: 50S ribosomal protein L36

Chain 19:  86% 14%



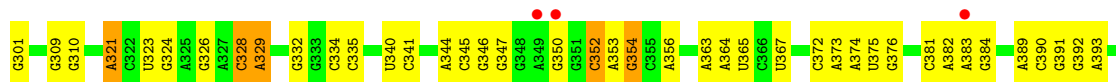
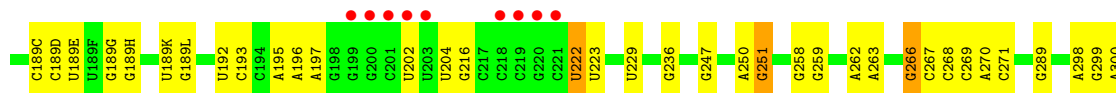
- Molecule 31: 50S ribosomal protein L36

Chain 29:  78% 19% .



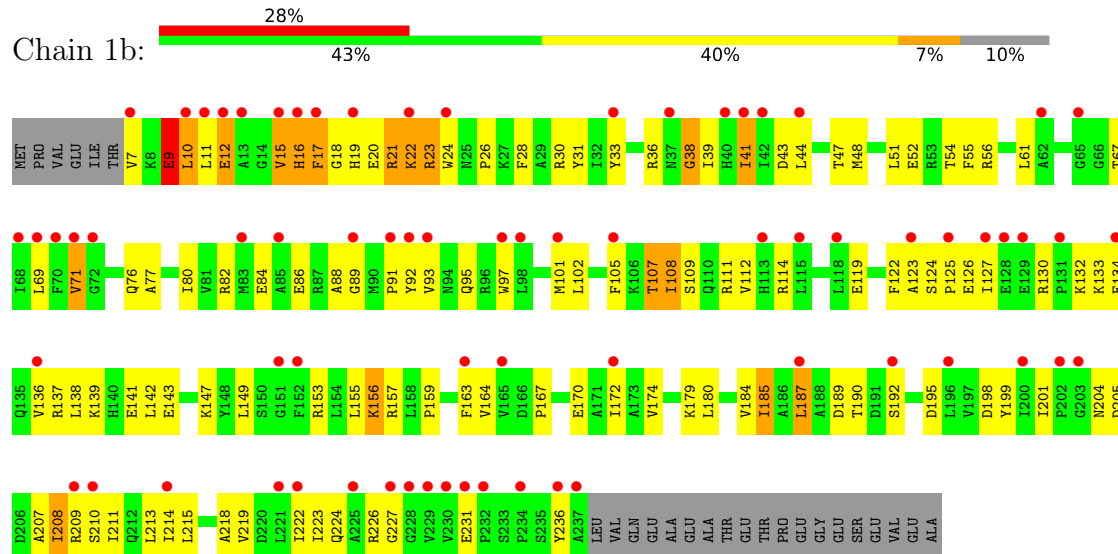
- Molecule 32: 16S Ribosomal RNA

Chain 1a:  59% 33% 7% .

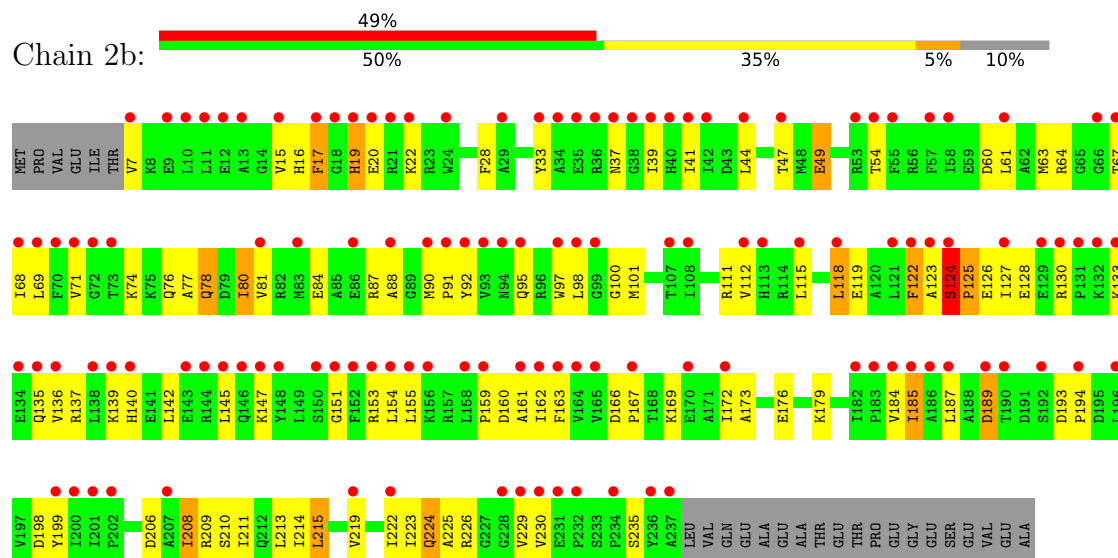


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A1499	C1369	A1225	U1150	U1085	U1020	G703	A576	G475	C201
	G1370	C1226	U1151	U1086	G1021	G577	G577	G476	U202
A1503	U1371	A1227	A1152	G1089	G1022	G713	G577	G477	U203
G1504	U1372	C1228	A1157	U1090	G1024	G714	A583	U358	U204
G1505	G1373	U1234	U1158	U1091	U1025	A715	G584	U359	G216
U1506	A1374	U1235	U1159	A1092	G1026		G584	A482	G217
A1507	U1375	A1236	G1160	A1093	C1027	U723	G595	C483	C218
	U1376	C1237	G1161	G1094	C1028	G724	C596	G485	C219
U1510	A1377	A1238	G1162	U1095	C1029	A728	G597	U367	G220
G1511	U1378	A1239	C1163	C1096	C1030	A729	A495	C372	C221
U1512	G1379	C1164	G1164	C1097	G1030A		A496	U222	U223
A1513	U1380	U1240	A1168	C1098	C1030B		A498		
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C1515	G1310	C1242	A1170	C1100	A1030D		A509	A383	
G1516	U1313	C1243	A1171	A1101	G1031		A510	G384	
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G1388	U1315		C1172	C1103	G1033		G505	G392	G248
G1389	G1316	A1248	G1173	G1104	U1034		A509	A393	U249
U1390	G1317	A1249	G1174	G1105	A1035		A510	A250	G251
U1391	C1317	A1250	G1175	G1106	G1036		C612	A397	
	A1320	A1251	G1176	A1111	C1037		G616	C398	G254
C1397	C1321	A1252	G1177	C1112	U1038		G629	G406	G255
A1398	C1322	G1254	G1178	C1113	C1039		G630	G406	U256
C1399	G1323	G1255	A1179	C1117	U1040		G631	G412	G258
G1400	A1324	U1256	A1180	G1116	A1041		G631	G413	
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C1403	C1326	U1258	G1182	G1118	C1043		G652	C422	C287
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	U1328	C1259	G1184	C1120	C1045		G654	G424	C289
C1407	A1329	C1260	G1187	U1121	A1046		G655	G425	G289
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G1422	A1332	C1263	G1191	G1124	G1057		G658	A298	A298
G1423	G1334	G1265	A1191	U1125	G1058		G659	G299	G299
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G1442	G1340	G1272	A1203	C1130	U1062		G664	A321	A321
G1442A	A1341	G1273	U1204	G1131	C1063		G665	C442	G326
A1442B	A1342	G1274	U1205	C1132	G1064		G665	A448	A327
	G1347	A1275	G1206	G1133	U1065		G666	A452	C328
U1446	U1348	C1276	G1207	G1134	C1066		G667	A452	A329
A1447	A1349	G1277	G1207	U1135	U1067		G673	C455	G332
C1452	C1352	U1278	U1211	U1136	C1068		G674	C455	G332
G1456	G1353	A1280	U1212	C1137	U1069		G674	C456	C335
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C1466	C1359	G1283	G1215	C1140	G1010		G677	C458	C345
G1467	A1360	C1284	G1216	C1141	U1011		G677	C458	
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	C1363	U1286	C1218	G1143	U1013		G677	C458	
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G1365	G1365	G1221	G1221	A1146	A1016		G677	C458	
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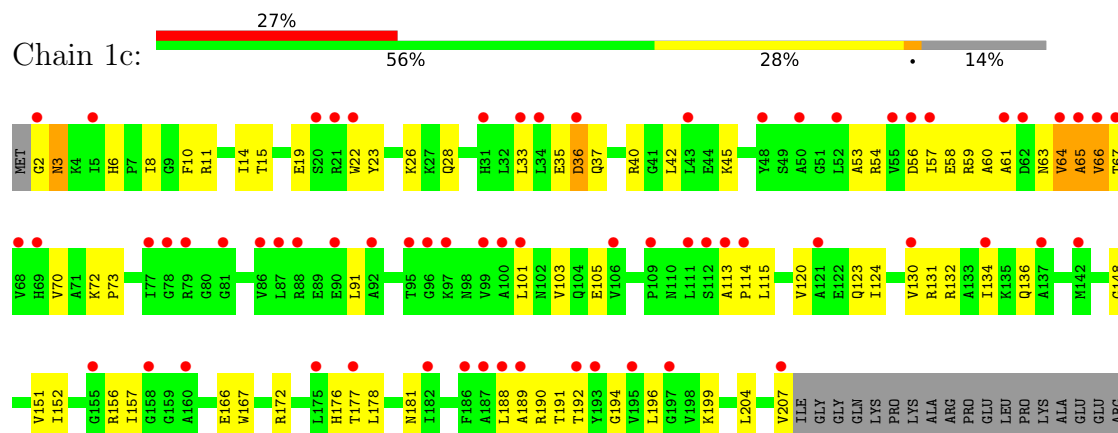
• Molecule 33: 30S ribosomal protein S2

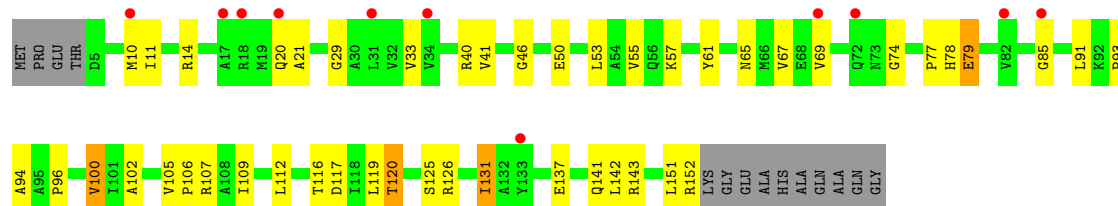


• Molecule 33: 30S ribosomal protein S2

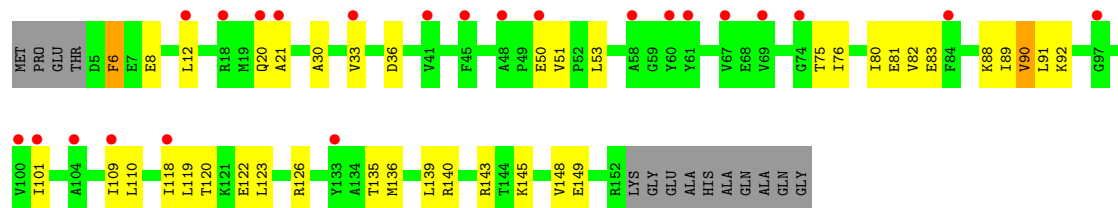


• Molecule 34: 30S ribosomal protein S3





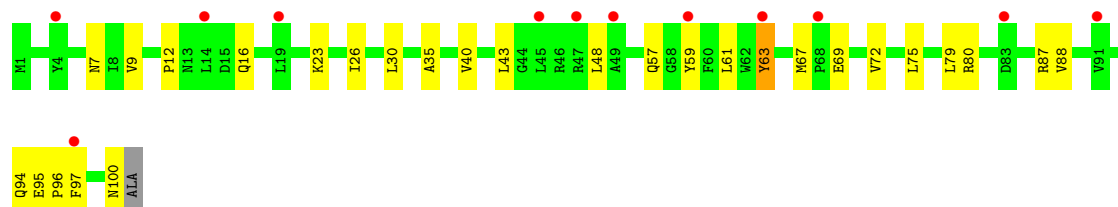
- Molecule 36: 30S ribosomal protein S5



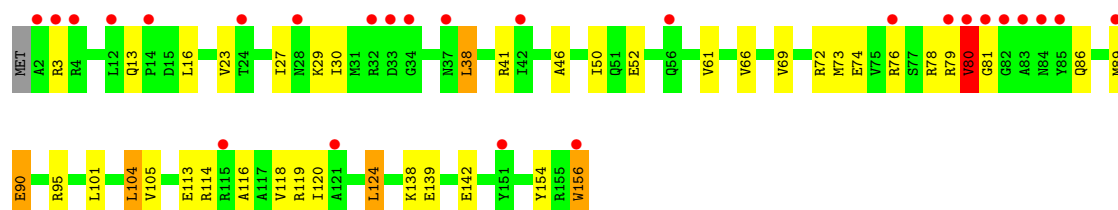
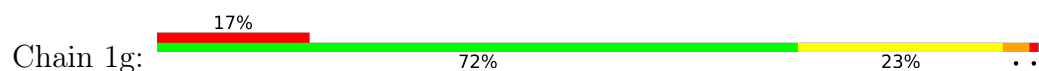
- Molecule 37: 30S ribosomal protein S6



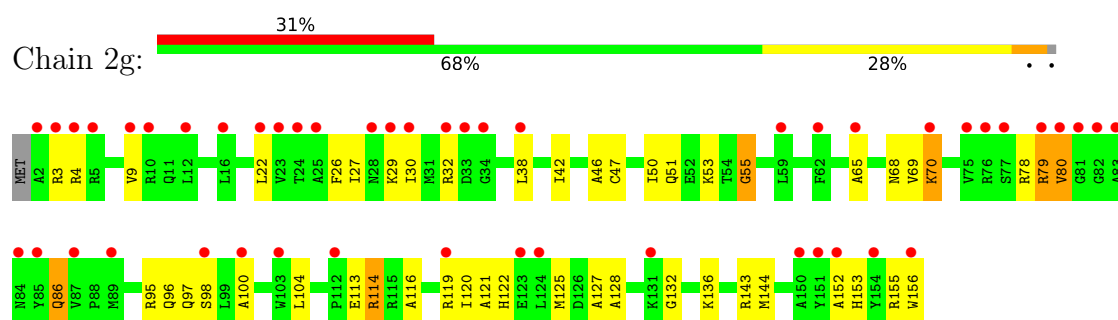
- Molecule 37: 30S ribosomal protein S6



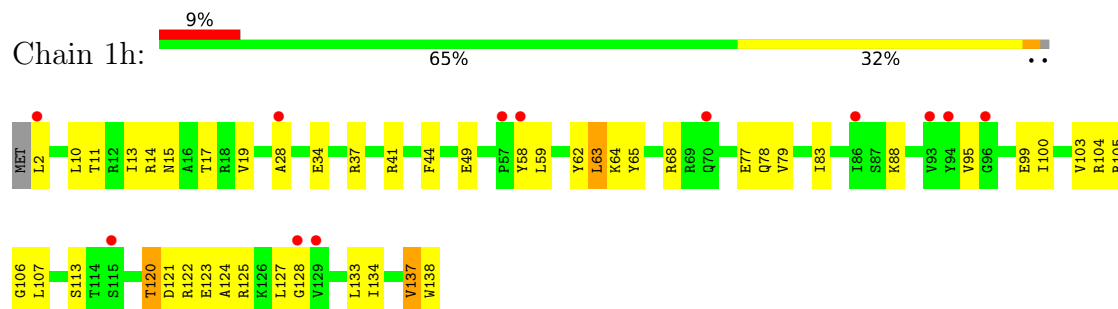
- Molecule 38: 30S ribosomal protein S7



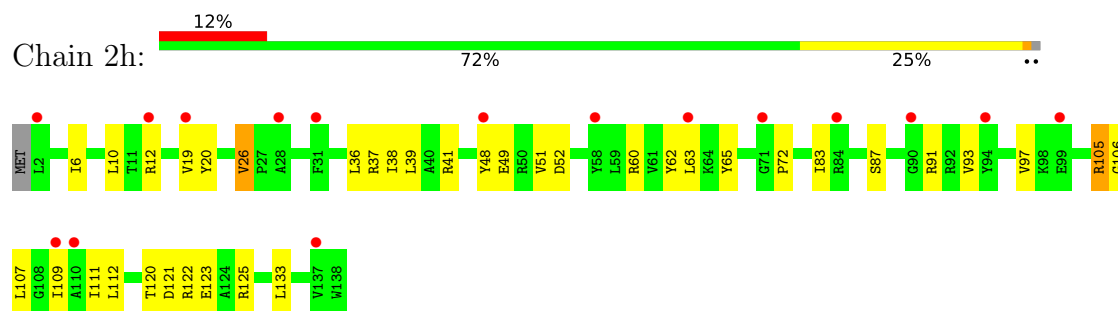
- Molecule 38: 30S ribosomal protein S7



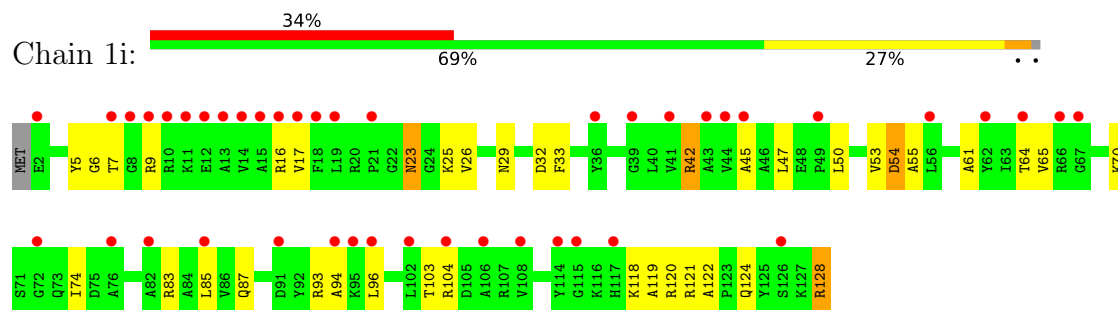
• Molecule 39: 30S ribosomal protein S8



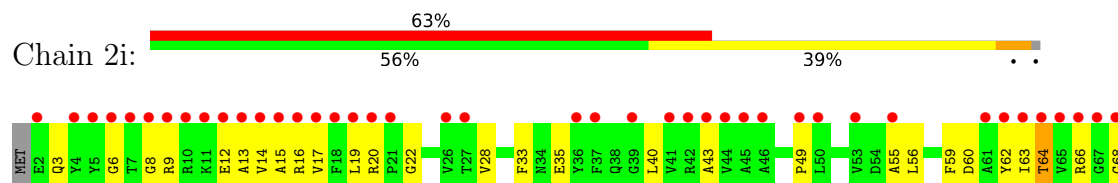
• Molecule 39: 30S ribosomal protein S8

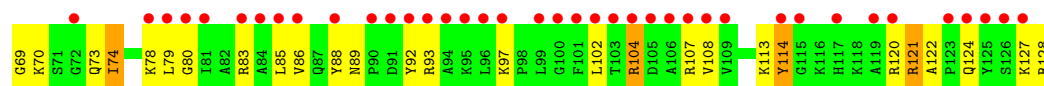


• Molecule 40: 30S ribosomal protein S9

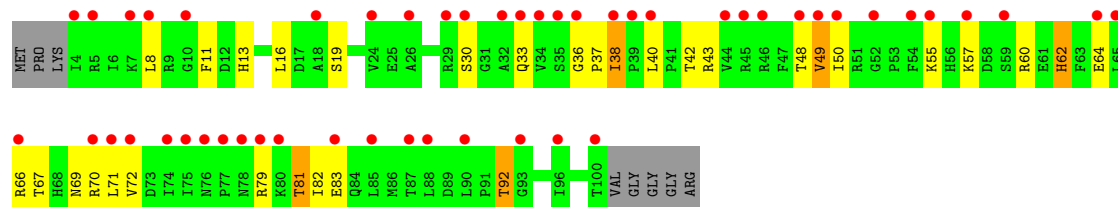


• Molecule 40: 30S ribosomal protein S9

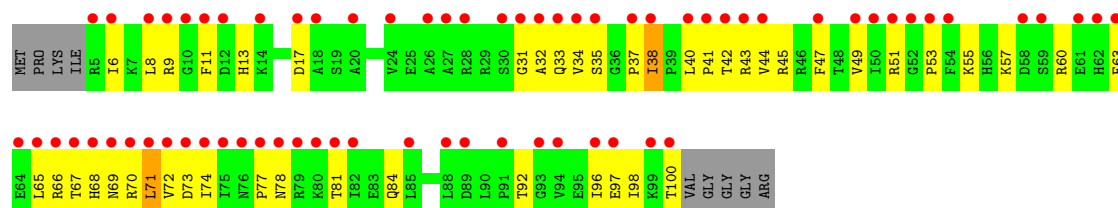




- Molecule 41: 30S ribosomal protein S10



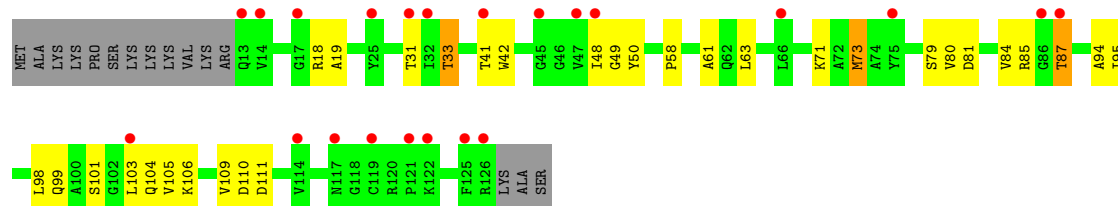
- Molecule 41: 30S ribosomal protein S10



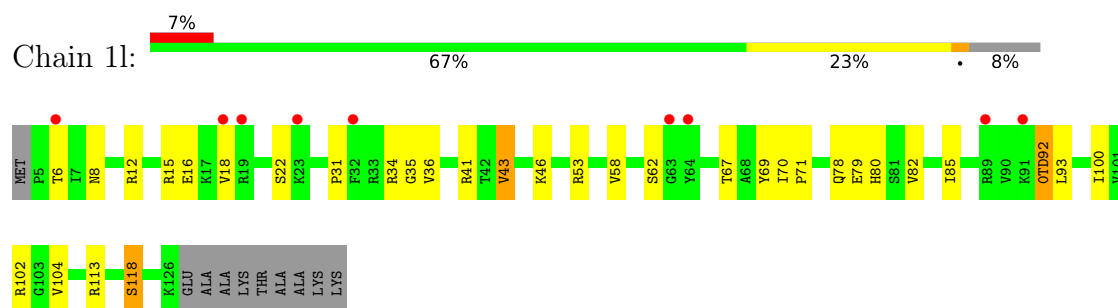
- Molecule 42: 30S ribosomal protein S11



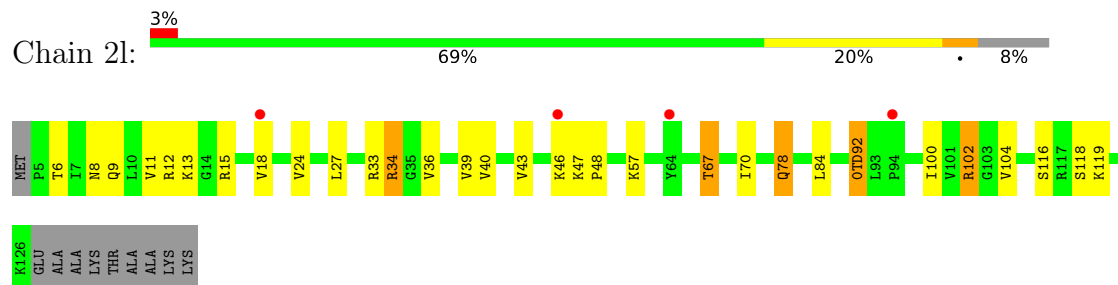
- Molecule 42: 30S ribosomal protein S11



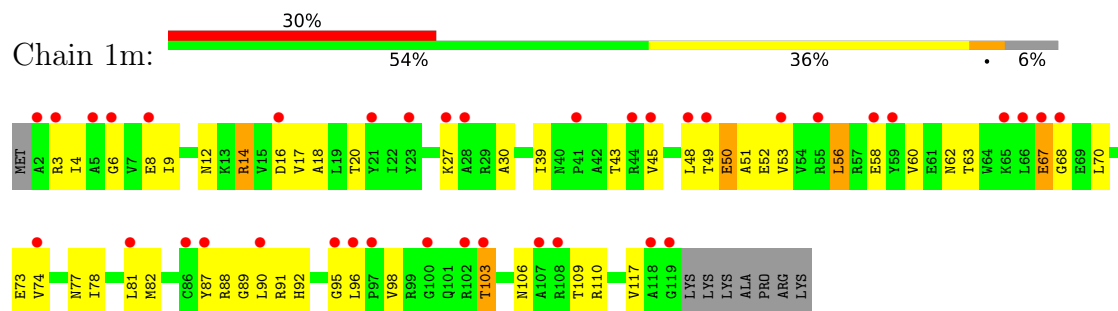
- Molecule 43: 30S ribosomal protein S12



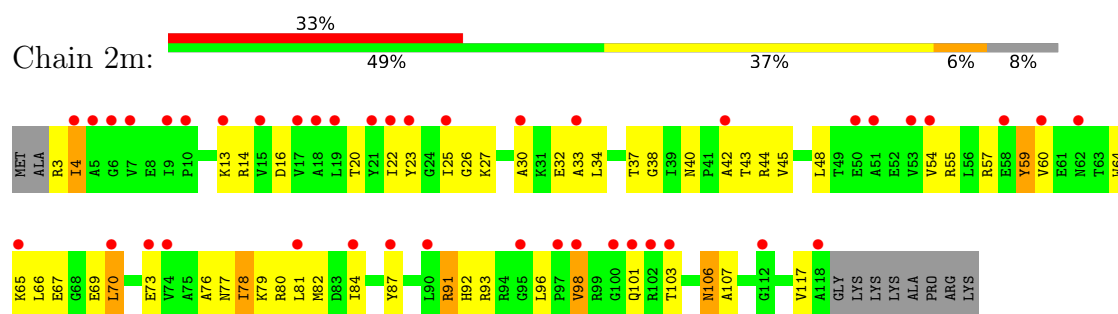
- Molecule 43: 30S ribosomal protein S12



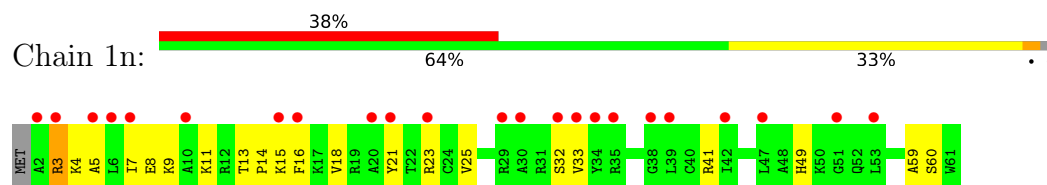
- Molecule 44: 30S ribosomal protein S13



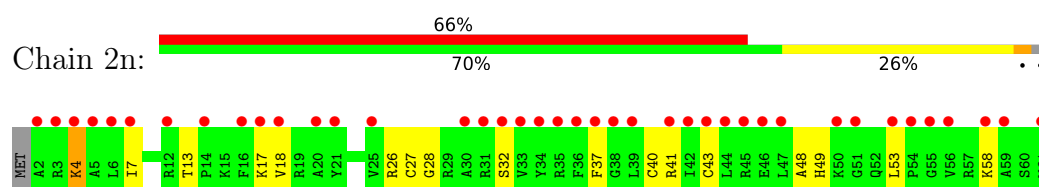
- Molecule 44: 30S ribosomal protein S13



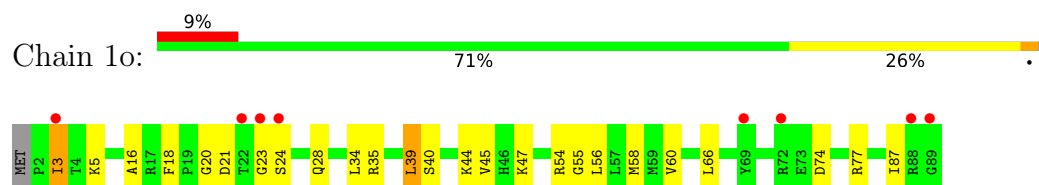
- Molecule 45: 30S ribosomal protein S14 type Z



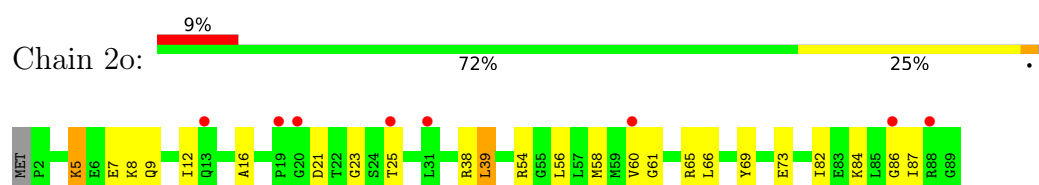
- Molecule 45: 30S ribosomal protein S14 type Z



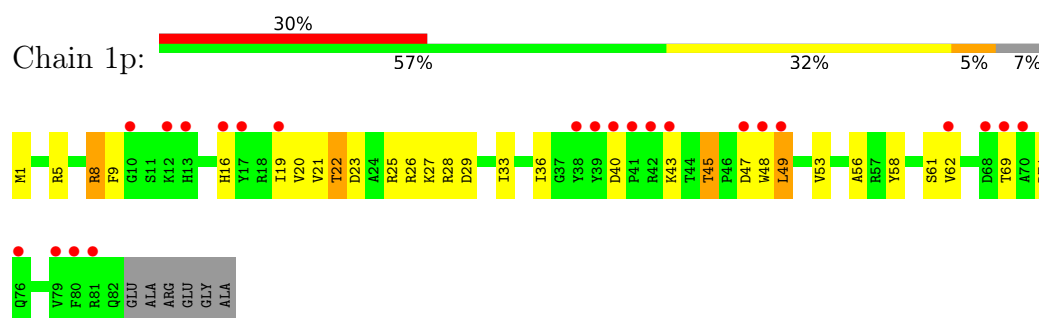
- Molecule 46: 30S ribosomal protein S15



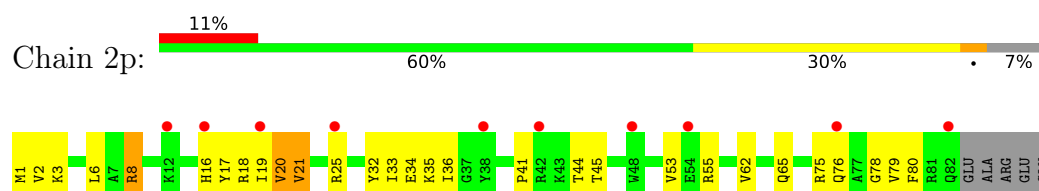
- Molecule 46: 30S ribosomal protein S15



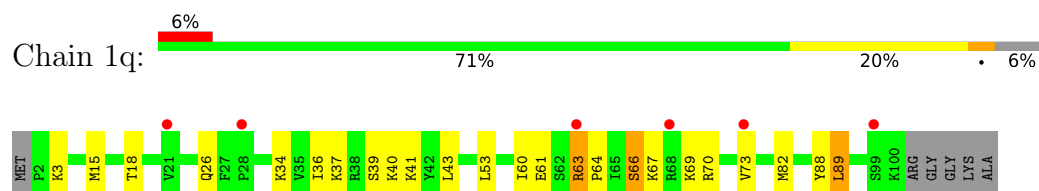
- Molecule 47: 30S ribosomal protein S16



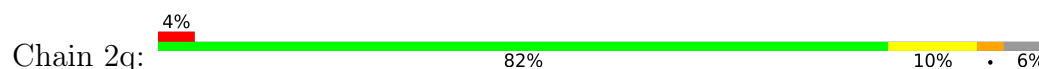
- Molecule 47: 30S ribosomal protein S16

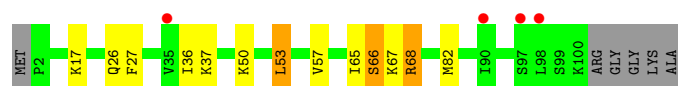


- Molecule 48: 30S ribosomal protein S17



- Molecule 48: 30S ribosomal protein S17

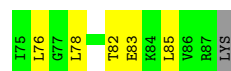
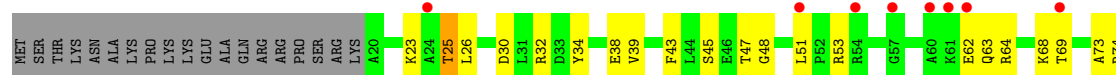




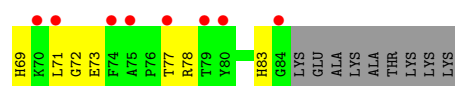
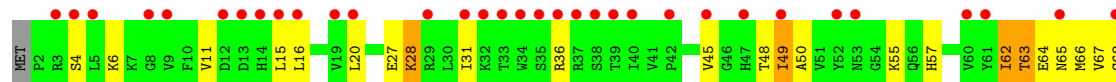
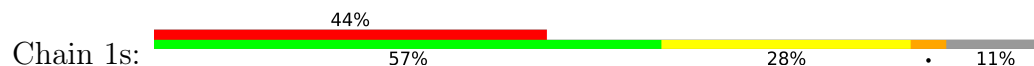
- Molecule 49: 30S ribosomal protein S18



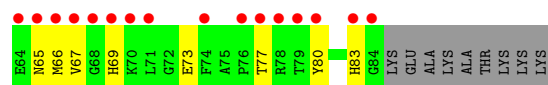
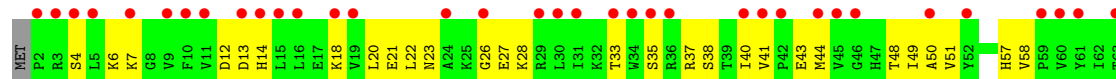
- Molecule 49: 30S ribosomal protein S18



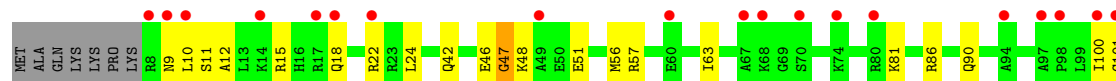
- Molecule 50: 30S ribosomal protein S19

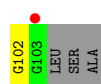


- Molecule 50: 30S ribosomal protein S19

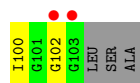
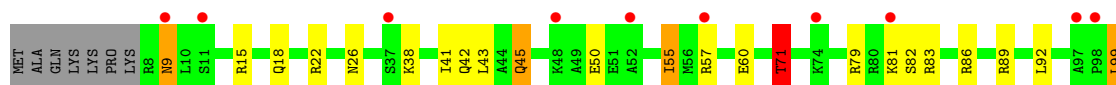


- Molecule 51: 30S ribosomal protein S20

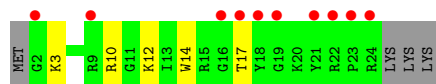
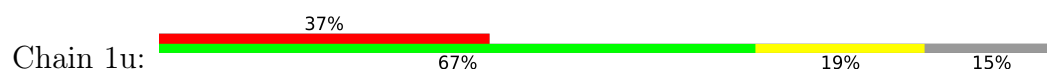




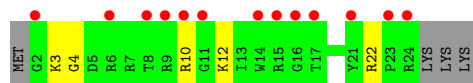
- Molecule 51: 30S ribosomal protein S20



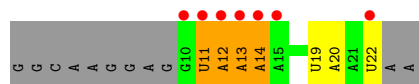
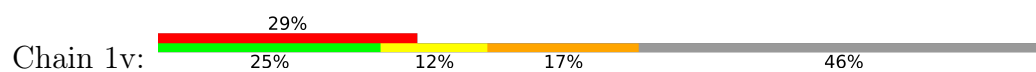
- Molecule 52: 30S ribosomal protein Thx



- Molecule 52: 30S ribosomal protein Thx



- Molecule 53: CYS-Stop mRNA

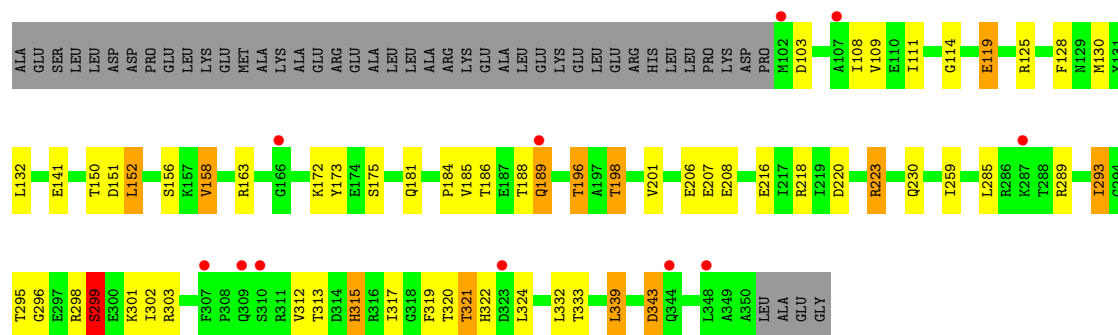


- Molecule 53: CYS-Stop mRNA

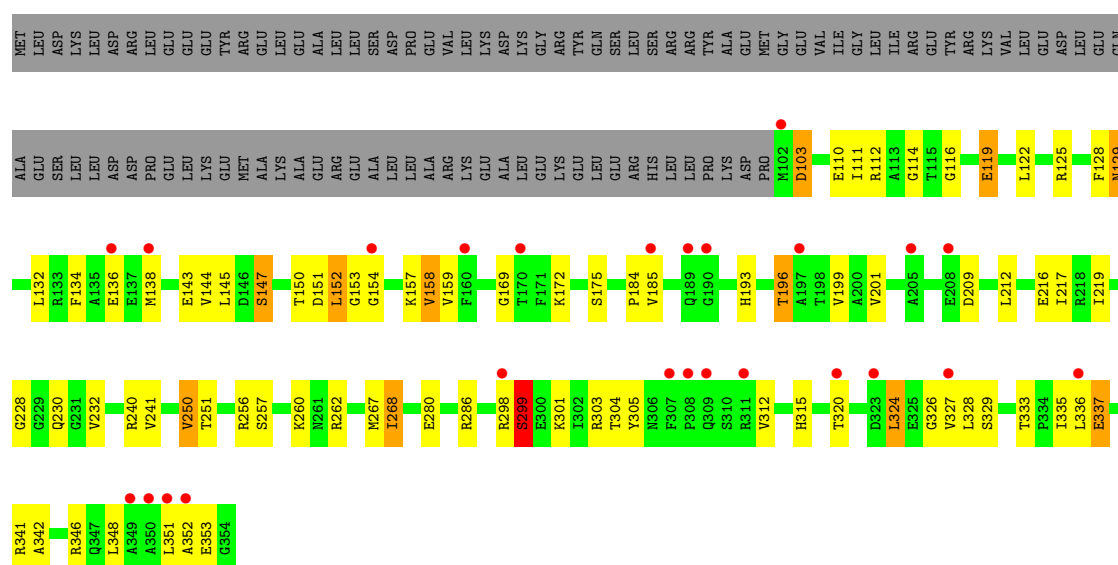


- Molecule 54: Peptide chain release factor 1

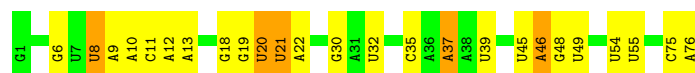




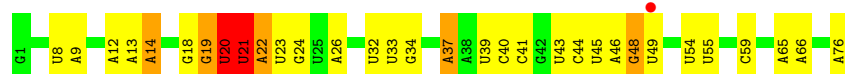
• Molecule 54: Peptide chain release factor 1



• Molecule 55: P-site Peptidyl-tRNA fMEAAAKC-tRNA_{cys} RNA-part



• Molecule 55: P-site Peptidyl-tRNA fMEAAAKC-tRNA_{cys} RNA-part

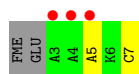
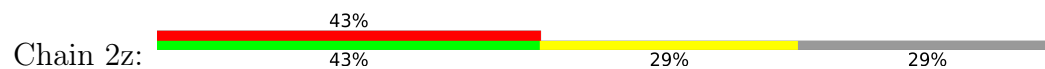


• Molecule 56: P-site Peptidyl-tRNA fMEAAAKC-tRNA_{cys} Peptide-part





- Molecule 56: P-site Peptidyl-tRNA fMEAAAKC-tRNAcys Peptide-part



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	210.49Å 452.41Å 626.59Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	366.79 – 2.70 366.79 – 2.70	Depositor EDS
% Data completeness (in resolution range)	99.4 (366.79-2.70) 99.5 (366.79-2.70)	Depositor EDS
R_{merge}	0.24	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.09 (at 2.69Å)	Xtriage
Refinement program	PHENIX 1.8.2	Depositor
R, R_{free}	0.218 , 0.262 0.216 , 0.259	Depositor DCC
R_{free} test set	80354 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	46.0	Xtriage
Anisotropy	0.102	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 138.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.43$, $\langle L^2 \rangle = 0.25$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.86	EDS
Total number of atoms	296409	wwPDB-VP
Average B, all atoms (Å ²)	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.62% 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: 2MA, MG, OMU, OMG, 2MG, K, OMC, 5MU, MA6, ZN, 5MC, SF4, PSU, M2G, MIA, UR3, 8AN, H2U, 4OC, G7M, 0TD, 4SU

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	0.27	0/69011	0.45	3/107720 (0.0%)
1	2A	0.21	0/67295	0.40	3/105042 (0.0%)
2	1B	0.21	0/2882	0.39	0/4494
2	2B	0.18	0/2879	0.35	0/4487
3	1D	0.26	0/2186	0.49	0/2944
3	2D	0.23	0/2186	0.45	0/2944
4	1E	0.26	0/1592	0.49	0/2149
4	2E	0.21	0/1592	0.46	0/2149
5	1F	0.25	0/1619	0.50	0/2193
5	2F	0.21	0/1615	0.42	0/2188
6	1G	0.21	0/1448	0.45	0/1957
6	2G	0.20	0/1453	0.46	0/1963
7	1H	0.22	0/1356	0.43	0/1834
7	2H	0.19	0/1356	0.38	0/1834
8	1I	0.19	0/1112	0.39	0/1514
8	2I	0.20	0/1079	0.39	0/1475
9	1N	0.25	0/1144	0.44	0/1543
9	2N	0.18	0/1144	0.39	0/1543
10	1O	0.25	0/943	0.44	0/1269
10	2O	0.22	0/943	0.44	0/1269
11	1P	0.27	0/1152	0.51	0/1533
11	2P	0.20	0/1152	0.45	0/1533
12	1Q	0.28	0/1143	0.51	0/1527
12	2Q	0.20	0/1143	0.42	0/1527
13	1R	0.26	0/982	0.51	0/1312
13	2R	0.21	0/982	0.41	0/1312
14	1S	0.22	0/883	0.44	0/1176
14	2S	0.20	0/880	0.48	0/1172
15	1T	0.23	0/1105	0.45	0/1477
15	2T	0.22	0/1097	0.48	0/1468
16	1U	0.28	0/977	0.48	0/1301

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
16	2U	0.20	0/977	0.41	0/1301
17	1V	0.24	0/782	0.46	0/1049
17	2V	0.19	0/782	0.39	0/1049
18	1W	0.27	0/897	0.46	0/1205
18	2W	0.21	0/897	0.42	0/1205
19	1X	0.26	0/764	0.51	0/1025
19	2X	0.19	0/764	0.49	2/1025 (0.2%)
20	1Y	0.23	0/819	0.46	0/1095
20	2Y	0.19	0/819	0.43	0/1095
21	1Z	0.23	0/1267	0.50	0/1717
21	2Z	0.21	0/1299	0.44	0/1763
22	10	0.25	0/612	0.45	0/816
22	20	0.20	0/612	0.44	0/816
23	11	0.25	0/762	0.42	0/1014
23	21	0.20	0/762	0.39	0/1014
24	12	0.22	0/590	0.42	0/781
24	22	0.19	0/590	0.38	0/781
25	13	0.26	0/474	0.49	0/635
25	23	0.21	0/469	0.40	0/630
26	14	0.26	0/565	0.55	0/761
26	24	0.23	0/545	0.52	0/737
27	15	0.27	0/469	0.49	0/635
27	25	0.23	0/469	0.47	0/635
28	16	0.26	0/460	0.48	0/613
28	26	0.19	0/456	0.45	0/608
29	17	0.31	0/426	0.52	0/561
29	27	0.25	0/426	0.52	0/561
30	18	0.26	0/525	0.47	0/691
30	28	0.21	0/525	0.41	0/691
31	19	0.25	0/310	0.46	0/407
31	29	0.20	0/310	0.40	0/407
32	1a	0.20	2/35795 (0.0%)	0.38	0/55864
32	2a	0.20	1/35886 (0.0%)	0.37	5/56005 (0.0%)
33	1b	0.24	0/1881	0.55	1/2542 (0.0%)
33	2b	0.23	0/1860	0.49	0/2518
34	1c	0.21	0/1572	0.45	0/2126
34	2c	0.21	0/1566	0.41	0/2119
35	1d	0.19	0/1685	0.41	0/2262
35	2d	0.20	0/1704	0.44	0/2284
36	1e	0.20	0/1145	0.44	0/1543
36	2e	0.21	0/1149	0.44	0/1548
37	1f	0.19	0/823	0.40	0/1115
37	2f	0.21	0/829	0.40	0/1123

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
38	1g	0.20	0/1250	0.42	0/1679
38	2g	0.21	0/1254	0.43	0/1683
39	1h	0.18	0/1108	0.40	0/1494
39	2h	0.18	0/1108	0.42	0/1494
40	1i	0.21	0/1002	0.48	0/1346
40	2i	0.23	0/997	0.46	0/1343
41	1j	0.25	0/722	0.46	0/982
41	2j	0.23	0/727	0.47	0/988
42	1k	0.18	0/844	0.43	0/1145
42	2k	0.18	0/848	0.39	0/1149
43	1l	0.21	0/937	0.43	0/1260
43	2l	0.18	0/937	0.42	0/1260
44	1m	0.19	0/929	0.48	0/1250
44	2m	0.23	0/917	0.48	0/1234
45	1n	0.19	0/501	0.46	0/664
45	2n	0.19	0/501	0.41	0/664
46	1o	0.20	0/739	0.38	0/985
46	2o	0.18	0/739	0.38	0/985
47	1p	0.20	0/697	0.45	0/939
47	2p	0.19	0/693	0.44	0/935
48	1q	0.18	0/836	0.39	0/1117
48	2q	0.17	0/836	0.42	0/1117
49	1r	0.19	0/560	0.41	0/746
49	2r	0.18	0/560	0.40	0/746
50	1s	0.22	0/667	0.48	0/900
50	2s	0.20	0/661	0.40	0/893
51	1t	0.19	0/730	0.42	0/965
51	2t	0.18	0/729	0.43	0/965
52	1u	0.21	0/203	0.45	0/266
52	2u	0.21	0/203	0.47	0/266
53	1v	0.26	0/310	0.45	0/480
53	2v	0.22	0/212	0.43	0/327
54	1w	0.20	0/1966	0.42	0/2649
54	2w	0.19	0/1984	0.40	0/2672
55	1x	0.23	0/1555	0.36	0/2419
55	2x	0.22	0/1555	0.40	0/2419
56	1z	0.32	0/29	0.58	0/37
56	2z	0.26	0/29	0.43	0/37
All	All	0.22	3/313725 (0.0%)	0.42	14/468721 (0.0%)

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

sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
21	1Z	0	1
33	1b	0	2
33	2b	0	1
All	All	0	4

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
32	2a	527	G7M	O3'-P	5.32	1.61	1.56
32	1a	1498	UR3	O3'-P	5.18	1.61	1.56
32	1a	527	G7M	O3'-P	5.15	1.61	1.56

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1A	1992	G	C2'-C3'-O3'	7.37	120.55	109.50
32	2a	1263	C	N1-C2-O2	6.90	139.59	118.90
1	2A	1992	G	C2'-C3'-O3'	6.74	119.62	109.50
32	2a	1272	G	N1-C2-N2	-6.74	95.98	116.20
32	2a	1272	G	N3-C2-N2	6.36	138.98	119.90
33	1b	38	GLY	N-CA-C	-6.06	107.30	115.36
32	2a	1272	G	C5-C6-O6	5.95	146.46	128.60
1	1A	1653	G	C2'-C3'-O3'	5.29	117.43	109.50
19	2X	94	GLY	CA-C-N	5.28	131.21	121.70
19	2X	94	GLY	C-N-CA	5.28	131.21	121.70
32	2a	1263	C	N3-C2-O2	-5.08	106.65	121.90
1	2A	1420	U	C2'-C3'-O3'	5.05	117.08	109.50
1	2A	1992	G	P-O3'-C3'	5.05	127.78	120.20
1	1A	2689	U	C2'-C3'-O3'	5.05	117.07	109.50

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
21	1Z	136	PHE	Peptide
33	1b	122	PHE	Peptide
33	1b	9	GLU	Peptide
33	2b	124	SER	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	61852	0	31194	445	0
1	2A	60322	0	30428	513	0
2	1B	2577	0	1305	11	0
2	2B	2575	0	1303	29	0
3	1D	2136	0	2218	33	0
3	2D	2136	0	2218	37	0
4	1E	1559	0	1618	18	0
4	2E	1559	0	1618	25	0
5	1F	1584	0	1625	38	0
5	2F	1580	0	1619	43	0
6	1G	1423	0	1436	22	0
6	2G	1428	0	1438	40	0
7	1H	1330	0	1407	29	0
7	2H	1330	0	1407	25	0
8	1I	1097	0	1140	29	0
8	2I	1064	0	1082	19	0
9	1N	1117	0	1184	10	0
9	2N	1117	0	1184	12	0
10	1O	933	0	996	10	0
10	2O	933	0	996	16	0
11	1P	1135	0	1212	18	0
11	2P	1135	0	1212	25	0
12	1Q	1122	0	1179	11	0
12	2Q	1122	0	1179	24	0
13	1R	968	0	1033	11	0
13	2R	968	0	1033	17	0
14	1S	873	0	927	17	0
14	2S	870	0	923	23	0
15	1T	1091	0	1151	19	0
15	2T	1083	0	1136	24	0
16	1U	959	0	1019	11	0
16	2U	959	0	1019	13	0
17	1V	771	0	830	6	0
17	2V	771	0	830	7	0
18	1W	886	0	940	7	0
18	2W	886	0	940	14	0
19	1X	750	0	814	15	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	2X	750	0	814	12	0
20	1Y	806	0	881	9	0
20	2Y	806	0	881	16	0
21	1Z	1240	0	1240	26	0
21	2Z	1271	0	1273	34	0
22	10	604	0	619	11	0
22	20	604	0	619	10	0
23	11	755	0	826	11	0
23	21	755	0	826	10	0
24	12	588	0	643	5	0
24	22	588	0	643	13	0
25	13	469	0	518	8	0
25	23	464	0	514	5	0
26	14	552	0	533	19	0
26	24	532	0	503	21	0
27	15	455	0	465	2	0
27	25	455	0	465	5	0
28	16	453	0	473	4	0
28	26	449	0	469	3	0
29	17	418	0	467	3	0
29	27	418	0	467	13	0
30	18	517	0	582	12	0
30	28	517	0	582	9	0
31	19	307	0	335	3	0
31	29	307	0	335	5	0
32	1a	32246	0	16294	336	0
32	2a	32327	0	16338	329	0
33	1b	1846	0	1867	70	0
33	2b	1825	0	1828	57	0
34	1c	1548	0	1535	42	0
34	2c	1542	0	1517	47	0
35	1d	1655	0	1672	46	0
35	2d	1674	0	1714	45	0
36	1e	1129	0	1185	37	0
36	2e	1133	0	1191	23	0
37	1f	810	0	804	14	0
37	2f	816	0	808	19	0
38	1g	1231	0	1238	30	0
38	2g	1235	0	1249	32	0
39	1h	1088	0	1126	32	0
39	2h	1088	0	1126	25	0
40	1i	983	0	986	28	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
40	2i	978	0	966	44	0
41	1j	709	0	650	21	0
41	2j	714	0	672	31	0
42	1k	829	0	825	19	0
42	2k	833	0	836	18	0
43	1l	932	0	981	22	0
43	2l	932	0	981	18	0
44	1m	919	0	951	26	0
44	2m	907	0	934	43	0
45	1n	492	0	529	12	0
45	2n	492	0	529	12	0
46	1o	728	0	760	14	0
46	2o	728	0	760	16	0
47	1p	681	0	697	28	0
47	2p	677	0	686	17	0
48	1q	823	0	891	12	0
48	2q	823	0	891	6	0
49	1r	555	0	618	9	0
49	2r	555	0	618	16	0
50	1s	652	0	662	18	0
50	2s	646	0	644	26	0
51	1t	728	0	798	15	0
51	2t	727	0	796	18	0
52	1u	199	0	208	4	0
52	2u	199	0	208	4	0
53	1v	277	0	140	5	0
53	2v	190	0	97	3	0
54	1w	1938	0	1923	31	0
54	2w	1956	0	1933	44	0
55	1x	1577	0	801	6	0
55	2x	1577	0	801	14	0
56	1z	30	0	32	3	0
56	2z	30	0	32	3	0
57	10	8	0	0	0	0
57	11	5	0	0	0	0
57	12	2	0	0	0	0
57	13	4	0	0	0	0
57	15	7	0	0	0	0
57	16	1	0	0	0	0
57	17	4	0	0	0	0
57	18	3	0	0	0	0
57	19	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
57	1A	1046	0	0	0	0
57	1B	38	0	0	0	0
57	1D	13	0	0	0	0
57	1E	12	0	0	0	0
57	1F	13	0	0	0	0
57	1G	5	0	0	0	0
57	1I	1	0	0	0	0
57	1N	6	0	0	0	0
57	1O	5	0	0	0	0
57	1P	3	0	0	0	0
57	1Q	7	0	0	0	0
57	1R	7	0	0	0	0
57	1S	3	0	0	0	0
57	1T	2	0	0	0	0
57	1U	10	0	0	0	0
57	1V	6	0	0	0	0
57	1W	9	0	0	0	0
57	1X	5	0	0	0	0
57	1Y	3	0	0	0	0
57	1Z	2	0	0	0	0
57	1a	205	0	0	0	0
57	1b	2	0	0	0	0
57	1d	1	0	0	0	0
57	1e	2	0	0	0	0
57	1f	1	0	0	0	0
57	1k	1	0	0	0	0
57	1l	2	0	0	0	0
57	1m	1	0	0	0	0
57	1n	2	0	0	0	0
57	1p	1	0	0	0	0
57	1r	1	0	0	0	0
57	1t	1	0	0	0	0
57	1v	2	0	0	0	0
57	1w	1	0	0	0	0
57	1x	11	0	0	0	0
57	20	1	0	0	0	0
57	21	1	0	0	0	0
57	23	1	0	0	0	0
57	25	6	0	0	0	0
57	26	1	0	0	0	0
57	27	1	0	0	0	0
57	28	3	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
57	2A	846	0	0	0	0
57	2B	19	0	0	0	0
57	2D	10	0	0	0	0
57	2E	7	0	0	0	0
57	2F	7	0	0	0	0
57	2G	1	0	0	0	0
57	2N	1	0	0	0	0
57	2O	2	0	0	0	0
57	2P	3	0	0	0	0
57	2Q	4	0	0	0	0
57	2R	2	0	0	0	0
57	2T	5	0	0	0	0
57	2U	1	0	0	0	0
57	2V	3	0	0	0	0
57	2W	2	0	0	0	0
57	2X	1	0	0	0	0
57	2Y	1	0	0	0	0
57	2Z	1	0	0	0	0
57	2a	171	0	0	0	0
57	2d	2	0	0	0	0
57	2e	1	0	0	0	0
57	2f	1	0	0	0	0
57	2i	1	0	0	0	0
57	2j	1	0	0	0	0
57	2k	1	0	0	0	0
57	2l	3	0	0	0	0
57	2n	1	0	0	0	0
57	2q	1	0	0	0	0
57	2t	2	0	0	0	0
57	2v	2	0	0	0	0
57	2x	7	0	0	0	0
58	1A	1	0	0	0	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

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
59	2Y	1	0	0	0	0
59	2n	1	0	0	0	0
60	1d	8	0	0	0	0
60	2d	8	0	0	0	0
61	10	11	0	0	0	0
61	11	8	0	0	0	0
61	12	3	0	0	1	0
61	13	6	0	0	0	0
61	14	1	0	0	0	0
61	15	6	0	0	0	0
61	17	7	0	0	0	0
61	18	9	0	0	1	0
61	1A	1729	0	0	66	0
61	1B	58	0	0	2	0
61	1D	23	0	0	0	0
61	1E	27	0	0	4	0
61	1F	15	0	0	0	0
61	1G	5	0	0	2	0
61	1H	2	0	0	0	0
61	1I	1	0	0	0	0
61	1N	7	0	0	0	0
61	1O	7	0	0	0	0
61	1P	20	0	0	0	0
61	1Q	8	0	0	0	0
61	1R	10	0	0	2	0
61	1S	3	0	0	1	0
61	1T	6	0	0	0	0
61	1U	13	0	0	0	0
61	1V	8	0	0	0	0
61	1W	12	0	0	1	0
61	1X	4	0	0	0	0
61	1Y	1	0	0	1	0
61	1Z	1	0	0	0	0
61	1a	211	0	0	10	0
61	1b	1	0	0	0	0
61	1i	1	0	0	0	0
61	1l	2	0	0	0	0
61	1q	3	0	0	0	0
61	1v	4	0	0	0	0
61	1w	2	0	0	1	0
61	1x	19	0	0	1	0
61	1z	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
61	20	3	0	0	0	0
61	21	9	0	0	0	0
61	22	1	0	0	0	0
61	23	2	0	0	1	0
61	25	2	0	0	0	0
61	27	1	0	0	0	0
61	28	5	0	0	0	0
61	29	1	0	0	0	0
61	2A	974	0	0	74	0
61	2B	20	0	0	3	0
61	2D	18	0	0	1	0
61	2E	15	0	0	0	0
61	2F	10	0	0	0	0
61	2I	1	0	0	0	0
61	2N	1	0	0	0	0
61	2O	2	0	0	0	0
61	2P	14	0	0	0	0
61	2Q	1	0	0	0	0
61	2R	2	0	0	0	0
61	2T	5	0	0	0	0
61	2U	3	0	0	0	0
61	2V	1	0	0	0	0
61	2W	2	0	0	0	0
61	2X	4	0	0	0	0
61	2Z	2	0	0	0	0
61	2a	120	0	0	5	0
61	2d	2	0	0	0	0
61	2e	1	0	0	0	0
61	2j	4	0	0	1	0
61	2l	4	0	0	0	0
61	2n	1	0	0	0	0
61	2q	2	0	0	0	0
61	2w	1	0	0	0	0
61	2x	12	0	0	0	0
All	All	296409	0	197094	3257	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 7.

All (3257) 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:O4	1:1A:1086:A:N1	1.84	1.10
1:2A:784:A:OP2	61:2A:3903:HOH:O	1.83	0.96
1:1A:1041:C:H42	1:1A:1114:G:H1	1.17	0.91
1:2A:1798:U:H5'	3:2D:259:THR:HG22	1.51	0.91
33:2b:185:ILE:HG22	33:2b:199:TYR:HB2	1.51	0.90
1:2A:2129:C:H42	1:2A:2159:G:H1	1.18	0.90
51:1t:57:ARG:HH12	51:1t:100:ILE:HD12	1.36	0.88
40:1i:53:VAL:O	40:1i:55:ALA:N	2.07	0.88
1:2A:783:A:OP2	61:2A:3903:HOH:O	1.92	0.88
32:2a:922:G:H4'	36:2e:20:GLN:HA	1.53	0.87
1:1A:1082:U:C4	1:1A:1086:A:N1	2.41	0.87
1:1A:1082:U:N3	1:1A:1086:A:N6	2.23	0.87
1:1A:1082:U:H3	1:1A:1086:A:H61	1.20	0.86
1:2A:2206:G:H3'	1:2A:2207:G:C8	2.10	0.86
5:2F:53:THR:HG23	5:2F:55:GLY:H	1.38	0.86
1:2A:1689:A:H62	1:2A:1698:A:H2	1.23	0.85
14:1S:61:ASN:HD22	14:1S:64:GLU:H	1.25	0.85
1:2A:1604:C:OP2	61:2A:3905:HOH:O	1.94	0.84
1:2A:981:A:OP1	61:2A:3904:HOH:O	1.94	0.84
32:2a:1286:A:H8	32:2a:1287:A:H4'	1.42	0.84
32:1a:1286:A:H8	32:1a:1287:A:H4'	1.42	0.84
54:1w:119:GLU:HG3	54:1w:184:PRO:HB3	1.57	0.84
1:2A:195:A:N7	61:2A:3915:HOH:O	2.09	0.83
1:1A:1060:U:H3	1:1A:1088:A:H8	1.27	0.83
1:1A:2134:A:H1'	1:1A:2159:G:H1'	1.61	0.82
1:2A:2822:G:OP2	61:2A:3906:HOH:O	1.96	0.82
33:2b:76:GLN:HB3	33:2b:208:ILE:HG12	1.62	0.82
1:1A:2427:C:OP1	61:1A:4104:HOH:O	1.97	0.81
1:1A:1332:G:OP1	61:1A:4106:HOH:O	1.99	0.81
1:1A:1865:G:OP1	61:1A:4105:HOH:O	1.98	0.81
1:1A:1798:U:H5'	3:1D:259:THR:HG22	1.60	0.81
1:2A:890:A:H2'	1:2A:892:G:H8	1.45	0.81
32:2a:1271:G:N2	32:2a:1272:G:N7	2.29	0.80
41:2j:49:VAL:HG23	45:2n:41:ARG:HB2	1.61	0.80
1:1A:826:U:OP1	61:1A:4104:HOH:O	2.00	0.80
40:2i:16:ARG:HB2	40:2i:64:THR:HG22	1.63	0.80
32:1a:1381:U:H1'	38:1g:79:ARG:HG2	1.64	0.80
1:1A:2161:C:HO2'	1:1A:2162:G:H8	1.30	0.80
14:1S:31:SER:HB2	14:1S:34:HIS:H	1.46	0.79
1:2A:948:G:OP1	61:2A:3907:HOH:O	2.00	0.79
32:2a:677:U:H3	32:2a:713:G:H22	1.29	0.79
32:1a:975:A:H4'	32:1a:976:G:H5''	1.64	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:1q:66:SER:O	48:1q:70:ARG:NH1	2.17	0.78
1:2A:1648:C:OP1	61:2A:3908:HOH:O	2.01	0.78
1:2A:2589:A:OP1	61:2A:3903:HOH:O	2.01	0.78
32:2a:664:G:H22	32:2a:741:G:H1	1.30	0.78
32:2a:1055:A:N3	34:2c:156:ARG:NH1	2.31	0.78
19:2X:40:LYS:HG3	19:2X:51:VAL:HB	1.65	0.77
1:1A:2447:G:OP2	61:1A:4107:HOH:O	2.02	0.77
1:2A:1022:G:H22	1:2A:1142(A):A:H2	1.30	0.77
8:1I:75:LEU:HD22	8:1I:105:HIS:HD2	1.49	0.77
32:2a:1352:C:OP1	52:2u:3:LYS:NZ	2.15	0.77
1:2A:1271:G:OP2	61:2A:3908:HOH:O	2.01	0.77
38:1g:69:VAL:HG21	38:1g:104:LEU:HD21	1.66	0.77
37:2f:61:LEU:HB3	37:2f:63:TYR:HE2	1.50	0.77
32:1a:1226:C:H3'	44:1m:96:LEU:HD21	1.67	0.77
35:2d:122:ARG:NH1	35:2d:134:ASP:O	2.17	0.77
38:2g:113:GLU:HB2	38:2g:119:ARG:HG2	1.65	0.77
39:2h:106:GLY:O	39:2h:122:ARG:NH2	2.17	0.76
50:2s:18:LYS:HA	50:2s:21:GLU:HB2	1.66	0.76
1:1A:1352:U:OP2	61:1A:4109:HOH:O	2.03	0.76
1:1A:1670:C:OP2	61:1A:4108:HOH:O	2.03	0.76
1:1A:2615:U:OP1	61:1A:4110:HOH:O	2.03	0.76
1:2A:1395:A:OP1	61:2A:3905:HOH:O	2.03	0.76
34:2c:78:GLY:HA3	34:2c:83:ARG:H	1.48	0.76
1:2A:1021:A:H62	1:2A:1141:U:H3	1.31	0.76
32:2a:1518:MA6:H93	32:2a:1519:MA6:H92	1.64	0.76
1:1A:9:U:H3	1:1A:2629:A:H2	1.34	0.76
37:2f:7:ASN:HD21	49:2r:34:TYR:HE1	1.34	0.76
1:2A:1204:A:H2	1:2A:1241:A:H62	1.33	0.76
32:1a:542:G:OP1	35:1d:10:ARG:NH2	2.18	0.76
41:1j:30:SER:HB3	41:1j:81:THR:HG23	1.67	0.76
25:23:5:LYS:NZ	25:23:34:GLU:OE2	2.19	0.75
1:1A:1082:U:H3	1:1A:1086:A:N6	1.83	0.75
50:1s:50:ALA:HB1	50:1s:57:HIS:HB3	1.68	0.75
1:2A:1828:G:OP1	61:2A:3909:HOH:O	2.04	0.75
1:1A:883:G:H21	1:1A:893:C:H42	1.35	0.75
48:1q:53:LEU:HB3	48:1q:82:MET:HE1	1.67	0.75
26:24:64:GLY:O	26:24:66:SER:N	2.19	0.75
34:2c:70:VAL:HG12	34:2c:72:LYS:H	1.52	0.75
1:1A:2702:U:OP2	61:1A:4111:HOH:O	2.05	0.75
32:2a:673:G:H2'	32:2a:674:G:C8	2.21	0.75
1:2A:994:C:OP1	16:2U:53:ARG:NH2	2.20	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:2m:13:LYS:HA	44:2m:44:ARG:HH11	1.50	0.75
1:1A:642:G:OP2	61:1A:4112:HOH:O	2.05	0.74
37:1f:35:ALA:HB1	37:1f:65:VAL:HG11	1.68	0.74
1:2A:921:G:O6	61:2A:3910:HOH:O	2.05	0.74
32:2a:542:G:OP1	35:2d:10:ARG:NH2	2.19	0.74
39:2h:36:LEU:HA	39:2h:39:LEU:HD12	1.69	0.74
54:1w:175:SER:HB3	54:1w:201:VAL:HG22	1.70	0.74
34:2c:58:GLU:HB3	41:2j:92:THR:HG21	1.70	0.74
1:1A:2550:G:OP1	61:1A:4108:HOH:O	2.06	0.74
1:2A:892:G:H2'	1:2A:893:C:H4'	1.68	0.74
32:1a:573:A:OP2	61:1a:1901:HOH:O	2.06	0.73
32:2a:559:A:OP1	36:2e:126:ARG:NH2	2.20	0.73
1:2A:882:G:H1	1:2A:894:C:H42	1.36	0.73
10:2O:49:ARG:NH2	32:2a:1423:G:OP1	2.15	0.73
36:2e:122:GLU:O	36:2e:126:ARG:NH1	2.21	0.73
1:1A:1185:C:OP2	61:1A:4113:HOH:O	2.06	0.73
1:1A:2789:C:O2	1:1A:2894:G:N1	2.18	0.73
1:2A:2104:G:H1	1:2A:2185:C:H42	1.36	0.73
33:2b:189:ASP:OD1	33:2b:189:ASP:N	2.20	0.73
1:1A:2121:G:O6	1:1A:2176:A:N6	2.20	0.73
1:2A:2110:G:H3'	1:2A:2111:C:H5'	1.71	0.73
1:2A:2313:C:H4'	6:2G:91:ARG:HG3	1.70	0.73
33:1b:54:THR:HG23	33:1b:199:TYR:HB3	1.71	0.72
23:11:52:ARG:NH1	23:11:55:GLY:O	2.21	0.72
1:2A:2129:C:N4	1:2A:2159:G:H1	1.86	0.72
8:1I:4:ILE:HG12	8:1I:18:VAL:HG12	1.71	0.72
1:2A:1762:A:N1	61:2A:3954:HOH:O	2.22	0.72
32:2a:1286:A:C8	32:2a:1287:A:H4'	2.25	0.72
34:2c:63:ASN:HB2	34:2c:98:ASN:HB2	1.71	0.72
32:1a:1441:G:H5''	32:1a:1442:G:H5'	1.71	0.72
35:1d:122:ARG:NH1	35:1d:134:ASP:O	2.22	0.72
11:2P:91:PHE:O	11:2P:121:LYS:NZ	2.23	0.72
12:2Q:11:LYS:NZ	12:2Q:88:GLY:O	2.23	0.72
34:2c:180:ALA:HB1	34:2c:203:PHE:HE1	1.53	0.72
40:2i:128:ARG:NH2	55:2x:33:U:OP2	2.22	0.72
1:2A:399:G:OP2	61:2A:3912:HOH:O	2.07	0.72
1:2A:2518:A:OP2	61:2A:3913:HOH:O	2.08	0.72
32:2a:1129:C:OP1	40:2i:66:ARG:NH1	2.23	0.72
5:2F:185:ASP:HA	5:2F:188:ARG:HD3	1.72	0.72
21:1Z:146:ILE:N	21:1Z:148:ASP:H	1.87	0.71
32:1a:1401:G:OP1	61:1a:1902:HOH:O	2.07	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2B:103:G:O6	61:2B:301:HOH:O	2.07	0.71
1:1A:1455:G:OP2	61:1A:4114:HOH:O	2.07	0.71
1:2A:962:G:OP1	61:2A:3907:HOH:O	2.08	0.71
44:2m:33:ALA:O	44:2m:37:THR:OG1	2.09	0.71
32:1a:1402:4OC:OP2	61:1a:1902:HOH:O	2.09	0.71
1:2A:955:C:OP1	12:2Q:87:LYS:NZ	2.21	0.71
1:2A:2125:G:H1'	1:2A:2173:A:H61	1.56	0.71
48:2q:26:GLN:HG2	48:2q:37:LYS:HG2	1.72	0.71
32:1a:972:C:O2'	41:1j:55:LYS:O	2.09	0.71
1:2A:2118:U:O4	1:2A:2148:G:N2	2.16	0.71
44:2m:60:VAL:HG23	44:2m:64:TRP:HE3	1.55	0.71
1:2A:818:G:OP2	61:2A:3911:HOH:O	2.07	0.71
2:2B:43:C:O2	6:2G:95:ARG:NH2	2.19	0.71
1:2A:323:G:HO2'	1:2A:1205:U:H3	1.38	0.70
32:2a:972:C:OP1	61:2a:1801:HOH:O	2.07	0.70
54:2w:169:GLY:HA2	54:2w:172:LYS:HE3	1.73	0.70
1:2A:1670:C:OP1	61:2A:3914:HOH:O	2.08	0.70
32:2a:1162:C:H42	32:2a:1174:G:H1	1.40	0.70
32:2a:1257:U:O4	45:2n:17:LYS:NZ	2.24	0.70
1:1A:993:G:OP1	16:1U:50:ARG:NH2	2.25	0.70
1:1A:2306:C:O2	61:1A:4115:HOH:O	2.09	0.70
10:1O:2:ILE:HD12	10:1O:6:THR:HG21	1.73	0.70
15:1T:41:ARG:NH2	32:1a:346:G:OP1	2.20	0.70
1:1A:1072:C:H1'	1:1A:1092:C:H41	1.56	0.70
32:1a:964:A:OP1	61:1a:1903:HOH:O	2.08	0.70
5:2F:70:THR:HG22	5:2F:72:ARG:H	1.57	0.70
1:2A:2296:U:OP2	14:2S:9:ARG:NH2	2.25	0.70
10:1O:48:PRO:HB3	32:1a:1422:G:H5''	1.73	0.70
34:2c:79:ARG:H	34:2c:82:GLU:HB3	1.56	0.70
1:1A:1092:C:H3'	1:1A:1094:U:H5	1.57	0.69
1:1A:1669:A:OP2	61:1A:4108:HOH:O	2.10	0.69
10:1O:64:ARG:HG2	10:1O:79:PHE:CG	2.27	0.69
61:1a:1902:HOH:O	53:1v:19:U:OP1	2.10	0.69
1:2A:1830:C:OP2	61:2A:3918:HOH:O	2.10	0.69
1:2A:1973:G:OP1	61:2A:3919:HOH:O	2.10	0.69
1:2A:2504:U:OP2	61:2A:3917:HOH:O	2.09	0.69
38:2g:153:HIS:CE1	42:2k:58:PRO:HD2	2.27	0.69
1:2A:198:C:OP2	61:2A:3915:HOH:O	2.10	0.69
35:2d:103:ASN:OD1	35:2d:114:ARG:NH2	2.24	0.69
1:1A:1064:C:N3	1:1A:1074:G:O6	2.25	0.69
5:1F:185:ASP:HA	5:1F:188:ARG:HD3	1.73	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:1d:12:CYS:HA	35:1d:19:LEU:HD12	1.73	0.69
54:1w:150:THR:HG22	54:1w:152:LEU:H	1.57	0.69
1:1A:998:C:OP1	61:1A:4117:HOH:O	2.10	0.69
1:1A:1253:A:OP1	61:1A:4116:HOH:O	2.09	0.69
1:1A:2062:A:C2	56:1z:5:ALA:HB1	2.28	0.69
32:1a:1025:U:H3	32:1a:1036:G:H1	1.38	0.69
32:2a:1129:C:H2'	32:2a:1139:G:N7	2.07	0.69
42:2k:18:ARG:HB2	42:2k:33:THR:HG23	1.73	0.69
42:2k:79:SER:HB2	42:2k:106:LYS:HD3	1.75	0.69
32:1a:1145:C:H4'	32:1a:1146:A:H5'	1.74	0.69
43:1l:70:ILE:HG12	43:1l:100:ILE:HD12	1.74	0.69
1:2A:2499:C:OP2	61:2A:3916:HOH:O	2.09	0.69
1:1A:1057:A:H61	1:1A:1081:U:H3	1.41	0.69
50:1s:27:GLU:HB2	50:1s:28:LYS:HA	1.74	0.69
33:2b:119:GLU:HG3	33:2b:153:ARG:HH12	1.58	0.69
38:2g:22:LEU:HD12	38:2g:97:GLN:HE22	1.57	0.69
54:2w:240:ARG:HB2	54:2w:251:THR:HG22	1.75	0.69
33:1b:195:ASP:O	39:1h:68:ARG:NH2	2.25	0.69
5:2F:153:SER:HB2	5:2F:190:GLU:H	1.57	0.69
13:2R:103:ARG:NH1	13:2R:108:GLY:O	2.25	0.69
21:2Z:145:GLU:HG3	21:2Z:146:ILE:H	1.57	0.69
35:2d:7:PRO:HB2	35:2d:10:ARG:HD2	1.74	0.69
42:2k:48:ILE:O	42:2k:50:TYR:N	2.25	0.69
1:1A:1381:G:N7	61:1A:4159:HOH:O	2.26	0.69
1:1A:1648:C:OP1	61:1A:4120:HOH:O	2.11	0.69
2:1B:7:G:N7	61:1B:302:HOH:O	2.26	0.69
32:1a:1035:A:H2'	32:1a:1036:G:H21	1.57	0.69
33:2b:155:LEU:HD21	33:2b:159:PRO:HD3	1.72	0.69
39:2h:87:SER:HB2	39:2h:93:VAL:H	1.58	0.69
1:2A:1981:A:N7	61:2A:3973:HOH:O	2.26	0.68
36:2e:89:ILE:HG12	36:2e:135:THR:HG22	1.75	0.68
1:1A:2499:C:OP1	61:1A:4118:HOH:O	2.10	0.68
54:1w:317:ILE:HG13	54:1w:319:PHE:H	1.58	0.68
32:2a:1272:G:N2	32:2a:1273:G:C5	2.61	0.68
33:2b:184:VAL:HG13	33:2b:198:ASP:H	1.56	0.68
1:2A:135:G:N7	61:2A:3975:HOH:O	2.26	0.68
1:2A:2006:C:OP2	61:2A:3921:HOH:O	2.11	0.68
1:2A:2839:G:H5'	13:2R:46:GLY:HA2	1.74	0.68
61:1A:4115:HOH:O	6:1G:45:GLU:OE2	2.10	0.68
1:2A:271(R):G:OP1	23:21:76:ARG:NH2	2.26	0.68
1:2A:2805:G:H2'	1:2A:2807:G:C8	2.28	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:544:G:OP1	35:2d:62:GLN:NE2	2.16	0.68
5:1F:53:THR:HG22	5:1F:55:GLY:H	1.58	0.68
32:1a:1366:C:O2'	41:1j:60:ARG:NH1	2.27	0.68
1:2A:1346:G:OP2	61:2A:3920:HOH:O	2.11	0.68
2:2B:8:U:H5'	14:2S:15:ARG:HH12	1.57	0.68
1:1A:1264:G:OP1	27:15:19:ARG:NH2	2.22	0.68
1:1A:1342:A:OP2	61:1A:4124:HOH:O	2.12	0.68
1:2A:2150:U:H2'	1:2A:2151:G:H8	1.59	0.68
32:1a:664:G:H22	32:1a:741:G:H1	1.42	0.68
32:1a:1086:U:H3	32:1a:1099:G:H22	1.42	0.68
35:1d:140:VAL:HG11	35:1d:146:ILE:HD11	1.74	0.68
54:1w:130:MET:HE3	54:1w:332:LEU:HD11	1.75	0.68
1:1A:762:U:OP1	61:1A:4121:HOH:O	2.11	0.67
34:1c:70:VAL:HG12	34:1c:72:LYS:H	1.59	0.67
1:2A:943:U:OP2	61:2A:3924:HOH:O	2.12	0.67
1:2A:1264:G:OP1	27:25:19:ARG:NH2	2.27	0.67
1:1A:2552:OMU:OP2	61:1A:4122:HOH:O	2.12	0.67
32:2a:768:A:OP2	61:2a:1802:HOH:O	2.10	0.67
1:1A:947:G:OP2	61:1A:4126:HOH:O	2.12	0.67
1:1A:2733:A:OP1	61:1A:4123:HOH:O	2.12	0.67
32:1a:559:A:OP1	36:1e:126:ARG:NH2	2.27	0.67
1:2A:1817:G:OP1	3:2D:88:ARG:NH2	2.27	0.67
39:2h:37:ARG:HH21	39:2h:38:ILE:HD11	1.58	0.67
32:1a:56:U:H2'	32:1a:57:G:C8	2.30	0.67
32:1a:677:U:H3	32:1a:713:G:H22	1.42	0.67
1:2A:1452:A:OP2	61:2A:3922:HOH:O	2.12	0.67
4:2E:181:LEU:HD11	15:2T:6:LEU:HD12	1.76	0.67
1:1A:120:U:OP2	61:1A:4129:HOH:O	2.13	0.67
1:1A:792:G:O6	61:1A:4119:HOH:O	2.10	0.67
1:1A:1271:G:OP2	61:1A:4120:HOH:O	2.12	0.67
32:1a:1356:G:H2'	32:1a:1357:A:C8	2.29	0.67
1:2A:963:U:OP2	61:2A:3907:HOH:O	2.10	0.67
43:2l:40:VAL:HG21	43:2l:78:GLN:HA	1.76	0.67
39:1h:124:ALA:O	39:1h:128:GLY:N	2.25	0.67
41:1j:49:VAL:HG23	45:1n:41:ARG:HB2	1.76	0.67
47:1p:49:LEU:HD11	47:1p:73:LEU:HB3	1.77	0.67
1:2A:1299:G:N7	61:2A:3978:HOH:O	2.27	0.67
1:2A:1970:A:OP1	61:2A:3925:HOH:O	2.13	0.67
32:1a:812:C:N3	61:1a:1914:HOH:O	2.28	0.67
33:1b:21:ARG:HB3	33:1b:39:ILE:HG12	1.76	0.67
36:1e:74:GLY:HA3	36:1e:116:THR:HG22	1.77	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:2r:32:ARG:HA	49:2r:69:THR:HG21	1.76	0.66
1:1A:242:G:OP1	61:1A:4125:HOH:O	2.12	0.66
32:1a:1521:G:N3	61:1a:1913:HOH:O	2.28	0.66
40:1i:121:ARG:NH1	40:1i:122:ALA:O	2.28	0.66
1:2A:2448:A:OP1	61:2A:3923:HOH:O	2.12	0.66
1:1A:2327:A:H2'	1:1A:2328:A:C8	2.30	0.66
5:1F:188:ARG:HA	11:1P:3:LEU:HD11	1.78	0.66
6:1G:41:GLN:NE2	6:1G:154:GLY:O	2.28	0.66
40:1i:50:LEU:HD23	40:1i:85:LEU:HD11	1.78	0.66
10:2O:48:PRO:HB3	32:2a:1422:G:H5''	1.76	0.66
1:1A:1385:G:O2'	1:1A:1396:U:O2	2.12	0.66
1:1A:1647:G:OP1	61:1A:4120:HOH:O	2.13	0.66
1:2A:248:G:OP1	61:2A:3926:HOH:O	2.13	0.66
1:2A:752:A:H3'	29:27:1:MET:HE1	1.78	0.66
1:1A:1073:A:H2'	1:1A:1074:G:H8	1.60	0.66
46:1o:16:ALA:HB1	46:1o:21:ASP:HB3	1.77	0.66
23:21:77:ALA:HA	23:21:80:LEU:HD12	1.76	0.66
26:24:16:CYS:SG	26:24:17:GLY:N	2.68	0.66
32:2a:953:G:H5'	32:2a:965:A:H61	1.61	0.66
36:2e:92:LYS:HB3	36:2e:119:LEU:HB2	1.77	0.66
40:1i:128:ARG:NH1	55:1x:35:C:OP1	2.29	0.66
42:1k:48:ILE:O	42:1k:50:TYR:N	2.27	0.66
32:2a:975:A:H4'	32:2a:976:G:H5''	1.77	0.66
1:1A:2810:A:N6	1:1A:2891:G:O2'	2.29	0.66
4:1E:110:GLY:O	61:1R:301:HOH:O	2.13	0.66
8:1I:92:VAL:HG13	8:1I:120:ILE:HB	1.78	0.66
26:14:55:ARG:O	26:14:57:GLU:N	2.28	0.66
1:1A:392:C:OP1	61:1A:4128:HOH:O	2.13	0.66
33:1b:33:TYR:HB2	33:1b:43:ASP:HB2	1.77	0.66
32:1a:953:G:H5'	32:1a:965:A:H61	1.60	0.66
1:2A:1721:G:H8	1:2A:1741:A:H62	1.43	0.66
1:2A:2379:G:O2'	14:2S:17:ARG:NH1	2.28	0.66
31:29:25:VAL:HB	31:29:34:GLN:HB2	1.78	0.66
32:2a:1083:U:OP2	61:2a:1803:HOH:O	2.14	0.66
32:1a:1226:C:OP2	44:1m:91:ARG:NH2	2.29	0.65
32:2a:1347:G:H5''	40:2i:107:ARG:HB3	1.77	0.65
1:1A:1970:A:OP1	61:1A:4130:HOH:O	2.14	0.65
38:1g:78:ARG:HG2	38:1g:79:ARG:H	1.61	0.65
2:2B:101:G:OP2	61:2B:302:HOH:O	2.14	0.65
6:2G:11:TYR:OH	6:2G:16:ARG:NH1	2.29	0.65
22:20:11:ARG:O	22:20:14:ARG:NH2	2.29	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
61:1A:4312:HOH:O	11:1P:37:GLY:HA3	1.96	0.65
8:1I:31:LEU:HD21	8:1I:38:LEU:HG	1.76	0.65
32:1a:1402:4OC:HM22	32:1a:1403:C:H5'	1.78	0.65
35:1d:98:GLU:HG3	35:1d:194:LEU:HD21	1.77	0.65
23:21:21:ARG:HD3	23:21:35:THR:HG21	1.77	0.65
32:2a:1492:A:C8	43:2l:47:LYS:HG3	2.32	0.65
1:1A:588:U:OP2	61:1A:4133:HOH:O	2.15	0.65
1:1A:1093:G:H3'	1:1A:1094:U:H5''	1.78	0.65
1:1A:2116:G:H2'	1:1A:2117:A:C5	2.31	0.65
32:1a:537:G:H5''	43:1l:113:ARG:NH1	2.10	0.65
32:1a:673:G:H2'	32:1a:674:G:C8	2.32	0.65
1:2A:2138:C:H42	1:2A:2153:G:H1	1.45	0.65
32:2a:316:G:OP2	32:2a:351:G:O2'	2.13	0.65
34:1c:131:ARG:HH11	34:1c:166:GLU:HG3	1.62	0.65
18:2W:78:GLU:OE2	18:2W:99:ARG:NH1	2.28	0.65
1:1A:740:U:OP2	61:1A:4131:HOH:O	2.14	0.65
1:1A:2069:G:OP2	61:1A:4132:HOH:O	2.15	0.65
1:1A:2705:A:O2'	61:1A:4127:HOH:O	2.13	0.65
37:2f:35:ALA:HA	37:2f:67:MET:HB3	1.78	0.65
1:1A:1939:5MU:OP1	1:1A:2604:U:O2'	2.14	0.65
7:1H:40:GLU:OE1	7:1H:61:HIS:NE2	2.28	0.65
42:1k:15:ALA:HA	42:1k:77:MET:HA	1.77	0.65
2:2B:50:G:OP1	14:2S:63:THR:OG1	2.15	0.65
32:2a:113:G:H1'	32:2a:354:G:H5'	1.77	0.65
38:2g:70:LYS:HG2	38:2g:96:GLN:HB3	1.78	0.65
19:1X:31:HIS:CD2	19:1X:33:LYS:H	2.15	0.65
32:1a:976:G:H5'	32:1a:1358:U:O2'	1.97	0.65
32:1a:1518:MA6:H93	32:1a:1519:MA6:H92	1.78	0.65
41:2j:11:PHE:HE1	41:2j:67:THR:HG22	1.61	0.65
42:2k:98:LEU:O	42:2k:101:SER:OG	2.14	0.65
26:14:61:ARG:HG2	26:14:62:ARG:N	2.12	0.64
33:2b:166:ASP:HB3	33:2b:169:LYS:HB3	1.79	0.64
36:1e:78:HIS:CD2	39:1h:104:ARG:HD2	2.32	0.64
1:2A:2268:A:OP1	61:2A:3930:HOH:O	2.15	0.64
1:2A:2292:C:OP1	14:2S:17:ARG:NH2	2.27	0.64
46:2o:5:LYS:NZ	46:2o:5:LYS:H	1.95	0.64
20:1Y:34:LYS:NZ	61:1Y:301:HOH:O	2.30	0.64
32:1a:933:G:O6	38:1g:3:ARG:NH2	2.28	0.64
23:11:21:ARG:HD3	23:11:35:THR:HG21	1.79	0.64
42:1k:84:VAL:HG23	42:1k:110:ASP:HA	1.79	0.64
55:1x:12:A:OP2	61:1x:6501:HOH:O	2.14	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1865:G:OP1	61:2A:3927:HOH:O	2.14	0.64
1:1A:2181:G:H2'	1:1A:2182:G:C8	2.32	0.64
34:1c:3:ASN:OD1	34:1c:3:ASN:N	2.29	0.64
6:2G:8:LYS:NZ	6:2G:97:ASP:OD1	2.26	0.64
35:2d:191:ARG:NE	35:2d:200:GLU:OE2	2.28	0.64
46:1o:3:ILE:HG21	46:1o:34:LEU:HD21	1.78	0.64
32:2a:771:G:N7	61:2a:1812:HOH:O	2.30	0.64
34:2c:108:ASN:HD21	34:2c:144:SER:HB3	1.63	0.64
1:1A:1796:U:H2'	1:1A:1797:C:C6	2.33	0.64
1:1A:2155:G:H3'	1:1A:2156:G:H8	1.63	0.64
6:1G:109:VAL:HG11	26:14:14:ILE:HG21	1.80	0.64
19:1X:31:HIS:HD2	19:1X:33:LYS:H	1.45	0.64
25:23:13:ILE:O	61:23:201:HOH:O	2.13	0.64
1:1A:2206:G:H5''	1:1A:2207:G:N7	2.12	0.64
32:1a:17:U:H2'	32:1a:18:C:C6	2.33	0.64
32:1a:382:A:H2'	32:1a:383:A:C8	2.32	0.64
54:1w:111:ILE:HB	54:1w:158:VAL:HG23	1.80	0.64
1:2A:890:A:H2'	1:2A:892:G:C8	2.31	0.64
1:2A:2498:C:OP2	61:2A:3916:HOH:O	2.15	0.64
32:2a:1141:C:H2'	32:2a:1142:G:H8	1.62	0.64
34:2c:127:ARG:HH12	34:2c:191:THR:HB	1.62	0.64
36:1e:142:LEU:O	36:1e:143:ARG:NH1	2.31	0.64
38:1g:139:GLU:HA	38:1g:142:GLU:HB2	1.79	0.64
1:2A:1356:G:OP2	61:2A:3928:HOH:O	2.15	0.64
43:2l:57:LYS:HG3	43:2l:67:THR:HG23	1.80	0.64
1:1A:1800:C:OP1	3:1D:264:LYS:NZ	2.26	0.64
4:1E:127:ASP:OD2	61:1E:401:HOH:O	2.14	0.64
1:2A:1334:G:N7	61:2A:3990:HOH:O	2.30	0.64
1:2A:2306:C:N4	6:2G:42:GLY:O	2.31	0.64
1:1A:2206:G:H3'	1:1A:2207:G:C8	2.33	0.63
46:2o:16:ALA:HB1	46:2o:21:ASP:HB3	1.80	0.63
49:2r:48:GLY:O	49:2r:74:ARG:NH2	2.31	0.63
1:1A:505:A:OP2	61:1A:4134:HOH:O	2.15	0.63
1:2A:2327:A:H2'	1:2A:2328:A:C8	2.32	0.63
5:2F:188:ARG:HA	11:2P:3:LEU:HD11	1.80	0.63
32:1a:1031:G:H2'	32:1a:1032:G:C8	2.34	0.63
54:1w:188:THR:HB	54:1w:189:GLN:HE21	1.64	0.63
1:2A:749:C:OP2	61:2A:3931:HOH:O	2.15	0.63
18:1W:92:ARG:NH2	61:1W:301:HOH:O	2.31	0.63
1:2A:301:G:OP2	20:2Y:84:ARG:NH2	2.32	0.63
1:2A:2576:G:OP1	61:2A:3929:HOH:O	2.15	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:2H:37:VAL:HG22	7:2H:68:THR:HG22	1.80	0.63
32:2a:17:U:H2'	32:2a:18:C:C6	2.33	0.63
32:2a:972:C:O2'	41:2j:55:LYS:O	2.15	0.63
44:2m:45:VAL:HA	44:2m:48:LEU:HD12	1.80	0.63
1:1A:530:G:N1	1:1A:2023:G:OP1	2.24	0.63
1:1A:2206:G:H3'	1:1A:2207:G:H8	1.64	0.63
33:1b:82:ARG:NH1	33:1b:92:TYR:OH	2.31	0.63
1:2A:893:C:H2'	1:2A:894:C:C5	2.33	0.63
32:2a:1404:5MC:O2	32:2a:1519:MA6:O2'	2.16	0.63
34:2c:58:GLU:HB2	34:2c:65:ALA:HB3	1.80	0.63
21:1Z:1:MET:HG2	21:1Z:135:GLU:HG2	1.80	0.63
1:2A:468:G:O2'	5:2F:62:ARG:NH2	2.29	0.63
1:2A:1024:G:OP2	61:2A:3932:HOH:O	2.16	0.63
32:2a:1060:C:C5	34:2c:2:GLY:HA3	2.34	0.63
41:2j:6:ILE:HG12	41:2j:98:ILE:HD12	1.80	0.63
37:1f:82:ARG:HB2	37:1f:85:VAL:HG23	1.81	0.62
10:2O:115:VAL:HG13	10:2O:121:VAL:HG21	1.79	0.62
54:2w:147:SER:HB2	54:2w:158:VAL:HG12	1.81	0.62
34:1c:124:ILE:HD11	34:1c:189:ALA:HB3	1.81	0.62
32:2a:1510:U:H2'	32:2a:1511:G:C8	2.33	0.62
51:2t:22:ARG:O	51:2t:26:ASN:ND2	2.32	0.62
36:1e:100:VAL:HB	36:1e:107:ARG:HH12	1.64	0.62
1:2A:2169:A:H2'	1:2A:2170:A:C8	2.33	0.62
36:2e:80:ILE:HG22	36:2e:91:LEU:HB2	1.80	0.62
1:1A:81:G:H21	20:1Y:1:MET:HE1	1.64	0.62
1:1A:1045:A:H1'	1:1A:1047:G:N3	2.15	0.62
10:1O:120:GLU:OE1	15:1T:67:SER:OG	2.17	0.62
39:1h:34:GLU:OE1	39:1h:37:ARG:NH1	2.32	0.62
32:2a:1239:A:H4'	32:2a:1240:U:H5'	1.81	0.62
18:1W:4:LYS:HD2	18:1W:6:ILE:HD11	1.80	0.62
30:18:33:ASN:HA	30:18:36:LYS:HD2	1.81	0.62
34:2c:42:LEU:HA	34:2c:45:LYS:HD2	1.81	0.62
51:2t:9:ASN:OD1	51:2t:9:ASN:N	2.31	0.62
24:12:55:ARG:NH2	61:12:201:HOH:O	2.25	0.62
32:1a:1456:G:N2	51:1t:51:GLU:OE2	2.28	0.62
7:2H:159:GLU:HG3	7:2H:169:VAL:HG11	1.81	0.62
25:23:8:LEU:HB2	25:23:28:LEU:HD22	1.81	0.62
32:2a:56:U:H2'	32:2a:57:G:C8	2.35	0.62
32:2a:437:U:H5'	35:2d:155:LEU:HD21	1.81	0.62
40:2i:6:GLY:HA3	40:2i:80:GLY:O	2.00	0.62
42:2k:110:ASP:HB3	49:2r:85:LEU:HB3	1.82	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:1b:71:VAL:HG22	33:1b:164:VAL:HA	1.82	0.62
1:2A:1153:C:OP1	16:2U:92:ARG:NH2	2.33	0.62
1:2A:2788:C:OP1	4:2E:61:ARG:NH2	2.33	0.62
33:2b:115:LEU:HA	33:2b:118:LEU:HB2	1.81	0.62
9:1N:67:LEU:HD23	9:1N:87:LEU:HD13	1.81	0.61
32:1a:656:C:O2'	46:1o:28:GLN:OE1	2.12	0.61
14:2S:3:ARG:NH1	14:2S:4:LEU:O	2.33	0.61
38:2g:70:LYS:HG3	38:2g:100:ALA:HB2	1.81	0.61
40:2i:8:GLY:HA3	40:2i:15:ALA:HB3	1.81	0.61
1:1A:1045:A:H1'	1:1A:1047:G:C4	2.35	0.61
1:1A:2155:G:H3'	1:1A:2156:G:C8	2.35	0.61
32:1a:451:A:H61	32:1a:481:G:H5'	1.66	0.61
36:1e:78:HIS:HD2	39:1h:104:ARG:HD2	1.64	0.61
38:1g:113:GLU:HB3	38:1g:118:VAL:HG13	1.82	0.61
34:2c:11:ARG:HB3	34:2c:15:THR:HB	1.82	0.61
32:1a:601:C:H2'	32:1a:602:A:H8	1.64	0.61
2:2B:8:U:H5'	14:2S:15:ARG:NH1	2.15	0.61
35:2d:102:ASP:OD2	35:2d:118:ARG:NH1	2.33	0.61
1:1A:500:G:N7	61:1A:4178:HOH:O	2.30	0.61
2:1B:103:G:H21	21:1Z:73:GLN:HE22	1.48	0.61
32:1a:328:C:H4'	32:1a:329:A:H5''	1.83	0.61
33:1b:16:HIS:HB3	33:1b:210:SER:HB2	1.82	0.61
33:1b:21:ARG:O	33:1b:23:ARG:N	2.27	0.61
1:2A:993:G:OP1	16:2U:50:ARG:NH2	2.34	0.61
26:24:61:ARG:HH12	50:2s:41:VAL:HG12	1.65	0.61
5:1F:29:ASN:HB3	5:1F:112:MET:HE1	1.82	0.61
8:2I:87:LYS:H	8:2I:87:LYS:HD3	1.66	0.61
32:2a:202:U:H5''	32:2a:203:U:H5	1.64	0.61
32:2a:1402:4OC:HM22	32:2a:1403:C:H5'	1.83	0.61
36:2e:110:LEU:HD13	36:2e:118:ILE:HG21	1.81	0.61
40:2i:86:VAL:HG11	40:2i:93:ARG:HD3	1.82	0.61
1:1A:2124:G:H3'	1:1A:2125:G:H8	1.66	0.61
5:1F:155:LEU:HD11	5:1F:176:LEU:HD12	1.81	0.61
8:1I:75:LEU:HD22	8:1I:105:HIS:CD2	2.34	0.61
39:1h:106:GLY:O	39:1h:122:ARG:NH2	2.34	0.61
1:2A:1667:G:O2'	1:2A:1991:U:O4	2.17	0.61
34:2c:116:VAL:HG21	34:2c:202:ILE:HD11	1.82	0.61
40:2i:9:ARG:HB3	40:2i:104:ARG:HH11	1.65	0.61
41:2j:40:LEU:HB2	41:2j:69:ASN:HB3	1.83	0.61
1:1A:2749:A:OP1	7:1H:3:ARG:NH1	2.34	0.61
33:1b:112:VAL:HG12	33:1b:149:LEU:HD13	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:1h:95:VAL:HB	39:1h:99:GLU:HB2	1.83	0.61
44:1m:58:GLU:O	44:1m:62:ASN:ND2	2.20	0.61
32:2a:35:G:O2'	43:2l:118:SER:O	2.17	0.61
1:1A:1071:G:H1'	1:1A:1089:G:C5	2.36	0.61
54:2w:312:VAL:HG21	54:2w:327:VAL:HG21	1.83	0.61
33:1b:47:THR:O	33:1b:51:LEU:N	2.27	0.61
1:2A:586:A:N1	1:2A:809:G:O2'	2.27	0.61
5:2F:28:ILE:HD12	5:2F:119:ARG:HH21	1.65	0.61
35:2d:111:ALA:HA	35:2d:161:ASN:HD22	1.65	0.61
32:1a:961:U:OP2	32:1a:1223:C:O2'	2.10	0.61
32:2a:1288:A:N1	32:2a:1371:G:H1'	2.16	0.61
32:1a:1002:G:H3'	32:1a:1003:G:H4'	1.83	0.60
43:1l:6:THR:HG22	43:1l:8:ASN:N	2.16	0.60
6:2G:179:PRO:HB2	26:24:42:PHE:HE2	1.66	0.60
43:1l:6:THR:HG22	43:1l:8:ASN:H	1.66	0.60
47:1p:43:LYS:HA	47:1p:48:TRP:CD1	2.36	0.60
34:2c:11:ARG:NH2	34:2c:177:THR:O	2.28	0.60
49:2r:53:ARG:HG3	49:2r:63:GLN:HE21	1.65	0.60
1:1A:1071:G:H1'	1:1A:1089:G:C6	2.36	0.60
32:1a:363:A:OP2	43:1l:34:ARG:NH1	2.34	0.60
49:1r:25:THR:O	49:1r:25:THR:OG1	2.17	0.60
8:2I:31:LEU:HD21	8:2I:38:LEU:HG	1.83	0.60
11:2P:3:LEU:H	11:2P:3:LEU:HD12	1.66	0.60
32:1a:986:A:H1'	50:1s:55:LYS:HA	1.84	0.60
32:1a:1286:A:C8	32:1a:1287:A:H4'	2.30	0.60
1:2A:668:G:H5'	1:2A:669:G:OP2	2.02	0.60
1:2A:1786:A:H1'	1:2A:1938:A:N6	2.15	0.60
33:2b:124:SER:HB3	33:2b:125:PRO:HD3	1.82	0.60
33:1b:88:ALA:HB2	33:1b:219:VAL:HG13	1.83	0.60
32:1a:532:A:N6	32:1a:1206:G:O2'	2.34	0.60
54:1w:141:GLU:O	54:1w:163:ARG:N	2.31	0.60
44:2m:79:LYS:HA	44:2m:82:MET:HE2	1.83	0.60
11:1P:63:PRO:HD3	30:18:27:THR:HG22	1.84	0.60
32:1a:41:G:H2'	32:1a:42:G:H8	1.66	0.60
40:2i:79:LEU:HG	40:2i:83:ARG:HD2	1.82	0.60
32:1a:1030(C):G:N7	32:1a:1031:G:N2	2.46	0.60
32:1a:1435:G:H2'	32:1a:1436:U:C6	2.37	0.60
8:2I:63:ALA:HA	8:2I:66:GLU:HB2	1.83	0.60
21:2Z:69:THR:HG22	21:2Z:90:VAL:HA	1.84	0.60
36:2e:81:GLU:HG2	36:2e:90:VAL:HG13	1.84	0.60
40:1i:23:ASN:ND2	40:1i:23:ASN:H	2.00	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:2N:30:ILE:HG22	9:2N:34:LEU:HD22	1.84	0.60
32:2a:1022:G:H2'	32:2a:1023:G:C8	2.37	0.60
50:2s:33:THR:HG22	50:2s:35:SER:H	1.67	0.60
39:1h:10:LEU:HD22	39:1h:83:ILE:HD11	1.83	0.60
1:2A:875:G:H5''	21:2Z:149:SER:HB3	1.83	0.60
32:2a:619:U:N3	35:2d:134:ASP:OD1	2.33	0.60
16:1U:69:CYS:HB3	16:1U:74:LEU:HD13	1.84	0.59
32:2a:663:A:O3'	49:2r:64:ARG:NH2	2.34	0.59
33:2b:84:GLU:HB3	33:2b:219:VAL:HG21	1.84	0.59
1:2A:1693:U:O2'	3:2D:14:ARG:NH2	2.36	0.59
15:2T:109:GLU:HG2	15:2T:112:ARG:HH22	1.66	0.59
26:24:34:GLU:HG2	26:24:35:VAL:HG23	1.83	0.59
44:2m:60:VAL:HG23	44:2m:64:TRP:CE3	2.36	0.59
19:1X:57:LEU:HD11	19:1X:78:LYS:HE2	1.83	0.59
33:1b:21:ARG:HA	33:1b:39:ILE:HA	1.85	0.59
47:1p:45:THR:HG23	47:1p:47:ASP:H	1.68	0.59
32:1a:1055:A:N7	32:1a:1200:C:N4	2.50	0.59
1:2A:2189:U:H2'	1:2A:2190:G:C8	2.38	0.59
2:2B:66:A:H61	2:2B:109:C:H5'	1.67	0.59
32:2a:67:C:H2'	32:2a:68:G:C8	2.37	0.59
32:2a:1133:G:H2'	32:2a:1134:G:H8	1.66	0.59
1:1A:588:U:H2'	1:1A:589:C:C6	2.36	0.59
1:2A:336:C:O2'	20:2Y:35:TYR:OH	2.20	0.59
18:2W:25:ARG:NH2	18:2W:74:ALA:O	2.32	0.59
1:1A:1064:C:O2	1:1A:1074:G:N1	2.33	0.59
32:1a:601:C:H2'	32:1a:602:A:C8	2.38	0.59
19:2X:94:GLY:H	19:2X:95:LEU:HB2	1.68	0.59
21:2Z:52:SER:OG	21:2Z:53:ILE:N	2.32	0.59
1:1A:1859:A:N6	1:1A:1883:G:O2'	2.35	0.59
1:1A:2469:A:O2'	12:1Q:56:ARG:NE	2.35	0.59
32:1a:160:A:H2'	32:1a:161:A:O4'	2.03	0.59
1:2A:628:G:H5''	30:28:18:ALA:HB2	1.84	0.59
24:22:49:LYS:HA	24:22:52:ASP:HB2	1.84	0.59
32:2a:176:C:H2'	32:2a:177:C:H6	1.66	0.59
32:2a:926:G:N2	53:2v:15:A:OP2	2.35	0.59
1:1A:1059:G:H2'	1:1A:1060:U:C5	2.37	0.59
1:1A:2106:G:H2'	1:1A:2107:C:C6	2.37	0.59
1:1A:2166:G:H2'	1:1A:2167:U:C5	2.38	0.59
32:1a:1412:C:H2'	32:1a:1413:A:C8	2.38	0.59
34:1c:15:THR:HG21	34:1c:181:ASN:HA	1.84	0.59
6:2G:106:LEU:HA	6:2G:110:ALA:HB3	1.85	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1347:G:N2	32:2a:1373:G:H2'	2.18	0.59
1:1A:2312:U:H5'	6:1G:88:ILE:HD11	1.85	0.59
5:1F:101:LEU:HD12	5:1F:102:PRO:HD2	1.85	0.59
6:2G:47:LYS:NZ	6:2G:80:PHE:O	2.26	0.59
12:2Q:110:THR:HB	12:2Q:113:GLN:H	1.67	0.59
19:2X:57:LEU:HD11	19:2X:78:LYS:HE2	1.85	0.59
32:2a:222:U:H2'	32:2a:223:U:C6	2.37	0.59
32:1a:757:U:H2'	32:1a:758:G:O4'	2.03	0.59
51:1t:57:ARG:NH1	51:1t:100:ILE:HD12	2.15	0.59
1:1A:1023:U:OP2	61:1A:4136:HOH:O	2.17	0.58
1:1A:1025:G:C4	1:1A:1135:C:H1'	2.38	0.58
1:1A:1469:A:OP2	61:1A:4139:HOH:O	2.17	0.58
1:1A:2023:G:H5'	1:1A:2617:C:H4'	1.85	0.58
1:1A:2331:G:O2'	1:1A:2336:A:N1	2.35	0.58
26:24:43:TYR:O	26:24:45:GLY:N	2.36	0.58
46:2o:7:GLU:OE1	46:2o:38:ARG:NH2	2.36	0.58
32:1a:1391:U:H2'	32:1a:1392:G:C8	2.38	0.58
33:1b:16:HIS:HD2	33:1b:18:GLY:H	1.51	0.58
33:1b:48:MET:HA	33:1b:51:LEU:HB2	1.85	0.58
34:1c:191:THR:OG1	34:1c:194:GLY:O	2.20	0.58
43:1l:53:ARG:HB3	43:1l:69:TYR:HE1	1.68	0.58
11:2P:19:VAL:HG12	11:2P:27:HIS:HB3	1.86	0.58
32:2a:1263:C:N3	32:2a:1272:G:O6	2.35	0.58
33:2b:124:SER:HB3	33:2b:125:PRO:CD	2.33	0.58
51:2t:57:ARG:HH22	51:2t:100:ILE:HD12	1.67	0.58
1:1A:991:C:OP2	61:1A:4135:HOH:O	2.17	0.58
21:2Z:72:ARG:NH2	21:2Z:97:GLU:O	2.35	0.58
32:2a:1492:A:N6	43:2l:48:PRO:O	2.36	0.58
1:1A:2127:G:H21	1:1A:2173:A:H1'	1.68	0.58
32:1a:1314:C:OP1	50:1s:6:LYS:NZ	2.33	0.58
42:2k:31:THR:HG22	42:2k:42:TRP:HB2	1.84	0.58
1:2A:1019:U:H3	1:2A:1142(A):A:H62	1.51	0.58
5:2F:167:ALA:HB1	5:2F:173:VAL:HG11	1.85	0.58
32:2a:1005:A:OP2	32:2a:1024:G:N2	2.37	0.58
32:2a:1133:G:H2'	32:2a:1134:G:C8	2.38	0.58
50:2s:27:GLU:HB2	50:2s:28:LYS:HB3	1.84	0.58
1:1A:2328:A:H2'	1:1A:2329:G:C8	2.39	0.58
14:2S:83:LYS:HG3	14:2S:84:GLN:H	1.69	0.58
33:2b:69:LEU:HB3	33:2b:162:ILE:HG22	1.85	0.58
35:1d:61:LYS:NZ	35:1d:72:GLU:OE1	2.37	0.58
37:1f:38:GLU:OE1	37:1f:64:GLN:NE2	2.37	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:154(A):C:H42	1:2A:171:G:H1	1.50	0.58
26:24:48:ARG:O	26:24:50:VAL:N	2.33	0.58
26:24:62:ARG:HA	26:24:62:ARG:NE	2.18	0.58
32:2a:256:U:OP1	48:2q:17:LYS:NZ	2.37	0.58
32:2a:1086:U:H3	32:2a:1099:G:H22	1.52	0.58
7:1H:3:ARG:HH11	7:1H:4:ILE:H	1.52	0.58
52:1u:3:LYS:HB3	52:1u:14:TRP:CD1	2.39	0.58
40:2i:28:VAL:HG12	40:2i:63:ILE:HB	1.86	0.58
1:1A:1093:G:H1'	1:1A:1098:A:N6	2.19	0.58
1:1A:2614:A:OP1	61:1A:4138:HOH:O	2.17	0.58
32:1a:64:G:H4'	32:1a:65:U:H3'	1.86	0.58
50:1s:63:THR:OG1	50:1s:65:ASN:OD1	2.22	0.58
1:2A:323:G:O2'	1:2A:1205:U:N3	2.30	0.58
1:2A:959:A:N3	1:2A:2457:U:O2'	2.36	0.58
1:2A:2646:C:OP2	1:2A:2732:G:O2'	2.22	0.58
15:2T:60:THR:HG22	15:2T:77:PRO:HA	1.86	0.58
32:2a:1251:A:H2'	32:2a:1252:A:C8	2.39	0.58
5:1F:167:ALA:HB1	5:1F:173:VAL:HG11	1.85	0.58
42:1k:14:VAL:HG22	42:1k:16:SER:H	1.69	0.58
1:2A:1434:A:H61	1:2A:1558:A:H62	1.51	0.58
1:2A:2611:U:C4	27:25:3:LYS:HG2	2.39	0.58
32:1a:624:C:H2'	32:1a:625:G:H8	1.69	0.57
49:2r:25:THR:O	49:2r:25:THR:OG1	2.22	0.57
1:1A:2139:C:H2'	1:1A:2140:C:O4'	2.04	0.57
32:1a:189(K):U:H2'	32:1a:189(L):G:C8	2.40	0.57
32:1a:1033:G:H2'	32:1a:1034:G:C8	2.39	0.57
34:1c:35:GLU:OE2	34:1c:59:ARG:NH2	2.34	0.57
32:2a:1310:G:H5'	44:2m:77:ASN:HD21	1.69	0.57
34:2c:32:LEU:HD23	34:2c:59:ARG:HD3	1.85	0.57
50:2s:50:ALA:HB1	50:2s:57:HIS:HB3	1.86	0.57
15:1T:39:ARG:NH2	32:1a:345:C:OP2	2.38	0.57
32:1a:381:C:H2'	32:1a:382:A:O4'	2.04	0.57
32:1a:1277:C:O2'	32:1a:1279:A:H1'	2.03	0.57
46:1o:54:ARG:HG2	46:1o:58:MET:HE2	1.86	0.57
32:2a:64:G:H4'	32:2a:65:U:H3'	1.85	0.57
32:2a:134:A:H61	47:2p:25:ARG:HH12	1.50	0.57
32:2a:564:C:O2'	39:2h:91:ARG:NH1	2.34	0.57
33:1b:15:VAL:HG11	33:1b:213:LEU:HD12	1.85	0.57
35:1d:105:VAL:HG21	35:1d:126:ILE:HD13	1.86	0.57
1:2A:625:G:O6	11:2P:107:LYS:NZ	2.38	0.57
1:2A:1309:G:H4'	29:27:7:PRO:HB2	1.84	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1191:A:OP2	34:2c:3:ASN:ND2	2.37	0.57
44:2m:40:ASN:HD22	44:2m:43:THR:HG23	1.68	0.57
1:1A:2107:C:N4	1:1A:2108:C:N3	2.53	0.57
11:2P:63:PRO:HD3	30:28:27:THR:HG22	1.86	0.57
32:2a:1068:G:N2	32:2a:1191:A:N3	2.51	0.57
4:1E:9:VAL:HG13	15:1T:3:ARG:HG2	1.87	0.57
32:1a:310:G:OP2	47:1p:27:LYS:NZ	2.32	0.57
1:1A:2336:A:H61	22:10:43:THR:CG2	2.17	0.57
33:1b:134:GLU:O	33:1b:138:LEU:HG	2.05	0.57
36:1e:78:HIS:HE1	36:1e:142:LEU:HA	1.70	0.57
11:2P:94:GLU:HG3	11:2P:124:LYS:HD2	1.86	0.57
15:2T:117:ASP:OD2	15:2T:120:ARG:NE	2.35	0.57
35:2d:153:ARG:HH11	35:2d:181:MET:HE3	1.70	0.57
38:2g:68:ASN:HD22	38:2g:128:ALA:HA	1.70	0.57
1:1A:1292:U:H2'	1:1A:1293:C:C6	2.40	0.57
1:2A:307:G:H21	1:2A:330:A:H62	1.51	0.57
19:2X:60:ARG:HH22	29:27:47:ARG:HH12	1.52	0.57
32:2a:1320:C:H2'	32:2a:1321:C:O4'	2.04	0.57
35:2d:122:ARG:HH12	35:2d:134:ASP:HB2	1.70	0.57
5:1F:53:THR:CG2	5:1F:55:GLY:H	2.17	0.57
22:10:11:ARG:O	22:10:14:ARG:NH2	2.38	0.57
32:1a:1151:A:O3'	41:1j:70:ARG:NH2	2.38	0.57
28:26:6:ARG:NH1	28:26:26:ASN:HB2	2.20	0.57
36:2e:6:PHE:HE1	36:2e:36:ASP:HB3	1.69	0.57
54:2w:219:ILE:HG12	54:2w:241:VAL:HG12	1.87	0.57
1:1A:1823:G:OP1	3:1D:54:ARG:NH1	2.38	0.57
32:1a:1305:G:N2	32:1a:1331:G:H1'	2.20	0.57
36:1e:137:GLU:HG3	36:1e:141:GLN:HE21	1.69	0.57
1:2A:1482:G:H2'	1:2A:1484:G:H8	1.69	0.57
1:2A:1530:C:H42	1:2A:1539:G:H1	1.51	0.57
1:2A:2321:G:H5''	1:2A:2322:A:OP2	2.05	0.57
21:2Z:125:LEU:HG	21:2Z:164:ALA:HB3	1.87	0.57
33:2b:81:VAL:HG12	33:2b:215:LEU:HD21	1.87	0.57
1:1A:2334:G:H5'	14:1S:9:ARG:HG2	1.87	0.56
32:1a:434:U:H2'	32:1a:435:C:C6	2.40	0.56
1:2A:2138:C:N4	1:2A:2153:G:H1	2.02	0.56
32:2a:461:A:O2'	32:2a:471:G:N7	2.32	0.56
1:1A:1266:G:O5'	18:1W:15:ARG:NH2	2.38	0.56
1:1A:1783:A:OP1	61:1A:4131:HOH:O	2.18	0.56
32:1a:67:C:H2'	32:1a:68:G:C8	2.40	0.56
32:1a:1240:U:OP2	38:1g:116:ALA:N	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:1b:133:LYS:O	33:1b:136:VAL:HG22	2.05	0.56
49:1r:32:ARG:HA	49:1r:69:THR:HG21	1.87	0.56
1:2A:1621:U:OP1	61:2A:3937:HOH:O	2.17	0.56
1:1A:1235:G:OP1	61:1A:4134:HOH:O	2.18	0.56
1:1A:1783:A:N7	61:1A:4185:HOH:O	2.32	0.56
8:1I:62:LYS:HE2	8:1I:133:HIS:HE1	1.70	0.56
20:1Y:38:ILE:HD11	20:1Y:66:PRO:HG3	1.88	0.56
32:1a:501:C:H1'	32:1a:549:C:H1'	1.87	0.56
32:1a:1530:G:H2'	32:1a:1531:A:C8	2.40	0.56
33:1b:163:PHE:HA	33:1b:185:ILE:HG12	1.86	0.56
43:1l:79:GLU:HG2	43:1l:80:HIS:HD2	1.71	0.56
1:2A:1607:C:N4	1:2A:1622:G:OP2	2.37	0.56
6:2G:145:THR:HB	6:2G:148:MET:HG2	1.87	0.56
22:20:23:VAL:HG22	22:20:38:VAL:HG22	1.85	0.56
24:22:35:LEU:HD13	24:22:53:LEU:HD12	1.86	0.56
26:24:40:HIS:HB3	26:24:43:TYR:HD2	1.70	0.56
35:2d:107:ARG:HH21	35:2d:194:LEU:HD23	1.70	0.56
39:2h:51:VAL:HG21	39:2h:60:ARG:HE	1.70	0.56
48:2q:67:LYS:O	48:2q:68:ARG:HB2	2.05	0.56
1:1A:602:G:O2'	1:1A:655:A:N6	2.39	0.56
3:1D:148:GLU:HB2	3:1D:151:LYS:HD2	1.87	0.56
17:1V:76:LYS:HB2	17:1V:81:TYR:HB3	1.87	0.56
30:18:42:ARG:HD2	61:18:203:HOH:O	2.05	0.56
1:2A:643:A:N1	1:2A:2369:A:O2'	2.38	0.56
30:28:28:GLY:O	30:28:36:LYS:NZ	2.36	0.56
32:2a:56:U:H2'	32:2a:57:G:H8	1.67	0.56
1:1A:271(M):G:N3	8:1I:50:ARG:NH1	2.54	0.56
32:1a:41:G:H2'	32:1a:42:G:C8	2.41	0.56
36:1e:50:GLU:HB2	36:1e:53:LEU:HD13	1.88	0.56
54:1w:198:THR:HG21	54:1w:293:ILE:HG23	1.87	0.56
42:2k:84:VAL:HG21	42:2k:95:ILE:HD11	1.88	0.56
1:2A:302:C:OP2	20:2Y:73:ARG:NH1	2.38	0.56
1:2A:2143:C:H2'	1:2A:2144:U:O4'	2.05	0.56
3:2D:71:ASP:HB3	3:2D:103:ARG:HH12	1.70	0.56
32:2a:1002:G:C6	32:2a:1003:G:H1'	2.41	0.56
32:2a:1218:C:H2'	32:2a:1219:U:C6	2.40	0.56
42:2k:41:THR:HG21	42:2k:71:LYS:HB3	1.87	0.56
51:2t:60:GLU:HG3	51:2t:81:LYS:HD2	1.86	0.56
1:1A:886:C:H2'	1:1A:887:A:H5''	1.88	0.56
1:1A:2840:C:OP1	61:1A:4137:HOH:O	2.17	0.56
32:1a:56:U:H2'	32:1a:57:G:H8	1.68	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1v:20:A:N6	54:1w:186:THR:OG1	2.39	0.56
16:2U:49:HIS:HA	16:2U:52:ARG:HG2	1.88	0.56
24:22:22:GLU:OE2	24:22:68:ARG:NH2	2.27	0.56
33:2b:33:TYR:HB3	33:2b:41:ILE:HD11	1.87	0.56
38:2g:69:VAL:HG21	38:2g:104:LEU:HD21	1.88	0.56
1:1A:1779:U:H2'	61:1A:4185:HOH:O	2.06	0.56
2:1B:28:C:OP1	14:1S:36:TYR:OH	2.23	0.56
33:1b:24:TRP:CD1	33:1b:24:TRP:H	2.24	0.56
35:1d:64:LEU:HB2	35:1d:198:VAL:HG11	1.88	0.56
42:1k:31:THR:HG22	42:1k:42:TRP:HB2	1.88	0.56
1:2A:2502:G:N7	61:2A:3997:HOH:O	2.32	0.56
3:2D:148:GLU:HB2	3:2D:151:LYS:HD2	1.88	0.56
14:2S:62:LYS:HB3	14:2S:97:ARG:NE	2.20	0.56
3:1D:71:ASP:CB	3:1D:103:ARG:HH12	2.18	0.56
40:1i:118:LYS:HB2	40:1i:121:ARG:HB3	1.88	0.56
1:2A:1472:A:N6	1:2A:1519:G:O2'	2.38	0.56
8:2I:14:ASP:OD1	8:2I:15:VAL:N	2.38	0.56
1:1A:686:G:OP1	29:17:11:LYS:NZ	2.39	0.56
7:1H:24:VAL:HG22	7:1H:35:VAL:HB	1.89	0.56
25:13:7:LYS:HB2	25:13:34:GLU:HG2	1.88	0.56
34:1c:91:LEU:HD22	34:1c:101:LEU:HD12	1.88	0.56
4:2E:174:ASP:OD1	4:2E:175:VAL:N	2.37	0.56
18:2W:30:GLU:O	18:2W:34:ASN:ND2	2.39	0.56
32:2a:266:G:H5''	32:2a:268:C:H41	1.70	0.56
32:2a:269:C:H2'	32:2a:270:A:C8	2.41	0.56
32:2a:750:G:N3	46:2o:23:GLY:HA3	2.21	0.56
32:2a:939:G:OP1	38:2g:95:ARG:NH2	2.34	0.56
1:1A:1580:A:OP2	1:1A:1580:A:H8	1.88	0.55
14:1S:27:SER:HA	14:1S:88:ASP:HB3	1.88	0.55
15:1T:108:ARG:NH2	15:1T:112:ARG:HD3	2.21	0.55
40:1i:6:GLY:HA3	40:1i:83:ARG:HB3	1.88	0.55
6:2G:36:LYS:NZ	6:2G:95:ARG:HH12	2.04	0.55
32:2a:1305:G:H22	32:2a:1331:G:H1'	1.71	0.55
40:2i:97:LYS:HA	40:2i:102:LEU:HD22	1.87	0.55
55:2x:19:G:O2'	55:2x:20:H2U:OP1	2.22	0.55
1:1A:1693:U:O2'	3:1D:14:ARG:NH2	2.39	0.55
21:1Z:138:GLU:H	21:1Z:156:LYS:NZ	2.04	0.55
26:14:58:ARG:O	26:14:61:ARG:HB3	2.05	0.55
1:2A:247:G:H4'	1:2A:386:G:C5	2.41	0.55
14:2S:39:ILE:HB	14:2S:49:VAL:HG12	1.87	0.55
32:2a:1052:U:O2'	32:2a:1055:A:OP2	2.16	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1073:A:H2'	1:1A:1074:G:C8	2.41	0.55
26:14:53:GLU:HB2	26:14:55:ARG:H	1.72	0.55
32:1a:1442:G:H2'	32:1a:1442:G:N3	2.20	0.55
38:1g:16:LEU:HD11	40:1i:45:ALA:HB2	1.88	0.55
44:1m:49:THR:HG22	44:1m:51:ALA:H	1.72	0.55
18:2W:65:LEU:HB2	18:2W:68:ARG:HG3	1.88	0.55
7:1H:3:ARG:NH1	7:1H:4:ILE:H	2.04	0.55
32:1a:1292:U:OP2	38:1g:41:ARG:NH2	2.39	0.55
1:2A:1141:U:OP2	9:2N:63:THR:OG1	2.24	0.55
1:2A:1503:U:H2'	1:2A:1504:C:C6	2.41	0.55
1:2A:1633:G:OP2	61:2A:3938:HOH:O	2.18	0.55
1:2A:2033:A:OP1	61:2A:3941:HOH:O	2.18	0.55
21:2Z:8:TYR:HB2	21:2Z:38:TYR:CE2	2.42	0.55
33:2b:172:ILE:HD12	33:2b:172:ILE:H	1.71	0.55
1:1A:2134:A:H2'	1:1A:2135:A:C8	2.41	0.55
1:1A:2483:C:N3	12:1Q:124:LYS:NZ	2.53	0.55
7:1H:41:MET:HE2	7:1H:65:HIS:HA	1.88	0.55
1:2A:2100:G:H1	1:2A:2189:U:H3	1.53	0.55
45:2n:32:SER:O	45:2n:40:CYS:HA	2.06	0.55
35:1d:101:LEU:HB2	35:1d:138:TYR:HB3	1.89	0.55
55:1x:8:4SU:O2'	55:1x:46:A:N3	2.38	0.55
1:2A:796:C:H2'	1:2A:797:C:C6	2.41	0.55
32:2a:1070:U:H2'	32:2a:1071:C:C6	2.42	0.55
32:2a:1240:U:C2	38:2g:32:ARG:HD2	2.42	0.55
54:2w:119:GLU:HA	54:2w:122:LEU:HD12	1.87	0.55
32:1a:1223:C:OP2	50:1s:78:ARG:NH2	2.35	0.55
1:2A:1847:A:H3'	1:2A:1848:A:H5'	1.87	0.55
1:2A:2023:G:H5'	1:2A:2617:C:H4'	1.87	0.55
1:2A:2285:C:OP2	28:26:6:ARG:NH1	2.39	0.55
4:2E:48:GLN:HA	4:2E:80:GLU:HA	1.88	0.55
14:2S:15:ARG:HB3	14:2S:19:LYS:HE3	1.89	0.55
32:2a:1187:G:OP1	40:2i:113:LYS:NZ	2.40	0.55
37:2f:97:PHE:HE2	49:2r:62:GLU:HG2	1.71	0.55
42:2k:48:ILE:HG12	42:2k:63:LEU:HB3	1.89	0.55
45:2n:48:ALA:HB2	45:2n:53:LEU:HD12	1.89	0.55
1:1A:1056:G:H4'	1:1A:1086:A:C8	2.42	0.55
1:1A:1267:U:OP1	61:1A:4143:HOH:O	2.18	0.55
15:1T:108:ARG:HH22	15:1T:112:ARG:HD3	1.71	0.55
15:1T:127:ALA:C	15:1T:129:ARG:H	2.14	0.55
32:1a:1355:G:H2'	32:1a:1356:G:C8	2.42	0.55
1:2A:300:A:OP1	20:2Y:86:ARG:NH2	2.39	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1226:C:H2'	44:2m:103:THR:HB	1.88	0.55
34:1c:53:ALA:HB2	34:1c:115:LEU:HG	1.88	0.55
1:2A:1796:U:H2'	1:2A:1797:C:C6	2.41	0.55
1:2A:2445:G:OP1	5:2F:74:ARG:NH2	2.35	0.55
32:2a:1280:A:H5'	41:2j:40:LEU:HD22	1.88	0.55
46:2o:39:LEU:HD13	46:2o:56:LEU:HB2	1.88	0.55
54:2w:348:LEU:HA	54:2w:352:ALA:HB3	1.89	0.55
1:1A:2126:A:N6	1:1A:2163:C:O4'	2.39	0.55
21:1Z:52:SER:C	21:1Z:54:HIS:H	2.15	0.55
21:1Z:72:ARG:NH2	21:1Z:97:GLU:O	2.39	0.55
32:1a:1356:G:H2'	32:1a:1357:A:H8	1.72	0.55
33:1b:185:ILE:HG22	33:1b:199:TYR:HD2	1.72	0.55
1:2A:1664:A:OP1	61:2A:3942:HOH:O	2.18	0.55
21:2Z:11:GLU:O	21:2Z:36:LYS:NZ	2.31	0.55
32:2a:1206:G:O4'	34:2c:194:GLY:N	2.40	0.55
49:2r:73:ALA:HB1	49:2r:78:LEU:HB2	1.89	0.55
1:1A:1379:A:H4'	1:1A:1380:G:OP2	2.06	0.54
6:1G:12:TYR:HA	6:1G:16:ARG:HG3	1.89	0.54
36:1e:33:VAL:HG21	36:1e:109:ILE:HA	1.90	0.54
32:2a:1435:G:H2'	32:2a:1436:U:C6	2.42	0.54
33:2b:98:LEU:HG	33:2b:101:MET:HE3	1.90	0.54
1:1A:536:A:H2'	1:1A:537:C:C6	2.42	0.54
26:14:24:THR:OG1	26:14:25:TYR:N	2.40	0.54
32:1a:1218:C:OP2	45:1n:9:LYS:NZ	2.41	0.54
1:2A:11:G:H2'	1:2A:12:U:H5'	1.89	0.54
1:2A:1237:A:OP1	61:2A:3940:HOH:O	2.18	0.54
2:2B:9:G:P	14:2S:25:ARG:HH22	2.30	0.54
21:2Z:98:MET:HE2	21:2Z:100:VAL:HG22	1.88	0.54
32:2a:1141:C:H2'	32:2a:1142:G:C8	2.40	0.54
46:2o:54:ARG:HG2	46:2o:58:MET:HE2	1.89	0.54
55:2x:19:G:H3'	55:2x:20:H2U:H5''	1.89	0.54
7:1H:150:ALA:HA	7:1H:153:LYS:HE3	1.90	0.54
1:2A:1579:A:H2'	1:2A:1580:A:C8	2.43	0.54
32:2a:45:U:H2'	32:2a:46:G:C8	2.43	0.54
33:2b:61:LEU:HD21	33:2b:160:ASP:HB2	1.89	0.54
33:2b:167:PRO:HD3	33:2b:187:LEU:O	2.08	0.54
1:1A:881:G:H2'	1:1A:882:G:O4'	2.07	0.54
1:1A:1528:A:OP2	61:1A:4144:HOH:O	2.18	0.54
1:1A:2305:A:H5''	6:1G:134:GLY:HA3	1.90	0.54
19:1X:44:GLU:HG2	19:1X:49:VAL:O	2.07	0.54
19:1X:44:GLU:HG3	19:1X:51:VAL:HG23	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:100:C:H2'	32:1a:101:A:C8	2.42	0.54
33:1b:201:ILE:HG21	33:1b:214:ILE:HG21	1.89	0.54
1:2A:2206:G:H3'	1:2A:2207:G:N7	2.21	0.54
3:2D:39:LYS:NZ	3:2D:57:GLY:O	2.40	0.54
32:2a:1119:C:H2'	32:2a:1120:G:H8	1.73	0.54
32:2a:1279:A:OP1	41:2j:9:ARG:NH2	2.40	0.54
39:2h:41:ARG:NH2	39:2h:123:GLU:OE2	2.40	0.54
1:1A:1005:C:H5''	61:1A:4154:HOH:O	2.08	0.54
1:1A:1068:G:H2'	1:1A:1096:A:O2'	2.08	0.54
1:1A:1786:A:H1'	1:1A:1938:A:N6	2.23	0.54
1:1A:2138:C:H42	1:1A:2153:G:H1	1.55	0.54
1:1A:2494:G:O2'	12:1Q:80:GLU:HA	2.06	0.54
32:2a:363:A:OP2	43:2l:34:ARG:NH1	2.40	0.54
34:2c:181:ASN:ND2	34:2c:204:LEU:HD12	2.22	0.54
38:2g:65:ALA:HB1	38:2g:127:ALA:HB3	1.90	0.54
44:2m:3:ARG:HG2	44:2m:4:ILE:HG22	1.88	0.54
47:2p:19:ILE:HG22	47:2p:36:ILE:HG13	1.88	0.54
3:1D:108:PRO:HD2	3:1D:111:LEU:HD22	1.90	0.54
26:14:59:PHE:CD1	26:14:60:GLN:HG2	2.43	0.54
32:1a:60:A:N1	32:1a:107:G:O2'	2.38	0.54
32:1a:1055:A:H2'	34:1c:156:ARG:HD2	1.88	0.54
7:2H:3:ARG:NH1	7:2H:4:ILE:H	2.05	0.54
29:27:24:THR:HG22	29:27:27:GLY:H	1.72	0.54
41:2j:32:ALA:HB3	41:2j:74:ILE:HD11	1.89	0.54
49:2r:26:LEU:HD21	49:2r:39:VAL:HG13	1.90	0.54
1:1A:2166:G:H2'	1:1A:2167:U:H5	1.71	0.54
5:1F:32:LEU:HD23	5:1F:112:MET:HE2	1.89	0.54
42:1k:91:ARG:HH21	49:1r:87:ARG:NH2	2.06	0.54
47:1p:22:THR:OG1	47:1p:23:ASP:N	2.41	0.54
1:2A:120:U:OP2	61:2A:3939:HOH:O	2.18	0.54
1:2A:2171:A:N3	1:2A:2172:U:N3	2.55	0.54
1:1A:2115:G:H1	1:1A:2119:A:P	2.31	0.54
19:1X:41:ASN:O	19:1X:45:THR:HG23	2.08	0.54
32:1a:1123:A:O2'	41:1j:37:PRO:O	2.24	0.54
35:1d:108:LEU:HD21	35:1d:183:GLY:HA3	1.90	0.54
54:1w:223:ARG:HB2	54:1w:223:ARG:HH11	1.73	0.54
1:2A:2758:A:C4	7:2H:67:LEU:HD21	2.42	0.54
32:2a:501:C:H2'	32:2a:502:G:C8	2.42	0.54
32:2a:1132:C:H2'	32:2a:1133:G:H8	1.72	0.54
1:1A:2161:C:O2'	1:1A:2162:G:H8	1.88	0.54
1:1A:2774:C:OP2	61:1A:4141:HOH:O	2.18	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:1G:137:GLU:HB3	6:1G:139:LEU:HD12	1.89	0.54
1:2A:322:A:OP1	5:2F:168:ARG:HD2	2.08	0.54
14:2S:49:VAL:HG11	14:2S:77:ALA:HB2	1.90	0.54
32:2a:959:A:O2'	32:2a:984:C:O2'	2.19	0.54
32:2a:1163:C:H2'	32:2a:1164:G:C8	2.42	0.54
33:2b:28:PHE:CD1	33:2b:194:PRO:HG3	2.42	0.54
34:2c:181:ASN:HD22	34:2c:204:LEU:HD12	1.73	0.54
35:2d:150:GLU:HA	35:2d:153:ARG:HG3	1.89	0.54
38:2g:27:ILE:HA	38:2g:30:ILE:HD12	1.89	0.54
39:2h:12:ARG:HD2	39:2h:26:VAL:HG13	1.88	0.54
1:1A:185:U:H4'	1:1A:218:A:H4'	1.90	0.54
12:1Q:111:GLU:O	12:1Q:115:MET:HG2	2.08	0.54
34:1c:56:ASP:HB2	34:1c:67:THR:HB	1.89	0.54
35:1d:28:SER:OG	35:1d:30:LYS:HG2	2.08	0.54
39:1h:121:ASP:HB2	39:1h:125:ARG:NH2	2.23	0.54
24:22:16:LEU:HD13	24:22:20:GLU:HB3	1.90	0.54
35:2d:122:ARG:HH11	35:2d:122:ARG:HA	1.72	0.54
1:1A:184:C:H2'	1:1A:185:U:C6	2.44	0.53
1:1A:1518:U:H2'	1:1A:1519:G:O4'	2.08	0.53
1:1A:2109:U:O4	1:1A:2179:C:N4	2.41	0.53
3:1D:163:ALA:HB1	3:1D:175:LEU:HD22	1.90	0.53
32:1a:1140:C:H2'	32:1a:1141:C:H6	1.73	0.53
39:1h:120:THR:H	39:1h:123:GLU:HB2	1.73	0.53
1:2A:602:G:O2'	1:2A:655:A:N6	2.41	0.53
1:2A:2135:A:C4	1:2A:2136:C:H5	2.26	0.53
1:2A:2396:G:OP1	23:21:25:LYS:NZ	2.33	0.53
1:2A:2602:A:OP1	61:2A:3946:HOH:O	2.19	0.53
5:2F:197:ASP:OD1	5:2F:197:ASP:N	2.35	0.53
32:2a:652:U:O4	32:2a:752:G:O2'	2.22	0.53
1:1A:1187:G:H5''	17:1V:81:TYR:CE1	2.44	0.53
8:1I:95:LYS:NZ	8:1I:99:GLU:OE2	2.42	0.53
32:1a:946:A:H2'	32:1a:947:G:C8	2.43	0.53
32:1a:1060:C:C5	34:1c:2:GLY:HA3	2.43	0.53
54:1w:151:ASP:OD1	54:1w:151:ASP:N	2.41	0.53
1:2A:131:G:OP1	61:2A:3944:HOH:O	2.18	0.53
33:2b:135:GLN:O	33:2b:139:LYS:HG3	2.09	0.53
40:2i:49:PRO:HD3	40:2i:78:LYS:HG3	1.91	0.53
54:2w:324:LEU:HA	54:2w:327:VAL:HG22	1.90	0.53
9:1N:13:TRP:HB3	9:1N:135:PRO:HB3	1.89	0.53
32:1a:148:G:H2'	32:1a:149:A:C8	2.44	0.53
35:1d:175:SER:HB3	35:1d:184:LYS:HB3	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:1h:14:ARG:NH2	39:1h:83:ILE:O	2.36	0.53
1:2A:1915:5MU:O2	54:2w:286:ARG:NH1	2.42	0.53
33:2b:37:ASN:O	33:2b:39:ILE:HG12	2.09	0.53
43:2l:70:ILE:HG12	43:2l:100:ILE:HD12	1.90	0.53
1:1A:883:G:N2	1:1A:893:C:H42	2.04	0.53
1:1A:2120:G:H2'	1:1A:2121:G:C8	2.43	0.53
22:10:32:ARG:H	22:10:35:ASN:ND2	2.06	0.53
34:2c:131:ARG:NH2	36:2e:50:GLU:HG3	2.24	0.53
35:2d:146:ILE:HD12	35:2d:146:ILE:H	1.72	0.53
32:1a:1144:G:N2	32:1a:1146:A:H62	2.06	0.53
34:1c:60:ALA:HB2	41:1j:92:THR:HG22	1.90	0.53
44:1m:74:VAL:O	44:1m:78:ILE:HG13	2.09	0.53
1:2A:361:G:O2'	1:2A:362:U:H5'	2.09	0.53
1:2A:636:G:OP1	11:2P:132:LYS:NZ	2.34	0.53
1:2A:2022:U:O2'	1:2A:2617:C:H5'	2.08	0.53
19:2X:72:LYS:NZ	19:2X:75:ASP:OD1	2.32	0.53
1:1A:2163:C:H2'	1:1A:2164:C:H5'	1.89	0.53
7:1H:98:LEU:HG	7:1H:125:VAL:HG23	1.90	0.53
11:1P:3:LEU:H	11:1P:3:LEU:HD12	1.73	0.53
22:10:10:THR:HG22	22:10:12:ASN:H	1.74	0.53
32:1a:1108:G:O6	61:1a:1904:HOH:O	2.14	0.53
44:1m:56:LEU:O	44:1m:60:VAL:HG23	2.09	0.53
1:2A:271(H):G:H2'	1:2A:271(I):G:C8	2.43	0.53
3:2D:12:SER:HB3	3:2D:208:LYS:HB3	1.90	0.53
1:1A:2062:A:N1	56:1z:5:ALA:HB1	2.24	0.53
46:1o:39:LEU:HD13	46:1o:56:LEU:HB2	1.90	0.53
54:1w:196:THR:HG21	54:1w:296:GLY:O	2.08	0.53
1:2A:1890:A:OP2	61:2A:3948:HOH:O	2.19	0.53
4:2E:167:VAL:HG12	4:2E:170:LEU:HD11	1.91	0.53
8:2I:40:THR:O	8:2I:44:LEU:HB2	2.09	0.53
35:2d:108:LEU:HD23	35:2d:170:VAL:HG21	1.89	0.53
40:2i:19:LEU:HD11	40:2i:59:PHE:HB3	1.91	0.53
1:1A:1430:C:H2'	1:1A:1431:U:C6	2.43	0.53
32:1a:1263:C:H2'	32:1a:1264:C:C6	2.44	0.53
36:1e:100:VAL:HB	36:1e:107:ARG:NH1	2.23	0.53
1:2A:805:G:OP1	61:2A:3945:HOH:O	2.19	0.53
1:2A:2887:U:H2'	1:2A:2888:C:H6	1.74	0.53
32:2a:501:C:H2'	32:2a:502:G:H8	1.73	0.53
38:2g:26:PHE:CE2	38:2g:30:ILE:HD11	2.44	0.53
1:1A:305:U:H2'	1:1A:306:U:C6	2.44	0.53
1:1A:2508:G:OP1	54:1w:223:ARG:NH2	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:1P:50:ARG:HD3	30:18:7:HIS:CD2	2.43	0.53
32:1a:1068:G:H8	32:1a:1068:G:OP2	1.92	0.53
1:2A:531:C:H4'	1:2A:532:A:H5''	1.91	0.53
1:2A:1187:G:H5''	17:2V:81:TYR:CE1	2.44	0.53
8:2I:75:LEU:HD11	8:2I:105:HIS:ND1	2.24	0.53
24:22:1:MET:SD	24:22:56:GLN:NE2	2.82	0.53
32:2a:352:C:H4'	32:2a:354:G:OP1	2.09	0.53
39:2h:51:VAL:HG11	39:2h:60:ARG:NH2	2.23	0.53
6:1G:47:LYS:HG3	6:1G:48:GLU:H	1.74	0.53
34:1c:148:GLY:HA3	34:1c:172:ARG:H	1.74	0.53
1:2A:2498:C:OP1	61:2A:3950:HOH:O	2.19	0.53
12:2Q:65:PHE:HB2	12:2Q:105:GLU:HB2	1.90	0.53
32:2a:176:C:H2'	32:2a:177:C:C6	2.43	0.53
44:2m:78:ILE:HA	44:2m:81:LEU:HD12	1.91	0.53
1:1A:2430:A:N3	1:1A:2430:A:H2'	2.24	0.52
32:1a:142:G:H2'	32:1a:143:A:C8	2.43	0.52
32:1a:537:G:H5''	43:1I:113:ARG:HH12	1.72	0.52
1:2A:1889:A:H2'	1:2A:1890:A:C8	2.44	0.52
1:2A:2062:A:H2	56:2z:5:ALA:HB1	1.74	0.52
1:2A:2115:G:H4'	1:2A:2167:U:C2	2.44	0.52
6:2G:61:ALA:O	6:2G:65:GLY:N	2.42	0.52
13:2R:38:VAL:HG22	13:2R:112:ALA:HB2	1.90	0.52
32:2a:1005:A:H5''	32:2a:1006:C:H5	1.73	0.52
32:2a:1119:C:H2'	32:2a:1120:G:C8	2.45	0.52
33:2b:162:ILE:O	33:2b:185:ILE:HG12	2.08	0.52
1:1A:1309:G:H4'	29:17:7:PRO:HB2	1.91	0.52
11:1P:95:VAL:HG12	11:1P:99:LEU:HD23	1.90	0.52
16:1U:58:ARG:HA	16:1U:61:TRP:CE3	2.44	0.52
32:1a:35:G:O2'	43:1I:118:SER:O	2.27	0.52
32:1a:1346:A:N1	32:1a:1374:A:H5''	2.24	0.52
33:1b:93:VAL:HG21	33:1b:97:TRP:CD1	2.45	0.52
38:1g:29:LYS:HB3	38:1g:105:VAL:HG21	1.91	0.52
44:1m:50:GLU:HA	44:1m:53:VAL:HB	1.90	0.52
44:1m:81:LEU:HD22	44:1m:88:ARG:HB2	1.91	0.52
1:2A:2318:G:H21	14:2S:3:ARG:NE	2.08	0.52
10:2O:68:GLU:OE1	10:2O:78:ARG:NH1	2.42	0.52
33:2b:77:ALA:HB2	33:2b:211:ILE:HD13	1.91	0.52
34:2c:123:GLN:HB3	34:2c:128:PHE:HD2	1.74	0.52
40:2i:13:ALA:HB2	40:2i:68:GLY:HA3	1.90	0.52
44:2m:54:VAL:HA	44:2m:57:ARG:HB3	1.91	0.52
50:2s:22:LEU:O	50:2s:26:GLY:N	2.41	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:39:C:O2	5:1F:46:ARG:NH2	2.43	0.52
1:1A:1453:U:O2'	1:1A:1455:G:N7	2.42	0.52
32:1a:1131:G:H1	32:1a:1143:G:H21	1.56	0.52
50:1s:36:ARG:HB3	50:1s:72:GLY:HA3	1.90	0.52
32:2a:41:G:H2'	32:2a:42:G:C8	2.44	0.52
39:2h:10:LEU:HD22	39:2h:83:ILE:HD11	1.91	0.52
42:2k:79:SER:HA	42:2k:104:GLN:HB3	1.90	0.52
50:2s:4:SER:HB3	50:2s:7:LYS:HD2	1.90	0.52
5:1F:157:VAL:HB	5:1F:194:MET:HG2	1.91	0.52
32:1a:474:G:H2'	32:1a:475:G:C8	2.44	0.52
1:2A:1170:G:H1	1:2A:1179:C:H42	1.57	0.52
15:2T:26:ASP:O	15:2T:49:VAL:HG22	2.09	0.52
32:2a:110:C:H2'	32:2a:111:G:O4'	2.08	0.52
1:1A:214:G:O2'	1:1A:216:A:O2'	2.24	0.52
1:1A:323:G:C8	5:1F:171:PRO:HG3	2.45	0.52
1:1A:1364:G:N7	23:11:3:LYS:HD2	2.25	0.52
1:1A:2127:G:N2	1:1A:2173:A:H1'	2.25	0.52
1:1A:2131:G:H21	1:1A:2133:G:H1'	1.75	0.52
15:1T:74:ARG:HG2	15:1T:76:PHE:CZ	2.45	0.52
34:1c:22:TRP:HB3	34:1c:59:ARG:HB2	1.92	0.52
38:1g:38:LEU:HA	38:1g:41:ARG:HD2	1.90	0.52
40:1i:32:ASP:OD1	40:1i:33:PHE:N	2.43	0.52
1:2A:122:G:N3	61:2A:4005:HOH:O	2.34	0.52
1:2A:1342:A:OP2	61:2A:3949:HOH:O	2.19	0.52
1:2A:2176:A:H2'	1:2A:2177:C:C6	2.44	0.52
5:2F:132:VAL:HG21	5:2F:163:VAL:HG22	1.91	0.52
5:2F:178:PRO:HB3	5:2F:198:ALA:HA	1.91	0.52
32:2a:1148:U:O2'	40:2i:66:ARG:NH2	2.42	0.52
33:2b:90:MET:HE2	33:2b:226:ARG:HH22	1.75	0.52
41:2j:11:PHE:CE1	41:2j:67:THR:HG22	2.42	0.52
5:1F:129:PHE:CD2	5:1F:163:VAL:HG21	2.45	0.52
16:2U:76:TYR:CE2	16:2U:80:ILE:HG13	2.44	0.52
17:2V:76:LYS:HB2	17:2V:81:TYR:HB3	1.91	0.52
32:2a:769:G:H4'	32:2a:1513:A:H4'	1.92	0.52
32:2a:1062:U:H2'	32:2a:1063:C:C6	2.45	0.52
43:2l:47:LYS:HG2	43:2l:48:PRO:HA	1.92	0.52
51:2t:50:GLU:HG3	51:2t:100:ILE:HD13	1.92	0.52
1:1A:747:U:H1'	18:1W:92:ARG:HH22	1.75	0.52
1:1A:990:A:OP2	61:1A:4135:HOH:O	2.19	0.52
1:1A:1069:A:H1'	1:1A:1096:A:H4'	1.92	0.52
8:1I:14:ASP:OD1	8:1I:15:VAL:N	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:652:U:O4	32:1a:752:G:O2'	2.24	0.52
32:1a:750:G:N3	46:1o:23:GLY:HA3	2.24	0.52
35:1d:86:LYS:HE2	35:1d:87:GLY:H	1.75	0.52
36:1e:102:ALA:HB1	36:1e:106:PRO:HB2	1.92	0.52
44:1m:17:VAL:O	44:1m:20:THR:OG1	2.21	0.52
1:2A:288:C:H2'	1:2A:289:A:H8	1.75	0.52
1:2A:2062:A:C2	56:2z:5:ALA:HB1	2.44	0.52
6:2G:179:PRO:HG3	26:24:43:TYR:CZ	2.45	0.52
12:2Q:111:GLU:O	12:2Q:115:MET:HG2	2.09	0.52
32:2a:583:A:N6	32:2a:758:G:O2'	2.41	0.52
32:2a:840:C:H4'	32:2a:841:U:OP1	2.09	0.52
25:13:6:VAL:HG12	25:13:54:VAL:HG21	1.91	0.52
25:13:39:ASP:OD2	25:13:44:ARG:NH2	2.43	0.52
28:16:13:CYS:SG	28:16:47:THR:HG21	2.50	0.52
32:1a:737:A:H2'	32:1a:738:C:C6	2.44	0.52
39:1h:113:SER:HB2	39:1h:134:ILE:HD11	1.91	0.52
1:2A:2887:U:H2'	1:2A:2888:C:C6	2.45	0.52
32:2a:1014:A:C2	32:2a:1219:U:H1'	2.44	0.52
36:2e:136:MET:HA	36:2e:139:LEU:HD12	1.91	0.52
54:2w:134:PHE:O	54:2w:138:MET:HG2	2.10	0.52
1:1A:1188:U:H4'	17:1V:79:VAL:HG22	1.92	0.52
1:1A:1800:C:OP1	3:1D:260:ARG:NH2	2.43	0.52
1:1A:2611:U:C4	27:15:3:LYS:HG2	2.45	0.52
3:1D:125:ILE:HB	37:1f:81:ILE:HD11	1.91	0.52
26:14:56:VAL:O	26:14:60:GLN:HB2	2.09	0.52
32:1a:1059:C:OP2	34:1c:199:LYS:NZ	2.41	0.52
47:1p:53:VAL:HA	47:1p:56:ALA:HB3	1.92	0.52
54:1w:312:VAL:HG22	54:1w:324:LEU:HD13	1.92	0.52
1:2A:839:U:H2'	1:2A:840:C:C6	2.44	0.52
1:2A:887:A:H2'	1:2A:887:A:N3	2.24	0.52
4:2E:116:VAL:HG13	4:2E:122:PHE:HB2	1.92	0.52
6:2G:15:VAL:HG21	6:2G:176:LEU:HD23	1.90	0.52
12:2Q:58:PHE:HB3	12:2Q:61:GLY:O	2.10	0.52
32:2a:254:G:OP1	48:2q:66:SER:OG	2.27	0.52
50:2s:22:LEU:HD22	50:2s:27:GLU:HA	1.91	0.52
1:1A:2177:C:H2'	1:1A:2178:C:O4'	2.10	0.52
21:1Z:1:MET:SD	21:1Z:1:MET:N	2.83	0.52
32:1a:958:A:N3	32:1a:985:C:O2'	2.39	0.52
1:2A:607:U:OP1	5:2F:102:PRO:HA	2.10	0.52
1:2A:1833:U:OP1	61:2A:3947:HOH:O	2.19	0.52
19:2X:60:ARG:HH22	29:27:47:ARG:NH1	2.07	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:2b:88:ALA:HB1	33:2b:222:ILE:HG21	1.92	0.52
34:2c:180:ALA:HB1	34:2c:203:PHE:CE1	2.41	0.52
38:2g:47:CYS:O	38:2g:50:ILE:HG22	2.09	0.52
38:2g:78:ARG:HG2	38:2g:79:ARG:H	1.75	0.52
32:1a:708:C:H2'	32:1a:709:G:H8	1.76	0.51
1:2A:229:A:H2'	1:2A:229:A:N3	2.25	0.51
1:2A:639:U:H2'	1:2A:640:C:C6	2.45	0.51
1:2A:888:C:H2'	1:2A:889:C:C4	2.45	0.51
1:2A:2164:C:N4	1:2A:2165:G:N3	2.57	0.51
19:2X:53:LYS:HB3	19:2X:82:GLN:HB3	1.92	0.51
32:2a:448:A:P	32:2a:485:G:H22	2.33	0.51
1:1A:1882:C:H2'	1:1A:1883:G:O4'	2.10	0.51
32:1a:959:A:HO2'	32:1a:984:C:HO2'	1.58	0.51
34:1c:42:LEU:HA	34:1c:45:LYS:HG2	1.92	0.51
1:2A:363(B):G:H2'	1:2A:363(C):G:H8	1.76	0.51
26:24:24:THR:OG1	26:24:25:TYR:N	2.43	0.51
26:24:40:HIS:HD2	26:24:41:PRO:HD2	1.75	0.51
34:2c:6:HIS:ND1	45:2n:49:HIS:HB3	2.25	0.51
32:1a:789:U:O2'	32:1a:791:G:N7	2.38	0.51
33:1b:138:LEU:O	33:1b:142:LEU:N	2.38	0.51
33:1b:167:PRO:HG2	33:1b:192:SER:HB3	1.92	0.51
34:1c:35:GLU:CD	34:1c:59:ARG:HH22	2.18	0.51
1:2A:657:U:H2'	1:2A:658:C:C6	2.45	0.51
8:2I:86:THR:HG23	8:2I:87:LYS:HD3	1.91	0.51
32:2a:1064:G:O2'	32:2a:1190:G:N2	2.43	0.51
6:1G:125:PHE:N	61:1G:301:HOH:O	2.43	0.51
6:1G:179:PRO:HG3	26:14:43:TYR:OH	2.10	0.51
33:1b:16:HIS:HB2	33:1b:204:ASN:HB3	1.92	0.51
35:1d:111:ALA:HB2	35:1d:120:LEU:HD12	1.91	0.51
41:1j:81:THR:C	41:1j:83:GLU:H	2.18	0.51
1:2A:2870:C:H2'	1:2A:2871:C:O4'	2.11	0.51
2:2B:14:U:H1'	2:2B:108:U:O2'	2.10	0.51
5:2F:101:LEU:HD12	5:2F:102:PRO:HD2	1.93	0.51
32:2a:137:C:H2'	32:2a:138:G:C8	2.45	0.51
32:2a:950:U:H2'	32:2a:951:G:C8	2.45	0.51
34:2c:52:LEU:HD11	34:2c:55:VAL:HG23	1.91	0.51
35:2d:112:VAL:HG22	35:2d:116:GLN:NE2	2.25	0.51
40:2i:55:ALA:HB1	40:2i:59:PHE:HD2	1.75	0.51
53:2v:19:U:N3	54:2w:116:GLY:O	2.38	0.51
1:1A:1173:G:O2'	1:1A:1174:A:O4'	2.29	0.51
6:1G:16:ARG:HB2	6:1G:17:PRO:HD3	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:976:G:OP1	45:1n:32:SER:N	2.33	0.51
34:1c:23:TYR:HA	41:1j:11:PHE:CE2	2.46	0.51
1:2A:577:G:O2'	1:2A:1254:A:OP1	2.29	0.51
30:28:33:ASN:HA	30:28:36:LYS:HD2	1.91	0.51
32:2a:384:G:H2'	32:2a:385:C:C6	2.45	0.51
32:2a:973:G:H3'	32:2a:974:A:H5''	1.93	0.51
32:2a:1118:C:H1'	32:2a:1179:A:C4	2.45	0.51
32:2a:1305:G:N2	32:2a:1331:G:H1'	2.26	0.51
47:2p:6:LEU:HD23	47:2p:17:TYR:CG	2.46	0.51
13:1R:104:ARG:HD2	13:1R:109:ALA:HB3	1.91	0.51
31:19:25:VAL:HB	31:19:34:GLN:HB2	1.93	0.51
1:2A:856:C:H2'	1:2A:857:C:C6	2.46	0.51
1:2A:1507:A:O2'	1:2A:1508:A:O5'	2.29	0.51
13:2R:9:LYS:O	13:2R:17:ARG:HD3	2.10	0.51
32:2a:108:G:N1	51:2t:15:ARG:HG2	2.25	0.51
32:2a:959:A:HO2'	32:2a:984:C:HO2'	1.45	0.51
32:2a:1162:C:N4	32:2a:1174:G:H1	2.06	0.51
34:2c:91:LEU:HD22	34:2c:101:LEU:HG	1.92	0.51
35:2d:140:VAL:HG11	35:2d:146:ILE:HD11	1.93	0.51
41:2j:98:ILE:O	61:2j:302:HOH:O	2.19	0.51
4:1E:33:VAL:HG13	4:1E:47:VAL:HG23	1.93	0.51
32:1a:600:C:H2'	32:1a:601:C:C6	2.45	0.51
4:2E:36:ARG:NH1	4:2E:85:ASN:OD1	2.44	0.51
12:2Q:75:THR:HG21	12:2Q:87:LYS:HE3	1.93	0.51
32:2a:1272:G:N2	32:2a:1273:G:N7	2.56	0.51
41:2j:81:THR:HA	41:2j:84:GLN:HB3	1.92	0.51
1:1A:1429:G:H2'	1:1A:1430:C:C6	2.46	0.51
5:1F:95:ARG:HD3	5:1F:97:TYR:CZ	2.46	0.51
33:1b:52:GLU:HG2	33:1b:56:ARG:HH12	1.75	0.51
1:2A:392:C:H5''	1:2A:409:C:H5''	1.93	0.51
1:2A:1371:G:O6	61:2A:3936:HOH:O	2.17	0.51
3:2D:146:GLU:HB2	3:2D:189:CYS:HB3	1.92	0.51
32:2a:433:C:H2'	32:2a:434:U:H6	1.74	0.51
32:2a:1117:G:H4'	40:2i:104:ARG:NH2	2.26	0.51
45:2n:26:ARG:HB3	45:2n:43:CYS:SG	2.51	0.51
32:1a:826:C:H2'	32:1a:827:U:C6	2.46	0.51
32:1a:1033:G:H2'	32:1a:1034:G:H8	1.75	0.51
1:2A:2537:U:H2'	1:2A:2538:C:C6	2.45	0.51
1:1A:1105:U:H2'	1:1A:1106:G:H8	1.76	0.51
1:1A:1364:G:C8	23:11:3:LYS:HD2	2.46	0.51
1:1A:2286:A:H4'	1:1A:2287:A:O4'	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:1F:8:GLN:HE22	5:1F:21:ALA:HB2	1.76	0.51
32:1a:352:C:O2'	32:1a:354:G:OP1	2.19	0.51
33:1b:55:PHE:HE1	33:1b:218:ALA:HA	1.74	0.51
34:1c:58:GLU:HB2	34:1c:65:ALA:HB3	1.93	0.51
42:1k:93:GLN:HA	42:1k:93:GLN:HE21	1.76	0.51
1:2A:299:A:N1	1:2A:322:A:O2'	2.37	0.51
1:2A:2001:A:H2'	1:2A:2002:G:C8	2.46	0.51
7:2H:56:SER:HB3	7:2H:61:HIS:ND1	2.26	0.51
15:2T:39:ARG:NH2	32:2a:345:C:OP2	2.41	0.51
32:2a:137:C:H2'	32:2a:138:G:H8	1.76	0.51
32:2a:1323:G:H2'	32:2a:1324:A:C8	2.46	0.51
33:2b:15:VAL:HG13	33:2b:209:ARG:HG2	1.93	0.51
1:1A:271(K):U:O2	8:1I:50:ARG:HG3	2.11	0.50
8:1I:116:LEU:HD11	8:1I:120:ILE:HG13	1.93	0.50
25:13:3:ARG:NH1	25:13:60:GLU:OE2	2.45	0.50
32:1a:991:U:H4'	32:1a:992:U:OP1	2.11	0.50
39:1h:41:ARG:NH2	39:1h:123:GLU:OE2	2.44	0.50
40:1i:5:TYR:H	40:1i:87:GLN:NE2	2.09	0.50
48:1q:26:GLN:HE21	48:1q:37:LYS:HD3	1.76	0.50
1:2A:1193:G:OP1	11:2P:14:LYS:NZ	2.38	0.50
32:2a:1259:C:C4	32:2a:1260:C:H1'	2.46	0.50
32:2a:1308:U:H5''	44:2m:98:VAL:HG23	1.93	0.50
1:1A:1045:A:H8	1:1A:1047:G:N2	2.09	0.50
4:1E:89:ASP:OD1	4:1E:89:ASP:N	2.44	0.50
5:1F:32:LEU:HD11	5:1F:105:VAL:HG13	1.92	0.50
12:1Q:32:TYR:OH	12:1Q:111:GLU:OE2	2.24	0.50
1:2A:2682:U:O2'	15:2T:58:ASN:ND2	2.44	0.50
29:27:12:ARG:NH2	29:27:44:PRO:HB3	2.27	0.50
32:2a:1285:A:H5'	32:2a:1286:A:C2	2.46	0.50
40:2i:17:VAL:HG22	40:2i:63:ILE:HD12	1.92	0.50
42:2k:99:GLN:HG2	42:2k:105:VAL:HG11	1.92	0.50
1:1A:443:A:H1'	1:1A:1201:C:O4'	2.11	0.50
7:1H:124:GLU:HB2	7:1H:132:ARG:HB3	1.92	0.50
21:1Z:54:HIS:ND1	21:1Z:101:PRO:HG3	2.26	0.50
32:1a:1152:A:H5'	41:1j:13:HIS:CD2	2.46	0.50
1:2A:1493:C:N4	1:2A:2206:G:O2'	2.39	0.50
1:2A:2111:C:N4	1:2A:2144:U:H4'	2.27	0.50
1:2A:2316:C:H4'	6:2G:128:ARG:NH1	2.27	0.50
1:2A:2483:C:N3	12:2Q:124:LYS:NZ	2.59	0.50
29:27:24:THR:HG22	29:27:26:GLY:N	2.25	0.50
32:2a:448:A:OP2	32:2a:485:G:N1	2.34	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:2d:111:ALA:HB2	35:2d:120:LEU:HD22	1.92	0.50
39:2h:121:ASP:N	39:2h:121:ASP:OD1	2.43	0.50
1:1A:2619:C:H4'	4:1E:151:TYR:O	2.11	0.50
32:1a:160:A:H1'	32:1a:344:A:C5	2.46	0.50
32:1a:562:C:H1'	43:1l:15:ARG:HB3	1.94	0.50
33:1b:76:GLN:HB3	33:1b:208:ILE:HG23	1.94	0.50
33:1b:218:ALA:O	33:1b:222:ILE:HG13	2.10	0.50
34:1c:59:ARG:HG2	34:1c:64:VAL:HB	1.92	0.50
51:1t:42:GLN:NE2	51:1t:46:GLU:OE2	2.44	0.50
1:2A:1803:A:O2'	3:2D:259:THR:HG21	2.12	0.50
1:2A:2785:C:OP1	4:2E:41:LYS:HE3	2.11	0.50
2:2B:119:G:H5'	2:2B:120:A:OP2	2.12	0.50
32:2a:1132:C:H2'	32:2a:1133:G:C8	2.47	0.50
32:2a:1225:A:H2'	32:2a:1225:A:N3	2.26	0.50
33:2b:179:LYS:HD3	39:2h:72:PRO:HG3	1.93	0.50
36:1e:78:HIS:CE1	36:1e:142:LEU:HD23	2.47	0.50
50:1s:45:VAL:HG11	50:1s:64:GLU:HG3	1.93	0.50
1:2A:500:G:N1	1:2A:503:A:OP2	2.43	0.50
1:2A:1932:A:H2'	1:2A:1933:G:O4'	2.12	0.50
1:2A:2430:A:H2'	1:2A:2430:A:N3	2.24	0.50
1:2A:2693:A:H2'	1:2A:2694:G:H8	1.76	0.50
3:2D:20:ASP:OD1	3:2D:20:ASP:N	2.32	0.50
6:2G:113:ARG:NH2	6:2G:139:LEU:O	2.44	0.50
32:2a:612:C:O2	32:2a:629:G:N2	2.45	0.50
32:2a:1070:U:H2'	32:2a:1071:C:H6	1.77	0.50
32:2a:1320:C:H1'	50:2s:73:GLU:HG3	1.92	0.50
1:1A:382:G:O6	61:1A:4142:HOH:O	2.18	0.50
1:1A:582:G:H2'	1:1A:583:G:C8	2.47	0.50
11:1P:65:ARG:HD2	30:18:25:MET:SD	2.51	0.50
21:1Z:1:MET:N	21:1Z:2:GLU:HA	2.27	0.50
32:1a:684:A:H1'	42:1k:39:PRO:HD2	1.94	0.50
39:1h:83:ILE:HB	39:1h:137:VAL:HG13	1.92	0.50
1:2A:698:C:O2'	1:2A:734:A:N6	2.45	0.50
1:2A:800:A:H8	1:2A:800:A:OP1	1.95	0.50
1:2A:2115:G:H4'	1:2A:2167:U:N3	2.26	0.50
7:2H:46:GLU:HG2	7:2H:47:GLU:H	1.75	0.50
32:2a:933:G:O6	38:2g:3:ARG:NH2	2.45	0.50
33:2b:74:LYS:O	33:2b:78:GLN:HG2	2.11	0.50
33:2b:213:LEU:HD22	33:2b:214:ILE:HD13	1.92	0.50
1:1A:2243:U:H2'	1:1A:2244:U:C6	2.46	0.50
7:1H:154:PRO:HB3	7:1H:163:TYR:CZ	2.47	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2154:G:H2'	1:2A:2155:G:H5''	1.92	0.50
1:2A:2472:G:H2'	1:2A:2475:C:H42	1.77	0.50
32:2a:936:C:H2'	32:2a:937:A:O4'	2.11	0.50
1:1A:1178:C:H2'	1:1A:1179:C:C6	2.46	0.50
32:1a:713:G:H2'	32:1a:714:G:C8	2.46	0.50
32:1a:1221:G:OP1	32:1a:1320:C:N4	2.42	0.50
38:1g:73:MET:HE3	38:1g:90:GLU:HG3	1.92	0.50
41:1j:38:ILE:HD12	41:1j:71:LEU:HD23	1.93	0.50
1:2A:1025:G:C4	1:2A:1135:C:H1'	2.46	0.50
6:2G:11:TYR:HA	6:2G:15:VAL:HB	1.93	0.50
37:2f:79:LEU:HB3	37:2f:88:VAL:HG21	1.93	0.50
3:1D:166:GLN:HB2	3:1D:174:ILE:HG22	1.94	0.50
1:2A:958:U:OP1	12:2Q:74:TYR:OH	2.27	0.50
1:2A:1669:A:O2'	1:2A:2549:G:OP1	2.28	0.50
21:2Z:39:VAL:HG21	21:2Z:44:PHE:HB2	1.94	0.50
32:2a:583:A:H2'	32:2a:584:G:O4'	2.12	0.50
1:1A:2165:G:N2	1:1A:2166:G:O6	2.45	0.49
1:1A:2377:A:H2'	1:1A:2378:A:C8	2.47	0.49
32:1a:112:G:P	47:1p:27:LYS:HD3	2.52	0.49
32:1a:620:C:H2'	32:1a:621:A:O4'	2.12	0.49
32:1a:1027:C:C2	32:1a:1034:G:N2	2.74	0.49
38:1g:89:MET:HG3	38:1g:156:TRP:HE1	1.77	0.49
50:1s:49:ILE:HD12	50:1s:71:LEU:HD11	1.94	0.49
53:1v:11:U:H2'	53:1v:12:A:C5	2.46	0.49
2:2B:12:C:O2	22:20:74:ARG:NH2	2.36	0.49
5:2F:25:PRO:HD2	5:2F:115:ALA:HB2	1.93	0.49
35:2d:18:LYS:NZ	35:2d:31:CYS:SG	2.74	0.49
44:2m:33:ALA:HA	44:2m:59:TYR:CE2	2.47	0.49
16:1U:76:TYR:CZ	16:1U:80:ILE:HG13	2.47	0.49
39:1h:11:THR:HG22	39:1h:15:ASN:ND2	2.27	0.49
44:1m:3:ARG:H	44:1m:8:GLU:HA	1.76	0.49
1:2A:483:A:O2'	20:2Y:49:VAL:O	2.15	0.49
1:2A:908:C:OP1	12:2Q:22:LYS:HE2	2.12	0.49
1:2A:2198:A:OP1	8:2I:33:ARG:NH2	2.44	0.49
3:2D:108:PRO:HD2	3:2D:111:LEU:HD22	1.94	0.49
14:2S:27:SER:HA	14:2S:88:ASP:HB3	1.93	0.49
1:1A:526:A:OP1	61:1A:4146:HOH:O	2.20	0.49
1:1A:747:U:O2	1:1A:2014:A:H1'	2.13	0.49
1:1A:1364:G:OP2	23:11:3:LYS:HG3	2.12	0.49
1:1A:2445:G:OP1	5:1F:74:ARG:NH2	2.43	0.49
1:1A:2682:U:O2'	15:1T:58:ASN:ND2	2.45	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:1T:84:GLN:HG2	15:1T:85:LYS:HG2	1.94	0.49
16:1U:49:HIS:HA	16:1U:52:ARG:HG2	1.94	0.49
32:1a:514:C:H42	32:1a:537:G:H1	1.58	0.49
32:1a:1051:C:H2'	32:1a:1052:U:C6	2.47	0.49
38:1g:78:ARG:NH1	38:1g:154:TYR:O	2.41	0.49
46:1o:5:LYS:H	46:1o:5:LYS:HD2	1.76	0.49
1:2A:479:A:N3	1:2A:481:G:H5''	2.26	0.49
19:2X:12:VAL:HG22	19:2X:29:TRP:CE2	2.48	0.49
24:22:10:LEU:HD11	24:22:59:ARG:HD3	1.94	0.49
27:25:41:PRO:O	27:25:44:THR:OG1	2.24	0.49
32:2a:974:A:H8	32:2a:974:A:OP1	1.96	0.49
32:2a:1265:G:C2	32:2a:1271:G:C2	3.00	0.49
1:1A:774:A:N3	1:1A:774:A:H2'	2.28	0.49
16:1U:28:ARG:NH1	16:1U:38:THR:OG1	2.44	0.49
25:13:59:VAL:O	25:13:60:GLU:HG2	2.13	0.49
32:1a:474:G:H2'	32:1a:475:G:H8	1.77	0.49
32:1a:1333:A:H2'	32:1a:1334:G:O4'	2.13	0.49
36:1e:67:VAL:HG22	36:1e:69:VAL:H	1.77	0.49
54:1w:230:GLN:NE2	56:1z:6:LYS:HG2	2.28	0.49
1:2A:1113:U:H2'	1:2A:1114:G:C8	2.47	0.49
7:2H:95:ARG:HH12	7:2H:97:ARG:HD3	1.77	0.49
11:2P:106:LEU:HD22	11:2P:112:LEU:HB2	1.94	0.49
32:2a:1151:A:H5''	41:2j:40:LEU:O	2.13	0.49
32:2a:1352:C:H2'	32:2a:1353:G:C8	2.47	0.49
44:2m:37:THR:O	44:2m:55:ARG:NH1	2.45	0.49
44:2m:66:LEU:C	44:2m:70:LEU:HB2	2.38	0.49
1:1A:1899:G:N3	1:1A:1899:G:H2'	2.27	0.49
1:1A:2080:G:O6	61:1A:4140:HOH:O	2.17	0.49
5:1F:181:LEU:O	5:1F:205:ARG:NH2	2.46	0.49
8:1I:72:LEU:HD23	8:1I:75:LEU:HD21	1.95	0.49
14:1S:61:ASN:HD22	14:1S:64:GLU:N	2.02	0.49
33:1b:77:ALA:HB2	33:1b:211:ILE:HD13	1.94	0.49
41:1j:81:THR:O	41:1j:83:GLU:N	2.44	0.49
43:1l:53:ARG:HG3	43:1l:93:LEU:HD21	1.93	0.49
1:2A:2624:G:N7	61:2A:4007:HOH:O	2.35	0.49
32:2a:392:G:H2'	32:2a:393:A:C8	2.48	0.49
37:2f:61:LEU:HB3	37:2f:63:TYR:CE2	2.39	0.49
38:2g:50:ILE:HG13	38:2g:125:MET:HE2	1.94	0.49
1:1A:2646:C:H2'	1:1A:2647:U:O4'	2.12	0.49
5:1F:63:LYS:HA	5:1F:76:GLY:O	2.12	0.49
34:1c:130:VAL:HG12	34:1c:134:ILE:HD11	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:1p:58:TYR:O	47:1p:61:SER:OG	2.26	0.49
1:2A:632:A:H2'	1:2A:633:A:C8	2.47	0.49
6:2G:179:PRO:HG3	26:24:43:TYR:OH	2.12	0.49
7:2H:41:MET:HE2	7:2H:65:HIS:HA	1.95	0.49
9:2N:42:TRP:HA	9:2N:48:MET:SD	2.53	0.49
21:2Z:9:TYR:OH	21:2Z:61:LEU:HD23	2.13	0.49
32:2a:1275:A:H2'	32:2a:1276:G:O4'	2.13	0.49
33:2b:90:MET:HE2	33:2b:226:ARG:NH2	2.27	0.49
36:2e:6:PHE:CE1	36:2e:36:ASP:HB3	2.48	0.49
40:2i:33:PHE:HE2	40:2i:43:ALA:HB1	1.77	0.49
1:1A:271(O):C:H2'	1:1A:271(P):C:C6	2.48	0.49
1:1A:1557:C:H5''	1:1A:1558:A:OP2	2.13	0.49
1:1A:1673:U:OP1	61:1A:4122:HOH:O	2.20	0.49
1:1A:2336:A:H61	22:10:43:THR:HG22	1.78	0.49
1:1A:2626:C:H2'	1:1A:2627:G:O4'	2.12	0.49
32:1a:1478:C:H2'	32:1a:1479:C:C6	2.48	0.49
36:1e:93:PRO:HG2	39:1h:105:ARG:NH1	2.28	0.49
38:1g:113:GLU:HB2	38:1g:119:ARG:HG2	1.94	0.49
1:2A:10:G:H2'	1:2A:11:G:C8	2.48	0.49
1:2A:1899:G:H2'	1:2A:1899:G:N3	2.28	0.49
1:2A:2116:G:N7	1:2A:2166:G:N2	2.61	0.49
3:2D:71:ASP:CG	3:2D:103:ARG:HH22	2.20	0.49
10:2O:22:ILE:HG23	10:2O:41:ALA:HA	1.95	0.49
17:2V:10:LYS:NZ	17:2V:23:GLU:OE2	2.34	0.49
30:28:23:VAL:HG12	30:28:47:LYS:HB3	1.93	0.49
32:2a:202:U:H3'	32:2a:203:U:C6	2.48	0.49
32:2a:977:A:O2'	32:2a:979:C:OP2	2.27	0.49
32:2a:1239:A:H4'	32:2a:1240:U:C5'	2.42	0.49
35:2d:100:ARG:HH21	35:2d:118:ARG:HH12	1.61	0.49
46:2o:5:LYS:H	46:2o:5:LYS:HZ2	1.60	0.49
54:2w:150:THR:C	54:2w:152:LEU:H	2.19	0.49
1:1A:668:G:H5'	1:1A:669:G:OP2	2.13	0.49
8:1I:4:ILE:HD11	8:1I:44:LEU:HD23	1.93	0.49
19:1X:12:VAL:HG22	19:1X:29:TRP:CE2	2.48	0.49
32:1a:134:A:H61	47:1p:25:ARG:NH1	2.11	0.49
32:1a:911:U:H2'	32:1a:912:C:C6	2.48	0.49
32:1a:1118:C:H1'	32:1a:1179:A:C4	2.48	0.49
32:1a:1209:C:O2'	32:1a:1214:C:N4	2.33	0.49
32:1a:1346:A:OP1	40:1i:120:ARG:NH1	2.28	0.49
32:1a:1353:G:OP1	52:1u:10:ARG:NH1	2.45	0.49
33:1b:16:HIS:CD2	33:1b:18:GLY:H	2.29	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:1d:112:VAL:HG22	35:1d:116:GLN:OE1	2.13	0.49
39:1h:49:GLU:OE2	39:1h:62:TYR:OH	2.22	0.49
1:2A:223:A:O2'	1:2A:420:C:O2	2.30	0.49
1:2A:1359:A:H2'	1:2A:1360:A:H5'	1.95	0.49
1:2A:2487:G:H2'	1:2A:2488:A:C8	2.48	0.49
29:27:5:TRP:NE1	29:27:7:PRO:HG3	2.27	0.49
32:2a:41:G:H2'	32:2a:42:G:H8	1.78	0.49
32:2a:1176:A:H2'	32:2a:1177:G:C8	2.47	0.49
33:2b:97:TRP:CH2	33:2b:173:ALA:HA	2.48	0.49
44:2m:80:ARG:HH12	50:2s:69:HIS:HE1	1.59	0.49
1:1A:1062:G:O5'	1:1A:1070:A:O2'	2.30	0.49
32:1a:1305:G:H22	32:1a:1331:G:H1'	1.76	0.49
37:1f:4:TYR:HD1	37:1f:92:LYS:HA	1.78	0.49
44:1m:82:MET:HG2	44:1m:89:GLY:O	2.13	0.49
47:1p:71:ARG:HA	47:1p:74:LEU:HD12	1.94	0.49
1:2A:288:C:H2'	1:2A:289:A:C8	2.47	0.49
1:2A:1023:U:OP2	61:2A:3932:HOH:O	2.20	0.49
1:2A:1345:C:OP2	61:2A:3920:HOH:O	2.19	0.49
1:2A:1952:A:OP1	10:2O:42:SER:OG	2.29	0.49
1:2A:2693:A:H2'	1:2A:2694:G:C8	2.48	0.49
9:2N:38:HIS:NE2	9:2N:50:ASP:OD2	2.44	0.49
12:2Q:35:VAL:HG22	12:2Q:102:VAL:HG22	1.95	0.49
32:2a:728:A:H2'	32:2a:729:A:C8	2.48	0.49
32:2a:1172:C:H2'	32:2a:1173:G:C8	2.48	0.49
40:2i:85:LEU:O	40:2i:88:TYR:HB3	2.13	0.49
1:1A:271(L):U:H4'	8:1I:50:ARG:HH22	1.78	0.49
1:1A:1059:G:H2'	1:1A:1060:U:H5	1.78	0.49
1:1A:1091:G:C2	1:1A:1101:U:H1'	2.47	0.49
1:1A:1359:A:H2	1:1A:1372:U:O4	1.96	0.49
5:1F:64:ILE:HG21	5:1F:78:ILE:HG23	1.95	0.49
7:1H:149:ARG:NH1	7:1H:167:GLU:OE2	2.44	0.49
14:1S:25:ARG:HD3	14:1S:42:ASP:OD1	2.12	0.49
23:11:64:ALA:HA	23:11:67:ILE:HG13	1.93	0.49
32:1a:828:A:H2'	32:1a:829:G:O4'	2.13	0.49
33:1b:15:VAL:HB	33:1b:209:ARG:HG2	1.94	0.49
41:1j:50:ILE:HD11	41:1j:57:LYS:HD3	1.95	0.49
42:1k:21:ILE:HG12	42:1k:30:VAL:HG22	1.95	0.49
1:2A:2074:U:H2'	1:2A:2075:U:C6	2.48	0.49
2:2B:75:G:H22	21:2Z:73:GLN:NE2	2.10	0.49
5:2F:126:VAL:HG21	5:2F:129:PHE:CZ	2.47	0.49
7:2H:80:SER:OG	7:2H:81:GLU:N	2.44	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1118:C:OP1	40:2i:104:ARG:NH1	2.46	0.49
44:2m:82:MET:HB3	44:2m:93:ARG:HD2	1.94	0.49
33:1b:24:TRP:H	33:1b:24:TRP:HD1	1.61	0.48
1:2A:1568:G:N7	61:2A:4009:HOH:O	2.35	0.48
1:2A:1815:A:OP2	3:2D:54:ARG:NH2	2.47	0.48
32:2a:624:C:H2'	32:2a:625:G:H8	1.77	0.48
42:2k:61:ALA:HB1	42:2k:94:ALA:HB2	1.95	0.48
1:1A:248:G:OP1	61:1A:4145:HOH:O	2.20	0.48
1:1A:271(L):U:H4'	8:1I:50:ARG:NH2	2.28	0.48
1:1A:839:U:H2'	1:1A:840:C:C6	2.48	0.48
1:1A:2099:U:H3	1:1A:2190:G:H1	1.60	0.48
1:1A:2107:C:H42	1:1A:2182:G:H1	1.60	0.48
7:1H:119:GLU:O	7:1H:140:LYS:NZ	2.45	0.48
32:1a:460:G:N2	32:1a:471:G:N7	2.61	0.48
32:1a:617:G:H1	32:1a:623:C:H42	1.60	0.48
39:1h:100:ILE:HB	39:1h:125:ARG:HH12	1.78	0.48
1:2A:644:A:H4'	1:2A:645:C:C5	2.48	0.48
1:2A:2185:C:H2'	1:2A:2186:G:O4'	2.13	0.48
6:2G:36:LYS:HZ3	6:2G:95:ARG:HH12	1.61	0.48
14:2S:18:ILE:O	14:2S:21:THR:HG23	2.12	0.48
21:2Z:28:MET:HE1	21:2Z:61:LEU:HD21	1.95	0.48
32:2a:993:G:H4'	32:2a:994:A:OP2	2.13	0.48
40:2i:88:TYR:HD2	40:2i:89:ASN:HD22	1.61	0.48
44:2m:80:ARG:HH12	50:2s:69:HIS:CE1	2.31	0.48
1:1A:579:G:H2'	1:1A:580:C:C6	2.49	0.48
1:1A:607:U:OP1	5:1F:102:PRO:HA	2.12	0.48
1:1A:2687:U:H2'	1:1A:2688:U:O4'	2.12	0.48
8:1I:101:LEU:HG	8:1I:107:VAL:HB	1.96	0.48
25:13:3:ARG:HH11	25:13:60:GLU:CD	2.21	0.48
32:1a:447:G:O6	32:1a:485:G:O2'	2.30	0.48
32:1a:1493:A:H4'	53:1v:19:U:O2	2.13	0.48
39:1h:11:THR:HG22	39:1h:15:ASN:HD21	1.78	0.48
1:2A:614(C):A:C4	5:2F:180:GLY:HA2	2.48	0.48
1:2A:817:C:O2'	1:2A:839:U:OP1	2.26	0.48
1:2A:875:G:H2'	1:2A:876:C:O4'	2.13	0.48
1:2A:2183:C:H2'	1:2A:2184:G:H8	1.77	0.48
1:2A:2637:U:OP1	4:2E:82:ARG:NH1	2.45	0.48
1:2A:2847:U:OP1	15:2T:98:LYS:NZ	2.46	0.48
25:23:46:ASN:O	25:23:50:VAL:HG22	2.14	0.48
32:2a:601:C:H2'	32:2a:602:A:C8	2.48	0.48
32:2a:1256:A:H61	32:2a:1278:U:H1'	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:2e:90:VAL:O	36:2e:120:THR:HA	2.14	0.48
40:2i:20:ARG:HH12	40:2i:62:TYR:HB3	1.78	0.48
40:2i:114:TYR:HE1	41:2j:60:ARG:H	1.61	0.48
1:1A:583:G:OP2	16:1U:10:ARG:NH1	2.42	0.48
1:1A:1996:C:H4'	1:1A:1997:G:OP1	2.13	0.48
1:1A:2162:G:C2'	1:1A:2163:C:H5'	2.42	0.48
6:1G:79:ASN:OD1	6:1G:79:ASN:N	2.47	0.48
15:1T:112:ARG:HG3	15:1T:115:ARG:NH2	2.28	0.48
32:1a:434:U:H2'	32:1a:435:C:H6	1.78	0.48
32:1a:508:C:OP1	35:1d:209:ARG:NH2	2.47	0.48
32:1a:1248:A:N3	40:1i:70:LYS:HE2	2.27	0.48
1:2A:271(A):A:N1	1:2A:272(D):G:O2'	2.42	0.48
1:2A:882:G:H1	1:2A:894:C:N4	2.08	0.48
1:2A:1410:G:H2'	1:2A:1411:C:C6	2.48	0.48
4:2E:176:ILE:HB	4:2E:181:LEU:HB2	1.95	0.48
6:2G:64:THR:HB	6:2G:94:LEU:HD21	1.96	0.48
11:2P:57:THR:O	11:2P:61:ARG:HG3	2.13	0.48
40:2i:40:LEU:HD21	40:2i:70:LYS:HD2	1.95	0.48
54:2w:110:GLU:OE1	54:2w:112:ARG:NH1	2.45	0.48
1:1A:1815:A:H8	1:1A:1815:A:OP1	1.97	0.48
32:1a:1298:C:H2'	38:1g:114:ARG:NH2	2.28	0.48
40:2i:69:GLY:O	40:2i:73:GLN:N	2.40	0.48
46:2o:5:LYS:O	46:2o:9:GLN:HG2	2.13	0.48
1:1A:2537:U:H2'	1:1A:2538:C:C6	2.49	0.48
21:1Z:1:MET:N	21:1Z:55:HIS:HB3	2.29	0.48
32:1a:1178:G:OP1	40:1i:93:ARG:NH1	2.46	0.48
51:1t:9:ASN:O	51:1t:10:LEU:HB2	2.12	0.48
54:1w:172:LYS:HA	54:1w:201:VAL:HG21	1.93	0.48
54:1w:299:SER:O	54:1w:301:LYS:N	2.47	0.48
54:1w:317:ILE:HD13	54:1w:339:LEU:HG	1.96	0.48
1:2A:271(F):C:H2'	1:2A:271(G):C:O4'	2.14	0.48
1:2A:863:A:H2'	1:2A:864:G:C8	2.49	0.48
1:2A:1815:A:P	3:2D:54:ARG:HH22	2.36	0.48
1:2A:2127:G:O2'	1:2A:2173:A:N3	2.46	0.48
1:2A:2467:C:H4'	12:2Q:123:HIS:CD2	2.47	0.48
21:2Z:130:PRO:HA	21:2Z:133:ILE:HD11	1.95	0.48
32:2a:1183:A:O2'	32:2a:1184:G:OP1	2.30	0.48
32:2a:1241:G:H2'	32:2a:1242:C:C6	2.49	0.48
40:2i:9:ARG:HB3	40:2i:104:ARG:NH1	2.28	0.48
1:1A:2105:C:H2'	1:1A:2106:G:O4'	2.14	0.48
1:1A:2189:U:H2'	1:1A:2190:G:H8	1.79	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2567:G:H2'	1:1A:2568:C:C6	2.49	0.48
15:1T:29:ARG:HG3	15:1T:46:GLU:HB2	1.96	0.48
15:1T:65:LYS:HE2	15:1T:67:SER:HB2	1.94	0.48
32:1a:691:G:H2'	32:1a:692:U:C6	2.49	0.48
32:1a:1016:A:H2'	32:1a:1017:G:O4'	2.14	0.48
34:1c:181:ASN:HD21	34:1c:204:LEU:HD12	1.79	0.48
35:1d:20:TYR:HD1	35:1d:26:CYS:HB3	1.77	0.48
1:2A:458:G:O2'	1:2A:469:G:O6	2.32	0.48
1:2A:646:A:H2'	1:2A:647:G:O4'	2.14	0.48
1:2A:2630:G:H2'	1:2A:2631:G:H8	1.79	0.48
12:2Q:31:ASP:HA	12:2Q:134:ARG:HH11	1.77	0.48
32:2a:1111:A:N1	34:2c:177:THR:OG1	2.36	0.48
40:2i:17:VAL:HG21	40:2i:80:GLY:HA3	1.95	0.48
47:2p:18:ARG:HD3	47:2p:35:LYS:HE3	1.95	0.48
1:1A:534:U:H2'	1:1A:535:C:C6	2.48	0.48
1:1A:969:U:H2'	1:1A:970:C:C6	2.49	0.48
1:1A:1406:U:H2'	1:1A:1407:C:C6	2.49	0.48
34:1c:36:ASP:OD1	34:1c:57:ILE:HG21	2.14	0.48
35:1d:50:ARG:NH2	36:1e:10:MET:HB2	2.29	0.48
44:1m:87:TYR:HA	44:1m:90:LEU:HD12	1.96	0.48
51:1t:47:GLY:N	51:1t:48:LYS:HB2	2.29	0.48
54:1w:128:PHE:CZ	54:1w:132:LEU:HD11	2.48	0.48
1:2A:307:G:N1	1:2A:310:A:OP2	2.46	0.48
1:2A:686:G:N2	1:2A:788:A:H61	2.12	0.48
1:2A:911:A:OP1	61:2A:3951:HOH:O	2.20	0.48
1:2A:1592:C:H2'	1:2A:1593:G:C8	2.48	0.48
1:2A:2117:A:O2'	1:2A:2118:U:H5''	2.14	0.48
1:2A:2164:C:C4	1:2A:2165:G:H1'	2.49	0.48
1:2A:2487:G:H2'	1:2A:2488:A:H8	1.78	0.48
1:2A:2711:A:OP2	61:2A:3953:HOH:O	2.20	0.48
6:2G:135:LEU:HD11	6:2G:157:ILE:HD11	1.94	0.48
13:2R:67:LEU:HG	13:2R:76:VAL:HG21	1.96	0.48
21:2Z:30:ASN:HB3	21:2Z:90:VAL:HB	1.95	0.48
32:2a:1030:C:H5'	32:2a:1030(A):G:OP2	2.14	0.48
32:2a:1376:U:OP1	38:2g:98:SER:OG	2.28	0.48
35:2d:119:GLN:HG3	35:2d:123:HIS:CE1	2.49	0.48
40:2i:9:ARG:HG2	40:2i:14:VAL:HG12	1.94	0.48
1:1A:197:A:N6	1:1A:2430:A:O2'	2.47	0.48
1:1A:1036:G:OP2	7:1H:59:ARG:NH1	2.46	0.48
1:1A:2119:A:H61	1:1A:2168:G:H8	1.55	0.48
1:1A:2183:C:H2'	1:1A:2184:G:H8	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2320:A:H2'	1:1A:2320:A:N3	2.29	0.48
1:1A:2869:G:H2'	1:1A:2870:C:O4'	2.13	0.48
21:1Z:1:MET:H1	21:1Z:55:HIS:HB3	1.79	0.48
48:1q:3:LYS:HD2	48:1q:60:ILE:HD11	1.95	0.48
1:2A:885:C:H2'	1:2A:886:C:O4'	2.14	0.48
6:2G:39:ILE:HD11	6:2G:102:PHE:CZ	2.49	0.48
32:2a:382:A:H2'	32:2a:383:A:C8	2.48	0.48
32:2a:643:C:H2'	32:2a:644:G:H8	1.78	0.48
32:2a:838:G:H3'	32:2a:840:C:H41	1.79	0.48
43:2l:24:VAL:HB	43:2l:27:LEU:HG	1.94	0.48
54:2w:228:GLY:HA3	54:2w:232:VAL:HB	1.96	0.48
55:2x:13:A:H2'	55:2x:14:A:H5''	1.96	0.48
19:1X:94:GLY:H	19:1X:95:LEU:C	2.21	0.48
32:1a:266:G:H2'	32:1a:266:G:N3	2.28	0.48
32:1a:1324:A:H4'	32:1a:1362:C:H4'	1.95	0.48
32:1a:1368:G:C2'	32:1a:1369:C:H5'	2.44	0.48
1:2A:774:A:H2'	1:2A:774:A:N3	2.29	0.48
36:2e:88:LYS:HB3	36:2e:123:LEU:HB2	1.96	0.48
51:2t:89:ARG:HE	51:2t:89:ARG:HB3	1.54	0.48
1:1A:27:G:N2	1:1A:512:G:H1'	2.29	0.47
6:1G:16:ARG:O	6:1G:20:ILE:HG13	2.14	0.47
8:1I:87:LYS:HD3	8:1I:87:LYS:H	1.79	0.47
20:1Y:9:LYS:HA	20:1Y:10:GLY:HA2	1.66	0.47
32:1a:1239:A:C4	32:1a:1298:C:N4	2.82	0.47
32:1a:1314:C:OP2	50:1s:4:SER:OG	2.21	0.47
40:1i:29:ASN:OD1	40:1i:64:THR:HA	2.13	0.47
42:1k:52:GLY:H	42:1k:55:LYS:HE2	1.78	0.47
1:2A:459:U:H5''	29:27:40:TRP:CD2	2.48	0.47
1:2A:529:A:H62	1:2A:2041:U:H3	1.62	0.47
1:2A:1324:G:O6	61:2A:3943:HOH:O	2.18	0.47
1:2A:2336:A:H61	22:20:43:THR:HG22	1.79	0.47
6:2G:122:PRO:HB3	6:2G:170:ARG:HH12	1.79	0.47
8:2I:5:LEU:HD22	8:2I:9:LEU:HD23	1.94	0.47
32:2a:426:G:OP1	35:2d:38:TYR:OH	2.29	0.47
32:2a:1376:U:H2'	32:2a:1377:A:C8	2.49	0.47
37:2f:80:ARG:NH1	37:2f:88:VAL:O	2.47	0.47
40:2i:85:LEU:HB3	40:2i:92:TYR:HD2	1.79	0.47
43:2l:102:ARG:HE	43:2l:102:ARG:HB3	1.49	0.47
44:2m:87:TYR:CZ	44:2m:91:ARG:HD2	2.49	0.47
54:2w:150:THR:N	54:2w:154:GLY:O	2.44	0.47
54:2w:326:GLY:HA2	54:2w:329:SER:HB3	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:548:A:H1'	1:1A:549:G:OP1	2.15	0.47
1:1A:2791:C:H2'	1:1A:2792:G:C8	2.49	0.47
3:1D:20:ASP:OD1	3:1D:20:ASP:N	2.41	0.47
32:1a:976:G:OP2	32:1a:1358:U:O2'	2.28	0.47
33:1b:208:ILE:HD12	33:1b:209:ARG:N	2.30	0.47
35:1d:177:ASP:O	35:1d:180:GLY:N	2.47	0.47
54:1w:173:TYR:OH	54:1w:343:ASP:OD2	2.22	0.47
1:2A:699:A:H2'	1:2A:700:G:O4'	2.14	0.47
1:2A:2849:U:H4'	1:2A:2868:A:C2	2.49	0.47
2:2B:72:G:O2'	2:2B:105:A:N6	2.47	0.47
11:2P:121:LYS:O	11:2P:123:LEU:N	2.47	0.47
20:2Y:85:VAL:HG13	20:2Y:97:ARG:HB3	1.96	0.47
32:2a:1279:A:H5''	32:2a:1280:A:OP1	2.14	0.47
34:2c:55:VAL:HG22	34:2c:68:VAL:HG22	1.96	0.47
34:2c:79:ARG:N	34:2c:82:GLU:HB3	2.28	0.47
36:2e:101:ILE:O	36:2e:120:THR:HB	2.13	0.47
40:2i:3:GLN:HE21	40:2i:20:ARG:HH21	1.62	0.47
41:2j:63:PHE:HE1	45:2n:58:LYS:HG3	1.79	0.47
45:2n:27:CYS:SG	45:2n:28:GLY:N	2.87	0.47
54:2w:257:SER:HB3	54:2w:260:LYS:HB2	1.96	0.47
1:1A:205:G:O6	23:11:39:LYS:NZ	2.44	0.47
25:13:8:LEU:HG	25:13:31:LEU:HD23	1.96	0.47
32:1a:128:G:O2'	48:1q:3:LYS:NZ	2.47	0.47
32:1a:1140:C:H2'	32:1a:1141:C:C6	2.48	0.47
36:1e:20:GLN:NE2	36:1e:21:ALA:O	2.47	0.47
39:1h:17:THR:HG22	39:1h:63:LEU:HG	1.96	0.47
1:2A:1530:C:O2'	1:2A:1531:C:O5'	2.23	0.47
1:2A:2646:C:H2'	1:2A:2647:U:O4'	2.13	0.47
5:2F:110:LEU:HD11	5:2F:181:LEU:HG	1.94	0.47
15:2T:24:PRO:HA	15:2T:49:VAL:HG23	1.96	0.47
32:2a:1068:G:H8	32:2a:1068:G:OP2	1.96	0.47
32:2a:1273:G:C6	32:2a:1274:G:C4	3.03	0.47
35:2d:22:LYS:HB2	35:2d:26:CYS:SG	2.54	0.47
54:2w:337:GLU:O	54:2w:341:ARG:N	2.45	0.47
1:1A:601:C:OP1	5:1F:108:LYS:HE3	2.14	0.47
1:1A:2001:A:H2'	1:1A:2002:G:C8	2.48	0.47
1:1A:2343:C:HO2'	1:1A:2373:G:HO2'	1.61	0.47
1:1A:2478:A:OP2	31:19:2:LYS:NZ	2.40	0.47
1:1A:2727:G:O2'	10:1O:70:LYS:NZ	2.45	0.47
4:1E:93:VAL:N	61:1E:402:HOH:O	2.25	0.47
32:1a:148:G:H2'	32:1a:149:A:H8	1.78	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1010:G:C2	32:1a:1020:U:H1'	2.49	0.47
32:1a:1401:G:C2	32:1a:1402:4OC:H1'	2.49	0.47
1:2A:1161:C:H2'	1:2A:1162:G:C8	2.49	0.47
1:2A:2104:G:H1	1:2A:2185:C:N4	2.06	0.47
1:2A:2552:OMU:OP2	61:2A:3952:HOH:O	2.20	0.47
5:2F:184:TYR:CE2	5:2F:188:ARG:HD2	2.49	0.47
9:2N:96:GLU:CD	9:2N:96:GLU:H	2.22	0.47
32:2a:1072:G:H2'	32:2a:1073:U:C6	2.50	0.47
35:2d:115:ARG:H	35:2d:115:ARG:HG3	1.52	0.47
38:2g:79:ARG:NH2	38:2g:80:VAL:HA	2.29	0.47
49:2r:47:THR:HA	49:2r:83:GLU:HB2	1.95	0.47
1:1A:8:A:H2'	1:1A:9:U:C6	2.49	0.47
1:1A:226:G:H21	1:1A:228:A:H62	1.61	0.47
5:1F:123:LEU:HD13	5:1F:192:LEU:HD13	1.96	0.47
32:1a:78:G:O2'	32:1a:79:G:O4'	2.33	0.47
32:1a:1084:G:C5	32:1a:1085:U:C4	3.03	0.47
47:1p:19:ILE:HG22	47:1p:36:ILE:HG13	1.97	0.47
1:2A:2145:C:O2'	1:2A:2147:G:N7	2.44	0.47
1:2A:2328:A:H2'	1:2A:2329:G:C8	2.49	0.47
6:2G:68:PRO:HB3	6:2G:92:VAL:HB	1.96	0.47
22:20:38:VAL:HG12	22:20:40:GLN:HG2	1.97	0.47
31:29:29:ASN:HD22	31:29:32:HIS:CE1	2.33	0.47
32:2a:1151:A:H5''	41:2j:41:PRO:HA	1.95	0.47
38:2g:38:LEU:O	38:2g:42:ILE:HG12	2.14	0.47
41:2j:8:LEU:HB3	41:2j:96:ILE:HG23	1.96	0.47
43:2l:6:THR:HG22	43:2l:8:ASN:H	1.80	0.47
45:2n:4:LYS:HA	45:2n:7:ILE:HG22	1.96	0.47
1:1A:1354:A:H2'	1:1A:1355:G:O4'	2.14	0.47
1:1A:1359:A:C2	1:1A:1372:U:O4	2.68	0.47
6:1G:115:ARG:NH1	44:1m:6:GLY:O	2.45	0.47
35:1d:155:LEU:O	35:1d:159:ARG:HG2	2.13	0.47
40:1i:23:ASN:HB2	40:1i:25:LYS:HE3	1.97	0.47
1:2A:468:G:N7	29:27:39:ARG:NH2	2.60	0.47
1:2A:2320:A:N3	1:2A:2320:A:H2'	2.29	0.47
3:2D:242:ARG:HD3	3:2D:242:ARG:N	2.30	0.47
7:2H:175:LYS:HD3	7:2H:175:LYS:HA	1.68	0.47
32:2a:1179:A:H2'	32:2a:1180:A:O4'	2.14	0.47
35:2d:60:GLU:HG3	35:2d:202:LEU:HD12	1.95	0.47
51:2t:42:GLN:O	51:2t:45:GLN:HB3	2.15	0.47
1:1A:154(A):C:H42	1:1A:171:G:H1	1.60	0.47
1:1A:2120:G:H2'	1:1A:2121:G:H8	1.78	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2304:G:H22	1:1A:2312:U:H3	1.62	0.47
1:1A:2406:U:H2'	1:1A:2406:U:OP2	2.14	0.47
1:1A:2646:C:OP2	1:1A:2732:G:O2'	2.21	0.47
4:1E:101:ARG:NH2	4:1E:171:GLU:HB2	2.29	0.47
21:1Z:138:GLU:H	21:1Z:156:LYS:HZ3	1.62	0.47
26:14:26:SER:OG	26:14:27:THR:N	2.48	0.47
30:18:23:VAL:HG11	30:18:47:LYS:HD3	1.96	0.47
32:1a:70:G:H1	32:1a:99:U:H3	1.62	0.47
32:1a:108:G:C6	51:1t:15:ARG:HG2	2.49	0.47
32:1a:389:A:C6	32:1a:390:C:H1'	2.50	0.47
32:1a:523:A:H61	43:1l:92:0TD:CG	2.28	0.47
32:1a:1125:U:O2'	32:1a:1127:G:N7	2.44	0.47
32:1a:1148:U:H2'	32:1a:1149:C:O4'	2.15	0.47
33:1b:102:LEU:HB3	33:1b:180:LEU:HD11	1.96	0.47
36:1e:57:LYS:HG2	36:1e:61:TYR:CE2	2.50	0.47
37:1f:27:GLN:HA	37:1f:30:LEU:HD12	1.97	0.47
48:1q:88:TYR:HD2	48:1q:89:LEU:HD23	1.79	0.47
53:1v:13:A:H3'	53:1v:14:A:C5'	2.44	0.47
54:1w:259:ILE:HB	61:1w:502:HOH:O	2.15	0.47
1:2A:855:G:O6	61:2A:3910:HOH:O	2.18	0.47
1:2A:1508:A:H4'	1:2A:1509(A):A:C5	2.50	0.47
2:2B:103:G:H21	21:2Z:73:GLN:HE22	1.62	0.47
5:2F:150:GLY:HA2	5:2F:172:TRP:CD2	2.49	0.47
5:2F:157:VAL:HB	5:2F:194:MET:HG2	1.97	0.47
11:2P:121:LYS:HE2	11:2P:121:LYS:HB3	1.69	0.47
14:2S:74:ALA:HB3	14:2S:108:GLY:HA3	1.95	0.47
32:2a:173:U:H5''	32:2a:197:A:O4'	2.14	0.47
32:2a:954:G:H2'	32:2a:955:U:C6	2.50	0.47
32:2a:1353:G:OP1	52:2u:10:ARG:NH1	2.47	0.47
32:2a:1513:A:H2'	32:2a:1514:C:C6	2.50	0.47
37:2f:26:ILE:O	37:2f:30:LEU:HG	2.15	0.47
37:2f:67:MET:HE1	37:2f:75:LEU:HD23	1.97	0.47
55:2x:40:C:H2'	55:2x:41:C:H6	1.80	0.47
1:1A:284:U:H2'	1:1A:285:C:C6	2.49	0.47
1:1A:1858:G:N2	1:1A:1883:G:H2'	2.30	0.47
1:1A:2821:A:OP2	61:1R:301:HOH:O	2.20	0.47
6:1G:3:LEU:HD13	26:14:25:TYR:CZ	2.49	0.47
32:1a:258:G:H2'	32:1a:259:G:H8	1.78	0.47
32:1a:877:C:OP1	39:1h:88:LYS:NZ	2.31	0.47
32:1a:994:A:N1	32:1a:1047:G:H4'	2.30	0.47
32:1a:1005:A:H1'	32:1a:1036:G:O6	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:271(E):U:H2'	1:2A:271(F):C:C6	2.50	0.47
1:2A:1778:U:H2'	1:2A:1784:A:N6	2.30	0.47
1:2A:2125:G:H1'	1:2A:2173:A:N6	2.28	0.47
1:2A:2162:G:O2'	1:2A:2172:U:H5'	2.15	0.47
1:2A:2315:G:H2'	1:2A:2316:C:C6	2.50	0.47
5:2F:129:PHE:CD2	5:2F:163:VAL:HG21	2.50	0.47
8:2I:84:GLY:C	8:2I:86:THR:H	2.23	0.47
32:2a:1346:A:OP1	40:2i:120:ARG:NH1	2.47	0.47
1:1A:271(H):G:H2'	1:1A:271(I):G:C8	2.50	0.47
1:1A:2086:U:H2'	1:1A:2087:G:C8	2.50	0.47
9:1N:75:TYR:HA	9:1N:81:GLY:O	2.15	0.47
21:1Z:121:HIS:HB2	21:1Z:171:ILE:HG22	1.97	0.47
32:1a:985:C:H2'	32:1a:986:A:H8	1.80	0.47
35:1d:98:GLU:OE1	35:1d:103:ASN:ND2	2.47	0.47
38:1g:79:ARG:HD2	38:1g:80:VAL:N	2.30	0.47
40:1i:128:ARG:HH12	55:1x:35:C:P	2.37	0.47
1:2A:30:G:H2'	1:2A:31:C:C6	2.50	0.47
12:2Q:66:ILE:HG12	12:2Q:104:PHE:CD1	2.50	0.47
21:2Z:97:GLU:HB3	21:2Z:125:LEU:HD11	1.97	0.47
32:2a:1040:U:H2'	32:2a:1041:A:O4'	2.13	0.47
47:2p:75:ARG:HB2	47:2p:80:PHE:CD2	2.49	0.47
50:2s:20:LEU:HD23	50:2s:23:ASN:HD22	1.79	0.47
54:2w:134:PHE:HZ	54:2w:336:LEU:HD22	1.80	0.47
55:2x:46:A:H2'	55:2x:48:G:C8	2.50	0.47
5:1F:178:PRO:HB2	5:1F:201:VAL:CG2	2.45	0.47
28:16:18:ARG:HD2	28:16:42:TRP:CD1	2.49	0.47
1:2A:2161:C:H2'	1:2A:2162:G:O4'	2.15	0.47
6:2G:114:ILE:HB	6:2G:117:PHE:HB2	1.97	0.47
12:2Q:133:ARG:HG2	12:2Q:134:ARG:N	2.29	0.47
21:2Z:144:LEU:HD23	21:2Z:144:LEU:HA	1.77	0.47
32:2a:328:C:H4'	32:2a:329:A:H5'	1.97	0.47
32:2a:1310:G:H5'	44:2m:77:ASN:ND2	2.29	0.47
32:2a:1316:G:N2	32:2a:1318:A:H3'	2.30	0.47
32:2a:1320:C:C1'	50:2s:73:GLU:HG3	2.45	0.47
33:2b:68:ILE:HG12	33:2b:161:ALA:HB3	1.97	0.47
39:2h:105:ARG:HA	39:2h:105:ARG:HD2	1.73	0.47
49:2r:43:PHE:C	49:2r:51:LEU:HD12	2.39	0.47
51:2t:57:ARG:HH12	51:2t:100:ILE:HG13	1.80	0.47
1:1A:1405:U:H2'	1:1A:1406:U:C6	2.50	0.46
32:1a:920:U:H2'	32:1a:921:U:C6	2.50	0.46
32:1a:1009:G:H2'	32:1a:1010:G:H5'	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:1c:6:HIS:ND1	45:1n:49:HIS:HB3	2.31	0.46
39:1h:100:ILE:HB	39:1h:125:ARG:NH1	2.30	0.46
41:1j:40:LEU:HB2	41:1j:69:ASN:HB2	1.97	0.46
1:2A:748:G:O6	18:2W:90:ARG:NH1	2.49	0.46
1:2A:2133:G:N2	1:2A:2157:G:N7	2.64	0.46
1:2A:2206:G:H3'	1:2A:2207:G:H8	1.71	0.46
1:2A:2352:A:N6	1:2A:2365:G:O2'	2.48	0.46
1:2A:2690:C:OP1	13:2R:17:ARG:NH2	2.47	0.46
3:2D:70:TRP:HB3	3:2D:190:TYR:CE2	2.49	0.46
20:2Y:38:ILE:HD11	20:2Y:66:PRO:HG3	1.97	0.46
32:2a:392:G:H2'	32:2a:393:A:H8	1.78	0.46
1:1A:2629:A:O2'	1:1A:2630:G:OP2	2.25	0.46
4:1E:143:ASN:HD22	4:1E:147:PRO:HD3	1.80	0.46
32:1a:512:U:H2'	32:1a:513:C:C6	2.49	0.46
33:1b:187:LEU:HD23	33:1b:201:ILE:O	2.16	0.46
40:1i:94:ALA:C	40:1i:96:LEU:H	2.22	0.46
1:2A:373:U:H2'	1:2A:374:A:H8	1.80	0.46
1:2A:1557:C:OP2	1:2A:1558:A:O2'	2.27	0.46
2:2B:45:A:O4'	6:2G:95:ARG:NH1	2.48	0.46
2:2B:58:A:H2'	2:2B:59:A:O4'	2.15	0.46
3:2D:5:LYS:HE3	3:2D:5:LYS:HB3	1.83	0.46
7:2H:8:PRO:HB3	7:2H:51:ARG:HG2	1.96	0.46
32:2a:881:G:OP2	43:2l:12:ARG:NH2	2.48	0.46
47:2p:3:LYS:HD3	47:2p:65:GLN:O	2.15	0.46
1:1A:226:G:N2	1:1A:228:A:H62	2.13	0.46
1:1A:1091:G:H2'	1:1A:1092:C:C6	2.50	0.46
1:1A:1803:A:O2'	3:1D:259:THR:HG21	2.15	0.46
12:1Q:10:ARG:HH11	12:1Q:11:LYS:HE2	1.81	0.46
32:1a:222:U:H2'	32:1a:223:U:C6	2.51	0.46
32:1a:458:C:N3	32:1a:474:G:N1	2.63	0.46
36:1e:79:GLU:H	36:1e:79:GLU:HG3	1.56	0.46
46:1o:74:ASP:HB3	46:1o:77:ARG:HB2	1.97	0.46
1:2A:196:A:OP2	11:2P:46:LYS:NZ	2.49	0.46
1:2A:414:C:H2'	1:2A:415:A:C8	2.50	0.46
1:2A:829:A:N7	1:2A:2248:C:H5'	2.31	0.46
1:2A:848:G:H2'	1:2A:849:A:C8	2.50	0.46
1:2A:2820:A:O2'	1:2A:2821:A:OP1	2.33	0.46
2:2B:20:C:H42	2:2B:63:G:H1	1.63	0.46
15:2T:11:GLU:O	15:2T:15:VAL:HG23	2.15	0.46
22:20:50:ASN:HB3	22:20:63:VAL:HG22	1.96	0.46
32:2a:266:G:H2'	32:2a:266:G:N3	2.30	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:662:G:H2'	32:2a:663:A:C8	2.50	0.46
32:2a:731:G:H5'	32:2a:766:A:H4'	1.96	0.46
33:2b:54:THR:HG22	33:2b:199:TYR:HB3	1.97	0.46
1:1A:576:U:H2'	1:1A:577:G:C8	2.51	0.46
1:1A:1093:G:C2	1:1A:1098:A:C8	3.04	0.46
1:1A:2462:U:H1'	1:1A:2491:U:O4	2.16	0.46
32:1a:989:C:H42	32:1a:1216:G:H1	1.63	0.46
33:1b:16:HIS:HB2	33:1b:204:ASN:CB	2.46	0.46
34:1c:73:PRO:HB3	34:1c:103:VAL:HG11	1.97	0.46
38:1g:120:ILE:HG22	38:1g:124:LEU:HD11	1.97	0.46
54:1w:141:GLU:HB3	54:1w:163:ARG:HB2	1.97	0.46
1:2A:118:A:N3	1:2A:178:G:H1'	2.30	0.46
1:2A:1636:C:H2'	1:2A:1637:A:C8	2.51	0.46
1:2A:2317:C:H2'	1:2A:2318:G:H5'	1.98	0.46
15:2T:74:ARG:HG2	15:2T:76:PHE:CZ	2.50	0.46
30:28:38:GLY:O	30:28:42:ARG:HB2	2.16	0.46
31:29:7:VAL:HG12	31:29:34:GLN:HB3	1.98	0.46
32:2a:744:C:O2'	32:2a:851:G:N2	2.47	0.46
47:2p:21:VAL:HG22	47:2p:33:ILE:HD12	1.97	0.46
54:2w:129:ASN:HA	54:2w:132:LEU:HB2	1.96	0.46
1:1A:2319:G:N2	14:1S:3:ARG:HA	2.30	0.46
4:1E:3:GLY:HA3	4:1E:81:ILE:HD12	1.97	0.46
7:1H:3:ARG:HH22	7:1H:66:GLY:N	2.14	0.46
26:14:57:GLU:HA	26:14:58:ARG:HA	1.76	0.46
32:1a:189(C):C:H2'	32:1a:189(D):C:O4'	2.16	0.46
32:1a:974:A:P	45:1n:41:ARG:HH21	2.38	0.46
32:1a:1317:C:H2'	32:1a:1318:A:O4'	2.15	0.46
32:1a:1530:G:H4'	32:1a:1530:G:OP1	2.14	0.46
40:1i:26:VAL:HG13	40:1i:61:ALA:HB3	1.97	0.46
43:1l:79:GLU:HG2	43:1l:80:HIS:CD2	2.51	0.46
1:2A:801:G:O6	5:2F:53:THR:OG1	2.34	0.46
1:2A:922:U:H2'	1:2A:923:C:C6	2.50	0.46
7:2H:59:ARG:O	7:2H:63:SER:OG	2.33	0.46
10:2O:35:VAL:HG13	10:2O:65:THR:HG23	1.97	0.46
18:2W:4:LYS:HB2	18:2W:106:ILE:HG12	1.98	0.46
32:2a:358:U:H2'	32:2a:359:U:H6	1.80	0.46
32:2a:460:G:H2'	32:2a:461:A:H2'	1.98	0.46
41:2j:35:SER:HB3	41:2j:73:ASP:HB2	1.97	0.46
54:2w:230:GLN:HG2	56:2z:7:CYS:O	2.15	0.46
1:1A:2126:A:C2	1:1A:2127:G:H1'	2.51	0.46
1:1A:2499:C:N3	61:1A:4201:HOH:O	2.36	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2753:A:N3	31:19:15:LYS:NZ	2.56	0.46
1:1A:2788:C:OP1	4:1E:61:ARG:NH2	2.48	0.46
2:1B:25:A:OP2	61:1B:301:HOH:O	2.20	0.46
11:1P:59:LEU:HD21	30:18:10:ALA:HB2	1.97	0.46
11:1P:124:LYS:HE2	11:1P:146:VAL:HG21	1.96	0.46
22:10:27:GLU:HB2	22:10:69:PHE:HD1	1.80	0.46
32:1a:149:A:H2'	32:1a:150:C:C6	2.50	0.46
32:1a:769:G:H4'	32:1a:1513:A:H4'	1.97	0.46
32:1a:995:C:H2'	32:1a:996:A:H8	1.80	0.46
32:1a:1320:C:H2'	32:1a:1321:C:O4'	2.15	0.46
33:1b:28:PHE:CD2	33:1b:190:THR:HA	2.51	0.46
42:1k:31:THR:HG22	42:1k:42:TRP:CB	2.46	0.46
48:1q:66:SER:OG	48:1q:67:LYS:N	2.48	0.46
54:1w:315:HIS:H	54:1w:315:HIS:HD1	1.62	0.46
1:2A:2127:G:H2'	1:2A:2128:C:C5	2.51	0.46
3:2D:71:ASP:CB	3:2D:103:ARG:HH12	2.28	0.46
16:2U:76:TYR:CZ	16:2U:80:ILE:HG13	2.50	0.46
32:2a:881:G:P	43:2l:12:ARG:HH22	2.39	0.46
32:2a:939:G:H2'	32:2a:940:C:C6	2.51	0.46
32:2a:1240:U:OP2	38:2g:116:ALA:N	2.47	0.46
32:2a:1318:A:O2'	50:2s:37:ARG:HD2	2.15	0.46
54:2w:128:PHE:CZ	54:2w:132:LEU:HD11	2.50	0.46
1:1A:956:G:H2'	1:1A:957:A:H2'	1.97	0.46
1:1A:1056:G:C2'	1:1A:1103:A:H61	2.28	0.46
1:1A:1069:A:H4'	1:1A:1070:A:H5''	1.98	0.46
1:1A:1653:G:H3'	13:1R:2:ARG:HD3	1.97	0.46
1:1A:2879:C:OP2	61:1A:4149:HOH:O	2.21	0.46
26:14:43:TYR:O	26:14:45:GLY:N	2.49	0.46
32:1a:1109:C:OP2	34:1c:176:HIS:ND1	2.49	0.46
33:1b:55:PHE:CE1	33:1b:218:ALA:HA	2.50	0.46
36:1e:11:ILE:HG23	36:1e:105:VAL:HG22	1.98	0.46
38:1g:120:ILE:O	38:1g:124:LEU:HD12	2.15	0.46
41:1j:62:HIS:HB3	45:1n:59:ALA:HB3	1.97	0.46
43:1l:53:ARG:HB2	43:1l:93:LEU:HD11	1.98	0.46
51:1t:11:SER:O	51:1t:15:ARG:N	2.48	0.46
9:2N:4:TYR:CD2	16:2U:100:VAL:HG11	2.50	0.46
13:2R:92:GLY:HA2	13:2R:94:TYR:CZ	2.51	0.46
1:1A:271(H):G:H2'	1:1A:271(I):G:H8	1.80	0.46
1:1A:667:U:O2	30:18:2:PRO:HD2	2.15	0.46
1:1A:882:G:H1	1:1A:894:C:N4	2.14	0.46
1:1A:2203:U:O2'	1:1A:2205:C:H5'	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:1I:88:ILE:HG22	8:1I:90:GLY:H	1.79	0.46
32:1a:309:G:O2'	32:1a:607:A:N1	2.49	0.46
32:1a:728:A:H2'	32:1a:729:A:C8	2.51	0.46
32:1a:1074:G:O2'	32:1a:1101:A:N1	2.46	0.46
35:1d:15:GLU:OE2	35:1d:66:ARG:NH1	2.48	0.46
41:1j:43:ARG:HB3	41:1j:67:THR:OG1	2.16	0.46
1:2A:2166:G:N7	1:2A:2168:G:N2	2.63	0.46
5:2F:36:VAL:O	5:2F:40:GLN:HG3	2.14	0.46
5:2F:108:LYS:HG2	5:2F:112:MET:HE2	1.97	0.46
6:2G:125:PHE:HB3	6:2G:166:ASP:CG	2.41	0.46
24:22:16:LEU:O	24:22:67:LYS:NZ	2.44	0.46
32:2a:189(I):G:H2'	32:2a:189(J):G:O4'	2.16	0.46
32:2a:532:A:N6	32:2a:1206:G:O2'	2.49	0.46
38:2g:113:GLU:O	38:2g:119:ARG:HD3	2.15	0.46
41:2j:63:PHE:CE1	45:2n:58:LYS:HG3	2.51	0.46
42:2k:19:ALA:N	42:2k:81:ASP:O	2.49	0.46
44:2m:73:GLU:O	44:2m:77:ASN:HB2	2.16	0.46
50:2s:27:GLU:HA	50:2s:28:LYS:HA	1.77	0.46
1:1A:2147:G:H3'	1:1A:2147:G:N3	2.31	0.46
1:1A:2289:G:OP1	61:1A:4147:HOH:O	2.20	0.46
1:1A:2811:G:N2	1:1A:2891:G:H1'	2.30	0.46
4:1E:27:LEU:HD12	4:1E:180:ASN:O	2.16	0.46
7:1H:13:LYS:HA	7:1H:14:GLY:HA2	1.63	0.46
14:1S:92:TYR:OH	61:1S:301:HOH:O	2.16	0.46
16:1U:76:TYR:CE2	16:1U:80:ILE:HG13	2.51	0.46
32:1a:487:A:H2'	32:1a:488:C:O4'	2.16	0.46
33:1b:208:ILE:H	33:1b:208:ILE:HG13	1.55	0.46
46:1o:55:GLY:HA2	46:1o:58:MET:HE3	1.97	0.46
55:1x:12:A:H2'	55:1x:13:A:O4'	2.16	0.46
1:2A:1518:U:H2'	1:2A:1519:G:O4'	2.16	0.46
1:2A:2162:G:H2'	1:2A:2163:C:O4'	2.16	0.46
5:2F:31:HIS:HB2	11:2P:9:ASN:OD1	2.15	0.46
6:2G:131:TYR:HB3	6:2G:159:VAL:HG13	1.98	0.46
32:2a:772:U:H2'	32:2a:773:G:O4'	2.16	0.46
1:1A:2206:G:H5''	1:1A:2207:G:C8	2.50	0.46
1:1A:2331:G:O2'	22:10:43:THR:HG22	2.16	0.46
1:1A:2705:A:O2'	1:1A:2852:G:OP1	2.28	0.46
1:1A:2747:G:OP1	7:1H:138:LYS:NZ	2.49	0.46
20:1Y:21:LYS:HE2	20:1Y:21:LYS:HB3	1.70	0.46
20:1Y:35:TYR:CE2	20:1Y:69:ALA:HB3	2.51	0.46
25:13:4:LEU:O	25:13:36:VAL:HA	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:624:C:H2'	32:1a:625:G:C8	2.51	0.46
52:1u:12:LYS:HB3	52:1u:17:THR:O	2.16	0.46
1:2A:1036:G:H1	1:2A:1119:C:H42	1.64	0.46
1:2A:1405:U:H2'	1:2A:1406:U:C6	2.51	0.46
1:2A:2111:C:H6	1:2A:2111:C:OP2	2.00	0.46
1:2A:2176:A:H2'	1:2A:2177:C:H6	1.81	0.46
7:2H:41:MET:HE1	7:2H:54:ARG:HB3	1.98	0.46
8:2I:38:LEU:H	8:2I:38:LEU:HD12	1.81	0.46
32:2a:167:G:H2'	32:2a:168:G:H8	1.81	0.46
32:2a:189:G:C6	32:2a:189(L):G:C6	3.04	0.46
32:2a:1095:U:H2'	32:2a:1096:C:O4'	2.16	0.46
35:2d:68:TYR:OH	35:2d:98:GLU:OE2	2.29	0.46
38:2g:70:LYS:HB2	38:2g:70:LYS:HE3	1.67	0.46
41:2j:49:VAL:O	41:2j:60:ARG:HB3	2.17	0.46
44:2m:20:THR:C	44:2m:22:ILE:H	2.24	0.46
1:1A:1359:A:H2'	1:1A:1360:A:H5'	1.98	0.45
7:1H:3:ARG:NH1	7:1H:5:GLY:H	2.15	0.45
7:1H:3:ARG:HH21	7:1H:65:HIS:HB3	1.80	0.45
32:1a:407:G:H5''	35:1d:115:ARG:HB3	1.97	0.45
32:1a:1531:A:H8	32:1a:1531:A:O5'	1.99	0.45
33:1b:132:LYS:O	33:1b:136:VAL:HG13	2.16	0.45
35:1d:79:PHE:CE1	35:1d:204:ILE:HD13	2.50	0.45
35:1d:146:ILE:H	35:1d:146:ILE:HD12	1.81	0.45
35:1d:201:GLN:HE21	35:1d:201:GLN:HB3	1.49	0.45
37:1f:44:GLY:HA2	37:1f:59:TYR:CE1	2.51	0.45
37:1f:86:ARG:O	37:1f:87:ARG:HG2	2.16	0.45
54:1w:109:VAL:HG22	54:1w:201:VAL:HG12	1.97	0.45
1:2A:297:C:H2'	1:2A:298:G:O4'	2.16	0.45
1:2A:744:G:OP1	4:2E:132:HIS:ND1	2.45	0.45
1:2A:1530:C:N4	1:2A:1539:G:H1	2.14	0.45
1:2A:2128:C:H1'	1:2A:2173:A:O2'	2.17	0.45
1:2A:2776:A:H4'	1:2A:2777:G:H5''	1.97	0.45
13:2R:38:VAL:HG12	13:2R:42:LYS:HD2	1.98	0.45
32:2a:1206:G:C6	32:2a:1207:2MG:C5	3.04	0.45
32:2a:1330:U:H4'	44:2m:23:TYR:CE1	2.51	0.45
33:2b:16:HIS:CG	33:2b:17:PHE:N	2.84	0.45
35:2d:173:TRP:CD1	35:2d:189:PRO:HG3	2.51	0.45
1:1A:1071:G:H3'	1:1A:1072:C:C6	2.51	0.45
1:1A:2251:OMG:HM23	1:1A:2251:OMG:H1'	1.69	0.45
8:1I:6:LEU:C	8:1I:7:GLU:HG2	2.40	0.45
9:1N:1:MET:HE3	17:1V:13:ARG:HB3	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:258:G:H2'	32:1a:259:G:C8	2.51	0.45
32:1a:1005:A:OP2	32:1a:1006:C:N4	2.50	0.45
35:1d:98:GLU:OE2	35:1d:107:ARG:NH1	2.49	0.45
42:1k:77:MET:HE2	42:1k:77:MET:HB2	1.89	0.45
44:1m:74:VAL:HG12	44:1m:78:ILE:HD11	1.97	0.45
1:2A:197:A:N6	1:2A:2430:A:O2'	2.49	0.45
1:2A:2110:G:H3'	1:2A:2111:C:C5'	2.43	0.45
1:2A:2748:A:H5'	7:2H:4:ILE:HD12	1.98	0.45
9:2N:61:ARG:HD3	9:2N:61:ARG:HA	1.64	0.45
18:2W:45:TYR:CZ	18:2W:49:LYS:HE3	2.51	0.45
32:2a:664:G:P	49:2r:64:ARG:HH21	2.38	0.45
33:2b:115:LEU:HD13	33:2b:145:LEU:HB2	1.99	0.45
40:2i:17:VAL:HA	40:2i:63:ILE:HD13	1.96	0.45
44:2m:66:LEU:O	44:2m:70:LEU:N	2.48	0.45
46:2o:82:ILE:O	46:2o:86:GLY:N	2.48	0.45
47:2p:34:GLU:OE1	47:2p:55:ARG:NH2	2.32	0.45
54:2w:122:LEU:HD21	54:2w:152:LEU:HD23	1.98	0.45
12:1Q:18:LYS:HE2	12:1Q:18:LYS:HB2	1.78	0.45
15:1T:108:ARG:HG3	15:1T:109:GLU:N	2.31	0.45
32:1a:533:A:OP1	61:1a:1905:HOH:O	2.21	0.45
1:2A:1582:C:H2'	1:2A:1583:A:C8	2.52	0.45
11:2P:96:THR:O	11:2P:100:LEU:HD12	2.17	0.45
32:2a:950:U:H2'	32:2a:951:G:H8	1.81	0.45
38:2g:122:HIS:O	38:2g:125:MET:HG2	2.17	0.45
44:2m:101:GLN:OE1	44:2m:101:GLN:N	2.50	0.45
47:2p:17:TYR:HE2	47:2p:41:PRO:HG3	1.81	0.45
1:1A:251:A:C5	1:1A:252:G:H1'	2.51	0.45
1:1A:1999:C:H4'	1:1A:2723:C:O2	2.16	0.45
1:1A:2233:U:H2'	1:1A:2234:G:C8	2.51	0.45
11:1P:82:GLY:HA2	11:1P:113:LYS:O	2.17	0.45
32:1a:683:G:H2'	32:1a:684:A:C8	2.51	0.45
32:1a:1273:G:H3'	32:1a:1274:G:H8	1.81	0.45
33:1b:184:VAL:H	33:1b:198:ASP:HB2	1.81	0.45
36:1e:94:ALA:HB2	36:1e:119:LEU:HG	1.98	0.45
37:1f:100:ASN:HB2	49:1r:28:GLU:HA	1.98	0.45
51:1t:47:GLY:HA2	51:1t:48:LYS:C	2.42	0.45
1:2A:12:U:O2	1:2A:2626:C:H4'	2.17	0.45
1:2A:773:U:O2'	3:2D:48:ARG:HD3	2.16	0.45
1:2A:1035:U:H5''	7:2H:59:ARG:HD3	1.98	0.45
6:2G:112:PRO:HG3	26:24:43:TYR:CE2	2.52	0.45
32:2a:8:A:N6	35:2d:209:ARG:HB2	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:2f:30:LEU:HB3	37:2f:35:ALA:HB3	1.98	0.45
40:2i:102:LEU:H	40:2i:102:LEU:HD23	1.82	0.45
1:1A:272(J):C:H2'	1:1A:274:G:H8	1.82	0.45
1:1A:784:A:C6	3:1D:229:VAL:HG11	2.51	0.45
21:1Z:53:ILE:HG22	21:1Z:71:VAL:HG12	1.99	0.45
30:18:26:LYS:HD3	30:18:48:PHE:HB3	1.99	0.45
32:1a:19:C:OP1	36:1e:125:SER:OG	2.24	0.45
32:1a:509:A:O2'	32:1a:510:A:OP1	2.33	0.45
32:1a:859:A:H2'	32:1a:860:A:O4'	2.17	0.45
32:1a:1137:C:H5'	32:1a:1138:G:C4	2.51	0.45
32:1a:1355:G:H2'	32:1a:1356:G:H8	1.79	0.45
44:1m:95:GLY:O	44:1m:110:ARG:HG2	2.16	0.45
1:2A:2872:G:O2'	1:2A:2873:A:H5'	2.17	0.45
4:2E:134:ILE:HA	4:2E:137:HIS:CD2	2.51	0.45
6:2G:151:ALA:O	6:2G:153:ARG:NH1	2.50	0.45
7:2H:17:VAL:HG22	7:2H:26:VAL:HG22	1.98	0.45
26:24:1:MET:HE2	26:24:6:HIS:CD2	2.51	0.45
32:2a:1390:U:H2'	32:2a:1391:U:C6	2.51	0.45
32:2a:1499:A:H1'	32:2a:1520:G:H5'	1.97	0.45
54:2w:111:ILE:HG12	54:2w:199:VAL:HG22	1.99	0.45
32:1a:1030(A):G:H3'	32:1a:1030(B):C:H5''	1.99	0.45
32:1a:1034:G:H3'	32:1a:1035:A:H8	1.81	0.45
34:1c:178:LEU:HD23	34:1c:178:LEU:HA	1.72	0.45
35:1d:173:TRP:CE3	35:1d:174:LEU:HG	2.51	0.45
38:1g:16:LEU:HD12	40:1i:42:ARG:HA	1.97	0.45
44:1m:39:ILE:HG12	44:1m:52:GLU:HG2	1.98	0.45
1:2A:2391:G:O6	1:2A:2425:A:H8	1.99	0.45
1:2A:2734:A:H2'	1:2A:2735:G:O4'	2.17	0.45
1:2A:2881:C:H2'	1:2A:2882:A:O4'	2.16	0.45
6:2G:36:LYS:HG2	6:2G:95:ARG:NH1	2.31	0.45
32:2a:1250:A:N3	32:2a:1370:G:O2'	2.44	0.45
32:2a:1329:A:H5''	44:2m:26:GLY:H	1.82	0.45
35:2d:9:CYS:O	35:2d:13:ARG:HG3	2.16	0.45
42:2k:87:THR:O	42:2k:87:THR:OG1	2.26	0.45
51:2t:38:LYS:O	51:2t:42:GLN:N	2.36	0.45
51:2t:43:LEU:HD12	51:2t:55:ILE:HG13	1.98	0.45
54:2w:111:ILE:O	54:2w:157:LYS:HA	2.17	0.45
1:1A:1068:G:C5	1:1A:1096:A:H1'	2.52	0.45
1:1A:1094:U:H4'	1:1A:1097:U:O4	2.16	0.45
1:1A:1971:A:OP2	3:1D:242:ARG:NH2	2.49	0.45
1:1A:2107:C:C4	1:1A:2108:C:C2	3.05	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:1F:51:THR:HG23	5:1F:92:PRO:HD2	1.98	0.45
16:1U:34:LYS:HA	16:1U:34:LYS:HD2	1.56	0.45
39:1h:49:GLU:HG2	39:1h:62:TYR:HE2	1.81	0.45
47:1p:40:ASP:HB3	47:1p:48:TRP:HB3	1.98	0.45
11:2P:46:LYS:HB3	11:2P:46:LYS:HE2	1.75	0.45
21:2Z:7:ALA:O	21:2Z:62:PRO:HD3	2.16	0.45
21:2Z:52:SER:C	21:2Z:54:HIS:H	2.24	0.45
32:2a:1032:G:H2'	32:2a:1033:G:O4'	2.17	0.45
1:1A:388:G:O2'	1:1A:389:G:N7	2.49	0.45
1:1A:1178:C:H2'	1:1A:1179:C:H6	1.81	0.45
7:1H:164:TYR:HB2	7:1H:167:GLU:HB2	1.97	0.45
9:1N:42:TRP:HA	9:1N:48:MET:HE1	1.99	0.45
13:1R:118:GLU:H	13:1R:118:GLU:CD	2.25	0.45
14:1S:93:LYS:HE2	14:1S:95:HIS:HB2	1.99	0.45
21:1Z:93:ASP:CB	21:1Z:131:ARG:HH22	2.30	0.45
21:1Z:146:ILE:N	21:1Z:147:GLY:HA2	2.32	0.45
32:1a:674:G:H2'	32:1a:675:A:H8	1.80	0.45
35:1d:57:ARG:HH22	36:1e:107:ARG:HD3	1.82	0.45
1:2A:265:A:C8	1:2A:266:G:H1'	2.51	0.45
2:2B:106:G:OP1	21:2Z:31:ARG:HG3	2.17	0.45
7:2H:84:SER:HB3	7:2H:134:SER:HB3	1.99	0.45
21:2Z:146:ILE:HA	21:2Z:147:GLY:HA2	1.54	0.45
32:2a:141:A:H1'	32:2a:182:U:H1'	1.99	0.45
32:2a:1023:G:H3'	32:2a:1024:G:C8	2.52	0.45
32:2a:1278:U:H5'	32:2a:1279:A:H5'	1.99	0.45
32:2a:1333:A:H2'	32:2a:1334:G:O4'	2.16	0.45
35:2d:122:ARG:NH1	35:2d:134:ASP:HB2	2.32	0.45
35:2d:173:TRP:CD1	35:2d:174:LEU:HG	2.51	0.45
37:2f:100:ASN:OD1	49:2r:23:LYS:HG2	2.17	0.45
39:2h:121:ASP:HB2	39:2h:125:ARG:NH2	2.32	0.45
42:2k:73:MET:HG3	42:2k:103:LEU:HD21	1.98	0.45
44:2m:66:LEU:O	44:2m:70:LEU:HB2	2.17	0.45
1:1A:271(A):A:N1	1:1A:272(D):G:O2'	2.49	0.45
1:1A:1364:G:P	23:11:3:LYS:HG3	2.57	0.45
1:1A:2146:C:H4'	1:1A:2147:G:H5''	1.99	0.45
2:1B:105:A:OP1	21:1Z:72:ARG:NH1	2.49	0.45
7:1H:25:LYS:HG2	7:1H:34:GLU:HG2	1.97	0.45
14:1S:61:ASN:HD21	14:1S:63:THR:HB	1.82	0.45
30:18:38:GLY:O	30:18:42:ARG:HB2	2.17	0.45
32:1a:7:G:H5'	32:1a:298:A:O4'	2.16	0.45
32:1a:340:U:H2'	32:1a:341:C:C6	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:1b:41:ILE:HD13	33:1b:41:ILE:HA	1.79	0.45
36:1e:96:PRO:HA	36:1e:117:ASP:OD2	2.16	0.45
38:1g:23:VAL:O	38:1g:27:ILE:HG13	2.17	0.45
39:1h:121:ASP:OD1	39:1h:121:ASP:N	2.49	0.45
1:2A:363(B):G:H2'	1:2A:363(C):G:C8	2.51	0.45
1:2A:1593:G:H2'	1:2A:1594:G:C8	2.52	0.45
5:2F:120:GLU:HB3	5:2F:122:LYS:HG2	1.99	0.45
9:2N:97:ARG:HA	9:2N:100:GLU:HB2	1.99	0.45
13:2R:51:LEU:HD22	13:2R:66:VAL:HG13	1.98	0.45
15:2T:6:LEU:O	15:2T:10:VAL:HG23	2.17	0.45
15:2T:6:LEU:HD13	15:2T:6:LEU:HA	1.73	0.45
32:2a:298:A:C6	32:2a:299:G:C2	3.05	0.45
32:2a:1265:G:C4	32:2a:1271:G:N2	2.85	0.45
39:2h:121:ASP:HB2	39:2h:125:ARG:HH22	1.81	0.45
41:2j:17:ASP:OD1	41:2j:70:ARG:NE	2.49	0.45
44:2m:27:LYS:HD2	44:2m:27:LYS:HA	1.79	0.45
47:2p:20:VAL:HG21	47:2p:32:TYR:CD2	2.52	0.45
1:1A:1889:A:N1	1:1A:2234:G:H1'	2.32	0.45
32:1a:499:A:H4'	32:1a:500:G:OP1	2.17	0.45
32:1a:1272:G:H2'	32:1a:1273:G:O4'	2.17	0.45
35:1d:19:LEU:O	35:1d:21:LEU:N	2.49	0.45
43:1l:41:ARG:HE	43:1l:43:VAL:HG13	1.81	0.45
1:2A:205:G:O6	23:21:39:LYS:NZ	2.48	0.45
1:2A:272:G:H4'	1:2A:272(A):U:H5''	1.99	0.45
1:2A:2648:C:H2'	1:2A:2649:U:C6	2.52	0.45
6:2G:54:GLU:O	6:2G:58:GLN:N	2.47	0.45
9:2N:58:ASP:OD1	9:2N:58:ASP:N	2.50	0.45
11:2P:2:LYS:HE3	11:2P:4:SER:HB2	1.99	0.45
32:2a:67:C:H2'	32:2a:68:G:H8	1.78	0.45
32:2a:148:G:H2'	32:2a:149:A:C8	2.51	0.45
32:2a:966:M2G:HM22	55:2x:34:G:H5'	1.99	0.45
32:2a:977:A:O3'	32:2a:980:C:N4	2.50	0.45
32:2a:1163:C:H2'	32:2a:1164:G:H8	1.82	0.45
1:1A:9:U:N3	1:1A:2629:A:H2	2.10	0.44
5:1F:178:PRO:HB2	5:1F:201:VAL:HG21	1.99	0.44
32:1a:501:C:H2'	32:1a:502:G:C8	2.52	0.44
34:1c:188:LEU:HD23	34:1c:190:ARG:CZ	2.48	0.44
43:1l:36:VAL:HG22	43:1l:82:VAL:HG22	1.98	0.44
1:2A:271(H):G:H2'	1:2A:271(I):G:H8	1.81	0.44
1:2A:582:G:H2'	1:2A:583:G:C8	2.52	0.44
1:2A:2134:A:C2	1:2A:2159:G:H1'	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2150:U:H2'	1:2A:2151:G:C8	2.46	0.44
5:2F:165:ARG:HG2	5:2F:168:ARG:NH2	2.32	0.44
21:2Z:91:LEU:HD13	21:2Z:91:LEU:HA	1.77	0.44
35:2d:158:ILE:HG23	35:2d:162:LEU:HD12	1.98	0.44
1:1A:551:G:O2'	1:1A:1220:A:N3	2.44	0.44
1:1A:729:G:C6	3:1D:208:LYS:HB2	2.52	0.44
1:1A:971:C:H2'	1:1A:972:G:O4'	2.17	0.44
1:1A:1339:G:H5''	19:1X:16:LYS:HD3	1.99	0.44
1:1A:2169:A:H2'	1:1A:2169:A:N3	2.33	0.44
6:1G:106:LEU:HA	6:1G:110:ALA:HB3	1.99	0.44
20:1Y:14:LEU:HD12	20:1Y:23:ARG:O	2.17	0.44
21:1Z:45:ASP:O	21:1Z:49:ARG:HB2	2.17	0.44
21:1Z:67:LEU:HD23	21:1Z:67:LEU:HA	1.77	0.44
33:1b:185:ILE:HG22	33:1b:199:TYR:CD2	2.50	0.44
54:1w:303:ARG:HA	54:1w:313:THR:O	2.17	0.44
1:2A:751:A:H5'	18:2W:90:ARG:HA	1.99	0.44
1:2A:784:A:C6	3:2D:229:VAL:HG11	2.53	0.44
1:2A:1028:A:N6	1:2A:1125:G:H2'	2.32	0.44
1:2A:1149:G:H2'	1:2A:1150:C:C6	2.53	0.44
1:2A:1607:C:H5''	1:2A:1608:A:H5'	1.99	0.44
29:27:24:THR:HG22	29:27:26:GLY:H	1.81	0.44
32:2a:1097:C:O2'	32:2a:1169:A:N3	2.46	0.44
32:2a:1252:A:H2'	32:2a:1253:G:O4'	2.17	0.44
54:2w:303:ARG:HD2	54:2w:305:TYR:OH	2.16	0.44
1:1A:2183:C:H2'	1:1A:2184:G:C8	2.52	0.44
20:1Y:95:LYS:HB3	20:1Y:95:LYS:HE2	1.86	0.44
21:1Z:155:LEU:HD23	21:1Z:155:LEU:HA	1.80	0.44
26:14:69:LYS:HD3	50:1s:20:LEU:HD13	1.99	0.44
29:17:5:TRP:NE1	29:17:7:PRO:HG3	2.32	0.44
32:1a:473:G:H2'	32:1a:474:G:H8	1.82	0.44
33:1b:119:GLU:OE2	33:1b:153:ARG:NH1	2.50	0.44
35:1d:60:GLU:OE1	35:1d:199:ASN:N	2.40	0.44
36:1e:33:VAL:HG13	36:1e:112:LEU:HD12	1.99	0.44
1:2A:660:G:H5'	5:2F:99:TYR:CE1	2.53	0.44
1:2A:2563:U:O2	1:2A:2565:A:H8	2.00	0.44
14:2S:10:ARG:HG2	14:2S:91:PRO:HA	1.98	0.44
28:26:3:SER:OG	28:26:4:GLU:N	2.50	0.44
32:2a:1014:A:H4'	50:2s:14:HIS:NE2	2.32	0.44
33:2b:61:LEU:HA	33:2b:64:ARG:HB2	1.99	0.44
40:2i:22:GLY:HA3	40:2i:60:ASP:OD2	2.17	0.44
54:1w:218:ARG:NH1	54:1w:220:ASP:OD2	2.47	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2405:G:H5'	11:2P:75:ILE:HD13	1.99	0.44
1:2A:2557:G:O4'	54:2w:240:ARG:NH2	2.51	0.44
2:2B:120:A:H5''	61:2B:314:HOH:O	2.17	0.44
4:2E:59:VAL:HG21	4:2E:74:PRO:HB3	2.00	0.44
7:2H:152:ARG:HA	7:2H:152:ARG:HD3	1.85	0.44
16:2U:78:THR:O	16:2U:117:GLN:NE2	2.51	0.44
21:2Z:93:ASP:HA	21:2Z:130:PRO:HG2	2.00	0.44
41:2j:38:ILE:HD13	41:2j:71:LEU:HD22	1.98	0.44
1:1A:174:C:H2'	1:1A:175:G:O4'	2.17	0.44
1:1A:428:A:H8	1:1A:428:A:OP2	2.00	0.44
1:1A:2336:A:H61	22:10:43:THR:HG21	1.83	0.44
4:1E:101:ARG:CZ	4:1E:171:GLU:HB2	2.48	0.44
13:1R:72:ASP:HB3	13:1R:75:LEU:HB3	1.99	0.44
32:1a:402:G:OP1	35:1d:74:GLN:HG2	2.17	0.44
45:1n:3:ARG:HA	45:1n:3:ARG:HD3	1.51	0.44
1:2A:118:A:H1'	1:2A:178:G:O4'	2.18	0.44
1:2A:811:U:H2'	11:2P:21:ARG:HA	2.00	0.44
1:2A:1026:U:H4'	1:2A:1027:A:OP1	2.18	0.44
1:2A:2291:U:H2'	1:2A:2292:C:C6	2.53	0.44
3:2D:132:PRO:HD3	3:2D:190:TYR:CZ	2.52	0.44
6:2G:96:ARG:N	6:2G:99:MET:HE2	2.31	0.44
15:2T:65:LYS:HE2	15:2T:65:LYS:HB3	1.71	0.44
32:2a:576:G:N2	32:2a:760:G:OP2	2.51	0.44
32:2a:1387:G:H2'	32:2a:1388:C:C6	2.52	0.44
32:2a:1442:G:H2'	32:2a:1442:G:N3	2.33	0.44
54:2w:212:LEU:HD22	54:2w:217:ILE:HD11	1.99	0.44
1:1A:1652:A:C2'	1:1A:1653:G:H5'	2.47	0.44
1:1A:2121:G:H1	1:1A:2177:C:H42	1.66	0.44
1:1A:2127:G:H2'	1:1A:2128:C:C6	2.53	0.44
11:1P:126:VAL:HG12	11:1P:148:LEU:HD13	1.99	0.44
12:1Q:45:GLN:OE1	12:1Q:45:GLN:N	2.44	0.44
12:1Q:58:PHE:HB3	12:1Q:61:GLY:O	2.18	0.44
32:1a:865:A:H2	32:1a:918:A:H4'	1.83	0.44
32:1a:959:A:O2'	32:1a:984:C:O2'	2.26	0.44
32:1a:1126:U:O2	32:1a:1280:A:H2'	2.17	0.44
32:1a:1252:A:H2'	32:1a:1253:G:O4'	2.18	0.44
32:1a:1513:A:H2'	32:1a:1514:C:C6	2.53	0.44
35:1d:98:GLU:HA	35:1d:103:ASN:ND2	2.33	0.44
35:1d:157:LEU:O	35:1d:161:ASN:ND2	2.51	0.44
40:1i:93:ARG:HE	40:1i:93:ARG:HB2	1.61	0.44
41:1j:50:ILE:HA	41:1j:60:ARG:HG2	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:1p:58:TYR:O	47:1p:62:VAL:HG23	2.17	0.44
1:2A:784:A:H5'	1:2A:785:G:OP1	2.18	0.44
1:2A:2136:C:C4	1:2A:2155:G:O6	2.71	0.44
2:2B:24:G:H4'	2:2B:25:A:C8	2.52	0.44
5:2F:116:ASP:OD1	5:2F:119:ARG:NH2	2.51	0.44
6:2G:111:LEU:HB2	6:2G:112:PRO:HD3	1.99	0.44
18:2W:1:MET:HA	18:2W:1:MET:HE3	2.00	0.44
22:20:43:THR:HG23	22:20:43:THR:O	2.17	0.44
32:2a:757:U:H2'	32:2a:758:G:O4'	2.17	0.44
34:2c:35:GLU:O	34:2c:39:ILE:HG12	2.18	0.44
42:2k:85:ARG:HE	42:2k:111:ASP:HB3	1.83	0.44
48:2q:53:LEU:HD23	48:2q:82:MET:HE1	1.98	0.44
1:1A:1568:G:H5''	3:1D:61:LEU:HG	1.99	0.44
1:1A:2188:C:H2'	1:1A:2189:U:O4'	2.17	0.44
1:1A:2224:G:H4'	1:1A:2226:C:C2	2.53	0.44
35:1d:9:CYS:O	35:1d:13:ARG:HG3	2.18	0.44
38:1g:72:ARG:NH2	38:1g:142:GLU:OE1	2.51	0.44
1:2A:981:A:N1	1:2A:2027:G:O2'	2.45	0.44
1:2A:2064:C:H2'	1:2A:2065:C:C6	2.53	0.44
1:2A:2165:G:H2'	1:2A:2166:G:H5''	2.00	0.44
1:2A:2471:C:H2'	1:2A:2472:G:O4'	2.18	0.44
21:2Z:36:LYS:HB2	21:2Z:36:LYS:HE3	1.72	0.44
32:2a:1004:A:H1'	32:2a:1038:C:H1'	2.00	0.44
33:2b:91:PRO:HG3	33:2b:154:LEU:HB3	1.99	0.44
35:2d:128:VAL:HG12	35:2d:129:ASN:HD22	1.83	0.44
36:2e:12:LEU:O	36:2e:30:ALA:HA	2.17	0.44
38:2g:86:GLN:HE21	38:2g:86:GLN:HA	1.83	0.44
39:2h:20:TYR:HA	39:2h:65:TYR:CZ	2.53	0.44
41:2j:45:ARG:O	41:2j:65:LEU:N	2.38	0.44
44:2m:30:ALA:O	44:2m:34:LEU:HG	2.18	0.44
44:2m:65:LYS:HG3	44:2m:69:GLU:CD	2.42	0.44
54:2w:241:VAL:HG23	54:2w:250:VAL:HG13	2.00	0.44
1:1A:883:G:H2'	1:1A:884:C:C5	2.51	0.44
1:1A:1274:A:N3	1:1A:1297:C:H1'	2.33	0.44
5:1F:117:ARG:NH2	5:1F:189:THR:O	2.42	0.44
14:1S:105:ALA:HB1	14:1S:110:LEU:HD12	1.99	0.44
32:1a:165:C:H2'	32:1a:166:G:H8	1.82	0.44
32:1a:444:C:H2'	32:1a:445:G:H8	1.83	0.44
32:1a:966:M2G:HM13	32:1a:967:5MC:H1'	2.00	0.44
36:1e:29:GLY:HA2	36:1e:46:GLY:O	2.18	0.44
36:1e:131:ILE:HD13	36:1e:131:ILE:HA	1.86	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:1h:64:LYS:HG2	39:1h:79:VAL:HG21	2.00	0.44
39:1h:77:GLU:HG2	39:1h:78:GLN:H	1.83	0.44
42:1k:72:ALA:HB1	42:1k:77:MET:HE3	2.00	0.44
54:1w:285:LEU:HG	54:1w:289:ARG:NH1	2.33	0.44
1:2A:489:G:H2'	1:2A:491:G:O4'	2.18	0.44
1:2A:493:G:H2'	1:2A:494:G:O4'	2.18	0.44
1:2A:721:C:H2'	1:2A:722:A:C8	2.53	0.44
1:2A:927:G:H2'	1:2A:928:G:O4'	2.16	0.44
1:2A:1250:G:N7	11:2P:18:ARG:NH2	2.66	0.44
1:2A:1364:G:P	23:21:3:LYS:HG3	2.58	0.44
1:2A:2238:G:H2'	1:2A:2238:G:N3	2.32	0.44
4:2E:89:ASP:OD1	4:2E:89:ASP:N	2.50	0.44
12:2Q:83:MET:HE2	12:2Q:83:MET:HA	1.98	0.44
32:2a:54:C:N4	32:2a:353:A:OP2	2.46	0.44
39:2h:51:VAL:HG11	39:2h:60:ARG:HH21	1.83	0.44
55:2x:21:H2U:HO2'	55:2x:22:A:P	2.40	0.44
1:1A:223:A:O4'	1:1A:422:A:H5'	2.17	0.44
1:1A:1068:G:C8	1:1A:1096:A:H1'	2.52	0.44
1:1A:2116:G:H2'	1:1A:2117:A:C6	2.53	0.44
7:1H:153:LYS:HE2	7:1H:153:LYS:HB3	1.80	0.44
32:1a:250:A:H4'	32:1a:251:G:O5'	2.17	0.44
32:1a:857:C:H2'	32:1a:858:G:O4'	2.18	0.44
32:1a:1343:G:H4'	40:1i:122:ALA:HB3	2.00	0.44
33:1b:114:ARG:HH21	33:1b:141:GLU:CD	2.25	0.44
39:1h:17:THR:HB	39:1h:65:TYR:HE1	1.83	0.44
1:2A:1263:U:C4	1:2A:1264:G:C6	3.05	0.44
1:2A:1275:A:N1	1:2A:1295:C:O2'	2.49	0.44
1:2A:1453:U:O2'	1:2A:1455:G:N7	2.46	0.44
18:2W:56:ALA:O	18:2W:60:ASN:HB2	2.18	0.44
20:2Y:9:LYS:HA	20:2Y:10:GLY:HA2	1.52	0.44
32:2a:562:C:H1'	43:2l:15:ARG:HD2	1.99	0.44
32:2a:573:A:N3	32:2a:883:C:O2'	2.50	0.44
32:2a:991:U:O2'	32:2a:992:U:H5'	2.18	0.44
32:2a:1060:C:H5''	41:2j:51:ARG:HG2	2.00	0.44
35:2d:100:ARG:HH22	35:2d:118:ARG:HH22	1.64	0.44
54:2w:125:ARG:NE	54:2w:153:GLY:O	2.37	0.44
54:2w:184:PRO:HG3	54:2w:193:HIS:HB2	2.00	0.44
1:1A:721:C:H2'	1:1A:722:A:C8	2.53	0.43
1:1A:1803:A:H4'	3:1D:259:THR:HG23	1.99	0.43
1:1A:1916:A:H2'	1:1A:1917:PSU:O4'	2.18	0.43
4:1E:29:GLY:HA3	61:1E:402:HOH:O	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:1G:56:ALA:O	6:1G:59:GLU:HG2	2.18	0.43
9:1N:96:GLU:H	9:1N:96:GLU:CD	2.26	0.43
32:1a:413:G:N2	32:1a:428:G:H1'	2.32	0.43
32:1a:1015:A:H2'	32:1a:1016:A:C8	2.53	0.43
32:1a:1157:A:H61	32:1a:1178:G:H21	1.66	0.43
34:1c:33:LEU:O	34:1c:37:GLN:HG2	2.18	0.43
38:1g:46:ALA:O	38:1g:50:ILE:HD12	2.18	0.43
47:1p:5:ARG:HE	47:1p:22:THR:HG23	1.83	0.43
47:1p:8:ARG:O	47:1p:9:PHE:HD1	2.01	0.43
1:2A:2314:C:H2'	1:2A:2315:G:C8	2.53	0.43
4:2E:181:LEU:HD23	4:2E:181:LEU:HA	1.81	0.43
14:2S:36:TYR:CD2	14:2S:36:TYR:N	2.86	0.43
15:2T:27:THR:HB	15:2T:89:VAL:HG22	2.01	0.43
15:2T:96:ARG:CZ	15:2T:96:ARG:HB3	2.47	0.43
32:2a:269:C:H2'	32:2a:270:A:H8	1.82	0.43
32:2a:1271:G:C2	32:2a:1272:G:N7	2.84	0.43
38:2g:152:ALA:O	38:2g:155:ARG:HD3	2.18	0.43
44:2m:80:ARG:HH22	50:2s:69:HIS:CE1	2.35	0.43
1:1A:1068:G:H1'	1:1A:1096:A:N3	2.33	0.43
1:1A:1371:G:H2'	1:1A:1372:U:H5	1.83	0.43
26:14:46:GLN:HB2	26:14:48:ARG:NE	2.33	0.43
32:1a:175:C:H2'	32:1a:176:C:H6	1.83	0.43
32:1a:1030(D):A:C8	32:1a:1031:G:H1'	2.53	0.43
34:1c:8:ILE:C	34:1c:10:PHE:H	2.26	0.43
44:1m:70:LEU:HD23	44:1m:70:LEU:HA	1.79	0.43
49:1r:47:THR:HA	49:1r:83:GLU:HB2	1.99	0.43
1:2A:26:G:C6	1:2A:27:G:N1	2.86	0.43
1:2A:764:A:O4'	3:2D:213:ARG:HG3	2.18	0.43
1:2A:1125:G:H5'	31:29:37:GLY:HA2	2.00	0.43
1:2A:1665:A:H4'	10:2O:67:LYS:HB2	1.98	0.43
13:2R:72:ASP:O	13:2R:76:VAL:HG23	2.18	0.43
32:2a:109:A:C6	32:2a:326:G:C6	3.07	0.43
32:2a:714:G:H2'	32:2a:715:A:C8	2.53	0.43
32:2a:1138:G:C5	32:2a:1140:C:H1'	2.53	0.43
44:2m:14:ARG:NE	44:2m:42:ALA:HA	2.32	0.43
1:1A:730:C:H5'	61:1A:4321:HOH:O	2.19	0.43
1:1A:1607:C:N4	1:1A:1622:G:OP2	2.36	0.43
1:1A:1876:A:H2'	1:1A:1877:A:C8	2.52	0.43
1:1A:2168:G:H2'	1:1A:2170:A:N7	2.34	0.43
26:14:58:ARG:HE	50:1s:68:GLY:H	1.65	0.43
32:1a:236:G:OP1	48:1q:40:LYS:NZ	2.50	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1241:G:H2'	32:1a:1242:C:C6	2.53	0.43
32:1a:1273:G:C2	32:1a:1274:G:H1'	2.54	0.43
34:1c:131:ARG:NH1	34:1c:166:GLU:HG3	2.31	0.43
35:1d:57:ARG:NH2	36:1e:107:ARG:HD3	2.33	0.43
39:1h:44:PHE:HZ	39:1h:138:TRP:HA	1.82	0.43
46:1o:40:SER:O	46:1o:44:LYS:HG3	2.17	0.43
1:2A:1417:C:H2'	1:2A:1418:G:O4'	2.18	0.43
1:2A:1779:U:H2'	61:2A:4220:HOH:O	2.18	0.43
1:2A:2189:U:H2'	1:2A:2190:G:H8	1.82	0.43
8:2I:114:LEU:HD11	8:2I:128:LEU:HD13	2.00	0.43
32:2a:90:U:H2'	32:2a:91:C:H6	1.83	0.43
32:2a:1151:A:O2'	32:2a:1152:A:O5'	2.33	0.43
32:2a:1265:G:C6	32:2a:1266:G:C5	3.07	0.43
33:2b:16:HIS:HB3	33:2b:210:SER:HB2	2.00	0.43
41:2j:6:ILE:HA	41:2j:98:ILE:HG23	2.00	0.43
55:2x:65:A:H2'	55:2x:66:A:C8	2.54	0.43
1:1A:221:A:N1	1:1A:265:A:O2'	2.49	0.43
1:1A:2543:G:H2'	1:1A:2544:G:C8	2.53	0.43
1:1A:2649:U:H2'	1:1A:2650:U:C6	2.52	0.43
3:1D:26:LYS:HD3	3:1D:83:GLU:OE2	2.18	0.43
8:1I:69:LYS:HE2	8:1I:73:GLU:OE2	2.18	0.43
32:1a:374:A:C6	32:1a:375:U:C4	3.06	0.43
32:1a:933:G:C2	32:1a:1385:G:C2	3.06	0.43
32:1a:1323:G:H2'	32:1a:1324:A:C8	2.53	0.43
47:1p:28:ARG:HG3	47:1p:29:ASP:N	2.33	0.43
1:2A:1992:G:H1'	61:2A:3956:HOH:O	2.18	0.43
1:2A:2111:C:H42	1:2A:2144:U:H4'	1.82	0.43
1:2A:2322:A:H2'	1:2A:2323:G:O4'	2.19	0.43
3:2D:38:LYS:C	3:2D:38:LYS:HD3	2.43	0.43
7:2H:149:ARG:HD3	7:2H:164:TYR:CZ	2.54	0.43
15:2T:109:GLU:HG2	15:2T:112:ARG:NH2	2.32	0.43
24:22:6:VAL:O	24:22:10:LEU:HD12	2.18	0.43
26:24:40:HIS:O	26:24:43:TYR:N	2.51	0.43
32:2a:1271:G:N2	32:2a:1272:G:C8	2.87	0.43
32:2a:1387:G:H2'	32:2a:1388:C:H6	1.82	0.43
33:2b:74:LYS:NZ	33:2b:206:ASP:OD1	2.41	0.43
37:2f:9:VAL:HA	37:2f:59:TYR:O	2.19	0.43
37:2f:12:PRO:HG3	37:2f:57:GLN:O	2.17	0.43
54:2w:111:ILE:HB	54:2w:158:VAL:HG23	1.99	0.43
54:2w:299:SER:O	54:2w:301:LYS:N	2.51	0.43
1:1A:359:A:H2'	1:1A:360:G:O4'	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1035:U:H2'	1:1A:1036:G:C8	2.53	0.43
1:1A:2794:C:H42	1:1A:2802:G:H1	1.65	0.43
2:1B:14:U:OP2	2:1B:70:C:O2'	2.29	0.43
2:1B:106:G:H5'	21:1Z:31:ARG:HB3	2.00	0.43
32:1a:1080:A:H5'	36:1e:14:ARG:NH2	2.33	0.43
32:1a:1195:C:H5''	32:1a:1196:U:OP2	2.18	0.43
33:1b:9:GLU:O	33:1b:11:LEU:N	2.43	0.43
35:1d:20:TYR:CD1	35:1d:26:CYS:HB3	2.53	0.43
42:1k:33:THR:HA	42:1k:39:PRO:HA	2.01	0.43
44:1m:9:ILE:HG23	44:1m:18:ALA:HB1	2.01	0.43
46:1o:18:PHE:HD1	46:1o:20:GLY:H	1.66	0.43
1:2A:271(K):U:O2	8:2I:50:ARG:HD3	2.18	0.43
1:2A:2331:G:O2'	22:20:43:THR:HG22	2.17	0.43
3:2D:145:VAL:HG12	3:2D:146:GLU:O	2.18	0.43
14:2S:71:ARG:NH1	14:2S:107:GLU:OE2	2.50	0.43
18:2W:88:ARG:NH1	18:2W:94:ASP:OD2	2.51	0.43
32:2a:358:U:H2'	32:2a:359:U:C6	2.53	0.43
32:2a:903:G:OP1	61:2a:1804:HOH:O	2.21	0.43
32:2a:1023:G:H3'	32:2a:1024:G:H8	1.83	0.43
34:2c:19:GLU:HG2	34:2c:54:ARG:HE	1.84	0.43
47:2p:3:LYS:O	47:2p:21:VAL:HA	2.18	0.43
51:2t:18:GLN:O	51:2t:22:ARG:HG2	2.19	0.43
1:1A:911:A:H2'	12:1Q:9:TYR:OH	2.19	0.43
5:1F:9:ILE:HD13	5:1F:123:LEU:HD23	1.99	0.43
32:1a:109:A:C6	32:1a:326:G:C6	3.06	0.43
32:1a:1225:A:OP1	44:1m:103:THR:N	2.46	0.43
32:1a:1326:C:OP1	52:1u:12:LYS:NZ	2.43	0.43
33:1b:139:LYS:O	33:1b:143:GLU:HG3	2.18	0.43
34:1c:181:ASN:ND2	34:1c:204:LEU:HD12	2.34	0.43
44:1m:45:VAL:HG13	44:1m:48:LEU:HD12	2.00	0.43
1:2A:330:A:H2	1:2A:1210:A:H2'	1.83	0.43
1:2A:1153:C:H2'	1:2A:1154:G:O4'	2.19	0.43
1:2A:2032:G:O2'	4:2E:145:LYS:HE3	2.18	0.43
1:2A:2515:C:H2'	1:2A:2516:G:C8	2.54	0.43
6:2G:72:ARG:NH1	6:2G:87:PRO:HG3	2.33	0.43
6:2G:108:ASN:O	6:2G:112:PRO:HG2	2.18	0.43
16:2U:102:GLU:HB3	16:2U:104:GLN:HE22	1.83	0.43
20:2Y:87:LYS:HB3	20:2Y:95:LYS:HD2	1.99	0.43
32:2a:523:A:H61	43:2l:92:OTD:CG	2.32	0.43
32:2a:1256:A:N6	32:2a:1278:U:H1'	2.33	0.43
32:2a:1277:C:H1'	32:2a:1279:A:C8	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:7:G:H2'	1:1A:8:A:O4'	2.18	0.43
1:1A:11:G:H2'	1:1A:12:U:H5'	2.01	0.43
1:1A:741:G:OP2	61:1A:4148:HOH:O	2.21	0.43
1:1A:818:G:H4'	1:1A:838:C:O3'	2.18	0.43
1:1A:2133:G:O2'	1:1A:2157:G:N2	2.52	0.43
1:1A:2667:C:H2'	1:1A:2668:G:O4'	2.18	0.43
1:1A:2773:C:H2'	1:1A:2774:C:H6	1.83	0.43
9:1N:73:THR:HB	9:1N:82:LEU:HD11	2.01	0.43
13:1R:28:LEU:HD23	13:1R:48:VAL:HG21	2.00	0.43
13:1R:104:ARG:HG3	13:1R:111:LEU:HD11	2.00	0.43
24:12:2:LYS:O	24:12:6:VAL:HG23	2.18	0.43
32:1a:45:U:H2'	32:1a:46:G:C8	2.53	0.43
32:1a:134:A:H61	47:1p:25:ARG:HH12	1.67	0.43
32:1a:501:C:H2'	32:1a:502:G:H8	1.84	0.43
32:1a:978:A:OP2	32:1a:1363:C:N4	2.47	0.43
32:1a:1118:C:P	40:1i:104:ARG:HH11	2.41	0.43
32:1a:1148:U:O4'	40:1i:16:ARG:HD2	2.18	0.43
32:1a:1426:C:H2'	32:1a:1427:U:C6	2.54	0.43
33:1b:95:GLN:HE22	33:1b:147:LYS:NZ	2.17	0.43
33:1b:101:MET:HA	33:1b:108:ILE:HD12	2.01	0.43
34:1c:11:ARG:HB3	34:1c:15:THR:HB	2.01	0.43
41:1j:55:LYS:O	41:1j:57:LYS:N	2.52	0.43
1:2A:729:G:C8	3:2D:208:LYS:HD2	2.53	0.43
1:2A:1548:C:H2'	1:2A:1549:C:C6	2.53	0.43
1:2A:1794:U:H2'	1:2A:1795:C:C6	2.54	0.43
3:2D:233:HIS:HA	61:2D:403:HOH:O	2.18	0.43
8:2I:98:ALA:O	8:2I:101:LEU:N	2.52	0.43
9:2N:68:GLU:HG2	9:2N:88:GLU:OE2	2.18	0.43
17:2V:43:GLU:OE1	17:2V:43:GLU:N	2.51	0.43
23:21:3:LYS:HB2	23:21:61:ARG:HH22	1.83	0.43
32:2a:824:C:H2'	32:2a:825:G:C8	2.53	0.43
32:2a:1148:U:H2'	32:2a:1149:C:O4'	2.19	0.43
37:2f:35:ALA:CA	37:2f:67:MET:HB3	2.48	0.43
1:1A:271(D):G:H1	1:1A:271(T):C:H42	1.67	0.43
1:1A:272(J):C:H2'	1:1A:274:G:C8	2.53	0.43
1:1A:530:G:H4'	1:1A:531:C:OP1	2.18	0.43
1:1A:1105:U:H2'	1:1A:1106:G:C8	2.52	0.43
1:1A:1991:U:H2'	1:1A:1992:G:H5''	2.01	0.43
1:1A:2156:G:H2'	1:1A:2157:G:C2	2.53	0.43
11:1P:8:PRO:HB2	11:1P:12:ALA:HB3	2.00	0.43
17:1V:43:GLU:OE1	17:1V:43:GLU:N	2.50	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:1Z:52:SER:OG	21:1Z:53:ILE:N	2.51	0.43
33:1b:155:LEU:HD21	33:1b:159:PRO:HD3	2.01	0.43
33:1b:170:GLU:O	33:1b:174:VAL:HG13	2.19	0.43
34:1c:130:VAL:HG21	34:1c:157:ILE:HG23	2.00	0.43
37:1f:3:ARG:HA	37:1f:65:VAL:O	2.19	0.43
37:1f:97:PHE:CD2	49:1r:31:LEU:HD12	2.54	0.43
42:1k:85:ARG:HD3	42:1k:113:PRO:HD3	2.01	0.43
1:2A:295:G:H4'	20:2Y:1:MET:HE2	2.01	0.43
1:2A:384:U:H2'	1:2A:385:C:H6	1.84	0.43
33:2b:215:LEU:HD12	33:2b:215:LEU:HA	1.84	0.43
46:2o:8:LYS:O	46:2o:12:ILE:HG13	2.19	0.43
55:2x:23:U:H2'	55:2x:24:G:C8	2.53	0.43
1:1A:657:U:H2'	1:1A:658:C:C6	2.53	0.43
1:1A:1056:G:H5''	1:1A:1086:A:C8	2.54	0.43
1:1A:1399:C:OP1	19:1X:25:LYS:NZ	2.52	0.43
1:1A:2152:G:H2'	1:1A:2153:G:H8	1.84	0.43
5:1F:165:ARG:HA	5:1F:168:ARG:HD2	2.01	0.43
6:1G:123:ASN:O	61:1G:301:HOH:O	2.21	0.43
32:1a:509:A:N3	32:1a:543:C:O2'	2.44	0.43
35:1d:120:LEU:HB3	35:1d:126:ILE:HD11	2.00	0.43
38:1g:113:GLU:OE1	38:1g:113:GLU:N	2.43	0.43
1:2A:108:U:H2'	1:2A:109:G:H8	1.84	0.43
1:2A:484:C:H2'	1:2A:485:C:C6	2.54	0.43
1:2A:1448:G:H4'	1:2A:1542:A:OP1	2.19	0.43
1:2A:1653:G:H3'	13:2R:2:ARG:HD3	2.00	0.43
1:2A:1996:C:H4'	1:2A:1997:G:OP1	2.19	0.43
1:2A:2695:C:H2'	1:2A:2696:U:C6	2.54	0.43
1:2A:2807:G:N1	1:2A:2893:G:O6	2.46	0.43
13:2R:54:LEU:HB3	13:2R:62:ALA:HB1	2.01	0.43
14:2S:99:LYS:NZ	14:2S:103:GLU:OE2	2.34	0.43
21:2Z:4:ARG:CZ	21:2Z:4:ARG:HB3	2.48	0.43
23:21:52:ARG:NH1	23:21:55:GLY:O	2.51	0.43
29:27:1:MET:HE3	29:27:3:ARG:NH2	2.33	0.43
32:2a:429:U:H1'	32:2a:430:A:H5''	2.01	0.43
32:2a:814:A:H2'	32:2a:816:A:C5'	2.49	0.43
32:2a:1466:C:H2'	32:2a:1467:G:O4'	2.18	0.43
32:2a:1492:A:O2'	54:2w:298:ARG:NH2	2.50	0.43
33:2b:60:ASP:HA	33:2b:63:MET:HE2	2.00	0.43
35:2d:200:GLU:O	35:2d:203:VAL:HG22	2.19	0.43
54:2w:250:VAL:HG21	54:2w:268:ILE:HG12	2.00	0.43
1:1A:2105:C:H2'	1:1A:2106:G:H8	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:1D:175:LEU:HD12	3:1D:185:VAL:HG21	2.01	0.43
5:1F:39:TRP:CH2	5:1F:106:ARG:HD3	2.53	0.43
8:1I:42:SER:OG	8:1I:43:ASN:N	2.52	0.43
9:1N:62:VAL:HG22	9:1N:66:LYS:HD2	2.01	0.43
26:14:49:PHE:HB3	26:14:50:VAL:H	1.71	0.43
32:1a:323:U:O3'	51:1t:22:ARG:HD3	2.19	0.43
32:1a:1304:G:C6	32:1a:1305:G:N1	2.87	0.43
37:1f:4:TYR:HD2	37:1f:67:MET:HE3	1.84	0.43
54:1w:114:GLY:HA3	54:1w:196:THR:HG22	2.00	0.43
54:1w:299:SER:C	54:1w:301:LYS:N	2.75	0.43
1:2A:236:C:H2'	1:2A:237:C:H6	1.83	0.43
1:2A:784:A:C8	1:2A:792:G:C5	3.07	0.43
1:2A:1300:U:H4'	1:2A:1301:A:H5'	2.01	0.43
1:2A:1582:C:H2'	1:2A:1583:A:H8	1.83	0.43
1:2A:1877:A:H5'	1:2A:1878:G:OP2	2.19	0.43
1:2A:2477:C:N4	31:29:10:ILE:HG23	2.34	0.43
1:2A:2680:C:H1'	4:2E:187:ALA:HB1	2.01	0.43
4:2E:1:MET:HB3	4:2E:83:ASP:O	2.18	0.43
6:2G:72:ARG:HH12	6:2G:87:PRO:HG3	1.84	0.43
7:2H:3:ARG:HH22	7:2H:65:HIS:HB3	1.84	0.43
12:2Q:12:GLN:NE2	12:2Q:72:LYS:HG3	2.34	0.43
12:2Q:17:LEU:HB3	12:2Q:39:PRO:HB2	2.00	0.43
16:2U:106:PHE:O	16:2U:110:VAL:HG23	2.19	0.43
32:2a:433:C:H2'	32:2a:434:U:C6	2.53	0.43
32:2a:683:G:H2'	32:2a:684:A:C8	2.53	0.43
37:2f:30:LEU:HG	37:2f:30:LEU:H	1.63	0.43
40:2i:70:LYS:O	40:2i:74:ILE:N	2.46	0.43
43:2l:6:THR:HB	43:2l:9:GLN:HG3	2.00	0.43
46:2o:69:TYR:CZ	46:2o:73:GLU:HG3	2.54	0.43
50:2s:40:ILE:HA	50:2s:44:MET:SD	2.59	0.43
1:1A:247:G:H4'	1:1A:386:G:C5	2.54	0.42
1:1A:1645:G:H5''	1:1A:1646:C:H5'	2.00	0.42
3:1D:12:SER:HB3	3:1D:208:LYS:HB3	2.00	0.42
7:1H:27:LYS:HG2	7:1H:32:GLU:HG2	2.00	0.42
7:1H:88:LEU:HD23	7:1H:130:ARG:HG2	2.01	0.42
16:1U:47:TYR:HA	16:1U:50:ARG:NH2	2.34	0.42
23:11:67:ILE:N	23:11:68:PRO:HD2	2.33	0.42
32:1a:110:C:O2'	47:1p:25:ARG:O	2.31	0.42
32:1a:512:U:H2'	32:1a:513:C:H6	1.84	0.42
38:1g:74:GLU:OE2	38:1g:95:ARG:NE	2.52	0.42
50:1s:31:ILE:HD12	50:1s:48:THR:O	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:84:A:H5''	20:2Y:8:LYS:HD2	2.01	0.42
1:2A:251:A:C5	1:2A:252:G:H1'	2.54	0.42
1:2A:601:C:O2'	1:2A:605:C:H5''	2.18	0.42
1:2A:645:C:H5''	1:2A:646:A:OP2	2.19	0.42
1:2A:656:G:H2'	1:2A:657:U:O4'	2.19	0.42
1:2A:1514:U:H2'	1:2A:1515:G:C8	2.54	0.42
1:2A:1803:A:H4'	3:2D:259:THR:HG23	2.01	0.42
1:2A:2142:C:H2'	1:2A:2143:C:C6	2.54	0.42
7:2H:3:ARG:NH2	7:2H:65:HIS:HB3	2.34	0.42
7:2H:13:LYS:HA	7:2H:14:GLY:HA2	1.62	0.42
10:2O:76:ALA:HB3	15:2T:75:ILE:HB	2.00	0.42
21:2Z:53:ILE:HG22	21:2Z:71:VAL:HB	2.01	0.42
32:2a:458:C:H2'	32:2a:460:G:O4'	2.19	0.42
32:2a:860:A:H2'	32:2a:861:G:O4'	2.18	0.42
32:2a:1142:G:H3'	32:2a:1143:G:H8	1.84	0.42
34:2c:23:TYR:HA	41:2j:11:PHE:CD2	2.54	0.42
35:2d:200:GLU:O	35:2d:204:ILE:HG12	2.19	0.42
39:2h:51:VAL:HG12	39:2h:52:ASP:N	2.34	0.42
1:1A:389:G:O6	11:1P:70:GLN:HB2	2.19	0.42
1:1A:2347:C:H2'	1:1A:2348:U:C6	2.54	0.42
6:1G:137:GLU:HB2	6:1G:140:ILE:HD13	2.01	0.42
7:1H:3:ARG:HE	7:1H:54:ARG:HH12	1.66	0.42
8:1I:123:LEU:HA	8:1I:144:VAL:HG22	2.00	0.42
19:1X:53:LYS:HB3	19:1X:82:GLN:HB3	2.02	0.42
39:1h:58:TYR:O	39:1h:59:LEU:HD23	2.18	0.42
50:1s:11:VAL:HG11	50:1s:16:LEU:HB2	2.01	0.42
51:1t:57:ARG:HD3	51:1t:101:GLY:O	2.20	0.42
1:2A:1235:G:C6	1:2A:1236:G:N1	2.87	0.42
2:2B:87:G:N2	2:2B:90:A:OP2	2.41	0.42
9:2N:43:THR:HG22	9:2N:44:PRO:HD2	2.02	0.42
10:2O:2:ILE:HB	10:2O:33:ALA:HB3	2.01	0.42
13:2R:96:ARG:HD3	13:2R:98:LEU:HD11	2.01	0.42
15:2T:107:ASP:OD1	15:2T:111:ARG:NH1	2.52	0.42
19:2X:84:ALA:HB3	19:2X:87:GLN:NE2	2.34	0.42
33:2b:77:ALA:HA	33:2b:80:ILE:HG23	2.01	0.42
33:2b:122:PHE:HD2	33:2b:142:LEU:HD13	1.83	0.42
40:2i:114:TYR:H	40:2i:114:TYR:HD2	1.67	0.42
43:2l:118:SER:OG	43:2l:119:LYS:N	2.52	0.42
1:1A:1064:C:H2'	1:1A:1065:U:O4'	2.19	0.42
1:1A:1453:U:OP1	13:1R:77:ARG:NH1	2.52	0.42
1:1A:1930:G:O2'	1:1A:1968:G:O6	2.36	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2104:G:H2'	1:1A:2105:C:C6	2.54	0.42
1:1A:2162:G:O2'	1:1A:2163:C:H5'	2.19	0.42
1:1A:2206:G:OP2	1:1A:2206:G:H4'	2.20	0.42
1:1A:2238:G:N3	1:1A:2238:G:H2'	2.34	0.42
14:1S:61:ASN:ND2	14:1S:64:GLU:HG3	2.34	0.42
24:12:10:LEU:O	24:12:14:ARG:HG3	2.19	0.42
24:12:23:LYS:O	24:12:27:GLU:HG3	2.19	0.42
32:1a:269:C:H2'	32:1a:270:A:C8	2.55	0.42
32:1a:334:C:H2'	32:1a:335:C:C6	2.54	0.42
32:1a:742:G:OP2	46:1o:35:ARG:NH2	2.43	0.42
32:1a:1367:C:H4'	41:1j:48:THR:HG21	2.02	0.42
48:1q:66:SER:H	48:1q:69:LYS:HB3	1.84	0.42
1:2A:570:G:H2'	1:2A:2030:A:C5	2.53	0.42
1:2A:1005:C:H2'	1:2A:1006:C:C6	2.55	0.42
1:2A:2680:C:H5'	4:2E:189:PRO:HA	2.02	0.42
32:2a:222:U:H2'	32:2a:223:U:H6	1.80	0.42
32:2a:659:U:H5''	46:2o:9:GLN:HE22	1.84	0.42
32:2a:678:U:H2'	32:2a:679:C:C6	2.54	0.42
32:2a:1001:A:H2'	32:2a:1001(A):G:C8	2.54	0.42
32:2a:1375:A:H4'	38:2g:29:LYS:HE3	2.00	0.42
33:2b:163:PHE:CD1	33:2b:185:ILE:HG13	2.54	0.42
33:2b:223:ILE:HG13	33:2b:224:GLN:N	2.35	0.42
34:2c:42:LEU:O	34:2c:46:GLU:HG2	2.19	0.42
44:2m:87:TYR:N	50:2s:73:GLU:O	2.41	0.42
51:2t:82:SER:O	51:2t:86:ARG:HG3	2.20	0.42
1:1A:910:A:N1	1:1A:2277:G:H1'	2.35	0.42
1:1A:1082:U:C4	1:1A:1086:A:N6	2.83	0.42
1:1A:2126:A:H4'	1:1A:2127:G:OP1	2.18	0.42
5:1F:170:LEU:HD13	5:1F:172:TRP:CZ2	2.53	0.42
5:1F:181:LEU:HD12	5:1F:181:LEU:HA	1.92	0.42
6:1G:125:PHE:O	6:1G:127:GLY:N	2.53	0.42
32:1a:942:G:H21	40:1i:124:GLN:NE2	2.18	0.42
33:1b:84:GLU:HB3	33:1b:219:VAL:HG21	2.00	0.42
35:1d:68:TYR:CE1	35:1d:97:LEU:HB3	2.54	0.42
48:1q:63:ARG:HG2	48:1q:64:PRO:HD2	2.00	0.42
1:2A:280:C:C2	1:2A:361:G:C2	3.07	0.42
1:2A:947:G:H2'	1:2A:948:G:C8	2.53	0.42
1:2A:1161:C:H2'	1:2A:1162:G:H8	1.83	0.42
1:2A:1204:A:H2	1:2A:1241:A:N6	2.10	0.42
1:2A:2019:A:N7	27:25:9:LYS:HE2	2.34	0.42
1:2A:2096:U:H2'	1:2A:2097:C:C6	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2B:4:C:H42	2:2B:117:G:H1	1.66	0.42
8:2I:134:PRO:O	8:2I:136:VAL:HG23	2.18	0.42
10:2O:107:ARG:HG3	10:2O:112:MET:HE1	2.01	0.42
32:2a:946:A:H2'	32:2a:947:G:C8	2.55	0.42
33:2b:95:GLN:NE2	33:2b:147:LYS:O	2.51	0.42
1:1A:1010:A:N3	1:1A:1153:C:H1'	2.35	0.42
32:1a:375:U:OP1	47:1p:69:THR:HG21	2.19	0.42
32:1a:864:A:H2'	32:1a:865:A:C8	2.54	0.42
32:1a:1206:G:H2'	32:1a:1207:2MG:C8	2.54	0.42
33:1b:105:PHE:C	33:1b:107:THR:H	2.26	0.42
34:1c:113:ALA:HB3	34:1c:114:PRO:HD3	2.02	0.42
38:1g:69:VAL:O	38:1g:138:LYS:HG3	2.20	0.42
48:1q:18:THR:HG23	48:1q:69:LYS:HE3	2.01	0.42
1:2A:116:C:H2'	1:2A:117:G:O4'	2.20	0.42
1:2A:827:U:O2'	1:2A:2068:U:C2	2.68	0.42
1:2A:1592:C:H2'	1:2A:1593:G:H8	1.85	0.42
1:2A:1721:G:H2'	1:2A:1740:G:O6	2.19	0.42
1:2A:2629:A:H1'	1:2A:2630:G:H5''	2.02	0.42
1:2A:2839:G:H5'	13:2R:46:GLY:CA	2.47	0.42
6:2G:33:ARG:HH21	6:2G:162:THR:HG21	1.85	0.42
8:2I:12:LEU:O	8:2I:19:VAL:HG11	2.18	0.42
18:2W:68:ARG:HB2	18:2W:109:GLU:HG2	2.01	0.42
32:2a:9:G:H2'	32:2a:10:A:H8	1.85	0.42
32:2a:779:C:H2'	32:2a:780:A:O4'	2.19	0.42
35:2d:76:ARG:NH2	35:2d:80:GLU:OE2	2.50	0.42
44:2m:20:THR:HA	44:2m:25:ILE:O	2.19	0.42
1:1A:1550:C:OP1	1:1A:1720:U:O2'	2.27	0.42
1:1A:2155:G:H2'	1:1A:2156:G:H5'	2.02	0.42
1:1A:2790:A:H2'	1:1A:2790:A:N3	2.35	0.42
3:1D:152:GLY:O	3:1D:154:LYS:HG2	2.19	0.42
19:1X:92:LEU:O	19:1X:94:GLY:N	2.52	0.42
22:10:43:THR:O	22:10:43:THR:HG23	2.19	0.42
28:16:6:ARG:NH1	28:16:26:ASN:HB2	2.35	0.42
32:1a:175:C:H2'	32:1a:176:C:C6	2.55	0.42
32:1a:270:A:H2'	32:1a:271:C:O4'	2.19	0.42
32:1a:364:A:H2'	32:1a:365:U:O2	2.19	0.42
32:1a:1002:G:H3'	32:1a:1003:G:C4'	2.47	0.42
32:1a:1031:G:H2'	32:1a:1032:G:H8	1.84	0.42
33:1b:102:LEU:HB3	33:1b:180:LEU:CD1	2.49	0.42
47:1p:5:ARG:HE	47:1p:22:THR:CG2	2.31	0.42
50:1s:36:ARG:NH2	50:1s:72:GLY:O	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:1w:321:THR:OG1	54:1w:322:HIS:N	2.50	0.42
1:2A:839:U:H2'	1:2A:840:C:H6	1.85	0.42
1:2A:1604:C:H2'	1:2A:1605:C:C6	2.55	0.42
1:2A:2294:C:P	14:2S:89:ARG:HH22	2.42	0.42
1:2A:2630:G:H2'	1:2A:2631:G:C8	2.55	0.42
3:2D:137:PRO:O	3:2D:140:THR:OG1	2.34	0.42
11:2P:63:PRO:HG2	30:28:25:MET:HB2	2.01	0.42
13:2R:87:TYR:HD1	13:2R:90:ARG:HD2	1.85	0.42
15:2T:88:ILE:HG13	15:2T:91:ARG:NH2	2.35	0.42
30:28:32:LEU:O	30:28:36:LYS:HE3	2.19	0.42
32:2a:1226:C:H4'	50:2s:80:TYR:CZ	2.54	0.42
36:2e:145:LYS:O	36:2e:149:GLU:HB2	2.20	0.42
50:2s:23:ASN:HA	50:2s:27:GLU:HG2	2.01	0.42
1:1A:784:A:C5	3:1D:229:VAL:HG21	2.54	0.42
1:1A:1072:C:O2	1:1A:1092:C:N4	2.53	0.42
1:1A:2379:G:O2'	14:1S:17:ARG:NH2	2.50	0.42
3:1D:121:PRO:HB3	3:1D:135:PHE:CE2	2.54	0.42
7:1H:41:MET:HE1	7:1H:54:ARG:HB3	2.01	0.42
14:1S:3:ARG:C	14:1S:3:ARG:HD3	2.43	0.42
26:14:58:ARG:HG3	50:1s:67:VAL:HB	2.01	0.42
32:1a:375:U:O2	47:1p:28:ARG:NH1	2.52	0.42
32:1a:1211:U:H4'	32:1a:1213:A:O4'	2.20	0.42
32:1a:1370:G:C2	32:1a:1371:G:C8	3.08	0.42
33:1b:24:TRP:CD1	33:1b:24:TRP:N	2.86	0.42
34:1c:152:ILE:HG23	34:1c:167:TRP:HB3	2.02	0.42
44:1m:73:GLU:O	44:1m:77:ASN:ND2	2.51	0.42
1:2A:900:A:O2'	1:2A:901:A:OP1	2.32	0.42
1:2A:1464:C:H2'	1:2A:1465:G:C8	2.55	0.42
1:2A:2129:C:N3	1:2A:2159:G:N2	2.54	0.42
1:2A:2251:OMG:HM23	1:2A:2251:OMG:H1'	1.64	0.42
1:2A:2880:C:O3'	13:2R:90:ARG:NH1	2.52	0.42
2:2B:17:C:H2'	2:2B:18:G:O4'	2.19	0.42
5:2F:137:LYS:HA	5:2F:140:LEU:HD13	2.02	0.42
15:2T:33:LYS:HB3	15:2T:82:LEU:O	2.20	0.42
32:2a:686:U:O2'	32:2a:703:G:N2	2.53	0.42
32:2a:978:A:C6	32:2a:1318:A:C6	3.08	0.42
32:2a:1318:A:H1'	50:2s:37:ARG:HH11	1.85	0.42
34:2c:9:GLY:HA2	34:2c:12:LEU:HG	2.02	0.42
34:2c:36:ASP:O	34:2c:40:ARG:HG3	2.19	0.42
41:2j:42:THR:HG22	41:2j:68:HIS:HA	2.02	0.42
48:2q:27:PHE:CE1	48:2q:36:ILE:HD11	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:796:C:H2'	1:1A:797:C:C6	2.55	0.42
1:1A:839:U:H1'	1:1A:1191:G:H1'	2.02	0.42
1:1A:1093:G:H3'	1:1A:1094:U:C5'	2.46	0.42
1:1A:1165:U:H2'	1:1A:1166:C:C6	2.54	0.42
1:1A:2102:U:H2'	1:1A:2103:C:C6	2.55	0.42
1:1A:2882:A:H5'	13:1R:96:ARG:HG3	2.01	0.42
2:1B:13:A:N1	2:1B:69:G:O2'	2.53	0.42
2:1B:66:A:H61	2:1B:108:U:H2'	1.84	0.42
3:1D:26:LYS:NZ	3:1D:30:GLU:OE1	2.53	0.42
8:1I:109:ILE:HD13	8:1I:109:ILE:HA	1.88	0.42
11:1P:95:VAL:HG23	11:1P:125:VAL:HB	2.00	0.42
18:1W:5:ALA:C	18:1W:6:ILE:HG13	2.44	0.42
32:1a:1132:C:H2'	32:1a:1133:G:C8	2.54	0.42
32:1a:1226:C:P	44:1m:91:ARG:HH22	2.40	0.42
32:1a:1304:G:C5	32:1a:1305:G:C6	3.07	0.42
33:1b:69:LEU:HD13	33:1b:91:PRO:HB2	2.02	0.42
33:1b:127:ILE:HG12	33:1b:130:ARG:H	1.85	0.42
34:1c:73:PRO:HD3	34:1c:105:GLU:HG3	2.01	0.42
35:1d:63:LYS:HD2	35:1d:198:VAL:HG22	2.01	0.42
47:1p:26:ARG:HG3	47:1p:27:LYS:O	2.20	0.42
1:2A:1514:U:H2'	1:2A:1515:G:H8	1.85	0.42
1:2A:2115:G:C4	1:2A:2117:A:C8	3.07	0.42
5:2F:178:PRO:HG2	5:2F:179:GLU:OE2	2.19	0.42
6:2G:44:GLY:HA2	6:2G:88:ILE:HG22	2.01	0.42
12:2Q:36:ALA:HB2	12:2Q:103:MET:SD	2.60	0.42
16:2U:76:TYR:HH	16:2U:92:ARG:HE	1.61	0.42
19:2X:35:THR:O	19:2X:39:ILE:HG13	2.19	0.42
21:2Z:163:LEU:HD22	21:2Z:165:VAL:HG22	2.01	0.42
25:23:52:HIS:CD2	25:23:53:LEU:HG	2.55	0.42
32:2a:335:C:H2'	32:2a:336:C:C6	2.55	0.42
32:2a:685:G:C2	32:2a:686:U:C4	3.08	0.42
34:2c:33:LEU:HA	34:2c:36:ASP:HB2	2.02	0.42
36:2e:148:VAL:HG21	39:2h:107:LEU:HD23	2.02	0.42
44:2m:76:ALA:HA	44:2m:79:LYS:HB3	2.01	0.42
1:1A:2448:A:OP1	61:1A:4118:HOH:O	2.22	0.42
8:1I:77:LEU:HB3	8:1I:142:VAL:HG22	2.01	0.42
9:1N:108:PRO:O	9:1N:113:GLY:HA3	2.20	0.42
13:1R:97:VAL:HG22	13:1R:114:VAL:HG13	2.02	0.42
23:11:71:TYR:O	23:11:74:VAL:HG22	2.20	0.42
32:1a:229:U:H5''	47:1p:33:ILE:HD13	2.02	0.42
34:1c:19:GLU:HG2	34:1c:54:ARG:NH2	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:1c:61:ALA:C	34:1c:63:ASN:H	2.28	0.42
35:1d:8:VAL:HG22	35:1d:21:LEU:HD13	2.00	0.42
37:1f:76:ALA:O	37:1f:80:ARG:HG3	2.20	0.42
43:1l:53:ARG:CB	43:1l:93:LEU:HD11	2.49	0.42
49:1r:22:VAL:HA	49:1r:25:THR:HG23	2.01	0.42
50:1s:49:ILE:HG13	50:1s:62:ILE:HD11	2.00	0.42
1:2A:616:G:H4'	5:2F:205:ARG:HD2	2.01	0.42
1:2A:652:C:C2'	1:2A:652(A):A:H5'	2.50	0.42
1:2A:956:G:OP2	12:2Q:14:ARG:NH1	2.48	0.42
5:2F:176:LEU:HA	5:2F:176:LEU:HD23	1.82	0.42
24:22:21:LEU:HD11	24:22:63:VAL:HG12	2.02	0.42
26:24:57:GLU:CB	26:24:58:ARG:HA	2.49	0.42
32:2a:160:A:H2'	32:2a:161:A:O4'	2.19	0.42
32:2a:455:C:H2'	32:2a:456:C:C6	2.55	0.42
32:2a:1000:U:N3	32:2a:1001:A:N7	2.68	0.42
32:2a:1263:C:O2	32:2a:1273:G:C2	2.73	0.42
42:2k:41:THR:HG22	42:2k:42:TRP:N	2.35	0.42
54:2w:304:THR:CB	54:2w:315:HIS:HE1	2.33	0.42
1:1A:27:G:C2	1:1A:512:G:N3	2.88	0.42
1:1A:139(A):G:H2'	1:1A:140:G:C8	2.54	0.42
1:1A:272(I):U:H3	1:1A:363(A):A:H61	1.66	0.42
1:1A:1588:C:H2'	1:1A:1589:C:C6	2.55	0.42
1:1A:1932:A:H2'	1:1A:1933:G:O4'	2.20	0.42
1:1A:2341:G:H2'	1:1A:2342:C:O4'	2.20	0.42
1:1A:2791:C:H2'	1:1A:2792:G:H8	1.85	0.42
3:1D:5:LYS:HE3	3:1D:5:LYS:HB3	1.93	0.42
4:1E:93:VAL:HG22	61:1E:402:HOH:O	2.20	0.42
7:1H:113:VAL:HG11	7:1H:151:ILE:HD13	2.02	0.42
11:1P:116:GLY:O	11:1P:137:LYS:NZ	2.45	0.42
15:1T:51:ARG:HG3	15:1T:98:LYS:HD2	2.01	0.42
32:1a:923:A:OP1	36:1e:21:ALA:HB2	2.20	0.42
32:1a:983:A:H1'	32:1a:1049:U:O2	2.19	0.42
32:1a:1030:C:C4	32:1a:1030(A):G:H1'	2.55	0.42
32:1a:1264:C:H2'	32:1a:1265:G:C8	2.54	0.42
33:1b:36:ARG:C	33:1b:38:GLY:H	2.28	0.42
38:1g:89:MET:HG3	38:1g:156:TRP:NE1	2.35	0.42
44:1m:27:LYS:HA	44:1m:30:ALA:HB3	2.02	0.42
44:1m:67:GLU:HB3	44:1m:68:GLY:H	1.63	0.42
45:1n:14:PRO:HB2	45:1n:16:PHE:O	2.19	0.42
46:1o:24:SER:O	46:1o:28:GLN:HG3	2.20	0.42
51:1t:10:LEU:HB3	51:1t:12:ALA:H	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:11:G:C2'	1:2A:12:U:H5'	2.49	0.42
1:2A:236:C:H2'	1:2A:237:C:C6	2.54	0.42
1:2A:484:C:H2'	1:2A:485:C:H6	1.85	0.42
1:2A:492:A:H2'	1:2A:493:G:O4'	2.20	0.42
1:2A:1410:G:H2'	1:2A:1411:C:H6	1.83	0.42
1:2A:2752:C:H2'	1:2A:2753:A:O4'	2.20	0.42
2:2B:73:A:N1	21:2Z:34:ASN:ND2	2.68	0.42
21:2Z:150:LEU:HD23	21:2Z:150:LEU:HA	1.88	0.42
32:2a:555:C:H2'	32:2a:556:C:C6	2.55	0.42
32:2a:1104:G:O3'	33:2b:111:ARG:NH2	2.53	0.42
33:2b:92:TYR:CD2	33:2b:151:GLY:HA3	2.54	0.42
33:2b:133:LYS:O	33:2b:137:ARG:HG2	2.20	0.42
34:2c:139:GLN:HE21	34:2c:143:GLU:HG3	1.85	0.42
35:2d:156:GLU:HA	35:2d:159:ARG:CZ	2.50	0.42
37:2f:16:GLN:N	37:2f:16:GLN:OE1	2.53	0.42
39:2h:6:ILE:O	39:2h:10:LEU:HG	2.20	0.42
51:2t:38:LYS:HA	51:2t:41:ILE:HB	2.01	0.42
1:1A:566:U:H5''	11:1P:29:LYS:HE3	2.02	0.41
1:1A:1047:G:H2'	1:1A:1110:G:N2	2.35	0.41
1:1A:1338:G:O2'	1:1A:1393:A:N1	2.48	0.41
3:1D:77:ALA:HB2	3:1D:97:TYR:CD1	2.55	0.41
10:1O:100:GLY:O	10:1O:119:PRO:HD2	2.19	0.41
11:1P:95:VAL:HG23	11:1P:125:VAL:HA	2.00	0.41
13:1R:103:ARG:HD3	13:1R:108:GLY:O	2.19	0.41
20:1Y:6:HIS:HE1	20:1Y:72:VAL:O	2.03	0.41
32:1a:22:G:H4'	32:1a:885:G:C8	2.55	0.41
32:1a:631:G:H2'	32:1a:632:A:H8	1.85	0.41
32:1a:735:C:H2'	32:1a:736:C:H6	1.85	0.41
32:1a:814:A:H2'	32:1a:816:A:H5''	2.01	0.41
32:1a:1124:G:OP1	41:1j:36:GLY:N	2.49	0.41
33:1b:109:SER:O	33:1b:112:VAL:HG22	2.20	0.41
42:1k:91:ARG:NH2	42:1k:110:ASP:OD1	2.50	0.41
44:1m:3:ARG:HG2	44:1m:4:ILE:HG12	2.01	0.41
47:1p:43:LYS:HG2	47:1p:48:TRP:NE1	2.35	0.41
47:1p:47:ASP:OD1	47:1p:47:ASP:N	2.53	0.41
48:1q:3:LYS:HB3	48:1q:61:GLU:HB3	2.02	0.41
1:2A:1509(B):A:H2'	1:2A:1510:G:C8	2.55	0.41
1:2A:2106:G:C2	1:2A:2107:C:C2	3.08	0.41
1:2A:2360:A:H2'	1:2A:2361:A:O4'	2.20	0.41
3:2D:123:ALA:HB1	3:2D:129:ASN:HD22	1.85	0.41
4:2E:107:THR:O	4:2E:190:GLY:HA2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:2N:34:LEU:HD12	9:2N:34:LEU:HA	1.83	0.41
12:2Q:59:ARG:C	12:2Q:61:GLY:H	2.25	0.41
26:24:50:VAL:HG11	44:2m:65:LYS:HB2	2.01	0.41
32:2a:201:C:H42	32:2a:216:G:H1	1.68	0.41
32:2a:202:U:H5''	32:2a:203:U:C5	2.51	0.41
32:2a:955:U:H2'	32:2a:956:U:O4'	2.20	0.41
32:2a:1005:A:H8	32:2a:1024:G:H21	1.68	0.41
32:2a:1316:G:N1	32:2a:1319:A:OP2	2.52	0.41
33:2b:63:MET:HG3	33:2b:225:ALA:HB1	2.01	0.41
34:2c:97:LYS:O	34:2c:99:VAL:N	2.53	0.41
35:2d:49:ARG:HE	35:2d:49:ARG:HB2	1.62	0.41
40:2i:43:ALA:HA	40:2i:74:ILE:HD11	2.02	0.41
50:2s:50:ALA:HA	50:2s:58:VAL:O	2.18	0.41
55:2x:21:H2U:O2'	55:2x:22:A:P	2.77	0.41
1:1A:1686:C:H2'	1:1A:1687:G:O4'	2.20	0.41
1:1A:2124:G:H3'	1:1A:2125:G:C8	2.49	0.41
1:1A:2181:G:H2'	1:1A:2182:G:N7	2.35	0.41
1:1A:2271:G:OP1	22:10:18:ALA:HB1	2.19	0.41
5:1F:89:VAL:HG12	5:1F:90:PHE:CD2	2.55	0.41
18:1W:71:VAL:HA	18:1W:107:LEU:HD23	2.01	0.41
32:1a:344:A:O2'	61:1a:1906:HOH:O	2.22	0.41
32:1a:1216:G:H5''	45:1n:5:ALA:CB	2.51	0.41
32:1a:1299:A:H2'	32:1a:1299:A:N3	2.35	0.41
34:1c:132:ARG:HH11	34:1c:136:GLN:HE22	1.67	0.41
43:1l:71:PRO:O	43:1l:102:ARG:NH1	2.43	0.41
1:2A:658:C:H2'	1:2A:659:C:C6	2.55	0.41
1:2A:994:C:O2'	1:2A:996:A:OP1	2.28	0.41
1:2A:1472:A:H2'	1:2A:1473:G:O4'	2.20	0.41
1:2A:2109:U:H2'	1:2A:2110:G:O4'	2.21	0.41
1:2A:2849:U:O4	15:2T:23:ARG:NH1	2.46	0.41
3:2D:121:PRO:HB3	3:2D:135:PHE:CE2	2.55	0.41
8:2I:72:LEU:HD21	8:2I:107:VAL:HG11	2.03	0.41
32:2a:1057:G:OP1	34:2c:154:SER:OG	2.38	0.41
32:2a:1256:A:N6	32:2a:1278:U:O2'	2.53	0.41
32:2a:1263:C:C4	32:2a:1272:G:O6	2.73	0.41
33:2b:19:HIS:NE2	33:2b:206:ASP:HB2	2.35	0.41
34:2c:67:THR:HA	34:2c:102:ASN:HB2	2.02	0.41
40:2i:114:TYR:HD1	41:2j:60:ARG:HB2	1.85	0.41
40:2i:127:LYS:O	40:2i:128:ARG:HB3	2.20	0.41
41:2j:57:LYS:HE3	41:2j:60:ARG:NH2	2.36	0.41
47:2p:20:VAL:HG21	47:2p:32:TYR:CG	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:2w:337:GLU:O	54:2w:341:ARG:HG3	2.19	0.41
1:1A:848:G:H2'	1:1A:849:A:C8	2.56	0.41
1:1A:859:G:O2'	1:1A:916:G:O6	2.28	0.41
1:1A:1641:A:H2'	1:1A:1642:G:O4'	2.20	0.41
1:1A:2176:A:H2'	1:1A:2177:C:C6	2.56	0.41
1:1A:2693:A:H2'	1:1A:2694:G:C8	2.55	0.41
7:1H:61:HIS:O	7:1H:65:HIS:HB2	2.21	0.41
8:1I:140:LEU:HD23	8:1I:140:LEU:HA	1.73	0.41
14:1S:20:ARG:NH2	22:10:51:VAL:O	2.53	0.41
28:16:8:LYS:HG2	30:18:34:TRP:CD1	2.56	0.41
32:1a:1333:A:H3'	32:1a:1334:G:H8	1.85	0.41
33:1b:9:GLU:C	33:1b:10:LEU:HG	2.45	0.41
43:1l:35:GLY:HA3	43:1l:58:VAL:HG12	2.03	0.41
45:1n:15:LYS:HD2	45:1n:16:PHE:CE2	2.54	0.41
55:1x:10:A:H2'	55:1x:11:C:C6	2.55	0.41
1:2A:10:G:H2'	1:2A:11:G:H8	1.85	0.41
1:2A:330:A:HO2'	1:2A:331:A:H8	1.67	0.41
1:2A:856:C:O2'	1:2A:857:C:OP1	2.31	0.41
1:2A:1014:U:H2'	1:2A:1015:G:H8	1.85	0.41
1:2A:1359:A:C2	1:2A:1372:U:O4	2.73	0.41
2:2B:95:C:H2'	2:2B:96:U:C6	2.55	0.41
4:2E:50:GLY:HA2	4:2E:77:ILE:O	2.20	0.41
10:2O:48:PRO:CB	32:2a:1422:G:H5''	2.47	0.41
14:2S:14:VAL:O	14:2S:18:ILE:HG12	2.20	0.41
21:2Z:152:ALA:O	21:2Z:155:LEU:HB2	2.20	0.41
21:2Z:163:LEU:HD23	21:2Z:163:LEU:HA	1.81	0.41
32:2a:782:A:O3'	32:2a:1515:C:H4'	2.20	0.41
32:2a:975:A:H5'	32:2a:975:A:H8	1.85	0.41
35:2d:59:ARG:NH2	35:2d:62:GLN:HG3	2.35	0.41
37:2f:7:ASN:HD22	49:2r:76:LEU:HD11	1.85	0.41
39:2h:49:GLU:OE2	39:2h:62:TYR:OH	2.34	0.41
40:2i:19:LEU:HD12	40:2i:60:ASP:O	2.20	0.41
51:2t:50:GLU:HB2	51:2t:99:LEU:HD13	2.02	0.41
1:1A:1179:C:H2'	1:1A:1180:C:H6	1.85	0.41
1:1A:2100:G:H2'	1:1A:2101:G:O4'	2.20	0.41
1:1A:2116:G:H3'	1:1A:2117:A:C8	2.56	0.41
3:1D:145:VAL:HG12	3:1D:146:GLU:O	2.20	0.41
3:1D:208:LYS:HG3	3:1D:210:GLY:H	1.84	0.41
4:1E:170:LEU:HB3	4:1E:184:VAL:CG2	2.50	0.41
32:1a:115:G:H4'	32:1a:116:A:O5'	2.19	0.41
32:1a:299:G:C6	32:1a:300:A:C6	3.09	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:390:C:H2'	32:1a:391:G:C8	2.55	0.41
32:1a:515:G:H2'	32:1a:516:PSU:O4'	2.20	0.41
32:1a:688:G:H5'	42:1k:46:GLY:C	2.45	0.41
32:1a:1075:C:OP1	33:1b:179:LYS:NZ	2.48	0.41
32:1a:1179:A:O3'	40:1i:103:THR:OG1	2.32	0.41
32:1a:1434:A:H2'	32:1a:1435:G:O4'	2.20	0.41
33:1b:156:LYS:HD2	33:1b:156:LYS:HA	1.85	0.41
35:1d:86:LYS:HD2	35:1d:86:LYS:HA	1.81	0.41
35:1d:104:VAL:O	35:1d:108:LEU:N	2.48	0.41
40:1i:7:THR:O	40:1i:83:ARG:HD2	2.21	0.41
1:2A:720:C:H2'	1:2A:721:C:C6	2.55	0.41
1:2A:1796:U:H2'	1:2A:1797:C:H6	1.83	0.41
1:2A:1930:G:O2'	1:2A:1968:G:O6	2.33	0.41
1:2A:2152:G:H2'	1:2A:2153:G:O4'	2.20	0.41
11:2P:6:LEU:HD23	11:2P:6:LEU:HA	1.84	0.41
32:2a:4:U:O4	39:2h:105:ARG:HA	2.19	0.41
32:2a:1058:G:N2	41:2j:53:PRO:HG3	2.35	0.41
32:2a:1172:C:H2'	32:2a:1173:G:H8	1.85	0.41
32:2a:1264:C:N3	32:2a:1272:G:O6	2.54	0.41
33:2b:125:PRO:HB2	33:2b:126:GLU:H	1.72	0.41
36:2e:140:ARG:O	36:2e:143:ARG:NH1	2.30	0.41
38:2g:132:GLY:O	38:2g:136:LYS:HG2	2.20	0.41
39:2h:51:VAL:HG12	39:2h:52:ASP:H	1.84	0.41
1:1A:1753:G:N1	1:1A:1756:G:OP2	2.51	0.41
1:1A:2103:C:H42	1:1A:2186:G:H1	1.67	0.41
1:1A:2128:C:O2'	1:1A:2174:C:H4'	2.20	0.41
26:14:59:PHE:HD1	26:14:60:GLN:HG2	1.82	0.41
32:1a:8:A:N6	35:1d:209:ARG:HB2	2.35	0.41
32:1a:674:G:H2'	32:1a:675:A:C8	2.55	0.41
32:1a:933:G:OP2	38:1g:3:ARG:HB2	2.20	0.41
32:1a:977:A:H1'	32:1a:982:U:O4	2.20	0.41
32:1a:987:G:H1	32:1a:1218:C:H42	1.68	0.41
32:1a:1111:A:N1	34:1c:177:THR:OG1	2.45	0.41
32:1a:1511:G:H2'	32:1a:1512:U:O4'	2.20	0.41
1:2A:76:C:O3'	24:22:59:ARG:HG3	2.19	0.41
1:2A:212:G:H2'	1:2A:213:A:O4'	2.19	0.41
1:2A:443:A:H1'	1:2A:1201:C:O4'	2.20	0.41
4:2E:163:GLU:HG2	4:2E:164:ARG:N	2.36	0.41
26:24:58:ARG:HG3	50:2s:65:ASN:C	2.45	0.41
32:2a:576:G:O6	32:2a:880:C:O2'	2.34	0.41
32:2a:923:A:OP1	36:2e:21:ALA:HB2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1004:A:N6	32:2a:1037:C:C2	2.89	0.41
32:2a:1030(D):A:H8	32:2a:1031:G:C8	2.38	0.41
36:2e:33:VAL:HG21	36:2e:109:ILE:HA	2.01	0.41
38:2g:51:GLN:O	38:2g:55:GLY:HA2	2.21	0.41
51:2t:92:LEU:HD23	51:2t:92:LEU:HA	1.90	0.41
54:2w:298:ARG:HB2	54:2w:298:ARG:HH11	1.85	0.41
1:1A:1056:G:H5'	1:1A:1086:A:H8	1.85	0.41
1:1A:1448:G:H4'	1:1A:1542:A:OP1	2.20	0.41
1:1A:1588:C:H2'	1:1A:1589:C:H6	1.85	0.41
1:1A:1805:U:O2	3:1D:50:THR:HB	2.20	0.41
1:1A:2364:C:H2'	1:1A:2365:G:O4'	2.20	0.41
3:1D:43:ARG:HA	3:1D:48:ARG:O	2.20	0.41
10:1O:90:GLN:OE1	10:1O:90:GLN:N	2.54	0.41
15:1T:107:ASP:O	15:1T:111:ARG:HG3	2.20	0.41
17:1V:98:GLU:CD	17:1V:100:ARG:HH11	2.29	0.41
32:1a:881:G:OP2	43:1l:12:ARG:NH2	2.53	0.41
32:1a:1057:G:H2'	32:1a:1058:G:O4'	2.21	0.41
32:1a:1466:C:H2'	32:1a:1467:G:O4'	2.21	0.41
44:1m:14:ARG:NH2	44:1m:16:ASP:OD2	2.46	0.41
45:1n:8:GLU:HA	45:1n:11:LYS:HE2	2.01	0.41
1:2A:244:A:C2	1:2A:255:A:C4	3.09	0.41
1:2A:1027:A:C2	1:2A:2488:A:H5'	2.55	0.41
1:2A:1268:A:H2'	1:2A:1269:A:O4'	2.21	0.41
1:2A:1316:U:H2'	1:2A:1317:A:C8	2.55	0.41
1:2A:1355:G:P	3:2D:38:LYS:HE2	2.61	0.41
1:2A:2123:G:H2'	1:2A:2124:G:C8	2.55	0.41
1:2A:2162:G:H3'	1:2A:2163:C:C6	2.56	0.41
1:2A:2273:A:H2'	1:2A:2274:A:C8	2.55	0.41
1:2A:2648:C:H2'	1:2A:2649:U:H6	1.85	0.41
6:2G:108:ASN:HA	26:24:37:SER:HB2	2.01	0.41
21:2Z:126:VAL:HG13	21:2Z:161:VAL:HG13	2.03	0.41
24:22:25:VAL:HG13	24:22:57:ILE:HG23	2.03	0.41
32:2a:1530:G:H4'	32:2a:1530:G:OP1	2.21	0.41
33:2b:80:ILE:O	33:2b:84:GLU:HG2	2.21	0.41
34:2c:3:ASN:N	34:2c:3:ASN:OD1	2.53	0.41
37:2f:9:VAL:HB	37:2f:87:ARG:HB2	2.00	0.41
47:2p:34:GLU:HG2	47:2p:35:LYS:H	1.85	0.41
1:1A:1093:G:P	1:1A:1094:U:H5'	2.61	0.41
1:1A:2163:C:OP1	1:1A:2165:G:N2	2.54	0.41
5:1F:54:ARG:NH2	5:1F:77:ASP:OD1	2.52	0.41
5:1F:184:TYR:CE2	5:1F:188:ARG:HD2	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:1I:88:ILE:HG22	8:1I:90:GLY:N	2.35	0.41
10:1O:64:ARG:O	10:1O:82:ASN:HA	2.20	0.41
11:1P:46:LYS:HB3	11:1P:46:LYS:HE2	1.79	0.41
24:12:53:LEU:HD23	24:12:53:LEU:HA	1.82	0.41
32:1a:192:U:H2'	32:1a:193:C:C6	2.56	0.41
32:1a:392:G:H2'	32:1a:393:A:H8	1.86	0.41
32:1a:1010:G:N2	32:1a:1020:U:H1'	2.35	0.41
32:1a:1032:G:H2'	32:1a:1033:G:C8	2.55	0.41
32:1a:1375:A:C6	32:1a:1376:U:C4	3.09	0.41
33:1b:48:MET:HA	33:1b:51:LEU:HD12	2.02	0.41
36:1e:77:PRO:HG2	36:1e:142:LEU:HD22	2.01	0.41
36:1e:91:LEU:HD23	36:1e:120:THR:HB	2.03	0.41
36:1e:137:GLU:HG3	36:1e:141:GLN:NE2	2.33	0.41
46:1o:56:LEU:O	46:1o:60:VAL:HG23	2.20	0.41
1:2A:898:C:H2'	1:2A:899:A:O4'	2.20	0.41
2:2B:11:C:H3'	2:2B:12:C:H6	1.85	0.41
5:2F:23:ASP:O	5:2F:24:LEU:HD23	2.20	0.41
5:2F:53:THR:HG22	5:2F:56:GLU:HG3	2.02	0.41
5:2F:117:ARG:HH12	11:2P:1:MET:N	2.18	0.41
15:2T:107:ASP:HA	15:2T:110:ILE:HD12	2.02	0.41
16:2U:55:ARG:O	16:2U:59:ARG:HG3	2.21	0.41
32:2a:9:G:H2'	32:2a:10:A:C8	2.55	0.41
32:2a:457:C:H2'	32:2a:458:C:C6	2.56	0.41
32:2a:664:G:N2	32:2a:741:G:H1	2.09	0.41
32:2a:1349:A:H1'	32:2a:1374:A:N6	2.36	0.41
39:2h:111:ILE:C	39:2h:112:LEU:HD12	2.45	0.41
44:2m:82:MET:HE3	44:2m:82:MET:HB2	1.81	0.41
46:2o:56:LEU:O	46:2o:60:VAL:HG23	2.20	0.41
54:2w:114:GLY:HA3	54:2w:196:THR:HG22	2.02	0.41
54:2w:342:ALA:O	54:2w:346:ARG:N	2.54	0.41
1:1A:239:U:H2'	1:1A:240:G:O4'	2.21	0.41
1:1A:994:C:OP1	16:1U:53:ARG:NH2	2.54	0.41
1:1A:2165:G:H2'	1:1A:2166:G:H5''	2.03	0.41
3:1D:70:TRP:HB3	3:1D:190:TYR:CZ	2.56	0.41
3:1D:206:LEU:HA	3:1D:206:LEU:HD23	1.74	0.41
8:1I:109:ILE:HD12	8:1I:130:TYR:CE2	2.56	0.41
13:1R:67:LEU:HG	13:1R:76:VAL:HG21	2.02	0.41
15:1T:105:LEU:HA	15:1T:105:LEU:HD23	1.78	0.41
19:1X:92:LEU:O	19:1X:95:LEU:HB2	2.21	0.41
32:1a:321:A:N7	32:1a:328:C:O2'	2.50	0.41
32:1a:363:A:C5	43:1I:31:PRO:HD2	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:593:G:H1	32:1a:646:U:H3	1.68	0.41
32:1a:1017:G:H2'	32:1a:1018:C:C6	2.56	0.41
33:1b:86:GLU:C	33:1b:89:GLY:H	2.28	0.41
35:1d:121:VAL:O	35:1d:134:ASP:HA	2.21	0.41
36:1e:152:ARG:NH2	39:1h:107:LEU:O	2.53	0.41
1:2A:581:C:H2'	1:2A:582:G:C8	2.56	0.41
1:2A:792:G:O2'	1:2A:2440:C:N3	2.40	0.41
1:2A:878:A:C5	1:2A:900:A:C5	3.08	0.41
1:2A:1364:G:OP2	23:21:3:LYS:HG3	2.21	0.41
1:2A:2747:G:O6	1:2A:2755:C:H5''	2.21	0.41
2:2B:105:A:H5'	2:2B:106:G:OP2	2.21	0.41
3:2D:173:VAL:HG23	3:2D:185:VAL:O	2.20	0.41
3:2D:182:LEU:HB2	3:2D:272:ALA:HB3	2.02	0.41
3:2D:218:ARG:HB3	3:2D:219:PRO:HD2	2.03	0.41
30:28:52:LYS:O	30:28:56:GLU:HG3	2.21	0.41
32:2a:134:A:H61	47:2p:25:ARG:NH1	2.18	0.41
32:2a:164:U:H2'	32:2a:165:C:C6	2.56	0.41
32:2a:985:C:H2'	32:2a:986:A:C8	2.55	0.41
32:2a:1168:A:C6	32:2a:1169:A:C6	3.08	0.41
32:2a:1365:G:H2'	32:2a:1366:C:O4'	2.21	0.41
36:2e:6:PHE:HD1	36:2e:6:PHE:HA	1.70	0.41
40:2i:121:ARG:NH1	40:2i:122:ALA:O	2.54	0.41
1:1A:375:C:H2'	1:1A:376:C:C6	2.55	0.41
1:1A:582:G:N7	61:1A:4210:HOH:O	2.37	0.41
1:1A:887:A:H4'	1:1A:888:C:H5''	2.02	0.41
1:1A:1665:A:H2'	1:1A:1666:G:O4'	2.21	0.41
1:1A:1796:U:H2'	1:1A:1797:C:H6	1.84	0.41
1:1A:2564:A:C2	1:1A:2647:U:H4'	2.56	0.41
1:1A:2572:A:C8	4:1E:144:ARG:HD3	2.55	0.41
1:1A:2849:U:H4'	1:1A:2868:A:C2	2.55	0.41
7:1H:152:ARG:HD3	7:1H:152:ARG:HA	1.79	0.41
8:1I:109:ILE:HG23	8:1I:130:TYR:CE1	2.56	0.41
10:1O:107:ARG:CZ	15:1T:36:GLU:HG3	2.51	0.41
15:1T:126:ALA:O	15:1T:129:ARG:HB2	2.20	0.41
18:1W:92:ARG:HG2	18:1W:93:ALA:N	2.36	0.41
19:1X:40:LYS:HG3	19:1X:51:VAL:HB	2.02	0.41
21:1Z:158:PRO:HG2	21:1Z:161:VAL:HG11	2.01	0.41
32:1a:1092:A:N3	32:1a:1183:A:N6	2.69	0.41
38:1g:101:LEU:O	38:1g:105:VAL:HG23	2.21	0.41
39:1h:13:ILE:O	39:1h:17:THR:HG23	2.21	0.41
40:1i:118:LYS:HB3	40:1i:119:ALA:H	1.63	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:1k:21:ILE:HB	42:1k:84:VAL:HG12	2.02	0.41
49:1r:84:LYS:HE3	49:1r:84:LYS:HB2	1.83	0.41
1:2A:195:A:H5''	1:2A:196:A:O5'	2.21	0.41
1:2A:208:C:H2'	1:2A:209:C:H6	1.86	0.41
1:2A:647:G:N3	1:2A:2350:C:O2'	2.54	0.41
1:2A:652(B):A:N3	1:2A:652(B):A:H2'	2.35	0.41
1:2A:858:U:O2	1:2A:2268:A:H2'	2.21	0.41
1:2A:1366:A:H2'	1:2A:1367:A:O4'	2.21	0.41
1:2A:1506:C:H2'	1:2A:1507:A:H5'	2.03	0.41
1:2A:2134:A:H2	1:2A:2159:G:H1'	1.86	0.41
1:2A:2510:C:C4	1:2A:2511:U:C4	3.09	0.41
1:2A:2690:C:OP2	13:2R:14:SER:HB3	2.20	0.41
1:2A:2836:U:H2'	1:2A:2837:G:C8	2.56	0.41
3:2D:70:TRP:HB3	3:2D:190:TYR:CZ	2.56	0.41
5:2F:33:LEU:HD21	5:2F:112:MET:HB3	2.03	0.41
7:2H:71:LEU:HA	7:2H:71:LEU:HD23	1.83	0.41
8:2I:12:LEU:HA	8:2I:12:LEU:HD23	1.81	0.41
10:2O:87:ILE:HD12	10:2O:91:LEU:HA	2.02	0.41
15:2T:18:ASP:OD1	15:2T:18:ASP:N	2.54	0.41
18:2W:18:ARG:HG2	18:2W:76:VAL:HB	2.03	0.41
32:2a:73:G:H1	32:2a:96:U:H3	1.69	0.41
32:2a:296:U:O2'	32:2a:556:C:O2	2.36	0.41
32:2a:353:A:H5'	32:2a:353:A:H8	1.85	0.41
32:2a:557:G:C6	32:2a:558:G:C6	3.09	0.41
32:2a:918:A:H2'	32:2a:919:A:O4'	2.21	0.41
32:2a:967:5MC:H2'	32:2a:968:A:N7	2.35	0.41
32:2a:1250:A:H4'	40:2i:68:GLY:N	2.36	0.41
32:2a:1305:G:H5'	52:2u:4:GLY:HA3	2.03	0.41
33:2b:49:GLU:H	33:2b:49:GLU:HG2	1.57	0.41
34:2c:36:ASP:OD1	34:2c:59:ARG:NH2	2.54	0.41
34:2c:131:ARG:HH22	36:2e:50:GLU:HG3	1.86	0.41
43:2l:84:LEU:HB3	43:2l:104:VAL:HG21	2.02	0.41
44:2m:92:HIS:CE1	44:2m:98:VAL:HG11	2.55	0.41
44:2m:106:ASN:HB2	44:2m:107:ALA:H	1.52	0.41
45:2n:37:PHE:CE1	45:2n:53:LEU:HD13	2.55	0.41
46:2o:61:GLY:O	46:2o:65:ARG:HG3	2.21	0.41
50:2s:40:ILE:HB	50:2s:67:VAL:O	2.20	0.41
54:2w:328:LEU:HD23	54:2w:328:LEU:HA	1.87	0.41
1:1A:1005:C:O2'	9:1N:28:THR:HG21	2.20	0.41
1:1A:1057:A:N7	1:1A:1086:A:H2'	2.35	0.41
1:1A:2267:A:H5''	1:1A:2268:A:H5'	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:1G:15:VAL:HG21	6:1G:176:LEU:HD23	2.02	0.41
8:1I:93:THR:O	8:1I:97:ILE:HG13	2.21	0.41
21:1Z:46:LYS:HE2	21:1Z:46:LYS:HB3	1.89	0.41
32:1a:111:G:H5''	47:1p:27:LYS:HB3	2.03	0.41
32:1a:711:G:H2'	32:1a:712:A:C8	2.56	0.41
32:1a:1292:U:P	38:1g:41:ARG:HH22	2.43	0.41
32:1a:1442:G:O2'	32:1a:1442(A):G:O5'	2.37	0.41
33:1b:12:GLU:HA	33:1b:15:VAL:HG22	2.02	0.41
1:2A:39:C:O2	5:2F:46:ARG:NH2	2.54	0.41
1:2A:1266:G:O5'	18:2W:15:ARG:NH2	2.53	0.41
1:2A:2712(A):A:OP2	61:2A:3953:HOH:O	2.21	0.41
3:2D:16:MET:HG3	3:2D:206:LEU:O	2.20	0.41
6:2G:82:LEU:HA	6:2G:86:MET:SD	2.61	0.41
17:2V:16:PRO:HD3	17:2V:99:ILE:HD11	2.02	0.41
17:2V:81:TYR:C	17:2V:82:ARG:HD2	2.45	0.41
32:2a:755:G:OP2	46:2o:65:ARG:HD2	2.21	0.41
32:2a:995:C:O2'	32:2a:996:A:H5'	2.21	0.41
32:2a:1004:A:N3	32:2a:1038:C:C2	2.89	0.41
32:2a:1123:A:H4'	41:2j:37:PRO:HD2	2.03	0.41
32:2a:1126:U:H6	32:2a:1281:U:C2	2.39	0.41
32:2a:1327:C:OP1	52:2u:12:LYS:HE3	2.20	0.41
54:2w:103:ASP:HB3	54:2w:169:GLY:CA	2.50	0.41
54:2w:145:LEU:HB2	54:2w:159:VAL:HG12	2.02	0.41
1:1A:1593:G:H2'	1:1A:1594:G:C8	2.56	0.40
1:1A:2023:G:H4'	1:1A:2617:C:O3'	2.21	0.40
1:1A:2040:C:H2'	1:1A:2041:U:O4'	2.21	0.40
1:1A:2632:A:O2'	1:1A:2811:G:O2'	2.23	0.40
4:1E:177:PRO:HD2	4:1E:178:GLU:OE1	2.20	0.40
10:1O:115:VAL:HG13	10:1O:121:VAL:HG21	2.02	0.40
14:1S:39:ILE:HB	14:1S:49:VAL:HG12	2.03	0.40
32:1a:562:C:O2	43:1l:16:GLU:N	2.41	0.40
32:1a:1021:G:O2'	32:1a:1022:G:P	2.79	0.40
36:1e:40:ARG:HA	36:1e:40:ARG:HD2	1.88	0.40
36:1e:100:VAL:O	36:1e:107:ARG:NH2	2.46	0.40
42:1k:73:MET:HG2	42:1k:103:LEU:HD21	2.02	0.40
51:1t:56:MET:HE2	51:1t:56:MET:HB3	1.99	0.40
1:2A:302:C:P	20:2Y:73:ARG:HH12	2.43	0.40
1:2A:958:U:H4'	61:2A:3968:HOH:O	2.21	0.40
1:2A:1739:U:O2'	1:2A:1740:G:H8	2.04	0.40
1:2A:1946:U:H2'	1:2A:1947:C:C6	2.56	0.40
1:2A:2561:A:H4'	10:2O:22:ILE:HD11	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2810:A:N6	1:2A:2891:G:O2'	2.45	0.40
61:2A:3906:HOH:O	4:2E:110:GLY:O	2.22	0.40
4:2E:28:ALA:HB3	4:2E:93:VAL:HG12	2.02	0.40
5:2F:183:VAL:O	5:2F:187:VAL:HG23	2.21	0.40
10:2O:4:PRO:O	10:2O:5:GLN:HB2	2.21	0.40
11:2P:50:ARG:O	11:2P:52:GLU:HG3	2.22	0.40
20:2Y:44:ILE:HA	20:2Y:63:LYS:O	2.21	0.40
20:2Y:44:ILE:CG2	20:2Y:62:GLU:HB3	2.51	0.40
21:2Z:30:ASN:HA	21:2Z:89:PHE:HE1	1.86	0.40
22:20:50:ASN:HA	22:20:62:LEU:HD12	2.03	0.40
24:22:13:ALA:HB1	24:22:21:LEU:HD21	2.02	0.40
34:2c:122:GLU:HA	34:2c:125:GLU:OE2	2.20	0.40
38:2g:78:ARG:NH1	38:2g:156:TRP:HB3	2.36	0.40
54:2w:260:LYS:HA	54:2w:260:LYS:HD3	1.79	0.40
1:1A:2218:U:O4'	23:11:52:ARG:NH2	2.55	0.40
7:1H:20:ALA:HB3	7:1H:23:ARG:HG3	2.02	0.40
32:1a:262:A:C6	32:1a:263:A:C6	3.10	0.40
32:1a:266:G:H5''	32:1a:268:C:H41	1.86	0.40
32:1a:376:G:O3'	47:1p:5:ARG:NH1	2.46	0.40
32:1a:491:G:H2'	32:1a:492:G:O4'	2.22	0.40
32:1a:741:G:H2'	32:1a:742:G:O4'	2.20	0.40
32:1a:945:G:C2	32:1a:946:A:C8	3.09	0.40
32:1a:1080:A:H5'	36:1e:14:ARG:HH21	1.86	0.40
37:1f:96:PRO:HB3	49:1r:30:ASP:CG	2.46	0.40
39:1h:28:ALA:HA	39:1h:59:LEU:HG	2.01	0.40
41:1j:13:HIS:HA	41:1j:16:LEU:HB3	2.04	0.40
1:2A:208:C:H2'	1:2A:209:C:C6	2.56	0.40
1:2A:601:C:O2	1:2A:605:C:H4'	2.21	0.40
1:2A:1188:U:H4'	17:2V:79:VAL:HG22	2.03	0.40
1:2A:1993:U:OP2	61:2A:3956:HOH:O	2.22	0.40
1:2A:2336:A:H61	22:20:43:THR:CG2	2.34	0.40
5:2F:126:VAL:O	5:2F:196:LEU:HG	2.21	0.40
12:2Q:31:ASP:HA	12:2Q:134:ARG:NH1	2.35	0.40
19:2X:5:TYR:CE1	24:22:30:ARG:HG3	2.57	0.40
32:2a:1006:C:H2'	32:2a:1007:C:O4'	2.21	0.40
33:2b:91:PRO:HG2	33:2b:155:LEU:HD13	2.03	0.40
33:2b:100:GLY:N	33:2b:176:GLU:OE2	2.44	0.40
38:2g:125:MET:HE2	38:2g:125:MET:HB3	1.98	0.40
44:2m:84:ILE:HG22	50:2s:66:MET:HE2	2.03	0.40
55:2x:12:A:H2'	55:2x:13:A:O4'	2.20	0.40
1:1A:118:A:O5'	1:1A:119:A:H5''	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1268:A:H2'	1:1A:1269:A:O4'	2.22	0.40
1:1A:1316:U:H2'	1:1A:1317:A:C8	2.56	0.40
1:1A:1697:G:OP2	1:1A:1698:A:O2'	2.33	0.40
1:1A:2438:U:O2'	1:1A:2440:C:OP1	2.33	0.40
2:1B:91:C:H5'	12:1Q:18:LYS:HA	2.02	0.40
5:1F:136:THR:HA	5:1F:166:ALA:O	2.21	0.40
5:1F:197:ASP:O	5:1F:201:VAL:HG13	2.22	0.40
32:1a:164:U:H2'	32:1a:165:C:C6	2.57	0.40
32:1a:448:A:P	32:1a:485:G:H22	2.44	0.40
32:1a:524:G:H2'	32:1a:525:C:C6	2.56	0.40
32:1a:987:G:O5'	32:1a:987:G:H8	2.04	0.40
32:1a:1314:C:H2'	32:1a:1315:U:C6	2.56	0.40
32:1a:1412:C:H2'	32:1a:1413:A:H8	1.85	0.40
33:1b:207:ALA:O	33:1b:211:ILE:HG13	2.21	0.40
35:1d:81:GLU:O	35:1d:85:LYS:HB2	2.20	0.40
45:1n:21:TYR:HE1	45:1n:23:ARG:NE	2.20	0.40
47:1p:40:ASP:HB3	47:1p:48:TRP:CB	2.51	0.40
51:1t:63:ILE:HG21	51:1t:81:LYS:HG3	2.02	0.40
51:1t:86:ARG:HB3	51:1t:90:GLN:NE2	2.37	0.40
1:2A:1364:G:C8	23:21:3:LYS:HD2	2.56	0.40
1:2A:1400:G:H2'	1:2A:1401:G:C8	2.56	0.40
1:2A:1495:A:H2'	1:2A:1496:A:C8	2.56	0.40
1:2A:2031:A:C6	1:2A:2498:C:H1'	2.56	0.40
12:2Q:1:MET:HE3	12:2Q:1:MET:HB2	1.72	0.40
16:2U:27:LEU:HD23	16:2U:27:LEU:HA	1.92	0.40
34:2c:5:ILE:HD11	45:2n:49:HIS:HE1	1.86	0.40
34:2c:133:ALA:HA	34:2c:136:GLN:HG2	2.02	0.40
35:2d:170:VAL:HG22	35:2d:171:GLY:H	1.87	0.40
44:2m:34:LEU:O	44:2m:38:GLY:N	2.52	0.40
55:2x:48:G:C4	55:2x:59:C:H1'	2.56	0.40
1:1A:32:C:O2'	1:1A:33:U:H5'	2.20	0.40
1:1A:922:U:H2'	1:1A:923:C:C6	2.57	0.40
1:1A:1062:G:N3	1:1A:1088:A:H2'	2.37	0.40
1:1A:2101:G:H3'	1:1A:2102:U:C6	2.56	0.40
1:1A:2189:U:H2'	1:1A:2190:G:C8	2.56	0.40
2:1B:33:G:H5'	6:1G:2:PRO:HG3	2.03	0.40
5:1F:7:TYR:CD2	5:1F:24:LEU:HB2	2.56	0.40
19:1X:64:LYS:HA	19:1X:64:LYS:HD3	1.90	0.40
21:1Z:124:ILE:HD12	21:1Z:124:ILE:HA	1.97	0.40
30:18:23:VAL:HG13	30:18:47:LYS:HB3	2.04	0.40
32:1a:444:C:H2'	32:1a:445:G:C8	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:486:U:H2'	32:1a:487:A:H8	1.86	0.40
32:1a:1446:U:H4'	32:1a:1447:A:C6	2.56	0.40
33:1b:24:TRP:CZ3	33:1b:26:PRO:HA	2.57	0.40
33:1b:211:ILE:HG13	33:1b:211:ILE:H	1.71	0.40
1:2A:516:C:OP1	27:25:13:LYS:NZ	2.45	0.40
1:2A:747:U:O2	1:2A:2014:A:H1'	2.21	0.40
1:2A:1448:G:H1'	1:2A:1528:A:N1	2.36	0.40
1:2A:1952:A:C2	10:2O:22:ILE:HD12	2.57	0.40
1:2A:2130:U:H5''	1:2A:2133:G:H5'	2.02	0.40
20:2Y:19:LYS:HB3	20:2Y:19:LYS:HE2	1.90	0.40
32:2a:457:C:C2	32:2a:475:G:C2	3.10	0.40
32:2a:559:A:H4'	32:2a:560:U:H5''	2.04	0.40
33:2b:128:GLU:HA	33:2b:135:GLN:NE2	2.36	0.40
35:2d:58:LEU:O	35:2d:62:GLN:HG2	2.22	0.40
38:2g:46:ALA:HB1	38:2g:121:ALA:HB2	2.03	0.40
39:2h:48:TYR:HA	39:2h:60:ARG:O	2.22	0.40
44:2m:16:ASP:OD1	44:2m:16:ASP:N	2.53	0.40
51:2t:26:ASN:HB3	51:2t:71:THR:HG23	2.03	0.40
51:2t:79:ARG:HD2	51:2t:83:ARG:HH21	1.86	0.40
55:2x:43:U:O2'	55:2x:44:C:H5'	2.22	0.40
1:1A:1039:G:H1	1:1A:1116:C:H42	1.70	0.40
1:1A:1570:A:H2'	1:1A:1571:A:C8	2.56	0.40
1:1A:1866:C:H2'	1:1A:1876:A:O4'	2.22	0.40
1:1A:1936:A:OP1	1:1A:1937:A:H5'	2.22	0.40
21:1Z:54:HIS:CG	21:1Z:101:PRO:HG3	2.57	0.40
32:1a:441:A:N7	32:1a:442:C:C2	2.90	0.40
32:1a:943:U:H1'	40:1i:124:GLN:HE22	1.86	0.40
32:1a:1006:C:H2'	32:1a:1007:C:C6	2.56	0.40
33:1b:30:ARG:HG3	33:1b:31:TYR:CE1	2.57	0.40
50:1s:69:HIS:HB3	50:1s:73:GLU:OE1	2.21	0.40
1:2A:328:U:H4'	20:2Y:68:HIS:CG	2.57	0.40
1:2A:702:G:C2	1:2A:731:C:C2	3.09	0.40
1:2A:729:G:C6	3:2D:208:LYS:HB2	2.57	0.40
1:2A:1469:A:H2'	1:2A:1470:G:O4'	2.21	0.40
1:2A:1608:A:H1'	1:2A:1610:A:OP2	2.22	0.40
1:2A:2406:U:H6	1:2A:2406:U:H2'	1.75	0.40
1:2A:2469:A:O2'	12:2Q:56:ARG:NE	2.55	0.40
1:2A:2748:A:N3	7:2H:63:SER:HB3	2.37	0.40
2:2B:20:C:N4	2:2B:63:G:H1	2.19	0.40
2:2B:66:A:N6	2:2B:109:C:H5'	2.36	0.40
4:2E:96:PHE:O	4:2E:175:VAL:HG21	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:2F:161:GLU:H	5:2F:161:GLU:HG2	1.58	0.40
7:2H:94:TYR:HA	7:2H:106:THR:O	2.21	0.40
8:2I:61:ARG:HE	8:2I:61:ARG:HB2	1.62	0.40
19:2X:11:PRO:HB2	19:2X:92:LEU:HD21	2.03	0.40
26:24:53:GLU:HB2	26:24:55:ARG:O	2.22	0.40
29:27:26:GLY:O	29:27:30:VAL:HG23	2.21	0.40
32:2a:430:A:OP1	35:2d:9:CYS:HB2	2.21	0.40
32:2a:922:G:N3	32:2a:1398:A:H2	2.20	0.40
32:2a:1278:U:H5'	32:2a:1279:A:C5'	2.52	0.40
32:2a:1298:C:H2'	38:2g:114:ARG:NH2	2.37	0.40
34:2c:190:ARG:HD2	34:2c:190:ARG:O	2.22	0.40
37:2f:96:PRO:HB3	49:2r:30:ASP:OD2	2.22	0.40
46:2o:84:LYS:HD3	46:2o:84:LYS:HA	1.94	0.40
47:2p:8:ARG:HG2	47:2p:17:TYR:CE1	2.56	0.40
47:2p:53:VAL:HG12	47:2p:79:VAL:HG22	2.04	0.40
47:2p:76:GLN:C	47:2p:78:GLY:H	2.28	0.40
53:2v:14:A:N3	53:2v:14:A:H2'	2.37	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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%)	262 (96%)	11 (4%)	0	100	100
3	2D	273/276 (99%)	257 (94%)	15 (6%)	1 (0%)	30	54
4	1E	202/206 (98%)	191 (95%)	10 (5%)	1 (0%)	24	48
4	2E	202/206 (98%)	190 (94%)	11 (5%)	1 (0%)	24	48
5	1F	201/210 (96%)	191 (95%)	8 (4%)	2 (1%)	12	32
5	2F	201/210 (96%)	185 (92%)	15 (8%)	1 (0%)	24	48
6	1G	179/182 (98%)	161 (90%)	15 (8%)	3 (2%)	7	19

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	2G	179/182 (98%)	154 (86%)	22 (12%)	3 (2%)	7	19
7	1H	172/180 (96%)	162 (94%)	10 (6%)	0	100	100
7	2H	172/180 (96%)	155 (90%)	13 (8%)	4 (2%)	5	13
8	1I	144/148 (97%)	126 (88%)	17 (12%)	1 (1%)	18	41
8	2I	144/148 (97%)	122 (85%)	21 (15%)	1 (1%)	18	41
9	1N	138/140 (99%)	134 (97%)	4 (3%)	0	100	100
9	2N	138/140 (99%)	135 (98%)	3 (2%)	0	100	100
10	1O	120/122 (98%)	112 (93%)	7 (6%)	1 (1%)	16	37
10	2O	120/122 (98%)	111 (92%)	8 (7%)	1 (1%)	16	37
11	1P	147/150 (98%)	139 (95%)	8 (5%)	0	100	100
11	2P	147/150 (98%)	139 (95%)	7 (5%)	1 (1%)	18	41
12	1Q	139/141 (99%)	133 (96%)	6 (4%)	0	100	100
12	2Q	139/141 (99%)	130 (94%)	8 (6%)	1 (1%)	18	41
13	1R	116/118 (98%)	111 (96%)	5 (4%)	0	100	100
13	2R	116/118 (98%)	110 (95%)	6 (5%)	0	100	100
14	1S	108/112 (96%)	104 (96%)	4 (4%)	0	100	100
14	2S	108/112 (96%)	95 (88%)	12 (11%)	1 (1%)	14	35
15	1T	129/146 (88%)	119 (92%)	9 (7%)	1 (1%)	16	37
15	2T	129/146 (88%)	121 (94%)	8 (6%)	0	100	100
16	1U	114/118 (97%)	113 (99%)	1 (1%)	0	100	100
16	2U	114/118 (97%)	108 (95%)	6 (5%)	0	100	100
17	1V	99/101 (98%)	97 (98%)	2 (2%)	0	100	100
17	2V	99/101 (98%)	89 (90%)	9 (9%)	1 (1%)	12	32
18	1W	110/113 (97%)	107 (97%)	3 (3%)	0	100	100
18	2W	110/113 (97%)	107 (97%)	3 (3%)	0	100	100
19	1X	93/96 (97%)	90 (97%)	1 (1%)	2 (2%)	5	14
19	2X	93/96 (97%)	87 (94%)	6 (6%)	0	100	100
20	1Y	105/110 (96%)	98 (93%)	7 (7%)	0	100	100
20	2Y	105/110 (96%)	98 (93%)	6 (6%)	1 (1%)	12	32
21	1Z	148/206 (72%)	134 (90%)	11 (7%)	3 (2%)	6	16
21	2Z	156/206 (76%)	137 (88%)	17 (11%)	2 (1%)	9	25

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
22	10	74/85 (87%)	72 (97%)	2 (3%)	0	100	100
22	20	74/85 (87%)	70 (95%)	4 (5%)	0	100	100
23	11	95/98 (97%)	91 (96%)	3 (3%)	1 (1%)	11	29
23	21	95/98 (97%)	93 (98%)	2 (2%)	0	100	100
24	12	68/72 (94%)	68 (100%)	0	0	100	100
24	22	68/72 (94%)	64 (94%)	4 (6%)	0	100	100
25	13	57/60 (95%)	55 (96%)	2 (4%)	0	100	100
25	23	57/60 (95%)	52 (91%)	4 (7%)	1 (2%)	6	18
26	14	67/71 (94%)	52 (78%)	10 (15%)	5 (8%)	1	1
26	24	67/71 (94%)	51 (76%)	10 (15%)	6 (9%)	0	0
27	15	57/60 (95%)	54 (95%)	3 (5%)	0	100	100
27	25	57/60 (95%)	53 (93%)	4 (7%)	0	100	100
28	16	51/54 (94%)	48 (94%)	3 (6%)	0	100	100
28	26	51/54 (94%)	49 (96%)	2 (4%)	0	100	100
29	17	46/49 (94%)	45 (98%)	1 (2%)	0	100	100
29	27	46/49 (94%)	44 (96%)	2 (4%)	0	100	100
30	18	62/65 (95%)	62 (100%)	0	0	100	100
30	28	62/65 (95%)	61 (98%)	1 (2%)	0	100	100
31	19	35/37 (95%)	34 (97%)	1 (3%)	0	100	100
31	29	35/37 (95%)	35 (100%)	0	0	100	100
33	1b	229/256 (90%)	196 (86%)	21 (9%)	12 (5%)	1	3
33	2b	229/256 (90%)	194 (85%)	28 (12%)	7 (3%)	3	8
34	1c	204/239 (85%)	181 (89%)	21 (10%)	2 (1%)	12	32
34	2c	204/239 (85%)	175 (86%)	27 (13%)	2 (1%)	12	32
35	1d	206/209 (99%)	183 (89%)	22 (11%)	1 (0%)	24	48
35	2d	206/209 (99%)	186 (90%)	20 (10%)	0	100	100
36	1e	146/162 (90%)	131 (90%)	14 (10%)	1 (1%)	18	41
36	2e	146/162 (90%)	138 (94%)	8 (6%)	0	100	100
37	1f	98/101 (97%)	90 (92%)	8 (8%)	0	100	100
37	2f	98/101 (97%)	88 (90%)	10 (10%)	0	100	100
38	1g	153/156 (98%)	134 (88%)	17 (11%)	2 (1%)	9	25

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
38	2g	153/156 (98%)	133 (87%)	17 (11%)	3 (2%)	6	16
39	1h	135/138 (98%)	126 (93%)	9 (7%)	0	100	100
39	2h	135/138 (98%)	130 (96%)	5 (4%)	0	100	100
40	1i	125/128 (98%)	107 (86%)	17 (14%)	1 (1%)	16	37
40	2i	125/128 (98%)	104 (83%)	20 (16%)	1 (1%)	16	37
41	1j	95/105 (90%)	84 (88%)	8 (8%)	3 (3%)	3	7
41	2j	94/105 (90%)	76 (81%)	14 (15%)	4 (4%)	2	4
42	1k	112/129 (87%)	102 (91%)	9 (8%)	1 (1%)	14	35
42	2k	112/129 (87%)	97 (87%)	14 (12%)	1 (1%)	14	35
43	1l	119/132 (90%)	113 (95%)	6 (5%)	0	100	100
43	2l	119/132 (90%)	111 (93%)	8 (7%)	0	100	100
44	1m	116/126 (92%)	106 (91%)	8 (7%)	2 (2%)	7	19
44	2m	114/126 (90%)	93 (82%)	19 (17%)	2 (2%)	6	18
45	1n	58/61 (95%)	51 (88%)	6 (10%)	1 (2%)	7	19
45	2n	58/61 (95%)	55 (95%)	3 (5%)	0	100	100
46	1o	86/89 (97%)	85 (99%)	1 (1%)	0	100	100
46	2o	86/89 (97%)	80 (93%)	6 (7%)	0	100	100
47	1p	80/88 (91%)	69 (86%)	11 (14%)	0	100	100
47	2p	80/88 (91%)	71 (89%)	9 (11%)	0	100	100
48	1q	97/105 (92%)	93 (96%)	4 (4%)	0	100	100
48	2q	97/105 (92%)	89 (92%)	7 (7%)	1 (1%)	12	32
49	1r	66/88 (75%)	63 (96%)	3 (4%)	0	100	100
49	2r	66/88 (75%)	63 (96%)	3 (4%)	0	100	100
50	1s	81/93 (87%)	69 (85%)	12 (15%)	0	100	100
50	2s	81/93 (87%)	69 (85%)	10 (12%)	2 (2%)	4	11
51	1t	94/106 (89%)	86 (92%)	6 (6%)	2 (2%)	5	15
51	2t	94/106 (89%)	85 (90%)	6 (6%)	3 (3%)	3	7
52	1u	21/27 (78%)	18 (86%)	3 (14%)	0	100	100
52	2u	21/27 (78%)	16 (76%)	5 (24%)	0	100	100
54	1w	247/354 (70%)	237 (96%)	8 (3%)	2 (1%)	16	37
54	2w	251/354 (71%)	234 (93%)	15 (6%)	2 (1%)	16	37

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
56	1z	3/7 (43%)	3 (100%)	0	0	100	100
56	2z	3/7 (43%)	3 (100%)	0	0	100	100
All	All	11849/12850 (92%)	10884 (92%)	861 (7%)	104 (1%)	14	35

All (104) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	1F	130	ALA
6	1G	126	ASP
19	1X	93	GLU
23	11	3	LYS
26	14	53	GLU
33	1b	10	LEU
33	1b	17	PHE
33	1b	22	LYS
33	1b	126	GLU
34	1c	66	VAL
38	1g	80	VAL
40	1i	54	ASP
44	1m	67	GLU
5	2F	130	ALA
6	2G	47	LYS
20	2Y	55	TYR
26	24	44	THR
26	24	65	ASP
33	2b	22	LYS
38	2g	4	ARG
38	2g	80	VAL
21	1Z	52	SER
26	14	49	PHE
33	1b	9	GLU
33	1b	227	GLY
41	1j	82	ILE
42	1k	49	GLY
44	1m	106	ASN
54	1w	299	SER
7	2H	47	GLU
7	2H	126	PRO
8	2I	42	SER
12	2Q	60	ARG
14	2S	96	GLY

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Mol	Chain	Res	Type
17	2V	79	VAL
26	24	39	CYS
26	24	50	VAL
33	2b	17	PHE
33	2b	78	GLN
33	2b	123	ALA
34	2c	98	ASN
38	2g	55	GLY
41	2j	33	GLN
42	2k	49	GLY
48	2q	68	ARG
50	2s	13	ASP
4	1E	52	LEU
5	1F	168	ARG
6	1G	43	LEU
26	14	56	VAL
33	1b	20	GLU
34	1c	65	ALA
45	1n	60	SER
54	1w	103	ASP
21	2Z	52	SER
26	24	62	ARG
26	24	64	GLY
41	2j	78	ASN
51	2t	71	THR
54	2w	299	SER
8	1I	117	GLU
10	1O	5	GLN
33	1b	125	PRO
36	1e	85	GLY
41	1j	33	GLN
41	1j	79	ARG
51	1t	47	GLY
51	1t	102	GLY
3	2D	199	ALA
4	2E	52	LEU
10	2O	5	GLN
11	2P	29	LYS
34	2c	91	LEU
40	2i	121	ARG
41	2j	31	GLY
44	2m	59	TYR

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Mol	Chain	Res	Type
50	2s	12	ASP
54	2w	209	ASP
6	1G	47	LYS
21	1Z	157	LEU
26	14	62	ARG
33	1b	16	HIS
33	1b	123	ALA
33	1b	231	GLU
6	2G	117	PHE
21	2Z	31	ARG
33	2b	20	GLU
33	2b	124	SER
33	2b	125	PRO
44	2m	91	ARG
26	14	44	THR
35	1d	178	VAL
51	2t	99	LEU
15	1T	37	GLY
38	1g	81	GLY
7	2H	21	PRO
6	2G	52	ILE
25	23	59	VAL
41	2j	77	PRO
51	2t	102	GLY
21	1Z	53	ILE
33	1b	124	SER
19	1X	94	GLY
7	2H	12	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	1D	215/218 (99%)	205 (95%)	10 (5%)	23	51
3	2D	215/218 (99%)	203 (94%)	12 (6%)	19	44
4	1E	164/166 (99%)	152 (93%)	12 (7%)	13	32

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	2E	164/166 (99%)	158 (96%)	6 (4%)	30	59
5	1F	160/166 (96%)	142 (89%)	18 (11%)	5	14
5	2F	159/166 (96%)	143 (90%)	16 (10%)	7	18
6	1G	143/156 (92%)	129 (90%)	14 (10%)	7	19
6	2G	143/156 (92%)	123 (86%)	20 (14%)	3	9
7	1H	144/148 (97%)	136 (94%)	8 (6%)	19	44
7	2H	144/148 (97%)	131 (91%)	13 (9%)	9	23
8	1I	113/124 (91%)	102 (90%)	11 (10%)	8	20
8	2I	105/124 (85%)	85 (81%)	20 (19%)	1	4
9	1N	118/119 (99%)	108 (92%)	10 (8%)	10	25
9	2N	118/119 (99%)	108 (92%)	10 (8%)	10	25
10	1O	100/100 (100%)	98 (98%)	2 (2%)	48	76
10	2O	100/100 (100%)	98 (98%)	2 (2%)	48	76
11	1P	115/116 (99%)	107 (93%)	8 (7%)	14	34
11	2P	115/116 (99%)	104 (90%)	11 (10%)	8	20
12	1Q	111/111 (100%)	107 (96%)	4 (4%)	31	60
12	2Q	111/111 (100%)	106 (96%)	5 (4%)	24	52
13	1R	101/101 (100%)	96 (95%)	5 (5%)	22	48
13	2R	101/101 (100%)	96 (95%)	5 (5%)	22	48
14	1S	86/88 (98%)	76 (88%)	10 (12%)	5	13
14	2S	85/88 (97%)	74 (87%)	11 (13%)	4	10
15	1T	115/127 (91%)	106 (92%)	9 (8%)	11	29
15	2T	113/127 (89%)	104 (92%)	9 (8%)	11	28
16	1U	93/94 (99%)	88 (95%)	5 (5%)	20	45
16	2U	93/94 (99%)	89 (96%)	4 (4%)	26	54
17	1V	80/82 (98%)	77 (96%)	3 (4%)	29	58
17	2V	80/82 (98%)	71 (89%)	9 (11%)	5	14
18	1W	90/92 (98%)	87 (97%)	3 (3%)	33	63
18	2W	90/92 (98%)	86 (96%)	4 (4%)	25	53
19	1X	77/78 (99%)	75 (97%)	2 (3%)	40	70
19	2X	77/78 (99%)	75 (97%)	2 (3%)	40	70

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
20	1Y	85/91 (93%)	78 (92%)	7 (8%)	10	27
20	2Y	85/91 (93%)	79 (93%)	6 (7%)	13	33
21	1Z	135/179 (75%)	121 (90%)	14 (10%)	7	17
21	2Z	137/179 (76%)	117 (85%)	20 (15%)	3	8
22	10	61/67 (91%)	61 (100%)	0	100	100
22	20	61/67 (91%)	59 (97%)	2 (3%)	33	63
23	11	80/83 (96%)	77 (96%)	3 (4%)	29	58
23	21	80/83 (96%)	74 (92%)	6 (8%)	12	31
24	12	65/67 (97%)	62 (95%)	3 (5%)	24	51
24	22	65/67 (97%)	54 (83%)	11 (17%)	2	6
25	13	51/52 (98%)	43 (84%)	8 (16%)	2	7
25	23	50/52 (96%)	46 (92%)	4 (8%)	11	28
26	14	59/63 (94%)	52 (88%)	7 (12%)	5	13
26	24	53/63 (84%)	48 (91%)	5 (9%)	8	21
27	15	50/52 (96%)	48 (96%)	2 (4%)	28	56
27	25	50/52 (96%)	47 (94%)	3 (6%)	17	41
28	16	51/52 (98%)	48 (94%)	3 (6%)	18	42
28	26	50/52 (96%)	44 (88%)	6 (12%)	5	12
29	17	41/42 (98%)	39 (95%)	2 (5%)	22	49
29	27	41/42 (98%)	36 (88%)	5 (12%)	5	12
30	18	54/55 (98%)	51 (94%)	3 (6%)	19	44
30	28	54/55 (98%)	52 (96%)	2 (4%)	30	59
31	19	34/34 (100%)	33 (97%)	1 (3%)	37	67
31	29	34/34 (100%)	32 (94%)	2 (6%)	18	42
33	1b	192/220 (87%)	161 (84%)	31 (16%)	2	6
33	2b	187/220 (85%)	161 (86%)	26 (14%)	3	9
34	1c	142/188 (76%)	128 (90%)	14 (10%)	7	19
34	2c	140/188 (74%)	131 (94%)	9 (6%)	16	38
35	1d	169/181 (93%)	156 (92%)	13 (8%)	12	30
35	2d	173/181 (96%)	158 (91%)	15 (9%)	9	24
36	1e	113/123 (92%)	105 (93%)	8 (7%)	13	33

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
36	2e	114/123 (93%)	105 (92%)	9 (8%)	11	28
37	1f	84/90 (93%)	78 (93%)	6 (7%)	13	33
37	2f	85/90 (94%)	76 (89%)	9 (11%)	6	17
38	1g	119/127 (94%)	106 (89%)	13 (11%)	6	16
38	2g	120/127 (94%)	111 (92%)	9 (8%)	12	31
39	1h	114/119 (96%)	106 (93%)	8 (7%)	14	34
39	2h	114/119 (96%)	106 (93%)	8 (7%)	14	34
40	1i	90/99 (91%)	81 (90%)	9 (10%)	7	19
40	2i	89/99 (90%)	80 (90%)	9 (10%)	7	18
41	1j	66/92 (72%)	55 (83%)	11 (17%)	2	6
41	2j	69/92 (75%)	58 (84%)	11 (16%)	2	7
42	1k	82/99 (83%)	73 (89%)	9 (11%)	6	15
42	2k	83/99 (84%)	78 (94%)	5 (6%)	17	41
43	1l	96/108 (89%)	86 (90%)	10 (10%)	7	17
43	2l	96/108 (89%)	83 (86%)	13 (14%)	4	9
44	1m	89/101 (88%)	78 (88%)	11 (12%)	4	11
44	2m	88/101 (87%)	79 (90%)	9 (10%)	7	18
45	1n	49/50 (98%)	42 (86%)	7 (14%)	3	8
45	2n	49/50 (98%)	46 (94%)	3 (6%)	17	40
46	1o	78/80 (98%)	72 (92%)	6 (8%)	12	30
46	2o	78/80 (98%)	73 (94%)	5 (6%)	16	38
47	1p	69/74 (93%)	61 (88%)	8 (12%)	5	13
47	2p	68/74 (92%)	59 (87%)	9 (13%)	4	10
48	1q	94/97 (97%)	84 (89%)	10 (11%)	6	17
48	2q	94/97 (97%)	89 (95%)	5 (5%)	20	46
49	1r	59/77 (77%)	51 (86%)	8 (14%)	3	9
49	2r	59/77 (77%)	54 (92%)	5 (8%)	10	25
50	1s	69/80 (86%)	61 (88%)	8 (12%)	5	13
50	2s	67/80 (84%)	59 (88%)	8 (12%)	5	13
51	1t	70/82 (85%)	68 (97%)	2 (3%)	37	67
51	2t	70/82 (85%)	66 (94%)	4 (6%)	18	43

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
52	1u	18/22 (82%)	18 (100%)	0	100	100
52	2u	18/22 (82%)	17 (94%)	1 (6%)	19	44
54	1w	204/299 (68%)	177 (87%)	27 (13%)	4	10
54	2w	204/299 (68%)	175 (86%)	29 (14%)	3	8
56	1z	2/3 (67%)	2 (100%)	0	100	100
56	2z	2/3 (67%)	2 (100%)	0	100	100
All	All	9699/10668 (91%)	8861 (91%)	838 (9%)	10	25

All (838) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	1D	3	VAL
3	1D	71	ASP
3	1D	105	ILE
3	1D	106	ILE
3	1D	113	VAL
3	1D	155	LEU
3	1D	183	ARG
3	1D	200	ASP
3	1D	229	VAL
3	1D	259	THR
4	1E	21	VAL
4	1E	41	LYS
4	1E	45	THR
4	1E	75	VAL
4	1E	89	ASP
4	1E	93	VAL
4	1E	94	GLU
4	1E	116	VAL
4	1E	170	LEU
4	1E	175	VAL
4	1E	182	LEU
4	1E	188	VAL
5	1F	18	ARG
5	1F	24	LEU
5	1F	28	ILE
5	1F	33	LEU
5	1F	53	THR
5	1F	57	VAL
5	1F	70	THR

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Mol	Chain	Res	Type
5	1F	72	ARG
5	1F	74	ARG
5	1F	127	GLU
5	1F	140	LEU
5	1F	157	VAL
5	1F	162	LEU
5	1F	173	VAL
5	1F	183	VAL
5	1F	192	LEU
5	1F	201	VAL
5	1F	205	ARG
6	1G	3	LEU
6	1G	28	VAL
6	1G	31	VAL
6	1G	41	GLN
6	1G	43	LEU
6	1G	66	GLN
6	1G	79	ASN
6	1G	133	LEU
6	1G	139	LEU
6	1G	140	ILE
6	1G	148	MET
6	1G	159	VAL
6	1G	161	THR
6	1G	162	THR
7	1H	24	VAL
7	1H	45	VAL
7	1H	47	GLU
7	1H	84	SER
7	1H	116	GLU
7	1H	119	GLU
7	1H	149	ARG
7	1H	153	LYS
8	1I	7	GLU
8	1I	41	GLU
8	1I	75	LEU
8	1I	78	THR
8	1I	87	LYS
8	1I	92	VAL
8	1I	120	ILE
8	1I	125	GLU
8	1I	139	GLN

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Mol	Chain	Res	Type
8	1I	140	LEU
8	1I	144	VAL
9	1N	1	MET
9	1N	8	GLN
9	1N	9	VAL
9	1N	28	THR
9	1N	34	LEU
9	1N	65	LYS
9	1N	87	LEU
9	1N	121	LYS
9	1N	137	LYS
9	1N	140	VAL
10	1O	22	ILE
10	1O	52	VAL
11	1P	15	ARG
11	1P	75	ILE
11	1P	95	VAL
11	1P	98	GLU
11	1P	125	VAL
11	1P	147	LEU
11	1P	148	LEU
11	1P	149	GLU
12	1Q	7	MET
12	1Q	8	LYS
12	1Q	59	ARG
12	1Q	75	THR
13	1R	6	SER
13	1R	8	ARG
13	1R	29	LEU
13	1R	113	LEU
13	1R	114	VAL
14	1S	3	ARG
14	1S	36	TYR
14	1S	46	VAL
14	1S	50	SER
14	1S	68	GLN
14	1S	76	LYS
14	1S	80	LEU
14	1S	83	LYS
14	1S	85	VAL
14	1S	93	LYS
15	1T	6	LEU

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Mol	Chain	Res	Type
15	1T	21	GLU
15	1T	23	ARG
15	1T	28	VAL
15	1T	36	GLU
15	1T	66	VAL
15	1T	96	ARG
15	1T	118	ARG
15	1T	128	GLU
16	1U	8	VAL
16	1U	74	LEU
16	1U	77	SER
16	1U	95	LEU
16	1U	108	GLU
17	1V	28	GLU
17	1V	46	VAL
17	1V	79	VAL
18	1W	4	LYS
18	1W	11	ARG
18	1W	17	VAL
19	1X	2	LYS
19	1X	92	LEU
20	1Y	21	LYS
20	1Y	40	GLU
20	1Y	67	LEU
20	1Y	70	SER
20	1Y	72	VAL
20	1Y	98	VAL
20	1Y	99	CYS
21	1Z	49	ARG
21	1Z	50	GLN
21	1Z	61	LEU
21	1Z	74	VAL
21	1Z	78	LYS
21	1Z	80	ARG
21	1Z	86	VAL
21	1Z	91	LEU
21	1Z	121	HIS
21	1Z	139	VAL
21	1Z	140	ASP
21	1Z	146	ILE
21	1Z	149	SER
21	1Z	161	VAL

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Mol	Chain	Res	Type
23	11	40	ARG
23	11	46	LEU
23	11	76	ARG
24	12	19	VAL
24	12	53	LEU
24	12	70	GLN
25	13	3	ARG
25	13	6	VAL
25	13	37	LEU
25	13	40	THR
25	13	54	VAL
25	13	56	VAL
25	13	57	GLU
25	13	58	VAL
26	14	14	ILE
26	14	27	THR
26	14	49	PHE
26	14	50	VAL
26	14	52	THR
26	14	58	ARG
26	14	61	ARG
27	15	6	VAL
27	15	60	VAL
28	16	9	LEU
28	16	48	VAL
28	16	52	VAL
29	17	43	THR
29	17	46	VAL
30	18	14	VAL
30	18	29	LYS
30	18	58	ILE
31	19	4	ARG
33	1b	7	VAL
33	1b	12	GLU
33	1b	15	VAL
33	1b	17	PHE
33	1b	19	HIS
33	1b	21	ARG
33	1b	22	LYS
33	1b	23	ARG
33	1b	41	ILE
33	1b	44	LEU

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Mol	Chain	Res	Type
33	1b	61	LEU
33	1b	67	THR
33	1b	71	VAL
33	1b	80	ILE
33	1b	107	THR
33	1b	108	ILE
33	1b	111	ARG
33	1b	137	ARG
33	1b	156	LYS
33	1b	157	ARG
33	1b	172	ILE
33	1b	185	ILE
33	1b	187	LEU
33	1b	189	ASP
33	1b	205	ASP
33	1b	208	ILE
33	1b	215	LEU
33	1b	223	ILE
33	1b	224	GLN
33	1b	226	ARG
33	1b	236	TYR
34	1c	3	ASN
34	1c	14	ILE
34	1c	26	LYS
34	1c	28	GLN
34	1c	36	ASP
34	1c	40	ARG
34	1c	64	VAL
34	1c	66	VAL
34	1c	120	VAL
34	1c	123	GLN
34	1c	151	VAL
34	1c	192	THR
34	1c	196	LEU
34	1c	207	VAL
35	1d	5	ILE
35	1d	8	VAL
35	1d	19	LEU
35	1d	31	CYS
35	1d	34	GLU
35	1d	70	ILE
35	1d	85	LYS

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Mol	Chain	Res	Type
35	1d	108	LEU
35	1d	135	LEU
35	1d	155	LEU
35	1d	160	GLN
35	1d	187	ARG
35	1d	201	GLN
36	1e	41	VAL
36	1e	55	VAL
36	1e	65	ASN
36	1e	79	GLU
36	1e	100	VAL
36	1e	120	THR
36	1e	131	ILE
36	1e	151	LEU
37	1f	40	VAL
37	1f	45	LEU
37	1f	55	ASP
37	1f	61	LEU
37	1f	63	TYR
37	1f	72	VAL
38	1g	13	GLN
38	1g	30	ILE
38	1g	38	LEU
38	1g	52	GLU
38	1g	61	VAL
38	1g	66	VAL
38	1g	76	ARG
38	1g	80	VAL
38	1g	86	GLN
38	1g	90	GLU
38	1g	104	LEU
38	1g	124	LEU
38	1g	156	TRP
39	1h	2	LEU
39	1h	19	VAL
39	1h	63	LEU
39	1h	103	VAL
39	1h	120	THR
39	1h	127	LEU
39	1h	133	LEU
39	1h	137	VAL
40	1i	9	ARG

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Mol	Chain	Res	Type
40	1i	17	VAL
40	1i	23	ASN
40	1i	42	ARG
40	1i	47	LEU
40	1i	54	ASP
40	1i	65	VAL
40	1i	74	ILE
40	1i	128	ARG
41	1j	8	LEU
41	1j	19	SER
41	1j	38	ILE
41	1j	42	THR
41	1j	49	VAL
41	1j	62	HIS
41	1j	64	GLU
41	1j	66	ARG
41	1j	72	VAL
41	1j	81	THR
41	1j	92	THR
42	1k	33	THR
42	1k	43	SER
42	1k	51	LYS
42	1k	84	VAL
42	1k	87	THR
42	1k	93	GLN
42	1k	96	ARG
42	1k	109	VAL
42	1k	117	ASN
43	1l	18	VAL
43	1l	22	SER
43	1l	43	VAL
43	1l	46	LYS
43	1l	62	SER
43	1l	67	THR
43	1l	78	GLN
43	1l	85	ILE
43	1l	104	VAL
43	1l	118	SER
44	1m	12	ASN
44	1m	14	ARG
44	1m	43	THR
44	1m	50	GLU

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Mol	Chain	Res	Type
44	1m	56	LEU
44	1m	63	THR
44	1m	92	HIS
44	1m	98	VAL
44	1m	103	THR
44	1m	109	THR
44	1m	117	VAL
45	1n	3	ARG
45	1n	4	LYS
45	1n	7	ILE
45	1n	13	THR
45	1n	18	VAL
45	1n	25	VAL
45	1n	33	VAL
46	1o	3	ILE
46	1o	39	LEU
46	1o	45	VAL
46	1o	47	LYS
46	1o	66	LEU
46	1o	87	ILE
47	1p	1	MET
47	1p	8	ARG
47	1p	16	HIS
47	1p	20	VAL
47	1p	21	VAL
47	1p	22	THR
47	1p	45	THR
47	1p	49	LEU
48	1q	15	MET
48	1q	34	LYS
48	1q	36	ILE
48	1q	39	SER
48	1q	41	LYS
48	1q	43	LEU
48	1q	63	ARG
48	1q	66	SER
48	1q	73	VAL
48	1q	89	LEU
49	1r	25	THR
49	1r	38	GLU
49	1r	39	VAL
49	1r	49	LYS

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Mol	Chain	Res	Type
49	1r	63	GLN
49	1r	65	ILE
49	1r	68	LYS
49	1r	85	LEU
50	1s	15	LEU
50	1s	28	LYS
50	1s	49	ILE
50	1s	62	ILE
50	1s	63	THR
50	1s	66	MET
50	1s	77	THR
50	1s	83	HIS
51	1t	18	GLN
51	1t	24	LEU
54	1w	108	ILE
54	1w	119	GLU
54	1w	125	ARG
54	1w	152	LEU
54	1w	156	SER
54	1w	158	VAL
54	1w	181	GLN
54	1w	185	VAL
54	1w	189	GLN
54	1w	196	THR
54	1w	198	THR
54	1w	206	GLU
54	1w	207	GLU
54	1w	208	GLU
54	1w	216	GLU
54	1w	223	ARG
54	1w	293	ILE
54	1w	295	THR
54	1w	298	ARG
54	1w	299	SER
54	1w	302	ILE
54	1w	315	HIS
54	1w	320	THR
54	1w	321	THR
54	1w	333	THR
54	1w	339	LEU
54	1w	343	ASP
3	2D	3	VAL

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Mol	Chain	Res	Type
3	2D	12	SER
3	2D	18	VAL
3	2D	20	ASP
3	2D	89	SER
3	2D	99	ASP
3	2D	113	VAL
3	2D	173	VAL
3	2D	183	ARG
3	2D	200	ASP
3	2D	229	VAL
3	2D	259	THR
4	2E	11	MET
4	2E	38	THR
4	2E	75	VAL
4	2E	107	THR
4	2E	116	VAL
4	2E	182	LEU
5	2F	19	GLU
5	2F	33	LEU
5	2F	57	VAL
5	2F	60	SER
5	2F	62	ARG
5	2F	70	THR
5	2F	74	ARG
5	2F	132	VAL
5	2F	158	THR
5	2F	161	GLU
5	2F	162	LEU
5	2F	175	THR
5	2F	183	VAL
5	2F	197	ASP
5	2F	201	VAL
5	2F	203	GLN
6	2G	5	VAL
6	2G	26	GLN
6	2G	31	VAL
6	2G	36	LYS
6	2G	60	LEU
6	2G	70	VAL
6	2G	75	LYS
6	2G	88	ILE
6	2G	90	LEU

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Mol	Chain	Res	Type
6	2G	91	ARG
6	2G	94	LEU
6	2G	109	VAL
6	2G	113	ARG
6	2G	124	SER
6	2G	135	LEU
6	2G	139	LEU
6	2G	140	ILE
6	2G	159	VAL
6	2G	162	THR
6	2G	165	THR
7	2H	6	ARG
7	2H	24	VAL
7	2H	32	GLU
7	2H	47	GLU
7	2H	49	VAL
7	2H	63	SER
7	2H	68	THR
7	2H	103	LEU
7	2H	114	VAL
7	2H	122	THR
7	2H	127	GLU
7	2H	134	SER
7	2H	175	LYS
8	2I	7	GLU
8	2I	18	VAL
8	2I	20	ASP
8	2I	38	LEU
8	2I	44	LEU
8	2I	47	LEU
8	2I	51	ILE
8	2I	58	LEU
8	2I	61	ARG
8	2I	68	LEU
8	2I	75	LEU
8	2I	77	LEU
8	2I	78	THR
8	2I	79	ILE
8	2I	86	THR
8	2I	87	LYS
8	2I	114	LEU
8	2I	127	VAL

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Mol	Chain	Res	Type
8	2I	133	HIS
8	2I	144	VAL
9	2N	10	GLU
9	2N	14	VAL
9	2N	28	THR
9	2N	34	LEU
9	2N	43	THR
9	2N	48	MET
9	2N	61	ARG
9	2N	62	VAL
9	2N	87	LEU
9	2N	89	LYS
10	2O	52	VAL
10	2O	78	ARG
11	2P	58	THR
11	2P	70	GLN
11	2P	71	VAL
11	2P	95	VAL
11	2P	96	THR
11	2P	98	GLU
11	2P	124	LYS
11	2P	133	SER
11	2P	138	LEU
11	2P	147	LEU
11	2P	149	GLU
12	2Q	38	GLU
12	2Q	59	ARG
12	2Q	75	THR
12	2Q	81	VAL
12	2Q	85	LYS
13	2R	29	LEU
13	2R	95	THR
13	2R	102	GLU
13	2R	114	VAL
13	2R	118	GLU
14	2S	4	LEU
14	2S	12	PHE
14	2S	21	THR
14	2S	23	ARG
14	2S	36	TYR
14	2S	48	LEU
14	2S	50	SER

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Mol	Chain	Res	Type
14	2S	69	VAL
14	2S	80	LEU
14	2S	85	VAL
14	2S	98	VAL
15	2T	6	LEU
15	2T	28	VAL
15	2T	33	LYS
15	2T	34	VAL
15	2T	40	THR
15	2T	75	ILE
15	2T	89	VAL
15	2T	118	ARG
15	2T	119	LYS
16	2U	8	VAL
16	2U	20	LEU
16	2U	70	ARG
16	2U	74	LEU
17	2V	7	THR
17	2V	15	GLU
17	2V	28	GLU
17	2V	32	THR
17	2V	46	VAL
17	2V	51	VAL
17	2V	53	GLU
17	2V	73	SER
17	2V	79	VAL
18	2W	11	ARG
18	2W	17	VAL
18	2W	60	ASN
18	2W	68	ARG
19	2X	83	VAL
19	2X	92	LEU
20	2Y	3	VAL
20	2Y	9	LYS
20	2Y	49	VAL
20	2Y	72	VAL
20	2Y	97	ARG
20	2Y	99	CYS
21	2Z	4	ARG
21	2Z	5	LEU
21	2Z	27	VAL
21	2Z	30	ASN

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Mol	Chain	Res	Type
21	2Z	33	LEU
21	2Z	36	LYS
21	2Z	42	VAL
21	2Z	50	GLN
21	2Z	60	GLU
21	2Z	70	LEU
21	2Z	71	VAL
21	2Z	72	ARG
21	2Z	91	LEU
21	2Z	121	HIS
21	2Z	123	ASP
21	2Z	126	VAL
21	2Z	128	VAL
21	2Z	132	ASN
21	2Z	154	ASP
21	2Z	174	VAL
22	20	10	THR
22	20	14	ARG
23	21	30	VAL
23	21	35	THR
23	21	40	ARG
23	21	46	LEU
23	21	53	VAL
23	21	74	VAL
24	22	10	LEU
24	22	19	VAL
24	22	35	LEU
24	22	40	SER
24	22	49	LYS
24	22	53	LEU
24	22	59	ARG
24	22	62	THR
24	22	65	ASN
24	22	66	GLU
24	22	67	LYS
25	23	31	LEU
25	23	34	GLU
25	23	54	VAL
25	23	59	VAL
26	24	3	GLU
26	24	49	PHE
26	24	50	VAL

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Mol	Chain	Res	Type
26	24	53	GLU
26	24	63	TYR
27	25	6	VAL
27	25	56	LYS
27	25	58	LEU
28	26	9	LEU
28	26	20	ASN
28	26	23	THR
28	26	32	ASN
28	26	48	VAL
28	26	52	VAL
29	27	1	MET
29	27	4	THR
29	27	32	LYS
29	27	41	ARG
29	27	43	THR
30	28	14	VAL
30	28	23	VAL
31	29	4	ARG
31	29	7	VAL
33	2b	7	VAL
33	2b	19	HIS
33	2b	44	LEU
33	2b	47	THR
33	2b	49	GLU
33	2b	67	THR
33	2b	71	VAL
33	2b	80	ILE
33	2b	87	ARG
33	2b	112	VAL
33	2b	118	LEU
33	2b	122	PHE
33	2b	124	SER
33	2b	127	ILE
33	2b	130	ARG
33	2b	136	VAL
33	2b	140	HIS
33	2b	185	ILE
33	2b	189	ASP
33	2b	193	ASP
33	2b	208	ILE
33	2b	215	LEU

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Mol	Chain	Res	Type
33	2b	224	GLN
33	2b	229	VAL
33	2b	230	VAL
33	2b	235	SER
34	2c	14	ILE
34	2c	17	ASP
34	2c	22	TRP
34	2c	36	ASP
34	2c	58	GLU
34	2c	102	ASN
34	2c	105	GLU
34	2c	130	VAL
34	2c	192	THR
35	2d	5	ILE
35	2d	28	SER
35	2d	34	GLU
35	2d	78	LEU
35	2d	96	LEU
35	2d	135	LEU
35	2d	140	VAL
35	2d	155	LEU
35	2d	158	ILE
35	2d	170	VAL
35	2d	175	SER
35	2d	178	VAL
35	2d	188	LEU
35	2d	194	LEU
35	2d	201	GLN
36	2e	6	PHE
36	2e	8	GLU
36	2e	51	VAL
36	2e	53	LEU
36	2e	75	THR
36	2e	76	ILE
36	2e	82	VAL
36	2e	83	GLU
36	2e	90	VAL
37	2f	23	LYS
37	2f	40	VAL
37	2f	43	LEU
37	2f	48	LEU
37	2f	63	TYR

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Mol	Chain	Res	Type
37	2f	69	GLU
37	2f	72	VAL
37	2f	94	GLN
37	2f	95	GLU
38	2g	9	VAL
38	2g	53	LYS
38	2g	70	LYS
38	2g	79	ARG
38	2g	86	GLN
38	2g	114	ARG
38	2g	120	ILE
38	2g	143	ARG
38	2g	144	MET
39	2h	19	VAL
39	2h	26	VAL
39	2h	63	LEU
39	2h	97	VAL
39	2h	105	ARG
39	2h	109	ILE
39	2h	120	THR
39	2h	133	LEU
40	2i	12	GLU
40	2i	35	GLU
40	2i	56	LEU
40	2i	64	THR
40	2i	74	ILE
40	2i	104	ARG
40	2i	108	VAL
40	2i	114	TYR
40	2i	124	GLN
41	2j	13	HIS
41	2j	34	VAL
41	2j	38	ILE
41	2j	43	ARG
41	2j	44	VAL
41	2j	47	PHE
41	2j	66	ARG
41	2j	71	LEU
41	2j	72	VAL
41	2j	97	GLU
41	2j	100	THR
42	2k	33	THR

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Mol	Chain	Res	Type
42	2k	73	MET
42	2k	80	VAL
42	2k	87	THR
42	2k	109	VAL
43	2l	11	VAL
43	2l	13	LYS
43	2l	18	VAL
43	2l	33	ARG
43	2l	34	ARG
43	2l	36	VAL
43	2l	39	VAL
43	2l	43	VAL
43	2l	46	LYS
43	2l	67	THR
43	2l	78	GLN
43	2l	102	ARG
43	2l	116	SER
44	2m	4	ILE
44	2m	32	GLU
44	2m	67	GLU
44	2m	70	LEU
44	2m	78	ILE
44	2m	96	LEU
44	2m	98	VAL
44	2m	106	ASN
44	2m	117	VAL
45	2n	4	LYS
45	2n	13	THR
45	2n	18	VAL
46	2o	5	LYS
46	2o	25	THR
46	2o	39	LEU
46	2o	66	LEU
46	2o	87	ILE
47	2p	1	MET
47	2p	2	VAL
47	2p	8	ARG
47	2p	16	HIS
47	2p	20	VAL
47	2p	21	VAL
47	2p	44	THR
47	2p	45	THR

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Mol	Chain	Res	Type
47	2p	62	VAL
48	2q	50	LYS
48	2q	53	LEU
48	2q	57	VAL
48	2q	65	ILE
48	2q	66	SER
49	2r	25	THR
49	2r	38	GLU
49	2r	45	SER
49	2r	68	LYS
49	2r	82	THR
50	2s	6	LYS
50	2s	38	SER
50	2s	43	GLU
50	2s	48	THR
50	2s	49	ILE
50	2s	51	VAL
50	2s	77	THR
50	2s	83	HIS
51	2t	9	ASN
51	2t	45	GLN
51	2t	55	ILE
51	2t	71	THR
52	2u	22	ARG
54	2w	103	ASP
54	2w	119	GLU
54	2w	129	ASN
54	2w	136	GLU
54	2w	143	GLU
54	2w	144	VAL
54	2w	147	SER
54	2w	151	ASP
54	2w	152	LEU
54	2w	158	VAL
54	2w	175	SER
54	2w	185	VAL
54	2w	196	THR
54	2w	201	VAL
54	2w	216	GLU
54	2w	250	VAL
54	2w	256	ARG
54	2w	262	ARG

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Mol	Chain	Res	Type
54	2w	267	MET
54	2w	268	ILE
54	2w	280	GLU
54	2w	299	SER
54	2w	320	THR
54	2w	324	LEU
54	2w	333	THR
54	2w	335	ILE
54	2w	337	GLU
54	2w	351	LEU
54	2w	353	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (148) such sidechains are listed below:

Mol	Chain	Res	Type
3	1D	115	GLN
3	1D	126	GLN
4	1E	143	ASN
5	1F	8	GLN
5	1F	69	HIS
5	1F	160	ASN
6	1G	26	GLN
6	1G	41	GLN
8	1I	54	GLN
8	1I	104	GLN
8	1I	105	HIS
8	1I	133	HIS
9	1N	94	HIS
9	1N	131	GLN
12	1Q	12	GLN
13	1R	24	GLN
14	1S	61	ASN
14	1S	84	GLN
15	1T	58	ASN
16	1U	94	ASN
19	1X	31	HIS
19	1X	82	GLN
20	1Y	6	HIS
21	1Z	73	GLN
22	10	35	ASN
26	14	46	GLN
30	18	35	GLN

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Mol	Chain	Res	Type
33	1b	16	HIS
33	1b	40	HIS
33	1b	78	GLN
33	1b	95	GLN
34	1c	98	ASN
34	1c	123	GLN
34	1c	170	GLN
34	1c	181	ASN
35	1d	77	ASN
35	1d	123	HIS
35	1d	125	HIS
35	1d	201	GLN
36	1e	65	ASN
36	1e	78	HIS
36	1e	141	GLN
37	1f	7	ASN
37	1f	57	GLN
37	1f	100	ASN
38	1g	28	ASN
38	1g	56	GLN
38	1g	109	ASN
38	1g	148	ASN
40	1i	23	ASN
40	1i	58	HIS
40	1i	73	GLN
40	1i	87	GLN
40	1i	124	GLN
41	1j	21	GLN
41	1j	56	HIS
41	1j	62	HIS
41	1j	69	ASN
42	1k	93	GLN
42	1k	116	HIS
43	1l	80	HIS
44	1m	92	HIS
44	1m	106	ASN
48	1q	26	GLN
48	1q	93	GLN
49	1r	63	GLN
50	1s	83	HIS
51	1t	9	ASN
51	1t	16	HIS

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Mol	Chain	Res	Type
51	1t	90	GLN
54	1w	129	ASN
54	1w	148	HIS
54	1w	181	GLN
54	1w	189	GLN
54	1w	230	GLN
54	1w	233	ASN
54	1w	309	GLN
54	1w	322	HIS
54	1w	347	GLN
3	2D	129	ASN
4	2E	48	GLN
4	2E	137	HIS
5	2F	69	HIS
6	2G	79	ASN
8	2I	43	ASN
9	2N	94	HIS
10	2O	3	GLN
10	2O	5	GLN
12	2Q	12	GLN
12	2Q	123	HIS
13	2R	24	GLN
13	2R	91	GLN
14	2S	68	GLN
15	2T	58	ASN
16	2U	94	ASN
19	2X	31	HIS
19	2X	82	GLN
20	2Y	6	HIS
21	2Z	34	ASN
21	2Z	50	GLN
21	2Z	73	GLN
21	2Z	132	ASN
24	22	56	GLN
26	24	40	HIS
26	24	46	GLN
28	26	20	ASN
33	2b	16	HIS
33	2b	224	GLN
34	2c	108	ASN
34	2c	123	GLN
34	2c	139	GLN

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Mol	Chain	Res	Type
34	2c	170	GLN
34	2c	176	HIS
34	2c	181	ASN
35	2d	45	GLN
35	2d	77	ASN
35	2d	116	GLN
35	2d	123	HIS
35	2d	161	ASN
35	2d	201	GLN
36	2e	20	GLN
37	2f	7	ASN
37	2f	100	ASN
38	2g	68	ASN
38	2g	86	GLN
38	2g	97	GLN
38	2g	109	ASN
40	2i	3	GLN
40	2i	89	ASN
41	2j	56	HIS
42	2k	99	GLN
43	2l	80	HIS
43	2l	99	HIS
44	2m	77	ASN
46	2o	9	GLN
46	2o	62	GLN
47	2p	13	HIS
48	2q	93	GLN
49	2r	63	GLN
50	2s	23	ASN
50	2s	47	HIS
50	2s	65	ASN
50	2s	69	HIS
50	2s	83	HIS
51	2t	75	ASN
54	2w	148	HIS
54	2w	193	HIS
54	2w	315	HIS

5.3.3 RNA ⓘ

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1A	2864/2915 (98%)	444 (15%)	30 (1%)
1	2A	2791/2915 (95%)	439 (15%)	23 (0%)
2	1B	119/121 (98%)	12 (10%)	0
2	2B	118/121 (97%)	18 (15%)	0
32	1a	1497/1521 (98%)	276 (18%)	0
32	2a	1501/1521 (98%)	299 (19%)	0
53	1v	10/24 (41%)	5 (50%)	0
53	2v	6/24 (25%)	2 (33%)	0
55	1x	72/74 (97%)	14 (19%)	0
55	2x	72/74 (97%)	12 (16%)	0
All	All	9050/9310 (97%)	1521 (16%)	53 (0%)

All (1521) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1A	12	U
1	1A	15	G
1	1A	34	C
1	1A	36	G
1	1A	45	C
1	1A	55	G
1	1A	63	U
1	1A	71	A
1	1A	74	A
1	1A	75	G
1	1A	78	A
1	1A	84	A
1	1A	95	G
1	1A	118	A
1	1A	119	A
1	1A	120	U
1	1A	125	G
1	1A	139(A)	G
1	1A	196	A
1	1A	197	A
1	1A	199	A
1	1A	200	U
1	1A	205	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	225	A
1	1A	228	A
1	1A	229	A
1	1A	233	A
1	1A	248	G
1	1A	265	A
1	1A	271(K)	U
1	1A	271(L)	U
1	1A	271(M)	G
1	1A	271(S)	G
1	1A	272(B)	G
1	1A	275	G
1	1A	279	C
1	1A	311	A
1	1A	329	G
1	1A	330	A
1	1A	331	A
1	1A	352	G
1	1A	362	U
1	1A	363	G
1	1A	363(A)	A
1	1A	363(B)	G
1	1A	370	G
1	1A	380	U
1	1A	386	G
1	1A	389	G
1	1A	395	U
1	1A	396	G
1	1A	405	U
1	1A	411	G
1	1A	412	A
1	1A	421	U
1	1A	428	A
1	1A	442	G
1	1A	444	C
1	1A	448	U
1	1A	454	A
1	1A	457	A
1	1A	481	G
1	1A	494	G
1	1A	504	U

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Mol	Chain	Res	Type
1	1A	505	A
1	1A	509	C
1	1A	528	A
1	1A	529	A
1	1A	530	G
1	1A	531	C
1	1A	532	A
1	1A	533	G
1	1A	545	G
1	1A	549	G
1	1A	563	G
1	1A	573	G
1	1A	575	A
1	1A	603	A
1	1A	604	G
1	1A	607	U
1	1A	614(A)	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	648	G
1	1A	652(E)	G
1	1A	652(T)	C
1	1A	654	A
1	1A	669	G
1	1A	686	G
1	1A	717	G
1	1A	730	C
1	1A	775	G
1	1A	776	G
1	1A	782	A
1	1A	784	A
1	1A	785	G
1	1A	792	G
1	1A	802	A
1	1A	805	G
1	1A	812	C
1	1A	827	U
1	1A	828	U

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Mol	Chain	Res	Type
1	1A	859	G
1	1A	866	A
1	1A	878	A
1	1A	885	C
1	1A	886	C
1	1A	887	A
1	1A	888	C
1	1A	889	C
1	1A	890	A
1	1A	896	A
1	1A	897	C
1	1A	899	A
1	1A	907	U
1	1A	910	A
1	1A	932	G
1	1A	938	G
1	1A	945	A
1	1A	946	G
1	1A	961	C
1	1A	963	U
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	1022	G
1	1A	1026	U
1	1A	1033	U
1	1A	1039	G
1	1A	1040	C
1	1A	1041	C
1	1A	1045	A
1	1A	1046	A
1	1A	1047	G
1	1A	1054	A
1	1A	1055	G
1	1A	1056	G
1	1A	1057	A
1	1A	1058	G
1	1A	1059	G
1	1A	1060	U

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Mol	Chain	Res	Type
1	1A	1063	G
1	1A	1065	U
1	1A	1066	U
1	1A	1067	A
1	1A	1068	G
1	1A	1071	G
1	1A	1072	C
1	1A	1073	A
1	1A	1074	G
1	1A	1075	C
1	1A	1076	C
1	1A	1078	U
1	1A	1079	C
1	1A	1080	C
1	1A	1083	U
1	1A	1085	A
1	1A	1086	A
1	1A	1089	G
1	1A	1090	U
1	1A	1093	G
1	1A	1094	U
1	1A	1095	A
1	1A	1096	A
1	1A	1100	C
1	1A	1106	G
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	1141	U
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	1211	U
1	1A	1218	C

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Mol	Chain	Res	Type
1	1A	1220	A
1	1A	1241	A
1	1A	1253	A
1	1A	1256	G
1	1A	1271	G
1	1A	1272	A
1	1A	1273	U
1	1A	1275	A
1	1A	1300	U
1	1A	1301	A
1	1A	1303	G
1	1A	1321	A
1	1A	1352	U
1	1A	1359	A
1	1A	1360	A
1	1A	1365	A
1	1A	1370	C
1	1A	1380	G
1	1A	1384	A
1	1A	1385	G
1	1A	1416	G
1	1A	1417	C
1	1A	1420	U
1	1A	1421	G
1	1A	1428	C
1	1A	1437	C
1	1A	1445	A
1	1A	1450	G
1	1A	1453	U
1	1A	1455	G
1	1A	1467	C
1	1A	1482	G
1	1A	1490	A
1	1A	1493	C
1	1A	1497	U
1	1A	1508	A
1	1A	1509	C
1	1A	1509(A)	A
1	1A	1541	G
1	1A	1543	C
1	1A	1558	A
1	1A	1566	A

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Mol	Chain	Res	Type
1	1A	1569	A
1	1A	1578	U
1	1A	1580	A
1	1A	1581	G
1	1A	1584	C
1	1A	1586	A
1	1A	1607	C
1	1A	1608	A
1	1A	1609	A
1	1A	1610	A
1	1A	1648	C
1	1A	1654	A
1	1A	1674	G
1	1A	1696	G
1	1A	1700	A
1	1A	1701	A
1	1A	1703	G
1	1A	1722	A
1	1A	1739	U
1	1A	1740	G
1	1A	1756	G
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	1811	G
1	1A	1812	A
1	1A	1816	G
1	1A	1828	G
1	1A	1829	A
1	1A	1847	A
1	1A	1878	G
1	1A	1889	A
1	1A	1900	A
1	1A	1906	G
1	1A	1914	C
1	1A	1929	G
1	1A	1930	G

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Mol	Chain	Res	Type
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	1992	G
1	1A	1993	U
1	1A	1997	G
1	1A	2020	A
1	1A	2023	G
1	1A	2031	A
1	1A	2033	A
1	1A	2039	C
1	1A	2043	C
1	1A	2055	C
1	1A	2056	G
1	1A	2057	A
1	1A	2060	A
1	1A	2061	G
1	1A	2069	G
1	1A	2100	G
1	1A	2102	U
1	1A	2104	G
1	1A	2105	C
1	1A	2106	G
1	1A	2108	C
1	1A	2112	G
1	1A	2113	U
1	1A	2115	G
1	1A	2116	G
1	1A	2117	A
1	1A	2119	A
1	1A	2120	G
1	1A	2122	U
1	1A	2123	G
1	1A	2124	G
1	1A	2126	A
1	1A	2127	G

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Mol	Chain	Res	Type
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	2144	U
1	1A	2146	C
1	1A	2147	G
1	1A	2150	U
1	1A	2151	G
1	1A	2154	G
1	1A	2156	G
1	1A	2157	G
1	1A	2158	A
1	1A	2162	G
1	1A	2163	C
1	1A	2165	G
1	1A	2166	G
1	1A	2168	G
1	1A	2169	A
1	1A	2170	A
1	1A	2171	A
1	1A	2172	U
1	1A	2173	A
1	1A	2175	C
1	1A	2176	A
1	1A	2182	G
1	1A	2184	G
1	1A	2188	C
1	1A	2198	A
1	1A	2206	G
1	1A	2207	G
1	1A	2208	A
1	1A	2225	A
1	1A	2238	G
1	1A	2239	G
1	1A	2268	A
1	1A	2280	G
1	1A	2283	C

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Mol	Chain	Res	Type
1	1A	2287	A
1	1A	2305	A
1	1A	2308	G
1	1A	2318	G
1	1A	2320	A
1	1A	2325	G
1	1A	2327	A
1	1A	2334	G
1	1A	2336	A
1	1A	2347	C
1	1A	2350	C
1	1A	2372	G
1	1A	2383	G
1	1A	2385	C
1	1A	2400	G
1	1A	2406	U
1	1A	2410	G
1	1A	2422	A
1	1A	2423	U
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	2441	C
1	1A	2448	A
1	1A	2468	G
1	1A	2476	A
1	1A	2478	A
1	1A	2502	G
1	1A	2505	G
1	1A	2506	U
1	1A	2518	A
1	1A	2525	G
1	1A	2529	G
1	1A	2535	G
1	1A	2549	G
1	1A	2554	U
1	1A	2566	A
1	1A	2567	G
1	1A	2573	C

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Mol	Chain	Res	Type
1	1A	2574	G
1	1A	2602	A
1	1A	2609	U
1	1A	2611	U
1	1A	2612	C
1	1A	2615	U
1	1A	2629	A
1	1A	2630	G
1	1A	2654	A
1	1A	2663	G
1	1A	2689	U
1	1A	2690	C
1	1A	2691	C
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	2757	A
1	1A	2764	A
1	1A	2765	A
1	1A	2778	A
1	1A	2780	G
1	1A	2790	A
1	1A	2791	C
1	1A	2794	C
1	1A	2802	G
1	1A	2805	G
1	1A	2807	G
1	1A	2820	A
1	1A	2821	A
1	1A	2833	G
1	1A	2835	A
1	1A	2836	U
1	1A	2872	G
1	1A	2880	C
1	1A	2892	A
1	1A	2894	G
1	1A	2895	U
2	1B	13	A
2	1B	15	A

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Mol	Chain	Res	Type
2	1B	25	A
2	1B	42	C
2	1B	45	A
2	1B	52	A
2	1B	56	G
2	1B	67	G
2	1B	73	A
2	1B	85	G
2	1B	106	G
2	1B	110	G
32	1a	5	U
32	1a	7	G
32	1a	9	G
32	1a	22	G
32	1a	31	G
32	1a	32	A
32	1a	39	G
32	1a	47	C
32	1a	48	C
32	1a	50	A
32	1a	51	A
32	1a	61	G
32	1a	65	U
32	1a	76	C
32	1a	78	G
32	1a	79	G
32	1a	91	C
32	1a	98	G
32	1a	101	A
32	1a	105	G
32	1a	116	A
32	1a	121	C
32	1a	131	C
32	1a	143	A
32	1a	144	G
32	1a	146	G
32	1a	163	C
32	1a	174	C
32	1a	182	U
32	1a	189(E)	U
32	1a	189(G)	G
32	1a	189(H)	G

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Mol	Chain	Res	Type
32	1a	195	A
32	1a	196	A
32	1a	197	A
32	1a	202	U
32	1a	204	U
32	1a	216	G
32	1a	222	U
32	1a	247	G
32	1a	251	G
32	1a	266	G
32	1a	267	C
32	1a	289	G
32	1a	301	G
32	1a	321	A
32	1a	324	G
32	1a	328	C
32	1a	329	A
32	1a	332	G
32	1a	347	G
32	1a	350	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	398	C
32	1a	406	G
32	1a	412	A
32	1a	413	G
32	1a	421	U
32	1a	423	G
32	1a	424	G
32	1a	429	U
32	1a	439	A
32	1a	442	C
32	1a	444	C
32	1a	445	G
32	1a	452	A

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Mol	Chain	Res	Type
32	1a	458	C
32	1a	461	A
32	1a	470	C
32	1a	474	G
32	1a	475	G
32	1a	485	G
32	1a	492	G
32	1a	496	A
32	1a	498	U
32	1a	505	G
32	1a	509	A
32	1a	510	A
32	1a	511	C
32	1a	518	C
32	1a	521	G
32	1a	524	G
32	1a	532	A
32	1a	547	A
32	1a	559	A
32	1a	561	U
32	1a	572	A
32	1a	573	A
32	1a	576	G
32	1a	577	G
32	1a	592	G
32	1a	596	C
32	1a	616	G
32	1a	618	C
32	1a	630	G
32	1a	631	G
32	1a	639	G
32	1a	650	G
32	1a	653	A
32	1a	665	A
32	1a	666	G
32	1a	673	G
32	1a	687	A
32	1a	688	G
32	1a	695	A
32	1a	702	A
32	1a	703	G
32	1a	723	U

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Mol	Chain	Res	Type
32	1a	749	C
32	1a	755	G
32	1a	777	A
32	1a	792	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	840	C
32	1a	841	U
32	1a	851	G
32	1a	853	G
32	1a	859	A
32	1a	870	U
32	1a	872	A
32	1a	885	G
32	1a	902	G
32	1a	913	A
32	1a	914	A
32	1a	926	G
32	1a	927	G
32	1a	934	C
32	1a	960	U
32	1a	961	U
32	1a	968	A
32	1a	969	A
32	1a	971	G
32	1a	975	A
32	1a	976	G
32	1a	977	A
32	1a	978	A
32	1a	982	U
32	1a	983	A
32	1a	991	U
32	1a	992	U
32	1a	993	G
32	1a	994	A
32	1a	997	U
32	1a	1000	U
32	1a	1003	G

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Mol	Chain	Res	Type
32	1a	1005	A
32	1a	1006	C
32	1a	1020	U
32	1a	1022	G
32	1a	1023	G
32	1a	1026	G
32	1a	1027	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	1031	G
32	1a	1032	G
32	1a	1033	G
32	1a	1035	A
32	1a	1036	G
32	1a	1038	C
32	1a	1042	G
32	1a	1043	C
32	1a	1044	A
32	1a	1045	C
32	1a	1050	G
32	1a	1053	G
32	1a	1054	C
32	1a	1065	U
32	1a	1066	C
32	1a	1068	G
32	1a	1081	G
32	1a	1086	U
32	1a	1088	G
32	1a	1094	G
32	1a	1095	U
32	1a	1101	A
32	1a	1122	U
32	1a	1123	A
32	1a	1125	U
32	1a	1126	U
32	1a	1132	C
32	1a	1134	G
32	1a	1136	U

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Mol	Chain	Res	Type
32	1a	1137	C
32	1a	1139	G
32	1a	1146	A
32	1a	1152	A
32	1a	1154	G
32	1a	1159	U
32	1a	1160	G
32	1a	1161	C
32	1a	1162	C
32	1a	1184	G
32	1a	1186	G
32	1a	1191	A
32	1a	1196	U
32	1a	1197	G
32	1a	1201	A
32	1a	1202	G
32	1a	1204	A
32	1a	1212	U
32	1a	1213	A
32	1a	1217	C
32	1a	1226	C
32	1a	1227	A
32	1a	1236	A
32	1a	1238	A
32	1a	1256	A
32	1a	1257	U
32	1a	1258	G
32	1a	1260	C
32	1a	1270	C
32	1a	1275	A
32	1a	1278	U
32	1a	1279	A
32	1a	1280	A
32	1a	1286	A
32	1a	1287	A
32	1a	1298	C
32	1a	1299	A
32	1a	1300	G
32	1a	1302	U
32	1a	1320	C
32	1a	1322	C
32	1a	1323	G

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Mol	Chain	Res	Type
32	1a	1340	A
32	1a	1346	A
32	1a	1347	G
32	1a	1353	G
32	1a	1363	C
32	1a	1363(A)	A
32	1a	1364	U
32	1a	1369	C
32	1a	1370	G
32	1a	1381	U
32	1a	1397	C
32	1a	1398	A
32	1a	1419	G
32	1a	1422	G
32	1a	1442	G
32	1a	1442(A)	G
32	1a	1442(B)	A
32	1a	1447	A
32	1a	1452	C
32	1a	1456	G
32	1a	1457	G
32	1a	1487	G
32	1a	1493	A
32	1a	1494	G
32	1a	1497	G
32	1a	1503	A
32	1a	1504	G
32	1a	1506	U
32	1a	1517	G
32	1a	1519	MA6
32	1a	1529	G
32	1a	1530	G
32	1a	1531	A
32	1a	1532	U
53	1v	11	U
53	1v	12	A
53	1v	13	A
53	1v	14	A
53	1v	22	U
55	1x	6	G
55	1x	9	A
55	1x	18	G

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Mol	Chain	Res	Type
55	1x	19	G
55	1x	20	H2U
55	1x	21	H2U
55	1x	22	A
55	1x	30	G
55	1x	37	MIA
55	1x	45	U
55	1x	46	A
55	1x	48	G
55	1x	49	U
55	1x	75	C
1	2A	8	A
1	2A	11	G
1	2A	12	U
1	2A	15	G
1	2A	34	C
1	2A	35	G
1	2A	45	C
1	2A	71	A
1	2A	74	A
1	2A	75	G
1	2A	77	C
1	2A	78	A
1	2A	79	G
1	2A	84	A
1	2A	90	U
1	2A	95	G
1	2A	100	G
1	2A	118	A
1	2A	119	A
1	2A	120	U
1	2A	141	A
1	2A	154(A)	C
1	2A	157	U
1	2A	181	A
1	2A	196	A
1	2A	197	A
1	2A	200	U
1	2A	205	G
1	2A	215	G
1	2A	216	A
1	2A	221	A

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Mol	Chain	Res	Type
1	2A	222	A
1	2A	225	A
1	2A	228	A
1	2A	229	A
1	2A	248	G
1	2A	249	C
1	2A	250	G
1	2A	271(G)	C
1	2A	271(J)	C
1	2A	271(K)	U
1	2A	271(L)	U
1	2A	271(M)	G
1	2A	271(O)	C
1	2A	271(U)	G
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	352	G
1	2A	362	U
1	2A	372	G
1	2A	386	G
1	2A	396	G
1	2A	405	U
1	2A	407	G
1	2A	411	G
1	2A	412	A
1	2A	435	C
1	2A	443	A
1	2A	444	C
1	2A	455	C
1	2A	456	C
1	2A	457	A
1	2A	481	G
1	2A	504	U
1	2A	505	A
1	2A	509	C

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Mol	Chain	Res	Type
1	2A	529	A
1	2A	530	G
1	2A	531	C
1	2A	532	A
1	2A	533	G
1	2A	551	G
1	2A	563	G
1	2A	573	G
1	2A	575	A
1	2A	586	A
1	2A	592	G
1	2A	603	A
1	2A	604	G
1	2A	607	U
1	2A	615	G
1	2A	627	A
1	2A	637	A
1	2A	645	C
1	2A	651	G
1	2A	652(A)	A
1	2A	652(B)	A
1	2A	652(U)	G
1	2A	653	A
1	2A	669	G
1	2A	686	G
1	2A	717	G
1	2A	730	C
1	2A	752	A
1	2A	753	C
1	2A	764	A
1	2A	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	819	A
1	2A	827	U
1	2A	828	U
1	2A	833	U

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Mol	Chain	Res	Type
1	2A	857	C
1	2A	859	G
1	2A	874	G
1	2A	878	A
1	2A	884	C
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	894	C
1	2A	895	U
1	2A	896	A
1	2A	898	C
1	2A	899	A
1	2A	900	A
1	2A	901	A
1	2A	910	A
1	2A	917	A
1	2A	932	G
1	2A	938	G
1	2A	941	A
1	2A	945	A
1	2A	946	G
1	2A	953	A
1	2A	959	A
1	2A	961	C
1	2A	968	G
1	2A	974	G
1	2A	975	C
1	2A	983	A
1	2A	996	A
1	2A	1006	C
1	2A	1012	U
1	2A	1013	C
1	2A	1022	G
1	2A	1026	U
1	2A	1030	G
1	2A	1033	U
1	2A	1039	G
1	2A	1040	C

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Mol	Chain	Res	Type
1	2A	1043	C
1	2A	1114	G
1	2A	1115	G
1	2A	1128	A
1	2A	1129	A
1	2A	1130	U
1	2A	1135	C
1	2A	1136	G
1	2A	1139	G
1	2A	1142(A)	A
1	2A	1205	U
1	2A	1210	A
1	2A	1211	U
1	2A	1220	A
1	2A	1249	U
1	2A	1253	A
1	2A	1256	G
1	2A	1271	G
1	2A	1272	A
1	2A	1273	U
1	2A	1300	U
1	2A	1301	A
1	2A	1314	C
1	2A	1352	U
1	2A	1359	A
1	2A	1360	A
1	2A	1365	A
1	2A	1370	C
1	2A	1380	G
1	2A	1384	A
1	2A	1385	G
1	2A	1400	G
1	2A	1416	G
1	2A	1417	C
1	2A	1419	A
1	2A	1420	U
1	2A	1421	G
1	2A	1428	C
1	2A	1435	G
1	2A	1437	C
1	2A	1445	A
1	2A	1449	A

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Mol	Chain	Res	Type
1	2A	1450	G
1	2A	1455	G
1	2A	1460	A
1	2A	1467	C
1	2A	1471	A
1	2A	1482	G
1	2A	1490	A
1	2A	1493	C
1	2A	1496	A
1	2A	1497	U
1	2A	1508	A
1	2A	1509(A)	A
1	2A	1531	C
1	2A	1532	C
1	2A	1543	C
1	2A	1545	A
1	2A	1547	C
1	2A	1558	A
1	2A	1566	A
1	2A	1569	A
1	2A	1578	U
1	2A	1580	A
1	2A	1583	A
1	2A	1584	C
1	2A	1586	A
1	2A	1587	A
1	2A	1608	A
1	2A	1609	A
1	2A	1613	G
1	2A	1640	C
1	2A	1647	G
1	2A	1648	C
1	2A	1654	A
1	2A	1674	G
1	2A	1700	A
1	2A	1721	G
1	2A	1722	A
1	2A	1746	G
1	2A	1756	G
1	2A	1762	A
1	2A	1763	G
1	2A	1764	G

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Mol	Chain	Res	Type
1	2A	1773	A
1	2A	1780	A
1	2A	1782	C
1	2A	1791	A
1	2A	1800	C
1	2A	1801	G
1	2A	1812	A
1	2A	1816	G
1	2A	1819	A
1	2A	1829	A
1	2A	1835	G
1	2A	1847	A
1	2A	1848	A
1	2A	1878	G
1	2A	1880	C
1	2A	1900	A
1	2A	1906	G
1	2A	1914	C
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	1965	C
1	2A	1967	C
1	2A	1970	A
1	2A	1971	A
1	2A	1972	A
1	2A	1984	G
1	2A	1992	G
1	2A	1993	U
1	2A	1997	G
1	2A	2020	A
1	2A	2023	G
1	2A	2031	A
1	2A	2032	G
1	2A	2033	A
1	2A	2036	C
1	2A	2043	C
1	2A	2055	C
1	2A	2056	G

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Mol	Chain	Res	Type
1	2A	2060	A
1	2A	2061	G
1	2A	2062	A
1	2A	2069	G
1	2A	2105	C
1	2A	2108	C
1	2A	2111	C
1	2A	2113	U
1	2A	2114	A
1	2A	2116	G
1	2A	2117	A
1	2A	2120	G
1	2A	2122	U
1	2A	2126	A
1	2A	2127	G
1	2A	2128	C
1	2A	2129	C
1	2A	2130	U
1	2A	2131	G
1	2A	2132	U
1	2A	2133	G
1	2A	2134	A
1	2A	2135	A
1	2A	2136	C
1	2A	2138	C
1	2A	2139	C
1	2A	2142	C
1	2A	2146	C
1	2A	2148	G
1	2A	2150	U
1	2A	2153	G
1	2A	2154	G
1	2A	2155	G
1	2A	2156	G
1	2A	2157	G
1	2A	2158	A
1	2A	2161	C
1	2A	2162	G
1	2A	2165	G
1	2A	2166	G
1	2A	2167	U
1	2A	2168	G

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Mol	Chain	Res	Type
1	2A	2170	A
1	2A	2172	U
1	2A	2178	C
1	2A	2181	G
1	2A	2182	G
1	2A	2185	C
1	2A	2186	G
1	2A	2188	C
1	2A	2189	U
1	2A	2192	G
1	2A	2193	G
1	2A	2198	A
1	2A	2206	G
1	2A	2207	G
1	2A	2208	A
1	2A	2219	G
1	2A	2225	A
1	2A	2238	G
1	2A	2239	G
1	2A	2268	A
1	2A	2275	C
1	2A	2278	A
1	2A	2279	G
1	2A	2283	C
1	2A	2287	A
1	2A	2305	A
1	2A	2307	G
1	2A	2308	G
1	2A	2319	G
1	2A	2320	A
1	2A	2321	G
1	2A	2325	G
1	2A	2334	G
1	2A	2336	A
1	2A	2343	C
1	2A	2347	C
1	2A	2350	C
1	2A	2372	G
1	2A	2376	A
1	2A	2383	G
1	2A	2385	C
1	2A	2396	G

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Mol	Chain	Res	Type
1	2A	2406	U
1	2A	2410	G
1	2A	2414	G
1	2A	2422	A
1	2A	2424	C
1	2A	2425	A
1	2A	2429	G
1	2A	2430	A
1	2A	2431	U
1	2A	2435	A
1	2A	2439	A
1	2A	2441	C
1	2A	2448	A
1	2A	2469	A
1	2A	2476	A
1	2A	2490	G
1	2A	2502	G
1	2A	2505	G
1	2A	2506	U
1	2A	2507	C
1	2A	2518	A
1	2A	2529	G
1	2A	2549	G
1	2A	2554	U
1	2A	2566	A
1	2A	2567	G
1	2A	2573	C
1	2A	2574	G
1	2A	2602	A
1	2A	2609	U
1	2A	2611	U
1	2A	2612	C
1	2A	2630	G
1	2A	2646	C
1	2A	2654	A
1	2A	2673	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

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Mol	Chain	Res	Type
1	2A	2714	G
1	2A	2726	U
1	2A	2733	A
1	2A	2734	A
1	2A	2751	G
1	2A	2760	C
1	2A	2761	G
1	2A	2764	A
1	2A	2765	A
1	2A	2766	G
1	2A	2778	A
1	2A	2789	C
1	2A	2793	G
1	2A	2794	C
1	2A	2802	G
1	2A	2804	C
1	2A	2807	G
1	2A	2818	G
1	2A	2820	A
1	2A	2821	A
1	2A	2833	G
1	2A	2835	A
1	2A	2872	G
1	2A	2873	A
1	2A	2876	G
1	2A	2880	C
1	2A	2892	A
1	2A	2894	G
1	2A	2895	U
1	2A	2897	U
2	2B	2	C
2	2B	13	A
2	2B	24	G
2	2B	25	A
2	2B	30	C
2	2B	35	U
2	2B	41	U
2	2B	42	C
2	2B	53	A
2	2B	56	G
2	2B	67	G
2	2B	73	A

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Mol	Chain	Res	Type
2	2B	85	G
2	2B	106	G
2	2B	108	U
2	2B	110	G
2	2B	111	G
2	2B	120	A
32	2a	5	U
32	2a	9	G
32	2a	22	G
32	2a	29	G
32	2a	30	U
32	2a	32	A
32	2a	39	G
32	2a	47	C
32	2a	48	C
32	2a	50	A
32	2a	51	A
32	2a	54	C
32	2a	65	U
32	2a	66	G
32	2a	73	G
32	2a	80	G
32	2a	88	A
32	2a	89	C
32	2a	101	A
32	2a	115	G
32	2a	116	A
32	2a	121	C
32	2a	131	C
32	2a	142	G
32	2a	144	G
32	2a	146	G
32	2a	163	C
32	2a	174	C
32	2a	182	U
32	2a	189(E)	U
32	2a	189(F)	U
32	2a	189(J)	G
32	2a	195	A
32	2a	197	A
32	2a	201	C
32	2a	202	U

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Mol	Chain	Res	Type
32	2a	203	U
32	2a	204	U
32	2a	216	G
32	2a	220	G
32	2a	226	G
32	2a	247	G
32	2a	249	U
32	2a	251	G
32	2a	258	G
32	2a	266	G
32	2a	267	C
32	2a	289	G
32	2a	299	G
32	2a	301	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	384	G
32	2a	397	A
32	2a	398	C
32	2a	406	G
32	2a	412	A
32	2a	413	G
32	2a	421	U
32	2a	422	C
32	2a	424	G
32	2a	429	U
32	2a	430	A
32	2a	439	A
32	2a	442	C
32	2a	452	A
32	2a	461	A
32	2a	470	C
32	2a	471	G
32	2a	477	A
32	2a	482	A

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Mol	Chain	Res	Type
32	2a	484	G
32	2a	485	G
32	2a	495	A
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	512	U
32	2a	513	C
32	2a	518	C
32	2a	521	G
32	2a	531	U
32	2a	532	A
32	2a	536	C
32	2a	547	A
32	2a	559	A
32	2a	561	U
32	2a	568	G
32	2a	572	A
32	2a	573	A
32	2a	576	G
32	2a	577	G
32	2a	595	G
32	2a	596	C
32	2a	597	G
32	2a	616	G
32	2a	630	G
32	2a	650	G
32	2a	653	A
32	2a	655	A
32	2a	657	G
32	2a	665	A
32	2a	687	A
32	2a	688	G
32	2a	703	G
32	2a	723	U
32	2a	724	G
32	2a	731	G
32	2a	750	G
32	2a	752	G

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Mol	Chain	Res	Type
32	2a	753	A
32	2a	755	G
32	2a	760	G
32	2a	773	G
32	2a	774	G
32	2a	777	A
32	2a	792	A
32	2a	793	U
32	2a	794	A
32	2a	816	A
32	2a	817	C
32	2a	821	G
32	2a	828	A
32	2a	836	G
32	2a	840	C
32	2a	841	U
32	2a	851	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	932	C
32	2a	933	G
32	2a	934	C
32	2a	960	U
32	2a	961	U
32	2a	968	A
32	2a	969	A
32	2a	971	G
32	2a	972	C
32	2a	974	A
32	2a	975	A
32	2a	976	G
32	2a	977	A
32	2a	982	U
32	2a	989	C
32	2a	992	U
32	2a	993	G
32	2a	995	C
32	2a	1001(A)	G

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Mol	Chain	Res	Type
32	2a	1002	G
32	2a	1003	G
32	2a	1005	A
32	2a	1006	C
32	2a	1009	G
32	2a	1013	G
32	2a	1017	G
32	2a	1022	G
32	2a	1023	G
32	2a	1025	U
32	2a	1026	G
32	2a	1027	C
32	2a	1030(A)	G
32	2a	1030(D)	A
32	2a	1031	G
32	2a	1032	G
32	2a	1033	G
32	2a	1034	G
32	2a	1035	A
32	2a	1037	C
32	2a	1039	C
32	2a	1040	U
32	2a	1042	G
32	2a	1043	C
32	2a	1045	C
32	2a	1046	A
32	2a	1053	G
32	2a	1064	G
32	2a	1065	U
32	2a	1066	C
32	2a	1068	G
32	2a	1081	G
32	2a	1086	U
32	2a	1094	G
32	2a	1095	U
32	2a	1101	A
32	2a	1106	G
32	2a	1112	C
32	2a	1113	C
32	2a	1117	G
32	2a	1122	U
32	2a	1123	A

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Mol	Chain	Res	Type
32	2a	1125	U
32	2a	1127	G
32	2a	1129	C
32	2a	1130	A
32	2a	1136	U
32	2a	1137	C
32	2a	1138	G
32	2a	1139	G
32	2a	1141	C
32	2a	1143	G
32	2a	1146	A
32	2a	1151	A
32	2a	1152	A
32	2a	1157	A
32	2a	1159	U
32	2a	1170	A
32	2a	1171	G
32	2a	1182	G
32	2a	1183	A
32	2a	1184	G
32	2a	1196	U
32	2a	1197	G
32	2a	1202	G
32	2a	1204	A
32	2a	1211	U
32	2a	1212	U
32	2a	1214	C
32	2a	1215	G
32	2a	1225	A
32	2a	1227	A
32	2a	1228	C
32	2a	1236	A
32	2a	1238	A
32	2a	1240	U
32	2a	1253	G
32	2a	1256	A
32	2a	1257	U
32	2a	1258	G
32	2a	1260	C
32	2a	1262	C
32	2a	1270	C
32	2a	1272	G

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Mol	Chain	Res	Type
32	2a	1273	G
32	2a	1278	U
32	2a	1279	A
32	2a	1280	A
32	2a	1285	A
32	2a	1287	A
32	2a	1289	A
32	2a	1299	A
32	2a	1300	G
32	2a	1303	C
32	2a	1305	G
32	2a	1320	C
32	2a	1322	C
32	2a	1323	G
32	2a	1338	G
32	2a	1340	A
32	2a	1346	A
32	2a	1347	G
32	2a	1353	G
32	2a	1358	U
32	2a	1363	C
32	2a	1364	U
32	2a	1368	G
32	2a	1370	G
32	2a	1377	A
32	2a	1379	G
32	2a	1384	C
32	2a	1397	C
32	2a	1398	A
32	2a	1402	4OC
32	2a	1419	G
32	2a	1442	G
32	2a	1442(A)	G
32	2a	1442(B)	A
32	2a	1446	U
32	2a	1447	A
32	2a	1452	C
32	2a	1456	G
32	2a	1457	G
32	2a	1487	G
32	2a	1493	A
32	2a	1494	G

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Mol	Chain	Res	Type
32	2a	1497	G
32	2a	1499	A
32	2a	1504	G
32	2a	1506	U
32	2a	1507	A
32	2a	1517	G
32	2a	1520	G
32	2a	1529	G
32	2a	1530	G
32	2a	1531	A
32	2a	1532	U
53	2v	15	A
53	2v	22	U
55	2x	9	A
55	2x	14	A
55	2x	18	G
55	2x	19	G
55	2x	20	H2U
55	2x	21	H2U
55	2x	22	A
55	2x	26	A
55	2x	37	MIA
55	2x	45	U
55	2x	48	G
55	2x	49	U

All (53) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1A	196	A
1	1A	266	G
1	1A	271(K)	U
1	1A	278	A
1	1A	548	A
1	1A	746	A
1	1A	827	U
1	1A	974	G
1	1A	1065	U
1	1A	1067	A
1	1A	1174	A
1	1A	1176	G
1	1A	1379	A

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Mol	Chain	Res	Type
1	1A	1420	U
1	1A	1442	G
1	1A	1508	A
1	1A	1608	A
1	1A	1653	G
1	1A	1992	G
1	1A	2126	A
1	1A	2134	A
1	1A	2181	G
1	1A	2183	C
1	1A	2406	U
1	1A	2422	A
1	1A	2430	A
1	1A	2439	A
1	1A	2601	C
1	1A	2689	U
1	1A	2756	U
1	2A	196	A
1	2A	199	A
1	2A	266	G
1	2A	277	C
1	2A	310	A
1	2A	528	A
1	2A	669	G
1	2A	746	A
1	2A	752	A
1	2A	774	A
1	2A	827	U
1	2A	856	C
1	2A	893	C
1	2A	900	A
1	2A	1210	A
1	2A	1379	A
1	2A	1420	U
1	2A	1530	C
1	2A	1653	G
1	2A	1992	G
1	2A	2406	U
1	2A	2430	A
1	2A	2689	U

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

66 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$
32	M2G	1a	966	32	24,27,28	1.33	4 (16%)	33,40,43	1.88	6 (18%)
1	OMG	1A	2251	1,55,57	23,26,27	1.22	3 (13%)	32,38,41	2.07	8 (25%)
55	H2U	2x	20	55	18,21,22	0.94	2 (11%)	19,30,33	0.88	0
55	PSU	1x	39	55	18,21,22	1.38	2 (11%)	21,30,33	1.92	4 (19%)
1	PSU	2A	1917	1	18,21,22	1.40	2 (11%)	21,30,33	2.06	3 (14%)
43	0TD	2l	92	43	8,9,10	4.73	2 (25%)	6,11,13	4.15	2 (33%)
1	OMC	1A	1920	1	19,22,23	0.82	0	25,31,34	0.94	1 (4%)
1	5MC	2A	1942	1	19,22,23	1.63	3 (15%)	26,32,35	1.23	3 (11%)
1	OMU	2A	2552	1,57	19,22,23	1.19	3 (15%)	25,31,34	1.80	5 (20%)
32	4OC	2a	1402	32,57	20,23,24	0.80	0	25,32,35	1.06	2 (8%)
32	MA6	2a	1518	32	23,26,27	0.39	0	33,38,41	2.04	9 (27%)
55	PSU	1x	55	55	18,21,22	1.30	2 (11%)	21,30,33	2.07	4 (19%)
32	4OC	1a	1402	32,57	20,23,24	0.76	0	25,32,35	1.06	2 (8%)
32	5MC	1a	1407	32	19,22,23	1.87	3 (15%)	26,32,35	1.23	4 (15%)
55	MIA	1x	37	55	21,24,32	1.57	4 (19%)	30,35,47	2.08	8 (26%)
32	2MG	2a	1207	32	23,26,27	1.23	2 (8%)	33,38,41	2.12	7 (21%)
32	M2G	2a	966	32	24,27,28	1.29	4 (16%)	33,40,43	1.91	5 (15%)
1	PSU	1A	1917	1	18,21,22	1.42	3 (16%)	21,30,33	1.96	4 (19%)
1	5MC	1A	1942	1,57	19,22,23	1.59	3 (15%)	26,32,35	1.23	4 (15%)
1	PSU	2A	1911	1	18,21,22	1.37	2 (11%)	21,30,33	1.99	5 (23%)
55	4SU	2x	8	55	18,21,22	1.87	5 (27%)	25,30,33	2.09	5 (20%)
55	8AN	1x	76	55,57,56	21,24,25	1.38	3 (14%)	26,35,38	2.32	10 (38%)
32	5MC	1a	967	32	19,22,23	1.52	3 (15%)	26,32,35	1.12	2 (7%)
32	5MC	2a	967	32	19,22,23	1.76	3 (15%)	26,32,35	1.13	3 (11%)
55	PSU	1x	32	55,57	18,21,22	1.33	2 (11%)	21,30,33	2.00	3 (14%)
43	0TD	1l	92	43	8,9,10	4.62	1 (12%)	6,11,13	8.09	3 (50%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
32	PSU	2a	516	32	18,21,22	1.33	3 (16%)	21,30,33	2.09	5 (23%)
55	PSU	2x	39	55	18,21,22	1.42	2 (11%)	21,30,33	1.59	4 (19%)
1	PSU	2A	2605	1	18,21,22	1.40	2 (11%)	21,30,33	2.11	4 (19%)
32	UR3	1a	1498	32	19,22,23	1.02	1 (5%)	26,32,35	1.66	3 (11%)
55	5MU	1x	54	55,57	19,22,23	1.40	5 (26%)	27,32,35	1.72	5 (18%)
32	2MG	1a	1207	32	23,26,27	1.29	4 (17%)	33,38,41	2.10	6 (18%)
32	5MC	1a	1400	32	19,22,23	1.66	3 (15%)	26,32,35	1.25	4 (15%)
1	5MC	2A	1962	1	19,22,23	1.56	3 (15%)	26,32,35	1.08	2 (7%)
1	5MC	1A	1962	1,57	19,22,23	1.64	3 (15%)	26,32,35	1.19	3 (11%)
55	PSU	2x	55	55	18,21,22	1.38	2 (11%)	21,30,33	2.10	5 (23%)
32	PSU	1a	516	32,57	18,21,22	1.31	2 (11%)	21,30,33	1.99	5 (23%)
32	G7M	2a	527	32,57	23,26,27	1.49	3 (13%)	34,39,42	1.72	5 (14%)
55	5MU	2x	54	55	19,22,23	1.40	5 (26%)	27,32,35	2.22	6 (22%)
55	H2U	1x	21	55	18,21,22	1.00	2 (11%)	19,30,33	1.63	3 (15%)
32	5MC	2a	1400	32	19,22,23	1.73	3 (15%)	26,32,35	1.17	2 (7%)
1	PSU	1A	2605	1,57	18,21,22	1.41	4 (22%)	21,30,33	2.12	4 (19%)
1	OMU	1A	2552	1,57	19,22,23	1.29	3 (15%)	25,31,34	1.80	5 (20%)
1	2MA	1A	2503	1,57	22,25,26	1.50	4 (18%)	32,37,40	2.32	9 (28%)
32	5MC	1a	1404	32	19,22,23	1.72	3 (15%)	26,32,35	1.13	3 (11%)
32	MA6	1a	1518	32	23,26,27	0.40	0	33,38,41	2.14	10 (30%)
32	G7M	1a	527	32,57	23,26,27	1.52	3 (13%)	34,39,42	1.74	5 (14%)
32	MA6	1a	1519	32	23,26,27	0.41	0	33,38,41	2.02	9 (27%)
32	UR3	2a	1498	32	19,22,23	1.09	2 (10%)	26,32,35	1.67	3 (11%)
1	5MU	1A	1939	1	19,22,23	1.44	5 (26%)	27,32,35	2.07	6 (22%)
32	5MC	2a	1404	32	19,22,23	1.74	3 (15%)	26,32,35	1.15	2 (7%)
1	5MU	1A	1915	1	19,22,23	1.35	5 (26%)	27,32,35	2.24	6 (22%)
55	4SU	1x	8	55	18,21,22	1.88	4 (22%)	25,30,33	1.62	4 (16%)
55	H2U	2x	21	55	18,21,22	0.94	2 (11%)	19,30,33	1.09	1 (5%)
55	8AN	2x	76	55,57,56	21,24,25	1.36	3 (14%)	26,35,38	2.29	11 (42%)
1	5MU	2A	1939	1	19,22,23	1.44	5 (26%)	27,32,35	2.22	6 (22%)
1	OMG	2A	2251	1,55,57	23,26,27	1.18	3 (13%)	32,38,41	1.96	6 (18%)
32	5MC	2a	1407	32,57	19,22,23	1.62	3 (15%)	26,32,35	1.24	3 (11%)
1	5MU	2A	1915	1,57	19,22,23	1.52	6 (31%)	27,32,35	2.21	6 (22%)
55	MIA	2x	37	55	21,24,32	1.55	4 (19%)	30,35,47	2.05	9 (30%)
1	PSU	1A	1911	1	18,21,22	1.40	2 (11%)	21,30,33	2.06	5 (23%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	OMC	2A	1920	1,57	19,22,23	0.81	0	25,31,34	0.90	0
32	MA6	2a	1519	32	23,26,27	0.42	0	33,38,41	2.13	10 (30%)
55	H2U	1x	20	55	18,21,22	0.98	2 (11%)	19,30,33	0.97	2 (10%)
1	2MA	2A	2503	1,57	22,25,26	1.48	4 (18%)	32,37,40	2.35	8 (25%)
55	PSU	2x	32	55	18,21,22	1.37	2 (11%)	21,30,33	2.05	3 (14%)

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
32	M2G	1a	966	32	-	0/11/29/30	0/3/3/3
1	OMG	1A	2251	1,55,57	-	0/9/27/28	0/3/3/3
55	H2U	2x	20	55	-	3/7/38/39	0/2/2/2
55	PSU	1x	39	55	-	0/7/25/26	0/2/2/2
1	PSU	2A	1917	1	-	0/7/25/26	0/2/2/2
43	0TD	2l	92	43	-	2/7/12/14	-
1	OMC	1A	1920	1	-	0/9/27/28	0/2/2/2
1	5MC	2A	1942	1	-	0/7/25/26	0/2/2/2
1	OMU	2A	2552	1,57	-	0/9/27/28	0/2/2/2
32	4OC	2a	1402	32,57	-	3/9/29/30	0/2/2/2
32	MA6	2a	1518	32	-	0/11/29/30	0/3/3/3
55	PSU	1x	55	55	-	0/7/25/26	0/2/2/2
32	4OC	1a	1402	32,57	-	2/9/29/30	0/2/2/2
32	5MC	1a	1407	32	-	0/7/25/26	0/2/2/2
55	MIA	1x	37	55	-	2/7/25/34	0/3/3/3
32	2MG	2a	1207	32	-	2/9/27/28	0/3/3/3
32	M2G	2a	966	32	-	0/11/29/30	0/3/3/3
1	PSU	1A	1917	1	-	0/7/25/26	0/2/2/2
1	5MC	1A	1942	1,57	-	0/7/25/26	0/2/2/2
1	PSU	2A	1911	1	-	0/7/25/26	0/2/2/2
55	4SU	2x	8	55	-	0/7/25/26	0/2/2/2
55	8AN	1x	76	55,57,56	-	1/7/25/26	0/3/3/3
32	5MC	1a	967	32	-	1/7/25/26	0/2/2/2
32	5MC	2a	967	32	-	0/7/25/26	0/2/2/2
55	PSU	1x	32	55,57	-	0/7/25/26	0/2/2/2
43	0TD	1l	92	43	-	2/7/12/14	-
32	PSU	2a	516	32	-	0/7/25/26	0/2/2/2
55	PSU	2x	39	55	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	PSU	2A	2605	1	-	0/7/25/26	0/2/2/2
32	UR3	1a	1498	32	-	0/7/25/26	0/2/2/2
55	5MU	1x	54	55,57	-	0/7/25/26	0/2/2/2
32	2MG	1a	1207	32	-	0/9/27/28	0/3/3/3
32	5MC	1a	1400	32	-	0/7/25/26	0/2/2/2
1	5MC	2A	1962	1	-	0/7/25/26	0/2/2/2
1	5MC	1A	1962	1,57	-	0/7/25/26	0/2/2/2
55	PSU	2x	55	55	-	0/7/25/26	0/2/2/2
32	PSU	1a	516	32,57	-	0/7/25/26	0/2/2/2
32	G7M	2a	527	32,57	-	1/7/25/26	0/3/3/3
55	5MU	2x	54	55	-	0/7/25/26	0/2/2/2
55	H2U	1x	21	55	-	6/7/38/39	0/2/2/2
32	5MC	2a	1400	32	-	0/7/25/26	0/2/2/2
1	PSU	1A	2605	1,57	-	0/7/25/26	0/2/2/2
1	OMU	1A	2552	1,57	-	0/9/27/28	0/2/2/2
1	2MA	1A	2503	1,57	-	2/7/25/26	0/3/3/3
32	5MC	1a	1404	32	-	0/7/25/26	0/2/2/2
32	MA6	1a	1518	32	-	0/11/29/30	0/3/3/3
32	G7M	1a	527	32,57	-	3/7/25/26	0/3/3/3
32	MA6	1a	1519	32	-	3/11/29/30	0/3/3/3
32	UR3	2a	1498	32	-	0/7/25/26	0/2/2/2
1	5MU	1A	1939	1	-	0/7/25/26	0/2/2/2
32	5MC	2a	1404	32	-	0/7/25/26	0/2/2/2
1	5MU	1A	1915	1	-	0/7/25/26	0/2/2/2
55	4SU	1x	8	55	-	0/7/25/26	0/2/2/2
55	H2U	2x	21	55	-	4/7/38/39	0/2/2/2
55	8AN	2x	76	55,57,56	-	1/7/25/26	0/3/3/3
1	5MU	2A	1939	1	-	0/7/25/26	0/2/2/2
1	OMG	2A	2251	1,55,57	-	1/9/27/28	0/3/3/3
32	5MC	2a	1407	32,57	-	0/7/25/26	0/2/2/2
1	5MU	2A	1915	1,57	-	0/7/25/26	0/2/2/2
55	MIA	2x	37	55	-	2/7/25/34	0/3/3/3
1	PSU	1A	1911	1	-	0/7/25/26	0/2/2/2
1	OMC	2A	1920	1,57	-	0/9/27/28	0/2/2/2
32	MA6	2a	1519	32	-	3/11/29/30	0/3/3/3
55	H2U	1x	20	55	-	2/7/38/39	0/2/2/2
1	2MA	2A	2503	1,57	-	1/7/25/26	0/3/3/3
55	PSU	2x	32	55	-	0/7/25/26	0/2/2/2

All (176) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
43	2l	92	0TD	CB-SB	-12.69	1.69	1.82
43	1l	92	0TD	CB-SB	-12.62	1.69	1.82
32	1a	1407	5MC	C5-C4	7.11	1.49	1.44
32	2a	967	5MC	C5-C4	6.60	1.49	1.44
32	2a	1404	5MC	C5-C4	6.41	1.49	1.44
32	2a	1400	5MC	C5-C4	6.36	1.48	1.44
32	1a	1404	5MC	C5-C4	6.26	1.48	1.44
32	1a	1400	5MC	C5-C4	5.96	1.48	1.44
1	1A	1962	5MC	C5-C4	5.80	1.48	1.44
1	2A	1942	5MC	C5-C4	5.76	1.48	1.44
1	1A	1942	5MC	C5-C4	5.70	1.48	1.44
32	2a	1407	5MC	C5-C4	5.67	1.48	1.44
1	2A	1962	5MC	C5-C4	5.47	1.48	1.44
32	1a	967	5MC	C5-C4	5.33	1.48	1.44
55	2x	8	4SU	C4-S4	-5.15	1.59	1.68
55	1x	8	4SU	C4-S4	-4.85	1.60	1.68
32	1a	527	G7M	C5-N7	-4.72	1.33	1.39
55	2x	37	MIA	C5-C4	4.70	1.47	1.39
32	2a	527	G7M	C5-N7	-4.64	1.33	1.39
55	1x	37	MIA	C5-C4	4.63	1.47	1.39
1	2A	2503	2MA	C5-C4	4.53	1.47	1.39
1	1A	2503	2MA	C5-C4	4.46	1.47	1.39
55	1x	76	8AN	C5-N7	-4.09	1.31	1.39
55	1x	8	4SU	C4-N3	-3.84	1.33	1.37
55	2x	39	PSU	C6-C5	3.78	1.39	1.35
55	2x	55	PSU	C6-C5	3.78	1.39	1.35
1	1A	1911	PSU	C6-C5	3.74	1.39	1.35
55	2x	76	8AN	C5-N7	-3.72	1.32	1.39
55	2x	32	PSU	C6-C5	3.55	1.39	1.35
1	1A	1917	PSU	C6-C5	3.54	1.39	1.35
1	2A	1917	PSU	C6-C5	3.50	1.39	1.35
55	1x	39	PSU	C6-C5	3.45	1.39	1.35
1	2A	1911	PSU	C6-C5	3.44	1.39	1.35
55	1x	32	PSU	C6-C5	3.41	1.39	1.35
32	1a	516	PSU	C6-C5	3.36	1.39	1.35
32	1a	527	G7M	C5-C4	3.33	1.46	1.38
55	1x	55	PSU	C6-C5	3.31	1.39	1.35
1	2A	2605	PSU	C6-C5	3.23	1.38	1.35
32	1a	966	M2G	C5-C4	3.22	1.47	1.38
32	2a	1207	2MG	C5-C4	3.20	1.47	1.38
55	2x	76	8AN	C5-C4	-3.19	1.33	1.39
32	1a	1207	2MG	C5-C4	3.18	1.47	1.38
32	2a	966	M2G	C5-C4	3.17	1.47	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
32	2a	527	G7M	C5-C4	3.08	1.46	1.38
55	2x	8	4SU	C4-N3	-3.08	1.34	1.37
32	2a	516	PSU	C6-C5	3.07	1.38	1.35
1	2A	2251	OMG	C5-C4	3.05	1.47	1.38
32	1a	966	M2G	C2-N2	3.02	1.40	1.35
32	2a	1404	5MC	C6-C5	2.99	1.39	1.34
32	2a	1407	5MC	C6-C5	2.99	1.39	1.34
32	1a	1404	5MC	C6-C5	2.97	1.39	1.34
55	1x	54	5MU	C6-C5	2.92	1.39	1.34
1	2A	1915	5MU	C6-C5	2.89	1.39	1.34
1	1A	2251	OMG	C5-C4	2.88	1.46	1.38
1	2A	1915	5MU	C2-N1	2.87	1.43	1.38
55	2x	37	MIA	C5-C6	2.87	1.49	1.41
1	1A	1915	5MU	C4-N3	-2.87	1.33	1.38
1	1A	1911	PSU	C4-N3	-2.87	1.33	1.38
55	2x	8	4SU	C5-C4	-2.86	1.39	1.42
1	1A	1939	5MU	C4-N3	-2.84	1.33	1.38
55	1x	37	MIA	C5-C6	2.84	1.48	1.41
55	1x	8	4SU	C5-C4	-2.83	1.39	1.42
1	1A	2605	PSU	C6-C5	2.82	1.38	1.35
1	2A	1962	5MC	C6-C5	2.82	1.39	1.34
55	1x	76	8AN	C5-C4	-2.82	1.34	1.39
1	1A	2552	OMU	C4-N3	-2.81	1.33	1.38
55	1x	54	5MU	C4-N3	-2.81	1.33	1.38
1	1A	2251	OMG	C6-N1	-2.81	1.33	1.38
1	2A	1939	5MU	C4-N3	-2.81	1.33	1.38
1	1A	1942	5MC	C6-C5	2.81	1.39	1.34
1	1A	1917	PSU	C4-N3	-2.80	1.33	1.38
1	1A	1939	5MU	C6-C5	2.80	1.39	1.34
1	2A	2605	PSU	C4-N3	-2.78	1.33	1.38
1	2A	1911	PSU	C4-N3	-2.77	1.33	1.38
32	1a	967	5MC	C6-C5	2.77	1.39	1.34
55	1x	39	PSU	C4-N3	-2.77	1.33	1.38
32	1a	1400	5MC	C6-C5	2.76	1.39	1.34
1	1A	1962	5MC	C6-C5	2.75	1.39	1.34
1	2A	1942	5MC	C6-C5	2.75	1.39	1.34
1	2A	1939	5MU	C6-C5	2.74	1.39	1.34
43	2l	92	0TD	CB-CA	-2.74	1.53	1.54
32	2a	1400	5MC	C6-C5	2.74	1.39	1.34
55	2x	54	5MU	C6-C5	2.72	1.39	1.34
1	2A	1915	5MU	C4-N3	-2.70	1.33	1.38
32	2a	966	M2G	C2-N2	2.70	1.40	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	2A	1915	5MU	C4-C5	2.68	1.49	1.44
55	1x	20	H2U	C4-N3	-2.66	1.33	1.37
32	1a	1207	2MG	C6-N1	-2.66	1.33	1.38
55	2x	39	PSU	C4-N3	-2.65	1.33	1.38
1	1A	2605	PSU	C4-N3	-2.62	1.33	1.38
55	2x	54	5MU	C4-C5	2.62	1.49	1.44
55	2x	76	8AN	C5-C6	-2.62	1.33	1.41
32	2a	967	5MC	C6-C5	2.60	1.38	1.34
1	2A	2552	OMU	C4-N3	-2.58	1.34	1.38
55	2x	32	PSU	C4-N3	-2.58	1.34	1.38
1	2A	1917	PSU	C4-N3	-2.57	1.34	1.38
32	2a	527	G7M	C6-N1	-2.57	1.34	1.38
32	1a	516	PSU	C4-N3	-2.56	1.34	1.38
55	1x	20	H2U	C2-N3	-2.54	1.33	1.38
55	1x	76	8AN	C5-C6	-2.54	1.33	1.41
1	2A	2251	OMG	C6-N1	-2.53	1.34	1.38
1	1A	1915	5MU	C6-C5	2.52	1.38	1.34
32	1a	1407	5MC	C6-C5	2.51	1.38	1.34
1	1A	2503	2MA	C8-N7	2.51	1.36	1.31
55	2x	55	PSU	C4-N3	-2.50	1.34	1.38
55	2x	21	H2U	C2-N3	-2.50	1.33	1.38
55	2x	54	5MU	C4-N3	-2.49	1.34	1.38
1	1A	1939	5MU	C2-N3	-2.49	1.33	1.38
1	1A	2552	OMU	C2-N3	-2.48	1.33	1.38
1	1A	2503	2MA	C5-C6	2.47	1.47	1.41
1	1A	2503	2MA	C5-N7	-2.46	1.34	1.39
32	2a	966	M2G	C6-N1	-2.45	1.34	1.38
1	2A	2503	2MA	C5-N7	-2.45	1.34	1.39
55	2x	20	H2U	C2-N3	-2.45	1.33	1.38
1	1A	1962	5MC	C6-N1	-2.45	1.33	1.38
55	2x	37	MIA	C8-N7	2.44	1.36	1.31
55	1x	8	4SU	C2-N3	-2.44	1.33	1.38
1	2A	2503	2MA	C5-C6	2.43	1.47	1.41
32	2a	516	PSU	C4-N3	-2.43	1.34	1.38
1	2A	1942	5MC	C6-N1	-2.43	1.33	1.38
1	2A	1939	5MU	C4-C5	2.42	1.48	1.44
1	1A	1939	5MU	C6-N1	-2.41	1.33	1.38
1	2A	1939	5MU	C6-N1	-2.41	1.33	1.38
55	1x	37	MIA	C8-N7	2.40	1.36	1.31
1	2A	1939	5MU	C2-N3	-2.40	1.33	1.38
1	1A	2552	OMU	C5-C4	-2.39	1.38	1.43
55	1x	37	MIA	C5-N7	-2.38	1.34	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
32	2a	1498	UR3	C2-N1	2.37	1.41	1.38
32	1a	527	G7M	C6-N1	-2.36	1.34	1.38
55	1x	32	PSU	C4-N3	-2.36	1.34	1.38
32	2a	1207	2MG	C6-N1	-2.35	1.34	1.38
1	1A	2251	OMG	C5-N7	-2.35	1.34	1.39
32	1a	1400	5MC	C6-N1	-2.34	1.34	1.38
32	1a	1498	UR3	C2-N1	2.33	1.41	1.38
32	1a	1207	2MG	C2-N3	2.32	1.36	1.32
32	2a	967	5MC	C6-N1	-2.31	1.34	1.38
55	2x	54	5MU	C2-N1	2.31	1.42	1.38
55	1x	55	PSU	C4-N3	-2.30	1.34	1.38
55	1x	21	H2U	C2-N3	-2.30	1.34	1.38
1	1A	1942	5MC	C6-N1	-2.29	1.34	1.38
1	2A	2503	2MA	C8-N7	2.28	1.36	1.31
55	2x	8	4SU	C2-N1	2.27	1.42	1.38
32	2a	1404	5MC	C6-N1	-2.23	1.34	1.38
1	2A	1962	5MC	C6-N1	-2.22	1.34	1.38
32	1a	1407	5MC	C6-N1	-2.20	1.34	1.38
32	2a	1400	5MC	C6-N1	-2.20	1.34	1.38
1	2A	2552	OMU	C2-N3	-2.20	1.34	1.38
32	1a	1404	5MC	C6-N1	-2.20	1.34	1.38
55	2x	8	4SU	C2-N3	-2.19	1.34	1.38
1	1A	1915	5MU	C4-C5	2.18	1.48	1.44
32	1a	967	5MC	C6-N1	-2.17	1.34	1.38
32	2a	1407	5MC	C6-N1	-2.17	1.34	1.38
55	1x	54	5MU	C2-N3	-2.17	1.34	1.38
1	1A	1939	5MU	C4-C5	2.16	1.48	1.44
1	2A	1915	5MU	C6-N1	-2.14	1.34	1.38
1	2A	1915	5MU	C2-N3	-2.14	1.34	1.38
1	1A	1917	PSU	C2-N3	-2.14	1.34	1.37
32	2a	516	PSU	O4'-C1'	-2.13	1.40	1.43
1	1A	2605	PSU	C2-N1	-2.13	1.33	1.36
32	1a	1207	2MG	C5-N7	-2.11	1.34	1.39
1	1A	1915	5MU	C6-N1	-2.11	1.34	1.38
32	1a	966	M2G	C6-N1	-2.11	1.34	1.38
55	1x	21	H2U	C2-N1	-2.09	1.32	1.35
55	2x	21	H2U	C4-N3	-2.09	1.34	1.37
55	2x	54	5MU	C6-N1	-2.08	1.34	1.38
1	2A	2552	OMU	C6-C5	2.07	1.39	1.35
32	1a	966	M2G	C5-N7	-2.07	1.34	1.39
1	1A	1915	5MU	C2-N3	-2.06	1.34	1.38
1	2A	2251	OMG	C5-N7	-2.06	1.34	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
55	2x	37	MIA	C5-N7	-2.06	1.35	1.39
32	2a	966	M2G	C5-N7	-2.06	1.34	1.39
55	1x	54	5MU	C4-C5	2.05	1.48	1.44
1	1A	2605	PSU	C2-N3	-2.04	1.34	1.37
32	2a	1498	UR3	C6-C5	2.03	1.39	1.35
55	1x	54	5MU	C6-N1	-2.02	1.34	1.38
55	2x	20	H2U	C4-N3	-2.00	1.34	1.37

All (310) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
43	1l	92	0TD	CSB-SB-CB	-19.39	67.51	102.36
43	2l	92	0TD	CSB-SB-CB	-9.40	85.48	102.36
1	2A	2503	2MA	C5-C4-N3	-8.27	118.47	127.18
1	1A	2503	2MA	C5-C4-N3	-8.05	118.70	127.18
1	2A	2605	PSU	N1-C2-N3	6.85	122.39	115.17
1	2A	2503	2MA	N3-C4-N9	6.75	135.56	126.99
32	2a	1207	2MG	C2-N3-C4	6.71	120.39	112.00
1	1A	2605	PSU	N1-C2-N3	6.68	122.21	115.17
32	1a	1207	2MG	C2-N3-C4	6.65	120.32	112.00
55	2x	55	PSU	N1-C2-N3	6.64	122.18	115.17
32	2a	1498	UR3	C4-N3-C2	-6.59	119.28	124.58
32	1a	1498	UR3	C4-N3-C2	-6.57	119.30	124.58
55	2x	32	PSU	N1-C2-N3	6.43	121.95	115.17
1	1A	1911	PSU	N1-C2-N3	6.41	121.93	115.17
1	2A	1917	PSU	N1-C2-N3	6.40	121.92	115.17
1	1A	2503	2MA	N3-C4-N9	6.38	135.09	126.99
32	2a	966	M2G	C5-C4-N3	-6.38	118.24	128.39
55	1x	55	PSU	N1-C2-N3	6.24	121.75	115.17
32	2a	516	PSU	N1-C2-N3	6.15	121.66	115.17
55	1x	37	MIA	C5-C4-N3	-6.15	118.25	126.72
32	1a	966	M2G	C5-C4-N3	-6.15	118.61	128.39
55	2x	8	4SU	C5-C4-N3	6.13	120.45	114.75
1	1A	2251	OMG	C5-C4-N3	-6.07	118.73	128.39
1	1A	1917	PSU	N1-C2-N3	6.06	121.56	115.17
55	1x	39	PSU	N1-C2-N3	6.03	121.53	115.17
32	1a	1207	2MG	C5-C4-N3	-6.02	118.81	128.39
1	2A	2251	OMG	C5-C4-N3	-6.01	118.82	128.39
32	1a	516	PSU	N1-C2-N3	5.91	121.40	115.17
55	1x	32	PSU	N1-C2-N3	5.89	121.38	115.17
1	2A	1911	PSU	N1-C2-N3	5.77	121.26	115.17
55	2x	37	MIA	C5-C4-N3	-5.74	118.81	126.72

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
55	2x	76	8AN	N1-C2-N3	-5.72	119.92	128.58
32	1a	527	G7M	N9-C4-N3	5.71	137.36	125.95
55	2x	8	4SU	C4-N3-C2	-5.69	121.86	127.31
55	1x	76	8AN	N1-C2-N3	-5.63	120.06	128.58
1	2A	1915	5MU	N3-C2-N1	5.63	122.22	114.89
1	2A	1939	5MU	C4-N3-C2	-5.60	119.99	127.34
55	2x	54	5MU	C4-N3-C2	-5.56	120.05	127.34
32	2a	1207	2MG	C5-C4-N3	-5.56	119.54	128.39
55	2x	54	5MU	N3-C2-N1	5.52	122.08	114.89
1	1A	1915	5MU	C4-N3-C2	-5.51	120.11	127.34
1	2A	1915	5MU	C4-N3-C2	-5.49	120.14	127.34
1	2A	1939	5MU	N3-C2-N1	5.46	122.00	114.89
1	1A	1915	5MU	N3-C2-N1	5.40	121.92	114.89
1	1A	2251	OMG	C2-N3-C4	5.24	121.33	112.30
55	1x	21	H2U	N3-C2-N1	-5.22	111.41	116.65
32	1a	527	G7M	C5-C4-N3	-5.20	118.33	128.15
32	2a	527	G7M	C5-C4-N3	-5.16	118.39	128.15
55	2x	76	8AN	C5-C4-N3	-5.14	119.64	126.72
32	2a	527	G7M	N9-C4-N3	5.12	136.20	125.95
32	1a	1518	MA6	N1-C2-N3	-5.10	120.87	128.58
55	1x	8	4SU	C5-C4-N3	5.08	119.47	114.75
1	1A	1939	5MU	C4-N3-C2	-4.92	120.89	127.34
1	1A	2251	OMG	N9-C4-N3	4.84	135.64	125.95
32	2a	1519	MA6	C5-C4-N3	-4.84	120.05	126.72
32	2a	527	G7M	C2-N3-C4	4.78	120.54	112.30
1	2A	2552	OMU	C4-N3-C2	-4.78	120.68	126.61
55	1x	76	8AN	C5-C4-N3	-4.77	120.15	126.72
1	1A	1915	5MU	C5-C4-N3	4.77	119.47	115.32
32	2a	1518	MA6	N1-C2-N3	-4.76	121.37	128.58
1	1A	1939	5MU	N3-C2-N1	4.74	121.06	114.89
1	2A	2552	OMU	N3-C2-N1	4.74	121.06	114.89
1	1A	2552	OMU	C4-N3-C2	-4.73	120.73	126.61
32	2a	1518	MA6	C5-C4-N3	-4.73	120.20	126.72
32	1a	1518	MA6	C5-C4-N3	-4.70	120.24	126.72
1	2A	2251	OMG	C2-N3-C4	4.69	120.39	112.30
32	2a	1519	MA6	N1-C2-N3	-4.69	121.48	128.58
32	1a	1519	MA6	N1-C2-N3	-4.68	121.50	128.58
1	2A	2251	OMG	N9-C4-N3	4.68	135.31	125.95
32	1a	966	M2G	C2-N3-C4	4.63	121.08	112.51
32	2a	966	M2G	N9-C4-N3	4.62	135.20	125.95
55	2x	39	PSU	N1-C2-N3	4.61	120.03	115.17
1	2A	1939	5MU	C5-C4-N3	4.59	119.31	115.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
55	1x	37	MIA	N3-C4-N9	4.59	134.97	127.17
32	2a	966	M2G	C2-N3-C4	4.55	120.93	112.51
55	2x	54	5MU	C5-C4-N3	4.51	119.25	115.32
32	1a	1519	MA6	C5-C4-N3	-4.49	120.53	126.72
1	2A	1915	5MU	C5-C4-N3	4.46	119.20	115.32
32	1a	1207	2MG	N9-C4-N3	4.44	134.83	125.95
32	1a	527	G7M	C2-N3-C4	4.42	119.92	112.30
32	1a	966	M2G	N9-C4-N3	4.42	134.79	125.95
55	2x	37	MIA	N3-C4-N9	4.41	134.66	127.17
32	2a	516	PSU	C4-N3-C2	-4.35	120.38	126.37
1	2A	1911	PSU	C4-N3-C2	-4.33	120.40	126.37
1	1A	1939	5MU	C5-C4-N3	4.32	119.08	115.32
55	1x	55	PSU	C4-N3-C2	-4.31	120.43	126.37
1	2A	1939	5MU	C5-C6-N1	-4.31	118.63	123.31
32	1a	516	PSU	C4-N3-C2	-4.27	120.49	126.37
1	1A	1911	PSU	C4-N3-C2	-4.26	120.50	126.37
1	1A	1939	5MU	O4-C4-C5	-4.26	120.04	124.92
1	1A	1939	5MU	C5-C6-N1	-4.24	118.71	123.31
55	2x	55	PSU	C4-N3-C2	-4.22	120.55	126.37
55	1x	54	5MU	N3-C2-N1	4.20	120.35	114.89
1	1A	2605	PSU	C4-N3-C2	-4.16	120.63	126.37
1	2A	2605	PSU	C4-N3-C2	-4.15	120.65	126.37
32	2a	1519	MA6	C4-C5-N7	-4.15	105.83	110.58
55	1x	8	4SU	C4-N3-C2	-4.10	123.39	127.31
55	1x	76	8AN	O4'-C1'-N9	-4.10	100.22	108.09
32	1a	1518	MA6	C5-N7-C8	4.08	109.87	103.45
55	1x	32	PSU	C4-N3-C2	-4.03	120.82	126.37
1	2A	1939	5MU	O4-C4-C5	-4.03	120.31	124.92
1	2A	1917	PSU	C4-N3-C2	-4.01	120.84	126.37
1	1A	1915	5MU	O4-C4-C5	-4.01	120.33	124.92
55	2x	32	PSU	C4-N3-C2	-4.00	120.86	126.37
32	2a	1400	5MC	C5-C6-N1	-4.00	118.97	123.31
32	2a	1519	MA6	C5-N7-C8	3.99	109.71	103.45
1	1A	2552	OMU	C5-C4-N3	3.98	120.37	114.80
1	1A	1917	PSU	C4-N3-C2	-3.97	120.91	126.37
32	2a	1518	MA6	C2-N1-C6	3.94	121.45	111.83
32	1a	1519	MA6	C2-N1-C6	3.94	121.44	111.83
32	1a	1518	MA6	C2-N1-C6	3.93	121.42	111.83
55	2x	54	5MU	O4-C4-C5	-3.92	120.43	124.92
55	1x	32	PSU	O2-C2-N1	-3.92	118.75	122.79
1	2A	1917	PSU	O2-C2-N1	-3.90	118.77	122.79
55	1x	54	5MU	C4-N3-C2	-3.88	122.25	127.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1A	2552	OMU	N3-C2-N1	3.87	119.93	114.89
55	1x	37	MIA	C2-N3-C4	3.86	121.26	111.83
55	2x	8	4SU	C5-C4-S4	-3.84	119.91	124.31
55	1x	37	MIA	C4-C5-N7	-3.83	106.21	110.58
32	2a	1207	2MG	N9-C4-N3	3.82	133.59	125.95
32	2a	1518	MA6	C4-C5-N7	-3.82	106.22	110.58
55	2x	32	PSU	O2-C2-N1	-3.82	118.85	122.79
32	2a	1519	MA6	C2-N1-C6	3.81	121.14	111.83
32	1a	1518	MA6	C4-C5-N7	-3.81	106.23	110.58
32	1a	1518	MA6	N9-C8-N7	-3.78	108.57	113.94
55	2x	37	MIA	C2-N3-C4	3.77	121.04	111.83
32	2a	967	5MC	C5-C6-N1	-3.74	119.25	123.31
1	2A	1915	5MU	C5-C6-N1	-3.73	119.26	123.31
55	1x	54	5MU	C5-C4-N3	3.73	118.56	115.32
55	1x	39	PSU	C4-N3-C2	-3.73	121.24	126.37
1	1A	2605	PSU	O2-C2-N1	-3.71	118.97	122.79
55	2x	37	MIA	C4-C5-N7	-3.70	106.35	110.58
32	2a	1518	MA6	C5-N7-C8	3.70	109.27	103.45
32	1a	1519	MA6	C5-N7-C8	3.70	109.26	103.45
55	1x	55	PSU	O2-C2-N1	-3.67	119.00	122.79
32	1a	1519	MA6	C4-C5-N7	-3.67	106.38	110.58
32	1a	1518	MA6	C2-N3-C4	3.66	120.78	111.83
32	2a	516	PSU	O2-C2-N1	-3.63	119.05	122.79
1	1A	1915	5MU	C5-C6-N1	-3.62	119.38	123.31
32	2a	1207	2MG	C6-C5-N7	3.61	136.87	130.29
55	2x	37	MIA	N3-C2-N1	-3.59	123.15	128.58
1	2A	1962	5MC	C5-C6-N1	-3.56	119.45	123.31
32	1a	967	5MC	C5-C6-N1	-3.56	119.45	123.31
1	2A	2503	2MA	N6-C6-N1	3.53	121.80	117.03
55	1x	76	8AN	N9-C8-N7	-3.52	108.94	113.94
32	2a	1519	MA6	C2-N3-C4	3.52	120.43	111.83
32	2a	1404	5MC	C5-C6-N1	-3.51	119.50	123.31
55	1x	54	5MU	O4-C4-C5	-3.50	120.91	124.92
1	1A	1915	5MU	O2-C2-N1	-3.50	118.24	122.80
55	1x	37	MIA	N3-C2-N1	-3.49	123.30	128.58
55	2x	54	5MU	C5-C6-N1	-3.49	119.52	123.31
32	2a	1518	MA6	C2-N3-C4	3.46	120.28	111.83
1	2A	1915	5MU	O4-C4-C5	-3.44	120.98	124.92
55	2x	76	8AN	N9-C8-N7	-3.42	109.09	113.94
1	1A	1942	5MC	C5-C6-N1	-3.41	119.61	123.31
55	2x	76	8AN	C2-N3-C4	3.38	120.09	111.83
55	1x	76	8AN	C2-N3-C4	3.36	120.05	111.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1A	2503	2MA	C4-C5-N7	-3.35	106.75	110.58
1	1A	2552	OMU	O4-C4-C5	-3.35	119.39	125.16
32	1a	1519	MA6	C2-N3-C4	3.34	119.99	111.83
1	1A	1962	5MC	C5-C6-N1	-3.34	119.69	123.31
32	2a	1519	MA6	N9-C8-N7	-3.33	109.21	113.94
32	1a	966	M2G	C6-C5-N7	3.28	136.25	130.29
32	1a	1519	MA6	N9-C8-N7	-3.26	109.32	113.94
1	1A	2503	2MA	N6-C6-N1	3.24	121.39	117.03
1	2A	2552	OMU	C5-C4-N3	3.23	119.32	114.80
1	2A	2552	OMU	O2-C2-N1	-3.23	118.59	122.80
1	2A	2503	2MA	C4-C5-N7	-3.22	106.90	110.58
32	1a	1404	5MC	C5-C4-N3	-3.20	118.47	121.75
32	2a	1407	5MC	C5-C6-N1	-3.20	119.84	123.31
55	1x	39	PSU	O2-C2-N1	-3.17	119.52	122.79
1	2A	1942	5MC	C5-C4-N3	-3.17	118.51	121.75
32	2a	1498	UR3	C5-C4-N3	3.17	119.21	115.04
32	2a	966	M2G	C6-C5-N7	3.16	136.04	130.29
55	2x	55	PSU	O2-C2-N1	-3.15	119.54	122.79
32	1a	516	PSU	O2-C2-N1	-3.14	119.55	122.79
55	2x	8	4SU	N3-C2-N1	3.12	118.95	114.89
55	1x	76	8AN	C5-N7-C8	3.12	108.35	103.45
32	1a	1207	2MG	C6-C5-N7	3.12	135.96	130.29
43	1l	92	0TD	OD2-CG-CB	3.11	119.86	113.15
1	1A	1942	5MC	C5-C4-N3	-3.09	118.59	121.75
1	1A	2251	OMG	C6-C5-N7	3.09	135.91	130.29
32	1a	1400	5MC	C5-C6-N1	-3.09	119.96	123.31
32	1a	1518	MA6	N3-C4-N9	3.08	132.41	127.17
32	2a	1518	MA6	N9-C8-N7	-3.08	109.56	113.94
1	2A	2251	OMG	C6-C5-N7	3.08	135.89	130.29
1	2A	2605	PSU	O2-C2-N1	-3.04	119.66	122.79
55	2x	54	5MU	O2-C2-N1	-3.03	118.85	122.80
55	2x	76	8AN	C5-N7-C8	2.99	108.14	103.45
32	2a	1407	5MC	C5-C4-N3	-2.97	118.71	121.75
32	1a	1404	5MC	C5-C6-N1	-2.97	120.09	123.31
55	1x	76	8AN	C4'-O4'-C1'	-2.95	102.96	109.47
32	1a	1407	5MC	C5-C6-N1	-2.94	120.12	123.31
1	1A	2503	2MA	C4-N9-C8	2.94	108.82	105.74
32	2a	1407	5MC	O2-C2-N3	-2.93	117.71	122.33
1	1A	1911	PSU	O2-C2-N1	-2.93	119.77	122.79
55	1x	54	5MU	C5-C6-N1	-2.93	120.13	123.31
55	2x	76	8AN	C5-C4-N9	2.92	109.00	105.81
1	1A	1962	5MC	C5-C4-N3	-2.92	118.76	121.75

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
43	2l	92	0TD	OD2-CG-CB	2.91	119.44	113.15
1	1A	1917	PSU	O2-C2-N1	-2.91	119.79	122.79
32	1a	1498	UR3	C5-C4-N3	2.89	118.85	115.04
32	1a	1400	5MC	C5-C4-N3	-2.88	118.80	121.75
32	1a	1402	4OC	C6-C5-C4	2.86	120.44	117.00
55	2x	76	8AN	C4'-O4'-C1'	-2.85	103.18	109.47
32	1a	1407	5MC	C5-C4-N3	-2.84	118.85	121.75
32	2a	1518	MA6	C4-C5-C6	2.79	118.80	115.91
1	2A	2503	2MA	C4-N9-C8	2.77	108.65	105.74
1	2A	1911	PSU	O2-C2-N1	-2.77	119.93	122.79
32	2a	1518	MA6	N3-C4-N9	2.77	131.88	127.17
32	1a	1519	MA6	N3-C4-N9	2.77	131.88	127.17
32	2a	1519	MA6	N3-C4-N9	2.77	131.87	127.17
55	1x	21	H2U	C5-C6-N1	-2.76	103.16	111.52
32	2a	966	M2G	C4-C5-N7	-2.74	106.33	110.67
32	1a	967	5MC	C5-C4-N3	-2.73	118.95	121.75
32	2a	1207	2MG	C4-C5-N7	-2.72	106.36	110.67
1	2A	1942	5MC	C5-C6-N1	-2.71	120.37	123.31
55	1x	37	MIA	C5-N7-C8	2.71	107.70	103.45
32	1a	527	G7M	O6-C6-C5	-2.70	121.97	128.01
32	2a	1519	MA6	C4-C5-C6	2.70	118.70	115.91
55	2x	39	PSU	C4-N3-C2	-2.70	122.66	126.37
55	2x	37	MIA	C5-N7-C8	2.69	107.68	103.45
32	2a	1404	5MC	C5-C4-N3	-2.67	119.02	121.75
32	2a	1207	2MG	N1-C2-N2	2.67	119.28	116.56
32	1a	966	M2G	C4-C5-N7	-2.65	106.47	110.67
1	1A	2503	2MA	C5-N7-C8	2.64	107.60	103.45
1	1A	2251	OMG	O6-C6-C5	-2.64	119.57	126.53
32	1a	1407	5MC	O2-C2-N3	-2.62	118.20	122.33
55	1x	20	H2U	N3-C2-N1	2.62	119.28	116.65
55	1x	76	8AN	N3-C4-N9	2.59	131.57	127.17
32	1a	1400	5MC	O2-C2-N3	-2.58	118.26	122.33
1	1A	1939	5MU	O2-C2-N1	-2.58	119.44	122.80
55	2x	39	PSU	C6-C5-C4	-2.57	116.44	118.17
1	1A	2552	OMU	O2-C2-N1	-2.57	119.45	122.80
55	2x	37	MIA	C4-N9-C8	2.57	108.44	105.74
1	2A	2503	2MA	C5-N7-C8	2.56	107.48	103.45
32	1a	1207	2MG	C4-C5-N7	-2.56	106.62	110.67
1	2A	1962	5MC	C5-C4-N3	-2.55	119.14	121.75
32	1a	1519	MA6	C4-C5-C6	2.55	118.55	115.91
55	2x	55	PSU	C5-C6-N1	-2.52	118.64	122.14
55	1x	8	4SU	N3-C2-N1	2.52	118.17	114.89

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	2A	1939	5MU	O2-C2-N1	-2.52	119.52	122.80
1	2A	2251	OMG	C4-C5-N7	-2.51	106.69	110.67
32	2a	527	G7M	O6-C6-C5	-2.49	122.45	128.01
1	2A	1942	5MC	O2-C2-N3	-2.49	118.40	122.33
32	2a	516	PSU	O4'-C1'-C2'	2.49	108.59	105.15
32	1a	1407	5MC	CM5-C5-C6	-2.48	119.50	122.85
1	2A	1911	PSU	C6-C5-C4	-2.48	116.50	118.17
1	1A	2605	PSU	C5-C6-N1	-2.48	118.70	122.14
55	2x	76	8AN	N3-C4-N9	2.47	131.37	127.17
32	2a	516	PSU	C5-C6-N1	-2.46	118.72	122.14
32	2a	1402	4OC	C6-C5-C4	2.45	119.95	117.00
55	2x	76	8AN	C6-C5-C4	2.44	120.50	117.18
32	2a	1400	5MC	C5-C4-N3	-2.41	119.28	121.75
1	2A	2503	2MA	C2-N1-C6	2.41	121.80	118.10
32	2a	527	G7M	C5-C6-N1	2.38	116.76	111.84
32	1a	1498	UR3	C6-N1-C2	-2.36	119.87	121.80
32	2a	1207	2MG	N2-C2-N3	-2.35	117.51	120.51
55	1x	55	PSU	C5-C6-N1	-2.34	118.89	122.14
1	1A	2503	2MA	N9-C8-N7	-2.33	110.63	113.94
1	2A	2552	OMU	O4-C4-C5	-2.33	121.15	125.16
55	2x	8	4SU	C1'-N1-C2	2.32	121.77	117.59
55	2x	76	8AN	O4'-C1'-N9	-2.31	103.65	108.09
1	1A	2503	2MA	C6-C5-N7	2.29	136.50	132.09
32	2a	1402	4OC	O2-C2-N3	-2.28	118.73	122.33
55	2x	76	8AN	C4-C5-N7	-2.28	107.97	110.58
55	1x	76	8AN	C5-C4-N9	2.27	108.28	105.81
55	2x	37	MIA	C6-C5-N7	2.25	136.42	132.09
32	1a	516	PSU	C5-C6-N1	-2.24	119.03	122.14
55	1x	8	4SU	C5-C4-S4	-2.24	121.75	124.31
1	1A	2251	OMG	C5-C6-N1	2.23	118.94	113.25
32	2a	967	5MC	C5-C4-N3	-2.23	119.47	121.75
1	1A	2503	2MA	C2-N1-C6	2.21	121.50	118.10
55	2x	21	H2U	N3-C2-N1	-2.21	114.42	116.65
1	1A	1962	5MC	CM5-C5-C6	-2.21	119.86	122.85
32	1a	1518	MA6	C4-C5-C6	2.21	118.19	115.91
32	1a	966	M2G	O6-C6-C5	-2.21	120.71	126.53
1	2A	2605	PSU	O2-C2-N3	-2.20	117.95	121.86
1	2A	2251	OMG	O6-C6-C5	-2.19	120.75	126.53
1	2A	1915	5MU	O2-C2-N3	-2.16	117.50	121.49
55	1x	37	MIA	C4-N9-C8	2.15	108.00	105.74
1	1A	1917	PSU	C5-C6-N1	-2.15	119.16	122.14
32	1a	1518	MA6	C4-N9-C8	2.14	107.98	105.74

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
55	1x	21	H2U	O4-C4-N3	2.13	123.59	120.30
43	1l	92	0TD	OD1-CG-CB	-2.12	118.00	122.44
32	1a	1402	4OC	O2-C2-N3	-2.11	119.00	122.33
32	1a	1400	5MC	C1'-N1-C6	-2.11	117.68	121.15
1	1A	2251	OMG	C4-C5-N7	-2.11	107.33	110.67
1	1A	1942	5MC	N1-C2-N3	2.10	122.45	118.80
1	1A	1942	5MC	CM5-C5-C6	-2.10	120.01	122.85
1	1A	1920	OMC	O2-C2-N3	-2.09	119.03	122.33
1	1A	1911	PSU	C5-C6-N1	-2.09	119.24	122.14
1	2A	1911	PSU	C5-C6-N1	-2.09	119.25	122.14
55	1x	37	MIA	C6-C5-N7	2.08	136.09	132.09
32	2a	967	5MC	CM5-C5-C6	-2.07	120.05	122.85
32	2a	1519	MA6	C5-C4-N9	2.07	108.07	105.81
1	2A	2503	2MA	N9-C8-N7	-2.07	111.00	113.94
55	2x	37	MIA	N9-C8-N7	-2.06	111.01	113.94
32	1a	1207	2MG	C2-N1-C6	-2.06	122.06	124.55
1	1A	2251	OMG	CM2-O2'-C2'	-2.04	109.23	114.47
32	1a	516	PSU	O4'-C1'-C2'	2.04	107.97	105.15
55	1x	76	8AN	C4-C5-N7	-2.02	108.27	110.58
55	2x	39	PSU	O4'-C1'-C2'	2.02	107.94	105.15
55	1x	39	PSU	C5-C6-N1	-2.02	119.34	122.14
55	2x	55	PSU	O2-C2-N3	-2.01	118.28	121.86
32	1a	527	G7M	C5-C6-N1	2.01	116.00	111.84
32	2a	1498	UR3	C3U-N3-C2	2.01	120.83	117.33
1	1A	1911	PSU	O2-C2-N3	-2.00	118.31	121.86
55	1x	20	H2U	O2-C2-N1	-2.00	120.70	123.10
32	1a	1404	5MC	O2-C2-N3	-2.00	119.17	122.33

There are no chirality outliers.

All (47) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
32	1a	1519	MA6	O4'-C4'-C5'-O5'
43	1l	92	0TD	O-C-CA-CB
1	2A	2251	OMG	C1'-C2'-O2'-CM2
32	2a	1207	2MG	N1-C2-N2-CM2
32	2a	1207	2MG	N3-C2-N2-CM2
32	2a	1402	4OC	O4'-C4'-C5'-O5'
55	2x	20	H2U	C4'-C5'-O5'-P
55	1x	21	H2U	O4'-C1'-N1-C6
55	2x	21	H2U	O4'-C1'-N1-C6
55	1x	37	MIA	O4'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
55	2x	76	8AN	C4'-C5'-O5'-P
32	1a	527	G7M	C3'-C4'-C5'-O5'
32	1a	1402	4OC	O4'-C4'-C5'-O5'
55	2x	20	H2U	O4'-C4'-C5'-O5'
55	2x	20	H2U	C3'-C4'-C5'-O5'
55	2x	37	MIA	O4'-C4'-C5'-O5'
55	1x	20	H2U	O4'-C4'-C5'-O5'
55	1x	20	H2U	C3'-C4'-C5'-O5'
55	1x	21	H2U	C3'-C4'-C5'-O5'
32	1a	1519	MA6	C3'-C4'-C5'-O5'
32	2a	1402	4OC	C3'-C4'-C5'-O5'
55	1x	37	MIA	C3'-C4'-C5'-O5'
55	1x	21	H2U	C2'-C1'-N1-C2
32	1a	1402	4OC	C3'-C4'-C5'-O5'
32	2a	1519	MA6	O4'-C4'-C5'-O5'
55	2x	37	MIA	C3'-C4'-C5'-O5'
55	1x	76	8AN	C4'-C5'-O5'-P
32	1a	527	G7M	O4'-C4'-C5'-O5'
55	2x	21	H2U	C4'-C5'-O5'-P
55	1x	21	H2U	O4'-C1'-N1-C2
55	1x	21	H2U	O4'-C4'-C5'-O5'
43	2l	92	0TD	SB-CB-CG-OD1
55	1x	21	H2U	C2'-C1'-N1-C6
32	2a	527	G7M	C3'-C4'-C5'-O5'
32	1a	1519	MA6	C4'-C5'-O5'-P
1	2A	2503	2MA	O4'-C4'-C5'-O5'
32	1a	967	5MC	O4'-C4'-C5'-O5'
55	2x	21	H2U	O4'-C1'-N1-C2
1	1A	2503	2MA	O4'-C4'-C5'-O5'
43	1l	92	0TD	CG-CB-SB-CSB
43	2l	92	0TD	CG-CB-SB-CSB
32	2a	1519	MA6	C3'-C4'-C5'-O5'
32	2a	1519	MA6	C4'-C5'-O5'-P
32	2a	1402	4OC	C2'-C1'-N1-C2
1	1A	2503	2MA	C4'-C5'-O5'-P
32	1a	527	G7M	C4'-C5'-O5'-P
55	2x	21	H2U	C2'-C1'-N1-C2

There are no ring outliers.

26 monomers are involved in 27 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
32	1a	966	M2G	1	0
1	1A	2251	OMG	1	0
55	2x	20	H2U	2	0
43	2l	92	0TD	1	0
1	2A	2552	OMU	1	0
32	2a	1402	4OC	1	0
32	2a	1518	MA6	1	0
32	1a	1402	4OC	3	0
32	2a	1207	2MG	1	0
32	2a	966	M2G	1	0
1	1A	1917	PSU	1	0
32	1a	967	5MC	1	0
32	2a	967	5MC	1	0
43	1l	92	0TD	1	0
32	1a	1207	2MG	1	0
32	1a	516	PSU	1	0
1	1A	2552	OMU	1	0
32	1a	1518	MA6	1	0
32	1a	1519	MA6	1	0
1	1A	1939	5MU	1	0
32	2a	1404	5MC	1	0
55	1x	8	4SU	1	0
55	2x	21	H2U	2	0
1	2A	2251	OMG	1	0
1	2A	1915	5MU	1	0
32	2a	1519	MA6	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2604 ligands modelled in this entry, 2602 are monoatomic - leaving 2 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
60	SF4	2d	303	35	0,12,12	-	-	-		
60	SF4	1d	302	35	0,12,12	-	-	-		

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
60	SF4	2d	303	35	-	-	0/6/5/5
60	SF4	1d	302	35	-	-	0/6/5/5

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	2860/2915 (98%)	-0.37	202 (7%) 22 19	10, 26, 88, 100	0
1	2A	2789/2915 (95%)	0.11	169 (6%) 27 24	22, 45, 84, 99	0
2	1B	120/121 (99%)	-0.25	0 100 100	21, 41, 54, 78	0
2	2B	120/121 (99%)	0.93	6 (5%) 34 30	48, 66, 76, 87	0
3	1D	275/276 (99%)	-0.19	2 (0%) 84 83	14, 28, 44, 72	0
3	2D	275/276 (99%)	0.22	5 (1%) 67 65	20, 38, 51, 69	0
4	1E	204/206 (99%)	-0.18	2 (0%) 79 78	11, 28, 51, 64	0
4	2E	204/206 (99%)	0.28	5 (2%) 58 55	23, 45, 60, 75	0
5	1F	203/210 (96%)	-0.04	1 (0%) 87 86	11, 31, 58, 78	0
5	2F	203/210 (96%)	0.74	13 (6%) 25 22	26, 56, 68, 77	0
6	1G	181/182 (99%)	0.99	23 (12%) 8 7	36, 54, 68, 81	0
6	2G	181/182 (99%)	1.65	50 (27%) 1 1	58, 68, 77, 85	0
7	1H	174/180 (96%)	0.30	5 (2%) 53 50	27, 43, 55, 71	0
7	2H	174/180 (96%)	1.87	75 (43%) 0 0	57, 71, 80, 86	0
8	1I	146/148 (98%)	0.90	11 (7%) 20 17	32, 62, 72, 76	0
8	2I	146/148 (98%)	1.24	27 (18%) 3 3	45, 66, 72, 76	0
9	1N	140/140 (100%)	-0.12	1 (0%) 84 83	17, 27, 49, 63	0
9	2N	140/140 (100%)	0.71	10 (7%) 22 19	34, 51, 65, 72	0
10	1O	122/122 (100%)	0.01	3 (2%) 58 55	18, 31, 48, 55	0
10	2O	122/122 (100%)	0.35	3 (2%) 58 55	32, 43, 56, 65	0
11	1P	149/150 (99%)	0.02	3 (2%) 65 62	11, 34, 55, 63	0
11	2P	149/150 (99%)	0.74	6 (4%) 42 38	28, 56, 71, 76	0
12	1Q	141/141 (100%)	-0.02	2 (1%) 73 72	19, 29, 43, 53	0
12	2Q	141/141 (100%)	0.74	6 (4%) 40 36	36, 51, 62, 71	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
13	1R	118/118 (100%)	-0.31	0 100 100	16, 24, 37, 47	0
13	2R	118/118 (100%)	0.31	1 (0%) 82 81	29, 40, 53, 59	0
14	1S	110/112 (98%)	0.19	0 100 100	29, 40, 51, 59	0
14	2S	110/112 (98%)	1.41	22 (20%) 3 2	51, 61, 71, 75	0
15	1T	131/146 (89%)	0.09	4 (3%) 51 48	23, 34, 59, 65	0
15	2T	131/146 (89%)	0.35	7 (5%) 32 28	38, 47, 64, 72	0
16	1U	116/118 (98%)	-0.42	1 (0%) 81 80	13, 19, 36, 47	0
16	2U	116/118 (98%)	0.45	1 (0%) 81 80	30, 45, 62, 70	0
17	1V	101/101 (100%)	-0.30	0 100 100	12, 29, 48, 62	0
17	2V	101/101 (100%)	0.99	7 (6%) 23 20	32, 57, 67, 75	0
18	1W	112/113 (99%)	-0.37	0 100 100	15, 22, 39, 69	0
18	2W	112/113 (99%)	0.17	2 (1%) 67 65	30, 38, 54, 76	0
19	1X	95/96 (98%)	-0.10	2 (2%) 63 61	20, 28, 53, 69	0
19	2X	95/96 (98%)	0.71	8 (8%) 17 14	36, 50, 66, 75	0
20	1Y	107/110 (97%)	0.17	1 (0%) 81 80	24, 38, 57, 68	0
20	2Y	107/110 (97%)	1.15	18 (16%) 4 3	47, 59, 71, 82	0
21	1Z	154/206 (74%)	0.68	8 (5%) 33 29	30, 46, 60, 69	0
21	2Z	160/206 (77%)	1.52	35 (21%) 2 2	51, 67, 74, 78	0
22	10	76/85 (89%)	-0.06	3 (3%) 43 39	19, 27, 49, 55	0
22	20	76/85 (89%)	0.92	6 (7%) 18 16	37, 51, 62, 68	0
23	11	97/98 (98%)	0.18	2 (2%) 63 61	18, 33, 59, 64	0
23	21	97/98 (98%)	0.56	4 (4%) 41 37	30, 47, 65, 68	0
24	12	70/72 (97%)	0.25	3 (4%) 40 36	25, 39, 51, 65	0
24	22	70/72 (97%)	0.92	1 (1%) 73 72	49, 60, 68, 70	0
25	13	59/60 (98%)	-0.07	2 (3%) 48 44	16, 25, 48, 63	0
25	23	59/60 (98%)	0.72	5 (8%) 16 14	37, 48, 63, 69	0
26	14	69/71 (97%)	1.49	19 (27%) 1 1	48, 69, 82, 86	0
26	24	69/71 (97%)	2.00	30 (43%) 0 0	65, 75, 84, 88	0
27	15	59/60 (98%)	-0.38	1 (1%) 69 67	12, 22, 40, 55	0
27	25	59/60 (98%)	0.31	1 (1%) 69 67	25, 39, 57, 70	0
28	16	53/54 (98%)	-0.07	0 100 100	23, 32, 47, 54	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
28	26	53/54 (98%)	0.51	4 (7%) 20 17	39, 49, 55, 63	0
29	17	48/49 (97%)	-0.32	3 (6%) 26 23	14, 19, 52, 59	0
29	27	48/49 (97%)	0.13	2 (4%) 40 37	26, 33, 56, 65	0
30	18	64/65 (98%)	-0.46	0 100 100	18, 24, 32, 41	0
30	28	64/65 (98%)	0.33	1 (1%) 70 68	34, 43, 52, 57	0
31	19	37/37 (100%)	-0.29	0 100 100	21, 30, 50, 50	0
31	29	37/37 (100%)	0.69	3 (8%) 18 15	43, 53, 62, 62	0
32	1a	1488/1521 (97%)	0.81	147 (9%) 13 10	28, 64, 86, 100	0
32	2a	1491/1521 (98%)	0.91	196 (13%) 7 6	38, 66, 86, 100	0
33	1b	231/256 (90%)	1.74	71 (30%) 1 1	58, 70, 80, 85	0
33	2b	231/256 (90%)	2.08	125 (54%) 0 0	61, 74, 81, 88	0
34	1c	206/239 (86%)	1.72	65 (31%) 1 1	57, 70, 77, 80	0
34	2c	206/239 (86%)	2.19	110 (53%) 0 0	59, 74, 80, 86	0
35	1d	208/209 (99%)	1.63	63 (30%) 1 1	49, 66, 76, 78	0
35	2d	208/209 (99%)	1.40	43 (20%) 2 2	50, 63, 73, 76	0
36	1e	148/162 (91%)	0.93	11 (7%) 20 18	44, 58, 67, 75	0
36	2e	148/162 (91%)	1.27	23 (15%) 5 4	51, 63, 71, 78	0
37	1f	100/101 (99%)	0.97	3 (3%) 52 49	46, 60, 68, 72	0
37	2f	100/101 (99%)	1.18	12 (12%) 9 7	56, 64, 72, 73	0
38	1g	155/156 (99%)	1.37	26 (16%) 4 3	58, 66, 76, 84	0
38	2g	155/156 (99%)	1.72	48 (30%) 1 1	61, 71, 78, 83	0
39	1h	137/138 (99%)	1.05	12 (8%) 15 13	51, 61, 69, 74	0
39	2h	137/138 (99%)	1.22	16 (11%) 9 7	54, 64, 70, 74	0
40	1i	127/128 (99%)	1.79	43 (33%) 1 1	55, 69, 75, 78	0
40	2i	127/128 (99%)	2.46	81 (63%) 0 0	64, 74, 81, 83	0
41	1j	97/105 (92%)	2.04	50 (51%) 0 0	58, 73, 79, 80	0
41	2j	96/105 (91%)	2.53	69 (71%) 0 0	63, 76, 82, 86	0
42	1k	114/129 (88%)	1.04	11 (9%) 13 11	36, 58, 70, 75	0
42	2k	114/129 (88%)	1.47	22 (19%) 3 3	46, 63, 73, 78	0
43	1l	121/132 (91%)	0.87	9 (7%) 20 18	41, 52, 62, 68	0
43	2l	121/132 (91%)	0.66	4 (3%) 49 45	46, 53, 63, 69	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
44	1m	118/126 (93%)	1.73	38 (32%) 1 1	60, 69, 75, 81	0
44	2m	116/126 (92%)	1.89	42 (36%) 1 0	63, 73, 77, 81	0
45	1n	60/61 (98%)	1.90	23 (38%) 1 0	57, 68, 76, 80	0
45	2n	60/61 (98%)	2.56	40 (66%) 0 0	67, 74, 79, 80	0
46	1o	88/89 (98%)	0.94	8 (9%) 15 12	37, 57, 68, 72	0
46	2o	88/89 (98%)	1.08	8 (9%) 15 12	52, 63, 73, 79	0
47	1p	82/88 (93%)	1.67	26 (31%) 1 1	56, 65, 75, 81	0
47	2p	82/88 (93%)	1.30	10 (12%) 8 7	50, 61, 69, 75	0
48	1q	99/105 (94%)	0.96	6 (6%) 27 24	45, 57, 67, 75	0
48	2q	99/105 (94%)	0.81	4 (4%) 42 38	51, 60, 70, 73	0
49	1r	68/88 (77%)	0.94	5 (7%) 20 18	48, 58, 67, 71	0
49	2r	68/88 (77%)	1.34	8 (11%) 9 7	56, 65, 74, 77	0
50	1s	83/93 (89%)	2.21	41 (49%) 0 0	62, 72, 79, 80	0
50	2s	83/93 (89%)	2.28	51 (61%) 0 0	69, 76, 82, 88	0
51	1t	96/106 (90%)	1.35	20 (20%) 2 2	52, 61, 70, 77	0
51	2t	96/106 (90%)	0.96	12 (12%) 8 7	47, 60, 69, 72	0
52	1u	23/27 (85%)	2.19	10 (43%) 0 0	61, 68, 73, 75	0
52	2u	23/27 (85%)	2.22	13 (56%) 0 0	64, 72, 76, 78	0
53	1v	13/24 (54%)	1.43	7 (53%) 0 0	43, 54, 92, 92	0
53	2v	9/24 (37%)	1.17	2 (22%) 2 2	52, 57, 79, 84	0
54	1w	249/354 (70%)	0.58	11 (4%) 39 35	20, 52, 68, 81	0
54	2w	253/354 (71%)	1.03	25 (9%) 13 10	33, 60, 77, 87	0
55	1x	65/74 (87%)	0.08	0 100 100	19, 51, 68, 71	0
55	2x	65/74 (87%)	0.52	1 (1%) 72 70	32, 64, 78, 80	0
56	1z	5/7 (71%)	1.65	2 (40%) 1 0	27, 27, 49, 51	0
56	2z	5/7 (71%)	2.41	3 (60%) 0 0	38, 43, 56, 57	0
All	All	21079/22160 (95%)	0.60	2513 (11%) 9 7	10, 53, 79, 100	0

All (2513) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
45	2n	2	ALA	14.3
1	2A	2117	A	11.9

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Mol	Chain	Res	Type	RSRZ
1	1A	2116	G	9.5
45	1n	2	ALA	9.4
1	2A	2115	G	9.0
1	2A	2138	C	8.7
1	2A	2803	C	8.7
1	1A	2117	A	8.6
1	2A	2793	G	8.6
1	1A	1088	A	8.5
1	2A	2116	G	8.5
1	1A	2141	G	8.2
1	2A	2802	G	8.2
1	1A	1072	C	8.2
1	1A	2115	G	8.2
1	1A	2129	C	8.2
1	1A	2174	C	8.1
1	2A	2122	U	8.0
1	2A	2108	C	8.0
1	1A	2120	G	7.9
1	1A	2121	G	7.9
1	2A	2111	C	7.9
1	1A	1068	G	7.8
1	1A	2114	A	7.8
1	1A	2175	C	7.6
1	1A	2108	C	7.6
26	24	49	PHE	7.4
1	1A	1057	A	7.3
1	2A	2804	C	7.3
44	1m	2	ALA	7.3
1	2A	2137	C	7.2
1	1A	1069	A	7.2
1	2A	2147	G	7.2
1	1A	2178	C	7.2
1	1A	2113	U	7.1
1	2A	2120	G	7.1
1	1A	2119	A	7.1
1	1A	1093	G	7.1
1	1A	2112	G	6.9
1	2A	2121	G	6.8
1	1A	1071	G	6.8
1	2A	2174	C	6.8
32	1a	1003	G	6.6
1	2A	2135	A	6.6

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Mol	Chain	Res	Type	RSRZ
1	1A	2179	C	6.5
32	1a	1026	G	6.4
1	1A	2135	A	6.4
1	2A	2114	A	6.4
1	2A	2105	C	6.4
1	1A	1058	G	6.4
1	1A	2159	G	6.4
1	1A	2148	G	6.3
1	2A	2123	G	6.3
1	1A	1094	U	6.3
1	2A	2169	A	6.3
1	1A	1059	G	6.3
1	1A	2128	C	6.3
1	2A	2148	G	6.2
1	1A	2892	A	6.2
1	2A	2173	A	6.2
1	1A	2130	U	6.2
1	2A	2170	A	6.1
32	2a	1034	G	6.1
32	1a	1027	C	6.1
1	1A	2169	A	6.1
32	1a	1036	G	6.0
1	1A	1062	G	6.0
1	1A	2122	U	6.0
20	2Y	1	MET	6.0
21	2Z	174	VAL	6.0
1	1A	2170	A	6.0
32	1a	1000	U	5.9
1	1A	1097	U	5.9
32	1a	1025	U	5.9
1	2A	2155	G	5.9
1	2A	2110	G	5.9
32	1a	1029	C	5.8
1	1A	2125	G	5.8
1	2A	2165	G	5.8
50	1s	71	LEU	5.8
32	2a	1036	G	5.8
1	2A	2128	C	5.8
1	2A	2134	A	5.8
1	1A	2167	U	5.7
1	2A	2113	U	5.7
1	1A	2173	A	5.7

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Mol	Chain	Res	Type	RSRZ
1	2A	2177	C	5.7
54	2w	351	LEU	5.7
1	2A	2101	G	5.7
3	1D	276	LYS	5.7
7	2H	2	SER	5.7
1	1A	2110	G	5.7
1	2A	2100	G	5.7
38	2g	4	ARG	5.6
1	2A	2792	G	5.6
23	2l	2	SER	5.6
33	1b	230	VAL	5.6
56	1z	3	ALA	5.6
1	1A	1098	A	5.5
32	2a	1035	A	5.5
1	2A	2107	C	5.5
32	1a	1028	C	5.5
1	2A	2125	G	5.5
1	2A	2160	G	5.5
1	1A	2104	G	5.5
1	1A	1073	A	5.5
1	1A	1063	G	5.4
1	1A	2124	G	5.4
1	1A	2168	G	5.4
1	2A	2104	G	5.4
1	1A	2150	U	5.4
33	1b	229	VAL	5.4
1	1A	1067	A	5.4
1	1A	2145	C	5.4
1	2A	2136	C	5.4
1	1A	1087	G	5.4
1	2A	2112	G	5.4
38	2g	80	VAL	5.4
7	1H	2	SER	5.4
1	1A	1086	A	5.4
33	2b	93	VAL	5.4
1	2A	2118	U	5.3
1	2A	2167	U	5.3
32	1a	1024	G	5.3
34	2c	194	GLY	5.3
1	2A	2178	C	5.3
1	2A	2166	G	5.3
1	1A	2160	G	5.3

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Mol	Chain	Res	Type	RSRZ
1	2A	2182	G	5.3
44	2m	5	ALA	5.3
1	2A	2149	G	5.2
32	1a	1002	G	5.2
1	2A	2119	A	5.2
56	2z	3	ALA	5.2
1	1A	2165	G	5.2
32	2a	1033	G	5.2
1	1A	2109	U	5.2
36	2e	21	ALA	5.1
34	2c	2	GLY	5.1
1	1A	2118	U	5.1
1	1A	2136	C	5.1
1	2A	2139	C	5.1
1	1A	1100	C	5.1
44	2m	102	ARG	5.1
47	1p	42	ARG	5.1
34	1c	65	ALA	5.0
34	2c	71	ALA	5.0
8	2I	133	HIS	5.0
1	1A	2158	A	5.0
1	1A	1099	G	5.0
1	2A	2159	G	5.0
32	1a	1001(A)	G	5.0
1	2A	2129	C	5.0
40	2i	66	ARG	5.0
32	2a	1004	A	5.0
33	1b	227	GLY	5.0
1	1A	2181	G	5.0
1	1A	1064	C	4.9
35	1d	3	ARG	4.9
20	1Y	1	MET	4.9
1	2A	2801(A)	A	4.9
1	1A	2111	C	4.9
1	2A	2106	G	4.9
1	1A	1065	U	4.9
1	2A	2126	A	4.9
1	2A	2168	G	4.9
1	1A	2134	A	4.9
1	2A	2183	C	4.8
32	2a	1027	C	4.8
1	1A	2102	U	4.8

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Mol	Chain	Res	Type	RSRZ
32	1a	1286	A	4.8
40	2i	91	ASP	4.8
50	1s	13	ASP	4.8
35	1d	170	VAL	4.8
1	1A	2149	G	4.8
32	1a	1034	G	4.8
1	2A	11	G	4.8
32	1a	1032	G	4.8
50	2s	84	GLY	4.8
32	1a	1005	A	4.8
1	1A	1060	U	4.7
32	2a	1029	C	4.7
40	2i	7	THR	4.7
38	1g	81	GLY	4.7
1	1A	11	G	4.7
1	1A	2147	G	4.7
1	2A	2805	G	4.7
38	1g	82	GLY	4.7
40	2i	67	GLY	4.7
1	2A	2146	C	4.7
1	2A	2175	C	4.7
1	2A	2133	G	4.7
26	14	59	PHE	4.7
23	11	26	ARG	4.7
1	2A	1537	G	4.7
32	1a	1041	A	4.7
26	24	56	VAL	4.7
1	1A	1082	U	4.7
1	1A	1092	C	4.6
32	1a	1039	C	4.6
54	2w	190	GLY	4.6
1	2A	2162	G	4.6
40	1i	8	GLY	4.6
1	2A	2163	C	4.6
14	2S	32	LEU	4.6
7	2H	45	VAL	4.6
1	1A	2893	G	4.6
1	1A	2894	G	4.6
32	1a	1035	A	4.6
1	1A	1089	G	4.6
1	2A	2154	G	4.6
1	1A	2139	C	4.5

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Mol	Chain	Res	Type	RSRZ
38	1g	34	GLY	4.5
47	2p	82	GLN	4.5
1	1A	1074	G	4.5
1	1A	2151	G	4.5
1	2A	2130	U	4.5
1	1A	2123	G	4.5
1	2A	2124	G	4.5
32	2a	1001(A)	G	4.5
38	2g	83	ALA	4.5
1	1A	2177	C	4.5
1	1A	2803	C	4.5
1	2A	888	C	4.5
1	2A	2179	C	4.5
33	2b	7	VAL	4.5
44	2m	6	GLY	4.5
35	2d	122	ARG	4.5
44	2m	7	VAL	4.5
32	2a	1028	C	4.4
44	1m	97	PRO	4.4
33	1b	17	PHE	4.4
40	1i	15	ALA	4.4
44	2m	118	ALA	4.4
34	2c	159	GLY	4.4
41	2j	37	PRO	4.4
32	1a	1040	U	4.4
39	2h	2	LEU	4.4
34	1c	189	ALA	4.4
1	2A	2894	G	4.4
1	2A	2145	C	4.4
1	2A	2164	C	4.4
1	2A	2109	U	4.4
1	2A	2132	U	4.4
40	2i	102	LEU	4.4
33	2b	91	PRO	4.4
1	1A	2131	G	4.4
1	1A	2186	G	4.4
1	1A	2792	G	4.4
1	1A	2107	C	4.4
1	2A	2102	U	4.3
34	1c	62	ASP	4.3
1	1A	1070	A	4.3
1	2A	2158	A	4.3

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Mol	Chain	Res	Type	RSRZ
32	1a	1001	A	4.3
42	2k	126	ARG	4.3
1	1A	2190	G	4.3
40	2i	105	ASP	4.3
32	2a	1001	A	4.3
34	1c	193	TYR	4.3
41	2j	40	LEU	4.3
50	2s	13	ASP	4.3
12	2Q	60	ARG	4.3
50	1s	4	SER	4.3
1	1A	2156	G	4.3
1	1A	2172	U	4.3
1	1A	2176	A	4.3
1	2A	2176	A	4.3
50	1s	16	LEU	4.3
50	1s	35	SER	4.3
35	1d	23	GLY	4.3
1	2A	2150	U	4.3
32	2a	1219	U	4.3
1	1A	2133	G	4.3
1	1A	2142	C	4.3
33	2b	13	ALA	4.2
50	2s	2	PRO	4.2
32	2a	1218	C	4.2
1	1A	2805	G	4.2
52	1u	23	PRO	4.2
34	2c	195	VAL	4.2
6	2G	53	LEU	4.2
1	1A	2103	C	4.2
32	1a	76	C	4.2
42	2k	13	GLN	4.2
1	1A	2166	G	4.2
1	2A	2156	G	4.2
32	2a	1002	G	4.2
41	2j	49	VAL	4.2
35	2d	157	LEU	4.2
1	1A	1081	U	4.2
1	2A	2161	C	4.2
44	2m	54	VAL	4.2
1	1A	12	U	4.1
12	2Q	59	ARG	4.1
1	1A	2140	C	4.1

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Mol	Chain	Res	Type	RSRZ
32	2a	1038	C	4.1
38	1g	85	TYR	4.1
38	2g	156	TRP	4.1
52	1u	21	TYR	4.1
1	2A	2131	G	4.1
6	2G	50	ALA	4.1
45	2n	55	GLY	4.1
35	1d	115	ARG	4.1
1	2A	2103	C	4.1
1	2A	2171	A	4.1
32	1a	1038	C	4.1
32	2a	1256	A	4.1
6	1G	48	GLU	4.1
1	2A	2157	G	4.1
25	23	29	ARG	4.1
33	2b	36	ARG	4.1
40	2i	18	PHE	4.1
33	1b	97	TRP	4.1
32	1a	1447	A	4.1
32	2a	994	A	4.1
41	1j	4	ILE	4.1
34	1c	52	LEU	4.1
50	1s	20	LEU	4.1
40	2i	109	VAL	4.1
45	2n	18	VAL	4.1
1	1A	2154	G	4.0
1	2A	1113	U	4.0
26	14	67	TYR	4.0
26	24	67	TYR	4.0
36	1e	85	GLY	4.0
40	1i	9	ARG	4.0
34	2c	52	LEU	4.0
44	2m	98	VAL	4.0
1	1A	2146	C	4.0
42	2k	31	THR	4.0
1	1A	2127	G	4.0
1	1A	2793	G	4.0
32	2a	1030(A)	G	4.0
1	1A	2132	U	4.0
35	2d	115	ARG	4.0
38	2g	32	ARG	4.0
33	2b	133	LYS	4.0

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Mol	Chain	Res	Type	RSRZ
1	1A	2137	C	4.0
34	2c	79	ARG	4.0
44	1m	118	ALA	4.0
54	2w	350	ALA	4.0
21	2Z	146	ILE	4.0
52	2u	14	TRP	4.0
1	1A	2162	G	4.0
41	1j	24	VAL	4.0
34	2c	192	THR	4.0
1	1A	1177	A	4.0
7	2H	124	GLU	4.0
1	1A	2185	C	4.0
32	2a	1363	C	4.0
38	2g	81	GLY	4.0
40	2i	81	ILE	4.0
19	2X	92	LEU	4.0
51	1t	9	ASN	4.0
32	2a	1000	U	4.0
1	1A	2106	G	3.9
1	2A	2127	G	3.9
1	2A	2190	G	3.9
34	2c	190	ARG	3.9
33	2b	200	ILE	3.9
34	2c	168	ALA	3.9
1	1A	2801(A)	A	3.9
33	2b	33	TYR	3.9
1	1A	2794	C	3.9
1	2A	2896	C	3.9
32	1a	999	C	3.9
9	2N	8	GLN	3.9
33	1b	231	GLU	3.9
8	1I	45	LYS	3.9
51	1t	103	GLY	3.9
32	2a	1005	A	3.9
1	1A	2105	C	3.9
36	2e	20	GLN	3.9
1	2A	2172	U	3.9
21	2Z	136	PHE	3.9
40	2i	14	VAL	3.9
32	2a	1447	A	3.9
32	1a	1037	C	3.9
32	2a	1257	U	3.9

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Mol	Chain	Res	Type	RSRZ
50	1s	84	GLY	3.9
40	2i	103	THR	3.8
1	1A	2187	G	3.8
32	1a	1030(A)	G	3.8
32	1a	1224	G	3.8
1	1A	1077	A	3.8
40	1i	56	LEU	3.8
1	1A	2164	C	3.8
1	1A	1101	U	3.8
38	1g	80	VAL	3.8
4	2E	151	TYR	3.8
41	2j	6	ILE	3.8
1	2A	2186	G	3.8
32	1a	1021	G	3.8
32	2a	1023	G	3.8
34	2c	185	GLY	3.8
35	1d	171	GLY	3.8
1	1A	2163	C	3.8
1	2A	2140	C	3.8
1	2A	2142	C	3.8
38	2g	84	ASN	3.8
20	2Y	55	TYR	3.8
6	2G	62	LEU	3.8
35	1d	132	ARG	3.8
50	1s	45	VAL	3.8
32	2a	1024	G	3.8
40	1i	91	ASP	3.8
50	1s	12	ASP	3.8
1	1A	2161	C	3.8
1	2A	2143	C	3.8
38	1g	2	ALA	3.8
46	1o	89	GLY	3.8
6	1G	113	ARG	3.8
26	14	56	VAL	3.8
33	2b	44	LEU	3.7
50	2s	15	LEU	3.7
1	2A	652(T)	C	3.7
40	2i	11	LYS	3.7
45	2n	3	ARG	3.7
50	2s	9	VAL	3.7
34	2c	69	HIS	3.7
1	2A	652(B)	A	3.7

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Mol	Chain	Res	Type	RSRZ
15	1T	131	ALA	3.7
41	2j	30	SER	3.7
51	2t	103	GLY	3.7
1	1A	1066	U	3.7
38	2g	5	ARG	3.7
52	2u	6	ARG	3.7
32	1a	1023	G	3.7
21	1Z	141	VAL	3.7
45	2n	33	VAL	3.7
1	1A	1509	C	3.7
33	1b	129	GLU	3.7
34	2c	191	THR	3.7
41	1j	74	ILE	3.7
44	2m	23	TYR	3.7
34	2c	160	ALA	3.7
38	1g	4	ARG	3.7
40	2i	15	ALA	3.7
40	2i	126	SER	3.7
44	2m	100	GLY	3.7
26	24	59	PHE	3.7
40	1i	2	GLU	3.7
1	2A	2151	G	3.7
1	2A	2184	G	3.7
40	2i	96	LEU	3.7
51	1t	68	LYS	3.7
44	1m	107	ALA	3.7
7	2H	58	GLU	3.7
32	1a	1531	A	3.6
1	1A	2144	U	3.6
32	2a	1235	U	3.6
33	1b	19	HIS	3.6
34	2c	152	ILE	3.6
41	2j	75	ILE	3.6
29	27	48	LYS	3.6
32	1a	1031	G	3.6
32	1a	1033	G	3.6
1	1A	2188	C	3.6
20	2Y	58	GLY	3.6
34	2c	158	GLY	3.6
35	2d	6	GLY	3.6
45	2n	59	ALA	3.6
41	2j	44	VAL	3.6

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Mol	Chain	Res	Type	RSRZ
44	2m	58	GLU	3.6
40	1i	7	THR	3.6
45	2n	42	ILE	3.6
1	1A	883	G	3.6
1	2A	2206	G	3.6
22	20	9	SER	3.6
32	1a	1050	G	3.6
34	2c	8	ILE	3.6
35	1d	118	ARG	3.6
1	1A	2790	A	3.6
32	2a	1324	A	3.6
41	2j	77	PRO	3.6
33	2b	230	VAL	3.6
40	2i	127	LYS	3.6
1	2A	645	C	3.6
32	1a	630	G	3.6
32	2a	1258	G	3.6
41	2j	42	THR	3.6
41	2j	81	THR	3.6
50	1s	77	THR	3.6
34	1c	2	GLY	3.6
38	2g	2	ALA	3.6
41	1j	10	GLY	3.6
41	2j	93	GLY	3.6
1	1A	271(K)	U	3.6
32	2a	1025	U	3.6
32	2a	1150	U	3.6
53	2v	15	A	3.6
40	1i	14	VAL	3.6
11	2P	15	ARG	3.5
38	1g	42	ILE	3.5
40	2i	10	ARG	3.5
1	1A	1075	C	3.5
32	2a	1030	C	3.5
41	2j	78	ASN	3.5
32	2a	1003	G	3.5
33	2b	70	PHE	3.5
39	1h	93	VAL	3.5
32	1a	1257	U	3.5
32	2a	1040	U	3.5
45	1n	32	SER	3.5
46	1o	3	ILE	3.5

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Mol	Chain	Res	Type	RSRZ
38	1g	84	ASN	3.5
1	1A	1076	C	3.5
1	2A	2188	C	3.5
1	2A	2794	C	3.5
6	2G	29	TRP	3.5
21	2Z	145	GLU	3.5
36	2e	45	PHE	3.5
41	2j	47	PHE	3.5
1	2A	10	G	3.5
1	2A	1533	G	3.5
22	20	84	LEU	3.5
7	2H	3	ARG	3.5
7	2H	6	ARG	3.5
41	1j	70	ARG	3.5
45	1n	3	ARG	3.5
47	1p	81	ARG	3.5
52	1u	9	ARG	3.5
34	2c	62	ASP	3.5
40	2i	115	GLY	3.5
41	1j	32	ALA	3.5
45	1n	30	ALA	3.5
6	2G	35	GLU	3.5
35	1d	157	LEU	3.5
47	1p	80	PHE	3.5
40	2i	53	VAL	3.5
41	2j	68	HIS	3.5
38	2g	85	TYR	3.5
40	2i	9	ARG	3.5
45	2n	21	TYR	3.5
26	24	22	ILE	3.5
1	1A	2152	G	3.5
1	1A	2157	G	3.5
32	1a	78	G	3.5
32	2a	1032	G	3.5
50	2s	79	THR	3.5
32	1a	1030(D)	A	3.5
41	2j	69	ASN	3.5
52	1u	16	GLY	3.5
33	2b	170	GLU	3.5
41	2j	65	LEU	3.5
50	1s	5	LEU	3.5
33	1b	7	VAL	3.5

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Mol	Chain	Res	Type	RSRZ
26	14	55	ARG	3.5
33	2b	199	TYR	3.4
41	2j	38	ILE	3.4
42	2k	25	TYR	3.4
50	2s	35	SER	3.4
50	2s	77	THR	3.4
20	2Y	54	LYS	3.4
1	1A	2180	U	3.4
1	2A	892	G	3.4
32	2a	1124	G	3.4
33	1b	91	PRO	3.4
34	2c	100	ALA	3.4
40	1i	39	GLY	3.4
33	2b	11	LEU	3.4
33	2b	154	LEU	3.4
34	2c	196	LEU	3.4
45	2n	6	LEU	3.4
33	2b	71	VAL	3.4
45	2n	34	TYR	3.4
32	2a	1217	C	3.4
3	2D	2	ALA	3.4
6	1G	50	ALA	3.4
33	1b	232	PRO	3.4
1	2A	2141	G	3.4
1	2A	2153	G	3.4
32	2a	1026	G	3.4
33	2b	97	TRP	3.4
21	2Z	106	GLY	3.4
34	1c	187	ALA	3.4
35	1d	111	ALA	3.4
39	2h	99	GLU	3.4
42	2k	121	PRO	3.4
35	1d	174	LEU	3.4
38	2g	16	LEU	3.4
45	2n	5	ALA	3.4
23	2l	26	ARG	3.4
21	1Z	105	VAL	3.4
21	1Z	136	PHE	3.4
32	2a	1006	C	3.4
34	2c	193	TYR	3.4
40	2i	62	TYR	3.4
1	1A	1056	G	3.4

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Mol	Chain	Res	Type	RSRZ
1	2A	2893	G	3.4
22	20	10	THR	3.4
32	2a	1030(D)	A	3.4
40	1i	76	ALA	3.4
41	1j	36	GLY	3.4
41	2j	43	ARG	3.4
51	1t	10	LEU	3.4
56	1z	4	ALA	3.4
33	2b	19	HIS	3.4
6	1G	49	ASP	3.4
26	14	51	ASP	3.4
35	1d	134	ASP	3.4
9	2N	9	VAL	3.4
33	2b	163	PHE	3.4
40	2i	95	LYS	3.3
35	1d	38	TYR	3.3
41	2j	35	SER	3.3
42	1k	25	TYR	3.3
34	1c	192	THR	3.3
6	2G	139	LEU	3.3
33	2b	131	PRO	3.3
33	2b	134	GLU	3.3
35	2d	174	LEU	3.3
38	2g	76	ARG	3.3
40	2i	2	GLU	3.3
26	14	17	GLY	3.3
40	2i	42	ARG	3.3
43	1l	89	ARG	3.3
1	1A	2171	A	3.3
14	2S	34	HIS	3.3
33	2b	161	ALA	3.3
34	2c	187	ALA	3.3
40	1i	94	ALA	3.3
1	1A	1091	G	3.3
1	2A	2807	G	3.3
32	1a	102	G	3.3
42	2k	125	PHE	3.3
50	1s	9	VAL	3.3
50	1s	38	SER	3.3
50	2s	52	TYR	3.3
1	2A	1536	C	3.3
32	1a	1030	C	3.3

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Mol	Chain	Res	Type	RSRZ
32	2a	1119	C	3.3
6	1G	137	GLU	3.3
34	1c	87	LEU	3.3
41	2j	85	LEU	3.3
50	2s	16	LEU	3.3
40	2i	72	GLY	3.3
12	2Q	22	LYS	3.3
50	2s	67	VAL	3.3
7	2H	162	ILE	3.3
33	1b	127	ILE	3.3
1	1A	2802	G	3.3
32	1a	1042	G	3.3
22	20	11	ARG	3.3
49	2r	54	ARG	3.3
50	2s	4	SER	3.3
41	2j	8	LEU	3.3
1	2A	2144	U	3.3
35	2d	42	GLN	3.3
42	1k	13	GLN	3.3
45	2n	30	ALA	3.3
1	2A	893	C	3.3
33	2b	39	ILE	3.3
54	1w	323	ASP	3.3
1	1A	890	A	3.3
32	2a	1093	A	3.3
35	1d	173	TRP	3.3
1	1A	1173	G	3.3
1	1A	2101	G	3.3
1	2A	883	G	3.3
21	2Z	125	LEU	3.3
32	2a	1021	G	3.3
32	2a	1224	G	3.3
33	1b	134	GLU	3.3
52	2u	8	THR	3.3
6	2G	146	TYR	3.3
40	2i	5	TYR	3.3
26	14	54	GLY	3.3
33	2b	151	GLY	3.3
40	2i	8	GLY	3.3
34	1c	55	VAL	3.3
40	2i	63	ILE	3.3
50	1s	40	ILE	3.3

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Mol	Chain	Res	Type	RSRZ
32	2a	1018	C	3.2
35	1d	122	ARG	3.2
50	1s	29	ARG	3.2
54	2w	311	ARG	3.2
6	2G	2	PRO	3.2
32	2a	1236	A	3.2
37	2f	45	LEU	3.2
50	1s	15	LEU	3.2
33	2b	22	LYS	3.2
51	1t	18	GLN	3.2
6	1G	146	TYR	3.2
7	2H	163	TYR	3.2
52	2u	11	GLY	3.2
32	1a	1009	G	3.2
34	2c	116	VAL	3.2
44	2m	17	VAL	3.2
54	2w	185	VAL	3.2
1	2A	271(K)	U	3.2
50	2s	36	ARG	3.2
1	1A	645	C	3.2
1	2A	2789	C	3.2
20	2Y	5	MET	3.2
32	1a	1043	C	3.2
33	2b	90	MET	3.2
38	1g	12	LEU	3.2
7	2H	128	PRO	3.2
38	1g	156	TRP	3.2
40	2i	12	GLU	3.2
35	1d	116	GLN	3.2
35	1d	119	GLN	3.2
40	2i	39	GLY	3.2
1	2A	890	A	3.2
38	2g	151	TYR	3.2
40	2i	92	TYR	3.2
34	1c	64	VAL	3.2
34	2c	182	ILE	3.2
33	2b	37	ASN	3.2
1	2A	2152	G	3.2
32	2a	630	G	3.2
35	2d	3	ARG	3.2
47	1p	72	ARG	3.2
48	1q	68	ARG	3.2

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Mol	Chain	Res	Type	RSRZ
1	1A	1090	U	3.2
7	2H	85	LYS	3.2
6	2G	172	LEU	3.2
44	2m	19	LEU	3.2
41	2j	10	GLY	3.2
32	1a	1030(B)	C	3.2
32	2a	1325	C	3.2
34	2c	92	ALA	3.2
50	2s	24	ALA	3.2
7	2H	50	VAL	3.2
34	1c	5	ILE	3.2
40	2i	17	VAL	3.2
41	2j	63	PHE	3.2
53	1v	12	A	3.2
34	2c	12	LEU	3.2
41	2j	41	PRO	3.2
50	1s	42	PRO	3.2
1	1A	1083	U	3.2
1	1A	1176	G	3.2
1	1A	2155	G	3.2
1	2A	1171	G	3.2
32	1a	73	G	3.2
32	1a	1012	U	3.2
32	2a	1253	G	3.2
32	2a	1304	G	3.2
41	1j	33	GLN	3.2
12	2Q	61	GLY	3.2
7	2H	165	ALA	3.2
40	1i	106	ALA	3.2
20	2Y	89	PHE	3.2
34	1c	68	VAL	3.2
34	2c	48	TYR	3.2
1	2A	2185	C	3.1
32	2a	1259	C	3.1
41	1j	5	ARG	3.1
8	2I	87	LYS	3.1
1	1A	1095	A	3.1
33	2b	10	LEU	3.1
40	2i	19	LEU	3.1
41	1j	48	THR	3.1
33	2b	72	GLY	3.1
46	2o	86	GLY	3.1

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Mol	Chain	Res	Type	RSRZ
50	1s	34	TRP	3.1
41	2j	27	ALA	3.1
7	2H	136	ILE	3.1
35	2d	152	SER	3.1
50	2s	10	PHE	3.1
50	2s	60	VAL	3.1
32	2a	1323	G	3.1
47	1p	17	TYR	3.1
44	2m	13	LYS	3.1
1	1A	1079	C	3.1
1	1A	2143	C	3.1
1	2A	885	C	3.1
34	2c	33	LEU	3.1
45	2n	53	LEU	3.1
8	2I	48	GLU	3.1
41	1j	77	PRO	3.1
1	1A	548	A	3.1
1	1A	1046	A	3.1
1	1A	1096	A	3.1
32	2a	1130	A	3.1
34	1c	96	GLY	3.1
38	2g	82	GLY	3.1
42	2k	86	GLY	3.1
33	1b	222	ILE	3.1
34	2c	124	ILE	3.1
50	2s	50	ALA	3.1
7	2H	134	SER	3.1
33	2b	112	VAL	3.1
1	1A	1078	U	3.1
12	1Q	60	ARG	3.1
47	2p	25	ARG	3.1
52	1u	24	ARG	3.1
33	2b	236	TYR	3.1
44	1m	87	TYR	3.1
44	2m	87	TYR	3.1
33	1b	37	ASN	3.1
44	2m	70	LEU	3.1
1	1A	2184	G	3.1
32	2a	1022	G	3.1
34	1c	114	PRO	3.1
32	1a	219	C	3.1
32	2a	1019	C	3.1

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Mol	Chain	Res	Type	RSRZ
32	2a	1037	C	3.1
32	2a	1039	C	3.1
38	2g	25	ALA	3.1
40	1i	43	ALA	3.1
41	2j	50	ILE	3.1
41	2j	96	ILE	3.1
42	1k	42	TRP	3.1
7	2H	97	ARG	3.1
34	1c	66	VAL	3.1
40	2i	104	ARG	3.1
45	1n	16	PHE	3.1
50	2s	3	ARG	3.1
50	2s	29	ARG	3.1
34	1c	142	MET	3.1
26	24	32	TYR	3.1
1	2A	2895	U	3.1
45	1n	39	LEU	3.1
54	2w	208	GLU	3.1
40	2i	21	PRO	3.1
54	2w	308	PRO	3.1
16	1U	117	GLN	3.1
32	1a	1017	G	3.1
34	2c	25	GLY	3.1
7	2H	148	ILE	3.1
33	2b	34	ALA	3.1
34	2c	60	ALA	3.1
22	20	55	ARG	3.1
35	2d	112	VAL	3.1
43	2l	18	VAL	3.1
22	10	9	SER	3.1
1	1A	1085	A	3.0
2	2B	59	A	3.0
32	1a	1004	A	3.0
19	2X	69	TYR	3.0
33	2b	92	TYR	3.0
35	1d	101	LEU	3.0
42	1k	98	LEU	3.0
54	1w	348	LEU	3.0
50	1s	14	HIS	3.0
32	1a	1049	U	3.0
33	2b	66	GLY	3.0
34	2c	197	GLY	3.0

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Mol	Chain	Res	Type	RSRZ
41	2j	31	GLY	3.0
15	1T	39	ARG	3.0
21	1Z	51	ALA	3.0
21	2Z	103	ARG	3.0
34	2c	189	ALA	3.0
39	2h	28	ALA	3.0
40	1i	16	ARG	3.0
41	2j	20	ALA	3.0
52	2u	9	ARG	3.0
56	2z	4	ALA	3.0
33	1b	71	VAL	3.0
33	2b	219	VAL	3.0
43	1l	18	VAL	3.0
1	1A	271(M)	G	3.0
1	2A	171	G	3.0
32	1a	1048	G	3.0
14	2S	110	LEU	3.0
1	1A	2138	C	3.0
18	2W	60	ASN	3.0
5	2F	178	PRO	3.0
1	1A	2126	A	3.0
33	2b	135	GLN	3.0
41	2j	80	LYS	3.0
12	2Q	6	ARG	3.0
33	2b	83	MET	3.0
34	1c	88	ARG	3.0
35	1d	69	GLY	3.0
35	2d	10	ARG	3.0
46	1o	88	ARG	3.0
50	1s	68	GLY	3.0
52	2u	2	GLY	3.0
33	2b	237	ALA	3.0
34	1c	100	ALA	3.0
26	14	50	VAL	3.0
34	1c	106	VAL	3.0
41	2j	72	VAL	3.0
33	2b	69	LEU	3.0
34	2c	188	LEU	3.0
41	1j	8	LEU	3.0
7	2H	164	TYR	3.0
34	2c	7	PRO	3.0
52	1u	18	TYR	3.0

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Mol	Chain	Res	Type	RSRZ
1	1A	1171	G	3.0
32	2a	1370	G	3.0
1	1A	889	C	3.0
32	2a	470	C	3.0
32	2a	1092	A	3.0
21	1Z	146	ILE	3.0
41	1j	38	ILE	3.0
35	1d	195	ALA	3.0
32	1a	991	U	3.0
34	2c	76	VAL	3.0
41	2j	34	VAL	3.0
45	2n	36	PHE	3.0
54	2w	307	PHE	3.0
35	2d	155	LEU	3.0
41	2j	88	LEU	3.0
50	2s	34	TRP	3.0
7	2H	10	PRO	3.0
7	2H	12	PRO	3.0
7	1H	175	LYS	3.0
43	2l	64	TYR	3.0
54	1w	344	GLN	3.0
19	2X	68	ARG	3.0
33	2b	153	ARG	3.0
40	1i	104	ARG	3.0
44	1m	108	ARG	3.0
6	2G	52	ILE	3.0
41	1j	50	ILE	3.0
1	1A	2182	G	3.0
1	2A	2191	G	3.0
32	1a	79	G	3.0
32	2a	1117	G	3.0
1	1A	886	C	3.0
6	2G	171	ALA	3.0
32	1a	67	C	3.0
32	1a	989	C	3.0
32	2a	1149	C	3.0
51	1t	67	ALA	3.0
1	1A	1103	A	3.0
35	1d	105	VAL	3.0
34	2c	32	LEU	2.9
32	1a	96	U	2.9
26	24	30	GLU	2.9

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Mol	Chain	Res	Type	RSRZ
33	2b	86	GLU	2.9
34	2c	105	GLU	2.9
6	1G	76	SER	2.9
34	2c	135	LYS	2.9
33	2b	148	TYR	2.9
7	2H	42	ARG	2.9
41	2j	58	ASP	2.9
46	2o	88	ARG	2.9
42	1k	48	ILE	2.9
40	2i	6	GLY	2.9
34	1c	95	THR	2.9
7	2H	133	VAL	2.9
40	2i	26	VAL	2.9
33	1b	44	LEU	2.9
1	1A	1080	C	2.9
1	2A	1178	C	2.9
21	2Z	121	HIS	2.9
33	1b	113	HIS	2.9
10	2O	31	LYS	2.9
32	2a	1017	G	2.9
32	2a	1031	G	2.9
32	2a	1373	G	2.9
35	1d	192	GLU	2.9
53	1v	10	G	2.9
7	2H	16	SER	2.9
48	2q	97	SER	2.9
6	2G	95	ARG	2.9
40	2i	107	ARG	2.9
41	2j	79	ARG	2.9
21	2Z	9	TYR	2.9
21	2Z	29	TYR	2.9
44	1m	59	TYR	2.9
46	1o	69	TYR	2.9
7	2H	142	GLY	2.9
21	2Z	51	ALA	2.9
36	2e	48	ALA	2.9
6	2G	149	VAL	2.9
33	2b	184	VAL	2.9
7	2H	88	LEU	2.9
33	1b	11	LEU	2.9
33	2b	158	LEU	2.9
40	2i	50	LEU	2.9

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Mol	Chain	Res	Type	RSRZ
6	2G	105	LYS	2.9
33	2b	140	HIS	2.9
47	1p	12	LYS	2.9
50	2s	14	HIS	2.9
39	1h	57	PRO	2.9
40	1i	126	SER	2.9
54	1w	309	GLN	2.9
1	1A	2791	C	2.9
1	1A	2833	G	2.9
32	2a	1222	G	2.9
35	2d	171	GLY	2.9
14	2S	77	ALA	2.9
33	1b	85	ALA	2.9
34	1c	137	ALA	2.9
33	1b	69	LEU	2.9
33	2b	118	LEU	2.9
38	2g	38	LEU	2.9
40	2i	99	LEU	2.9
44	1m	53	VAL	2.9
41	2j	14	LYS	2.9
49	1r	29	PHE	2.9
6	2G	45	GLU	2.9
33	2b	231	GLU	2.9
21	2Z	1	MET	2.9
47	1p	48	TRP	2.9
47	2p	76	GLN	2.9
40	1i	10	ARG	2.9
41	2j	76	ASN	2.9
34	2c	202	ILE	2.9
1	1A	888	C	2.9
1	2A	2099	U	2.9
1	2A	2809	A	2.9
1	2A	2897	U	2.9
11	2P	116	GLY	2.9
32	1a	1006	C	2.9
32	1a	1446	U	2.9
32	2a	1030(B)	C	2.9
40	2i	125	TYR	2.9
45	2n	38	GLY	2.9
33	2b	107	THR	2.9
50	1s	33	THR	2.9
50	1s	39	THR	2.9

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Mol	Chain	Res	Type	RSRZ
32	1a	1215	G	2.9
47	2p	12	LYS	2.9
51	1t	14	LYS	2.9
34	2c	207	VAL	2.9
25	23	60	GLU	2.8
7	1H	3	ARG	2.8
52	2u	24	ARG	2.8
38	2g	77	SER	2.8
44	2m	9	ILE	2.8
45	1n	7	ILE	2.8
20	2Y	80	GLY	2.8
28	26	39	TYR	2.8
33	1b	151	GLY	2.8
39	1h	94	TYR	2.8
40	2i	36	TYR	2.8
44	1m	6	GLY	2.8
44	1m	65	LYS	2.8
45	2n	58	LYS	2.8
47	1p	43	LYS	2.8
51	2t	74	LYS	2.8
35	1d	21	LEU	2.8
44	2m	51	ALA	2.8
46	2o	25	THR	2.8
1	1A	1174	A	2.8
1	2A	272(A)	U	2.8
1	2A	2189	U	2.8
14	2S	28	VAL	2.8
32	1a	1044	A	2.8
32	1a	1299	A	2.8
32	2a	1090	U	2.8
33	2b	164	VAL	2.8
1	1A	154(A)	C	2.8
1	1A	2183	C	2.8
7	1H	58	GLU	2.8
44	1m	58	GLU	2.8
53	2v	14	A	2.8
32	2a	1043	C	2.8
32	2a	1249	C	2.8
1	2A	652(U)	G	2.8
1	2A	2192	G	2.8
20	2Y	57	GLN	2.8
32	1a	1030(C)	G	2.8

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Mol	Chain	Res	Type	RSRZ
32	2a	485	G	2.8
6	1G	114	ILE	2.8
38	1g	37	ASN	2.8
6	2G	36	LYS	2.8
7	2H	30	LYS	2.8
8	2I	34	GLY	2.8
12	1Q	61	GLY	2.8
14	2S	60	GLY	2.8
23	2I	28	GLY	2.8
34	1c	36	ASP	2.8
44	1m	100	GLY	2.8
26	14	52	THR	2.8
33	1b	236	TYR	2.8
40	1i	85	LEU	2.8
44	1m	103	THR	2.8
45	1n	5	ALA	2.8
7	2H	113	VAL	2.8
33	2b	152	PHE	2.8
40	1i	117	HIS	2.8
41	1j	64	GLU	2.8
1	1A	1175	U	2.8
32	1a	841	U	2.8
32	2a	1532	U	2.8
32	2a	1016	A	2.8
32	2a	1286	A	2.8
32	2a	1289	A	2.8
54	2w	309	GLN	2.8
1	2A	886	C	2.8
32	1a	1260	C	2.8
32	2a	1397	C	2.8
3	2D	38	LYS	2.8
6	2G	74	LYS	2.8
41	1j	75	ILE	2.8
23	11	2	SER	2.8
38	2g	98	SER	2.8
1	1A	10	G	2.8
15	1T	38	ASN	2.8
32	2a	1190	G	2.8
32	2a	1290	G	2.8
33	2b	94	ASN	2.8
41	1j	76	ASN	2.8
19	1X	95	LEU	2.8

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Mol	Chain	Res	Type	RSRZ
35	1d	120	LEU	2.8
44	1m	68	GLY	2.8
7	2H	102	ALA	2.8
34	2c	53	ALA	2.8
34	2c	55	VAL	2.8
34	2c	120	VAL	2.8
40	1i	45	ALA	2.8
44	1m	28	ALA	2.8
10	2O	108	GLU	2.8
50	1s	19	VAL	2.8
9	2N	134	ARG	2.8
33	2b	183	PRO	2.8
35	2d	118	ARG	2.8
1	1A	2189	U	2.8
29	17	48	LYS	2.8
43	1l	23	LYS	2.8
32	1a	1016	A	2.8
33	1b	214	ILE	2.8
45	2n	7	ILE	2.8
1	2A	889	C	2.8
35	2d	161	ASN	2.8
6	2G	3	LEU	2.8
33	2b	38	GLY	2.8
40	1i	102	LEU	2.8
40	2i	100	GLY	2.8
41	2j	52	GLY	2.8
47	1p	10	GLY	2.8
26	24	51	ASP	2.8
33	1b	16	HIS	2.8
35	1d	102	ASP	2.8
35	2d	123	HIS	2.8
47	1p	16	HIS	2.8
12	2Q	65	PHE	2.8
33	1b	93	VAL	2.8
37	1f	90	VAL	2.8
41	2j	67	THR	2.8
33	1b	105	PHE	2.8
1	2A	1042	G	2.8
34	2c	184	TYR	2.8
42	2k	75	TYR	2.8
44	1m	3	ARG	2.8
33	2b	234	PRO	2.7

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Mol	Chain	Res	Type	RSRZ
46	2o	13	GLN	2.7
32	1a	202	U	2.7
32	2a	1020	U	2.7
6	1G	82	LEU	2.7
41	1j	40	LEU	2.7
1	1A	529	A	2.7
35	2d	23	GLY	2.7
6	2G	48	GLU	2.7
6	2G	73	ALA	2.7
6	2G	158	ALA	2.7
8	1I	46	ALA	2.7
21	1Z	2	GLU	2.7
26	24	52	THR	2.7
18	2W	92	ARG	2.7
25	13	29	ARG	2.7
32	1a	1141	C	2.7
34	2c	106	VAL	2.7
35	1d	149	ALA	2.7
40	2i	13	ALA	2.7
41	2j	28	ARG	2.7
47	1p	75	ARG	2.7
26	24	25	TYR	2.7
33	2b	232	PRO	2.7
36	2e	133	TYR	2.7
9	1N	8	GLN	2.7
1	2A	2187	G	2.7
32	1a	631	G	2.7
32	2a	1013	G	2.7
32	2a	1220	G	2.7
34	1c	77	ILE	2.7
34	2c	134	ILE	2.7
6	2G	107	LEU	2.7
8	2I	38	LEU	2.7
38	2g	59	LEU	2.7
35	2d	2	GLY	2.7
1	2A	2180	U	2.7
32	2a	202	U	2.7
32	2a	961	U	2.7
32	2a	1148	U	2.7
7	2H	59	ARG	2.7
13	2R	68	ARG	2.7
34	1c	86	VAL	2.7

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Mol	Chain	Res	Type	RSRZ
34	1c	186	PHE	2.7
34	2c	68	VAL	2.7
34	2c	75	VAL	2.7
38	1g	3	ARG	2.7
41	1j	72	VAL	2.7
43	1l	6	THR	2.7
44	2m	33	ALA	2.7
45	1n	33	VAL	2.7
32	2a	1261	A	2.7
32	2a	1503	A	2.7
8	2l	89	TYR	2.7
34	2c	4	LYS	2.7
34	2c	170	GLN	2.7
38	1g	151	TYR	2.7
1	2A	277	C	2.7
32	2a	1103	C	2.7
33	2b	185	ILE	2.7
33	2b	145	LEU	2.7
41	2j	71	LEU	2.7
42	2k	103	LEU	2.7
44	1m	96	LEU	2.7
1	2A	100	G	2.7
1	2A	1112	G	2.7
1	2A	2181	G	2.7
32	2a	631	G	2.7
6	2G	100	TRP	2.7
11	1P	54	GLY	2.7
33	1b	192	SER	2.7
33	2b	9	GLU	2.7
45	1n	29	ARG	2.7
14	2S	55	ALA	2.7
33	1b	165	VAL	2.7
34	2c	65	ALA	2.7
34	2c	121	ALA	2.7
40	2i	46	ALA	2.7
40	2i	61	ALA	2.7
3	1D	275	LYS	2.7
9	2N	118	LYS	2.7
25	23	2	PRO	2.7
33	2b	132	LYS	2.7
34	1c	109	PRO	2.7
34	2c	104	GLN	2.7

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Mol	Chain	Res	Type	RSRZ
45	1n	34	TYR	2.7
1	2A	887	A	2.7
6	2G	20	ILE	2.7
33	2b	68	ILE	2.7
35	2d	9	CYS	2.7
41	2j	74	ILE	2.7
44	1m	86	CYS	2.7
1	2A	1509	C	2.7
32	1a	201	C	2.7
32	1a	1018	C	2.7
32	2a	1132	C	2.7
33	1b	118	LEU	2.7
38	2g	89	MET	2.7
6	1G	115	ARG	2.7
33	2b	130	ARG	2.7
34	2c	13	GLY	2.7
38	1g	115	ARG	2.7
40	1i	67	GLY	2.7
44	1m	102	ARG	2.7
5	2F	169	ASN	2.7
45	2n	46	GLU	2.7
14	2S	93	LYS	2.7
35	1d	17	VAL	2.7
35	1d	112	VAL	2.7
33	2b	190	THR	2.7
34	2c	67	THR	2.7
35	1d	89	THR	2.7
40	2i	43	ALA	2.7
41	1j	34	VAL	2.7
42	2k	14	VAL	2.7
50	2s	74	PHE	2.7
6	2G	142	PRO	2.7
20	2Y	107	ASP	2.7
33	1b	125	PRO	2.7
33	2b	189	ASP	2.7
38	1g	33	ASP	2.7
32	1a	97	G	2.6
32	1a	1258	G	2.6
32	2a	993	G	2.6
33	1b	33	TYR	2.6
36	2e	61	TYR	2.6
39	1h	58	TYR	2.6

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Mol	Chain	Res	Type	RSRZ
40	2i	88	TYR	2.6
14	2S	35	ILE	2.6
26	24	14	ILE	2.6
34	2c	5	ILE	2.6
34	2c	39	ILE	2.6
1	2A	2892	A	2.6
6	2G	152	LEU	2.6
34	1c	33	LEU	2.6
35	1d	155	LEU	2.6
53	1v	14	A	2.6
8	1I	52	ARG	2.6
40	2i	16	ARG	2.6
7	2H	5	GLY	2.6
50	2s	64	GLU	2.6
1	1A	1102	C	2.6
32	2a	979	C	2.6
42	1k	117	ASN	2.6
50	1s	65	ASN	2.6
6	2G	5	VAL	2.6
26	24	35	VAL	2.6
33	1b	70	PHE	2.6
33	2b	57	PHE	2.6
33	2b	88	ALA	2.6
36	1e	82	VAL	2.6
50	2s	45	VAL	2.6
51	1t	97	ALA	2.6
50	2s	59	PRO	2.6
52	1u	17	THR	2.6
41	2j	17	ASP	2.6
33	1b	41	ILE	2.6
34	1c	48	TYR	2.6
35	1d	158	ILE	2.6
43	1l	64	TYR	2.6
1	1A	2191	G	2.6
1	2A	12	U	2.6
1	2A	2833	G	2.6
2	2B	1	U	2.6
32	1a	199	G	2.6
32	1a	992	U	2.6
32	2a	950	U	2.6
32	2a	991	U	2.6
32	2a	1068	G	2.6

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Mol	Chain	Res	Type	RSRZ
32	2a	1126	U	2.6
32	2a	1171	G	2.6
33	2b	155	LEU	2.6
34	1c	101	LEU	2.6
50	2s	30	LEU	2.6
50	2s	71	LEU	2.6
21	1Z	103	ARG	2.6
38	1g	32	ARG	2.6
45	2n	12	ARG	2.6
45	2n	31	ARG	2.6
50	2s	69	HIS	2.6
52	1u	22	ARG	2.6
7	2H	175	LYS	2.6
1	1A	229	A	2.6
1	1A	887	A	2.6
14	2S	61	ASN	2.6
6	2G	76	SER	2.6
6	2G	160	VAL	2.6
7	2H	146	ALA	2.6
26	24	10	VAL	2.6
34	1c	207	VAL	2.6
34	2c	64	VAL	2.6
35	1d	133	VAL	2.6
35	2d	164	ALA	2.6
36	2e	41	VAL	2.6
40	2i	65	VAL	2.6
40	2i	86	VAL	2.6
35	1d	37	PRO	2.6
40	2i	94	ALA	2.6
1	2A	1043	C	2.6
32	2a	218	C	2.6
32	2a	1118	C	2.6
7	2H	4	ILE	2.6
34	2c	77	ILE	2.6
50	2s	31	ILE	2.6
14	2S	80	LEU	2.6
21	2Z	5	LEU	2.6
33	2b	138	LEU	2.6
34	2c	204	LEU	2.6
35	2d	4	TYR	2.6
40	2i	4	TYR	2.6
34	2c	6	HIS	2.6

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Mol	Chain	Res	Type	RSRZ
50	1s	37	ARG	2.6
1	1A	2897	U	2.6
32	1a	65	U	2.6
44	1m	8	GLU	2.6
44	1m	67	GLU	2.6
5	1F	16	GLY	2.6
50	2s	68	GLY	2.6
54	1w	166	GLY	2.6
1	2A	652(C)	G	2.6
32	1a	1274	G	2.6
32	2a	1057	G	2.6
33	1b	234	PRO	2.6
33	2b	123	ALA	2.6
33	2b	159	PRO	2.6
33	2b	165	VAL	2.6
36	2e	67	VAL	2.6
39	1h	28	ALA	2.6
42	1k	14	VAL	2.6
44	2m	60	VAL	2.6
50	2s	41	VAL	2.6
33	2b	17	PHE	2.6
34	1c	67	THR	2.6
1	2A	8	A	2.6
21	2Z	87	ASP	2.6
32	1a	994	A	2.6
32	2a	532	A	2.6
53	1v	15	A	2.6
54	1w	102	MET	2.6
26	24	31	ILE	2.6
42	2k	48	ILE	2.6
1	1A	2804	C	2.6
32	1a	979	C	2.6
32	2a	1145	C	2.6
40	1i	19	LEU	2.6
21	2Z	99	TYR	2.6
34	2c	21	ARG	2.6
44	1m	23	TYR	2.6
45	1n	21	TYR	2.6
34	1c	90	GLU	2.6
35	1d	156	GLU	2.6
8	1I	90	GLY	2.6
26	24	54	GLY	2.6

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Mol	Chain	Res	Type	RSRZ
35	2d	180	GLY	2.6
7	2H	44	VAL	2.6
33	1b	225	ALA	2.6
33	2b	167	PRO	2.6
40	2i	84	ALA	2.6
41	2j	18	ALA	2.6
47	1p	79	VAL	2.6
54	2w	189	GLN	2.6
41	1j	30	SER	2.5
1	1A	2192	G	2.5
6	2G	147	ASP	2.5
7	2H	41	MET	2.5
32	1a	1058	G	2.5
32	2a	1030(C)	G	2.5
32	2a	1305	G	2.5
38	1g	89	MET	2.5
50	2s	66	MET	2.5
7	2H	9	ILE	2.5
33	2b	222	ILE	2.5
35	1d	70	ILE	2.5
6	1G	139	LEU	2.5
32	2a	978	A	2.5
32	2a	1180	A	2.5
34	1c	34	LEU	2.5
48	2q	98	LEU	2.5
41	1j	55	LYS	2.5
45	2n	4	LYS	2.5
50	1s	32	LYS	2.5
50	2s	83	HIS	2.5
17	2V	91	TYR	2.5
36	1e	133	TYR	2.5
50	1s	80	TYR	2.5
1	1A	1053	C	2.5
32	1a	1214	C	2.5
32	2a	1045	C	2.5
40	2i	80	GLY	2.5
17	2V	52	VAL	2.5
34	2c	66	VAL	2.5
34	2c	114	PRO	2.5
35	1d	172	PRO	2.5
37	1f	88	VAL	2.5
44	2m	53	VAL	2.5

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Mol	Chain	Res	Type	RSRZ
47	1p	62	VAL	2.5
6	2G	117	PHE	2.5
33	1b	237	ALA	2.5
33	2b	186	ALA	2.5
34	1c	121	ALA	2.5
40	2i	106	ALA	2.5
47	1p	76	GLN	2.5
54	2w	349	ALA	2.5
34	2c	177	THR	2.5
41	1j	78	ASN	2.5
47	1p	69	THR	2.5
26	24	66	SER	2.5
32	2a	1125	U	2.5
36	1e	10	MET	2.5
41	1j	35	SER	2.5
41	2j	59	SER	2.5
34	2c	22	TRP	2.5
38	2g	33	ASP	2.5
33	1b	42	ILE	2.5
45	1n	42	ILE	2.5
11	2P	79	ARG	2.5
14	2S	3	ARG	2.5
14	2S	20	ARG	2.5
33	1b	98	LEU	2.5
34	2c	72	LYS	2.5
34	2c	178	LEU	2.5
35	2d	132	ARG	2.5
40	1i	95	LYS	2.5
40	2i	85	LEU	2.5
32	1a	993	G	2.5
32	2a	1216	G	2.5
32	2a	1272	G	2.5
32	2a	1283	G	2.5
5	2F	161	GLU	2.5
20	2Y	91	GLU	2.5
40	1i	12	GLU	2.5
51	1t	60	GLU	2.5
41	1j	52	GLY	2.5
44	2m	112	GLY	2.5
35	2d	40	PRO	2.5
44	1m	41	PRO	2.5
50	2s	76	PRO	2.5

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Mol	Chain	Res	Type	RSRZ
7	2H	11	VAL	2.5
21	2Z	96	VAL	2.5
25	23	58	VAL	2.5
35	2d	170	VAL	2.5
50	1s	60	VAL	2.5
26	14	49	PHE	2.5
26	24	60	GLN	2.5
34	2c	129	ALA	2.5
35	1d	32	ALA	2.5
35	2d	149	ALA	2.5
41	1j	18	ALA	2.5
45	1n	10	ALA	2.5
54	2w	160	PHE	2.5
54	2w	197	ALA	2.5
32	1a	218	C	2.5
32	1a	1045	C	2.5
32	2a	995	C	2.5
14	2S	31	SER	2.5
6	2G	4	ASP	2.5
8	2I	141	LYS	2.5
34	1c	97	LYS	2.5
34	2c	57	ILE	2.5
35	1d	5	ILE	2.5
45	2n	61	TRP	2.5
40	2i	120	ARG	2.5
48	2q	90	ILE	2.5
51	1t	100	ILE	2.5
1	1A	1026	U	2.5
21	2Z	33	LEU	2.5
34	1c	111	LEU	2.5
34	2c	34	LEU	2.5
35	1d	108	LEU	2.5
46	2o	31	LEU	2.5
53	1v	11	U	2.5
33	2b	40	HIS	2.5
8	2I	99	GLU	2.5
17	2V	93	GLU	2.5
33	1b	228	GLY	2.5
34	2c	155	GLY	2.5
49	2r	57	GLY	2.5
52	1u	2	GLY	2.5
48	1q	28	PRO	2.5

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Mol	Chain	Res	Type	RSRZ
52	2u	23	PRO	2.5
1	2A	6	A	2.5
1	2A	2319	G	2.5
3	2D	166	GLN	2.5
7	2H	35	VAL	2.5
7	2H	76	VAL	2.5
21	2Z	105	VAL	2.5
26	24	33	VAL	2.5
26	24	50	VAL	2.5
32	1a	152	A	2.5
32	1a	532	A	2.5
32	1a	988	G	2.5
32	2a	1131	G	2.5
33	2b	15	VAL	2.5
34	2c	99	VAL	2.5
34	2c	153	VAL	2.5
35	1d	42	GLN	2.5
40	1i	17	VAL	2.5
33	2b	73	THR	2.5
34	1c	177	THR	2.5
40	2i	64	THR	2.5
44	2m	62	ASN	2.5
4	2E	63	LEU	2.5
15	2T	93	ARG	2.5
26	24	15	ILE	2.5
34	2c	87	LEU	2.5
34	2c	175	LEU	2.5
44	2m	84	ILE	2.5
45	1n	6	LEU	2.5
45	2n	35	ARG	2.5
32	1a	470	C	2.5
32	2a	989	C	2.5
47	2p	48	TRP	2.5
34	1c	31	HIS	2.5
32	2a	1313	U	2.5
33	2b	228	GLY	2.5
37	2f	63	TYR	2.5
44	1m	119	GLY	2.5
44	2m	21	TYR	2.5
45	2n	54	PRO	2.5
47	1p	39	TYR	2.5
33	1b	101	MET	2.5

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Mol	Chain	Res	Type	RSRZ
34	1c	195	VAL	2.5
46	2o	60	VAL	2.5
15	1T	130	ALA	2.5
33	1b	62	ALA	2.5
34	1c	92	ALA	2.5
40	1i	82	ALA	2.5
41	2j	54	PHE	2.5
54	1w	307	PHE	2.5
14	2S	97	ARG	2.4
41	1j	79	ARG	2.4
43	1l	19	ARG	2.4
51	2t	57	ARG	2.4
8	1I	138	ILE	2.4
21	2Z	155	LEU	2.4
33	2b	172	ILE	2.4
40	1i	96	LEU	2.4
1	1A	2100	G	2.4
1	2A	2207	G	2.4
32	2a	1011	G	2.4
34	2c	144	SER	2.4
37	2f	83	ASP	2.4
49	2r	62	GLU	2.4
1	1A	2896	C	2.4
1	2A	1026	U	2.4
35	1d	180	GLY	2.4
40	1i	21	PRO	2.4
41	2j	53	PRO	2.4
41	2j	91	PRO	2.4
14	2S	92	TYR	2.4
7	2H	49	VAL	2.4
26	24	21	VAL	2.4
40	2i	41	VAL	2.4
40	2i	78	LYS	2.4
44	1m	27	LYS	2.4
49	1r	86	VAL	2.4
6	2G	102	PHE	2.4
49	2r	61	LYS	2.4
8	2I	146	ALA	2.4
34	2c	137	ALA	2.4
44	1m	5	ALA	2.4
54	1w	107	ALA	2.4
6	2G	145	THR	2.4

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Mol	Chain	Res	Type	RSRZ
33	2b	67	THR	2.4
38	1g	79	ARG	2.4
41	2j	66	ARG	2.4
42	2k	41	THR	2.4
50	1s	36	ARG	2.4
51	1t	22	ARG	2.4
6	2G	34	LEU	2.4
33	2b	127	ILE	2.4
39	1h	86	ILE	2.4
50	1s	31	ILE	2.4
46	1o	24	SER	2.4
32	1a	1357	A	2.4
10	1O	108	GLU	2.4
41	2j	97	GLU	2.4
47	2p	54	GLU	2.4
1	2A	271(M)	G	2.4
32	2a	1009	G	2.4
32	2a	1042	G	2.4
32	2a	1255	G	2.4
54	2w	102	MET	2.4
41	1j	93	GLY	2.4
43	1l	63	GLY	2.4
50	1s	8	GLY	2.4
19	2X	33	LYS	2.4
33	2b	139	LYS	2.4
51	2t	81	LYS	2.4
1	1A	652(S)	C	2.4
20	2Y	72	VAL	2.4
26	24	63	TYR	2.4
32	1a	984	C	2.4
32	1a	985	C	2.4
32	1a	1140	C	2.4
32	1a	1452	C	2.4
32	2a	999	C	2.4
32	2a	1137	C	2.4
33	1b	15	VAL	2.4
39	2h	48	TYR	2.4
42	2k	47	VAL	2.4
50	1s	61	TYR	2.4
8	2I	103	ARG	2.4
33	1b	123	ALA	2.4
40	2i	83	ARG	2.4

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Mol	Chain	Res	Type	RSRZ
41	1j	46	ARG	2.4
49	2r	60	ALA	2.4
51	2t	97	ALA	2.4
54	2w	205	ALA	2.4
7	2H	103	LEU	2.4
8	2I	101	LEU	2.4
33	1b	68	ILE	2.4
34	1c	175	LEU	2.4
35	1d	162	LEU	2.4
38	2g	124	LEU	2.4
46	1o	22	THR	2.4
50	1s	79	THR	2.4
21	2Z	34	ASN	2.4
33	1b	40	HIS	2.4
47	1p	13	HIS	2.4
48	1q	99	SER	2.4
21	2Z	148	ASP	2.4
1	2A	896	A	2.4
7	2H	25	LYS	2.4
17	2V	19	LYS	2.4
32	2a	975	A	2.4
35	2d	22	LYS	2.4
41	1j	39	PRO	2.4
42	2k	122	LYS	2.4
53	1v	13	A	2.4
9	2N	113	GLY	2.4
34	1c	155	GLY	2.4
34	2c	51	GLY	2.4
36	2e	74	GLY	2.4
40	1i	115	GLY	2.4
40	2i	49	PRO	2.4
44	2m	10	PRO	2.4
44	2m	95	GLY	2.4
52	1u	19	GLY	2.4
54	2w	154	GLY	2.4
7	2H	17	VAL	2.4
7	2H	169	VAL	2.4
8	2I	127	VAL	2.4
36	1e	69	VAL	2.4
38	2g	9	VAL	2.4
39	2h	137	VAL	2.4
40	2i	44	VAL	2.4

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Mol	Chain	Res	Type	RSRZ
1	1A	2153	G	2.4
14	2S	17	ARG	2.4
20	2Y	50	ARG	2.4
32	1a	77	G	2.4
32	1a	93	G	2.4
32	1a	104	G	2.4
32	2a	1094	G	2.4
32	2a	1221	G	2.4
34	2c	117	ALA	2.4
38	1g	83	ALA	2.4
40	2i	37	PHE	2.4
41	1j	26	ALA	2.4
41	2j	32	ALA	2.4
51	1t	49	ALA	2.4
1	2A	9	U	2.4
1	2A	362	U	2.4
1	2A	2808	U	2.4
6	2G	39	ILE	2.4
40	2i	79	LEU	2.4
44	2m	25	ILE	2.4
45	2n	39	LEU	2.4
49	1r	31	LEU	2.4
1	2A	652(V)	C	2.4
32	1a	203	U	2.4
41	1j	87	THR	2.4
32	1a	221	C	2.4
32	1a	848	C	2.4
32	1a	990	C	2.4
34	1c	69	HIS	2.4
38	2g	28	ASN	2.4
33	2b	20	GLU	2.4
33	2b	35	GLU	2.4
33	2b	150	SER	2.4
41	1j	80	LYS	2.4
45	2n	43	CYS	2.4
35	2d	7	PRO	2.4
40	1i	49	PRO	2.4
45	1n	38	GLY	2.4
46	1o	23	GLY	2.4
46	2o	20	GLY	2.4
5	2F	6	VAL	2.4
6	1G	160	VAL	2.4

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Mol	Chain	Res	Type	RSRZ
26	24	55	ARG	2.4
34	2c	11	ARG	2.4
35	2d	159	ARG	2.4
38	2g	75	VAL	2.4
39	1h	129	VAL	2.4
51	1t	80	ARG	2.4
1	1A	2629	A	2.4
38	2g	150	ALA	2.4
40	2i	45	ALA	2.4
8	2I	35	LEU	2.3
34	2c	29	TYR	2.3
41	1j	65	LEU	2.3
45	1n	47	LEU	2.3
52	2u	17	THR	2.3
32	1a	68	G	2.3
32	1a	852	G	2.3
8	1I	10	GLU	2.3
8	1I	41	GLU	2.3
32	1a	1020	U	2.3
32	1a	1219	U	2.3
35	1d	150	GLU	2.3
41	2j	61	GLU	2.3
32	1a	1137	C	2.3
32	2a	1214	C	2.3
32	2a	1326	C	2.3
33	2b	156	LYS	2.3
35	1d	113	SER	2.3
35	1d	208	SER	2.3
40	2i	97	LYS	2.3
41	2j	12	ASP	2.3
44	2m	65	LYS	2.3
45	2n	17	LYS	2.3
50	2s	18	LYS	2.3
33	1b	24	TRP	2.3
33	2b	24	TRP	2.3
7	2H	21	PRO	2.3
42	2k	119	CYS	2.3
6	1G	44	GLY	2.3
11	1P	69	GLY	2.3
36	2e	97	GLY	2.3
39	1h	96	GLY	2.3
45	1n	51	GLY	2.3

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Mol	Chain	Res	Type	RSRZ
4	2E	58	ARG	2.3
28	26	44	ARG	2.3
52	2u	15	ARG	2.3
8	2I	144	VAL	2.3
27	15	60	VAL	2.3
35	2d	104	VAL	2.3
42	2k	114	VAL	2.3
7	2H	20	ALA	2.3
35	1d	147	ALA	2.3
41	1j	54	PHE	2.3
41	1j	85	LEU	2.3
44	2m	18	ALA	2.3
45	2n	47	LEU	2.3
49	2r	24	ALA	2.3
6	2G	101	ILE	2.3
33	2b	41	ILE	2.3
39	2h	109	ILE	2.3
40	1i	62	TYR	2.3
44	1m	21	TYR	2.3
50	2s	61	TYR	2.3
32	2a	969	A	2.3
32	2a	1146	A	2.3
44	1m	49	THR	2.3
6	1G	84	LYS	2.3
38	2g	70	LYS	2.3
33	2b	192	SER	2.3
45	2n	32	SER	2.3
1	1A	9	U	2.3
32	1a	1278	U	2.3
1	1A	1106	G	2.3
25	13	2	PRO	2.3
32	1a	1010	G	2.3
32	1a	1222	G	2.3
32	2a	988	G	2.3
32	2a	998	G	2.3
32	2a	1160	G	2.3
32	2a	1182	G	2.3
1	1A	885	C	2.3
8	2I	67	ARG	2.3
32	2a	1147	C	2.3
32	2a	1314	C	2.3
34	1c	21	ARG	2.3

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Mol	Chain	Res	Type	RSRZ
36	1e	18	ARG	2.3
45	2n	51	GLY	2.3
52	2u	10	ARG	2.3
7	2H	115	VAL	2.3
34	1c	99	VAL	2.3
39	2h	19	VAL	2.3
40	1i	41	VAL	2.3
41	1j	44	VAL	2.3
28	26	11	LEU	2.3
34	1c	50	ALA	2.3
34	2c	101	LEU	2.3
37	2f	97	PHE	2.3
37	2f	49	ALA	2.3
38	2g	12	LEU	2.3
45	2n	16	PHE	2.3
38	2g	100	ALA	2.3
26	14	22	ILE	2.3
35	2d	5	ILE	2.3
47	1p	19	ILE	2.3
40	2i	117	HIS	2.3
7	2H	157	TYR	2.3
22	10	10	THR	2.3
22	20	26	TYR	2.3
35	2d	38	TYR	2.3
35	2d	68	TYR	2.3
44	2m	103	THR	2.3
49	1r	25	THR	2.3
52	2u	21	TYR	2.3
8	1I	87	LYS	2.3
14	2S	64	GLU	2.3
33	1b	128	GLU	2.3
35	1d	22	LYS	2.3
43	1l	91	LYS	2.3
51	1t	74	LYS	2.3
34	2c	108	ASN	2.3
1	1A	1460	A	2.3
1	2A	655	A	2.3
32	2a	959	A	2.3
32	2a	983	A	2.3
32	2a	1252	A	2.3
32	2a	1280	A	2.3
4	1E	61	ARG	2.3

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Mol	Chain	Res	Type	RSRZ
6	2G	115	ARG	2.3
6	2G	179	PRO	2.3
7	2H	126	PRO	2.3
19	2X	65	ARG	2.3
38	2g	10	ARG	2.3
49	1r	87	ARG	2.3
34	2c	28	GLN	2.3
50	2s	46	GLY	2.3
1	1A	2808	U	2.3
32	1a	961	U	2.3
32	2a	1446	U	2.3
21	2Z	56	VAL	2.3
38	2g	23	VAL	2.3
33	1b	163	PHE	2.3
34	2c	203	PHE	2.3
40	2i	101	PHE	2.3
45	2n	37	PHE	2.3
6	2G	57	ALA	2.3
33	1b	13	ALA	2.3
1	1A	2304	G	2.3
6	2G	140	ILE	2.3
8	2I	109	ILE	2.3
36	2e	109	ILE	2.3
40	2i	55	ALA	2.3
44	2m	42	ALA	2.3
32	1a	220	G	2.3
32	1a	1327	C	2.3
32	1a	1361	G	2.3
32	2a	990	C	2.3
32	2a	1007	C	2.3
32	2a	1295	G	2.3
32	2a	1316	G	2.3
50	2s	40	ILE	2.3
41	2j	62	HIS	2.3
4	2E	92	THR	2.3
24	22	8	LYS	2.3
38	2g	24	THR	2.3
41	2j	100	THR	2.3
50	2s	33	THR	2.3
54	2w	138	MET	2.3
21	2Z	38	TYR	2.3
34	2c	23	TYR	2.3

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Mol	Chain	Res	Type	RSRZ
35	1d	106	TYR	2.3
47	2p	38	TYR	2.3
7	2H	47	GLU	2.3
35	2d	150	GLU	2.3
42	2k	117	ASN	2.3
7	2H	55	PRO	2.3
7	2H	170	ARG	2.3
15	2T	111	ARG	2.3
15	2T	129	ARG	2.3
29	27	23	ARG	2.3
38	2g	3	ARG	2.3
39	2h	84	ARG	2.3
50	1s	3	ARG	2.3
50	2s	78	ARG	2.3
51	1t	8	ARG	2.3
7	2H	174	GLY	2.3
32	1a	632	A	2.3
32	1a	1306	A	2.3
32	2a	1360	A	2.3
32	2a	1531	A	2.3
38	1g	56	GLN	2.3
39	1h	70	GLN	2.3
40	2i	68	GLY	2.3
42	2k	17	GLY	2.3
6	2G	15	VAL	2.3
7	2H	98	LEU	2.3
8	2I	136	VAL	2.3
21	2Z	90	VAL	2.3
21	2Z	126	VAL	2.3
33	1b	136	VAL	2.3
33	1b	221	LEU	2.3
35	1d	140	VAL	2.3
38	2g	87	VAL	2.3
39	1h	2	LEU	2.3
42	2k	66	LEU	2.3
48	1q	73	VAL	2.3
50	1s	74	PHE	2.3
6	2G	46	ALA	2.2
21	2Z	173	ALA	2.2
32	2a	1095	U	2.2
41	2j	82	ILE	2.2
53	1v	22	U	2.2

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Mol	Chain	Res	Type	RSRZ
47	2p	16	HIS	2.2
33	1b	83	MET	2.2
43	2l	46	LYS	2.2
42	2k	87	THR	2.2
26	14	53	GLU	2.2
33	2b	12	GLU	2.2
33	2b	129	GLU	2.2
35	2d	20	TYR	2.2
40	2i	114	TYR	2.2
1	2A	1532	C	2.2
32	1a	1320	C	2.2
32	2a	1066	C	2.2
32	2a	1244	C	2.2
32	2a	1284	C	2.2
1	1A	2207	G	2.2
1	2A	1039	G	2.2
1	2A	1169	G	2.2
32	1a	945	G	2.2
32	1a	1143	G	2.2
32	2a	1215	G	2.2
5	2F	168	ARG	2.2
6	1G	181	ARG	2.2
33	2b	21	ARG	2.2
38	2g	119	ARG	2.2
40	1i	66	ARG	2.2
41	1j	29	ARG	2.2
41	2j	70	ARG	2.2
48	1q	63	ARG	2.2
33	2b	202	PRO	2.2
51	2t	98	PRO	2.2
36	1e	72	GLN	2.2
39	1h	115	SER	2.2
51	2t	37	SER	2.2
19	2X	94	GLY	2.2
33	2b	61	LEU	2.2
34	1c	22	TRP	2.2
34	1c	188	LEU	2.2
39	2h	63	LEU	2.2
42	1k	103	LEU	2.2
1	1A	653	A	2.2
1	2A	2629	A	2.2
3	2D	106	ILE	2.2

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Mol	Chain	Res	Type	RSRZ
11	1P	120	ALA	2.2
26	24	5	ILE	2.2
32	1a	383	A	2.2
33	1b	22	LYS	2.2
33	1b	152	PHE	2.2
34	1c	57	ILE	2.2
34	1c	61	ALA	2.2
34	1c	182	ILE	2.2
38	1g	121	ALA	2.2
39	2h	110	ALA	2.2
51	2t	52	ALA	2.2
33	1b	12	GLU	2.2
54	2w	170	THR	2.2
26	14	32	TYR	2.2
34	2c	201	TYR	2.2
37	2f	59	TYR	2.2
39	2h	94	TYR	2.2
7	1H	59	ARG	2.2
9	2N	45	ASN	2.2
26	24	58	ARG	2.2
33	1b	209	ARG	2.2
34	2c	127	ARG	2.2
41	2j	5	ARG	2.2
41	2j	51	ARG	2.2
43	2l	94	PRO	2.2
2	2B	62	C	2.2
32	1a	92	C	2.2
32	1a	456	C	2.2
34	2c	37	GLN	2.2
35	2d	160	GLN	2.2
40	2i	124	GLN	2.2
10	1O	110	GLY	2.2
21	2Z	153	SER	2.2
6	2G	111	LEU	2.2
32	1a	350	G	2.2
32	1a	476	G	2.2
32	1a	1133	G	2.2
32	2a	973	G	2.2
32	2a	1047	G	2.2
33	1b	65	GLY	2.2
54	2w	323	ASP	2.2
33	1b	10	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
33	2b	121	LEU	2.2
34	1c	43	LEU	2.2
35	1d	94	LEU	2.2
36	1e	31	LEU	2.2
37	2f	19	LEU	2.2
50	2s	5	LEU	2.2
34	2c	173	VAL	2.2
35	2d	8	VAL	2.2
38	2g	131	LYS	2.2
40	1i	44	VAL	2.2
40	2i	108	VAL	2.2
41	2j	24	VAL	2.2
42	1k	51	LYS	2.2
45	2n	56	VAL	2.2
48	2q	35	VAL	2.2
50	2s	7	LYS	2.2
50	2s	70	LYS	2.2
19	2X	1	MET	2.2
26	14	14	ILE	2.2
33	2b	122	PHE	2.2
34	1c	134	ILE	2.2
34	2c	186	PHE	2.2
36	2e	118	ILE	2.2
38	2g	30	ILE	2.2
39	2h	31	PHE	2.2
34	2c	180	ALA	2.2
45	1n	20	ALA	2.2
4	2E	87	GLU	2.2
6	1G	35	GLU	2.2
26	14	18	CYS	2.2
32	1a	1261	A	2.2
32	2a	1285	A	2.2
41	1j	100	THR	2.2
6	2G	12	TYR	2.2
32	1a	1532	U	2.2
32	2a	1281	U	2.2
35	2d	50	ARG	2.2
35	2d	73	ARG	2.2
36	2e	18	ARG	2.2
45	2n	45	ARG	2.2
46	1o	72	ARG	2.2
34	2c	181	ASN	2.2

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Mol	Chain	Res	Type	RSRZ
35	1d	4	TYR	2.2
40	1i	36	TYR	2.2
47	1p	38	TYR	2.2
20	2Y	66	PRO	2.2
33	1b	131	PRO	2.2
34	2c	73	PRO	2.2
35	1d	189	PRO	2.2
38	1g	14	PRO	2.2
50	2s	42	PRO	2.2
26	14	46	GLN	2.2
44	2m	101	GLN	2.2
6	1G	182	LYS	2.2
33	1b	89	GLY	2.2
33	1b	115	LEU	2.2
33	2b	99	GLY	2.2
34	2c	80	GLY	2.2
35	1d	176	LEU	2.2
35	2d	16	GLY	2.2
39	2h	71	GLY	2.2
44	1m	48	LEU	2.2
44	1m	81	LEU	2.2
47	1p	74	LEU	2.2
49	2r	51	LEU	2.2
51	1t	101	GLY	2.2
35	1d	152	SER	2.2
6	1G	149	VAL	2.2
8	2I	81	VAL	2.2
44	1m	45	VAL	2.2
45	2n	25	VAL	2.2
1	1A	1532	C	2.2
14	2S	29	PHE	2.2
32	1a	63	C	2.2
32	1a	436	C	2.2
40	1i	18	PHE	2.2
41	1j	96	ILE	2.2
50	1s	47	HIS	2.2
8	2I	94	ALA	2.2
34	1c	113	ALA	2.2
45	2n	20	ALA	2.2
47	1p	70	ALA	2.2
7	2H	127	GLU	2.2
32	2a	1174	G	2.2

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Mol	Chain	Res	Type	RSRZ
50	2s	63	THR	2.2
26	24	68	ARG	2.2
35	1d	10	ARG	2.2
41	1j	66	ARG	2.2
51	1t	17	ARG	2.2
54	2w	298	ARG	2.2
4	1E	151	TYR	2.2
7	2H	83	TYR	2.2
32	2a	1041	A	2.2
32	2a	1044	A	2.2
32	2a	1250	A	2.2
35	1d	20	TYR	2.2
37	2f	4	TYR	2.2
38	2g	154	TYR	2.2
47	1p	41	PRO	2.2
50	2s	65	ASN	2.2
9	2N	69	GLN	2.2
5	2F	135	LYS	2.2
20	2Y	81	LYS	2.2
24	12	15	LYS	2.2
32	2a	1083	U	2.2
32	2a	1091	U	2.2
41	2j	33	GLN	2.2
41	1j	7	LYS	2.2
45	1n	15	LYS	2.2
7	2H	120	GLY	2.2
8	1I	77	LEU	2.2
11	2P	109	GLY	2.2
19	2X	9	LEU	2.2
21	2Z	102	LEU	2.2
33	2b	98	LEU	2.2
33	2b	196	LEU	2.2
34	1c	78	GLY	2.2
34	1c	81	GLY	2.2
34	1c	158	GLY	2.2
34	1c	197	GLY	2.2
38	2g	34	GLY	2.2
40	1i	72	GLY	2.2
44	1m	95	GLY	2.2
44	2m	81	LEU	2.2
44	2m	90	LEU	2.2
50	2s	26	GLY	2.2

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Mol	Chain	Res	Type	RSRZ
41	2j	89	ASP	2.2
44	1m	16	ASP	2.2
47	1p	47	ASP	2.2
7	2H	19	VAL	2.2
7	2H	131	VAL	2.2
8	2I	79	ILE	2.2
33	2b	81	VAL	2.2
41	1j	49	VAL	2.2
44	2m	22	ILE	2.2
33	2b	55	PHE	2.2
43	1l	32	PHE	2.2
33	2b	29	ALA	2.1
38	2g	103	TRP	2.1
6	2G	30	GLU	2.1
24	12	12	GLU	2.1
41	1j	83	GLU	2.1
44	2m	73	GLU	2.1
1	1A	1104	C	2.1
8	2I	57	ARG	2.1
10	1O	97	ARG	2.1
32	1a	1223	C	2.1
32	2a	932	C	2.1
32	2a	980	C	2.1
32	2a	1054	C	2.1
32	2a	1113	C	2.1
32	2a	1116	C	2.1
40	2i	27	THR	2.1
45	2n	41	ARG	2.1
1	1A	652(C)	G	2.1
1	1A	1047	G	2.1
7	2H	118	PRO	2.1
32	1a	111	G	2.1
32	1a	1047	G	2.1
32	2a	1084	G	2.1
32	2a	1089	G	2.1
32	2a	1175	G	2.1
33	2b	194	PRO	2.1
37	2f	68	PRO	2.1
8	2I	95	LYS	2.1
33	2b	95	GLN	2.1
34	2c	3	ASN	2.1
38	1g	28	ASN	2.1

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Mol	Chain	Res	Type	RSRZ
50	1s	70	LYS	2.1
51	2t	9	ASN	2.1
50	2s	80	TYR	2.1
14	2S	54	LEU	2.1
34	2c	115	LEU	2.1
37	2f	14	LEU	2.1
38	2g	22	LEU	2.1
1	1A	878	A	2.1
7	2H	22	GLY	2.1
7	2H	78	GLY	2.1
34	2c	9	GLY	2.1
34	2c	74	GLY	2.1
39	1h	128	GLY	2.1
52	2u	16	GLY	2.1
1	1A	1105	U	2.1
1	2A	271(L)	U	2.1
1	2A	2098	U	2.1
5	2F	23	ASP	2.1
21	2Z	93	ASP	2.1
7	2H	84	SER	2.1
7	2H	110	SER	2.1
8	1I	136	VAL	2.1
9	2N	5	VAL	2.1
9	2N	140	VAL	2.1
33	2b	113	HIS	2.1
33	2b	201	ILE	2.1
33	2b	229	VAL	2.1
34	2c	56	ASP	2.1
36	2e	33	VAL	2.1
41	2j	73	ASP	2.1
33	1b	210	SER	2.1
21	2Z	89	PHE	2.1
8	1I	65	ALA	2.1
11	2P	120	ALA	2.1
15	2T	130	ALA	2.1
20	2Y	78	ALA	2.1
33	2b	207	ALA	2.1
38	2g	65	ALA	2.1
40	2i	119	ALA	2.1
44	2m	30	ALA	2.1
9	2N	10	GLU	2.1
15	2T	128	GLU	2.1

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Mol	Chain	Res	Type	RSRZ
41	2j	64	GLU	2.1
6	2G	9	ARG	2.1
26	14	58	ARG	2.1
27	25	15	ARG	2.1
33	2b	144	ARG	2.1
38	2g	79	ARG	2.1
40	2i	20	ARG	2.1
44	1m	44	ARG	2.1
33	2b	47	THR	2.1
49	2r	69	THR	2.1
7	2H	8	PRO	2.1
8	2I	8	PRO	2.1
38	2g	112	PRO	2.1
44	2m	97	PRO	2.1
45	2n	14	PRO	2.1
45	2n	50	LYS	2.1
51	1t	98	PRO	2.1
2	2B	109	C	2.1
32	1a	1147	C	2.1
32	2a	1097	C	2.1
32	2a	1129	C	2.1
32	2a	1234	C	2.1
32	2a	1296	C	2.1
20	2Y	90	LEU	2.1
33	1b	187	LEU	2.1
33	2b	115	LEU	2.1
33	2b	187	LEU	2.1
35	2d	120	LEU	2.1
42	1k	75	TYR	2.1
45	2n	44	LEU	2.1
20	2Y	93	GLY	2.1
33	2b	18	GLY	2.1
1	1A	2206	G	2.1
7	2H	79	VAL	2.1
7	2H	92	ILE	2.1
31	29	16	VAL	2.1
32	1a	1138	G	2.1
32	2a	1144	G	2.1
32	2a	1178	G	2.1
33	2b	58	ILE	2.1
34	2c	141	VAL	2.1
36	2e	100	VAL	2.1

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Mol	Chain	Res	Type	RSRZ
44	2m	4	ILE	2.1
44	2m	74	VAL	2.1
47	1p	40	ASP	2.1
47	2p	19	ILE	2.1
54	2w	327	VAL	2.1
33	2b	124	SER	2.1
34	2c	112	SER	2.1
36	2e	84	PHE	2.1
37	1f	60	PHE	2.1
41	2j	11	PHE	2.1
51	2t	11	SER	2.1
1	1A	1054	A	2.1
1	1A	2099	U	2.1
1	2A	1847	A	2.1
5	2F	166	ALA	2.1
6	1G	46	ALA	2.1
15	2T	131	ALA	2.1
21	2Z	172	ALA	2.1
32	1a	408	A	2.1
32	1a	1148	U	2.1
32	2a	1123	A	2.1
32	2a	1151	A	2.1
32	2a	1159	U	2.1
34	2c	113	ALA	2.1
34	2c	149	ALA	2.1
36	2e	104	ALA	2.1
40	1i	13	ALA	2.1
50	1s	75	ALA	2.1
36	2e	50	GLU	2.1
55	2x	49	U	2.1
7	2H	23	ARG	2.1
7	2H	132	ARG	2.1
31	29	22	ARG	2.1
33	2b	54	THR	2.1
33	2b	147	LYS	2.1
38	2g	29	LYS	2.1
41	2j	99	LYS	2.1
5	2F	171	PRO	2.1
26	24	29	PRO	2.1
35	1d	7	PRO	2.1
35	1d	29	PRO	2.1
24	12	70	GLN	2.1

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Mol	Chain	Res	Type	RSRZ
14	2S	78	LEU	2.1
21	1Z	150	LEU	2.1
41	1j	71	LEU	2.1
44	1m	90	LEU	2.1
11	2P	84	ASN	2.1
31	29	20	HIS	2.1
33	1b	203	GLY	2.1
35	2d	167	GLY	2.1
36	2e	60	TYR	2.1
39	2h	90	GLY	2.1
42	2k	45	GLY	2.1
50	1s	52	TYR	2.1
1	2A	1038	C	2.1
2	2B	5	C	2.1
7	2H	15	VAL	2.1
7	2H	26	VAL	2.1
7	2H	114	VAL	2.1
30	28	41	ILE	2.1
32	1a	72	C	2.1
32	1a	1059	C	2.1
32	2a	848	C	2.1
32	2a	1140	C	2.1
32	2a	1254	C	2.1
33	2b	108	ILE	2.1
34	1c	130	VAL	2.1
35	2d	204	ILE	2.1
36	1e	34	VAL	2.1
37	2f	91	VAL	2.1
41	2j	94	VAL	2.1
3	2D	122	ASP	2.1
23	21	38	SER	2.1
34	1c	79	ARG	2.1
34	1c	160	ALA	2.1
35	1d	71	SER	2.1
41	1j	59	SER	2.1
26	24	57	GLU	2.1
38	2g	123	GLU	2.1
39	2h	12	ARG	2.1
41	2j	26	ALA	2.1
32	1a	200	G	2.1
32	1a	1131	G	2.1
32	2a	953	G	2.1

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Mol	Chain	Res	Type	RSRZ
32	2a	1010	G	2.1
1	1A	2305	A	2.1
1	2A	614(A)	U	2.1
1	2A	1508	A	2.1
2	2B	52	A	2.1
8	2I	78	THR	2.1
32	1a	1014	A	2.1
32	1a	1015	A	2.1
32	1a	1111	A	2.1
32	1a	1287	A	2.1
32	2a	1183	A	2.1
32	2a	1299	A	2.1
40	1i	11	LYS	2.1
54	1w	287	LYS	2.1
40	1i	64	THR	2.1
54	2w	320	THR	2.1
21	2Z	95	PRO	2.1
35	1d	33	MET	2.1
36	1e	20	GLN	2.1
54	1w	189	GLN	2.1
7	2H	87	LEU	2.1
41	1j	90	LEU	2.1
47	1p	49	LEU	2.1
26	14	16	CYS	2.1
33	1b	72	GLY	2.1
51	2t	102	GLY	2.1
17	2V	99	ILE	2.1
33	2b	42	ILE	2.1
39	2h	58	TYR	2.1
40	1i	114	TYR	2.1
42	2k	32	ILE	2.1
7	2H	37	VAL	2.1
8	2I	142	VAL	2.1
16	2U	110	VAL	2.1
44	2m	15	VAL	2.1
6	1G	116	ASP	2.0
38	2g	62	PHE	2.1
42	1k	125	PHE	2.1
6	1G	136	ARG	2.0
15	2T	115	ARG	2.0
41	2j	9	ARG	2.0
45	1n	23	ARG	2.0

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Mol	Chain	Res	Type	RSRZ
47	1p	68	ASP	2.0
29	17	45	ALA	2.0
33	2b	143	GLU	2.0
34	1c	20	SER	2.0
36	2e	58	ALA	2.0
38	2g	152	ALA	2.0
51	1t	94	ALA	2.0
54	2w	136	GLU	2.0
54	1w	310	SER	2.0
56	2z	5	ALA	2.0
7	2H	153	LYS	2.0
17	2V	85	LYS	2.0
26	14	69	LYS	2.0
26	24	38	LYS	2.0
32	1a	150	C	2.0
32	2a	1060	C	2.0
32	2a	1112	C	2.0
32	2a	1282	C	2.0
32	2a	1303	C	2.0
41	1j	57	LYS	2.0
6	2G	161	THR	2.0
38	1g	24	THR	2.0
6	2G	32	PRO	2.0
33	1b	202	PRO	2.0
46	2o	19	PRO	2.0
50	2s	44	MET	2.0
5	2F	196	LEU	2.0
35	1d	19	LEU	2.0
36	2e	12	LEU	2.0
44	1m	66	LEU	2.0
54	2w	336	LEU	2.0
1	1A	1045	A	2.0
1	2A	530	G	2.0
1	2A	1142(A)	A	2.0
32	1a	64	G	2.0
32	1a	998	G	2.0
32	1a	1279	A	2.0
32	2a	976	G	2.0
32	2a	986	A	2.0
32	2a	1015	A	2.0
32	2a	1101	A	2.0
32	2a	1133	G	2.0

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Mol	Chain	Res	Type	RSRZ
28	26	20	ASN	2.0
7	2H	135	GLY	2.0
19	1X	94	GLY	2.0
21	2Z	124	ILE	2.0
33	1b	172	ILE	2.0
33	1b	200	ILE	2.0
50	1s	49	ILE	2.0
8	2I	29	TYR	2.0
29	17	46	VAL	2.0
33	2b	136	VAL	2.0
35	1d	9	CYS	2.0
36	2e	69	VAL	2.0
40	1i	108	VAL	2.0
48	1q	21	VAL	2.0
50	2s	11	VAL	2.0
17	2V	21	ARG	2.0
22	10	11	ARG	2.0
25	23	3	ARG	2.0
38	1g	76	ARG	2.0
5	2F	22	ALA	2.0
14	2S	88	ASP	2.0
34	1c	56	ASP	2.0
35	2d	24	GLU	2.0
44	2m	50	GLU	2.0
5	2F	137	LYS	2.0
6	1G	151	ALA	2.0
20	2Y	4	LYS	2.0
21	2Z	164	ALA	2.0
36	1e	17	ALA	2.0
51	2t	48	LYS	2.0
54	2w	352	ALA	2.0
34	1c	112	SER	2.0
51	1t	70	SER	2.0
5	2F	136	THR	2.0
8	2I	132	PRO	2.0
35	1d	127	THR	2.0
40	2i	90	PRO	2.0
40	2i	123	PRO	2.0
32	2a	1096	C	2.0
32	2a	1161	C	2.0
33	1b	196	LEU	2.0
33	2b	146	GLN	2.0

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Mol	Chain	Res	Type	RSRZ
41	1j	88	LEU	2.0
45	1n	53	LEU	2.0
10	2O	89	ASN	2.0
32	2a	204	U	2.0
32	2a	1122	U	2.0
26	24	17	GLY	2.0
33	2b	162	ILE	2.0
33	2b	182	ILE	2.0
34	2c	81	GLY	2.0
34	2c	205	GLY	2.0
36	2e	101	ILE	2.0
50	1s	53	ASN	2.0
6	1G	109	VAL	2.0
6	2G	51	ARG	2.0
21	2Z	141	VAL	2.0
32	1a	349	A	2.0
32	1a	461	A	2.0
32	1a	1046	A	2.0
32	2a	1176	A	2.0
32	2a	1248	A	2.0
33	2b	53	ARG	2.0
34	2c	138	VAL	2.0
34	2c	198	VAL	2.0
35	1d	35	ARG	2.0
37	2f	47	ARG	2.0
40	2i	93	ARG	2.0
41	1j	45	ARG	2.0
44	1m	55	ARG	2.0
44	1m	74	VAL	2.0
45	1n	35	ARG	2.0
47	2p	42	ARG	2.0
50	2s	19	VAL	2.0
33	1b	92	TYR	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($\text{\AA}^2$)	Q<0.9
55	H2U	2x	21	20/21	0.60	0.23	73,85,93,108	0
55	H2U	1x	21	20/21	0.64	0.19	74,85,92,103	0
55	H2U	2x	20	20/21	0.75	0.15	80,87,90,92	0
32	2MG	1a	1207	24/25	0.85	0.18	69,78,83,85	0
55	PSU	2x	55	20/21	0.85	0.12	65,70,78,87	0
55	H2U	1x	20	20/21	0.86	0.12	63,72,79,86	0
55	5MU	2x	54	21/22	0.87	0.14	67,72,83,90	0
43	0TD	1l	92	10/11	0.88	0.14	43,48,53,69	0
32	2MG	2a	1207	24/25	0.88	0.13	65,75,78,91	0
32	G7M	2a	527	24/25	0.91	0.12	51,55,61,64	0
32	M2G	2a	966	25/26	0.91	0.13	49,55,68,73	0
1	5MU	2A	1915	21/22	0.91	0.11	53,59,62,66	0
55	MIA	2x	37	22/30	0.91	0.11	45,60,63,64	0
55	5MU	1x	54	21/22	0.91	0.15	52,58,67,75	0
32	5MC	2a	1400	21/22	0.91	0.12	53,61,66,70	0
55	PSU	1x	55	20/21	0.91	0.16	53,58,71,77	0
32	PSU	2a	516	20/21	0.91	0.11	47,60,66,66	0
55	PSU	2x	32	20/21	0.92	0.10	57,65,69,71	0
43	0TD	2l	92	10/11	0.92	0.11	46,55,61,71	0
55	PSU	1x	32	20/21	0.92	0.12	50,58,62,67	0
32	5MC	2a	967	21/22	0.93	0.11	53,58,67,69	0
32	PSU	1a	516	20/21	0.93	0.11	50,61,66,68	0
32	5MC	1a	967	21/22	0.93	0.10	45,52,59,62	0
1	PSU	2A	1911	20/21	0.94	0.09	44,50,58,58	0
1	5MU	1A	1915	21/22	0.94	0.10	35,43,48,52	0
32	G7M	1a	527	24/25	0.94	0.10	42,49,53,57	0
32	M2G	1a	966	25/26	0.94	0.10	43,53,59,61	0
55	MIA	1x	37	22/30	0.95	0.09	43,49,55,58	0
32	4OC	2a	1402	22/23	0.95	0.11	43,48,53,59	0
55	PSU	1x	39	20/21	0.95	0.08	31,46,51,51	0
55	PSU	2x	39	20/21	0.95	0.08	49,59,69,70	0
32	5MC	2a	1404	21/22	0.95	0.10	38,42,45,50	0
1	PSU	1A	1911	20/21	0.95	0.09	37,42,46,50	0
55	4SU	2x	8	20/21	0.95	0.10	54,64,67,70	0
1	PSU	2A	1917	20/21	0.95	0.08	47,54,58,60	0
32	UR3	2a	1498	21/22	0.96	0.09	36,43,48,51	0
32	MA6	2a	1518	24/25	0.96	0.10	39,48,54,57	0
1	PSU	1A	1917	20/21	0.96	0.08	35,42,49,52	0
32	5MC	1a	1400	21/22	0.96	0.10	37,45,50,52	0
32	4OC	1a	1402	22/23	0.96	0.09	36,39,45,45	0
1	5MC	2A	1942	21/22	0.96	0.10	31,38,44,47	0
32	5MC	1a	1407	21/22	0.96	0.09	26,30,35,36	0
1	5MC	1A	1942	21/22	0.96	0.10	24,29,32,33	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
32	5MC	2a	1407	21/22	0.96	0.09	37,42,46,53	0
55	8AN	2x	76	22/23	0.96	0.08	31,36,41,45	0
1	5MC	2A	1962	21/22	0.97	0.07	28,35,43,50	0
55	4SU	1x	8	20/21	0.97	0.07	33,42,48,49	0
1	OMG	2A	2251	24/25	0.97	0.06	23,29,33,37	0
1	2MA	2A	2503	23/24	0.97	0.07	23,27,30,31	0
32	MA6	1a	1519	24/25	0.97	0.08	29,34,37,39	0
32	5MC	1a	1404	21/22	0.97	0.08	28,33,38,41	0
1	OMC	2A	1920	21/22	0.97	0.09	40,48,53,54	0
1	PSU	1A	2605	20/21	0.97	0.07	14,18,24,31	0
32	MA6	2a	1519	24/25	0.97	0.11	41,47,52,53	0
1	OMG	1A	2251	24/25	0.98	0.06	13,16,19,22	0
1	OMU	1A	2552	21/22	0.98	0.07	16,19,23,25	0
32	UR3	1a	1498	21/22	0.98	0.06	30,34,37,37	0
1	5MU	2A	1939	21/22	0.98	0.06	25,28,31,32	0
32	MA6	1a	1518	24/25	0.98	0.07	28,34,37,40	0
1	5MU	1A	1939	21/22	0.98	0.07	14,18,22,25	0
1	OMC	1A	1920	21/22	0.98	0.07	27,34,38,39	0
1	5MC	1A	1962	21/22	0.98	0.07	24,26,30,38	0
1	OMU	2A	2552	21/22	0.98	0.07	25,30,34,36	0
55	8AN	1x	76	22/23	0.98	0.07	16,23,25,28	0
1	PSU	2A	2605	20/21	0.98	0.06	18,25,33,33	0
1	2MA	1A	2503	23/24	0.99	0.05	9,12,14,15	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2a	1725	1/1	0.54	0.24	79,79,79,79	0
57	MG	2i	201	1/1	0.57	0.22	71,71,71,71	0
57	MG	1a	1750	1/1	0.61	0.21	65,65,65,65	0
57	MG	2A	3796	1/1	0.64	0.26	74,74,74,74	0
57	MG	1a	1771	1/1	0.65	0.27	76,76,76,76	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1A	3675	1/1	0.65	0.28	60,60,60,60	0
57	MG	2A	3744	1/1	0.66	0.30	47,47,47,47	0
57	MG	1A	3826	1/1	0.66	0.12	36,36,36,36	0
57	MG	1a	1660	1/1	0.66	0.16	77,77,77,77	0
57	MG	2A	3272	1/1	0.66	0.27	74,74,74,74	0
57	MG	2A	3644	1/1	0.67	0.27	57,57,57,57	0
57	MG	2A	3653	1/1	0.67	0.21	54,54,54,54	0
57	MG	2A	3337	1/1	0.68	0.17	71,71,71,71	0
57	MG	1a	1631	1/1	0.69	0.13	68,68,68,68	0
57	MG	2A	3239	1/1	0.69	0.43	66,66,66,66	0
57	MG	1A	4017	1/1	0.71	0.22	41,41,41,41	0
57	MG	2A	3420	1/1	0.72	0.28	71,71,71,71	0
57	MG	2A	3277	1/1	0.72	0.11	56,56,56,56	0
57	MG	1A	4007	1/1	0.72	0.17	59,59,59,59	0
57	MG	2A	3734	1/1	0.72	0.19	62,62,62,62	0
57	MG	2A	3301	1/1	0.73	0.22	57,57,57,57	0
57	MG	2a	1712	1/1	0.73	0.26	51,51,51,51	0
57	MG	2A	3528	1/1	0.73	0.15	63,63,63,63	0
57	MG	1A	4037	1/1	0.73	0.26	65,65,65,65	0
57	MG	2A	3284	1/1	0.74	0.11	60,60,60,60	0
57	MG	2E	306	1/1	0.74	0.14	52,52,52,52	0
57	MG	2A	3699	1/1	0.74	0.20	51,51,51,51	0
57	MG	1A	3760	1/1	0.74	0.17	52,52,52,52	0
57	MG	1A	3731	1/1	0.74	0.12	13,13,13,13	0
57	MG	2A	3431	1/1	0.75	0.13	58,58,58,58	0
57	MG	1a	1761	1/1	0.75	0.25	70,70,70,70	0
57	MG	1A	3671	1/1	0.75	0.22	48,48,48,48	0
57	MG	2A	3085	1/1	0.75	0.31	69,69,69,69	0
57	MG	1O	201	1/1	0.75	0.23	60,60,60,60	0
57	MG	2a	1759	1/1	0.75	0.25	59,59,59,59	0
57	MG	1W	209	1/1	0.75	0.17	47,47,47,47	0
57	MG	1a	1721	1/1	0.76	0.27	58,58,58,58	0
57	MG	2A	3677	1/1	0.76	0.23	51,51,51,51	0
57	MG	1a	1773	1/1	0.76	0.17	66,66,66,66	0
57	MG	1l	201	1/1	0.76	0.15	65,65,65,65	0
57	MG	2A	3062	1/1	0.76	0.17	70,70,70,70	0
57	MG	2A	3790	1/1	0.76	0.19	47,47,47,47	0
57	MG	1A	3969	1/1	0.76	0.26	54,54,54,54	0
57	MG	2A	3108	1/1	0.76	0.22	50,50,50,50	0
57	MG	2A	3227	1/1	0.76	0.34	69,69,69,69	0
57	MG	1A	3317	1/1	0.76	0.16	48,48,48,48	0
57	MG	2a	1755	1/1	0.76	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
57	MG	2a	1758	1/1	0.76	0.35	66,66,66,66	0
57	MG	2A	3250	1/1	0.76	0.12	60,60,60,60	0
57	MG	2A	3651	1/1	0.76	0.17	57,57,57,57	0
57	MG	2A	3304	1/1	0.77	0.34	67,67,67,67	0
57	MG	1b	302	1/1	0.77	0.17	80,80,80,80	0
57	MG	2B	219	1/1	0.77	0.25	66,66,66,66	0
57	MG	1a	1720	1/1	0.77	0.35	76,76,76,76	0
57	MG	2A	3668	1/1	0.77	0.18	53,53,53,53	0
57	MG	2A	3263	1/1	0.77	0.13	64,64,64,64	0
57	MG	2A	3458	1/1	0.77	0.14	58,58,58,58	0
57	MG	2A	3727	1/1	0.77	0.20	43,43,43,43	0
57	MG	2A	3462	1/1	0.77	0.27	63,63,63,63	0
57	MG	2a	1770	1/1	0.77	0.16	70,70,70,70	0
57	MG	2A	3265	1/1	0.77	0.13	56,56,56,56	0
57	MG	2A	3300	1/1	0.78	0.28	66,66,66,66	0
57	MG	1x	105	1/1	0.78	0.12	56,56,56,56	0
57	MG	2A	3687	1/1	0.78	0.29	67,67,67,67	0
57	MG	2a	1622	1/1	0.78	0.23	61,61,61,61	0
57	MG	2a	1669	1/1	0.78	0.29	64,64,64,64	0
57	MG	2A	3691	1/1	0.78	0.26	65,65,65,65	0
57	MG	2A	3698	1/1	0.78	0.24	56,56,56,56	0
57	MG	2A	3185	1/1	0.78	0.21	60,60,60,60	0
57	MG	2A	3618	1/1	0.78	0.21	66,66,66,66	0
57	MG	1A	3958	1/1	0.78	0.14	24,24,24,24	0
57	MG	1B	209	1/1	0.78	0.19	54,54,54,54	0
57	MG	2A	3106	1/1	0.78	0.23	59,59,59,59	0
57	MG	2v	101	1/1	0.78	0.29	58,58,58,58	0
57	MG	2A	3521	1/1	0.79	0.23	57,57,57,57	0
57	MG	2A	3738	1/1	0.79	0.17	59,59,59,59	0
57	MG	1a	1723	1/1	0.79	0.38	70,70,70,70	0
57	MG	2A	3767	1/1	0.79	0.16	63,63,63,63	0
57	MG	2A	3580	1/1	0.79	0.23	58,58,58,58	0
57	MG	1A	3836	1/1	0.79	0.27	59,59,59,59	0
57	MG	1a	1648	1/1	0.79	0.27	68,68,68,68	0
57	MG	2E	301	1/1	0.79	0.21	62,62,62,62	0
57	MG	2A	3649	1/1	0.79	0.17	70,70,70,70	0
57	MG	1A	3986	1/1	0.79	0.29	61,61,61,61	0
57	MG	2a	1625	1/1	0.79	0.31	66,66,66,66	0
57	MG	2A	3375	1/1	0.79	0.12	55,55,55,55	0
57	MG	1a	1670	1/1	0.79	0.26	58,58,58,58	0
57	MG	2A	3275	1/1	0.79	0.22	70,70,70,70	0
57	MG	2A	3432	1/1	0.79	0.28	58,58,58,58	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2A	3451	1/1	0.79	0.24	53,53,53,53	0
57	MG	1A	3870	1/1	0.79	0.20	40,40,40,40	0
57	MG	2a	1764	1/1	0.79	0.20	60,60,60,60	0
57	MG	1A	3607	1/1	0.79	0.25	60,60,60,60	0
57	MG	2A	3716	1/1	0.79	0.20	67,67,67,67	0
57	MG	2A	3498	1/1	0.79	0.15	48,48,48,48	0
57	MG	2a	1644	1/1	0.80	0.24	68,68,68,68	0
57	MG	1A	3647	1/1	0.80	0.12	40,40,40,40	0
57	MG	1a	1747	1/1	0.80	0.21	74,74,74,74	0
57	MG	2a	1722	1/1	0.80	0.21	70,70,70,70	0
57	MG	1a	1684	1/1	0.80	0.25	64,64,64,64	0
57	MG	1a	1654	1/1	0.80	0.18	65,65,65,65	0
57	MG	2A	3199	1/1	0.80	0.26	70,70,70,70	0
57	MG	2A	3313	1/1	0.80	0.18	77,77,77,77	0
57	MG	1A	3548	1/1	0.80	0.28	51,51,51,51	0
57	MG	2R	202	1/1	0.80	0.18	55,55,55,55	0
57	MG	2A	3347	1/1	0.80	0.19	43,43,43,43	0
57	MG	2A	3512	1/1	0.80	0.24	66,66,66,66	0
57	MG	2x	104	1/1	0.80	0.21	65,65,65,65	0
57	MG	2B	204	1/1	0.81	0.29	60,60,60,60	0
57	MG	1A	3545	1/1	0.81	0.16	50,50,50,50	0
57	MG	2A	3333	1/1	0.81	0.17	64,64,64,64	0
57	MG	1A	3441	1/1	0.81	0.14	51,51,51,51	0
57	MG	2A	3226	1/1	0.81	0.27	58,58,58,58	0
57	MG	1A	3990	1/1	0.81	0.11	47,47,47,47	0
57	MG	1A	3927	1/1	0.81	0.32	70,70,70,70	0
57	MG	1A	3474	1/1	0.81	0.24	68,68,68,68	0
57	MG	2a	1666	1/1	0.81	0.27	61,61,61,61	0
57	MG	2A	3007	1/1	0.81	0.22	50,50,50,50	0
57	MG	1a	1647	1/1	0.81	0.20	55,55,55,55	0
57	MG	1A	4025	1/1	0.81	0.12	59,59,59,59	0
57	MG	2A	3086	1/1	0.81	0.19	60,60,60,60	0
57	MG	2a	1732	1/1	0.81	0.18	52,52,52,52	0
57	MG	2a	1736	1/1	0.81	0.30	72,72,72,72	0
57	MG	1a	1652	1/1	0.81	0.17	62,62,62,62	0
57	MG	1A	4036	1/1	0.81	0.21	60,60,60,60	0
57	MG	2A	3297	1/1	0.81	0.12	47,47,47,47	0
57	MG	2A	3526	1/1	0.81	0.16	47,47,47,47	0
57	MG	2A	3113	1/1	0.81	0.19	58,58,58,58	0
57	MG	2A	3118	1/1	0.81	0.32	56,56,56,56	0
57	MG	2q	201	1/1	0.81	0.29	66,66,66,66	0
57	MG	2A	3159	1/1	0.81	0.19	55,55,55,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2A	3843	1/1	0.81	0.25	57,57,57,57	0
57	MG	2A	3830	1/1	0.82	0.18	52,52,52,52	0
57	MG	2A	3564	1/1	0.82	0.20	59,59,59,59	0
57	MG	2A	3845	1/1	0.82	0.23	59,59,59,59	0
57	MG	2A	3572	1/1	0.82	0.26	64,64,64,64	0
57	MG	2A	3164	1/1	0.82	0.20	70,70,70,70	0
57	MG	2A	3605	1/1	0.82	0.16	29,29,29,29	0
57	MG	1a	1621	1/1	0.82	0.20	63,63,63,63	0
57	MG	2A	3332	1/1	0.82	0.18	61,61,61,61	0
57	MG	2a	1618	1/1	0.82	0.25	60,60,60,60	0
57	MG	1A	3481	1/1	0.82	0.30	62,62,62,62	0
57	MG	1x	109	1/1	0.82	0.26	67,67,67,67	0
57	MG	1B	225	1/1	0.82	0.15	53,53,53,53	0
57	MG	2A	3667	1/1	0.82	0.20	64,64,64,64	0
57	MG	2A	3355	1/1	0.82	0.16	57,57,57,57	0
57	MG	2A	3232	1/1	0.82	0.10	62,62,62,62	0
57	MG	2A	3376	1/1	0.82	0.20	63,63,63,63	0
57	MG	2A	3031	1/1	0.82	0.16	54,54,54,54	0
57	MG	2A	3056	1/1	0.82	0.19	57,57,57,57	0
57	MG	1B	235	1/1	0.82	0.16	62,62,62,62	0
57	MG	2a	1743	1/1	0.82	0.23	64,64,64,64	0
57	MG	2a	1748	1/1	0.82	0.24	64,64,64,64	0
57	MG	1G	204	1/1	0.82	0.08	34,34,34,34	0
57	MG	2A	3719	1/1	0.82	0.22	62,62,62,62	0
57	MG	1A	3794	1/1	0.82	0.12	41,41,41,41	0
57	MG	1a	1767	1/1	0.82	0.33	70,70,70,70	0
57	MG	1A	3640	1/1	0.82	0.07	24,24,24,24	0
57	MG	1Y	202	1/1	0.82	0.15	53,53,53,53	0
57	MG	1a	1792	1/1	0.82	0.18	76,76,76,76	0
57	MG	2A	3120	1/1	0.82	0.11	57,57,57,57	0
57	MG	1Z	301	1/1	0.82	0.29	66,66,66,66	0
57	MG	2O	201	1/1	0.83	0.19	53,53,53,53	0
57	MG	1B	219	1/1	0.83	0.14	45,45,45,45	0
57	MG	2A	3121	1/1	0.83	0.12	65,65,65,65	0
57	MG	2A	3286	1/1	0.83	0.15	58,58,58,58	0
57	MG	1A	4000	1/1	0.83	0.19	53,53,53,53	0
57	MG	2A	3006	1/1	0.83	0.31	62,62,62,62	0
57	MG	1B	232	1/1	0.83	0.28	59,59,59,59	0
57	MG	2A	3017	1/1	0.83	0.33	57,57,57,57	0
57	MG	2a	1678	1/1	0.83	0.32	65,65,65,65	0
57	MG	2A	3225	1/1	0.83	0.25	66,66,66,66	0
57	MG	2A	3327	1/1	0.83	0.13	45,45,45,45	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1A	3872	1/1	0.83	0.21	42,42,42,42	0
57	MG	1B	237	1/1	0.83	0.15	40,40,40,40	0
57	MG	2A	3745	1/1	0.83	0.15	68,68,68,68	0
57	MG	2A	3761	1/1	0.83	0.13	66,66,66,66	0
57	MG	1A	3312	1/1	0.83	0.15	48,48,48,48	0
57	MG	2a	1751	1/1	0.83	0.15	58,58,58,58	0
57	MG	2A	3343	1/1	0.83	0.13	56,56,56,56	0
57	MG	1A	3708	1/1	0.83	0.15	49,49,49,49	0
57	MG	2A	3632	1/1	0.83	0.16	44,44,44,44	0
57	MG	1a	1665	1/1	0.83	0.18	56,56,56,56	0
57	MG	2a	1767	1/1	0.83	0.15	68,68,68,68	0
57	MG	1A	3377	1/1	0.83	0.15	44,44,44,44	0
57	MG	1a	1803	1/1	0.83	0.16	64,64,64,64	0
57	MG	2j	201	1/1	0.83	0.11	67,67,67,67	0
57	MG	2n	101	1/1	0.83	0.29	63,63,63,63	0
57	MG	2A	3400	1/1	0.83	0.29	52,52,52,52	0
57	MG	1A	3849	1/1	0.83	0.17	53,53,53,53	0
57	MG	1A	3403	1/1	0.83	0.10	48,48,48,48	0
57	MG	2A	3408	1/1	0.84	0.12	62,62,62,62	0
57	MG	1A	4044	1/1	0.84	0.13	50,50,50,50	0
57	MG	18	102	1/1	0.84	0.14	42,42,42,42	0
57	MG	2A	3772	1/1	0.84	0.15	39,39,39,39	0
57	MG	1A	3653	1/1	0.84	0.12	15,15,15,15	0
57	MG	2A	3243	1/1	0.84	0.24	56,56,56,56	0
57	MG	2A	3826	1/1	0.84	0.16	57,57,57,57	0
57	MG	2A	3049	1/1	0.84	0.33	58,58,58,58	0
57	MG	2A	3459	1/1	0.84	0.19	65,65,65,65	0
57	MG	1A	3767	1/1	0.84	0.16	44,44,44,44	0
57	MG	1a	1634	1/1	0.84	0.27	70,70,70,70	0
57	MG	2B	215	1/1	0.84	0.22	60,60,60,60	0
57	MG	2A	3271	1/1	0.84	0.21	60,60,60,60	0
57	MG	1a	1762	1/1	0.84	0.18	63,63,63,63	0
57	MG	2E	302	1/1	0.84	0.15	56,56,56,56	0
57	MG	1A	3247	1/1	0.84	0.24	60,60,60,60	0
57	MG	2A	3096	1/1	0.84	0.24	59,59,59,59	0
57	MG	2A	3279	1/1	0.84	0.17	48,48,48,48	0
57	MG	2a	1613	1/1	0.84	0.31	57,57,57,57	0
57	MG	2A	3571	1/1	0.84	0.13	51,51,51,51	0
57	MG	2A	3099	1/1	0.84	0.15	63,63,63,63	0
57	MG	1a	1769	1/1	0.84	0.19	53,53,53,53	0
57	MG	1A	3884	1/1	0.84	0.12	45,45,45,45	0
57	MG	1A	3908	1/1	0.84	0.10	37,37,37,37	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2A	3619	1/1	0.84	0.19	27,27,27,27	0
57	MG	2A	3116	1/1	0.84	0.15	53,53,53,53	0
57	MG	2a	1700	1/1	0.84	0.26	61,61,61,61	0
57	MG	2a	1706	1/1	0.84	0.27	59,59,59,59	0
57	MG	2A	3302	1/1	0.84	0.17	61,61,61,61	0
57	MG	2a	1720	1/1	0.84	0.16	55,55,55,55	0
57	MG	2A	3648	1/1	0.84	0.25	60,60,60,60	0
57	MG	1a	1780	1/1	0.84	0.23	59,59,59,59	0
57	MG	1A	3672	1/1	0.84	0.14	58,58,58,58	0
57	MG	2A	3315	1/1	0.84	0.16	54,54,54,54	0
57	MG	2a	1741	1/1	0.84	0.29	63,63,63,63	0
57	MG	2A	3318	1/1	0.84	0.22	73,73,73,73	0
57	MG	1a	1659	1/1	0.84	0.25	54,54,54,54	0
57	MG	2A	3670	1/1	0.84	0.18	43,43,43,43	0
57	MG	2A	3329	1/1	0.84	0.15	67,67,67,67	0
57	MG	2A	3331	1/1	0.84	0.10	58,58,58,58	0
57	MG	2A	3138	1/1	0.84	0.30	60,60,60,60	0
57	MG	1a	1805	1/1	0.84	0.21	71,71,71,71	0
57	MG	1A	3942	1/1	0.84	0.16	55,55,55,55	0
57	MG	2A	3713	1/1	0.84	0.25	69,69,69,69	0
57	MG	2A	3165	1/1	0.84	0.22	61,61,61,61	0
57	MG	1A	3947	1/1	0.84	0.15	23,23,23,23	0
57	MG	2l	201	1/1	0.84	0.16	63,63,63,63	0
57	MG	1U	205	1/1	0.84	0.17	37,37,37,37	0
57	MG	2A	3201	1/1	0.84	0.12	79,79,79,79	0
57	MG	1A	3750	1/1	0.84	0.20	52,52,52,52	0
57	MG	1A	4040	1/1	0.84	0.11	33,33,33,33	0
57	MG	2A	3832	1/1	0.85	0.15	44,44,44,44	0
57	MG	2A	3833	1/1	0.85	0.16	26,26,26,26	0
57	MG	2A	3538	1/1	0.85	0.12	28,28,28,28	0
57	MG	1A	3529	1/1	0.85	0.15	49,49,49,49	0
57	MG	1a	1676	1/1	0.85	0.11	43,43,43,43	0
57	MG	2B	208	1/1	0.85	0.26	60,60,60,60	0
57	MG	2A	3122	1/1	0.85	0.22	48,48,48,48	0
57	MG	1a	1680	1/1	0.85	0.35	63,63,63,63	0
57	MG	2D	308	1/1	0.85	0.16	62,62,62,62	0
57	MG	1A	3001	1/1	0.85	0.10	32,32,32,32	0
57	MG	1x	104	1/1	0.85	0.16	57,57,57,57	0
57	MG	2A	3321	1/1	0.85	0.18	51,51,51,51	0
57	MG	1a	1700	1/1	0.85	0.21	56,56,56,56	0
57	MG	2A	3636	1/1	0.85	0.13	66,66,66,66	0
57	MG	2a	1604	1/1	0.85	0.29	62,62,62,62	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2a	1611	1/1	0.85	0.34	66,66,66,66	0
57	MG	2A	3176	1/1	0.85	0.27	58,58,58,58	0
57	MG	1a	1709	1/1	0.85	0.24	61,61,61,61	0
57	MG	2A	3197	1/1	0.85	0.14	55,55,55,55	0
57	MG	1a	1719	1/1	0.85	0.15	58,58,58,58	0
57	MG	1B	223	1/1	0.85	0.18	51,51,51,51	0
57	MG	2A	3658	1/1	0.85	0.16	49,49,49,49	0
57	MG	2A	3008	1/1	0.85	0.17	49,49,49,49	0
57	MG	1a	1602	1/1	0.85	0.15	50,50,50,50	0
57	MG	2A	3348	1/1	0.85	0.07	26,26,26,26	0
57	MG	2A	3022	1/1	0.85	0.34	69,69,69,69	0
57	MG	2A	3358	1/1	0.85	0.15	45,45,45,45	0
57	MG	2A	3370	1/1	0.85	0.14	61,61,61,61	0
57	MG	1a	1604	1/1	0.85	0.12	66,66,66,66	0
57	MG	2A	3033	1/1	0.85	0.23	52,52,52,52	0
57	MG	1A	3358	1/1	0.85	0.15	46,46,46,46	0
57	MG	2a	1733	1/1	0.85	0.16	61,61,61,61	0
57	MG	2A	3404	1/1	0.85	0.23	56,56,56,56	0
57	MG	1A	3602	1/1	0.85	0.10	30,30,30,30	0
57	MG	2A	3724	1/1	0.85	0.13	52,52,52,52	0
57	MG	1A	3925	1/1	0.85	0.16	58,58,58,58	0
57	MG	2a	1750	1/1	0.85	0.23	59,59,59,59	0
57	MG	1A	3603	1/1	0.85	0.21	57,57,57,57	0
57	MG	1F	313	1/1	0.85	0.20	39,39,39,39	0
57	MG	1A	3831	1/1	0.85	0.28	37,37,37,37	0
57	MG	1G	205	1/1	0.85	0.16	52,52,52,52	0
57	MG	2A	3104	1/1	0.85	0.28	54,54,54,54	0
57	MG	2A	3763	1/1	0.85	0.10	58,58,58,58	0
57	MG	1A	3368	1/1	0.85	0.15	51,51,51,51	0
57	MG	2A	3281	1/1	0.85	0.14	61,61,61,61	0
57	MG	2A	3787	1/1	0.85	0.12	43,43,43,43	0
57	MG	1a	1774	1/1	0.85	0.20	65,65,65,65	0
57	MG	1a	1778	1/1	0.85	0.14	37,37,37,37	0
57	MG	2A	3814	1/1	0.85	0.28	54,54,54,54	0
57	MG	1A	3190	1/1	0.85	0.16	46,46,46,46	0
57	MG	1A	3854	1/1	0.85	0.13	51,51,51,51	0
57	MG	2x	106	1/1	0.85	0.16	46,46,46,46	0
57	MG	1f	201	1/1	0.86	0.24	57,57,57,57	0
57	MG	2B	206	1/1	0.86	0.20	61,61,61,61	0
57	MG	1A	3953	1/1	0.86	0.13	66,66,66,66	0
57	MG	2B	209	1/1	0.86	0.18	58,58,58,58	0
57	MG	1A	3471	1/1	0.86	0.11	44,44,44,44	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2B	216	1/1	0.86	0.15	65,65,65,65	0
57	MG	2A	3172	1/1	0.86	0.24	62,62,62,62	0
57	MG	1a	1701	1/1	0.86	0.20	59,59,59,59	0
57	MG	15	107	1/1	0.86	0.11	36,36,36,36	0
57	MG	2A	3186	1/1	0.86	0.12	52,52,52,52	0
57	MG	1A	3552	1/1	0.86	0.19	50,50,50,50	0
57	MG	1B	222	1/1	0.86	0.15	43,43,43,43	0
57	MG	2P	202	1/1	0.86	0.12	63,63,63,63	0
57	MG	1A	3871	1/1	0.86	0.15	36,36,36,36	0
57	MG	20	101	1/1	0.86	0.10	48,48,48,48	0
57	MG	2A	3216	1/1	0.86	0.22	49,49,49,49	0
57	MG	2A	3224	1/1	0.86	0.17	49,49,49,49	0
57	MG	1A	3668	1/1	0.86	0.16	20,20,20,20	0
57	MG	1a	1732	1/1	0.86	0.27	66,66,66,66	0
57	MG	1a	1733	1/1	0.86	0.18	64,64,64,64	0
57	MG	1B	227	1/1	0.86	0.13	63,63,63,63	0
57	MG	2a	1640	1/1	0.86	0.22	48,48,48,48	0
57	MG	2A	3690	1/1	0.86	0.14	27,27,27,27	0
57	MG	2A	3234	1/1	0.86	0.38	57,57,57,57	0
57	MG	1a	1749	1/1	0.86	0.17	54,54,54,54	0
57	MG	2A	3398	1/1	0.86	0.29	51,51,51,51	0
57	MG	2A	3707	1/1	0.86	0.21	59,59,59,59	0
57	MG	1A	3997	1/1	0.86	0.16	50,50,50,50	0
57	MG	2a	1710	1/1	0.86	0.19	61,61,61,61	0
57	MG	1a	1752	1/1	0.86	0.23	53,53,53,53	0
57	MG	2A	3252	1/1	0.86	0.16	51,51,51,51	0
57	MG	2A	3723	1/1	0.86	0.20	66,66,66,66	0
57	MG	2A	3255	1/1	0.86	0.23	49,49,49,49	0
57	MG	2a	1726	1/1	0.86	0.20	48,48,48,48	0
57	MG	1a	1637	1/1	0.86	0.25	55,55,55,55	0
57	MG	1a	1641	1/1	0.86	0.17	69,69,69,69	0
57	MG	2a	1734	1/1	0.86	0.20	59,59,59,59	0
57	MG	2A	3268	1/1	0.86	0.10	65,65,65,65	0
57	MG	2a	1738	1/1	0.86	0.20	49,49,49,49	0
57	MG	1A	3785	1/1	0.86	0.16	41,41,41,41	0
57	MG	1A	3892	1/1	0.86	0.18	45,45,45,45	0
57	MG	2a	1747	1/1	0.86	0.23	59,59,59,59	0
57	MG	2A	3746	1/1	0.86	0.12	62,62,62,62	0
57	MG	1D	311	1/1	0.86	0.25	47,47,47,47	0
57	MG	1A	3553	1/1	0.86	0.15	49,49,49,49	0
57	MG	2A	3504	1/1	0.86	0.11	18,18,18,18	0
57	MG	1A	3197	1/1	0.86	0.08	34,34,34,34	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2A	3774	1/1	0.86	0.10	63,63,63,63	0
57	MG	1A	4032	1/1	0.86	0.11	41,41,41,41	0
57	MG	1A	3459	1/1	0.86	0.18	61,61,61,61	0
57	MG	1a	1668	1/1	0.86	0.29	73,73,73,73	0
57	MG	2A	3797	1/1	0.86	0.13	27,27,27,27	0
57	MG	1a	1798	1/1	0.86	0.23	59,59,59,59	0
57	MG	2A	3548	1/1	0.86	0.12	26,26,26,26	0
57	MG	1Q	205	1/1	0.86	0.19	44,44,44,44	0
57	MG	1A	3460	1/1	0.86	0.12	39,39,39,39	0
57	MG	2A	3123	1/1	0.86	0.20	54,54,54,54	0
57	MG	2x	102	1/1	0.86	0.18	66,66,66,66	0
57	MG	2A	3574	1/1	0.86	0.11	54,54,54,54	0
57	MG	1A	3468	1/1	0.86	0.16	47,47,47,47	0
57	MG	2B	203	1/1	0.87	0.22	63,63,63,63	0
57	MG	1a	1772	1/1	0.87	0.17	63,63,63,63	0
57	MG	1F	312	1/1	0.87	0.11	45,45,45,45	0
57	MG	1A	3179	1/1	0.87	0.12	61,61,61,61	0
57	MG	2A	3600	1/1	0.87	0.12	42,42,42,42	0
57	MG	2A	3602	1/1	0.87	0.14	63,63,63,63	0
57	MG	1A	4014	1/1	0.87	0.12	37,37,37,37	0
57	MG	2A	3610	1/1	0.87	0.14	63,63,63,63	0
57	MG	1a	1663	1/1	0.87	0.18	55,55,55,55	0
57	MG	1A	3903	1/1	0.87	0.12	47,47,47,47	0
57	MG	2A	3141	1/1	0.87	0.20	35,35,35,35	0
57	MG	1N	205	1/1	0.87	0.17	44,44,44,44	0
57	MG	1a	1802	1/1	0.87	0.16	58,58,58,58	0
57	MG	1a	1669	1/1	0.87	0.17	65,65,65,65	0
57	MG	1A	3821	1/1	0.87	0.12	40,40,40,40	0
57	MG	2T	201	1/1	0.87	0.18	48,48,48,48	0
57	MG	1a	1673	1/1	0.87	0.39	64,64,64,64	0
57	MG	25	106	1/1	0.87	0.11	65,65,65,65	0
57	MG	26	101	1/1	0.87	0.19	64,64,64,64	0
57	MG	2a	1603	1/1	0.87	0.12	57,57,57,57	0
57	MG	1a	1675	1/1	0.87	0.15	66,66,66,66	0
57	MG	1O	203	1/1	0.87	0.23	64,64,64,64	0
57	MG	2A	3338	1/1	0.87	0.20	45,45,45,45	0
57	MG	1A	4029	1/1	0.87	0.12	54,54,54,54	0
57	MG	1A	3920	1/1	0.87	0.22	52,52,52,52	0
57	MG	1A	3674	1/1	0.87	0.14	55,55,55,55	0
57	MG	1A	3466	1/1	0.87	0.30	37,37,37,37	0
57	MG	2A	3217	1/1	0.87	0.20	57,57,57,57	0
57	MG	2A	3365	1/1	0.87	0.19	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2A	3693	1/1	0.87	0.11	52,52,52,52	0
57	MG	2a	1675	1/1	0.87	0.18	56,56,56,56	0
57	MG	2A	3366	1/1	0.87	0.25	57,57,57,57	0
57	MG	2a	1693	1/1	0.87	0.17	58,58,58,58	0
57	MG	1A	3931	1/1	0.87	0.11	59,59,59,59	0
57	MG	10	107	1/1	0.87	0.17	61,61,61,61	0
57	MG	2A	3710	1/1	0.87	0.14	53,53,53,53	0
57	MG	1A	3939	1/1	0.87	0.19	63,63,63,63	0
57	MG	2a	1715	1/1	0.87	0.23	62,62,62,62	0
57	MG	2A	3394	1/1	0.87	0.32	57,57,57,57	0
57	MG	1A	3679	1/1	0.87	0.13	44,44,44,44	0
57	MG	2A	3023	1/1	0.87	0.14	56,56,56,56	0
57	MG	2A	3028	1/1	0.87	0.19	54,54,54,54	0
57	MG	2A	3030	1/1	0.87	0.17	59,59,59,59	0
57	MG	2A	3732	1/1	0.87	0.26	42,42,42,42	0
57	MG	2A	3412	1/1	0.87	0.35	49,49,49,49	0
57	MG	1A	3629	1/1	0.87	0.13	29,29,29,29	0
57	MG	2A	3246	1/1	0.87	0.18	62,62,62,62	0
57	MG	1A	3406	1/1	0.87	0.23	48,48,48,48	0
57	MG	2A	3446	1/1	0.87	0.16	56,56,56,56	0
57	MG	2a	1745	1/1	0.87	0.13	55,55,55,55	0
57	MG	1a	1612	1/1	0.87	0.15	55,55,55,55	0
57	MG	2A	3454	1/1	0.87	0.10	55,55,55,55	0
57	MG	2a	1749	1/1	0.87	0.15	70,70,70,70	0
57	MG	2A	3764	1/1	0.87	0.10	40,40,40,40	0
57	MG	1A	3550	1/1	0.87	0.19	46,46,46,46	0
57	MG	1A	3335	1/1	0.87	0.15	53,53,53,53	0
57	MG	2A	3077	1/1	0.87	0.19	50,50,50,50	0
57	MG	1A	3983	1/1	0.87	0.12	53,53,53,53	0
57	MG	1A	3442	1/1	0.87	0.13	45,45,45,45	0
57	MG	2A	3088	1/1	0.87	0.10	46,46,46,46	0
57	MG	1a	1755	1/1	0.87	0.13	60,60,60,60	0
57	MG	2A	3803	1/1	0.87	0.16	54,54,54,54	0
57	MG	1A	3880	1/1	0.87	0.14	52,52,52,52	0
57	MG	2A	3819	1/1	0.87	0.11	57,57,57,57	0
57	MG	1a	1642	1/1	0.87	0.20	55,55,55,55	0
57	MG	1a	1763	1/1	0.87	0.23	56,56,56,56	0
57	MG	1A	3881	1/1	0.87	0.12	20,20,20,20	0
57	MG	2A	3551	1/1	0.87	0.22	45,45,45,45	0
57	MG	1A	3349	1/1	0.87	0.11	37,37,37,37	0
57	MG	1E	306	1/1	0.87	0.10	10,10,10,10	0
57	MG	2A	3477	1/1	0.88	0.26	57,57,57,57	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2A	3494	1/1	0.88	0.10	38,38,38,38	0
57	MG	2A	3496	1/1	0.88	0.20	59,59,59,59	0
57	MG	2A	3044	1/1	0.88	0.20	62,62,62,62	0
57	MG	2A	3499	1/1	0.88	0.13	26,26,26,26	0
57	MG	2A	3837	1/1	0.88	0.12	31,31,31,31	0
57	MG	1B	231	1/1	0.88	0.09	45,45,45,45	0
57	MG	2A	3256	1/1	0.88	0.08	49,49,49,49	0
57	MG	2B	201	1/1	0.88	0.13	67,67,67,67	0
57	MG	2A	3259	1/1	0.88	0.26	42,42,42,42	0
57	MG	2A	3260	1/1	0.88	0.13	38,38,38,38	0
57	MG	1A	3069	1/1	0.88	0.26	42,42,42,42	0
57	MG	2A	3537	1/1	0.88	0.08	32,32,32,32	0
57	MG	2A	3057	1/1	0.88	0.11	57,57,57,57	0
57	MG	2B	210	1/1	0.88	0.26	60,60,60,60	0
57	MG	2A	3266	1/1	0.88	0.08	49,49,49,49	0
57	MG	1A	3733	1/1	0.88	0.12	19,19,19,19	0
57	MG	2A	3558	1/1	0.88	0.15	27,27,27,27	0
57	MG	2A	3269	1/1	0.88	0.25	61,61,61,61	0
57	MG	2A	3063	1/1	0.88	0.21	57,57,57,57	0
57	MG	1a	1636	1/1	0.88	0.31	65,65,65,65	0
57	MG	1A	3425	1/1	0.88	0.16	63,63,63,63	0
57	MG	1A	3656	1/1	0.88	0.13	56,56,56,56	0
57	MG	1A	3660	1/1	0.88	0.10	24,24,24,24	0
57	MG	1a	1645	1/1	0.88	0.23	53,53,53,53	0
57	MG	1E	309	1/1	0.88	0.13	48,48,48,48	0
57	MG	2Z	301	1/1	0.88	0.20	61,61,61,61	0
57	MG	2A	3100	1/1	0.88	0.19	56,56,56,56	0
57	MG	1F	304	1/1	0.88	0.13	51,51,51,51	0
57	MG	1a	1768	1/1	0.88	0.14	71,71,71,71	0
57	MG	2A	3631	1/1	0.88	0.18	33,33,33,33	0
57	MG	1A	3781	1/1	0.88	0.13	30,30,30,30	0
57	MG	1A	3293	1/1	0.88	0.12	41,41,41,41	0
57	MG	1G	202	1/1	0.88	0.27	58,58,58,58	0
57	MG	2A	3312	1/1	0.88	0.12	68,68,68,68	0
57	MG	2a	1619	1/1	0.88	0.16	55,55,55,55	0
57	MG	1G	203	1/1	0.88	0.10	64,64,64,64	0
57	MG	2a	1624	1/1	0.88	0.29	58,58,58,58	0
57	MG	1A	3898	1/1	0.88	0.13	20,20,20,20	0
57	MG	1A	3789	1/1	0.88	0.13	51,51,51,51	0
57	MG	2a	1641	1/1	0.88	0.21	66,66,66,66	0
57	MG	1A	3790	1/1	0.88	0.12	61,61,61,61	0
57	MG	2a	1646	1/1	0.88	0.16	57,57,57,57	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2a	1654	1/1	0.88	0.21	54,54,54,54	0
57	MG	2a	1659	1/1	0.88	0.38	55,55,55,55	0
57	MG	2A	3323	1/1	0.88	0.15	59,59,59,59	0
57	MG	2a	1668	1/1	0.88	0.28	57,57,57,57	0
57	MG	1A	4030	1/1	0.88	0.11	60,60,60,60	0
57	MG	1a	1793	1/1	0.88	0.16	67,67,67,67	0
57	MG	2A	3330	1/1	0.88	0.21	65,65,65,65	0
57	MG	1A	3380	1/1	0.88	0.30	52,52,52,52	0
57	MG	2a	1695	1/1	0.88	0.25	55,55,55,55	0
57	MG	2A	3147	1/1	0.88	0.20	43,43,43,43	0
57	MG	2a	1701	1/1	0.88	0.21	68,68,68,68	0
57	MG	1A	3805	1/1	0.88	0.11	54,54,54,54	0
57	MG	1a	1674	1/1	0.88	0.17	56,56,56,56	0
57	MG	1T	202	1/1	0.88	0.13	48,48,48,48	0
57	MG	2a	1714	1/1	0.88	0.22	51,51,51,51	0
57	MG	1A	3809	1/1	0.88	0.13	67,67,67,67	0
57	MG	2A	3704	1/1	0.88	0.09	55,55,55,55	0
57	MG	1a	1677	1/1	0.88	0.30	60,60,60,60	0
57	MG	2A	3179	1/1	0.88	0.13	62,62,62,62	0
57	MG	1a	1679	1/1	0.88	0.15	62,62,62,62	0
57	MG	2a	1729	1/1	0.88	0.11	50,50,50,50	0
57	MG	1x	102	1/1	0.88	0.12	55,55,55,55	0
57	MG	2A	3188	1/1	0.88	0.24	59,59,59,59	0
57	MG	1A	3476	1/1	0.88	0.13	67,67,67,67	0
57	MG	2A	3369	1/1	0.88	0.11	51,51,51,51	0
57	MG	1A	3824	1/1	0.88	0.10	30,30,30,30	0
57	MG	2A	3729	1/1	0.88	0.11	49,49,49,49	0
57	MG	1B	208	1/1	0.88	0.14	57,57,57,57	0
57	MG	2A	3733	1/1	0.88	0.09	50,50,50,50	0
57	MG	2A	3211	1/1	0.88	0.17	49,49,49,49	0
57	MG	2A	3385	1/1	0.88	0.21	35,35,35,35	0
57	MG	1A	3454	1/1	0.88	0.12	46,46,46,46	0
57	MG	1A	3510	1/1	0.88	0.17	44,44,44,44	0
57	MG	2A	3219	1/1	0.88	0.14	34,34,34,34	0
57	MG	2a	1753	1/1	0.88	0.10	57,57,57,57	0
57	MG	2A	3750	1/1	0.88	0.18	60,60,60,60	0
57	MG	2A	3753	1/1	0.88	0.17	57,57,57,57	0
57	MG	1a	1717	1/1	0.88	0.23	56,56,56,56	0
57	MG	1A	3394	1/1	0.88	0.12	56,56,56,56	0
57	MG	2A	3019	1/1	0.88	0.15	50,50,50,50	0
57	MG	1A	3326	1/1	0.88	0.11	47,47,47,47	0
57	MG	2f	201	1/1	0.88	0.17	61,61,61,61	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2A	3230	1/1	0.88	0.20	59,59,59,59	0
57	MG	1A	3710	1/1	0.88	0.17	32,32,32,32	0
57	MG	1a	1611	1/1	0.88	0.19	69,69,69,69	0
57	MG	2A	3029	1/1	0.88	0.20	37,37,37,37	0
57	MG	2A	3240	1/1	0.88	0.11	52,52,52,52	0
57	MG	1a	1724	1/1	0.88	0.18	48,48,48,48	0
57	MG	1a	1730	1/1	0.88	0.17	56,56,56,56	0
57	MG	1A	3973	1/1	0.88	0.09	62,62,62,62	0
57	MG	2A	3817	1/1	0.88	0.15	60,60,60,60	0
57	MG	1a	1753	1/1	0.89	0.18	55,55,55,55	0
57	MG	1A	3452	1/1	0.89	0.31	43,43,43,43	0
57	MG	2A	3835	1/1	0.89	0.21	69,69,69,69	0
57	MG	2A	3518	1/1	0.89	0.10	32,32,32,32	0
57	MG	2A	3842	1/1	0.89	0.12	48,48,48,48	0
57	MG	1a	1759	1/1	0.89	0.14	54,54,54,54	0
57	MG	1A	3239	1/1	0.89	0.16	42,42,42,42	0
57	MG	1A	3938	1/1	0.89	0.12	27,27,27,27	0
57	MG	1A	3327	1/1	0.89	0.18	55,55,55,55	0
57	MG	2A	3280	1/1	0.89	0.14	44,44,44,44	0
57	MG	1a	1766	1/1	0.89	0.09	45,45,45,45	0
57	MG	1A	3626	1/1	0.89	0.11	45,45,45,45	0
57	MG	1A	3791	1/1	0.89	0.15	43,43,43,43	0
57	MG	1A	3793	1/1	0.89	0.09	44,44,44,44	0
57	MG	2A	3298	1/1	0.89	0.32	52,52,52,52	0
57	MG	1A	3246	1/1	0.89	0.21	45,45,45,45	0
57	MG	1A	3633	1/1	0.89	0.10	41,41,41,41	0
57	MG	1A	3147	1/1	0.89	0.17	31,31,31,31	0
57	MG	2A	3592	1/1	0.89	0.09	28,28,28,28	0
57	MG	2A	3596	1/1	0.89	0.11	54,54,54,54	0
57	MG	2A	3597	1/1	0.89	0.15	46,46,46,46	0
57	MG	2A	3598	1/1	0.89	0.13	57,57,57,57	0
57	MG	1A	3975	1/1	0.89	0.18	48,48,48,48	0
57	MG	2A	3305	1/1	0.89	0.12	43,43,43,43	0
57	MG	1a	1661	1/1	0.89	0.12	54,54,54,54	0
57	MG	2T	205	1/1	0.89	0.09	59,59,59,59	0
57	MG	2X	101	1/1	0.89	0.20	65,65,65,65	0
57	MG	2A	3609	1/1	0.89	0.15	40,40,40,40	0
57	MG	1A	3979	1/1	0.89	0.13	52,52,52,52	0
57	MG	2A	3617	1/1	0.89	0.09	28,28,28,28	0
57	MG	2A	3314	1/1	0.89	0.13	67,67,67,67	0
57	MG	2a	1602	1/1	0.89	0.13	45,45,45,45	0
57	MG	1a	1784	1/1	0.89	0.11	52,52,52,52	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2A	3317	1/1	0.89	0.27	59,59,59,59	0
57	MG	2a	1606	1/1	0.89	0.17	60,60,60,60	0
57	MG	2a	1609	1/1	0.89	0.11	65,65,65,65	0
57	MG	2A	3157	1/1	0.89	0.22	45,45,45,45	0
57	MG	2A	3319	1/1	0.89	0.16	49,49,49,49	0
57	MG	2A	3642	1/1	0.89	0.16	54,54,54,54	0
57	MG	1A	3275	1/1	0.89	0.09	34,34,34,34	0
57	MG	1A	3277	1/1	0.89	0.23	61,61,61,61	0
57	MG	2A	3324	1/1	0.89	0.28	55,55,55,55	0
57	MG	1A	3089	1/1	0.89	0.18	42,42,42,42	0
57	MG	2a	1637	1/1	0.89	0.21	51,51,51,51	0
57	MG	1A	3827	1/1	0.89	0.16	28,28,28,28	0
57	MG	2A	3175	1/1	0.89	0.16	45,45,45,45	0
57	MG	2A	3663	1/1	0.89	0.18	56,56,56,56	0
57	MG	1a	1671	1/1	0.89	0.30	67,67,67,67	0
57	MG	2A	3177	1/1	0.89	0.17	54,54,54,54	0
57	MG	1A	3294	1/1	0.89	0.20	46,46,46,46	0
57	MG	2a	1663	1/1	0.89	0.25	53,53,53,53	0
57	MG	2A	3182	1/1	0.89	0.21	52,52,52,52	0
57	MG	2A	3681	1/1	0.89	0.10	43,43,43,43	0
57	MG	2A	3686	1/1	0.89	0.18	77,77,77,77	0
57	MG	2a	1671	1/1	0.89	0.32	67,67,67,67	0
57	MG	2a	1674	1/1	0.89	0.20	52,52,52,52	0
57	MG	1A	3393	1/1	0.89	0.11	48,48,48,48	0
57	MG	2A	3339	1/1	0.89	0.15	60,60,60,60	0
57	MG	2a	1681	1/1	0.89	0.15	48,48,48,48	0
57	MG	2a	1686	1/1	0.89	0.18	61,61,61,61	0
57	MG	2a	1690	1/1	0.89	0.33	63,63,63,63	0
57	MG	1A	3492	1/1	0.89	0.07	43,43,43,43	0
57	MG	2A	3344	1/1	0.89	0.10	56,56,56,56	0
57	MG	2a	1697	1/1	0.89	0.18	46,46,46,46	0
57	MG	1A	3493	1/1	0.89	0.19	45,45,45,45	0
57	MG	1l	202	1/1	0.89	0.18	62,62,62,62	0
57	MG	2a	1703	1/1	0.89	0.20	49,49,49,49	0
57	MG	1n	101	1/1	0.89	0.33	69,69,69,69	0
57	MG	1n	102	1/1	0.89	0.20	61,61,61,61	0
57	MG	2A	3361	1/1	0.89	0.25	40,40,40,40	0
57	MG	2A	3362	1/1	0.89	0.14	56,56,56,56	0
57	MG	2A	3205	1/1	0.89	0.11	59,59,59,59	0
57	MG	1R	207	1/1	0.89	0.17	52,52,52,52	0
57	MG	1A	3855	1/1	0.89	0.08	43,43,43,43	0
57	MG	1A	4027	1/1	0.89	0.10	35,35,35,35	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2A	3725	1/1	0.89	0.15	59,59,59,59	0
57	MG	1a	1683	1/1	0.89	0.27	61,61,61,61	0
57	MG	2a	1730	1/1	0.89	0.20	58,58,58,58	0
57	MG	1A	3498	1/1	0.89	0.08	41,41,41,41	0
57	MG	1a	1687	1/1	0.89	0.15	63,63,63,63	0
57	MG	1a	1689	1/1	0.89	0.24	51,51,51,51	0
57	MG	1A	3304	1/1	0.89	0.16	43,43,43,43	0
57	MG	2A	3737	1/1	0.89	0.13	52,52,52,52	0
57	MG	1A	3511	1/1	0.89	0.23	44,44,44,44	0
57	MG	2a	1742	1/1	0.89	0.22	60,60,60,60	0
57	MG	1A	3704	1/1	0.89	0.09	11,11,11,11	0
57	MG	1A	3402	1/1	0.89	0.22	34,34,34,34	0
57	MG	1A	3208	1/1	0.89	0.16	49,49,49,49	0
57	MG	2A	3749	1/1	0.89	0.12	42,42,42,42	0
57	MG	2A	3417	1/1	0.89	0.22	50,50,50,50	0
57	MG	1A	3316	1/1	0.89	0.20	53,53,53,53	0
57	MG	1A	3233	1/1	0.89	0.14	36,36,36,36	0
57	MG	1A	3736	1/1	0.89	0.11	50,50,50,50	0
57	MG	2A	3247	1/1	0.89	0.14	61,61,61,61	0
57	MG	2A	3448	1/1	0.89	0.11	49,49,49,49	0
57	MG	1A	3322	1/1	0.89	0.15	54,54,54,54	0
57	MG	1a	1613	1/1	0.89	0.14	65,65,65,65	0
57	MG	1a	1731	1/1	0.89	0.23	51,51,51,51	0
57	MG	1a	1614	1/1	0.89	0.12	48,48,48,48	0
57	MG	1a	1618	1/1	0.89	0.09	40,40,40,40	0
57	MG	2A	3473	1/1	0.89	0.24	54,54,54,54	0
57	MG	1a	1734	1/1	0.89	0.25	57,57,57,57	0
57	MG	2A	3483	1/1	0.89	0.16	47,47,47,47	0
57	MG	1A	3323	1/1	0.89	0.24	46,46,46,46	0
57	MG	1a	1628	1/1	0.89	0.21	51,51,51,51	0
57	MG	2t	201	1/1	0.89	0.17	48,48,48,48	0
57	MG	2A	3824	1/1	0.89	0.14	23,23,23,23	0
57	MG	2x	101	1/1	0.89	0.19	60,60,60,60	0
57	MG	1A	3554	1/1	0.89	0.14	39,39,39,39	0
57	MG	2A	3827	1/1	0.89	0.10	20,20,20,20	0
57	MG	2x	105	1/1	0.89	0.28	57,57,57,57	0
57	MG	1B	224	1/1	0.89	0.12	53,53,53,53	0
57	MG	2A	3291	1/1	0.90	0.24	52,52,52,52	0
57	MG	1A	3336	1/1	0.90	0.11	33,33,33,33	0
57	MG	2A	3101	1/1	0.90	0.11	53,53,53,53	0
57	MG	1A	4006	1/1	0.90	0.12	38,38,38,38	0
57	MG	2A	3588	1/1	0.90	0.09	49,49,49,49	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1A	3417	1/1	0.90	0.18	61,61,61,61	0
57	MG	2A	3595	1/1	0.90	0.15	45,45,45,45	0
57	MG	1A	3494	1/1	0.90	0.15	43,43,43,43	0
57	MG	1a	1617	1/1	0.90	0.08	53,53,53,53	0
57	MG	1A	3292	1/1	0.90	0.11	33,33,33,33	0
57	MG	1a	1620	1/1	0.90	0.29	65,65,65,65	0
57	MG	1a	1760	1/1	0.90	0.07	52,52,52,52	0
57	MG	1A	4018	1/1	0.90	0.12	14,14,14,14	0
57	MG	1A	3426	1/1	0.90	0.12	47,47,47,47	0
57	MG	2A	3316	1/1	0.90	0.18	58,58,58,58	0
57	MG	1A	3351	1/1	0.90	0.14	50,50,50,50	0
57	MG	2P	203	1/1	0.90	0.09	49,49,49,49	0
57	MG	2A	3130	1/1	0.90	0.17	47,47,47,47	0
57	MG	1A	3164	1/1	0.90	0.23	43,43,43,43	0
57	MG	2T	202	1/1	0.90	0.13	58,58,58,58	0
57	MG	2A	3630	1/1	0.90	0.13	49,49,49,49	0
57	MG	1A	3847	1/1	0.90	0.08	19,19,19,19	0
57	MG	1A	3532	1/1	0.90	0.32	44,44,44,44	0
57	MG	2A	3151	1/1	0.90	0.17	42,42,42,42	0
57	MG	1A	3359	1/1	0.90	0.18	28,28,28,28	0
57	MG	1A	3453	1/1	0.90	0.13	57,57,57,57	0
57	MG	28	101	1/1	0.90	0.13	52,52,52,52	0
57	MG	2A	3647	1/1	0.90	0.15	52,52,52,52	0
57	MG	2A	3161	1/1	0.90	0.20	61,61,61,61	0
57	MG	1A	3858	1/1	0.90	0.11	33,33,33,33	0
57	MG	1A	3865	1/1	0.90	0.29	27,27,27,27	0
57	MG	2A	3652	1/1	0.90	0.11	34,34,34,34	0
57	MG	2A	3169	1/1	0.90	0.15	57,57,57,57	0
57	MG	1A	3318	1/1	0.90	0.08	39,39,39,39	0
57	MG	2a	1617	1/1	0.90	0.12	40,40,40,40	0
57	MG	2A	3659	1/1	0.90	0.18	52,52,52,52	0
57	MG	1A	3551	1/1	0.90	0.08	34,34,34,34	0
57	MG	2A	3665	1/1	0.90	0.18	64,64,64,64	0
57	MG	2A	3666	1/1	0.90	0.20	43,43,43,43	0
57	MG	1A	3696	1/1	0.90	0.13	52,52,52,52	0
57	MG	2a	1630	1/1	0.90	0.19	59,59,59,59	0
57	MG	2a	1636	1/1	0.90	0.24	54,54,54,54	0
57	MG	1a	1658	1/1	0.90	0.12	55,55,55,55	0
57	MG	1A	3874	1/1	0.90	0.09	25,25,25,25	0
57	MG	1A	3321	1/1	0.90	0.21	39,39,39,39	0
57	MG	1a	1795	1/1	0.90	0.14	62,62,62,62	0
57	MG	2A	3684	1/1	0.90	0.10	40,40,40,40	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1a	1796	1/1	0.90	0.19	51,51,51,51	0
57	MG	1A	3166	1/1	0.90	0.10	35,35,35,35	0
57	MG	2A	3190	1/1	0.90	0.25	49,49,49,49	0
57	MG	2A	3191	1/1	0.90	0.16	57,57,57,57	0
57	MG	1A	3386	1/1	0.90	0.14	54,54,54,54	0
57	MG	1A	3712	1/1	0.90	0.08	41,41,41,41	0
57	MG	2A	3368	1/1	0.90	0.09	45,45,45,45	0
57	MG	1A	3720	1/1	0.90	0.12	47,47,47,47	0
57	MG	2A	3204	1/1	0.90	0.20	51,51,51,51	0
57	MG	2a	1676	1/1	0.90	0.49	69,69,69,69	0
57	MG	2a	1677	1/1	0.90	0.18	58,58,58,58	0
57	MG	2A	3709	1/1	0.90	0.13	52,52,52,52	0
57	MG	1A	3722	1/1	0.90	0.10	9,9,9,9	0
57	MG	2A	3206	1/1	0.90	0.19	62,62,62,62	0
57	MG	2a	1688	1/1	0.90	0.25	58,58,58,58	0
57	MG	2A	3715	1/1	0.90	0.14	60,60,60,60	0
57	MG	2a	1692	1/1	0.90	0.22	55,55,55,55	0
57	MG	1A	3904	1/1	0.90	0.15	47,47,47,47	0
57	MG	1A	3556	1/1	0.90	0.25	57,57,57,57	0
57	MG	1A	3915	1/1	0.90	0.10	28,28,28,28	0
57	MG	1A	3562	1/1	0.90	0.20	50,50,50,50	0
57	MG	1A	3924	1/1	0.90	0.09	26,26,26,26	0
57	MG	1r	101	1/1	0.90	0.30	54,54,54,54	0
57	MG	2A	3728	1/1	0.90	0.10	49,49,49,49	0
57	MG	2a	1709	1/1	0.90	0.14	37,37,37,37	0
57	MG	1t	201	1/1	0.90	0.11	48,48,48,48	0
57	MG	1A	3563	1/1	0.90	0.14	46,46,46,46	0
57	MG	1A	3591	1/1	0.90	0.07	42,42,42,42	0
57	MG	2A	3422	1/1	0.90	0.25	58,58,58,58	0
57	MG	2A	3429	1/1	0.90	0.11	54,54,54,54	0
57	MG	1A	3592	1/1	0.90	0.06	22,22,22,22	0
57	MG	1A	3933	1/1	0.90	0.10	21,21,21,21	0
57	MG	1a	1682	1/1	0.90	0.13	54,54,54,54	0
57	MG	1A	3761	1/1	0.90	0.08	42,42,42,42	0
57	MG	1A	3593	1/1	0.90	0.11	31,31,31,31	0
57	MG	1A	3389	1/1	0.90	0.17	40,40,40,40	0
57	MG	1a	1688	1/1	0.90	0.08	65,65,65,65	0
57	MG	2A	3759	1/1	0.90	0.10	46,46,46,46	0
57	MG	2a	1735	1/1	0.90	0.21	50,50,50,50	0
57	MG	1A	3944	1/1	0.90	0.16	33,33,33,33	0
57	MG	1a	1698	1/1	0.90	0.09	65,65,65,65	0
57	MG	1A	3783	1/1	0.90	0.12	44,44,44,44	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1A	3784	1/1	0.90	0.11	47,47,47,47	0
57	MG	2A	3481	1/1	0.90	0.29	46,46,46,46	0
57	MG	2A	3773	1/1	0.90	0.12	38,38,38,38	0
57	MG	1A	3301	1/1	0.90	0.11	53,53,53,53	0
57	MG	2A	3484	1/1	0.90	0.25	54,54,54,54	0
57	MG	2A	3486	1/1	0.90	0.13	49,49,49,49	0
57	MG	1a	1713	1/1	0.90	0.22	60,60,60,60	0
57	MG	1A	3961	1/1	0.90	0.12	35,35,35,35	0
57	MG	2A	3800	1/1	0.90	0.08	43,43,43,43	0
57	MG	1A	3968	1/1	0.90	0.13	51,51,51,51	0
57	MG	2A	3805	1/1	0.90	0.12	48,48,48,48	0
57	MG	2A	3812	1/1	0.90	0.09	33,33,33,33	0
57	MG	1A	3606	1/1	0.90	0.21	47,47,47,47	0
57	MG	2A	3816	1/1	0.90	0.20	55,55,55,55	0
57	MG	2a	1769	1/1	0.90	0.22	58,58,58,58	0
57	MG	1A	3113	1/1	0.90	0.12	45,45,45,45	0
57	MG	2d	302	1/1	0.90	0.13	64,64,64,64	0
57	MG	2e	201	1/1	0.90	0.15	64,64,64,64	0
57	MG	2A	3818	1/1	0.90	0.15	52,52,52,52	0
57	MG	2A	3505	1/1	0.90	0.20	40,40,40,40	0
57	MG	1A	3610	1/1	0.90	0.06	16,16,16,16	0
57	MG	1A	3617	1/1	0.90	0.30	53,53,53,53	0
57	MG	1a	1727	1/1	0.90	0.17	48,48,48,48	0
57	MG	2A	3070	1/1	0.90	0.09	39,39,39,39	0
57	MG	1A	3982	1/1	0.90	0.15	46,46,46,46	0
57	MG	1A	3055	1/1	0.90	0.08	31,31,31,31	0
57	MG	1A	3803	1/1	0.90	0.10	44,44,44,44	0
57	MG	1A	3804	1/1	0.90	0.16	50,50,50,50	0
57	MG	1A	3315	1/1	0.90	0.18	41,41,41,41	0
57	MG	2A	3285	1/1	0.90	0.12	58,58,58,58	0
57	MG	1a	1743	1/1	0.90	0.12	48,48,48,48	0
57	MG	2x	107	1/1	0.90	0.24	61,61,61,61	0
57	MG	1A	3364	1/1	0.91	0.22	31,31,31,31	0
57	MG	1A	4034	1/1	0.91	0.24	36,36,36,36	0
57	MG	1a	1638	1/1	0.91	0.24	52,52,52,52	0
57	MG	1a	1779	1/1	0.91	0.15	50,50,50,50	0
57	MG	2A	3798	1/1	0.91	0.11	24,24,24,24	0
57	MG	2A	3799	1/1	0.91	0.14	46,46,46,46	0
57	MG	1a	1640	1/1	0.91	0.20	49,49,49,49	0
57	MG	1a	1781	1/1	0.91	0.11	39,39,39,39	0
57	MG	2A	3441	1/1	0.91	0.11	65,65,65,65	0
57	MG	2A	3442	1/1	0.91	0.16	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1a	1783	1/1	0.91	0.19	61,61,61,61	0
57	MG	1A	3558	1/1	0.91	0.13	47,47,47,47	0
57	MG	2A	3449	1/1	0.91	0.20	55,55,55,55	0
57	MG	1A	3049	1/1	0.91	0.16	25,25,25,25	0
57	MG	2A	3452	1/1	0.91	0.09	41,41,41,41	0
57	MG	1A	3095	1/1	0.91	0.15	48,48,48,48	0
57	MG	2A	3825	1/1	0.91	0.10	20,20,20,20	0
57	MG	1A	3729	1/1	0.91	0.10	19,19,19,19	0
57	MG	2A	3212	1/1	0.91	0.12	56,56,56,56	0
57	MG	2A	3214	1/1	0.91	0.11	37,37,37,37	0
57	MG	1B	202	1/1	0.91	0.14	42,42,42,42	0
57	MG	1a	1651	1/1	0.91	0.18	52,52,52,52	0
57	MG	1a	1799	1/1	0.91	0.07	59,59,59,59	0
57	MG	1A	3572	1/1	0.91	0.10	44,44,44,44	0
57	MG	1A	3573	1/1	0.91	0.12	24,24,24,24	0
57	MG	1a	1804	1/1	0.91	0.18	51,51,51,51	0
57	MG	2A	3844	1/1	0.91	0.17	50,50,50,50	0
57	MG	2A	3491	1/1	0.91	0.29	48,48,48,48	0
57	MG	1a	1656	1/1	0.91	0.20	71,71,71,71	0
57	MG	1b	301	1/1	0.91	0.09	69,69,69,69	0
57	MG	1B	211	1/1	0.91	0.10	30,30,30,30	0
57	MG	1B	212	1/1	0.91	0.33	65,65,65,65	0
57	MG	2A	3236	1/1	0.91	0.10	48,48,48,48	0
57	MG	1A	3583	1/1	0.91	0.07	38,38,38,38	0
57	MG	2A	3506	1/1	0.91	0.17	32,32,32,32	0
57	MG	2B	211	1/1	0.91	0.22	62,62,62,62	0
57	MG	2B	212	1/1	0.91	0.09	69,69,69,69	0
57	MG	1A	3463	1/1	0.91	0.18	57,57,57,57	0
57	MG	1A	3758	1/1	0.91	0.07	28,28,28,28	0
57	MG	2B	217	1/1	0.91	0.15	58,58,58,58	0
57	MG	1A	3104	1/1	0.91	0.11	37,37,37,37	0
57	MG	1a	1667	1/1	0.91	0.12	68,68,68,68	0
57	MG	2D	309	1/1	0.91	0.14	60,60,60,60	0
57	MG	2A	3527	1/1	0.91	0.16	44,44,44,44	0
57	MG	1A	3384	1/1	0.91	0.26	44,44,44,44	0
57	MG	2E	305	1/1	0.91	0.12	47,47,47,47	0
57	MG	1x	101	1/1	0.91	0.22	55,55,55,55	0
57	MG	2F	302	1/1	0.91	0.22	43,43,43,43	0
57	MG	2A	3253	1/1	0.91	0.17	54,54,54,54	0
57	MG	1A	3923	1/1	0.91	0.13	46,46,46,46	0
57	MG	2A	3549	1/1	0.91	0.12	42,42,42,42	0
57	MG	2Q	204	1/1	0.91	0.18	46,46,46,46	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1A	3597	1/1	0.91	0.24	54,54,54,54	0
57	MG	2A	3553	1/1	0.91	0.10	49,49,49,49	0
57	MG	2A	3554	1/1	0.91	0.07	28,28,28,28	0
57	MG	1A	3771	1/1	0.91	0.14	41,41,41,41	0
57	MG	2W	202	1/1	0.91	0.18	47,47,47,47	0
57	MG	2A	3560	1/1	0.91	0.14	25,25,25,25	0
57	MG	1x	107	1/1	0.91	0.15	45,45,45,45	0
57	MG	2A	3261	1/1	0.91	0.12	45,45,45,45	0
57	MG	25	103	1/1	0.91	0.07	39,39,39,39	0
57	MG	25	105	1/1	0.91	0.08	34,34,34,34	0
57	MG	1x	108	1/1	0.91	0.13	43,43,43,43	0
57	MG	1A	3470	1/1	0.91	0.10	42,42,42,42	0
57	MG	2A	3575	1/1	0.91	0.17	48,48,48,48	0
57	MG	2a	1601	1/1	0.91	0.17	48,48,48,48	0
57	MG	1A	3782	1/1	0.91	0.09	28,28,28,28	0
57	MG	1D	309	1/1	0.91	0.12	41,41,41,41	0
57	MG	1A	3006	1/1	0.91	0.13	46,46,46,46	0
57	MG	1E	303	1/1	0.91	0.20	31,31,31,31	0
57	MG	2a	1608	1/1	0.91	0.29	44,44,44,44	0
57	MG	1A	3604	1/1	0.91	0.09	7,7,7,7	0
57	MG	2a	1610	1/1	0.91	0.10	53,53,53,53	0
57	MG	1A	3286	1/1	0.91	0.18	33,33,33,33	0
57	MG	1a	1681	1/1	0.91	0.15	55,55,55,55	0
57	MG	1A	3940	1/1	0.91	0.08	32,32,32,32	0
57	MG	1F	309	1/1	0.91	0.14	55,55,55,55	0
57	MG	2A	3604	1/1	0.91	0.08	21,21,21,21	0
57	MG	1A	3475	1/1	0.91	0.10	51,51,51,51	0
57	MG	2A	3282	1/1	0.91	0.09	46,46,46,46	0
57	MG	1a	1686	1/1	0.91	0.16	58,58,58,58	0
57	MG	2A	3615	1/1	0.91	0.27	61,61,61,61	0
57	MG	2a	1632	1/1	0.91	0.16	49,49,49,49	0
57	MG	1A	3392	1/1	0.91	0.24	47,47,47,47	0
57	MG	1A	3613	1/1	0.91	0.08	40,40,40,40	0
57	MG	1A	3290	1/1	0.91	0.23	39,39,39,39	0
57	MG	2A	3294	1/1	0.91	0.23	61,61,61,61	0
57	MG	2A	3296	1/1	0.91	0.10	53,53,53,53	0
57	MG	2A	3052	1/1	0.91	0.11	45,45,45,45	0
57	MG	2a	1651	1/1	0.91	0.16	53,53,53,53	0
57	MG	2A	3633	1/1	0.91	0.14	47,47,47,47	0
57	MG	2a	1658	1/1	0.91	0.21	47,47,47,47	0
57	MG	2A	3055	1/1	0.91	0.10	57,57,57,57	0
57	MG	2a	1662	1/1	0.91	0.22	52,52,52,52	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2A	3640	1/1	0.91	0.20	53,53,53,53	0
57	MG	1a	1691	1/1	0.91	0.23	45,45,45,45	0
57	MG	1a	1694	1/1	0.91	0.24	45,45,45,45	0
57	MG	1A	3136	1/1	0.91	0.02	8,8,8,8	0
57	MG	2a	1670	1/1	0.91	0.26	56,56,56,56	0
57	MG	1A	3399	1/1	0.91	0.14	36,36,36,36	0
57	MG	2a	1673	1/1	0.91	0.17	57,57,57,57	0
57	MG	1N	202	1/1	0.91	0.07	30,30,30,30	0
57	MG	2A	3309	1/1	0.91	0.17	62,62,62,62	0
57	MG	2A	3310	1/1	0.91	0.23	55,55,55,55	0
57	MG	1A	3222	1/1	0.91	0.11	46,46,46,46	0
57	MG	1A	3328	1/1	0.91	0.22	48,48,48,48	0
57	MG	2a	1679	1/1	0.91	0.22	64,64,64,64	0
57	MG	1A	3970	1/1	0.91	0.12	44,44,44,44	0
57	MG	2a	1682	1/1	0.91	0.18	52,52,52,52	0
57	MG	2a	1684	1/1	0.91	0.12	58,58,58,58	0
57	MG	2A	3660	1/1	0.91	0.10	37,37,37,37	0
57	MG	2A	3087	1/1	0.91	0.11	62,62,62,62	0
57	MG	2A	3664	1/1	0.91	0.12	50,50,50,50	0
57	MG	1A	3645	1/1	0.91	0.13	48,48,48,48	0
57	MG	1A	3815	1/1	0.91	0.21	30,30,30,30	0
57	MG	1A	3509	1/1	0.91	0.09	67,67,67,67	0
57	MG	1A	3823	1/1	0.91	0.10	35,35,35,35	0
57	MG	2A	3669	1/1	0.91	0.14	58,58,58,58	0
57	MG	1A	3404	1/1	0.91	0.12	34,34,34,34	0
57	MG	2A	3672	1/1	0.91	0.17	43,43,43,43	0
57	MG	1Y	201	1/1	0.91	0.23	41,41,41,41	0
57	MG	1a	1728	1/1	0.91	0.24	50,50,50,50	0
57	MG	1a	1729	1/1	0.91	0.09	51,51,51,51	0
57	MG	2A	3111	1/1	0.91	0.15	45,45,45,45	0
57	MG	1A	3224	1/1	0.91	0.08	50,50,50,50	0
57	MG	1A	3408	1/1	0.91	0.09	48,48,48,48	0
57	MG	2a	1718	1/1	0.91	0.14	40,40,40,40	0
57	MG	1A	3993	1/1	0.91	0.11	23,23,23,23	0
57	MG	2A	3692	1/1	0.91	0.19	46,46,46,46	0
57	MG	12	101	1/1	0.91	0.09	42,42,42,42	0
57	MG	2A	3336	1/1	0.91	0.24	55,55,55,55	0
57	MG	1A	3663	1/1	0.91	0.17	55,55,55,55	0
57	MG	2A	3701	1/1	0.91	0.17	54,54,54,54	0
57	MG	1a	1737	1/1	0.91	0.15	50,50,50,50	0
57	MG	1a	1742	1/1	0.91	0.11	51,51,51,51	0
57	MG	17	103	1/1	0.91	0.18	34,34,34,34	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1A	3834	1/1	0.91	0.10	31,31,31,31	0
57	MG	1A	4002	1/1	0.91	0.12	52,52,52,52	0
57	MG	2A	3145	1/1	0.91	0.09	51,51,51,51	0
57	MG	2A	3349	1/1	0.91	0.24	45,45,45,45	0
57	MG	2A	3717	1/1	0.91	0.09	45,45,45,45	0
57	MG	1A	3037	1/1	0.91	0.07	37,37,37,37	0
57	MG	2A	3720	1/1	0.91	0.08	39,39,39,39	0
57	MG	1a	1605	1/1	0.91	0.14	59,59,59,59	0
57	MG	1A	3238	1/1	0.91	0.18	42,42,42,42	0
57	MG	2A	3158	1/1	0.91	0.19	32,32,32,32	0
57	MG	1A	4011	1/1	0.91	0.09	40,40,40,40	0
57	MG	2A	3160	1/1	0.91	0.14	54,54,54,54	0
57	MG	1A	3308	1/1	0.91	0.07	29,29,29,29	0
57	MG	1A	3427	1/1	0.91	0.15	56,56,56,56	0
57	MG	2a	1757	1/1	0.91	0.23	60,60,60,60	0
57	MG	1A	3085	1/1	0.91	0.10	35,35,35,35	0
57	MG	2A	3371	1/1	0.91	0.10	47,47,47,47	0
57	MG	2A	3372	1/1	0.91	0.13	49,49,49,49	0
57	MG	1A	4022	1/1	0.91	0.10	43,43,43,43	0
57	MG	2a	1768	1/1	0.91	0.22	50,50,50,50	0
57	MG	1A	3245	1/1	0.91	0.11	40,40,40,40	0
57	MG	2A	3377	1/1	0.91	0.15	51,51,51,51	0
57	MG	2A	3378	1/1	0.91	0.14	46,46,46,46	0
57	MG	2A	3383	1/1	0.91	0.20	38,38,38,38	0
57	MG	1A	3361	1/1	0.91	0.09	45,45,45,45	0
57	MG	1a	1623	1/1	0.91	0.32	65,65,65,65	0
57	MG	2A	3755	1/1	0.91	0.11	37,37,37,37	0
57	MG	1A	4028	1/1	0.91	0.10	19,19,19,19	0
57	MG	1A	3362	1/1	0.91	0.29	56,56,56,56	0
57	MG	2A	3181	1/1	0.91	0.09	54,54,54,54	0
57	MG	2A	3406	1/1	0.91	0.28	55,55,55,55	0
57	MG	2A	3407	1/1	0.91	0.19	40,40,40,40	0
57	MG	1A	3555	1/1	0.91	0.16	53,53,53,53	0
57	MG	2A	3409	1/1	0.91	0.22	45,45,45,45	0
57	MG	2x	103	1/1	0.91	0.17	35,35,35,35	0
57	MG	1a	1635	1/1	0.91	0.08	48,48,48,48	0
57	MG	2A	3779	1/1	0.91	0.13	59,59,59,59	0
57	MG	2A	3780	1/1	0.91	0.10	54,54,54,54	0
57	MG	2A	3781	1/1	0.91	0.09	63,63,63,63	0
57	MG	2A	3183	1/1	0.92	0.12	47,47,47,47	0
57	MG	1A	4020	1/1	0.92	0.12	37,37,37,37	0
57	MG	2A	3342	1/1	0.92	0.19	66,66,66,66	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1a	1692	1/1	0.92	0.20	50,50,50,50	0
57	MG	1A	3352	1/1	0.92	0.10	50,50,50,50	0
57	MG	2A	3189	1/1	0.92	0.12	41,41,41,41	0
57	MG	1A	3387	1/1	0.92	0.13	46,46,46,46	0
57	MG	2A	3635	1/1	0.92	0.10	48,48,48,48	0
57	MG	1A	4026	1/1	0.92	0.09	31,31,31,31	0
57	MG	2G	201	1/1	0.92	0.12	52,52,52,52	0
57	MG	2A	3192	1/1	0.92	0.27	46,46,46,46	0
57	MG	2A	3356	1/1	0.92	0.08	52,52,52,52	0
57	MG	1A	3162	1/1	0.92	0.08	27,27,27,27	0
57	MG	2A	3359	1/1	0.92	0.19	52,52,52,52	0
57	MG	2A	3360	1/1	0.92	0.10	48,48,48,48	0
57	MG	1A	3897	1/1	0.92	0.11	11,11,11,11	0
57	MG	2A	3200	1/1	0.92	0.09	44,44,44,44	0
57	MG	1A	3250	1/1	0.92	0.24	40,40,40,40	0
57	MG	2V	201	1/1	0.92	0.13	57,57,57,57	0
57	MG	2W	201	1/1	0.92	0.32	42,42,42,42	0
57	MG	1a	1715	1/1	0.92	0.20	56,56,56,56	0
57	MG	2A	3654	1/1	0.92	0.08	41,41,41,41	0
57	MG	2A	3657	1/1	0.92	0.10	48,48,48,48	0
57	MG	1a	1716	1/1	0.92	0.18	58,58,58,58	0
57	MG	1A	3899	1/1	0.92	0.09	50,50,50,50	0
57	MG	2A	3209	1/1	0.92	0.32	36,36,36,36	0
57	MG	1a	1718	1/1	0.92	0.19	53,53,53,53	0
57	MG	1A	3605	1/1	0.92	0.09	8,8,8,8	0
57	MG	1A	3681	1/1	0.92	0.14	37,37,37,37	0
57	MG	1A	4035	1/1	0.92	0.11	38,38,38,38	0
57	MG	1A	3429	1/1	0.92	0.12	44,44,44,44	0
57	MG	1A	3479	1/1	0.92	0.47	31,31,31,31	0
57	MG	2A	3223	1/1	0.92	0.13	44,44,44,44	0
57	MG	1A	3258	1/1	0.92	0.07	35,35,35,35	0
57	MG	2A	3387	1/1	0.92	0.23	46,46,46,46	0
57	MG	2A	3675	1/1	0.92	0.12	39,39,39,39	0
57	MG	2A	3388	1/1	0.92	0.29	51,51,51,51	0
57	MG	2A	3678	1/1	0.92	0.09	68,68,68,68	0
57	MG	1a	1619	1/1	0.92	0.13	43,43,43,43	0
57	MG	2a	1616	1/1	0.92	0.19	46,46,46,46	0
57	MG	1A	3921	1/1	0.92	0.09	44,44,44,44	0
57	MG	1A	3183	1/1	0.92	0.17	30,30,30,30	0
57	MG	1B	204	1/1	0.92	0.19	50,50,50,50	0
57	MG	2A	3689	1/1	0.92	0.10	68,68,68,68	0
57	MG	1B	207	1/1	0.92	0.15	54,54,54,54	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1A	3395	1/1	0.92	0.13	42,42,42,42	0
57	MG	2A	3035	1/1	0.92	0.11	31,31,31,31	0
57	MG	2A	3039	1/1	0.92	0.11	52,52,52,52	0
57	MG	2a	1635	1/1	0.92	0.15	46,46,46,46	0
57	MG	2A	3410	1/1	0.92	0.09	42,42,42,42	0
57	MG	2A	3040	1/1	0.92	0.10	38,38,38,38	0
57	MG	2A	3242	1/1	0.92	0.11	39,39,39,39	0
57	MG	2A	3042	1/1	0.92	0.23	48,48,48,48	0
57	MG	2a	1643	1/1	0.92	0.29	58,58,58,58	0
57	MG	1A	3806	1/1	0.92	0.18	37,37,37,37	0
57	MG	1a	1736	1/1	0.92	0.10	48,48,48,48	0
57	MG	2a	1648	1/1	0.92	0.27	57,57,57,57	0
57	MG	2a	1650	1/1	0.92	0.16	47,47,47,47	0
57	MG	1A	3926	1/1	0.92	0.12	54,54,54,54	0
57	MG	2a	1653	1/1	0.92	0.32	49,49,49,49	0
57	MG	1A	3240	1/1	0.92	0.28	48,48,48,48	0
57	MG	2A	3435	1/1	0.92	0.07	45,45,45,45	0
57	MG	1A	3813	1/1	0.92	0.10	20,20,20,20	0
57	MG	2A	3254	1/1	0.92	0.13	64,64,64,64	0
57	MG	2A	3718	1/1	0.92	0.20	40,40,40,40	0
57	MG	2a	1665	1/1	0.92	0.17	53,53,53,53	0
57	MG	1a	1744	1/1	0.92	0.13	51,51,51,51	0
57	MG	2A	3061	1/1	0.92	0.11	62,62,62,62	0
57	MG	2A	3258	1/1	0.92	0.43	53,53,53,53	0
57	MG	1B	221	1/1	0.92	0.07	22,22,22,22	0
57	MG	1A	3495	1/1	0.92	0.22	44,44,44,44	0
57	MG	2A	3065	1/1	0.92	0.12	52,52,52,52	0
57	MG	1A	3728	1/1	0.92	0.11	32,32,32,32	0
57	MG	1A	3822	1/1	0.92	0.08	14,14,14,14	0
57	MG	1A	3338	1/1	0.92	0.09	37,37,37,37	0
57	MG	2A	3463	1/1	0.92	0.16	41,41,41,41	0
57	MG	1A	3638	1/1	0.92	0.11	11,11,11,11	0
57	MG	2A	3475	1/1	0.92	0.06	42,42,42,42	0
57	MG	1A	3565	1/1	0.92	0.16	33,33,33,33	0
57	MG	2A	3739	1/1	0.92	0.17	47,47,47,47	0
57	MG	2A	3740	1/1	0.92	0.18	61,61,61,61	0
57	MG	1A	3945	1/1	0.92	0.08	53,53,53,53	0
57	MG	2A	3093	1/1	0.92	0.18	57,57,57,57	0
57	MG	1A	3642	1/1	0.92	0.15	43,43,43,43	0
57	MG	1A	3738	1/1	0.92	0.07	15,15,15,15	0
57	MG	2A	3487	1/1	0.92	0.42	51,51,51,51	0
57	MG	1a	1655	1/1	0.92	0.25	55,55,55,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2A	3754	1/1	0.92	0.08	44,44,44,44	0
57	MG	1a	1765	1/1	0.92	0.10	56,56,56,56	0
57	MG	2A	3495	1/1	0.92	0.08	34,34,34,34	0
57	MG	2a	1702	1/1	0.92	0.16	36,36,36,36	0
57	MG	1A	3744	1/1	0.92	0.10	63,63,63,63	0
57	MG	1A	3745	1/1	0.92	0.07	30,30,30,30	0
57	MG	1A	3837	1/1	0.92	0.09	10,10,10,10	0
57	MG	2A	3501	1/1	0.92	0.09	53,53,53,53	0
57	MG	1A	3840	1/1	0.92	0.10	20,20,20,20	0
57	MG	1A	3841	1/1	0.92	0.11	36,36,36,36	0
57	MG	2A	3287	1/1	0.92	0.30	40,40,40,40	0
57	MG	2a	1717	1/1	0.92	0.17	49,49,49,49	0
57	MG	2A	3778	1/1	0.92	0.10	55,55,55,55	0
57	MG	2A	3289	1/1	0.92	0.10	51,51,51,51	0
57	MG	2A	3290	1/1	0.92	0.08	51,51,51,51	0
57	MG	1A	3746	1/1	0.92	0.09	27,27,27,27	0
57	MG	2A	3524	1/1	0.92	0.30	51,51,51,51	0
57	MG	1A	3567	1/1	0.92	0.10	24,24,24,24	0
57	MG	2A	3795	1/1	0.92	0.16	47,47,47,47	0
57	MG	1A	3850	1/1	0.92	0.09	33,33,33,33	0
57	MG	1a	1777	1/1	0.92	0.18	56,56,56,56	0
57	MG	2A	3533	1/1	0.92	0.08	26,26,26,26	0
57	MG	1A	3371	1/1	0.92	0.20	47,47,47,47	0
57	MG	1A	3348	1/1	0.92	0.15	45,45,45,45	0
57	MG	1A	3856	1/1	0.92	0.12	44,44,44,44	0
57	MG	2a	1740	1/1	0.92	0.10	50,50,50,50	0
57	MG	2A	3133	1/1	0.92	0.16	51,51,51,51	0
57	MG	2A	3808	1/1	0.92	0.10	28,28,28,28	0
57	MG	2A	3137	1/1	0.92	0.19	44,44,44,44	0
57	MG	1A	3987	1/1	0.92	0.08	49,49,49,49	0
57	MG	1A	3090	1/1	0.92	0.22	48,48,48,48	0
57	MG	1A	3991	1/1	0.92	0.06	34,34,34,34	0
57	MG	1A	3860	1/1	0.92	0.07	38,38,38,38	0
57	MG	1A	3995	1/1	0.92	0.07	23,23,23,23	0
57	MG	1a	1794	1/1	0.92	0.09	54,54,54,54	0
57	MG	1A	3659	1/1	0.92	0.09	26,26,26,26	0
57	MG	1a	1678	1/1	0.92	0.10	44,44,44,44	0
57	MG	1Q	203	1/1	0.92	0.15	49,49,49,49	0
57	MG	2A	3828	1/1	0.92	0.12	56,56,56,56	0
57	MG	2A	3579	1/1	0.92	0.11	31,31,31,31	0
57	MG	1A	3160	1/1	0.92	0.10	33,33,33,33	0
57	MG	2a	1766	1/1	0.92	0.17	52,52,52,52	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2A	3582	1/1	0.92	0.13	43,43,43,43	0
57	MG	2A	3583	1/1	0.92	0.25	58,58,58,58	0
57	MG	1A	3772	1/1	0.92	0.15	53,53,53,53	0
57	MG	1A	3780	1/1	0.92	0.12	34,34,34,34	0
57	MG	2d	301	1/1	0.92	0.23	49,49,49,49	0
57	MG	2A	3594	1/1	0.92	0.12	48,48,48,48	0
57	MG	2A	3168	1/1	0.92	0.11	40,40,40,40	0
57	MG	1A	3873	1/1	0.92	0.14	56,56,56,56	0
57	MG	2A	3846	1/1	0.92	0.17	56,56,56,56	0
57	MG	2A	3170	1/1	0.92	0.10	56,56,56,56	0
57	MG	2k	201	1/1	0.92	0.21	53,53,53,53	0
57	MG	2B	202	1/1	0.92	0.07	63,63,63,63	0
57	MG	2l	203	1/1	0.92	0.12	56,56,56,56	0
57	MG	1A	3416	1/1	0.92	0.14	51,51,51,51	0
57	MG	1A	3875	1/1	0.92	0.15	51,51,51,51	0
57	MG	2B	205	1/1	0.92	0.17	60,60,60,60	0
57	MG	2A	3601	1/1	0.92	0.16	52,52,52,52	0
57	MG	1A	3876	1/1	0.92	0.09	38,38,38,38	0
57	MG	1e	201	1/1	0.92	0.35	59,59,59,59	0
57	MG	1e	202	1/1	0.92	0.16	57,57,57,57	0
57	MG	2A	3334	1/1	0.92	0.11	50,50,50,50	0
57	MG	1A	3544	1/1	0.92	0.08	38,38,38,38	0
57	MG	10	106	1/1	0.92	0.09	55,55,55,55	0
57	MG	2A	3616	1/1	0.92	0.09	39,39,39,39	0
57	MG	2A	3809	1/1	0.93	0.11	43,43,43,43	0
57	MG	1A	3484	1/1	0.93	0.15	40,40,40,40	0
57	MG	2A	3231	1/1	0.93	0.08	52,52,52,52	0
57	MG	1A	4042	1/1	0.93	0.19	43,43,43,43	0
57	MG	1A	3600	1/1	0.93	0.09	43,43,43,43	0
57	MG	1A	4045	1/1	0.93	0.13	37,37,37,37	0
57	MG	2A	3237	1/1	0.93	0.17	45,45,45,45	0
57	MG	1A	3485	1/1	0.93	0.18	27,27,27,27	0
57	MG	1A	3889	1/1	0.93	0.12	17,17,17,17	0
57	MG	1A	3488	1/1	0.93	0.38	54,54,54,54	0
57	MG	1p	101	1/1	0.93	0.24	46,46,46,46	0
57	MG	1A	3756	1/1	0.93	0.11	11,11,11,11	0
57	MG	1A	3491	1/1	0.93	0.19	37,37,37,37	0
57	MG	1B	210	1/1	0.93	0.13	33,33,33,33	0
57	MG	1A	3415	1/1	0.93	0.23	37,37,37,37	0
57	MG	1x	103	1/1	0.93	0.28	43,43,43,43	0
57	MG	2A	3509	1/1	0.93	0.15	43,43,43,43	0
57	MG	2A	3838	1/1	0.93	0.14	57,57,57,57	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2A	3839	1/1	0.93	0.13	29,29,29,29	0
57	MG	2A	3510	1/1	0.93	0.12	51,51,51,51	0
57	MG	1a	1664	1/1	0.93	0.16	52,52,52,52	0
57	MG	2A	3513	1/1	0.93	0.06	39,39,39,39	0
57	MG	1A	3176	1/1	0.93	0.19	48,48,48,48	0
57	MG	1a	1666	1/1	0.93	0.23	50,50,50,50	0
57	MG	1A	3289	1/1	0.93	0.11	38,38,38,38	0
57	MG	1A	3768	1/1	0.93	0.07	32,32,32,32	0
57	MG	2A	3002	1/1	0.93	0.25	48,48,48,48	0
57	MG	1A	3016	1/1	0.93	0.20	37,37,37,37	0
57	MG	2A	3530	1/1	0.93	0.11	49,49,49,49	0
57	MG	2A	3262	1/1	0.93	0.09	63,63,63,63	0
57	MG	1A	3916	1/1	0.93	0.06	32,32,32,32	0
57	MG	2A	3264	1/1	0.93	0.07	66,66,66,66	0
57	MG	2A	3545	1/1	0.93	0.12	52,52,52,52	0
57	MG	2A	3546	1/1	0.93	0.08	37,37,37,37	0
57	MG	1A	3291	1/1	0.93	0.08	48,48,48,48	0
57	MG	1A	3778	1/1	0.93	0.08	16,16,16,16	0
57	MG	2A	3550	1/1	0.93	0.13	26,26,26,26	0
57	MG	1A	3615	1/1	0.93	0.10	36,36,36,36	0
57	MG	2A	3552	1/1	0.93	0.22	50,50,50,50	0
57	MG	1A	3499	1/1	0.93	0.09	48,48,48,48	0
57	MG	1A	3622	1/1	0.93	0.07	16,16,16,16	0
57	MG	2D	310	1/1	0.93	0.10	57,57,57,57	0
57	MG	1B	233	1/1	0.93	0.09	49,49,49,49	0
57	MG	2A	3273	1/1	0.93	0.14	48,48,48,48	0
57	MG	2A	3563	1/1	0.93	0.08	36,36,36,36	0
57	MG	1B	234	1/1	0.93	0.12	40,40,40,40	0
57	MG	2A	3566	1/1	0.93	0.12	36,36,36,36	0
57	MG	2F	303	1/1	0.93	0.08	46,46,46,46	0
57	MG	2F	304	1/1	0.93	0.08	40,40,40,40	0
57	MG	2A	3570	1/1	0.93	0.15	47,47,47,47	0
57	MG	2A	3276	1/1	0.93	0.09	44,44,44,44	0
57	MG	1A	3623	1/1	0.93	0.10	11,11,11,11	0
57	MG	1B	236	1/1	0.93	0.11	46,46,46,46	0
57	MG	2Q	202	1/1	0.93	0.16	33,33,33,33	0
57	MG	1A	3625	1/1	0.93	0.06	15,15,15,15	0
57	MG	2A	3577	1/1	0.93	0.18	45,45,45,45	0
57	MG	1D	302	1/1	0.93	0.11	32,32,32,32	0
57	MG	2A	3037	1/1	0.93	0.12	38,38,38,38	0
57	MG	2T	203	1/1	0.93	0.19	39,39,39,39	0
57	MG	2T	204	1/1	0.93	0.13	51,51,51,51	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2A	3283	1/1	0.93	0.13	43,43,43,43	0
57	MG	1D	303	1/1	0.93	0.17	33,33,33,33	0
57	MG	2V	203	1/1	0.93	0.20	46,46,46,46	0
57	MG	2A	3586	1/1	0.93	0.12	55,55,55,55	0
57	MG	1A	3507	1/1	0.93	0.20	50,50,50,50	0
57	MG	2A	3590	1/1	0.93	0.26	51,51,51,51	0
57	MG	1A	3786	1/1	0.93	0.17	46,46,46,46	0
57	MG	1D	312	1/1	0.93	0.12	36,36,36,36	0
57	MG	2I	101	1/1	0.93	0.43	41,41,41,41	0
57	MG	25	101	1/1	0.93	0.24	46,46,46,46	0
57	MG	2A	3045	1/1	0.93	0.14	48,48,48,48	0
57	MG	1A	3934	1/1	0.93	0.11	23,23,23,23	0
57	MG	1E	304	1/1	0.93	0.14	45,45,45,45	0
57	MG	2A	3293	1/1	0.93	0.20	46,46,46,46	0
57	MG	2A	3053	1/1	0.93	0.10	54,54,54,54	0
57	MG	1a	1690	1/1	0.93	0.20	49,49,49,49	0
57	MG	1A	3935	1/1	0.93	0.11	25,25,25,25	0
57	MG	1A	3138	1/1	0.93	0.10	41,41,41,41	0
57	MG	2A	3299	1/1	0.93	0.40	57,57,57,57	0
57	MG	2A	3606	1/1	0.93	0.11	38,38,38,38	0
57	MG	1A	3372	1/1	0.93	0.10	34,34,34,34	0
57	MG	1a	1697	1/1	0.93	0.19	56,56,56,56	0
57	MG	2A	3614	1/1	0.93	0.07	30,30,30,30	0
57	MG	1A	3435	1/1	0.93	0.10	49,49,49,49	0
57	MG	1A	3516	1/1	0.93	0.12	47,47,47,47	0
57	MG	2a	1614	1/1	0.93	0.21	48,48,48,48	0
57	MG	1A	3436	1/1	0.93	0.18	56,56,56,56	0
57	MG	1a	1705	1/1	0.93	0.11	50,50,50,50	0
57	MG	1a	1706	1/1	0.93	0.17	60,60,60,60	0
57	MG	2A	3627	1/1	0.93	0.11	27,27,27,27	0
57	MG	2a	1620	1/1	0.93	0.10	39,39,39,39	0
57	MG	1A	3796	1/1	0.93	0.09	34,34,34,34	0
57	MG	1a	1711	1/1	0.93	0.14	52,52,52,52	0
57	MG	1A	3056	1/1	0.93	0.31	47,47,47,47	0
57	MG	2a	1627	1/1	0.93	0.29	59,59,59,59	0
57	MG	1A	3952	1/1	0.93	0.13	54,54,54,54	0
57	MG	1A	3536	1/1	0.93	0.13	49,49,49,49	0
57	MG	2A	3097	1/1	0.93	0.23	55,55,55,55	0
57	MG	1A	3538	1/1	0.93	0.12	45,45,45,45	0
57	MG	1A	3654	1/1	0.93	0.09	11,11,11,11	0
57	MG	2A	3320	1/1	0.93	0.11	61,61,61,61	0
57	MG	1A	3808	1/1	0.93	0.16	42,42,42,42	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2A	3102	1/1	0.93	0.15	51,51,51,51	0
57	MG	1A	3097	1/1	0.93	0.16	25,25,25,25	0
57	MG	2A	3650	1/1	0.93	0.11	47,47,47,47	0
57	MG	2A	3325	1/1	0.93	0.11	54,54,54,54	0
57	MG	1O	204	1/1	0.93	0.08	58,58,58,58	0
57	MG	1a	1722	1/1	0.93	0.17	48,48,48,48	0
57	MG	2A	3109	1/1	0.93	0.30	61,61,61,61	0
57	MG	1O	205	1/1	0.93	0.06	28,28,28,28	0
57	MG	1A	3447	1/1	0.93	0.13	57,57,57,57	0
57	MG	1A	3547	1/1	0.93	0.24	50,50,50,50	0
57	MG	2a	1660	1/1	0.93	0.17	56,56,56,56	0
57	MG	1A	3820	1/1	0.93	0.10	43,43,43,43	0
57	MG	2A	3662	1/1	0.93	0.09	56,56,56,56	0
57	MG	1S	203	1/1	0.93	0.07	50,50,50,50	0
57	MG	1A	3978	1/1	0.93	0.10	43,43,43,43	0
57	MG	1A	3451	1/1	0.93	0.14	34,34,34,34	0
57	MG	1V	202	1/1	0.93	0.23	37,37,37,37	0
57	MG	2A	3340	1/1	0.93	0.13	61,61,61,61	0
57	MG	2A	3124	1/1	0.93	0.11	47,47,47,47	0
57	MG	1V	204	1/1	0.93	0.18	41,41,41,41	0
57	MG	1A	3300	1/1	0.93	0.24	29,29,29,29	0
57	MG	2A	3134	1/1	0.93	0.18	51,51,51,51	0
57	MG	2A	3673	1/1	0.93	0.17	50,50,50,50	0
57	MG	2A	3674	1/1	0.93	0.09	41,41,41,41	0
57	MG	1A	3669	1/1	0.93	0.08	43,43,43,43	0
57	MG	1A	3985	1/1	0.93	0.12	47,47,47,47	0
57	MG	2A	3351	1/1	0.93	0.27	54,54,54,54	0
57	MG	2A	3680	1/1	0.93	0.07	64,64,64,64	0
57	MG	2a	1683	1/1	0.93	0.17	54,54,54,54	0
57	MG	2A	3354	1/1	0.93	0.22	53,53,53,53	0
57	MG	1a	1740	1/1	0.93	0.13	32,32,32,32	0
57	MG	2A	3144	1/1	0.93	0.31	52,52,52,52	0
57	MG	2a	1689	1/1	0.93	0.21	58,58,58,58	0
57	MG	1A	3087	1/1	0.93	0.14	50,50,50,50	0
57	MG	2A	3688	1/1	0.93	0.14	39,39,39,39	0
57	MG	1O	102	1/1	0.93	0.15	44,44,44,44	0
57	MG	2a	1694	1/1	0.93	0.23	50,50,50,50	0
57	MG	2A	3148	1/1	0.93	0.22	57,57,57,57	0
57	MG	1A	3303	1/1	0.93	0.14	40,40,40,40	0
57	MG	1A	3988	1/1	0.93	0.06	21,21,21,21	0
57	MG	2A	3363	1/1	0.93	0.11	55,55,55,55	0
57	MG	2A	3364	1/1	0.93	0.15	51,51,51,51	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1A	3989	1/1	0.93	0.10	31,31,31,31	0
57	MG	13	103	1/1	0.93	0.20	41,41,41,41	0
57	MG	2A	3367	1/1	0.93	0.22	51,51,51,51	0
57	MG	1a	1751	1/1	0.93	0.19	47,47,47,47	0
57	MG	15	106	1/1	0.93	0.15	31,31,31,31	0
57	MG	2A	3162	1/1	0.93	0.10	48,48,48,48	0
57	MG	1A	3455	1/1	0.93	0.15	43,43,43,43	0
57	MG	1a	1754	1/1	0.93	0.07	33,33,33,33	0
57	MG	17	101	1/1	0.93	0.09	29,29,29,29	0
57	MG	1a	1758	1/1	0.93	0.15	45,45,45,45	0
57	MG	1A	3249	1/1	0.93	0.16	38,38,38,38	0
57	MG	2a	1724	1/1	0.93	0.09	65,65,65,65	0
57	MG	1A	3833	1/1	0.93	0.11	23,23,23,23	0
57	MG	2A	3380	1/1	0.93	0.18	43,43,43,43	0
57	MG	2a	1728	1/1	0.93	0.12	44,44,44,44	0
57	MG	2A	3722	1/1	0.93	0.07	24,24,24,24	0
57	MG	19	101	1/1	0.93	0.14	46,46,46,46	0
57	MG	1A	3340	1/1	0.93	0.07	35,35,35,35	0
57	MG	1a	1603	1/1	0.93	0.15	45,45,45,45	0
57	MG	2A	3178	1/1	0.93	0.13	44,44,44,44	0
57	MG	1A	3996	1/1	0.93	0.13	34,34,34,34	0
57	MG	1A	3835	1/1	0.93	0.08	40,40,40,40	0
57	MG	1a	1608	1/1	0.93	0.09	55,55,55,55	0
57	MG	1A	3461	1/1	0.93	0.11	38,38,38,38	0
57	MG	1A	3682	1/1	0.93	0.08	32,32,32,32	0
57	MG	1a	1770	1/1	0.93	0.09	56,56,56,56	0
57	MG	1A	3689	1/1	0.93	0.07	35,35,35,35	0
57	MG	1A	3695	1/1	0.93	0.07	38,38,38,38	0
57	MG	1a	1615	1/1	0.93	0.12	63,63,63,63	0
57	MG	1A	3343	1/1	0.93	0.15	45,45,45,45	0
57	MG	2A	3413	1/1	0.93	0.10	52,52,52,52	0
57	MG	1A	3848	1/1	0.93	0.14	16,16,16,16	0
57	MG	2A	3747	1/1	0.93	0.12	58,58,58,58	0
57	MG	1A	4015	1/1	0.93	0.12	8,8,8,8	0
57	MG	1A	3699	1/1	0.93	0.07	34,34,34,34	0
57	MG	2A	3424	1/1	0.93	0.32	47,47,47,47	0
57	MG	2A	3425	1/1	0.93	0.12	37,37,37,37	0
57	MG	2A	3428	1/1	0.93	0.17	50,50,50,50	0
57	MG	1A	3345	1/1	0.93	0.09	36,36,36,36	0
57	MG	1A	3347	1/1	0.93	0.07	32,32,32,32	0
57	MG	1a	1627	1/1	0.93	0.14	43,43,43,43	0
57	MG	1A	3306	1/1	0.93	0.18	37,37,37,37	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2A	3437	1/1	0.93	0.15	45,45,45,45	0
57	MG	1A	3212	1/1	0.93	0.14	43,43,43,43	0
57	MG	2a	1771	1/1	0.93	0.17	63,63,63,63	0
57	MG	1A	3717	1/1	0.93	0.18	38,38,38,38	0
57	MG	1A	3569	1/1	0.93	0.11	20,20,20,20	0
57	MG	1A	3571	1/1	0.93	0.09	15,15,15,15	0
57	MG	2A	3213	1/1	0.93	0.09	28,28,28,28	0
57	MG	1A	3310	1/1	0.93	0.12	37,37,37,37	0
57	MG	1A	3110	1/1	0.93	0.32	32,32,32,32	0
57	MG	1A	3058	1/1	0.93	0.16	37,37,37,37	0
57	MG	2A	3788	1/1	0.93	0.08	35,35,35,35	0
57	MG	1A	3732	1/1	0.93	0.06	48,48,48,48	0
57	MG	2A	3793	1/1	0.93	0.17	38,38,38,38	0
57	MG	2A	3221	1/1	0.93	0.13	54,54,54,54	0
57	MG	2A	3461	1/1	0.93	0.16	50,50,50,50	0
57	MG	1A	3167	1/1	0.93	0.10	39,39,39,39	0
57	MG	1a	1644	1/1	0.93	0.09	53,53,53,53	0
57	MG	2A	3469	1/1	0.93	0.27	41,41,41,41	0
57	MG	2A	3472	1/1	0.93	0.13	54,54,54,54	0
57	MG	1A	3480	1/1	0.93	0.20	33,33,33,33	0
57	MG	1a	1646	1/1	0.93	0.12	50,50,50,50	0
57	MG	2A	3807	1/1	0.93	0.12	50,50,50,50	0
57	MG	1A	3412	1/1	0.93	0.10	49,49,49,49	0
57	MG	1A	3467	1/1	0.94	0.28	23,23,23,23	0
57	MG	2A	3457	1/1	0.94	0.16	41,41,41,41	0
57	MG	1A	3124	1/1	0.94	0.12	56,56,56,56	0
57	MG	1a	1786	1/1	0.94	0.10	42,42,42,42	0
57	MG	1a	1787	1/1	0.94	0.14	43,43,43,43	0
57	MG	1a	1788	1/1	0.94	0.10	48,48,48,48	0
57	MG	1A	3469	1/1	0.94	0.23	29,29,29,29	0
57	MG	2A	3465	1/1	0.94	0.12	40,40,40,40	0
57	MG	2A	3466	1/1	0.94	0.11	44,44,44,44	0
57	MG	2A	3467	1/1	0.94	0.11	44,44,44,44	0
57	MG	1a	1616	1/1	0.94	0.08	40,40,40,40	0
57	MG	2A	3470	1/1	0.94	0.14	45,45,45,45	0
57	MG	2A	3810	1/1	0.94	0.09	36,36,36,36	0
57	MG	2A	3471	1/1	0.94	0.10	52,52,52,52	0
57	MG	2A	3218	1/1	0.94	0.10	39,39,39,39	0
57	MG	1A	3795	1/1	0.94	0.08	32,32,32,32	0
57	MG	1A	3024	1/1	0.94	0.10	46,46,46,46	0
57	MG	1A	3800	1/1	0.94	0.08	50,50,50,50	0
57	MG	1A	3801	1/1	0.94	0.20	44,44,44,44	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2A	3482	1/1	0.94	0.17	38,38,38,38	0
57	MG	1A	3612	1/1	0.94	0.05	28,28,28,28	0
57	MG	1A	3998	1/1	0.94	0.07	41,41,41,41	0
57	MG	1a	1624	1/1	0.94	0.17	45,45,45,45	0
57	MG	1a	1626	1/1	0.94	0.15	42,42,42,42	0
57	MG	1A	3367	1/1	0.94	0.18	34,34,34,34	0
57	MG	1A	3473	1/1	0.94	0.09	36,36,36,36	0
57	MG	2A	3233	1/1	0.94	0.24	47,47,47,47	0
57	MG	1A	4004	1/1	0.94	0.08	31,31,31,31	0
57	MG	1d	301	1/1	0.94	0.23	35,35,35,35	0
57	MG	1A	3202	1/1	0.94	0.10	49,49,49,49	0
57	MG	1A	3369	1/1	0.94	0.11	41,41,41,41	0
57	MG	1A	3203	1/1	0.94	0.13	57,57,57,57	0
57	MG	2A	3241	1/1	0.94	0.13	46,46,46,46	0
57	MG	1A	3810	1/1	0.94	0.07	51,51,51,51	0
57	MG	2A	3508	1/1	0.94	0.16	55,55,55,55	0
57	MG	1A	3624	1/1	0.94	0.07	13,13,13,13	0
57	MG	1A	3477	1/1	0.94	0.26	39,39,39,39	0
57	MG	1A	3817	1/1	0.94	0.07	51,51,51,51	0
57	MG	2A	3249	1/1	0.94	0.22	49,49,49,49	0
57	MG	2A	3514	1/1	0.94	0.08	50,50,50,50	0
57	MG	1A	3298	1/1	0.94	0.09	51,51,51,51	0
57	MG	1A	3137	1/1	0.94	0.11	40,40,40,40	0
57	MG	2A	3522	1/1	0.94	0.06	25,25,25,25	0
57	MG	1A	3630	1/1	0.94	0.09	18,18,18,18	0
57	MG	2A	3525	1/1	0.94	0.15	44,44,44,44	0
57	MG	1A	3059	1/1	0.94	0.07	37,37,37,37	0
57	MG	1A	3302	1/1	0.94	0.19	30,30,30,30	0
57	MG	1A	3216	1/1	0.94	0.28	46,46,46,46	0
57	MG	1a	1650	1/1	0.94	0.12	51,51,51,51	0
57	MG	2A	3532	1/1	0.94	0.07	36,36,36,36	0
57	MG	1A	3221	1/1	0.94	0.14	43,43,43,43	0
57	MG	2D	306	1/1	0.94	0.32	40,40,40,40	0
57	MG	2A	3536	1/1	0.94	0.11	24,24,24,24	0
57	MG	1A	3489	1/1	0.94	0.24	42,42,42,42	0
57	MG	1A	3305	1/1	0.94	0.24	44,44,44,44	0
57	MG	1A	3390	1/1	0.94	0.13	34,34,34,34	0
57	MG	1A	3391	1/1	0.94	0.07	35,35,35,35	0
57	MG	2E	303	1/1	0.94	0.23	49,49,49,49	0
57	MG	1A	3139	1/1	0.94	0.09	27,27,27,27	0
57	MG	1A	3060	1/1	0.94	0.14	31,31,31,31	0
57	MG	2E	307	1/1	0.94	0.13	23,23,23,23	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1A	4039	1/1	0.94	0.14	35,35,35,35	0
57	MG	2A	3267	1/1	0.94	0.07	54,54,54,54	0
57	MG	2A	3010	1/1	0.94	0.14	36,36,36,36	0
57	MG	2F	306	1/1	0.94	0.13	34,34,34,34	0
57	MG	2A	3013	1/1	0.94	0.07	37,37,37,37	0
57	MG	2N	201	1/1	0.94	0.12	59,59,59,59	0
57	MG	2A	3270	1/1	0.94	0.25	57,57,57,57	0
57	MG	2P	201	1/1	0.94	0.21	47,47,47,47	0
57	MG	2A	3555	1/1	0.94	0.15	45,45,45,45	0
57	MG	2A	3016	1/1	0.94	0.31	56,56,56,56	0
57	MG	2A	3559	1/1	0.94	0.10	37,37,37,37	0
57	MG	1A	3152	1/1	0.94	0.07	27,27,27,27	0
57	MG	1a	1662	1/1	0.94	0.15	47,47,47,47	0
57	MG	2A	3274	1/1	0.94	0.28	53,53,53,53	0
57	MG	1A	3662	1/1	0.94	0.14	20,20,20,20	0
57	MG	1A	4043	1/1	0.94	0.11	36,36,36,36	0
57	MG	2A	3024	1/1	0.94	0.37	45,45,45,45	0
57	MG	2A	3025	1/1	0.94	0.14	36,36,36,36	0
57	MG	1A	3235	1/1	0.94	0.10	45,45,45,45	0
57	MG	1A	3664	1/1	0.94	0.09	19,19,19,19	0
57	MG	1A	3665	1/1	0.94	0.06	12,12,12,12	0
57	MG	1A	3158	1/1	0.94	0.17	38,38,38,38	0
57	MG	2A	3032	1/1	0.94	0.11	37,37,37,37	0
57	MG	1B	206	1/1	0.94	0.19	31,31,31,31	0
57	MG	1A	3851	1/1	0.94	0.10	32,32,32,32	0
57	MG	1A	3508	1/1	0.94	0.20	30,30,30,30	0
57	MG	2A	3288	1/1	0.94	0.07	43,43,43,43	0
57	MG	25	102	1/1	0.94	0.20	46,46,46,46	0
57	MG	2A	3589	1/1	0.94	0.10	55,55,55,55	0
57	MG	1A	3092	1/1	0.94	0.08	41,41,41,41	0
57	MG	2A	3591	1/1	0.94	0.20	49,49,49,49	0
57	MG	1A	3011	1/1	0.94	0.10	32,32,32,32	0
57	MG	1A	3241	1/1	0.94	0.07	24,24,24,24	0
57	MG	2A	3043	1/1	0.94	0.12	41,41,41,41	0
57	MG	1A	3515	1/1	0.94	0.10	17,17,17,17	0
57	MG	1A	3863	1/1	0.94	0.16	42,42,42,42	0
57	MG	1A	3163	1/1	0.94	0.15	33,33,33,33	0
57	MG	2a	1605	1/1	0.94	0.23	44,44,44,44	0
57	MG	2A	3599	1/1	0.94	0.09	39,39,39,39	0
57	MG	2A	3050	1/1	0.94	0.08	39,39,39,39	0
57	MG	1A	3866	1/1	0.94	0.42	29,29,29,29	0
57	MG	1A	3869	1/1	0.94	0.11	13,13,13,13	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1A	3082	1/1	0.94	0.27	38,38,38,38	0
57	MG	1A	3531	1/1	0.94	0.22	37,37,37,37	0
57	MG	1A	3684	1/1	0.94	0.06	52,52,52,52	0
57	MG	2a	1615	1/1	0.94	0.11	44,44,44,44	0
57	MG	2A	3607	1/1	0.94	0.10	31,31,31,31	0
57	MG	2A	3059	1/1	0.94	0.07	43,43,43,43	0
57	MG	2A	3306	1/1	0.94	0.08	41,41,41,41	0
57	MG	2A	3308	1/1	0.94	0.18	42,42,42,42	0
57	MG	1B	230	1/1	0.94	0.09	35,35,35,35	0
57	MG	1A	3409	1/1	0.94	0.13	47,47,47,47	0
57	MG	1A	3533	1/1	0.94	0.30	30,30,30,30	0
57	MG	1A	3534	1/1	0.94	0.12	48,48,48,48	0
57	MG	1A	3165	1/1	0.94	0.15	35,35,35,35	0
57	MG	2a	1628	1/1	0.94	0.10	37,37,37,37	0
57	MG	2A	3621	1/1	0.94	0.12	25,25,25,25	0
57	MG	1A	3248	1/1	0.94	0.10	61,61,61,61	0
57	MG	2a	1633	1/1	0.94	0.10	55,55,55,55	0
57	MG	2A	3629	1/1	0.94	0.09	29,29,29,29	0
57	MG	2A	3084	1/1	0.94	0.07	46,46,46,46	0
57	MG	1A	3705	1/1	0.94	0.08	25,25,25,25	0
57	MG	2a	1639	1/1	0.94	0.28	56,56,56,56	0
57	MG	1A	3707	1/1	0.94	0.07	10,10,10,10	0
57	MG	1A	3543	1/1	0.94	0.07	53,53,53,53	0
57	MG	1A	3083	1/1	0.94	0.08	41,41,41,41	0
57	MG	2A	3089	1/1	0.94	0.21	32,32,32,32	0
57	MG	2A	3092	1/1	0.94	0.07	28,28,28,28	0
57	MG	2a	1647	1/1	0.94	0.17	38,38,38,38	0
57	MG	1A	3896	1/1	0.94	0.07	42,42,42,42	0
57	MG	1A	3108	1/1	0.94	0.09	34,34,34,34	0
57	MG	2A	3646	1/1	0.94	0.09	51,51,51,51	0
57	MG	2A	3326	1/1	0.94	0.07	49,49,49,49	0
57	MG	1A	3715	1/1	0.94	0.08	18,18,18,18	0
57	MG	2a	1656	1/1	0.94	0.24	39,39,39,39	0
57	MG	1a	1703	1/1	0.94	0.09	53,53,53,53	0
57	MG	1A	3716	1/1	0.94	0.10	41,41,41,41	0
57	MG	1A	3424	1/1	0.94	0.08	67,67,67,67	0
57	MG	1a	1708	1/1	0.94	0.19	54,54,54,54	0
57	MG	1A	3329	1/1	0.94	0.23	35,35,35,35	0
57	MG	1A	3251	1/1	0.94	0.21	51,51,51,51	0
57	MG	2A	3655	1/1	0.94	0.10	55,55,55,55	0
57	MG	2a	1667	1/1	0.94	0.09	60,60,60,60	0
57	MG	1E	311	1/1	0.94	0.15	51,51,51,51	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1A	3909	1/1	0.94	0.05	25,25,25,25	0
57	MG	2A	3110	1/1	0.94	0.21	48,48,48,48	0
57	MG	1A	3912	1/1	0.94	0.08	41,41,41,41	0
57	MG	2A	3112	1/1	0.94	0.14	40,40,40,40	0
57	MG	1A	3726	1/1	0.94	0.07	10,10,10,10	0
57	MG	1A	3255	1/1	0.94	0.11	31,31,31,31	0
57	MG	1G	201	1/1	0.94	0.10	33,33,33,33	0
57	MG	1A	3917	1/1	0.94	0.11	46,46,46,46	0
57	MG	1A	3048	1/1	0.94	0.10	21,21,21,21	0
57	MG	1A	3730	1/1	0.94	0.08	22,22,22,22	0
57	MG	2a	1680	1/1	0.94	0.15	50,50,50,50	0
57	MG	1A	3430	1/1	0.94	0.28	49,49,49,49	0
57	MG	2A	3352	1/1	0.94	0.20	42,42,42,42	0
57	MG	1I	201	1/1	0.94	0.13	60,60,60,60	0
57	MG	1A	3431	1/1	0.94	0.16	45,45,45,45	0
57	MG	2a	1685	1/1	0.94	0.18	41,41,41,41	0
57	MG	1A	3434	1/1	0.94	0.12	28,28,28,28	0
57	MG	2a	1687	1/1	0.94	0.16	57,57,57,57	0
57	MG	1A	3735	1/1	0.94	0.09	34,34,34,34	0
57	MG	1A	3265	1/1	0.94	0.20	23,23,23,23	0
57	MG	1A	3557	1/1	0.94	0.11	45,45,45,45	0
57	MG	1A	3932	1/1	0.94	0.14	37,37,37,37	0
57	MG	2A	3142	1/1	0.94	0.06	28,28,28,28	0
57	MG	2A	3143	1/1	0.94	0.17	54,54,54,54	0
57	MG	1A	3341	1/1	0.94	0.23	45,45,45,45	0
57	MG	1A	3438	1/1	0.94	0.20	40,40,40,40	0
57	MG	1a	1735	1/1	0.94	0.12	51,51,51,51	0
57	MG	1R	206	1/1	0.94	0.13	26,26,26,26	0
57	MG	1A	3270	1/1	0.94	0.12	35,35,35,35	0
57	MG	2A	3155	1/1	0.94	0.14	40,40,40,40	0
57	MG	2a	1704	1/1	0.94	0.22	50,50,50,50	0
57	MG	1S	202	1/1	0.94	0.10	47,47,47,47	0
57	MG	1A	3564	1/1	0.94	0.10	33,33,33,33	0
57	MG	1A	3754	1/1	0.94	0.09	16,16,16,16	0
57	MG	2A	3373	1/1	0.94	0.07	43,43,43,43	0
57	MG	2A	3374	1/1	0.94	0.21	56,56,56,56	0
57	MG	1A	3344	1/1	0.94	0.19	43,43,43,43	0
57	MG	2A	3705	1/1	0.94	0.14	44,44,44,44	0
57	MG	2A	3706	1/1	0.94	0.11	22,22,22,22	0
57	MG	1A	3444	1/1	0.94	0.11	34,34,34,34	0
57	MG	1A	3445	1/1	0.94	0.14	40,40,40,40	0
57	MG	2a	1723	1/1	0.94	0.14	47,47,47,47	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1W	202	1/1	0.94	0.16	38,38,38,38	0
57	MG	2A	3712	1/1	0.94	0.09	43,43,43,43	0
57	MG	1A	3271	1/1	0.94	0.18	39,39,39,39	0
57	MG	2A	3382	1/1	0.94	0.20	31,31,31,31	0
57	MG	1X	101	1/1	0.94	0.35	32,32,32,32	0
57	MG	1A	3766	1/1	0.94	0.33	22,22,22,22	0
57	MG	2A	3386	1/1	0.94	0.15	44,44,44,44	0
57	MG	1A	3177	1/1	0.94	0.17	38,38,38,38	0
57	MG	1A	3276	1/1	0.94	0.09	38,38,38,38	0
57	MG	2A	3390	1/1	0.94	0.17	24,24,24,24	0
57	MG	1Z	302	1/1	0.94	0.14	44,44,44,44	0
57	MG	1A	3956	1/1	0.94	0.10	18,18,18,18	0
57	MG	2A	3399	1/1	0.94	0.29	54,54,54,54	0
57	MG	10	105	1/1	0.94	0.30	57,57,57,57	0
57	MG	2A	3401	1/1	0.94	0.18	46,46,46,46	0
57	MG	1A	3769	1/1	0.94	0.10	32,32,32,32	0
57	MG	1A	3577	1/1	0.94	0.10	46,46,46,46	0
57	MG	1A	3966	1/1	0.94	0.15	55,55,55,55	0
57	MG	1a	1764	1/1	0.94	0.12	57,57,57,57	0
57	MG	2A	3735	1/1	0.94	0.08	49,49,49,49	0
57	MG	1A	3178	1/1	0.94	0.08	45,45,45,45	0
57	MG	2A	3184	1/1	0.94	0.11	43,43,43,43	0
57	MG	13	104	1/1	0.94	0.09	44,44,44,44	0
57	MG	1A	3775	1/1	0.94	0.43	22,22,22,22	0
57	MG	2A	3741	1/1	0.94	0.10	51,51,51,51	0
57	MG	2A	3743	1/1	0.94	0.10	33,33,33,33	0
57	MG	2A	3415	1/1	0.94	0.09	42,42,42,42	0
57	MG	2a	1761	1/1	0.94	0.12	64,64,64,64	0
57	MG	2a	1762	1/1	0.94	0.14	67,67,67,67	0
57	MG	2A	3416	1/1	0.94	0.30	51,51,51,51	0
57	MG	2A	3187	1/1	0.94	0.17	47,47,47,47	0
57	MG	1A	3584	1/1	0.94	0.09	24,24,24,24	0
57	MG	1A	3971	1/1	0.94	0.09	62,62,62,62	0
57	MG	2A	3423	1/1	0.94	0.14	44,44,44,44	0
57	MG	2A	3751	1/1	0.94	0.13	51,51,51,51	0
57	MG	1A	3281	1/1	0.94	0.29	46,46,46,46	0
57	MG	1A	3974	1/1	0.94	0.13	48,48,48,48	0
57	MG	2A	3427	1/1	0.94	0.24	32,32,32,32	0
57	MG	2A	3757	1/1	0.94	0.08	51,51,51,51	0
57	MG	1A	3086	1/1	0.94	0.18	39,39,39,39	0
57	MG	2A	3760	1/1	0.94	0.11	51,51,51,51	0
57	MG	2A	3193	1/1	0.94	0.15	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2A	3195	1/1	0.94	0.14	47,47,47,47	0
57	MG	2A	3196	1/1	0.94	0.07	40,40,40,40	0
57	MG	1A	3457	1/1	0.94	0.13	45,45,45,45	0
57	MG	2A	3768	1/1	0.94	0.08	70,70,70,70	0
57	MG	1A	3595	1/1	0.94	0.09	22,22,22,22	0
57	MG	2A	3438	1/1	0.94	0.22	34,34,34,34	0
57	MG	2t	202	1/1	0.94	0.16	55,55,55,55	0
57	MG	2A	3440	1/1	0.94	0.09	44,44,44,44	0
57	MG	1A	3355	1/1	0.94	0.22	38,38,38,38	0
57	MG	1A	3287	1/1	0.94	0.17	40,40,40,40	0
57	MG	2A	3203	1/1	0.94	0.06	45,45,45,45	0
57	MG	1A	3181	1/1	0.94	0.10	44,44,44,44	0
57	MG	1A	3360	1/1	0.94	0.07	43,43,43,43	0
57	MG	1A	3114	1/1	0.94	0.10	31,31,31,31	0
57	MG	2A	3207	1/1	0.94	0.09	46,46,46,46	0
57	MG	1A	3963	1/1	0.95	0.05	19,19,19,19	0
57	MG	2A	3058	1/1	0.95	0.13	43,43,43,43	0
57	MG	1A	3964	1/1	0.95	0.07	34,34,34,34	0
57	MG	2A	3060	1/1	0.95	0.06	39,39,39,39	0
57	MG	1A	3814	1/1	0.95	0.10	43,43,43,43	0
57	MG	2A	3531	1/1	0.95	0.15	45,45,45,45	0
57	MG	1A	3967	1/1	0.95	0.07	40,40,40,40	0
57	MG	1A	3159	1/1	0.95	0.15	56,56,56,56	0
57	MG	2A	3534	1/1	0.95	0.08	48,48,48,48	0
57	MG	2A	3834	1/1	0.95	0.14	44,44,44,44	0
57	MG	1A	3816	1/1	0.95	0.11	45,45,45,45	0
57	MG	2A	3836	1/1	0.95	0.11	56,56,56,56	0
57	MG	2A	3066	1/1	0.95	0.17	41,41,41,41	0
57	MG	1a	1712	1/1	0.95	0.13	44,44,44,44	0
57	MG	2A	3541	1/1	0.95	0.14	38,38,38,38	0
57	MG	2A	3072	1/1	0.95	0.07	48,48,48,48	0
57	MG	1A	3686	1/1	0.95	0.14	48,48,48,48	0
57	MG	2A	3547	1/1	0.95	0.11	20,20,20,20	0
57	MG	2A	3079	1/1	0.95	0.17	48,48,48,48	0
57	MG	2A	3080	1/1	0.95	0.14	39,39,39,39	0
57	MG	2A	3081	1/1	0.95	0.08	49,49,49,49	0
57	MG	1A	3278	1/1	0.95	0.09	32,32,32,32	0
57	MG	1A	3033	1/1	0.95	0.18	24,24,24,24	0
57	MG	1Q	207	1/1	0.95	0.10	31,31,31,31	0
57	MG	1R	202	1/1	0.95	0.11	42,42,42,42	0
57	MG	1A	3319	1/1	0.95	0.15	51,51,51,51	0
57	MG	1A	3579	1/1	0.95	0.09	27,27,27,27	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1A	3977	1/1	0.95	0.06	39,39,39,39	0
57	MG	1A	3700	1/1	0.95	0.08	43,43,43,43	0
57	MG	2A	3561	1/1	0.95	0.08	41,41,41,41	0
57	MG	2A	3562	1/1	0.95	0.19	52,52,52,52	0
57	MG	2B	213	1/1	0.95	0.21	53,53,53,53	0
57	MG	1A	3701	1/1	0.95	0.07	36,36,36,36	0
57	MG	2A	3307	1/1	0.95	0.10	52,52,52,52	0
57	MG	2A	3565	1/1	0.95	0.11	37,37,37,37	0
57	MG	1A	3282	1/1	0.95	0.18	17,17,17,17	0
57	MG	1a	1726	1/1	0.95	0.28	61,61,61,61	0
57	MG	2D	307	1/1	0.95	0.12	41,41,41,41	0
57	MG	1U	210	1/1	0.95	0.17	34,34,34,34	0
57	MG	1A	3828	1/1	0.95	0.16	27,27,27,27	0
57	MG	2A	3573	1/1	0.95	0.10	14,14,14,14	0
57	MG	1A	3161	1/1	0.95	0.14	36,36,36,36	0
57	MG	1A	3832	1/1	0.95	0.23	22,22,22,22	0
57	MG	2A	3576	1/1	0.95	0.11	52,52,52,52	0
57	MG	1W	203	1/1	0.95	0.16	31,31,31,31	0
57	MG	1W	207	1/1	0.95	0.11	26,26,26,26	0
57	MG	1A	3706	1/1	0.95	0.07	31,31,31,31	0
57	MG	1A	3587	1/1	0.95	0.06	24,24,24,24	0
57	MG	1A	3589	1/1	0.95	0.10	42,42,42,42	0
57	MG	1A	3709	1/1	0.95	0.14	42,42,42,42	0
57	MG	2F	305	1/1	0.95	0.16	56,56,56,56	0
57	MG	2A	3587	1/1	0.95	0.18	48,48,48,48	0
57	MG	1A	3129	1/1	0.95	0.17	23,23,23,23	0
57	MG	1A	3992	1/1	0.95	0.08	25,25,25,25	0
57	MG	2A	3117	1/1	0.95	0.10	44,44,44,44	0
57	MG	1A	3376	1/1	0.95	0.13	37,37,37,37	0
57	MG	10	103	1/1	0.95	0.08	42,42,42,42	0
57	MG	1A	3437	1/1	0.95	0.14	36,36,36,36	0
57	MG	2Q	201	1/1	0.95	0.17	43,43,43,43	0
57	MG	2A	3328	1/1	0.95	0.15	48,48,48,48	0
57	MG	2Q	203	1/1	0.95	0.09	52,52,52,52	0
57	MG	1A	3845	1/1	0.95	0.05	12,12,12,12	0
57	MG	1A	3131	1/1	0.95	0.17	20,20,20,20	0
57	MG	11	104	1/1	0.95	0.08	34,34,34,34	0
57	MG	2A	3125	1/1	0.95	0.10	37,37,37,37	0
57	MG	2A	3127	1/1	0.95	0.11	35,35,35,35	0
57	MG	2A	3129	1/1	0.95	0.18	52,52,52,52	0
57	MG	2A	3335	1/1	0.95	0.12	53,53,53,53	0
57	MG	1A	3502	1/1	0.95	0.14	32,32,32,32	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2V	202	1/1	0.95	0.21	48,48,48,48	0
57	MG	1A	3719	1/1	0.95	0.09	7,7,7,7	0
57	MG	1A	3440	1/1	0.95	0.14	47,47,47,47	0
57	MG	15	105	1/1	0.95	0.12	20,20,20,20	0
57	MG	2A	3608	1/1	0.95	0.10	27,27,27,27	0
57	MG	2Y	201	1/1	0.95	0.08	53,53,53,53	0
57	MG	1A	4003	1/1	0.95	0.08	43,43,43,43	0
57	MG	2A	3341	1/1	0.95	0.19	38,38,38,38	0
57	MG	1A	3378	1/1	0.95	0.19	44,44,44,44	0
57	MG	23	101	1/1	0.95	0.10	48,48,48,48	0
57	MG	1A	4005	1/1	0.95	0.10	70,70,70,70	0
57	MG	1A	3723	1/1	0.95	0.11	33,33,33,33	0
57	MG	2A	3345	1/1	0.95	0.07	36,36,36,36	0
57	MG	2A	3346	1/1	0.95	0.29	51,51,51,51	0
57	MG	1A	3043	1/1	0.95	0.07	19,19,19,19	0
57	MG	2A	3620	1/1	0.95	0.09	44,44,44,44	0
57	MG	27	101	1/1	0.95	0.13	35,35,35,35	0
57	MG	18	103	1/1	0.95	0.10	35,35,35,35	0
57	MG	28	102	1/1	0.95	0.12	38,38,38,38	0
57	MG	2A	3625	1/1	0.95	0.15	29,29,29,29	0
57	MG	2A	3146	1/1	0.95	0.09	45,45,45,45	0
57	MG	1A	4008	1/1	0.95	0.07	27,27,27,27	0
57	MG	1A	3206	1/1	0.95	0.33	27,27,27,27	0
57	MG	2A	3353	1/1	0.95	0.23	46,46,46,46	0
57	MG	1A	3076	1/1	0.95	0.10	32,32,32,32	0
57	MG	2a	1607	1/1	0.95	0.22	39,39,39,39	0
57	MG	1A	3513	1/1	0.95	0.18	21,21,21,21	0
57	MG	2A	3156	1/1	0.95	0.27	57,57,57,57	0
57	MG	1A	3330	1/1	0.95	0.09	51,51,51,51	0
57	MG	1a	1607	1/1	0.95	0.16	45,45,45,45	0
57	MG	2a	1612	1/1	0.95	0.18	56,56,56,56	0
57	MG	1A	3448	1/1	0.95	0.16	36,36,36,36	0
57	MG	1a	1609	1/1	0.95	0.15	27,27,27,27	0
57	MG	1A	4019	1/1	0.95	0.08	39,39,39,39	0
57	MG	1A	3521	1/1	0.95	0.07	37,37,37,37	0
57	MG	2A	3163	1/1	0.95	0.18	50,50,50,50	0
57	MG	1A	3527	1/1	0.95	0.17	60,60,60,60	0
57	MG	1A	4023	1/1	0.95	0.08	24,24,24,24	0
57	MG	1a	1775	1/1	0.95	0.11	57,57,57,57	0
57	MG	1a	1776	1/1	0.95	0.17	43,43,43,43	0
57	MG	2a	1623	1/1	0.95	0.29	43,43,43,43	0
57	MG	1A	3388	1/1	0.95	0.12	45,45,45,45	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1A	3334	1/1	0.95	0.06	34,34,34,34	0
57	MG	2a	1626	1/1	0.95	0.30	52,52,52,52	0
57	MG	1A	3743	1/1	0.95	0.07	16,16,16,16	0
57	MG	1A	3621	1/1	0.95	0.12	37,37,37,37	0
57	MG	2a	1629	1/1	0.95	0.18	47,47,47,47	0
57	MG	1A	3211	1/1	0.95	0.27	31,31,31,31	0
57	MG	1a	1782	1/1	0.95	0.08	37,37,37,37	0
57	MG	1A	3105	1/1	0.95	0.18	25,25,25,25	0
57	MG	2A	3661	1/1	0.95	0.07	47,47,47,47	0
57	MG	1A	3747	1/1	0.95	0.07	34,34,34,34	0
57	MG	1a	1785	1/1	0.95	0.13	44,44,44,44	0
57	MG	1A	3295	1/1	0.95	0.12	37,37,37,37	0
57	MG	1A	3535	1/1	0.95	0.17	52,52,52,52	0
57	MG	2A	3381	1/1	0.95	0.16	34,34,34,34	0
57	MG	1A	3296	1/1	0.95	0.08	34,34,34,34	0
57	MG	1a	1789	1/1	0.95	0.06	60,60,60,60	0
57	MG	1A	3888	1/1	0.95	0.14	42,42,42,42	0
57	MG	1A	4038	1/1	0.95	0.14	64,64,64,64	0
57	MG	1A	3757	1/1	0.95	0.09	11,11,11,11	0
57	MG	1A	3627	1/1	0.95	0.08	31,31,31,31	0
57	MG	1A	3894	1/1	0.95	0.09	49,49,49,49	0
57	MG	2A	3393	1/1	0.95	0.30	47,47,47,47	0
57	MG	2A	3676	1/1	0.95	0.14	45,45,45,45	0
57	MG	1a	1797	1/1	0.95	0.10	44,44,44,44	0
57	MG	2a	1657	1/1	0.95	0.24	45,45,45,45	0
57	MG	2A	3397	1/1	0.95	0.24	54,54,54,54	0
57	MG	1A	3537	1/1	0.95	0.18	32,32,32,32	0
57	MG	2A	3194	1/1	0.95	0.13	48,48,48,48	0
57	MG	2A	3682	1/1	0.95	0.12	40,40,40,40	0
57	MG	1A	3077	1/1	0.95	0.15	31,31,31,31	0
57	MG	1a	1800	1/1	0.95	0.06	44,44,44,44	0
57	MG	1A	3539	1/1	0.95	0.14	45,45,45,45	0
57	MG	2A	3198	1/1	0.95	0.10	54,54,54,54	0
57	MG	1a	1639	1/1	0.95	0.34	56,56,56,56	0
57	MG	1A	4047	1/1	0.95	0.07	45,45,45,45	0
57	MG	1B	201	1/1	0.95	0.15	39,39,39,39	0
57	MG	1A	3542	1/1	0.95	0.07	34,34,34,34	0
57	MG	1A	3900	1/1	0.95	0.14	35,35,35,35	0
57	MG	2A	3696	1/1	0.95	0.10	23,23,23,23	0
57	MG	1A	3342	1/1	0.95	0.16	49,49,49,49	0
57	MG	1A	3175	1/1	0.95	0.12	30,30,30,30	0
57	MG	2A	3700	1/1	0.95	0.21	52,52,52,52	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1A	3905	1/1	0.95	0.09	47,47,47,47	0
57	MG	2A	3703	1/1	0.95	0.08	51,51,51,51	0
57	MG	1A	3907	1/1	0.95	0.08	43,43,43,43	0
57	MG	2A	3419	1/1	0.95	0.25	53,53,53,53	0
57	MG	1A	3644	1/1	0.95	0.05	19,19,19,19	0
57	MG	2A	3421	1/1	0.95	0.27	40,40,40,40	0
57	MG	1A	3143	1/1	0.95	0.20	41,41,41,41	0
57	MG	1A	3051	1/1	0.95	0.16	33,33,33,33	0
57	MG	1A	3649	1/1	0.95	0.12	36,36,36,36	0
57	MG	1A	3652	1/1	0.95	0.08	12,12,12,12	0
57	MG	2A	3714	1/1	0.95	0.16	51,51,51,51	0
57	MG	1A	3266	1/1	0.95	0.26	29,29,29,29	0
57	MG	1A	3268	1/1	0.95	0.10	33,33,33,33	0
57	MG	1A	3655	1/1	0.95	0.05	12,12,12,12	0
57	MG	2A	3220	1/1	0.95	0.14	44,44,44,44	0
57	MG	1A	3922	1/1	0.95	0.09	52,52,52,52	0
57	MG	2A	3222	1/1	0.95	0.12	55,55,55,55	0
57	MG	1B	226	1/1	0.95	0.06	43,43,43,43	0
57	MG	2a	1698	1/1	0.95	0.18	49,49,49,49	0
57	MG	2a	1699	1/1	0.95	0.14	44,44,44,44	0
57	MG	1A	3053	1/1	0.95	0.13	30,30,30,30	0
57	MG	1B	228	1/1	0.95	0.10	56,56,56,56	0
57	MG	1x	106	1/1	0.95	0.10	21,21,21,21	0
57	MG	1B	229	1/1	0.95	0.05	33,33,33,33	0
57	MG	2A	3445	1/1	0.95	0.17	50,50,50,50	0
57	MG	2A	3228	1/1	0.95	0.23	44,44,44,44	0
57	MG	2A	3730	1/1	0.95	0.10	28,28,28,28	0
57	MG	2A	3731	1/1	0.95	0.14	41,41,41,41	0
57	MG	2A	3447	1/1	0.95	0.10	39,39,39,39	0
57	MG	1A	3234	1/1	0.95	0.14	43,43,43,43	0
57	MG	1A	3272	1/1	0.95	0.12	38,38,38,38	0
57	MG	1A	3414	1/1	0.95	0.09	34,34,34,34	0
57	MG	2A	3003	1/1	0.95	0.21	42,42,42,42	0
57	MG	2a	1719	1/1	0.95	0.09	41,41,41,41	0
57	MG	2A	3005	1/1	0.95	0.24	52,52,52,52	0
57	MG	2A	3235	1/1	0.95	0.07	38,38,38,38	0
57	MG	1A	3273	1/1	0.95	0.14	38,38,38,38	0
57	MG	1A	3929	1/1	0.95	0.06	27,27,27,27	0
57	MG	2A	3238	1/1	0.95	0.23	43,43,43,43	0
57	MG	1A	3311	1/1	0.95	0.09	41,41,41,41	0
57	MG	1A	3792	1/1	0.95	0.06	29,29,29,29	0
57	MG	2A	3464	1/1	0.95	0.13	34,34,34,34	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1a	1672	1/1	0.95	0.20	47,47,47,47	0
57	MG	1A	3094	1/1	0.95	0.09	31,31,31,31	0
57	MG	1B	238	1/1	0.95	0.06	23,23,23,23	0
57	MG	1A	3418	1/1	0.95	0.13	41,41,41,41	0
57	MG	2A	3020	1/1	0.95	0.06	20,20,20,20	0
57	MG	2A	3248	1/1	0.95	0.17	60,60,60,60	0
57	MG	1A	3560	1/1	0.95	0.16	45,45,45,45	0
57	MG	2A	3756	1/1	0.95	0.11	46,46,46,46	0
57	MG	1A	3478	1/1	0.95	0.10	27,27,27,27	0
57	MG	2A	3251	1/1	0.95	0.13	55,55,55,55	0
57	MG	1A	3799	1/1	0.95	0.08	43,43,43,43	0
57	MG	1A	3421	1/1	0.95	0.14	37,37,37,37	0
57	MG	2A	3762	1/1	0.95	0.12	42,42,42,42	0
57	MG	2A	3026	1/1	0.95	0.13	37,37,37,37	0
57	MG	1A	3941	1/1	0.95	0.07	37,37,37,37	0
57	MG	2A	3766	1/1	0.95	0.07	55,55,55,55	0
57	MG	1A	3673	1/1	0.95	0.13	40,40,40,40	0
57	MG	2a	1752	1/1	0.95	0.19	53,53,53,53	0
57	MG	1A	3943	1/1	0.95	0.06	34,34,34,34	0
57	MG	2A	3770	1/1	0.95	0.13	43,43,43,43	0
57	MG	1E	307	1/1	0.95	0.11	35,35,35,35	0
57	MG	1A	3423	1/1	0.95	0.21	47,47,47,47	0
57	MG	1a	1685	1/1	0.95	0.26	48,48,48,48	0
57	MG	2a	1760	1/1	0.95	0.13	47,47,47,47	0
57	MG	2A	3777	1/1	0.95	0.09	39,39,39,39	0
57	MG	1A	3314	1/1	0.95	0.12	40,40,40,40	0
57	MG	1F	301	1/1	0.95	0.15	26,26,26,26	0
57	MG	2a	1765	1/1	0.95	0.17	41,41,41,41	0
57	MG	2A	3497	1/1	0.95	0.10	39,39,39,39	0
57	MG	2A	3038	1/1	0.95	0.17	25,25,25,25	0
57	MG	2A	3784	1/1	0.95	0.07	50,50,50,50	0
57	MG	2A	3785	1/1	0.95	0.11	39,39,39,39	0
57	MG	1A	3676	1/1	0.95	0.05	6,6,6,6	0
57	MG	1A	3948	1/1	0.95	0.08	8,8,8,8	0
57	MG	2A	3502	1/1	0.95	0.07	30,30,30,30	0
57	MG	2A	3503	1/1	0.95	0.12	46,46,46,46	0
57	MG	2A	3794	1/1	0.95	0.06	24,24,24,24	0
57	MG	1F	310	1/1	0.95	0.07	36,36,36,36	0
57	MG	1A	3949	1/1	0.95	0.18	29,29,29,29	0
57	MG	1A	3950	1/1	0.95	0.10	12,12,12,12	0
57	MG	1A	3677	1/1	0.95	0.11	40,40,40,40	0
57	MG	1a	1695	1/1	0.95	0.28	45,45,45,45	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2I	202	1/1	0.95	0.10	59,59,59,59	0
57	MG	1A	3566	1/1	0.95	0.06	11,11,11,11	0
57	MG	2A	3801	1/1	0.95	0.09	26,26,26,26	0
57	MG	2A	3511	1/1	0.95	0.08	36,36,36,36	0
57	MG	2A	3051	1/1	0.95	0.14	58,58,58,58	0
57	MG	1A	3680	1/1	0.95	0.09	46,46,46,46	0
57	MG	1a	1699	1/1	0.95	0.20	46,46,46,46	0
57	MG	2A	3517	1/1	0.95	0.12	25,25,25,25	0
57	MG	2A	3054	1/1	0.95	0.08	36,36,36,36	0
57	MG	2A	3520	1/1	0.95	0.14	55,55,55,55	0
57	MG	1A	3482	1/1	0.95	0.20	36,36,36,36	0
57	MG	2A	3278	1/1	0.95	0.12	62,62,62,62	0
57	MG	2A	3523	1/1	0.95	0.09	51,51,51,51	0
57	MG	1A	3236	1/1	0.95	0.10	51,51,51,51	0
58	K	1A	3512	1/1	0.95	0.12	74,74,74,74	0
57	MG	1A	3153	1/1	0.96	0.09	40,40,40,40	0
57	MG	1A	3198	1/1	0.96	0.09	16,16,16,16	0
57	MG	2A	3820	1/1	0.96	0.18	43,43,43,43	0
57	MG	1A	3365	1/1	0.96	0.08	45,45,45,45	0
57	MG	1E	308	1/1	0.96	0.12	13,13,13,13	0
57	MG	1A	3657	1/1	0.96	0.09	16,16,16,16	0
57	MG	1E	310	1/1	0.96	0.28	28,28,28,28	0
57	MG	1A	3366	1/1	0.96	0.08	31,31,31,31	0
57	MG	2A	3829	1/1	0.96	0.07	24,24,24,24	0
57	MG	1A	3541	1/1	0.96	0.15	42,42,42,42	0
57	MG	1F	303	1/1	0.96	0.18	23,23,23,23	0
57	MG	1a	1693	1/1	0.96	0.31	49,49,49,49	0
57	MG	1A	3661	1/1	0.96	0.09	21,21,21,21	0
57	MG	1A	3199	1/1	0.96	0.11	21,21,21,21	0
57	MG	1a	1696	1/1	0.96	0.27	38,38,38,38	0
57	MG	1A	3200	1/1	0.96	0.06	43,43,43,43	0
57	MG	1A	3254	1/1	0.96	0.12	36,36,36,36	0
57	MG	1A	3370	1/1	0.96	0.13	38,38,38,38	0
57	MG	2A	3840	1/1	0.96	0.05	36,36,36,36	0
57	MG	2A	3841	1/1	0.96	0.16	52,52,52,52	0
57	MG	2A	3068	1/1	0.96	0.22	41,41,41,41	0
57	MG	2A	3069	1/1	0.96	0.20	46,46,46,46	0
57	MG	1A	3955	1/1	0.96	0.04	23,23,23,23	0
57	MG	1A	3449	1/1	0.96	0.13	25,25,25,25	0
57	MG	2A	3074	1/1	0.96	0.07	31,31,31,31	0
57	MG	2A	3295	1/1	0.96	0.06	45,45,45,45	0
57	MG	2A	3076	1/1	0.96	0.11	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1a	1702	1/1	0.96	0.16	39,39,39,39	0
57	MG	1A	3025	1/1	0.96	0.15	30,30,30,30	0
57	MG	1a	1704	1/1	0.96	0.10	53,53,53,53	0
57	MG	1A	3959	1/1	0.96	0.12	17,17,17,17	0
57	MG	2B	207	1/1	0.96	0.15	51,51,51,51	0
57	MG	2A	3082	1/1	0.96	0.07	37,37,37,37	0
57	MG	1A	3670	1/1	0.96	0.13	23,23,23,23	0
57	MG	2A	3303	1/1	0.96	0.20	53,53,53,53	0
57	MG	1A	3962	1/1	0.96	0.11	23,23,23,23	0
57	MG	1A	3549	1/1	0.96	0.18	31,31,31,31	0
57	MG	1A	3256	1/1	0.96	0.17	39,39,39,39	0
57	MG	2B	214	1/1	0.96	0.09	60,60,60,60	0
57	MG	1N	206	1/1	0.96	0.12	34,34,34,34	0
57	MG	1A	3375	1/1	0.96	0.10	41,41,41,41	0
57	MG	1A	3811	1/1	0.96	0.09	11,11,11,11	0
57	MG	2A	3569	1/1	0.96	0.07	36,36,36,36	0
57	MG	2D	301	1/1	0.96	0.08	34,34,34,34	0
57	MG	2D	303	1/1	0.96	0.20	46,46,46,46	0
57	MG	1A	3313	1/1	0.96	0.16	44,44,44,44	0
57	MG	2A	3311	1/1	0.96	0.08	36,36,36,36	0
57	MG	1A	3257	1/1	0.96	0.11	26,26,26,26	0
57	MG	1P	203	1/1	0.96	0.18	33,33,33,33	0
57	MG	2A	3098	1/1	0.96	0.12	20,20,20,20	0
57	MG	1A	3074	1/1	0.96	0.08	26,26,26,26	0
57	MG	1Q	204	1/1	0.96	0.05	35,35,35,35	0
57	MG	1A	3458	1/1	0.96	0.06	30,30,30,30	0
57	MG	2E	304	1/1	0.96	0.10	37,37,37,37	0
57	MG	1A	3972	1/1	0.96	0.08	41,41,41,41	0
57	MG	1A	3678	1/1	0.96	0.08	23,23,23,23	0
57	MG	2A	3105	1/1	0.96	0.20	43,43,43,43	0
57	MG	1R	203	1/1	0.96	0.18	28,28,28,28	0
57	MG	2A	3107	1/1	0.96	0.12	44,44,44,44	0
57	MG	1a	1725	1/1	0.96	0.23	55,55,55,55	0
57	MG	1A	3818	1/1	0.96	0.08	41,41,41,41	0
57	MG	1A	3262	1/1	0.96	0.17	17,17,17,17	0
57	MG	1S	201	1/1	0.96	0.12	35,35,35,35	0
57	MG	1A	3381	1/1	0.96	0.29	35,35,35,35	0
57	MG	1A	3383	1/1	0.96	0.08	29,29,29,29	0
57	MG	2O	202	1/1	0.96	0.21	49,49,49,49	0
57	MG	1T	201	1/1	0.96	0.06	49,49,49,49	0
57	MG	1A	3462	1/1	0.96	0.15	38,38,38,38	0
57	MG	1U	204	1/1	0.96	0.08	23,23,23,23	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2A	3119	1/1	0.96	0.07	48,48,48,48	0
57	MG	1A	3264	1/1	0.96	0.48	31,31,31,31	0
57	MG	1U	207	1/1	0.96	0.51	27,27,27,27	0
57	MG	1A	3825	1/1	0.96	0.10	28,28,28,28	0
57	MG	2R	201	1/1	0.96	0.12	45,45,45,45	0
57	MG	1A	3385	1/1	0.96	0.17	38,38,38,38	0
57	MG	1a	1738	1/1	0.96	0.10	44,44,44,44	0
57	MG	2A	3603	1/1	0.96	0.09	55,55,55,55	0
57	MG	1a	1739	1/1	0.96	0.07	29,29,29,29	0
57	MG	1A	3047	1/1	0.96	0.21	26,26,26,26	0
57	MG	2A	3128	1/1	0.96	0.05	34,34,34,34	0
57	MG	2U	201	1/1	0.96	0.10	45,45,45,45	0
57	MG	1A	3692	1/1	0.96	0.11	17,17,17,17	0
57	MG	1A	3031	1/1	0.96	0.18	28,28,28,28	0
57	MG	1W	204	1/1	0.96	0.06	32,32,32,32	0
57	MG	1A	3116	1/1	0.96	0.12	24,24,24,24	0
57	MG	2A	3611	1/1	0.96	0.11	42,42,42,42	0
57	MG	2A	3136	1/1	0.96	0.15	29,29,29,29	0
57	MG	1a	1748	1/1	0.96	0.09	39,39,39,39	0
57	MG	1W	208	1/1	0.96	0.05	21,21,21,21	0
57	MG	2A	3139	1/1	0.96	0.17	53,53,53,53	0
57	MG	2A	3140	1/1	0.96	0.18	45,45,45,45	0
57	MG	1A	3122	1/1	0.96	0.11	42,42,42,42	0
57	MG	1A	3213	1/1	0.96	0.07	23,23,23,23	0
57	MG	1X	104	1/1	0.96	0.11	35,35,35,35	0
57	MG	2A	3624	1/1	0.96	0.08	26,26,26,26	0
57	MG	1A	3324	1/1	0.96	0.10	36,36,36,36	0
57	MG	1A	3703	1/1	0.96	0.10	38,38,38,38	0
57	MG	2A	3628	1/1	0.96	0.10	37,37,37,37	0
57	MG	2A	3357	1/1	0.96	0.15	53,53,53,53	0
57	MG	1Y	203	1/1	0.96	0.13	38,38,38,38	0
57	MG	1a	1757	1/1	0.96	0.10	40,40,40,40	0
57	MG	28	103	1/1	0.96	0.20	40,40,40,40	0
57	MG	1A	3994	1/1	0.96	0.09	12,12,12,12	0
57	MG	1A	3078	1/1	0.96	0.11	29,29,29,29	0
57	MG	2A	3634	1/1	0.96	0.13	33,33,33,33	0
57	MG	2A	3152	1/1	0.96	0.08	49,49,49,49	0
57	MG	2A	3153	1/1	0.96	0.14	42,42,42,42	0
57	MG	2A	3637	1/1	0.96	0.15	37,37,37,37	0
57	MG	2A	3154	1/1	0.96	0.11	49,49,49,49	0
57	MG	2A	3641	1/1	0.96	0.21	45,45,45,45	0
57	MG	1A	3838	1/1	0.96	0.06	16,16,16,16	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2A	3643	1/1	0.96	0.18	45,45,45,45	0
57	MG	1A	3219	1/1	0.96	0.22	23,23,23,23	0
57	MG	2A	3645	1/1	0.96	0.15	41,41,41,41	0
57	MG	10	104	1/1	0.96	0.36	34,34,34,34	0
57	MG	1A	3574	1/1	0.96	0.09	39,39,39,39	0
57	MG	1A	3576	1/1	0.96	0.09	35,35,35,35	0
57	MG	1A	4001	1/1	0.96	0.07	14,14,14,14	0
57	MG	11	102	1/1	0.96	0.16	40,40,40,40	0
57	MG	11	103	1/1	0.96	0.06	23,23,23,23	0
57	MG	1A	3220	1/1	0.96	0.41	24,24,24,24	0
57	MG	1A	3128	1/1	0.96	0.09	29,29,29,29	0
57	MG	1A	3396	1/1	0.96	0.28	34,34,34,34	0
57	MG	2A	3166	1/1	0.96	0.05	44,44,44,44	0
57	MG	2A	3656	1/1	0.96	0.06	25,25,25,25	0
57	MG	2A	3167	1/1	0.96	0.15	30,30,30,30	0
57	MG	1A	3398	1/1	0.96	0.11	33,33,33,33	0
57	MG	15	104	1/1	0.96	0.14	28,28,28,28	0
57	MG	1A	3022	1/1	0.96	0.11	33,33,33,33	0
57	MG	2A	3171	1/1	0.96	0.14	39,39,39,39	0
57	MG	1A	3853	1/1	0.96	0.08	28,28,28,28	0
57	MG	2A	3384	1/1	0.96	0.21	32,32,32,32	0
57	MG	1A	3400	1/1	0.96	0.20	31,31,31,31	0
57	MG	2a	1634	1/1	0.96	0.13	48,48,48,48	0
57	MG	1A	3331	1/1	0.96	0.10	46,46,46,46	0
57	MG	1A	4012	1/1	0.96	0.11	39,39,39,39	0
57	MG	1A	3483	1/1	0.96	0.13	27,27,27,27	0
57	MG	2a	1638	1/1	0.96	0.14	40,40,40,40	0
57	MG	2A	3389	1/1	0.96	0.22	38,38,38,38	0
57	MG	1A	3223	1/1	0.96	0.28	32,32,32,32	0
57	MG	2A	3391	1/1	0.96	0.11	30,30,30,30	0
57	MG	2a	1642	1/1	0.96	0.18	45,45,45,45	0
57	MG	2A	3671	1/1	0.96	0.10	44,44,44,44	0
57	MG	2A	3392	1/1	0.96	0.06	36,36,36,36	0
57	MG	2a	1645	1/1	0.96	0.17	27,27,27,27	0
57	MG	2A	3180	1/1	0.96	0.11	52,52,52,52	0
57	MG	1A	3594	1/1	0.96	0.05	11,11,11,11	0
57	MG	2A	3395	1/1	0.96	0.13	35,35,35,35	0
57	MG	2a	1649	1/1	0.96	0.14	54,54,54,54	0
57	MG	1A	3280	1/1	0.96	0.14	33,33,33,33	0
57	MG	1A	3724	1/1	0.96	0.10	17,17,17,17	0
57	MG	1A	3486	1/1	0.96	0.19	32,32,32,32	0
57	MG	1A	3727	1/1	0.96	0.10	15,15,15,15	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1a	1606	1/1	0.96	0.19	59,59,59,59	0
57	MG	2A	3402	1/1	0.96	0.15	41,41,41,41	0
57	MG	2A	3683	1/1	0.96	0.09	45,45,45,45	0
57	MG	2A	3403	1/1	0.96	0.21	39,39,39,39	0
57	MG	1A	3599	1/1	0.96	0.06	13,13,13,13	0
57	MG	1A	3487	1/1	0.96	0.14	41,41,41,41	0
57	MG	1A	3405	1/1	0.96	0.05	37,37,37,37	0
57	MG	2a	1664	1/1	0.96	0.21	53,53,53,53	0
57	MG	1a	1610	1/1	0.96	0.14	55,55,55,55	0
57	MG	1a	1790	1/1	0.96	0.05	40,40,40,40	0
57	MG	1A	3050	1/1	0.96	0.13	52,52,52,52	0
57	MG	1A	3407	1/1	0.96	0.12	32,32,32,32	0
57	MG	1A	3337	1/1	0.96	0.12	40,40,40,40	0
57	MG	2A	3694	1/1	0.96	0.09	37,37,37,37	0
57	MG	2A	3414	1/1	0.96	0.18	32,32,32,32	0
57	MG	2A	3697	1/1	0.96	0.15	43,43,43,43	0
57	MG	1A	3734	1/1	0.96	0.10	12,12,12,12	0
57	MG	1A	4031	1/1	0.96	0.08	35,35,35,35	0
57	MG	1A	3879	1/1	0.96	0.07	41,41,41,41	0
57	MG	1A	4033	1/1	0.96	0.05	39,39,39,39	0
57	MG	2A	3702	1/1	0.96	0.06	35,35,35,35	0
57	MG	1A	3228	1/1	0.96	0.13	23,23,23,23	0
57	MG	1A	3410	1/1	0.96	0.12	44,44,44,44	0
57	MG	1A	3883	1/1	0.96	0.08	35,35,35,35	0
57	MG	1A	3284	1/1	0.96	0.07	24,24,24,24	0
57	MG	1A	3740	1/1	0.96	0.07	22,22,22,22	0
57	MG	1A	3611	1/1	0.96	0.07	24,24,24,24	0
57	MG	2A	3426	1/1	0.96	0.06	51,51,51,51	0
57	MG	1A	3497	1/1	0.96	0.10	53,53,53,53	0
57	MG	1A	3413	1/1	0.96	0.09	35,35,35,35	0
57	MG	2A	3208	1/1	0.96	0.06	48,48,48,48	0
57	MG	1A	3614	1/1	0.96	0.07	33,33,33,33	0
57	MG	2A	3210	1/1	0.96	0.16	57,57,57,57	0
57	MG	2a	1691	1/1	0.96	0.07	49,49,49,49	0
57	MG	2A	3434	1/1	0.96	0.06	48,48,48,48	0
57	MG	1a	1630	1/1	0.96	0.28	56,56,56,56	0
57	MG	1A	3229	1/1	0.96	0.16	27,27,27,27	0
57	MG	1A	3748	1/1	0.96	0.06	31,31,31,31	0
57	MG	2A	3721	1/1	0.96	0.09	62,62,62,62	0
57	MG	1k	201	1/1	0.96	0.11	42,42,42,42	0
57	MG	1A	3098	1/1	0.96	0.16	27,27,27,27	0
57	MG	1A	3752	1/1	0.96	0.12	42,42,42,42	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2A	3443	1/1	0.96	0.14	30,30,30,30	0
57	MG	2A	3444	1/1	0.96	0.10	56,56,56,56	0
57	MG	1A	3902	1/1	0.96	0.13	49,49,49,49	0
57	MG	1B	203	1/1	0.96	0.11	42,42,42,42	0
57	MG	2a	1705	1/1	0.96	0.06	35,35,35,35	0
57	MG	1A	3506	1/1	0.96	0.20	23,23,23,23	0
57	MG	2a	1707	1/1	0.96	0.19	30,30,30,30	0
57	MG	1A	3099	1/1	0.96	0.11	33,33,33,33	0
57	MG	1A	3100	1/1	0.96	0.10	27,27,27,27	0
57	MG	2A	3450	1/1	0.96	0.08	56,56,56,56	0
57	MG	1v	102	1/1	0.96	0.09	44,44,44,44	0
57	MG	1A	3906	1/1	0.96	0.10	36,36,36,36	0
57	MG	2A	3736	1/1	0.96	0.11	55,55,55,55	0
57	MG	2A	3453	1/1	0.96	0.06	34,34,34,34	0
57	MG	1a	1643	1/1	0.96	0.30	50,50,50,50	0
57	MG	2A	3455	1/1	0.96	0.12	35,35,35,35	0
57	MG	2A	3456	1/1	0.96	0.18	55,55,55,55	0
57	MG	1A	3101	1/1	0.96	0.09	19,19,19,19	0
57	MG	2A	3742	1/1	0.96	0.12	28,28,28,28	0
57	MG	1A	3237	1/1	0.96	0.26	26,26,26,26	0
57	MG	1A	3102	1/1	0.96	0.27	31,31,31,31	0
57	MG	2a	1727	1/1	0.96	0.16	73,73,73,73	0
57	MG	2A	3229	1/1	0.96	0.12	55,55,55,55	0
57	MG	1A	3910	1/1	0.96	0.05	42,42,42,42	0
57	MG	1B	214	1/1	0.96	0.14	48,48,48,48	0
57	MG	2a	1731	1/1	0.96	0.17	54,54,54,54	0
57	MG	1a	1649	1/1	0.96	0.15	38,38,38,38	0
57	MG	1B	215	1/1	0.96	0.10	45,45,45,45	0
57	MG	1x	111	1/1	0.96	0.15	48,48,48,48	0
57	MG	1B	217	1/1	0.96	0.08	46,46,46,46	0
57	MG	2A	3468	1/1	0.96	0.09	48,48,48,48	0
57	MG	1B	218	1/1	0.96	0.06	30,30,30,30	0
57	MG	2A	3004	1/1	0.96	0.23	45,45,45,45	0
57	MG	1a	1653	1/1	0.96	0.06	42,42,42,42	0
57	MG	1A	3911	1/1	0.96	0.09	12,12,12,12	0
57	MG	1B	220	1/1	0.96	0.11	30,30,30,30	0
57	MG	2a	1744	1/1	0.96	0.24	54,54,54,54	0
57	MG	1A	3762	1/1	0.96	0.11	38,38,38,38	0
57	MG	2A	3476	1/1	0.96	0.10	41,41,41,41	0
57	MG	1a	1657	1/1	0.96	0.14	53,53,53,53	0
57	MG	2A	3479	1/1	0.96	0.16	55,55,55,55	0
57	MG	2A	3480	1/1	0.96	0.06	40,40,40,40	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2A	3011	1/1	0.96	0.07	31,31,31,31	0
57	MG	2A	3244	1/1	0.96	0.14	49,49,49,49	0
57	MG	2A	3769	1/1	0.96	0.15	36,36,36,36	0
57	MG	2A	3245	1/1	0.96	0.08	52,52,52,52	0
57	MG	2a	1756	1/1	0.96	0.17	45,45,45,45	0
57	MG	2A	3771	1/1	0.96	0.06	32,32,32,32	0
57	MG	1A	3146	1/1	0.96	0.18	31,31,31,31	0
57	MG	1A	3514	1/1	0.96	0.07	23,23,23,23	0
57	MG	1A	3008	1/1	0.96	0.06	13,13,13,13	0
57	MG	2A	3776	1/1	0.96	0.14	59,59,59,59	0
57	MG	2A	3489	1/1	0.96	0.11	50,50,50,50	0
57	MG	2a	1763	1/1	0.96	0.16	45,45,45,45	0
57	MG	2A	3490	1/1	0.96	0.17	39,39,39,39	0
57	MG	1A	3918	1/1	0.96	0.12	45,45,45,45	0
57	MG	2A	3492	1/1	0.96	0.14	49,49,49,49	0
57	MG	1A	3184	1/1	0.96	0.23	31,31,31,31	0
57	MG	1A	3637	1/1	0.96	0.06	13,13,13,13	0
57	MG	1A	3353	1/1	0.96	0.25	39,39,39,39	0
57	MG	1A	3773	1/1	0.96	0.16	24,24,24,24	0
57	MG	1A	3524	1/1	0.96	0.24	28,28,28,28	0
57	MG	1A	3776	1/1	0.96	0.07	34,34,34,34	0
57	MG	2A	3792	1/1	0.96	0.17	46,46,46,46	0
57	MG	2A	3500	1/1	0.96	0.09	35,35,35,35	0
57	MG	1A	3777	1/1	0.96	0.12	36,36,36,36	0
57	MG	2A	3257	1/1	0.96	0.10	52,52,52,52	0
57	MG	1A	3354	1/1	0.96	0.08	36,36,36,36	0
57	MG	1A	3928	1/1	0.96	0.07	34,34,34,34	0
57	MG	1A	3779	1/1	0.96	0.04	20,20,20,20	0
57	MG	1A	3930	1/1	0.96	0.07	47,47,47,47	0
57	MG	1A	3643	1/1	0.96	0.07	46,46,46,46	0
57	MG	1A	3242	1/1	0.96	0.09	17,17,17,17	0
57	MG	1A	3356	1/1	0.96	0.24	24,24,24,24	0
57	MG	2A	3804	1/1	0.96	0.07	38,38,38,38	0
57	MG	1A	3646	1/1	0.96	0.05	16,16,16,16	0
57	MG	2A	3806	1/1	0.96	0.23	37,37,37,37	0
57	MG	2v	102	1/1	0.96	0.13	49,49,49,49	0
57	MG	1D	305	1/1	0.96	0.07	31,31,31,31	0
57	MG	1A	3243	1/1	0.96	0.06	27,27,27,27	0
57	MG	1A	3064	1/1	0.96	0.08	37,37,37,37	0
57	MG	2A	3515	1/1	0.96	0.07	20,20,20,20	0
57	MG	1A	3192	1/1	0.96	0.19	31,31,31,31	0
57	MG	1E	301	1/1	0.96	0.14	33,33,33,33	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1E	302	1/1	0.96	0.22	31,31,31,31	0
57	MG	1A	3193	1/1	0.96	0.05	28,28,28,28	0
59	ZN	14	501	1/1	0.96	0.06	92,92,92,92	0
59	ZN	24	501	1/1	0.96	0.07	103,103,103,103	0
57	MG	1A	3021	1/1	0.97	0.05	20,20,20,20	0
57	MG	1F	305	1/1	0.97	0.05	31,31,31,31	0
57	MG	1F	307	1/1	0.97	0.06	17,17,17,17	0
57	MG	1A	3694	1/1	0.97	0.05	53,53,53,53	0
57	MG	1A	3196	1/1	0.97	0.15	30,30,30,30	0
57	MG	2A	3405	1/1	0.97	0.09	37,37,37,37	0
57	MG	1A	3140	1/1	0.97	0.16	23,23,23,23	0
57	MG	2A	3638	1/1	0.97	0.06	35,35,35,35	0
57	MG	2A	3639	1/1	0.97	0.07	42,42,42,42	0
57	MG	1A	3141	1/1	0.97	0.20	19,19,19,19	0
57	MG	1A	3142	1/1	0.97	0.06	25,25,25,25	0
57	MG	2F	307	1/1	0.97	0.22	42,42,42,42	0
57	MG	2A	3012	1/1	0.97	0.04	29,29,29,29	0
57	MG	1A	3259	1/1	0.97	0.09	37,37,37,37	0
57	MG	2A	3215	1/1	0.97	0.10	36,36,36,36	0
57	MG	2A	3014	1/1	0.97	0.12	33,33,33,33	0
57	MG	2A	3015	1/1	0.97	0.20	32,32,32,32	0
57	MG	1A	3260	1/1	0.97	0.06	34,34,34,34	0
57	MG	1A	3581	1/1	0.97	0.15	16,16,16,16	0
57	MG	1A	3582	1/1	0.97	0.05	28,28,28,28	0
57	MG	1A	3261	1/1	0.97	0.12	29,29,29,29	0
57	MG	2A	3021	1/1	0.97	0.18	30,30,30,30	0
57	MG	1N	201	1/1	0.97	0.23	33,33,33,33	0
57	MG	1A	3052	1/1	0.97	0.13	29,29,29,29	0
57	MG	1N	203	1/1	0.97	0.06	30,30,30,30	0
57	MG	1A	3585	1/1	0.97	0.06	21,21,21,21	0
57	MG	1A	3332	1/1	0.97	0.06	36,36,36,36	0
57	MG	1A	3333	1/1	0.97	0.07	47,47,47,47	0
57	MG	1O	202	1/1	0.97	0.10	42,42,42,42	0
57	MG	1A	3711	1/1	0.97	0.12	32,32,32,32	0
57	MG	1A	3590	1/1	0.97	0.06	12,12,12,12	0
57	MG	1A	3714	1/1	0.97	0.04	27,27,27,27	0
57	MG	1A	3263	1/1	0.97	0.12	19,19,19,19	0
57	MG	2A	3034	1/1	0.97	0.10	44,44,44,44	0
57	MG	1Q	201	1/1	0.97	0.16	26,26,26,26	0
57	MG	2A	3436	1/1	0.97	0.07	39,39,39,39	0
57	MG	2A	3036	1/1	0.97	0.14	32,32,32,32	0
57	MG	1A	3843	1/1	0.97	0.07	28,28,28,28	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1A	3844	1/1	0.97	0.14	10,10,10,10	0
57	MG	1A	3201	1/1	0.97	0.08	30,30,30,30	0
57	MG	1Q	206	1/1	0.97	0.05	37,37,37,37	0
57	MG	2A	3041	1/1	0.97	0.21	39,39,39,39	0
57	MG	1A	3490	1/1	0.97	0.10	15,15,15,15	0
57	MG	1A	3103	1/1	0.97	0.14	24,24,24,24	0
57	MG	1A	3411	1/1	0.97	0.06	44,44,44,44	0
57	MG	25	104	1/1	0.97	0.16	39,39,39,39	0
57	MG	1R	205	1/1	0.97	0.17	35,35,35,35	0
57	MG	2A	3046	1/1	0.97	0.16	42,42,42,42	0
57	MG	2A	3047	1/1	0.97	0.17	52,52,52,52	0
57	MG	1A	3596	1/1	0.97	0.05	10,10,10,10	0
57	MG	2A	3679	1/1	0.97	0.10	19,19,19,19	0
57	MG	1A	3081	1/1	0.97	0.20	33,33,33,33	0
57	MG	1A	3852	1/1	0.97	0.06	36,36,36,36	0
57	MG	1A	3149	1/1	0.97	0.34	39,39,39,39	0
57	MG	1A	3269	1/1	0.97	0.07	37,37,37,37	0
57	MG	1A	3496	1/1	0.97	0.11	42,42,42,42	0
57	MG	2A	3685	1/1	0.97	0.06	58,58,58,58	0
57	MG	1A	3207	1/1	0.97	0.08	32,32,32,32	0
57	MG	1a	1707	1/1	0.97	0.09	34,34,34,34	0
57	MG	1A	3150	1/1	0.97	0.05	21,21,21,21	0
57	MG	1A	3859	1/1	0.97	0.12	45,45,45,45	0
57	MG	1a	1710	1/1	0.97	0.21	33,33,33,33	0
57	MG	1A	3209	1/1	0.97	0.09	44,44,44,44	0
57	MG	1U	208	1/1	0.97	0.18	29,29,29,29	0
57	MG	1A	3862	1/1	0.97	0.06	30,30,30,30	0
57	MG	1a	1714	1/1	0.97	0.18	43,43,43,43	0
57	MG	2A	3064	1/1	0.97	0.21	41,41,41,41	0
57	MG	1A	3500	1/1	0.97	0.06	48,48,48,48	0
57	MG	1A	3864	1/1	0.97	0.09	58,58,58,58	0
57	MG	1V	205	1/1	0.97	0.06	27,27,27,27	0
57	MG	1V	206	1/1	0.97	0.05	43,43,43,43	0
57	MG	1A	3501	1/1	0.97	0.30	28,28,28,28	0
57	MG	2A	3071	1/1	0.97	0.08	42,42,42,42	0
57	MG	1A	3210	1/1	0.97	0.17	33,33,33,33	0
57	MG	2A	3474	1/1	0.97	0.23	45,45,45,45	0
57	MG	2A	3073	1/1	0.97	0.22	39,39,39,39	0
57	MG	1A	4010	1/1	0.97	0.04	32,32,32,32	0
57	MG	2A	3075	1/1	0.97	0.09	23,23,23,23	0
57	MG	1A	3503	1/1	0.97	0.11	38,38,38,38	0
57	MG	1A	3504	1/1	0.97	0.16	13,13,13,13	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2A	3711	1/1	0.97	0.06	35,35,35,35	0
57	MG	2A	3078	1/1	0.97	0.24	43,43,43,43	0
57	MG	1A	3419	1/1	0.97	0.12	30,30,30,30	0
57	MG	1A	3737	1/1	0.97	0.05	29,29,29,29	0
57	MG	1X	102	1/1	0.97	0.07	33,33,33,33	0
57	MG	2A	3485	1/1	0.97	0.25	45,45,45,45	0
57	MG	1A	3009	1/1	0.97	0.05	17,17,17,17	0
57	MG	2A	3083	1/1	0.97	0.05	42,42,42,42	0
57	MG	2A	3488	1/1	0.97	0.12	36,36,36,36	0
57	MG	1X	105	1/1	0.97	0.09	42,42,42,42	0
57	MG	1A	3422	1/1	0.97	0.07	41,41,41,41	0
57	MG	1A	3741	1/1	0.97	0.08	34,34,34,34	0
57	MG	1A	3742	1/1	0.97	0.06	37,37,37,37	0
57	MG	1A	3878	1/1	0.97	0.16	50,50,50,50	0
57	MG	1A	3038	1/1	0.97	0.05	21,21,21,21	0
57	MG	2A	3090	1/1	0.97	0.29	35,35,35,35	0
57	MG	10	101	1/1	0.97	0.04	27,27,27,27	0
57	MG	1A	3618	1/1	0.97	0.05	50,50,50,50	0
57	MG	2A	3095	1/1	0.97	0.12	49,49,49,49	0
57	MG	2A	3292	1/1	0.97	0.05	50,50,50,50	0
57	MG	1A	3154	1/1	0.97	0.20	23,23,23,23	0
57	MG	1A	3214	1/1	0.97	0.10	40,40,40,40	0
57	MG	2a	1652	1/1	0.97	0.14	41,41,41,41	0
57	MG	1A	3156	1/1	0.97	0.17	23,23,23,23	0
57	MG	1A	3885	1/1	0.97	0.05	27,27,27,27	0
57	MG	2a	1655	1/1	0.97	0.09	65,65,65,65	0
57	MG	1A	3886	1/1	0.97	0.06	26,26,26,26	0
57	MG	1a	1741	1/1	0.97	0.07	33,33,33,33	0
57	MG	10	108	1/1	0.97	0.12	35,35,35,35	0
57	MG	1A	3887	1/1	0.97	0.05	9,9,9,9	0
57	MG	1A	3217	1/1	0.97	0.24	33,33,33,33	0
57	MG	2a	1661	1/1	0.97	0.32	48,48,48,48	0
57	MG	1a	1745	1/1	0.97	0.08	31,31,31,31	0
57	MG	1A	3041	1/1	0.97	0.06	25,25,25,25	0
57	MG	1A	3002	1/1	0.97	0.05	33,33,33,33	0
57	MG	13	101	1/1	0.97	0.23	28,28,28,28	0
57	MG	13	102	1/1	0.97	0.10	34,34,34,34	0
57	MG	2A	3516	1/1	0.97	0.12	41,41,41,41	0
57	MG	1A	3753	1/1	0.97	0.06	42,42,42,42	0
57	MG	1A	3895	1/1	0.97	0.10	40,40,40,40	0
57	MG	2A	3519	1/1	0.97	0.08	25,25,25,25	0
57	MG	15	101	1/1	0.97	0.30	25,25,25,25	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2a	1672	1/1	0.97	0.22	43,43,43,43	0
57	MG	2A	3752	1/1	0.97	0.13	32,32,32,32	0
57	MG	2A	3115	1/1	0.97	0.12	30,30,30,30	0
57	MG	15	102	1/1	0.97	0.23	22,22,22,22	0
57	MG	1A	3518	1/1	0.97	0.22	33,33,33,33	0
57	MG	1a	1756	1/1	0.97	0.10	52,52,52,52	0
57	MG	1A	3519	1/1	0.97	0.07	21,21,21,21	0
57	MG	2A	3758	1/1	0.97	0.06	22,22,22,22	0
57	MG	1A	3520	1/1	0.97	0.12	33,33,33,33	0
57	MG	1A	3632	1/1	0.97	0.07	18,18,18,18	0
57	MG	1A	4041	1/1	0.97	0.10	41,41,41,41	0
57	MG	2A	3529	1/1	0.97	0.12	32,32,32,32	0
57	MG	17	102	1/1	0.97	0.06	18,18,18,18	0
57	MG	1A	3759	1/1	0.97	0.09	34,34,34,34	0
57	MG	2A	3765	1/1	0.97	0.07	38,38,38,38	0
57	MG	17	104	1/1	0.97	0.06	31,31,31,31	0
57	MG	2A	3126	1/1	0.97	0.06	41,41,41,41	0
57	MG	2A	3322	1/1	0.97	0.31	40,40,40,40	0
57	MG	2A	3535	1/1	0.97	0.09	29,29,29,29	0
57	MG	1A	3044	1/1	0.97	0.09	25,25,25,25	0
57	MG	1A	3115	1/1	0.97	0.19	35,35,35,35	0
57	MG	1A	3525	1/1	0.97	0.09	28,28,28,28	0
57	MG	2A	3539	1/1	0.97	0.08	29,29,29,29	0
57	MG	2A	3540	1/1	0.97	0.08	20,20,20,20	0
57	MG	1A	3763	1/1	0.97	0.06	15,15,15,15	0
57	MG	2A	3543	1/1	0.97	0.12	25,25,25,25	0
57	MG	2A	3544	1/1	0.97	0.19	32,32,32,32	0
57	MG	2A	3132	1/1	0.97	0.12	40,40,40,40	0
57	MG	1A	3639	1/1	0.97	0.05	12,12,12,12	0
57	MG	1A	3288	1/1	0.97	0.07	20,20,20,20	0
57	MG	2A	3782	1/1	0.97	0.07	30,30,30,30	0
57	MG	2A	3783	1/1	0.97	0.07	37,37,37,37	0
57	MG	2A	3135	1/1	0.97	0.19	45,45,45,45	0
57	MG	1A	3045	1/1	0.97	0.10	27,27,27,27	0
57	MG	2A	3786	1/1	0.97	0.05	42,42,42,42	0
57	MG	2a	1708	1/1	0.97	0.16	48,48,48,48	0
57	MG	1A	3530	1/1	0.97	0.06	32,32,32,32	0
57	MG	1B	205	1/1	0.97	0.06	34,34,34,34	0
57	MG	1A	3770	1/1	0.97	0.06	37,37,37,37	0
57	MG	2a	1713	1/1	0.97	0.20	43,43,43,43	0
57	MG	1A	3117	1/1	0.97	0.17	31,31,31,31	0
57	MG	1A	3225	1/1	0.97	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
57	MG	2a	1716	1/1	0.97	0.11	45,45,45,45	0
57	MG	1A	3913	1/1	0.97	0.05	31,31,31,31	0
57	MG	1A	3439	1/1	0.97	0.08	41,41,41,41	0
57	MG	1A	3774	1/1	0.97	0.05	44,44,44,44	0
57	MG	1A	3227	1/1	0.97	0.12	27,27,27,27	0
57	MG	2a	1721	1/1	0.97	0.12	42,42,42,42	0
57	MG	1A	3363	1/1	0.97	0.18	29,29,29,29	0
57	MG	1A	3919	1/1	0.97	0.07	46,46,46,46	0
57	MG	1B	216	1/1	0.97	0.04	30,30,30,30	0
57	MG	2A	3149	1/1	0.97	0.15	34,34,34,34	0
57	MG	1A	3650	1/1	0.97	0.05	20,20,20,20	0
57	MG	1A	3119	1/1	0.97	0.34	31,31,31,31	0
57	MG	2A	3567	1/1	0.97	0.06	26,26,26,26	0
57	MG	1A	3120	1/1	0.97	0.25	23,23,23,23	0
57	MG	1A	3232	1/1	0.97	0.15	27,27,27,27	0
57	MG	1a	1622	1/1	0.97	0.06	45,45,45,45	0
57	MG	2A	3350	1/1	0.97	0.05	32,32,32,32	0
57	MG	1A	3015	1/1	0.97	0.27	23,23,23,23	0
57	MG	1A	3123	1/1	0.97	0.09	29,29,29,29	0
57	MG	2A	3813	1/1	0.97	0.06	22,22,22,22	0
57	MG	1a	1625	1/1	0.97	0.16	40,40,40,40	0
57	MG	2a	1737	1/1	0.97	0.07	32,32,32,32	0
57	MG	2A	3815	1/1	0.97	0.05	53,53,53,53	0
57	MG	2a	1739	1/1	0.97	0.12	41,41,41,41	0
57	MG	1a	1791	1/1	0.97	0.19	40,40,40,40	0
57	MG	1A	3299	1/1	0.97	0.07	22,22,22,22	0
57	MG	2A	3578	1/1	0.97	0.10	38,38,38,38	0
57	MG	1A	3168	1/1	0.97	0.07	28,28,28,28	0
57	MG	1A	3173	1/1	0.97	0.06	8,8,8,8	0
57	MG	2A	3821	1/1	0.97	0.07	54,54,54,54	0
57	MG	2a	1746	1/1	0.97	0.21	44,44,44,44	0
57	MG	2A	3823	1/1	0.97	0.04	46,46,46,46	0
57	MG	2A	3581	1/1	0.97	0.07	46,46,46,46	0
57	MG	1a	1629	1/1	0.97	0.12	53,53,53,53	0
57	MG	1A	3066	1/1	0.97	0.05	8,8,8,8	0
57	MG	1A	3787	1/1	0.97	0.14	42,42,42,42	0
57	MG	1A	3374	1/1	0.97	0.09	37,37,37,37	0
57	MG	1A	3125	1/1	0.97	0.08	27,27,27,27	0
57	MG	2a	1754	1/1	0.97	0.16	44,44,44,44	0
57	MG	1A	3126	1/1	0.97	0.10	27,27,27,27	0
57	MG	1A	3067	1/1	0.97	0.09	27,27,27,27	0
57	MG	1A	3666	1/1	0.97	0.09	7,7,7,7	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1A	3936	1/1	0.97	0.07	8,8,8,8	0
57	MG	2A	3593	1/1	0.97	0.14	49,49,49,49	0
57	MG	1A	3937	1/1	0.97	0.10	19,19,19,19	0
57	MG	2A	3174	1/1	0.97	0.10	31,31,31,31	0
57	MG	1A	3026	1/1	0.97	0.06	34,34,34,34	0
57	MG	1A	3307	1/1	0.97	0.29	43,43,43,43	0
57	MG	1A	3180	1/1	0.97	0.15	29,29,29,29	0
57	MG	1A	3070	1/1	0.97	0.04	23,23,23,23	0
57	MG	1A	3244	1/1	0.97	0.06	33,33,33,33	0
57	MG	1A	3134	1/1	0.97	0.16	30,30,30,30	0
57	MG	1A	3071	1/1	0.97	0.05	23,23,23,23	0
57	MG	1D	307	1/1	0.97	0.05	26,26,26,26	0
57	MG	1A	3187	1/1	0.97	0.05	30,30,30,30	0
57	MG	1A	3946	1/1	0.97	0.05	23,23,23,23	0
57	MG	2A	3379	1/1	0.97	0.09	34,34,34,34	0
57	MG	1A	3559	1/1	0.97	0.12	39,39,39,39	0
57	MG	1D	313	1/1	0.97	0.07	23,23,23,23	0
57	MG	1A	3189	1/1	0.97	0.17	21,21,21,21	0
57	MG	1A	3561	1/1	0.97	0.12	26,26,26,26	0
57	MG	1A	3028	1/1	0.97	0.18	21,21,21,21	0
57	MG	2A	3612	1/1	0.97	0.11	37,37,37,37	0
57	MG	2A	3613	1/1	0.97	0.11	26,26,26,26	0
57	MG	1w	401	1/1	0.97	0.11	27,27,27,27	0
57	MG	1A	3191	1/1	0.97	0.06	30,30,30,30	0
57	MG	1A	3472	1/1	0.97	0.06	39,39,39,39	0
57	MG	1A	3004	1/1	0.97	0.11	18,18,18,18	0
57	MG	1A	3252	1/1	0.97	0.09	33,33,33,33	0
57	MG	1A	3957	1/1	0.97	0.05	11,11,11,11	0
57	MG	1A	3685	1/1	0.97	0.09	48,48,48,48	0
57	MG	1A	3320	1/1	0.97	0.07	33,33,33,33	0
57	MG	2A	3622	1/1	0.97	0.11	43,43,43,43	0
57	MG	2A	3623	1/1	0.97	0.11	51,51,51,51	0
57	MG	2D	302	1/1	0.97	0.18	35,35,35,35	0
57	MG	1E	312	1/1	0.97	0.07	29,29,29,29	0
57	MG	1A	3253	1/1	0.97	0.30	49,49,49,49	0
57	MG	2A	3626	1/1	0.97	0.06	33,33,33,33	0
57	MG	1x	110	1/1	0.97	0.23	36,36,36,36	0
57	MG	1F	302	1/1	0.97	0.23	26,26,26,26	0
57	MG	2A	3001	1/1	0.97	0.32	45,45,45,45	0
57	MG	1A	3691	1/1	0.97	0.04	30,30,30,30	0
59	ZN	2n	102	1/1	0.97	0.05	86,86,86,86	0
60	SF4	1d	302	8/8	0.97	0.06	61,65,77,79	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1A	3018	1/1	0.98	0.07	18,18,18,18	0
57	MG	1A	3080	1/1	0.98	0.17	19,19,19,19	0
57	MG	2A	3556	1/1	0.98	0.05	21,21,21,21	0
57	MG	1A	3397	1/1	0.98	0.09	28,28,28,28	0
57	MG	1A	3118	1/1	0.98	0.27	24,24,24,24	0
57	MG	1A	3032	1/1	0.98	0.06	35,35,35,35	0
57	MG	1A	3020	1/1	0.98	0.04	26,26,26,26	0
57	MG	1A	3401	1/1	0.98	0.11	29,29,29,29	0
57	MG	1A	3169	1/1	0.98	0.24	25,25,25,25	0
57	MG	1A	3279	1/1	0.98	0.06	29,29,29,29	0
57	MG	1A	3171	1/1	0.98	0.07	22,22,22,22	0
57	MG	2A	3048	1/1	0.98	0.12	25,25,25,25	0
57	MG	1A	3339	1/1	0.98	0.06	35,35,35,35	0
57	MG	2A	3568	1/1	0.98	0.06	26,26,26,26	0
57	MG	1A	3226	1/1	0.98	0.05	15,15,15,15	0
57	MG	1A	3172	1/1	0.98	0.07	15,15,15,15	0
57	MG	1A	3283	1/1	0.98	0.12	37,37,37,37	0
57	MG	2a	1621	1/1	0.98	0.08	49,49,49,49	0
57	MG	1A	4046	1/1	0.98	0.08	33,33,33,33	0
57	MG	11	101	1/1	0.98	0.28	28,28,28,28	0
57	MG	1A	3121	1/1	0.98	0.18	28,28,28,28	0
57	MG	1A	3568	1/1	0.98	0.06	30,30,30,30	0
57	MG	1A	3914	1/1	0.98	0.08	12,12,12,12	0
57	MG	11	105	1/1	0.98	0.05	41,41,41,41	0
57	MG	2A	3396	1/1	0.98	0.06	39,39,39,39	0
57	MG	1A	3035	1/1	0.98	0.24	28,28,28,28	0
57	MG	12	102	1/1	0.98	0.07	38,38,38,38	0
57	MG	2a	1631	1/1	0.98	0.28	46,46,46,46	0
57	MG	1A	3570	1/1	0.98	0.07	30,30,30,30	0
57	MG	1A	3230	1/1	0.98	0.21	25,25,25,25	0
57	MG	1A	3346	1/1	0.98	0.18	34,34,34,34	0
57	MG	1A	3231	1/1	0.98	0.15	24,24,24,24	0
57	MG	1A	3084	1/1	0.98	0.15	31,31,31,31	0
57	MG	1A	3054	1/1	0.98	0.06	17,17,17,17	0
57	MG	2A	3067	1/1	0.98	0.04	21,21,21,21	0
57	MG	15	103	1/1	0.98	0.16	11,11,11,11	0
57	MG	2A	3775	1/1	0.98	0.07	60,60,60,60	0
57	MG	1A	3350	1/1	0.98	0.15	19,19,19,19	0
57	MG	1A	3578	1/1	0.98	0.07	12,12,12,12	0
57	MG	1A	3036	1/1	0.98	0.26	23,23,23,23	0
57	MG	1B	213	1/1	0.98	0.08	60,60,60,60	0
57	MG	2A	3411	1/1	0.98	0.06	28,28,28,28	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	16	101	1/1	0.98	0.15	29,29,29,29	0
57	MG	1A	3003	1/1	0.98	0.05	14,14,14,14	0
57	MG	1A	3797	1/1	0.98	0.12	44,44,44,44	0
57	MG	1A	3798	1/1	0.98	0.04	25,25,25,25	0
57	MG	1A	3088	1/1	0.98	0.10	14,14,14,14	0
57	MG	18	101	1/1	0.98	0.17	28,28,28,28	0
57	MG	2A	3418	1/1	0.98	0.09	33,33,33,33	0
57	MG	1A	3420	1/1	0.98	0.19	28,28,28,28	0
57	MG	2A	3789	1/1	0.98	0.04	23,23,23,23	0
57	MG	1A	3057	1/1	0.98	0.05	36,36,36,36	0
57	MG	2A	3791	1/1	0.98	0.06	22,22,22,22	0
57	MG	1A	3687	1/1	0.98	0.13	45,45,45,45	0
57	MG	1a	1601	1/1	0.98	0.06	42,42,42,42	0
57	MG	1A	3688	1/1	0.98	0.04	35,35,35,35	0
57	MG	1A	3182	1/1	0.98	0.07	33,33,33,33	0
57	MG	1A	3690	1/1	0.98	0.06	37,37,37,37	0
57	MG	1A	3807	1/1	0.98	0.06	9,9,9,9	0
57	MG	1A	3586	1/1	0.98	0.07	16,16,16,16	0
57	MG	1A	3013	1/1	0.98	0.21	18,18,18,18	0
57	MG	1A	3588	1/1	0.98	0.10	54,54,54,54	0
57	MG	2A	3430	1/1	0.98	0.07	35,35,35,35	0
57	MG	2A	3802	1/1	0.98	0.05	23,23,23,23	0
57	MG	1A	3357	1/1	0.98	0.28	19,19,19,19	0
57	MG	2A	3091	1/1	0.98	0.07	33,33,33,33	0
57	MG	1A	3812	1/1	0.98	0.10	15,15,15,15	0
57	MG	1A	3297	1/1	0.98	0.05	36,36,36,36	0
57	MG	2A	3094	1/1	0.98	0.13	37,37,37,37	0
57	MG	1A	3697	1/1	0.98	0.05	49,49,49,49	0
57	MG	1A	3698	1/1	0.98	0.05	37,37,37,37	0
57	MG	2A	3439	1/1	0.98	0.22	39,39,39,39	0
57	MG	1A	3133	1/1	0.98	0.08	37,37,37,37	0
57	MG	1A	3185	1/1	0.98	0.17	23,23,23,23	0
57	MG	1A	3428	1/1	0.98	0.15	30,30,30,30	0
57	MG	1A	3702	1/1	0.98	0.04	41,41,41,41	0
57	MG	1A	3505	1/1	0.98	0.13	21,21,21,21	0
57	MG	1A	3091	1/1	0.98	0.14	31,31,31,31	0
57	MG	2A	3103	1/1	0.98	0.04	34,34,34,34	0
57	MG	1A	3188	1/1	0.98	0.17	26,26,26,26	0
57	MG	1A	3951	1/1	0.98	0.06	14,14,14,14	0
57	MG	1D	304	1/1	0.98	0.07	12,12,12,12	0
57	MG	2A	3822	1/1	0.98	0.05	15,15,15,15	0
57	MG	1A	3135	1/1	0.98	0.25	29,29,29,29	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1D	306	1/1	0.98	0.05	31,31,31,31	0
57	MG	1A	3598	1/1	0.98	0.06	13,13,13,13	0
57	MG	1D	308	1/1	0.98	0.09	35,35,35,35	0
57	MG	1A	3954	1/1	0.98	0.13	37,37,37,37	0
57	MG	1A	3432	1/1	0.98	0.06	35,35,35,35	0
57	MG	1A	3039	1/1	0.98	0.10	25,25,25,25	0
57	MG	1A	3601	1/1	0.98	0.06	27,27,27,27	0
57	MG	2A	3831	1/1	0.98	0.05	34,34,34,34	0
57	MG	2a	1696	1/1	0.98	0.17	43,43,43,43	0
57	MG	1A	3830	1/1	0.98	0.16	15,15,15,15	0
57	MG	1a	1632	1/1	0.98	0.14	22,22,22,22	0
57	MG	2A	3460	1/1	0.98	0.14	32,32,32,32	0
57	MG	1a	1633	1/1	0.98	0.13	38,38,38,38	0
57	MG	1A	3040	1/1	0.98	0.23	26,26,26,26	0
57	MG	1A	3960	1/1	0.98	0.04	24,24,24,24	0
57	MG	1A	3062	1/1	0.98	0.08	25,25,25,25	0
57	MG	1E	305	1/1	0.98	0.03	21,21,21,21	0
57	MG	1A	3713	1/1	0.98	0.06	38,38,38,38	0
57	MG	1A	3096	1/1	0.98	0.06	32,32,32,32	0
57	MG	1A	3194	1/1	0.98	0.13	13,13,13,13	0
57	MG	1A	3965	1/1	0.98	0.06	35,35,35,35	0
57	MG	1A	3063	1/1	0.98	0.04	22,22,22,22	0
57	MG	1A	3309	1/1	0.98	0.12	33,33,33,33	0
57	MG	1A	3718	1/1	0.98	0.05	34,34,34,34	0
57	MG	1A	3608	1/1	0.98	0.14	14,14,14,14	0
57	MG	2A	3131	1/1	0.98	0.11	28,28,28,28	0
57	MG	1A	3609	1/1	0.98	0.08	15,15,15,15	0
57	MG	1a	1801	1/1	0.98	0.14	36,36,36,36	0
57	MG	1A	3842	1/1	0.98	0.07	44,44,44,44	0
57	MG	2A	3478	1/1	0.98	0.13	37,37,37,37	0
57	MG	1A	3721	1/1	0.98	0.05	25,25,25,25	0
57	MG	1A	3023	1/1	0.98	0.08	8,8,8,8	0
57	MG	1F	306	1/1	0.98	0.06	31,31,31,31	0
57	MG	1A	3065	1/1	0.98	0.10	19,19,19,19	0
57	MG	1F	308	1/1	0.98	0.15	25,25,25,25	0
57	MG	1A	3443	1/1	0.98	0.19	28,28,28,28	0
57	MG	1A	3976	1/1	0.98	0.06	28,28,28,28	0
57	MG	1F	311	1/1	0.98	0.10	26,26,26,26	0
57	MG	1A	3725	1/1	0.98	0.04	28,28,28,28	0
57	MG	1A	3522	1/1	0.98	0.23	25,25,25,25	0
57	MG	1A	3373	1/1	0.98	0.16	29,29,29,29	0
57	MG	2B	218	1/1	0.98	0.08	45,45,45,45	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1A	3980	1/1	0.98	0.09	29,29,29,29	0
57	MG	1m	3001	1/1	0.98	0.09	53,53,53,53	0
57	MG	1A	3981	1/1	0.98	0.05	15,15,15,15	0
57	MG	2A	3493	1/1	0.98	0.07	37,37,37,37	0
57	MG	2D	304	1/1	0.98	0.05	38,38,38,38	0
57	MG	2D	305	1/1	0.98	0.04	21,21,21,21	0
57	MG	1A	3042	1/1	0.98	0.06	26,26,26,26	0
57	MG	2A	3150	1/1	0.98	0.05	43,43,43,43	0
57	MG	1A	3616	1/1	0.98	0.04	29,29,29,29	0
57	MG	1A	3984	1/1	0.98	0.07	46,46,46,46	0
57	MG	1A	3526	1/1	0.98	0.13	25,25,25,25	0
57	MG	1v	101	1/1	0.98	0.15	55,55,55,55	0
57	MG	1A	3446	1/1	0.98	0.14	32,32,32,32	0
57	MG	1A	3619	1/1	0.98	0.07	21,21,21,21	0
57	MG	1N	204	1/1	0.98	0.23	37,37,37,37	0
57	MG	1A	3620	1/1	0.98	0.13	28,28,28,28	0
57	MG	1A	3857	1/1	0.98	0.06	31,31,31,31	0
57	MG	1A	3528	1/1	0.98	0.17	23,23,23,23	0
57	MG	2F	301	1/1	0.98	0.15	35,35,35,35	0
57	MG	1A	3014	1/1	0.98	0.10	21,21,21,21	0
57	MG	2A	3507	1/1	0.98	0.06	28,28,28,28	0
57	MG	1A	3068	1/1	0.98	0.10	7,7,7,7	0
57	MG	1A	3007	1/1	0.98	0.06	26,26,26,26	0
57	MG	1A	3010	1/1	0.98	0.08	30,30,30,30	0
57	MG	1A	3739	1/1	0.98	0.05	11,11,11,11	0
57	MG	1A	3379	1/1	0.98	0.04	24,24,24,24	0
57	MG	1A	3205	1/1	0.98	0.09	32,32,32,32	0
57	MG	1A	3628	1/1	0.98	0.09	28,28,28,28	0
57	MG	1A	3999	1/1	0.98	0.08	11,11,11,11	0
57	MG	1A	3046	1/1	0.98	0.07	15,15,15,15	0
57	MG	1A	3382	1/1	0.98	0.14	26,26,26,26	0
57	MG	1A	3631	1/1	0.98	0.04	8,8,8,8	0
57	MG	2A	3173	1/1	0.98	0.07	39,39,39,39	0
57	MG	1A	3456	1/1	0.98	0.07	46,46,46,46	0
57	MG	1A	3106	1/1	0.98	0.13	21,21,21,21	0
57	MG	1A	3072	1/1	0.98	0.19	31,31,31,31	0
57	MG	2A	3009	1/1	0.98	0.05	32,32,32,32	0
57	MG	2A	3708	1/1	0.98	0.05	31,31,31,31	0
57	MG	1A	3540	1/1	0.98	0.12	18,18,18,18	0
57	MG	1A	3877	1/1	0.98	0.06	41,41,41,41	0
57	MG	1A	3751	1/1	0.98	0.08	48,48,48,48	0
57	MG	1A	3109	1/1	0.98	0.15	29,29,29,29	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1A	3157	1/1	0.98	0.23	22,22,22,22	0
57	MG	1A	3641	1/1	0.98	0.06	20,20,20,20	0
57	MG	1A	3882	1/1	0.98	0.06	29,29,29,29	0
57	MG	1A	3027	1/1	0.98	0.21	24,24,24,24	0
57	MG	2A	3018	1/1	0.98	0.08	36,36,36,36	0
57	MG	1U	206	1/1	0.98	0.07	24,24,24,24	0
57	MG	1A	4016	1/1	0.98	0.09	14,14,14,14	0
57	MG	1A	3111	1/1	0.98	0.22	18,18,18,18	0
57	MG	1A	3325	1/1	0.98	0.29	26,26,26,26	0
57	MG	1A	3546	1/1	0.98	0.17	16,16,16,16	0
57	MG	1A	3465	1/1	0.98	0.15	21,21,21,21	0
57	MG	1A	4021	1/1	0.98	0.07	23,23,23,23	0
57	MG	1A	3112	1/1	0.98	0.15	33,33,33,33	0
57	MG	2A	3726	1/1	0.98	0.05	34,34,34,34	0
57	MG	2A	3027	1/1	0.98	0.16	35,35,35,35	0
57	MG	2A	3542	1/1	0.98	0.09	21,21,21,21	0
57	MG	1W	201	1/1	0.98	0.23	30,30,30,30	0
57	MG	1A	3075	1/1	0.98	0.14	26,26,26,26	0
57	MG	1A	3890	1/1	0.98	0.05	18,18,18,18	0
57	MG	1A	3891	1/1	0.98	0.12	31,31,31,31	0
57	MG	1A	3017	1/1	0.98	0.08	47,47,47,47	0
57	MG	1A	3893	1/1	0.98	0.09	24,24,24,24	0
57	MG	2A	3202	1/1	0.98	0.19	41,41,41,41	0
57	MG	1A	3651	1/1	0.98	0.05	12,12,12,12	0
59	ZN	1n	103	1/1	0.98	0.04	76,76,76,76	0
59	ZN	2Y	202	1/1	0.98	0.04	83,83,83,83	0
57	MG	1A	3029	1/1	0.98	0.14	19,19,19,19	0
57	MG	1A	3218	1/1	0.98	0.20	31,31,31,31	0
57	MG	1X	103	1/1	0.98	0.08	35,35,35,35	0
60	SF4	2d	303	8/8	0.98	0.05	56,61,73,74	0
57	MG	1A	3523	1/1	0.99	0.09	21,21,21,21	0
57	MG	1A	3155	1/1	0.99	0.13	16,16,16,16	0
57	MG	1A	3433	1/1	0.99	0.06	38,38,38,38	0
57	MG	1U	201	1/1	0.99	0.26	23,23,23,23	0
57	MG	1U	202	1/1	0.99	0.30	20,20,20,20	0
57	MG	1U	203	1/1	0.99	0.21	25,25,25,25	0
57	MG	1A	3079	1/1	0.99	0.09	20,20,20,20	0
57	MG	1A	3749	1/1	0.99	0.06	9,9,9,9	0
57	MG	1A	3464	1/1	0.99	0.24	18,18,18,18	0
57	MG	2A	3114	1/1	0.99	0.08	18,18,18,18	0
57	MG	1A	3667	1/1	0.99	0.07	21,21,21,21	0
57	MG	1A	3030	1/1	0.99	0.15	22,22,22,22	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1U	209	1/1	0.99	0.07	21,21,21,21	0
57	MG	1A	3127	1/1	0.99	0.14	22,22,22,22	0
57	MG	1V	201	1/1	0.99	0.19	17,17,17,17	0
57	MG	1a	1746	1/1	0.99	0.07	23,23,23,23	0
57	MG	1A	3901	1/1	0.99	0.04	18,18,18,18	0
57	MG	1V	203	1/1	0.99	0.15	22,22,22,22	0
57	MG	1A	3274	1/1	0.99	0.14	18,18,18,18	0
57	MG	1A	3755	1/1	0.99	0.03	11,11,11,11	0
57	MG	1A	3802	1/1	0.99	0.04	35,35,35,35	0
57	MG	1A	3107	1/1	0.99	0.06	25,25,25,25	0
57	MG	1A	3073	1/1	0.99	0.09	23,23,23,23	0
57	MG	1A	3130	1/1	0.99	0.03	25,25,25,25	0
57	MG	1A	3634	1/1	0.99	0.03	23,23,23,23	0
57	MG	1W	205	1/1	0.99	0.10	27,27,27,27	0
57	MG	1W	206	1/1	0.99	0.06	23,23,23,23	0
57	MG	1A	4009	1/1	0.99	0.07	7,7,7,7	0
57	MG	1A	3635	1/1	0.99	0.06	12,12,12,12	0
57	MG	1A	3636	1/1	0.99	0.06	12,12,12,12	0
57	MG	2A	3557	1/1	0.99	0.07	28,28,28,28	0
57	MG	1A	3204	1/1	0.99	0.07	23,23,23,23	0
57	MG	1A	4013	1/1	0.99	0.06	34,34,34,34	0
57	MG	1A	3144	1/1	0.99	0.16	17,17,17,17	0
57	MG	1A	3861	1/1	0.99	0.10	28,28,28,28	0
57	MG	1A	3764	1/1	0.99	0.05	24,24,24,24	0
57	MG	1A	3145	1/1	0.99	0.24	27,27,27,27	0
57	MG	1A	3061	1/1	0.99	0.11	27,27,27,27	0
57	MG	1A	3132	1/1	0.99	0.11	20,20,20,20	0
57	MG	1A	3186	1/1	0.99	0.14	24,24,24,24	0
57	MG	1A	3683	1/1	0.99	0.03	15,15,15,15	0
57	MG	1A	3148	1/1	0.99	0.05	23,23,23,23	0
57	MG	1A	3285	1/1	0.99	0.10	14,14,14,14	0
57	MG	1A	4024	1/1	0.99	0.04	35,35,35,35	0
57	MG	1A	3819	1/1	0.99	0.08	43,43,43,43	0
57	MG	1A	3012	1/1	0.99	0.04	21,21,21,21	0
57	MG	1A	3575	1/1	0.99	0.04	24,24,24,24	0
57	MG	1A	3450	1/1	0.99	0.15	25,25,25,25	0
57	MG	1A	3648	1/1	0.99	0.03	16,16,16,16	0
57	MG	2A	3433	1/1	0.99	0.11	15,15,15,15	0
57	MG	1A	3019	1/1	0.99	0.17	30,30,30,30	0
57	MG	1A	3151	1/1	0.99	0.17	27,27,27,27	0
57	MG	1A	3170	1/1	0.99	0.16	20,20,20,20	0
57	MG	1P	201	1/1	0.99	0.21	21,21,21,21	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1P	202	1/1	0.99	0.25	23,23,23,23	0
57	MG	1D	301	1/1	0.99	0.10	18,18,18,18	0
57	MG	1A	3580	1/1	0.99	0.09	8,8,8,8	0
57	MG	2A	3584	1/1	0.99	0.08	24,24,24,24	0
57	MG	2A	3585	1/1	0.99	0.08	29,29,29,29	0
57	MG	1Q	202	1/1	0.99	0.07	29,29,29,29	0
57	MG	2A	3811	1/1	0.99	0.10	43,43,43,43	0
57	MG	1A	3215	1/1	0.99	0.07	27,27,27,27	0
57	MG	2a	1711	1/1	0.99	0.03	49,49,49,49	0
57	MG	1A	3829	1/1	0.99	0.14	23,23,23,23	0
57	MG	1A	3093	1/1	0.99	0.17	13,13,13,13	0
57	MG	1A	3517	1/1	0.99	0.14	23,23,23,23	0
57	MG	1A	3005	1/1	0.99	0.07	28,28,28,28	0
57	MG	1R	201	1/1	0.99	0.05	36,36,36,36	0
57	MG	1A	3034	1/1	0.99	0.16	15,15,15,15	0
57	MG	1A	3658	1/1	0.99	0.06	30,30,30,30	0
59	ZN	1Y	204	1/1	0.99	0.03	55,55,55,55	0
57	MG	1R	204	1/1	0.99	0.08	25,25,25,25	0
59	ZN	15	108	1/1	0.99	0.09	44,44,44,44	0
59	ZN	16	102	1/1	0.99	0.07	42,42,42,42	0
59	ZN	19	102	1/1	0.99	0.04	31,31,31,31	0
57	MG	1D	310	1/1	0.99	0.15	13,13,13,13	0
57	MG	1A	3267	1/1	0.99	0.17	21,21,21,21	0
57	MG	1A	3788	1/1	0.99	0.05	41,41,41,41	0
59	ZN	25	107	1/1	0.99	0.05	41,41,41,41	0
59	ZN	26	102	1/1	0.99	0.03	52,52,52,52	0
59	ZN	29	501	1/1	0.99	0.04	50,50,50,50	0
57	MG	2A	3748	1/1	0.99	0.04	46,46,46,46	0
57	MG	1A	3195	1/1	0.99	0.03	29,29,29,29	0
57	MG	1A	3174	1/1	0.99	0.02	17,17,17,17	0
57	MG	1A	3868	1/1	1.00	0.04	20,20,20,20	0
57	MG	1A	3765	1/1	1.00	0.05	13,13,13,13	0
57	MG	1A	3693	1/1	1.00	0.06	9,9,9,9	0
57	MG	2A	3695	1/1	1.00	0.05	20,20,20,20	0
57	MG	1A	3839	1/1	1.00	0.02	16,16,16,16	0
57	MG	1A	3846	1/1	1.00	0.06	15,15,15,15	0
57	MG	1A	3867	1/1	1.00	0.01	12,12,12,12	0

6.5 Other polymers ⓘ

There are no such residues in this entry.