



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 11:50 AM UTC

PDB ID : 4ZER / pdb_00004zer
Title : Crystal structure of the Onc112 antimicrobial peptide bound to the *Thermus thermophilus* 70S ribosome
Authors : Seefeldt, A.C.; Nguyen, F.; Antunes, S.; Perebaskine, N.; Graf, M.; Arenz, S.; Inampudi, K.K.; Douat, C.; Guichard, G.; Wilson, D.N.; Innis, C.A.
Deposited on : 2015-04-20
Resolution : 3.10 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

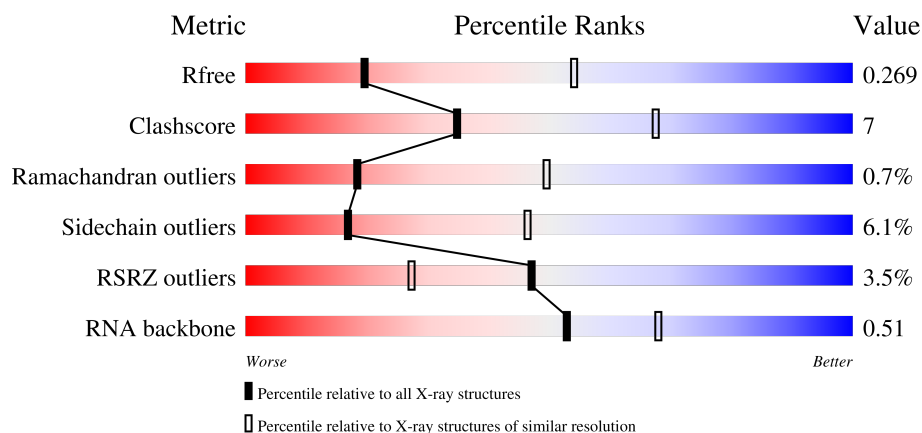
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.10 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.



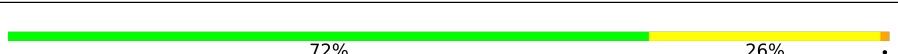
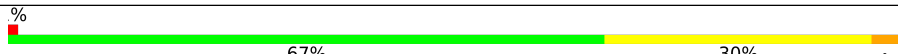
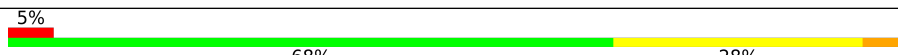
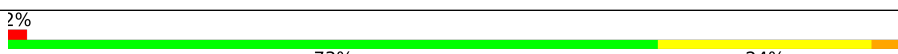
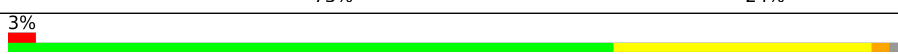
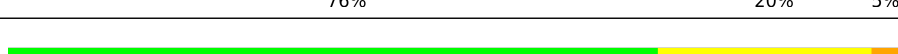
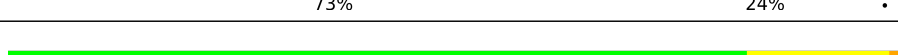
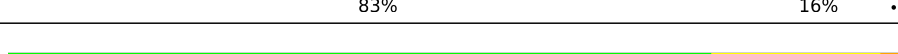
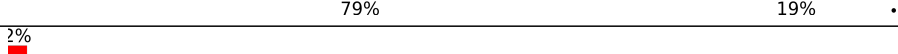
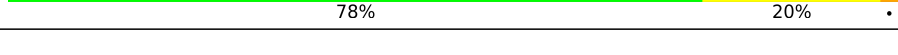
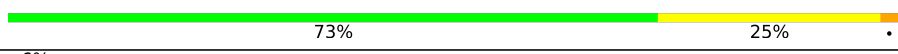
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1456 (3.10-3.10)
Clashscore	190562	1539 (3.10-3.10)
Ramachandran outliers	187476	1467 (3.10-3.10)
Sidechain outliers	187428	1467 (3.10-3.10)
RSRZ outliers	180081	1456 (3.10-3.10)
RNA backbone	3983	1022 (3.32-2.88)

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	3% 63% 29% 5%
1	2A	2915	4% 62% 30% 7%
2	1B	120	63% 32%
2	2B	120	70% 27%

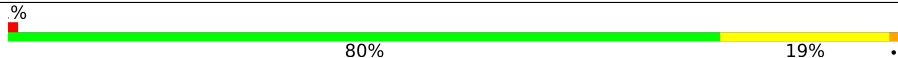
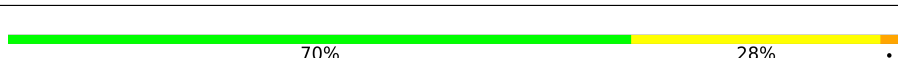
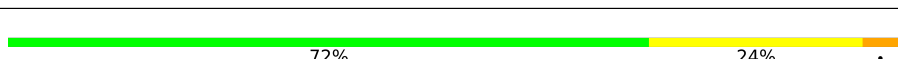
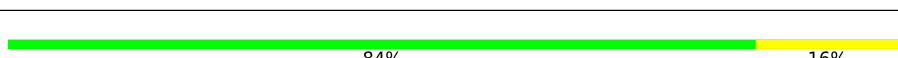
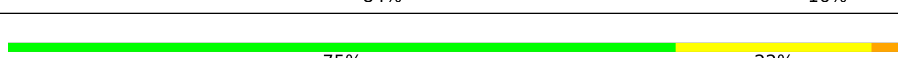
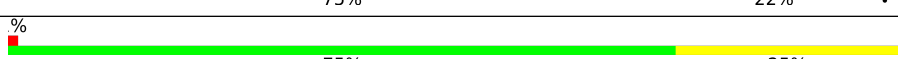
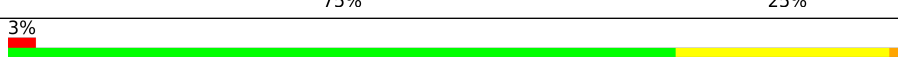
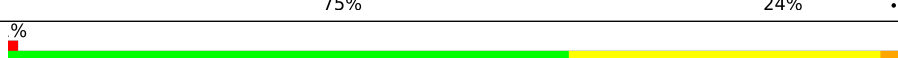
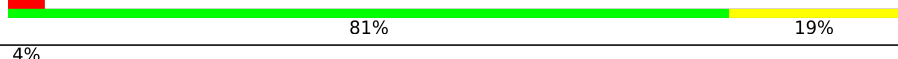
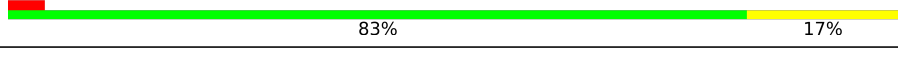
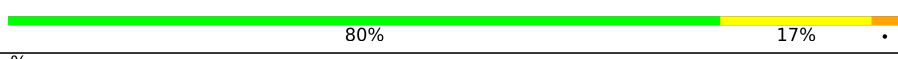
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Mol	Chain	Length	Quality of chain
3	1D	275	
3	2D	275	
4	1E	204	
4	2E	204	
5	1F	203	
5	2F	203	
6	1G	181	
6	2G	181	
7	1H	174	
7	2H	174	
8	1I	147	
8	2I	147	
9	1N	140	
9	2N	140	
10	1O	122	
10	2O	122	
11	1P	149	
11	2P	149	
12	1Q	141	
12	2Q	141	
13	1R	118	
13	2R	118	
14	1S	110	
14	2S	110	
15	1T	131	

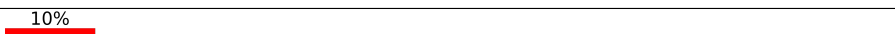
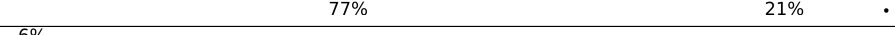
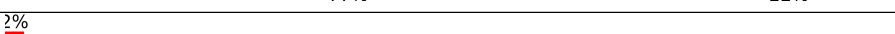
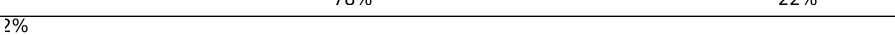
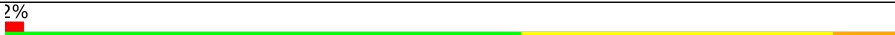
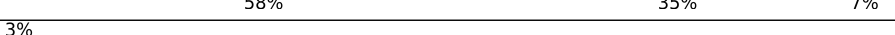
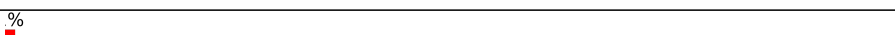
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Mol	Chain	Length	Quality of chain	
15	2T	131		
16	1U	116		.
16	2U	116		.
17	1V	101		.
17	2V	101		.
18	1W	112		
18	2W	112		.
19	1X	95		
19	2X	95		.
20	1Y	107		.
20	2Y	107		.
21	1Z	203		.
21	2Z	203		..
22	10	77		.
22	20	77		
23	11	97		
23	21	97		
24	12	70		
24	22	70		
25	13	59		
25	23	59		.
26	14	69		.
26	24	69		
27	15	59		.
27	25	59		

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Mol	Chain	Length	Quality of chain
28	16	53	
28	26	53	
29	17	48	
29	27	48	
30	18	64	
30	28	64	
31	19	37	
31	29	37	
32	1a	1521	
32	2a	1521	
33	1b	231	
33	2b	231	
34	1c	206	
34	2c	206	
35	1d	208	
35	2d	208	
36	1e	148	
36	2e	148	
37	1f	100	
37	2f	100	
38	1g	155	
38	2g	155	
39	1h	137	
39	2h	137	
40	1i	127	

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Mol	Chain	Length	Quality of chain
40	2i	127	
41	1j	97	
41	2j	97	
42	1k	114	
42	2k	114	
43	1l	122	
43	2l	122	
44	1m	116	
44	2m	116	
45	1n	60	
45	2n	60	
46	1o	88	
46	2o	88	
47	1p	82	
47	2p	82	
48	1q	99	
48	2q	99	
49	1r	68	
49	2r	68	
50	1s	83	
50	2s	83	
51	1t	98	
51	2t	98	
52	1u	23	
52	2u	23	

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Mol	Chain	Length	Quality of chain
53	1x	76	
53	2x	76	
54	1y	19	
54	2y	19	
55	A	27	
55	B	27	

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
56	MG	1a	1667	-	-	-	X
56	MG	1a	1713	-	-	-	X
56	MG	1a	1732	-	-	-	X
56	MG	2A	3081	-	-	-	X
56	MG	2D	302	-	-	-	X
56	MG	2a	1606	-	-	-	X
56	MG	2a	1608	-	-	-	X
56	MG	2a	1630	-	-	-	X
56	MG	2a	1639	-	-	-	X
56	MG	2a	1640	-	-	-	X
56	MG	2a	1675	-	-	-	X
56	MG	2p	101	-	-	-	X

2 Entry composition [i](#)

There are 63 unique types of molecules in this entry. The entry contains 293672 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	2824	Total	C	N	O	P	0	0	0
			60842	27081	11388	19550	2823			
1	2A	2869	Total	C	N	O	P	0	0	0
			61801	27510	11560	19864	2867			

- Molecule 2 is a RNA chain called 5s ribosomal RNA.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	10	77	Total	C	N	O	S	0	0	0
			608	375	129	103	1			
22	20	77	Total	C	N	O	S	0	0	0
			608	375	129	103	1			

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 32 is a RNA chain called 16s ribosomal RNA.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 53 is a RNA chain called tRNA met.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
53	1x	76	Total	C	N	O	P	S	0	0	0
			1625	725	294	529	76	1			
53	2x	76	Total	C	N	O	P	S	0	0	0
			1625	725	294	529	76	1			

- Molecule 54 is a protein called Onc112.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
54	1y	12	Total	C	N	O	0	0	0
			101	67	19	15			
54	2y	12	Total	C	N	O	0	0	0
			101	67	19	15			

- Molecule 55 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
55	A	3	Total	C	N	O	P	0	0	0
			65	29	12	21	3			
55	B	3	Total	C	N	O	P	0	0	0
			65	29	12	21	3			

- Molecule 56 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	1A	946	Total	Mg	0	0
			946	946		
56	1B	29	Total	Mg	0	0
			29	29		
56	1D	21	Total	Mg	0	0
			21	21		
56	1E	6	Total	Mg	0	0
			6	6		
56	1F	9	Total	Mg	0	0
			9	9		
56	1G	4	Total	Mg	0	0
			4	4		
56	1H	2	Total	Mg	0	0
			2	2		
56	1N	3	Total	Mg	0	0
			3	3		
56	1O	1	Total	Mg	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	1P	2	Total 2	Mg 2	0	0
56	1Q	4	Total 4	Mg 4	0	0
56	1R	4	Total 4	Mg 4	0	0
56	1T	2	Total 2	Mg 2	0	0
56	1U	5	Total 5	Mg 5	0	0
56	1V	3	Total 3	Mg 3	0	0
56	1W	3	Total 3	Mg 3	0	0
56	1X	1	Total 1	Mg 1	0	0
56	1Y	1	Total 1	Mg 1	0	0
56	1Z	1	Total 1	Mg 1	0	0
56	10	7	Total 7	Mg 7	0	0
56	11	3	Total 3	Mg 3	0	0
56	13	3	Total 3	Mg 3	0	0
56	15	3	Total 3	Mg 3	0	0
56	17	2	Total 2	Mg 2	0	0
56	18	1	Total 1	Mg 1	0	0
56	19	2	Total 2	Mg 2	0	0
56	1a	261	Total 261	Mg 261	0	0
56	1b	1	Total 1	Mg 1	0	0
56	1d	4	Total 4	Mg 4	0	0
56	1e	4	Total 4	Mg 4	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	1f	1	Total 1	Mg 1	0	0
56	1g	1	Total 1	Mg 1	0	0
56	1i	1	Total 1	Mg 1	0	0
56	1l	1	Total 1	Mg 1	0	0
56	1n	1	Total 1	Mg 1	0	0
56	1o	2	Total 2	Mg 2	0	0
56	1r	1	Total 1	Mg 1	0	0
56	1t	1	Total 1	Mg 1	0	0
56	1x	12	Total 12	Mg 12	0	0
56	2A	679	Total 679	Mg 679	0	0
56	2B	17	Total 17	Mg 17	0	0
56	2D	8	Total 8	Mg 8	0	0
56	2E	7	Total 7	Mg 7	0	0
56	2F	3	Total 3	Mg 3	0	0
56	2G	2	Total 2	Mg 2	0	0
56	2I	1	Total 1	Mg 1	0	0
56	2N	1	Total 1	Mg 1	0	0
56	2O	2	Total 2	Mg 2	0	0
56	2P	1	Total 1	Mg 1	0	0
56	2Q	2	Total 2	Mg 2	0	0
56	2R	1	Total 1	Mg 1	0	0

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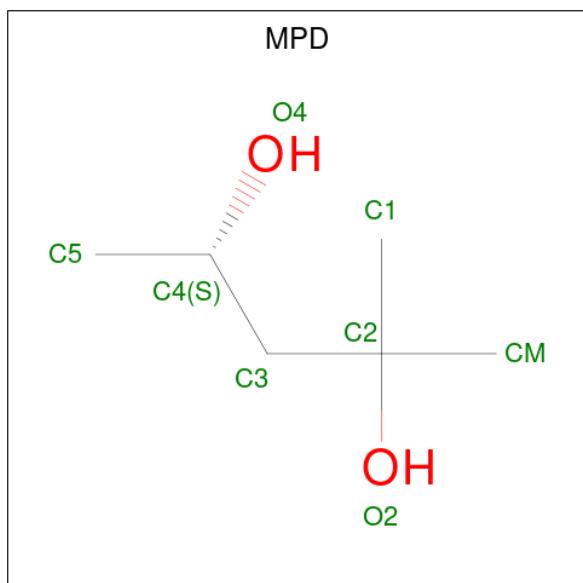
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	2T	4	Total 4	Mg 4	0	0
56	2U	2	Total 2	Mg 2	0	0
56	2V	3	Total 3	Mg 3	0	0
56	2W	1	Total 1	Mg 1	0	0
56	2X	1	Total 1	Mg 1	0	0
56	2Y	1	Total 1	Mg 1	0	0
56	20	1	Total 1	Mg 1	0	0
56	21	1	Total 1	Mg 1	0	0
56	23	1	Total 1	Mg 1	0	0
56	28	2	Total 2	Mg 2	0	0
56	2a	183	Total 183	Mg 183	0	0
56	2e	1	Total 1	Mg 1	0	0
56	2f	1	Total 1	Mg 1	0	0
56	2j	1	Total 1	Mg 1	0	0
56	2k	1	Total 1	Mg 1	0	0
56	2l	1	Total 1	Mg 1	0	0
56	2n	1	Total 1	Mg 1	0	0
56	2p	1	Total 1	Mg 1	0	0
56	2q	1	Total 1	Mg 1	0	0
56	2t	1	Total 1	Mg 1	0	0
56	2x	10	Total 10	Mg 10	0	0

- Molecule 57 is UNKNOWN ATOM OR ION (CCD ID: UNX) (formula: X).

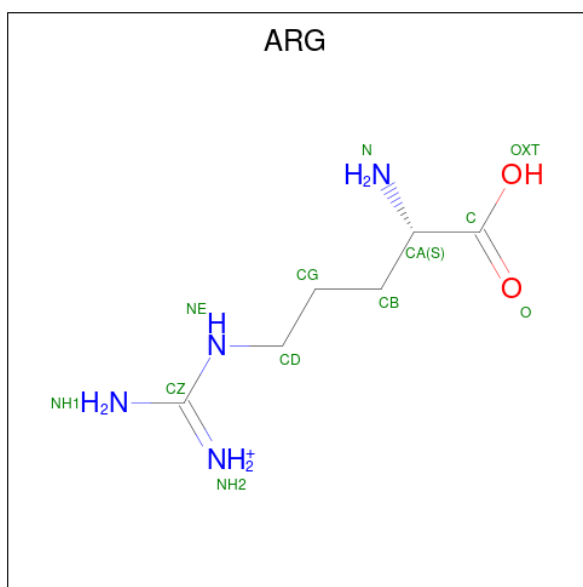
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
57	1A	1	Total	X	0	0
			1	1		
57	2A	1	Total	X	0	0
			1	1		

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



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

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



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

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

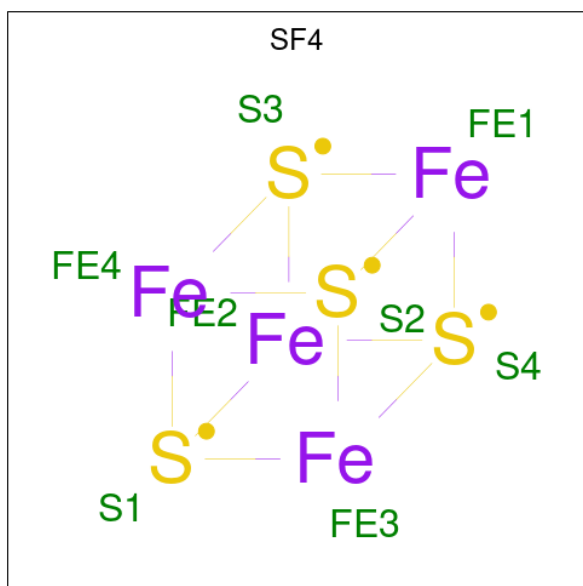
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
60	1Y	1	Total	Zn	0	0
			1	1		
60	14	1	Total	Zn	0	0
			1	1		
60	15	1	Total	Zn	0	0
			1	1		
60	16	1	Total	Zn	0	0
			1	1		
60	19	1	Total	Zn	0	0
			1	1		
60	1n	1	Total	Zn	0	0
			1	1		
60	2Y	1	Total	Zn	0	0
			1	1		
60	24	1	Total	Zn	0	0
			1	1		
60	25	1	Total	Zn	0	0
			1	1		
60	26	1	Total	Zn	0	0
			1	1		
60	29	1	Total	Zn	0	0
			1	1		

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

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



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

- Molecule 62 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
62	2A	1	Total	K	0	0
			1	1		

- Molecule 63 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
63	1A	1632	Total	O	0	0
			1632	1632		
63	1B	50	Total	O	0	0
			50	50		
63	1D	20	Total	O	0	0
			20	20		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
63	1E	17	Total	O	0	0
			17	17		
63	1F	14	Total	O	0	0
			14	14		
63	1G	5	Total	O	0	0
			5	5		
63	1H	4	Total	O	0	0
			4	4		
63	1N	7	Total	O	0	0
			7	7		
63	1O	2	Total	O	0	0
			2	2		
63	1P	18	Total	O	0	0
			18	18		
63	1Q	5	Total	O	0	0
			5	5		
63	1R	7	Total	O	0	0
			7	7		
63	1T	4	Total	O	0	0
			4	4		
63	1U	3	Total	O	0	0
			3	3		
63	1V	3	Total	O	0	0
			3	3		
63	1X	6	Total	O	0	0
			6	6		
63	1Y	2	Total	O	0	0
			2	2		
63	10	4	Total	O	0	0
			4	4		
63	11	3	Total	O	0	0
			3	3		
63	13	6	Total	O	0	0
			6	6		
63	15	2	Total	O	0	0
			2	2		
63	16	3	Total	O	0	0
			3	3		
63	18	7	Total	O	0	0
			7	7		
63	19	3	Total	O	0	0
			3	3		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
63	1a	369	Total 369	O 369	0	0
63	1c	1	Total 1	O 1	0	0
63	1d	6	Total 6	O 6	0	0
63	1e	3	Total 3	O 3	0	0
63	1f	1	Total 1	O 1	0	0
63	1h	1	Total 1	O 1	0	0
63	1l	3	Total 3	O 3	0	0
63	1m	1	Total 1	O 1	0	0
63	1n	1	Total 1	O 1	0	0
63	1o	2	Total 2	O 2	0	0
63	1p	1	Total 1	O 1	0	0
63	1t	1	Total 1	O 1	0	0
63	1x	2	Total 2	O 2	0	0
63	2A	1221	Total 1221	O 1221	0	0
63	2B	33	Total 33	O 33	0	0
63	2D	13	Total 13	O 13	0	0
63	2E	12	Total 12	O 12	0	0
63	2F	4	Total 4	O 4	0	0
63	2N	2	Total 2	O 2	0	0
63	2O	4	Total 4	O 4	0	0
63	2P	7	Total 7	O 7	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
63	2Q	5	Total 5	O 5	0	0
63	2R	2	Total 2	O 2	0	0
63	2T	2	Total 2	O 2	0	0
63	2U	3	Total 3	O 3	0	0
63	2X	4	Total 4	O 4	0	0
63	2Y	1	Total 1	O 1	0	0
63	20	2	Total 2	O 2	0	0
63	21	2	Total 2	O 2	0	0
63	23	2	Total 2	O 2	0	0
63	25	1	Total 1	O 1	0	0
63	26	2	Total 2	O 2	0	0
63	28	5	Total 5	O 5	0	0
63	2a	305	Total 305	O 305	0	0
63	2d	3	Total 3	O 3	0	0
63	2e	1	Total 1	O 1	0	0
63	2j	2	Total 2	O 2	0	0
63	2l	1	Total 1	O 1	0	0
63	2n	1	Total 1	O 1	0	0
63	2p	1	Total 1	O 1	0	0
63	2r	1	Total 1	O 1	0	0
63	2t	1	Total 1	O 1	0	0

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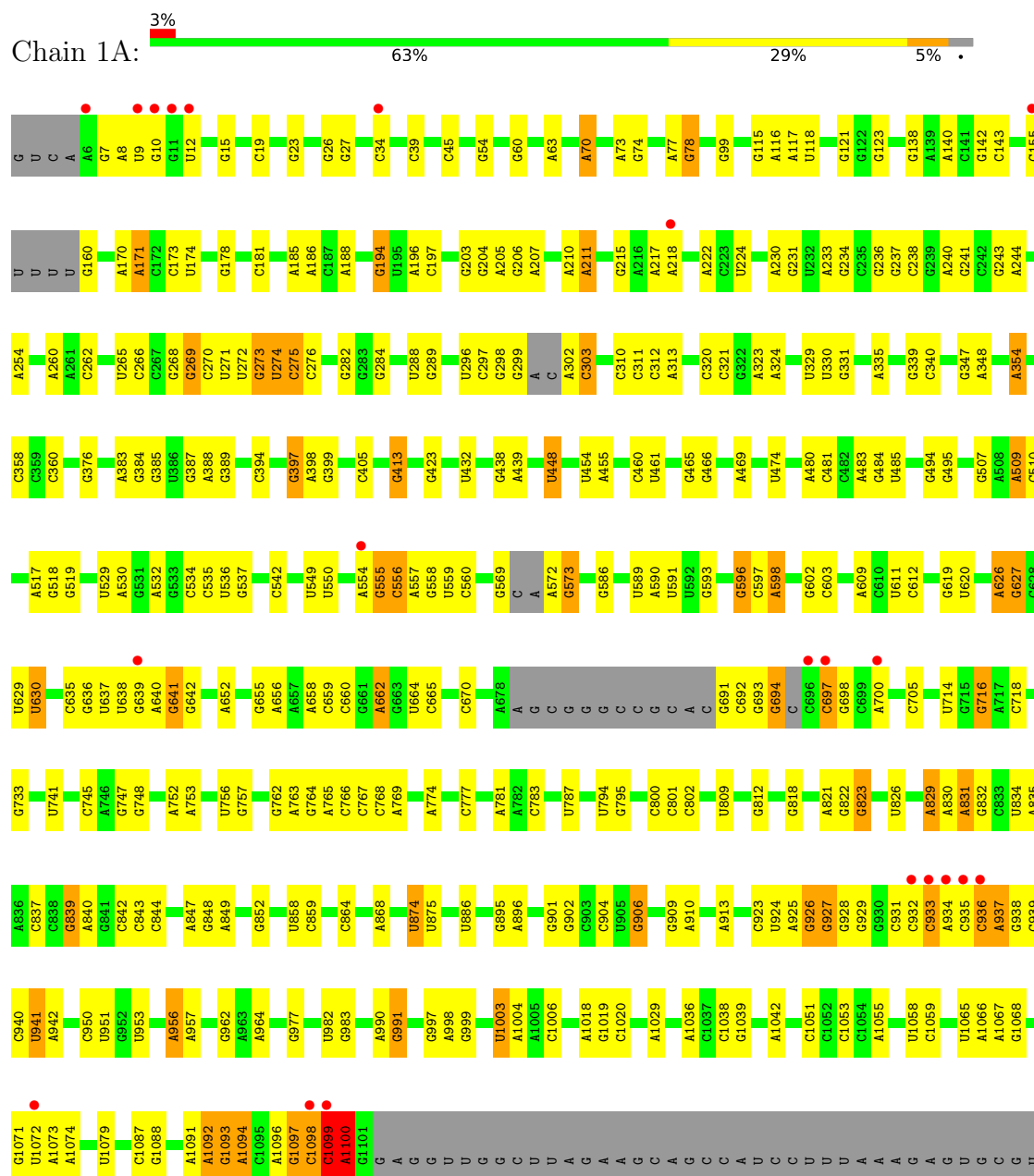
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
63	2x	2	Total	O	0	0
			2	2		
63	A	1	Total	O	0	0
			1	1		

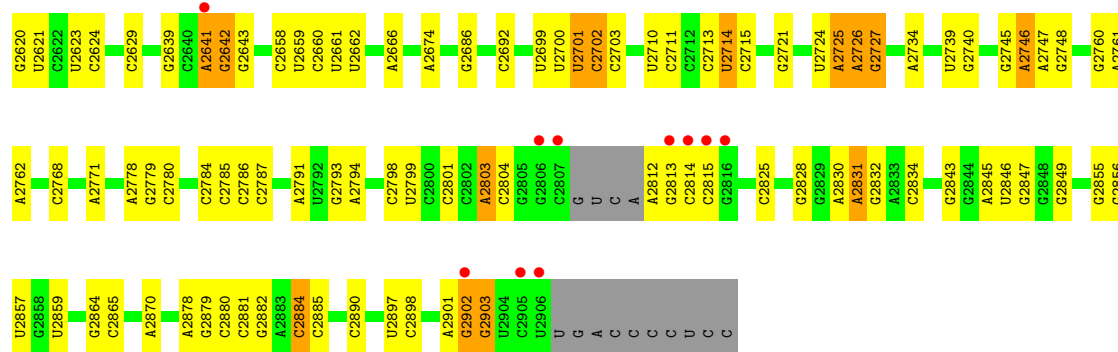
3 Residue-property plots [i](#)

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

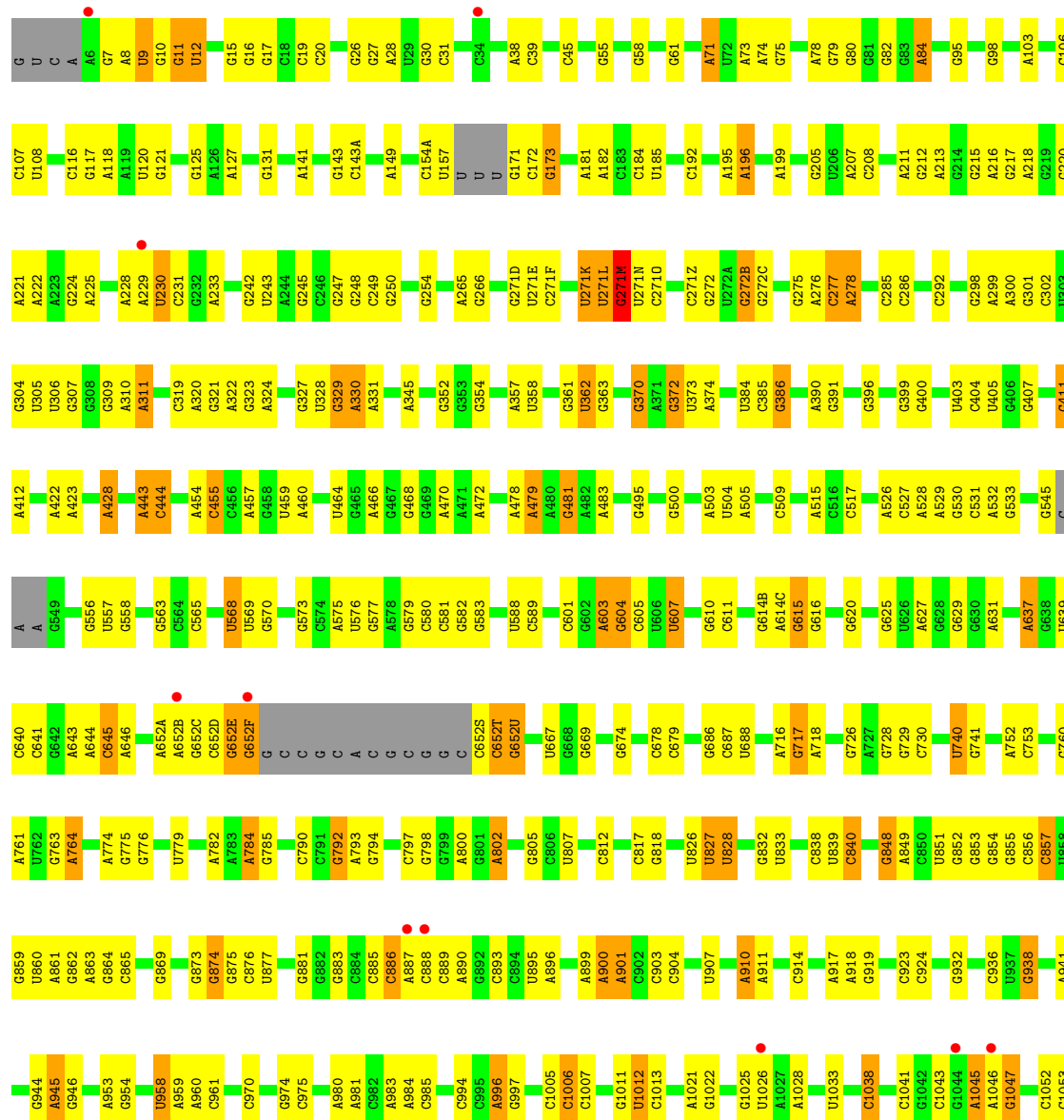
- Molecule 1: 23s ribosomal RNA



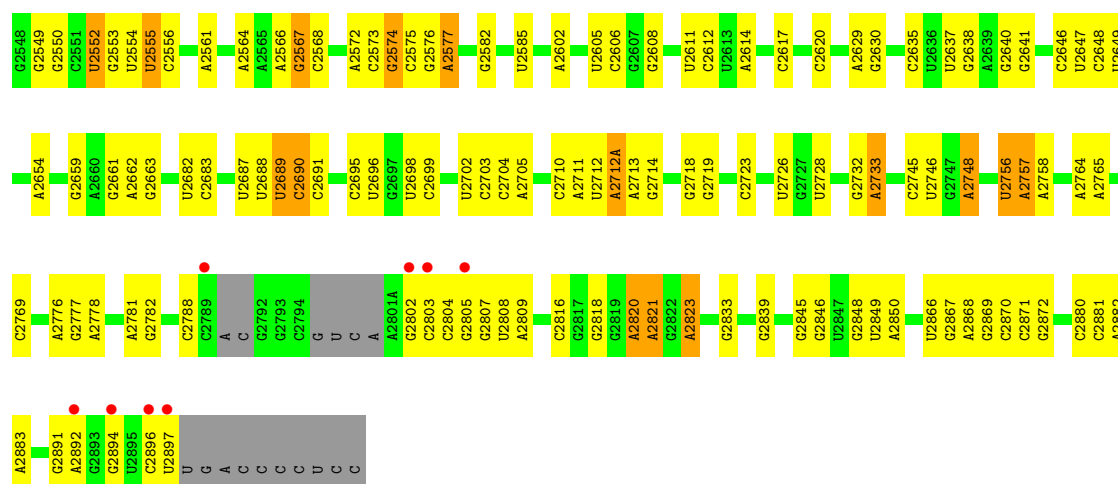
G2510	G2395	A2300	G2307	G2145	A2052	U1933	A1701	A1575	G1473	C1361	G1232	A
G2511	G2396	G2301	G2208	G2146	A2053	A1934	C1704	A1579	C1474	U1362	U1233	A
G2512	G2397	G2302	G2209	G2147	A2054	A1935	C1705	G	A1234	A1363	A1234	U
G2513	G2398	G2303	G2210	A2148	A2055	C1936	C1706	U	C1245	G1378	C1245	A
G2514	U2402	G2304	G2211	G2149	G2060	U1937	G1710	A	C1246	U1386	G1246	C
G2515	G2405	G2305	G2212	G2150	G2061	A1938	A1711	C	C1247	U1387	C1247	U
G2516	A2406	G2306	G2213	G2151	C2062	U1939	A1712	G1584	G1248	U1388	G1248	C
G2517	G2407	G2307	G2214	U2152	U2063	A1940	G1713	G1585		G1389		
U2518		U2308	G2215	G2153	G2064	A1941	A1715	G1586		G1390		
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G2541		A2332	G2232	C2163		A1958	A1736	A1605		U1286		
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- Molecule 1: 23s ribosomal RNA

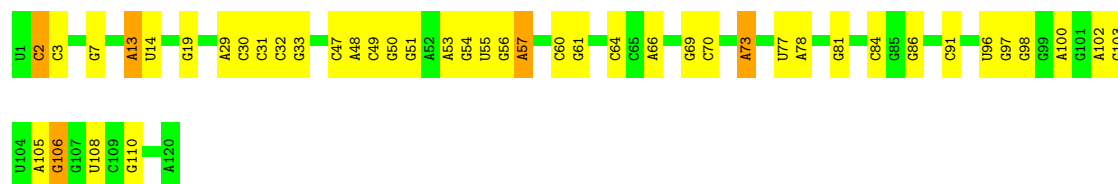


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• Molecule 2: 5s ribosomal RNA

Chain 1B: 63% 32% .



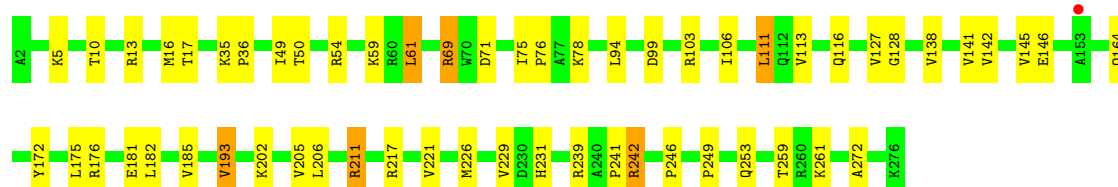
• Molecule 2: 5s ribosomal RNA

Chain 2B: 70% 27% .



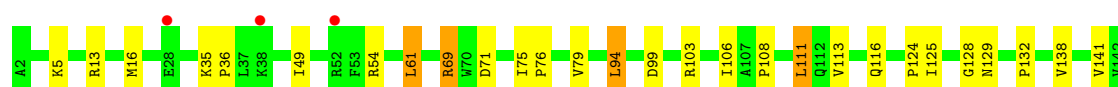
• Molecule 3: 50S ribosomal protein L2

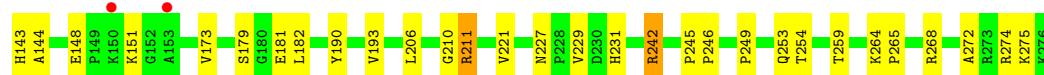
Chain 1D: 79% 19% .



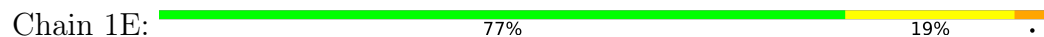
• Molecule 3: 50S ribosomal protein L2

Chain 2D: 2% 79% 19% .

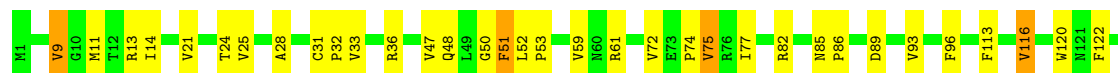
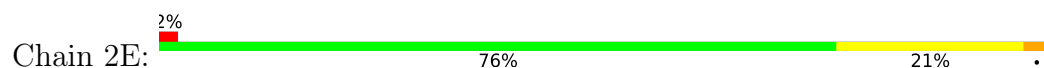




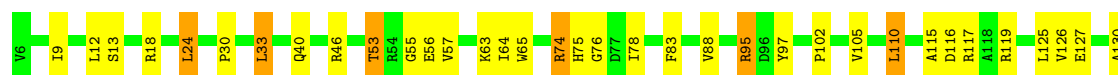
- Molecule 4: 50S ribosomal protein L3



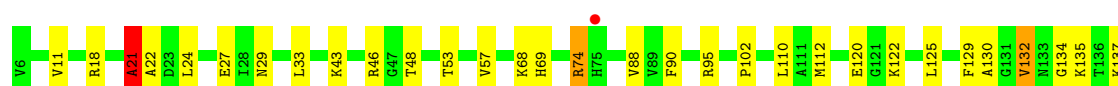
- Molecule 4: 50S ribosomal protein L3



- Molecule 5: 50S ribosomal protein L4

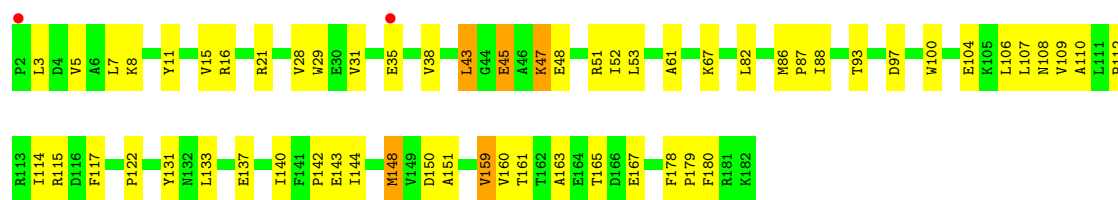


- Molecule 5: 50S ribosomal protein L4

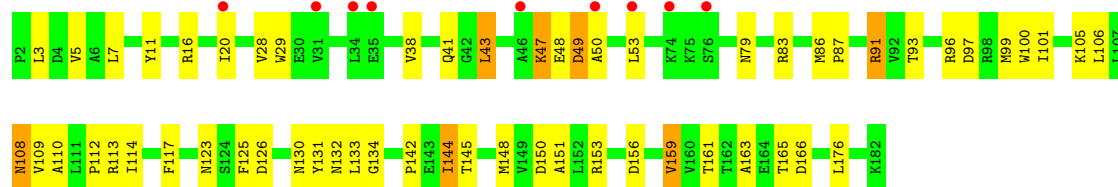


- Molecule 6: 50S ribosomal protein L5

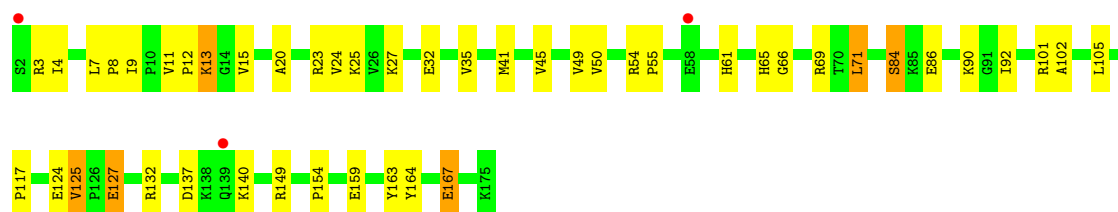
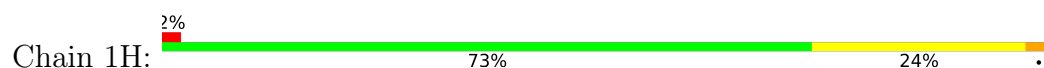




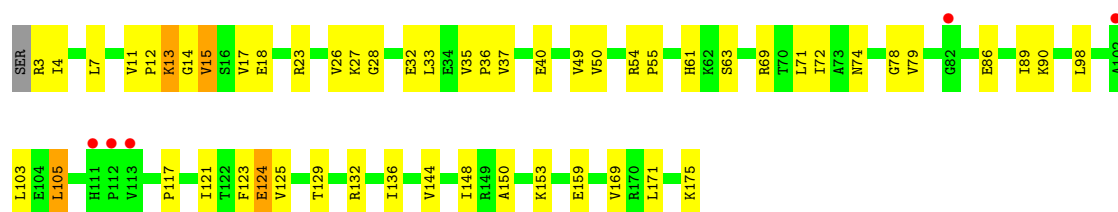
• Molecule 6: 50S ribosomal protein L5



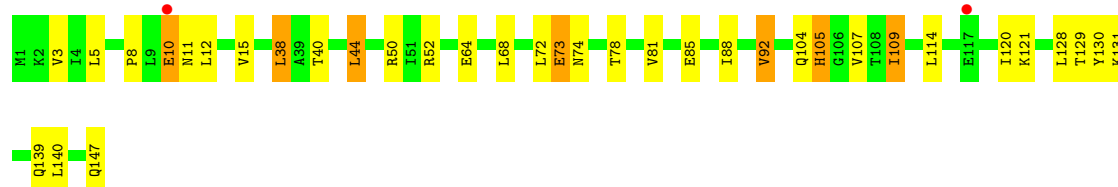
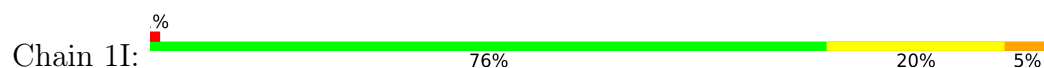
• Molecule 7: 50S ribosomal protein L6



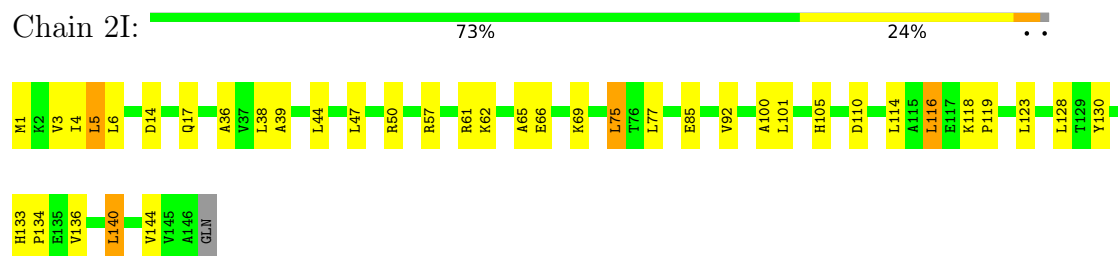
• Molecule 7: 50S ribosomal protein L6



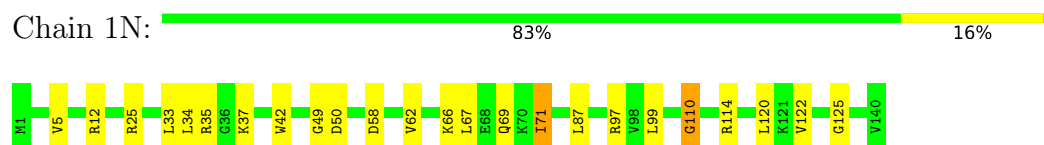
• Molecule 8: 50S ribosomal protein L9



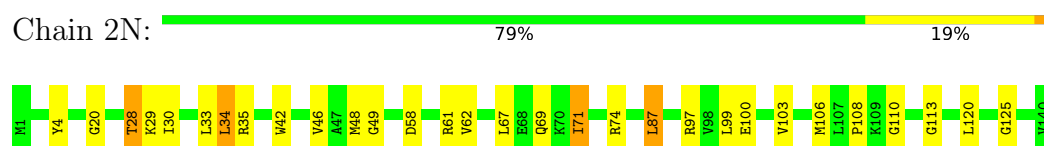
- Molecule 8: 50S ribosomal protein L9



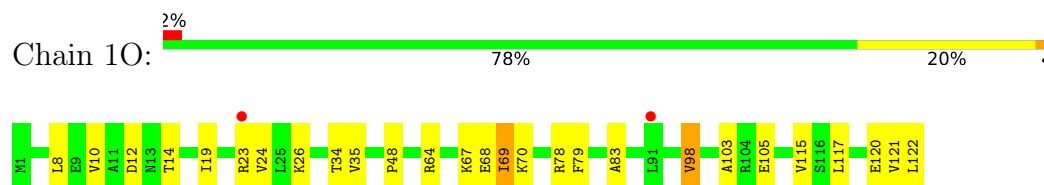
- Molecule 9: 50S ribosomal protein L13



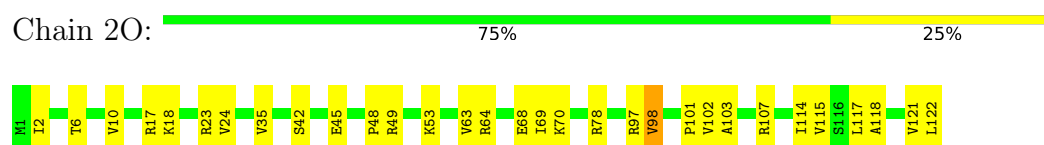
- Molecule 9: 50S ribosomal protein L13



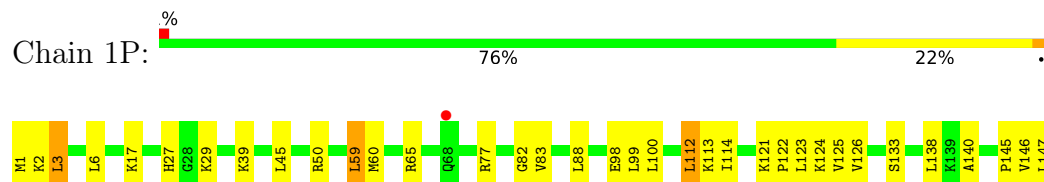
- Molecule 10: 50S ribosomal protein L14



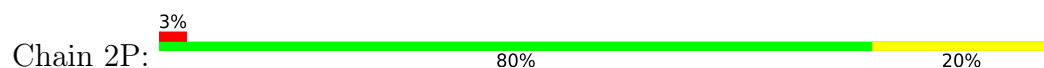
- Molecule 10: 50S ribosomal protein L14



- Molecule 11: 50S ribosomal protein L15

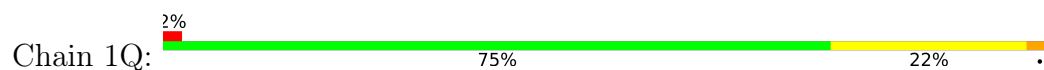


- Molecule 11: 50S ribosomal protein L15

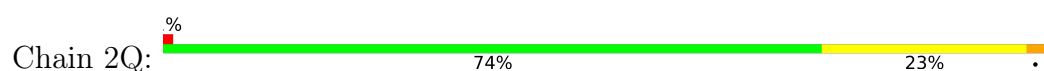




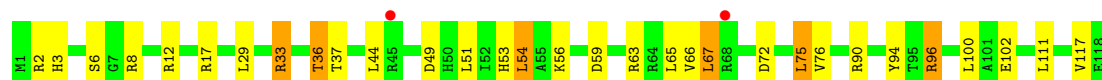
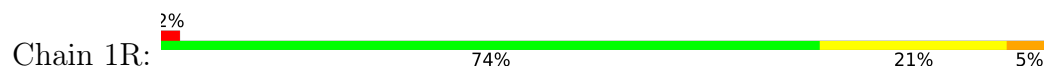
- Molecule 12: 50S ribosomal protein L16



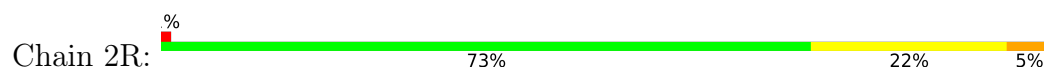
- Molecule 12: 50S ribosomal protein L16



- Molecule 13: 50S ribosomal protein L17



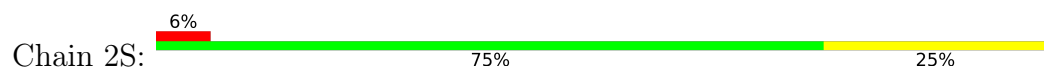
- Molecule 13: 50S ribosomal protein L17



- Molecule 14: 50S ribosomal protein L18

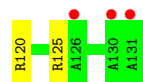
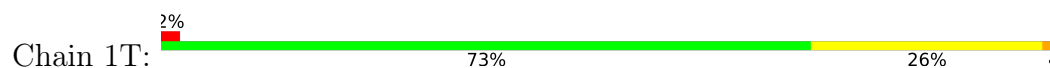


- Molecule 14: 50S ribosomal protein L18

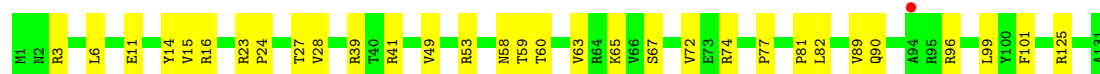
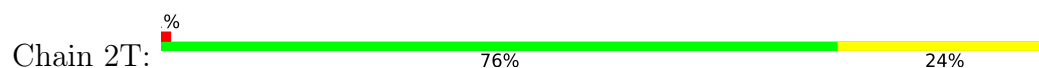




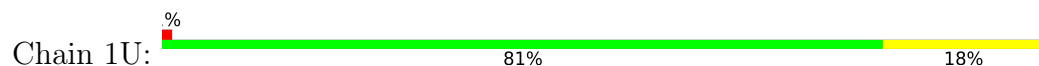
- Molecule 15: 50S ribosomal protein L19



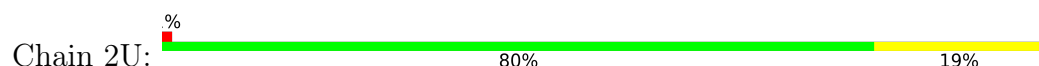
- Molecule 15: 50S ribosomal protein L19



- Molecule 16: 50S ribosomal protein L20



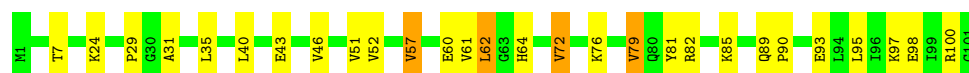
- Molecule 16: 50S ribosomal protein L20



- Molecule 17: 50S ribosomal protein L21

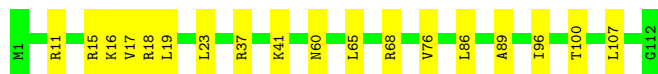


- Molecule 17: 50S ribosomal protein L21



- Molecule 18: 50S ribosomal protein L22

Chain 1W:  84% 16%



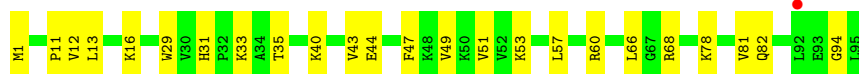
- Molecule 18: 50S ribosomal protein L22

Chain 2W:  75% 22% .



- Molecule 19: 50S ribosomal protein L23

Chain 1X:  % 75% 25%



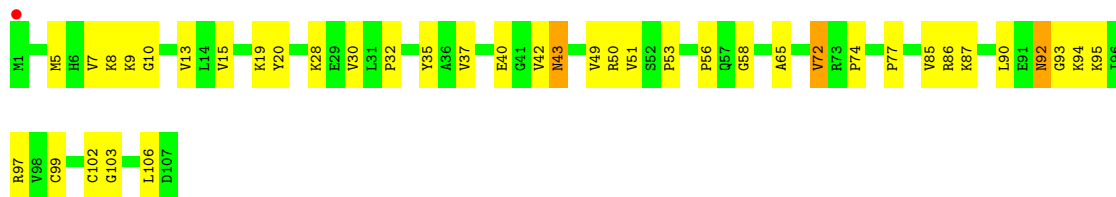
- Molecule 19: 50S ribosomal protein L23

Chain 2X:  3% 75% 24% .



- Molecule 20: 50S ribosomal protein L24

Chain 1Y:  % 63% 35%



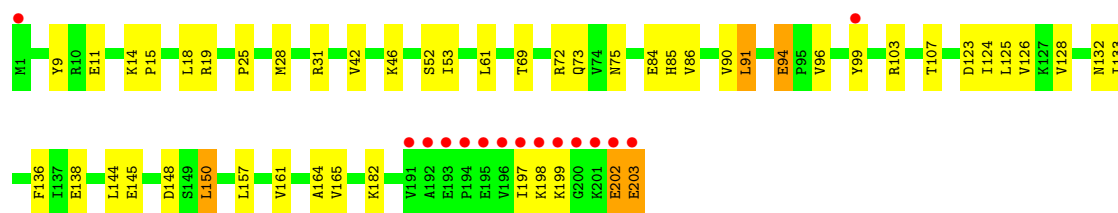
- Molecule 20: 50S ribosomal protein L24

Chain 2Y:  6% 69% 30% .

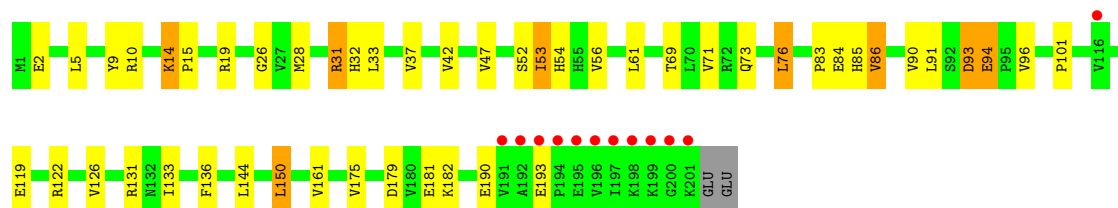
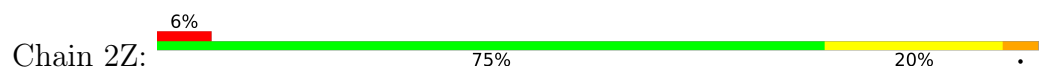


- Molecule 21: 50S ribosomal protein L25

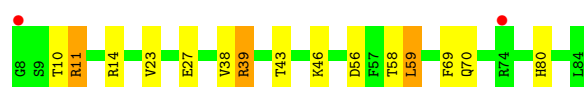
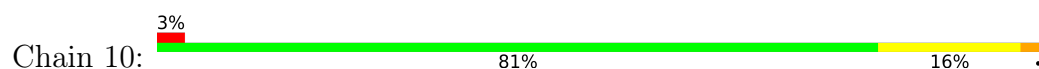
Chain 1Z:  7% 75% 23%



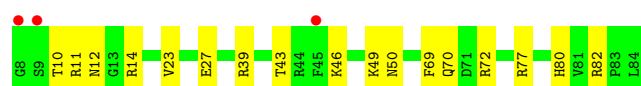
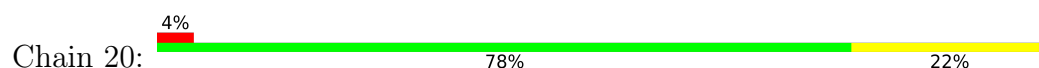
- Molecule 21: 50S ribosomal protein L25



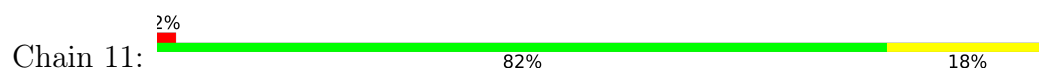
- Molecule 22: 50S ribosomal protein L27



- Molecule 22: 50S ribosomal protein L27



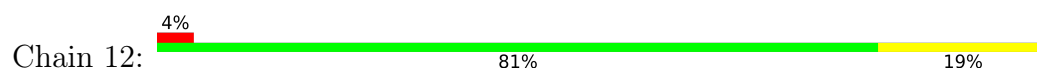
- Molecule 23: 50S ribosomal protein L28



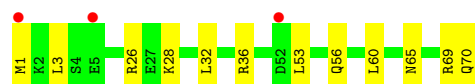
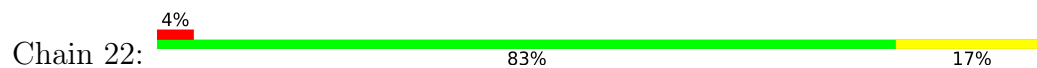
- Molecule 23: 50S ribosomal protein L28



- Molecule 24: 50S ribosomal protein L29



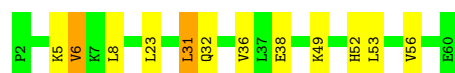
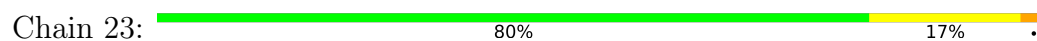
- Molecule 24: 50S ribosomal protein L29



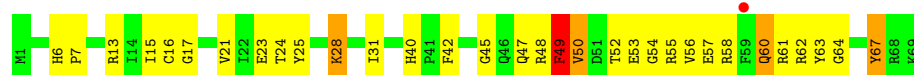
- Molecule 25: 50S ribosomal protein L30



- Molecule 25: 50S ribosomal protein L30



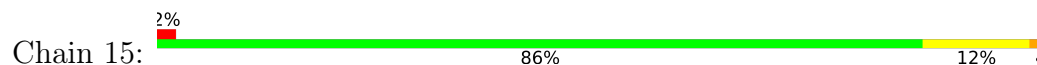
- Molecule 26: 50S ribosomal protein L31



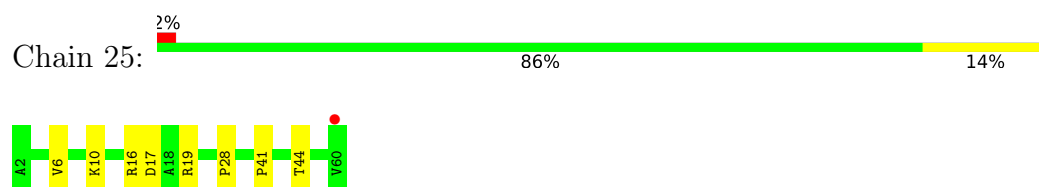
- Molecule 26: 50S ribosomal protein L31



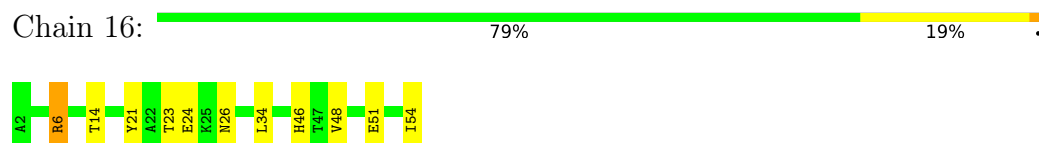
- Molecule 27: 50S ribosomal protein L32



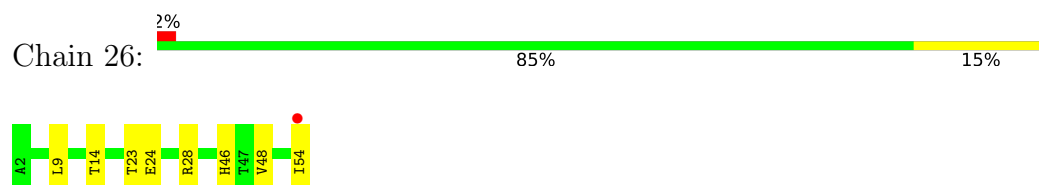
- Molecule 27: 50S ribosomal protein L32



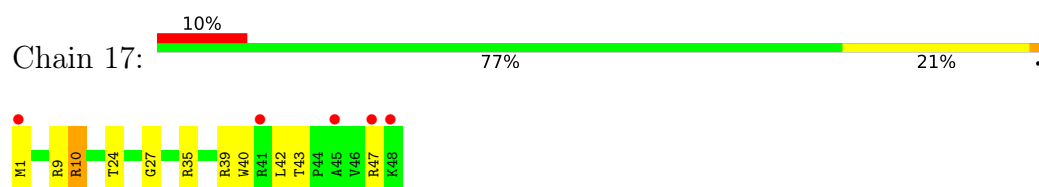
- Molecule 28: 50S ribosomal protein L33



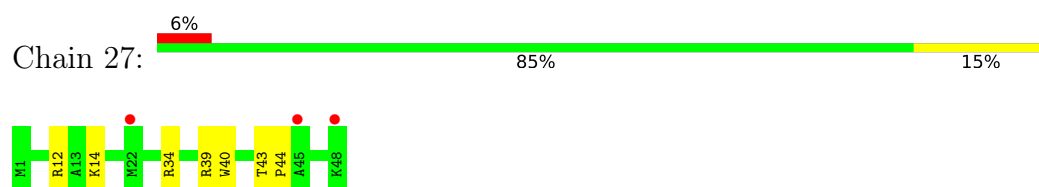
- Molecule 28: 50S ribosomal protein L33



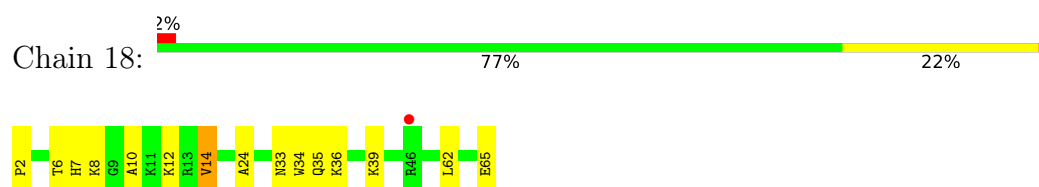
- Molecule 29: 50S ribosomal protein L34



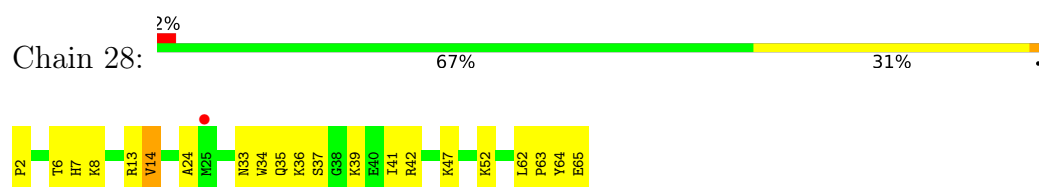
- Molecule 29: 50S ribosomal protein L34



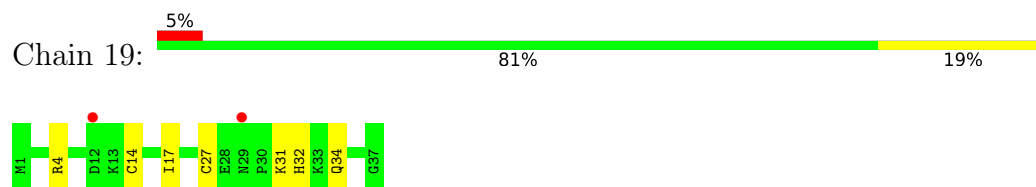
- Molecule 30: 50S ribosomal protein L35



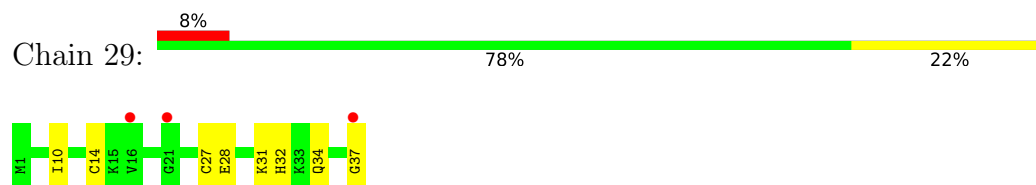
- Molecule 30: 50S ribosomal protein L35



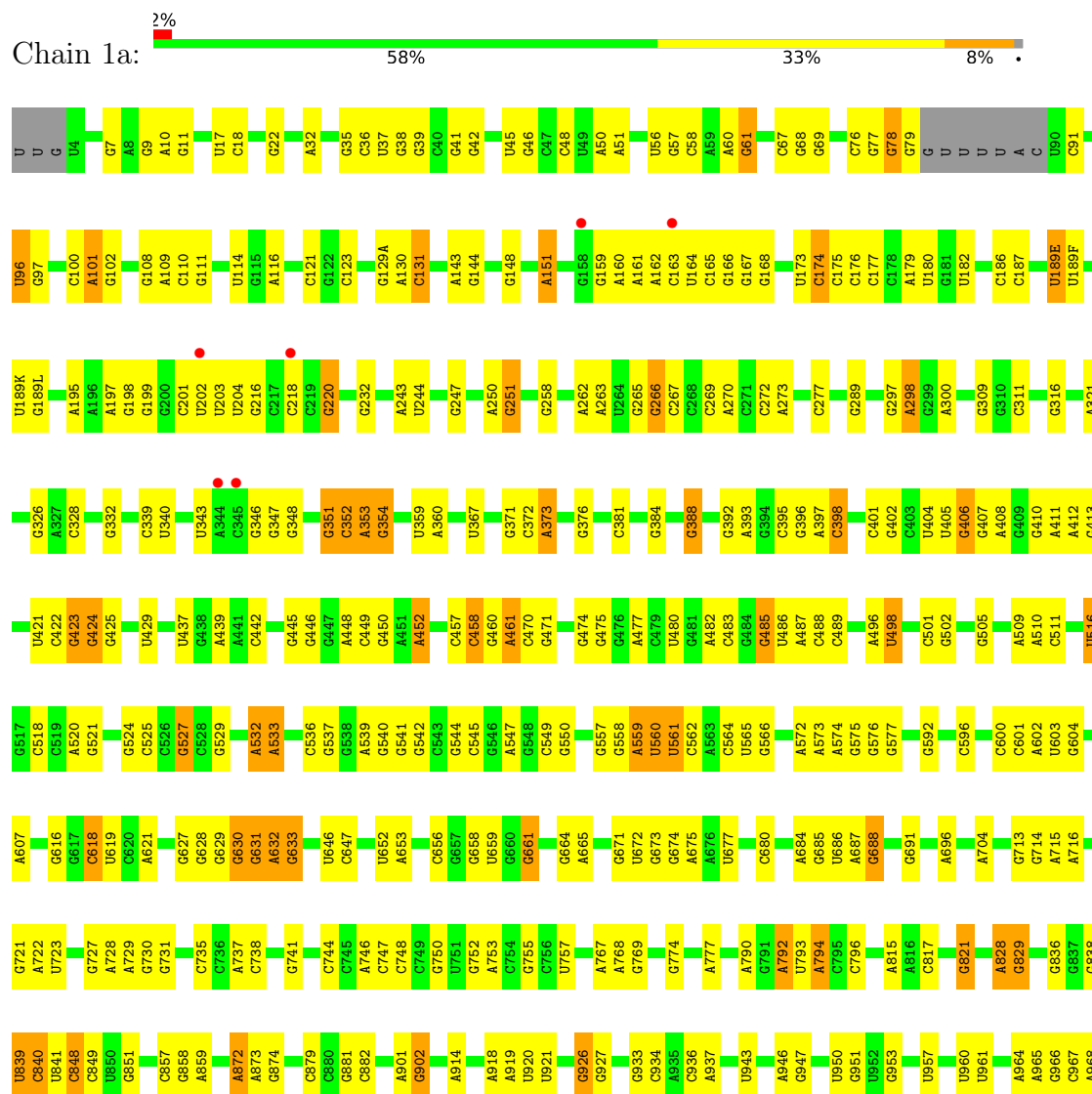
- Molecule 31: 50S ribosomal protein L36

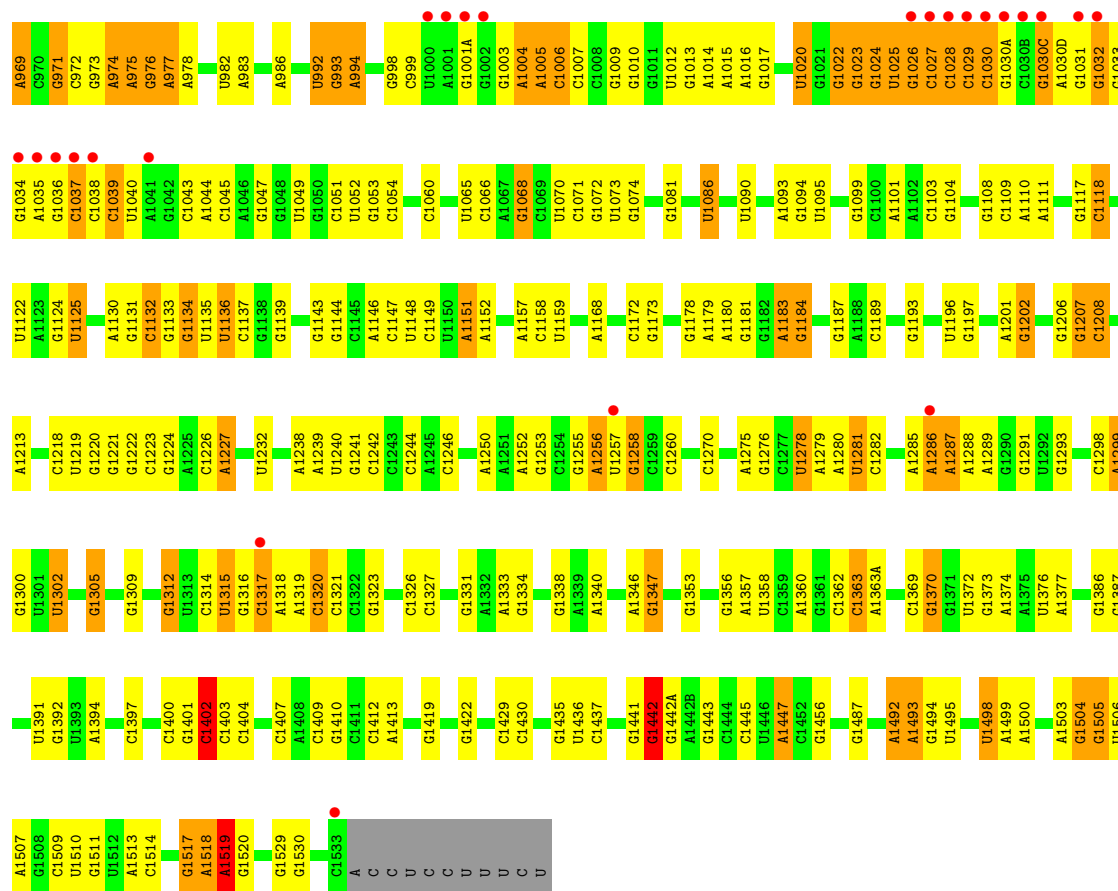


- Molecule 31: 50S ribosomal protein L36

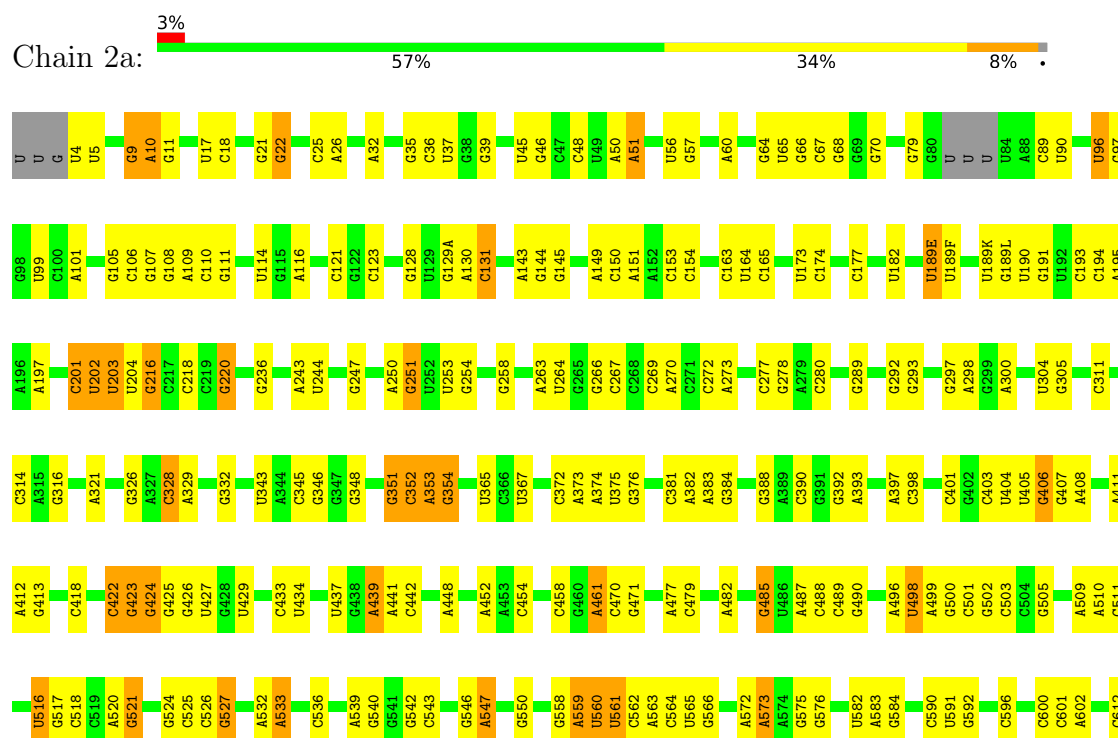


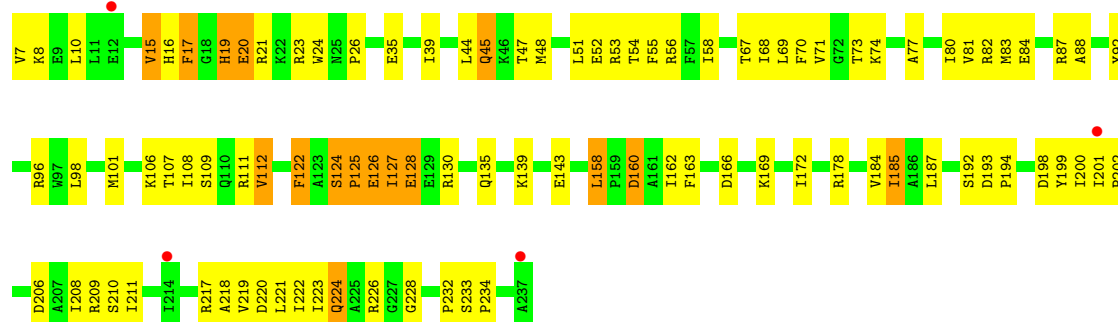
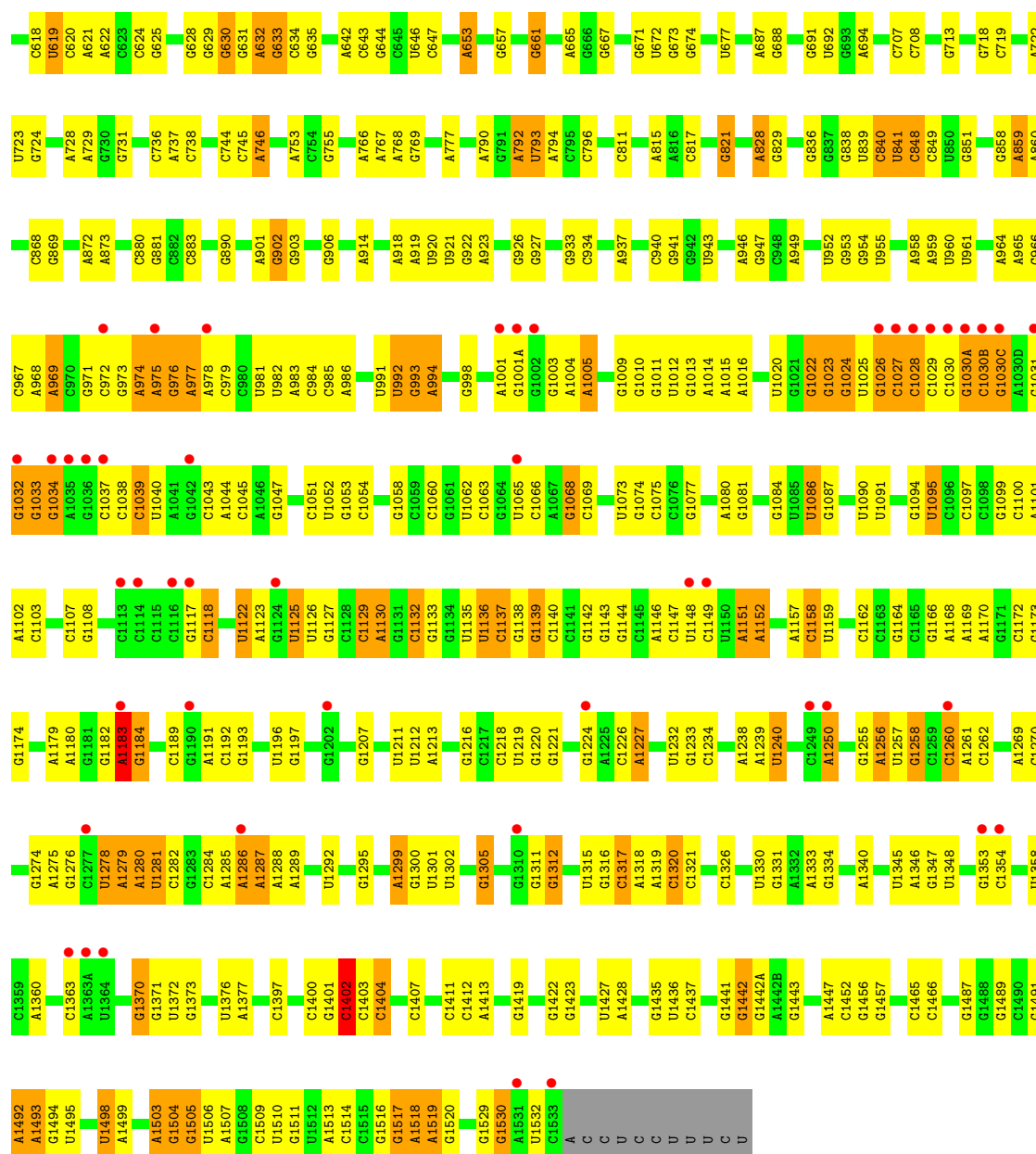
- Molecule 32: 16s ribosomal RNA



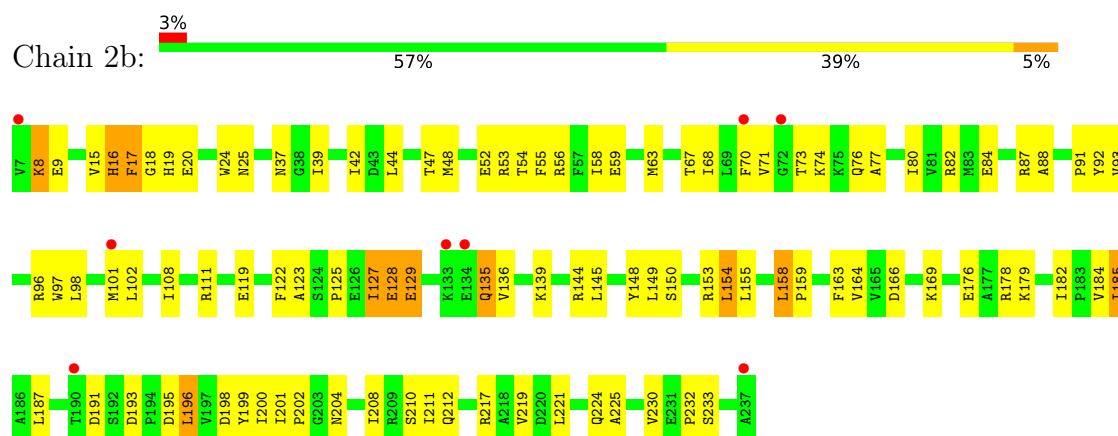


- Molecule 32: 16s ribosomal RNA

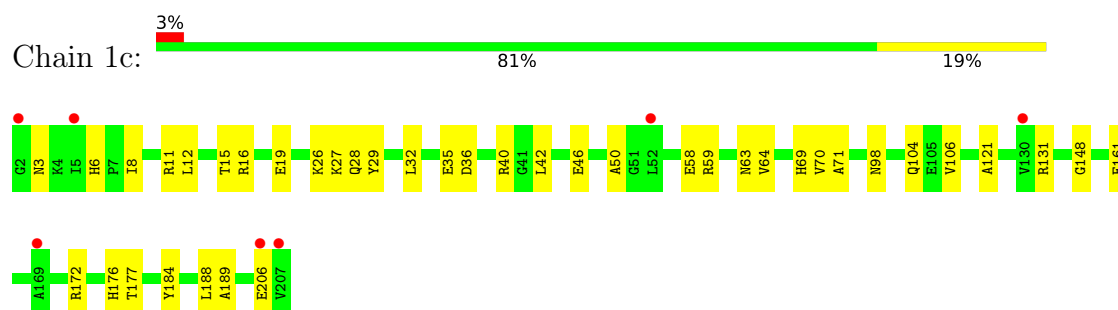




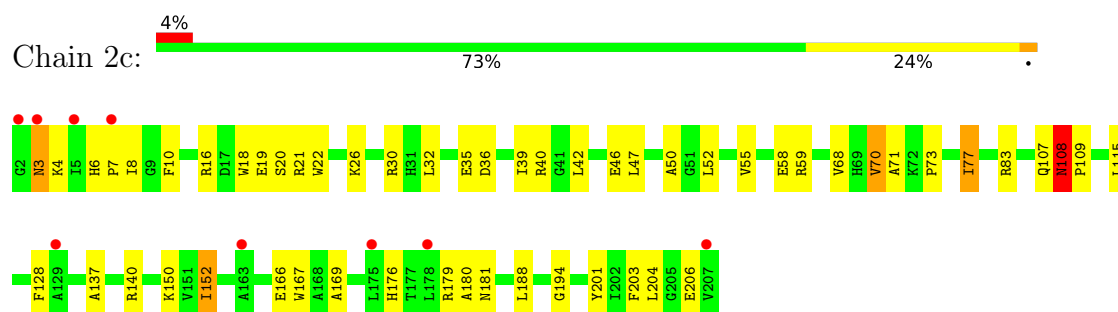
- Molecule 33: 30S ribosomal protein S2



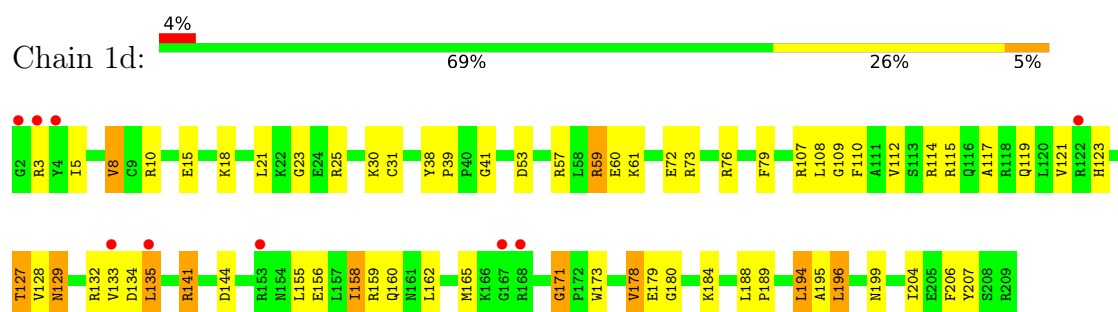
- Molecule 34: 30S ribosomal protein S3



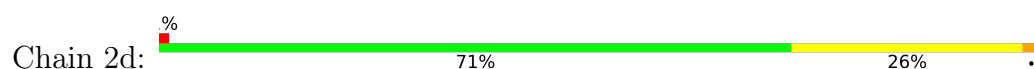
- Molecule 34: 30S ribosomal protein S3

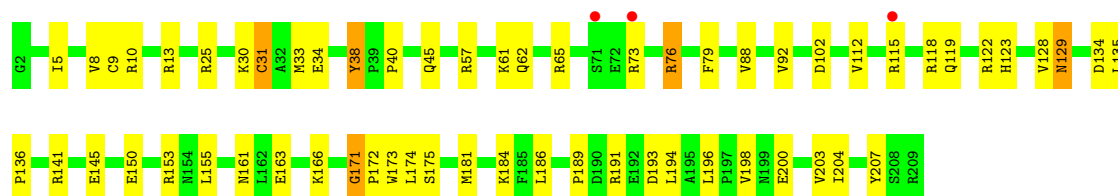


- Molecule 35: 30S ribosomal protein S4

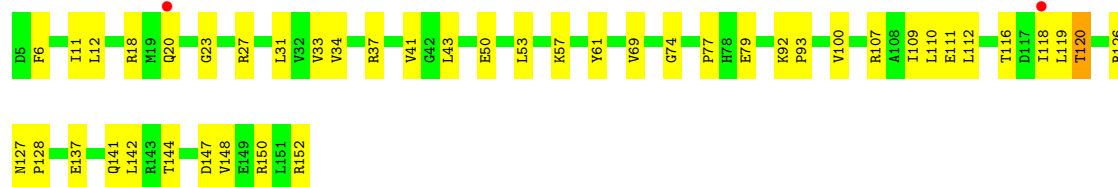


- Molecule 35: 30S ribosomal protein S4

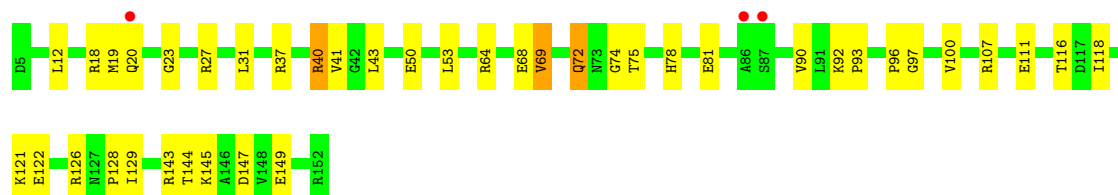
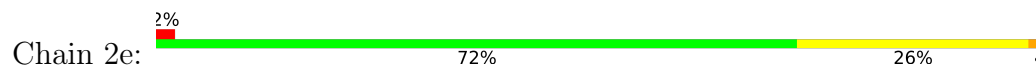




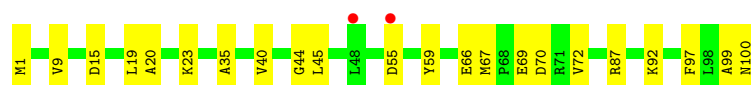
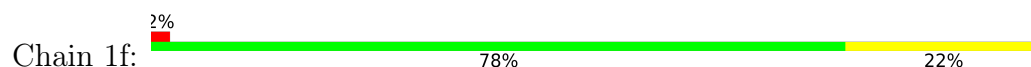
- Molecule 36: 30S ribosomal protein S5



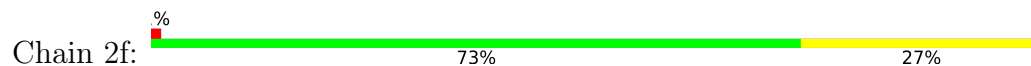
- Molecule 36: 30S ribosomal protein S5



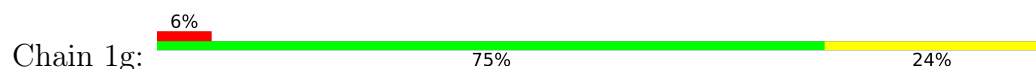
- Molecule 37: 30S ribosomal protein S6



- Molecule 37: 30S ribosomal protein S6

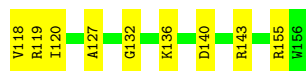
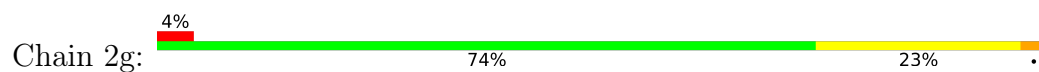


- Molecule 38: 30S ribosomal protein S7

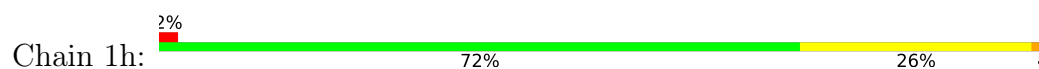




- Molecule 38: 30S ribosomal protein S7



- Molecule 39: 30S ribosomal protein S8



- Molecule 39: 30S ribosomal protein S8

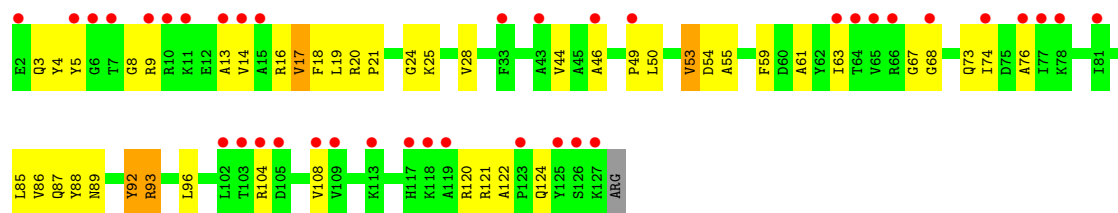


- Molecule 40: 30S ribosomal protein S9

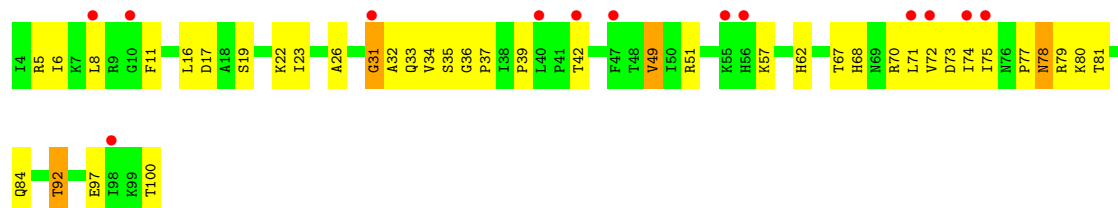


- Molecule 40: 30S ribosomal protein S9

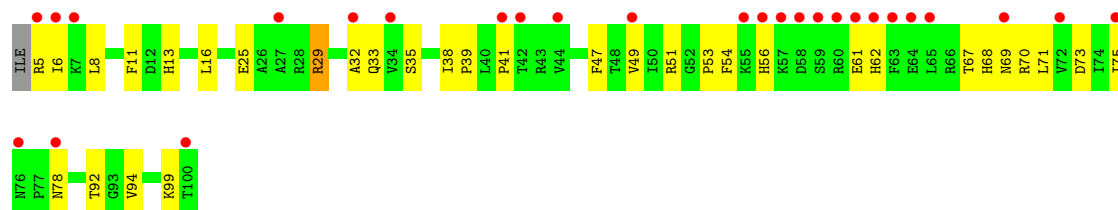




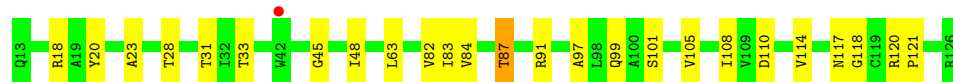
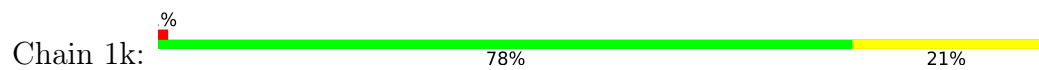
• Molecule 41: 30S ribosomal protein S10



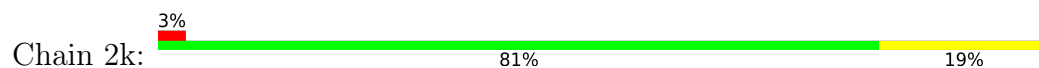
• Molecule 41: 30S ribosomal protein S10



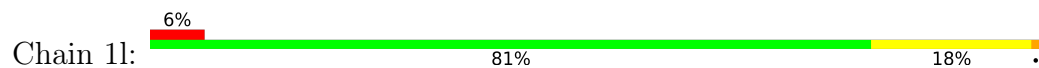
• Molecule 42: 30S ribosomal protein S11



• Molecule 42: 30S ribosomal protein S11

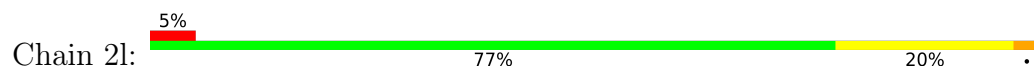


• Molecule 43: 30S ribosomal protein S12

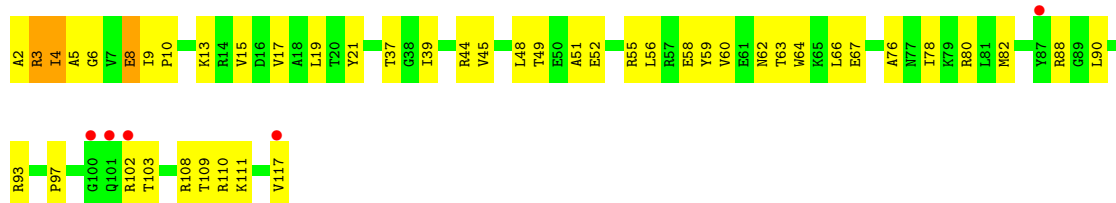




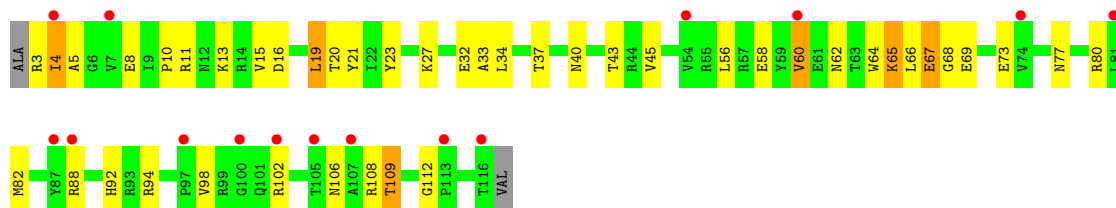
- Molecule 43: 30S ribosomal protein S12



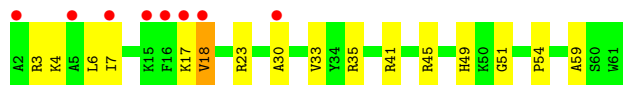
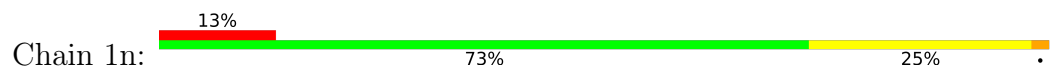
- Molecule 44: 30S ribosomal protein S13



- Molecule 44: 30S ribosomal protein S13



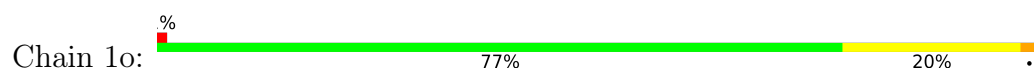
- Molecule 45: 30S ribosomal protein S14 type Z



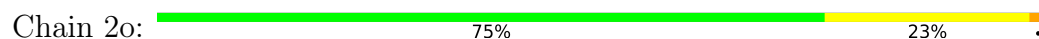
- Molecule 45: 30S ribosomal protein S14 type Z



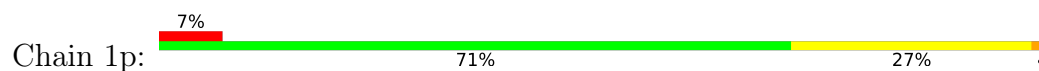
- Molecule 46: 30S ribosomal protein S15



- Molecule 46: 30S ribosomal protein S15



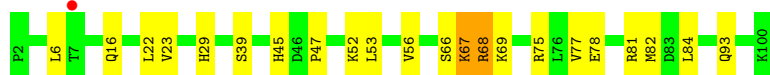
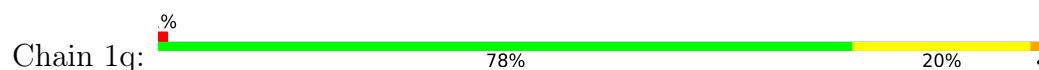
- Molecule 47: 30S ribosomal protein S16



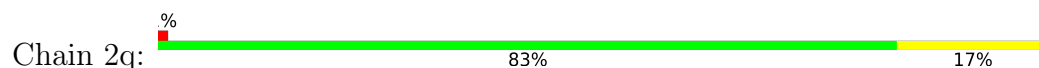
- Molecule 47: 30S ribosomal protein S16



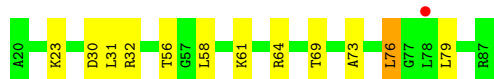
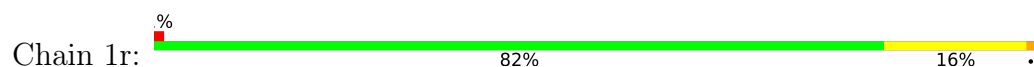
- Molecule 48: 30S ribosomal protein S17



- Molecule 48: 30S ribosomal protein S17



- Molecule 49: 30S ribosomal protein S18



- Molecule 49: 30S ribosomal protein S18

Chain 2r:  65% 34% .



- Molecule 50: 30S ribosomal protein S19

Chain 1s:  8% 65% 30% 5%



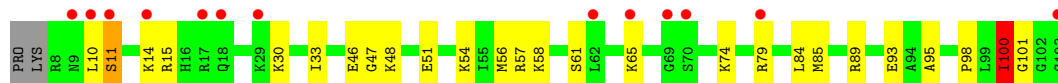
- Molecule 50: 30S ribosomal protein S19

Chain 2s:  14% 69% 30%



- Molecule 51: 30S ribosomal protein S20

Chain 1t:  13% 71% 24% ..

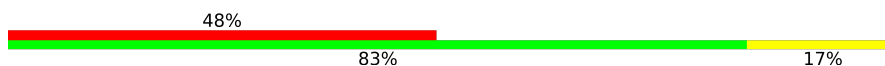


- Molecule 51: 30S ribosomal protein S20

Chain 2t:  5% 87% 12%



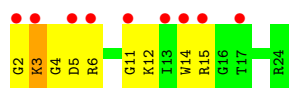
- Molecule 52: 30S ribosomal protein Thx

Chain 1u:  48% 83% 17%

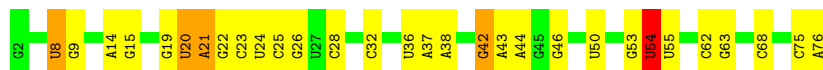


- Molecule 52: 30S ribosomal protein Thx

Chain 2u:  39% 61% 35%



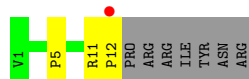
- Molecule 53: tRNA met



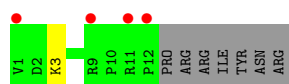
- Molecule 53: tRNA met



- Molecule 54: Onc112



- Molecule 54: Onc112



- Molecule 55: mRNA



- Molecule 55: mRNA



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	209.30Å 452.29Å 625.12Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.72 – 3.10 49.72 – 3.10	Depositor EDS
% Data completeness (in resolution range)	99.1 (49.72-3.10) 99.0 (49.72-3.10)	Depositor EDS
R_{merge}	0.22	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.30 (at 3.12Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.231 , 0.271 0.230 , 0.269	Depositor DCC
R_{free} test set	52535 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	71.9	Xtriage
Anisotropy	0.244	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.26 , 29.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.26$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	293672	wwPDB-VP
Average B, all atoms (Å ²)	61.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.57% 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: ZN, 2MG, MA6, 0TD, OMU, OMG, MG, 4OC, OMC, K, M2G, G7M, PSU, UR3, 5MU, MPD, SF4, 5MC, UNX, 4SU, 2MA

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	0.25	1/67879 (0.0%)	0.39	4/105953 (0.0%)
1	2A	0.19	1/68951 (0.0%)	0.36	2/107627 (0.0%)
2	1B	0.23	0/2876	0.49	0/4486
2	2B	0.19	0/2878	0.34	0/4490
3	1D	0.42	0/2181	0.84	0/2940
3	2D	0.37	0/2186	0.84	1/2944 (0.0%)
4	1E	0.42	0/1592	0.86	4/2149 (0.2%)
4	2E	0.37	0/1592	0.87	1/2149 (0.0%)
5	1F	0.42	0/1619	0.82	2/2193 (0.1%)
5	2F	0.36	0/1615	0.86	2/2188 (0.1%)
6	1G	0.35	0/1451	0.84	2/1961 (0.1%)
6	2G	0.36	0/1449	0.85	1/1957 (0.1%)
7	1H	0.40	0/1356	0.90	5/1834 (0.3%)
7	2H	0.38	0/1350	0.93	5/1826 (0.3%)
8	1I	0.38	0/1109	0.87	0/1512
8	2I	0.36	0/1091	0.85	2/1490 (0.1%)
9	1N	0.39	0/1148	0.84	4/1547 (0.3%)
9	2N	0.33	0/1144	0.88	4/1543 (0.3%)
10	1O	0.44	0/943	0.80	0/1269
10	2O	0.38	0/943	0.80	0/1269
11	1P	0.42	0/1152	0.79	0/1533
11	2P	0.32	0/1152	0.79	0/1533
12	1Q	0.42	0/1143	0.77	0/1527
12	2Q	0.34	0/1143	0.73	0/1527
13	1R	0.43	0/982	0.76	0/1312
13	2R	0.36	0/982	0.72	0/1312
14	1S	0.36	0/887	0.83	1/1180 (0.1%)
14	2S	0.33	0/880	0.86	0/1172
15	1T	0.41	0/1105	0.82	0/1477
15	2T	0.33	0/1097	0.80	0/1468
16	1U	0.46	0/977	0.80	2/1301 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
16	2U	0.35	0/977	0.78	1/1301 (0.1%)
17	1V	0.39	0/786	0.76	0/1053
17	2V	0.33	0/782	0.79	0/1049
18	1W	0.47	0/897	0.81	0/1205
18	2W	0.38	0/897	0.79	2/1205 (0.2%)
19	1X	0.41	0/764	0.78	0/1025
19	2X	0.33	0/764	0.78	0/1025
20	1Y	0.40	0/823	0.80	1/1099 (0.1%)
20	2Y	0.31	0/823	0.79	0/1100
21	1Z	0.38	0/1620	0.91	6/2200 (0.3%)
21	2Z	0.35	0/1590	0.89	3/2162 (0.1%)
22	10	0.39	0/616	0.81	0/821
22	20	0.34	0/616	0.89	5/821 (0.6%)
23	11	0.38	0/761	0.77	0/1013
23	21	0.36	0/766	0.79	0/1018
24	12	0.39	0/590	0.77	0/781
24	22	0.30	0/594	0.74	0/785
25	13	0.41	0/474	0.77	0/635
25	23	0.31	0/469	0.78	0/630
26	14	0.38	0/559	0.99	6/754 (0.8%)
26	24	0.47	0/549	1.03	6/741 (0.8%)
27	15	0.46	0/473	0.72	0/639
27	25	0.39	0/469	0.74	0/635
28	16	0.36	0/460	0.69	0/613
28	26	0.32	0/456	0.69	0/608
29	17	0.45	0/426	0.81	0/561
29	27	0.38	0/426	0.77	0/561
30	18	0.41	0/525	0.74	0/691
30	28	0.35	0/525	0.72	0/691
31	19	0.38	0/310	0.78	0/407
31	29	0.31	0/310	0.77	0/407
32	1a	0.19	1/35795 (0.0%)	0.37	2/55864 (0.0%)
32	2a	0.19	0/35890	0.36	1/56012 (0.0%)
33	1b	0.35	0/1876	0.94	6/2533 (0.2%)
33	2b	0.37	0/1860	0.89	7/2518 (0.3%)
34	1c	0.36	0/1582	0.84	0/2137
34	2c	0.38	0/1566	0.88	3/2119 (0.1%)
35	1d	0.37	0/1695	0.88	6/2274 (0.3%)
35	2d	0.34	0/1698	0.84	2/2277 (0.1%)
36	1e	0.34	0/1149	0.85	3/1548 (0.2%)
36	2e	0.34	0/1149	0.87	3/1548 (0.2%)
37	1f	0.32	0/827	0.77	2/1120 (0.2%)
37	2f	0.34	0/829	0.78	0/1123

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
38	1g	0.32	0/1254	0.83	0/1683
38	2g	0.33	0/1248	0.82	0/1676
39	1h	0.32	0/1118	0.84	3/1506 (0.2%)
39	2h	0.30	0/1108	0.82	0/1494
40	1i	0.37	0/1005	0.82	0/1351
40	2i	0.40	0/985	0.83	0/1329
41	1j	0.40	0/732	0.96	2/993 (0.2%)
41	2j	0.42	0/723	0.90	0/984
42	1k	0.36	0/849	0.76	0/1150
42	2k	0.38	0/848	0.87	1/1149 (0.1%)
43	1l	0.33	0/937	0.80	0/1260
43	2l	0.34	0/937	0.85	2/1260 (0.2%)
44	1m	0.33	0/924	0.84	1/1242 (0.1%)
44	2m	0.39	0/905	0.88	3/1217 (0.2%)
45	1n	0.32	0/501	0.77	0/664
45	2n	0.32	0/501	0.77	0/664
46	1o	0.34	0/739	0.80	0/985
46	2o	0.33	0/739	0.81	0/985
47	1p	0.36	0/697	0.78	0/939
47	2p	0.34	0/693	0.80	0/935
48	1q	0.31	0/836	0.81	3/1117 (0.3%)
48	2q	0.29	0/836	0.79	2/1117 (0.2%)
49	1r	0.34	0/560	0.78	0/746
49	2r	0.34	0/560	0.74	0/746
50	1s	0.35	0/663	0.88	1/895 (0.1%)
50	2s	0.38	0/660	0.91	1/893 (0.1%)
51	1t	0.33	0/734	0.86	1/969 (0.1%)
51	2t	0.34	0/736	0.81	0/976
52	1u	0.32	0/203	0.85	0/266
52	2u	0.35	0/203	0.80	0/266
53	1x	0.25	0/1725	0.45	0/2689
53	2x	0.25	1/1725 (0.1%)	0.43	0/2689
54	1y	0.41	0/106	1.01	0/146
54	2y	0.39	0/106	1.10	0/146
55	A	0.27	0/72	0.42	0/110
55	B	0.24	0/72	0.38	0/110
All	All	0.27	4/311106 (0.0%)	0.54	127/465325 (0.0%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	2A	2552	OMU	O3'-P	5.15	1.61	1.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1A	2564	OMU	O3'-P	5.13	1.61	1.56
32	1a	1498	UR3	O3'-P	5.09	1.61	1.56
53	2x	8	4SU	O3'-P	5.09	1.61	1.56

All (127) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1A	1099	C	OP1-P-O3'	-11.84	72.47	108.00
1	1A	1099	C	OP2-P-O3'	-10.78	75.67	108.00
1	1A	1100	A	OP1-P-OP2	8.46	144.98	119.60
50	2s	67	VAL	N-CA-C	7.46	117.54	110.53
35	1d	38	TYR	CA-C-N	7.20	124.92	119.66
35	1d	38	TYR	C-N-CA	7.20	124.92	119.66
33	1b	128	GLU	N-CA-C	-7.06	104.40	113.16
48	1q	67	LYS	N-CA-C	-6.64	102.24	110.41
9	2N	125	GLY	CA-C-N	6.62	126.31	119.82
9	2N	125	GLY	C-N-CA	6.62	126.31	119.82
34	2c	194	GLY	N-CA-C	6.55	119.16	111.63
21	1Z	133	ILE	N-CA-C	6.52	113.49	107.56
33	1b	158	LEU	CA-C-N	6.39	126.41	119.89
33	1b	158	LEU	C-N-CA	6.39	126.41	119.89
39	1h	79	VAL	N-CA-C	-6.38	106.33	111.81
16	2U	9	VAL	N-CA-C	6.38	116.54	110.42
7	2H	125	VAL	CA-C-N	6.22	125.44	118.97
7	2H	125	VAL	C-N-CA	6.22	125.44	118.97
21	2Z	133	ILE	N-CA-C	6.12	113.94	107.76
18	2W	13	SER	CA-C-N	6.11	126.28	119.32
18	2W	13	SER	C-N-CA	6.11	126.28	119.32
44	2m	66	LEU	N-CA-C	6.10	117.81	108.30
7	1H	167	GLU	CA-C-N	6.08	126.39	119.83
7	1H	167	GLU	C-N-CA	6.08	126.39	119.83
6	1G	45	GLU	N-CA-C	-6.02	105.93	113.28
9	2N	110	GLY	CA-C-N	6.01	126.17	119.32
9	2N	110	GLY	C-N-CA	6.01	126.17	119.32
43	2l	28	LYS	N-CA-C	5.98	119.65	111.39
7	2H	35	VAL	N-CA-C	5.96	114.53	107.73
42	2k	40	ILE	N-CA-C	-5.95	107.08	111.90
21	1Z	107	THR	CA-C-N	5.88	125.89	119.89
21	1Z	107	THR	C-N-CA	5.88	125.89	119.89
35	1d	39	PRO	N-CA-C	5.84	116.08	110.47
26	14	28	LYS	CA-C-N	5.81	125.50	119.05
26	14	28	LYS	C-N-CA	5.81	125.50	119.05

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
33	1b	193	ASP	CA-C-N	5.80	125.49	119.05
33	1b	193	ASP	C-N-CA	5.80	125.49	119.05
4	1E	188	VAL	CA-C-N	5.79	125.79	119.89
4	1E	188	VAL	C-N-CA	5.79	125.79	119.89
5	1F	194	MET	N-CA-C	5.78	118.33	108.90
7	2H	28	GLY	CA-C-N	5.78	125.48	119.82
7	2H	28	GLY	C-N-CA	5.78	125.48	119.82
48	2q	29	HIS	CA-C-N	5.77	125.89	119.32
48	2q	29	HIS	C-N-CA	5.77	125.89	119.32
48	1q	29	HIS	CA-C-N	5.76	126.15	119.47
48	1q	29	HIS	C-N-CA	5.76	126.15	119.47
21	2Z	14	LYS	CA-C-N	5.76	126.15	119.47
21	2Z	14	LYS	C-N-CA	5.76	126.15	119.47
50	1s	10	PHE	N-CA-C	5.74	117.65	108.41
22	20	12	ASN	CB-CA-C	-5.72	108.83	117.07
41	1j	36	GLY	CA-C-N	5.63	126.88	119.84
41	1j	36	GLY	C-N-CA	5.63	126.88	119.84
36	2e	69	VAL	CA-C-N	5.63	126.88	119.84
36	2e	69	VAL	C-N-CA	5.63	126.88	119.84
51	1t	11	SER	N-CA-C	-5.62	106.08	113.17
6	1G	51	ARG	N-CA-C	-5.61	105.70	112.54
32	1a	839	U	P-O3'-C3'	5.56	128.55	120.20
36	1e	23	GLY	N-CA-C	5.48	118.01	110.56
1	2A	271(M)	G	P-O3'-C3'	5.48	126.28	119.70
22	20	12	ASN	CA-C-O	5.48	121.12	117.94
20	1Y	92	ASN	N-CA-C	5.47	117.67	111.11
26	24	40	HIS	CA-C-N	5.47	126.68	119.84
26	24	40	HIS	C-N-CA	5.47	126.68	119.84
1	2A	271(M)	G	OP1-P-O3'	5.46	117.22	105.20
8	2I	118	LYS	CA-C-N	5.46	125.39	119.76
8	2I	118	LYS	C-N-CA	5.46	125.39	119.76
5	2F	21	ALA	CA-C-N	5.44	131.50	121.70
5	2F	21	ALA	C-N-CA	5.44	131.50	121.70
3	2D	275	LYS	N-CA-C	-5.43	100.82	109.07
33	2b	158	LEU	CA-C-N	5.41	125.41	119.89
33	2b	158	LEU	C-N-CA	5.41	125.41	119.89
39	1h	71	GLY	CA-C-N	5.40	124.92	119.19
39	1h	71	GLY	C-N-CA	5.40	124.92	119.19
6	2G	144	ILE	N-CA-C	5.39	114.50	106.85
9	1N	110	GLY	CA-C-N	5.38	125.46	119.32
9	1N	110	GLY	C-N-CA	5.38	125.46	119.32
44	2m	112	GLY	CA-C-N	5.38	125.38	119.89

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	2m	112	GLY	C-N-CA	5.38	125.38	119.89
35	1d	171	GLY	CA-C-N	5.38	126.56	119.84
35	1d	171	GLY	C-N-CA	5.38	126.56	119.84
7	1H	92	ILE	N-CA-C	5.38	115.82	110.23
22	20	82	ARG	CA-C-N	5.37	125.37	119.89
22	20	82	ARG	C-N-CA	5.37	125.37	119.89
21	1Z	157	LEU	N-CA-C	5.35	116.81	110.07
36	2e	23	GLY	N-CA-C	5.33	117.81	110.56
16	1U	102	GLU	CA-C-N	5.32	124.83	119.19
16	1U	102	GLU	C-N-CA	5.32	124.83	119.19
32	2a	1183	A	C2'-C3'-O3'	5.31	117.46	109.50
26	14	52	THR	N-CA-C	-5.30	107.35	112.97
9	1N	125	GLY	CA-C-N	5.29	125.00	119.82
9	1N	125	GLY	C-N-CA	5.29	125.00	119.82
14	1S	59	LYS	N-CA-C	5.27	122.02	110.80
1	1A	1100	A	O5'-P-OP1	-5.26	92.23	108.00
33	2b	25	ASN	CA-C-N	5.25	124.91	119.56
33	2b	25	ASN	C-N-CA	5.25	124.91	119.56
34	2c	108	ASN	CA-C-N	5.24	124.85	119.56
34	2c	108	ASN	C-N-CA	5.24	124.85	119.56
26	14	40	HIS	CA-C-N	5.23	126.38	119.84
26	14	40	HIS	C-N-CA	5.23	126.38	119.84
4	2E	72	VAL	N-CA-C	5.23	115.43	108.11
37	1f	55	ASP	CA-C-N	5.22	124.88	119.56
37	1f	55	ASP	C-N-CA	5.22	124.88	119.56
7	1H	127	GLU	CA-C-N	-5.22	113.32	119.84
7	1H	127	GLU	C-N-CA	-5.22	113.32	119.84
33	1b	23	ARG	N-CA-C	-5.20	104.11	110.61
21	1Z	157	LEU	CA-C-N	5.20	125.73	120.38
21	1Z	157	LEU	C-N-CA	5.20	125.73	120.38
35	1d	171	GLY	N-CA-C	5.15	122.85	112.34
22	20	12	ASN	N-CA-C	5.14	113.00	108.78
4	1E	176	ILE	CA-C-N	5.13	124.92	119.28
4	1E	176	ILE	C-N-CA	5.13	124.92	119.28
33	2b	193	ASP	CA-C-N	5.13	124.74	119.05
33	2b	193	ASP	C-N-CA	5.13	124.74	119.05
35	2d	38	TYR	CA-C-N	5.12	123.40	119.66
35	2d	38	TYR	C-N-CA	5.12	123.40	119.66
43	2l	119	LYS	N-CA-C	-5.12	102.81	110.23
26	24	59	PHE	CA-C-N	5.11	130.90	121.70
26	24	59	PHE	C-N-CA	5.11	130.90	121.70
44	1m	6	GLY	N-CA-C	-5.09	107.95	114.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	14	53	GLU	N-CA-C	5.09	116.52	111.07
33	2b	129	GLU	N-CA-C	-5.09	106.85	113.16
26	24	28	LYS	CA-C-N	5.08	124.68	119.05
26	24	28	LYS	C-N-CA	5.08	124.68	119.05
32	1a	1442	G	P-O3'-C3'	5.06	125.77	119.70
36	1e	127	ASN	CA-C-N	5.04	124.48	119.24
36	1e	127	ASN	C-N-CA	5.04	124.48	119.24
5	1F	24	LEU	N-CA-C	-5.01	103.88	110.39

There are no chirality outliers.

There are no planarity outliers.

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	60842	0	30688	535	0
1	2A	61801	0	31173	620	0
2	1B	2572	0	1305	33	0
2	2B	2573	0	1306	28	0
3	1D	2131	0	2207	41	0
3	2D	2136	0	2218	46	0
4	1E	1559	0	1618	28	0
4	2E	1559	0	1618	33	0
5	1F	1584	0	1625	38	0
5	2F	1580	0	1619	34	0
6	1G	1426	0	1445	32	0
6	2G	1424	0	1441	37	0
7	1H	1330	0	1407	32	0
7	2H	1324	0	1402	31	0
8	1I	1094	0	1127	23	0
8	2I	1076	0	1094	23	0
9	1N	1121	0	1194	11	0
9	2N	1117	0	1184	20	0
10	1O	933	0	996	21	0
10	2O	933	0	996	23	0
11	1P	1135	0	1212	23	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
11	2P	1135	0	1212	18	0
12	1Q	1122	0	1179	23	0
12	2Q	1122	0	1179	25	0
13	1R	968	0	1033	19	0
13	2R	968	0	1033	20	0
14	1S	877	0	938	24	0
14	2S	870	0	923	22	0
15	1T	1091	0	1151	20	0
15	2T	1083	0	1136	20	0
16	1U	959	0	1019	13	0
16	2U	959	0	1019	12	0
17	1V	775	0	841	13	0
17	2V	771	0	829	13	0
18	1W	886	0	940	8	0
18	2W	886	0	940	19	0
19	1X	750	0	814	19	0
19	2X	750	0	814	14	0
20	1Y	810	0	892	25	0
20	2Y	810	0	887	23	0
21	1Z	1587	0	1598	34	0
21	2Z	1557	0	1564	30	0
22	10	608	0	622	10	0
22	20	608	0	622	10	0
23	11	754	0	823	10	0
23	21	759	0	837	17	0
24	12	588	0	643	11	0
24	22	592	0	654	7	0
25	13	469	0	518	12	0
25	23	464	0	514	7	0
26	14	546	0	522	23	0
26	24	536	0	514	22	0
27	15	459	0	476	6	0
27	25	455	0	465	6	0
28	16	453	0	473	8	0
28	26	449	0	469	6	0
29	17	418	0	467	10	0
29	27	418	0	467	6	0
30	18	517	0	582	10	0
30	28	517	0	582	16	0
31	19	307	0	335	4	0
31	29	307	0	335	6	0
32	1a	32246	0	16294	395	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
32	2a	32331	0	16338	423	0
33	1b	1842	0	1862	60	0
33	2b	1825	0	1828	66	0
34	1c	1558	0	1557	23	0
34	2c	1542	0	1517	34	0
35	1d	1665	0	1687	49	0
35	2d	1668	0	1703	53	0
36	1e	1133	0	1191	26	0
36	2e	1133	0	1191	30	0
37	1f	814	0	808	14	0
37	2f	816	0	808	23	0
38	1g	1235	0	1249	25	0
38	2g	1229	0	1238	24	0
39	1h	1098	0	1143	26	0
39	2h	1088	0	1126	31	0
40	1i	986	0	990	30	0
40	2i	966	0	953	33	0
41	1j	719	0	672	25	0
41	2j	710	0	661	26	0
42	1k	834	0	838	14	0
42	2k	833	0	836	11	0
43	1l	932	0	981	14	0
43	2l	932	0	981	18	0
44	1m	914	0	954	29	0
44	2m	895	0	920	27	0
45	1n	492	0	529	14	0
45	2n	492	0	529	24	0
46	1o	728	0	760	15	0
46	2o	728	0	760	15	0
47	1p	681	0	697	15	0
47	2p	677	0	686	15	0
48	1q	823	0	891	12	0
48	2q	823	0	891	10	0
49	1r	555	0	618	10	0
49	2r	555	0	618	21	0
50	1s	648	0	658	24	0
50	2s	645	0	635	22	0
51	1t	732	0	809	17	0
51	2t	733	0	795	6	0
52	1u	199	0	208	3	0
52	2u	199	0	208	6	0
53	1x	1625	0	829	24	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
53	2x	1625	0	829	17	0
54	1y	101	0	109	2	0
54	2y	101	0	109	1	0
55	A	65	0	33	4	0
55	B	65	0	33	4	0
56	10	7	0	0	0	0
56	11	3	0	0	0	0
56	13	3	0	0	0	0
56	15	3	0	0	0	0
56	17	2	0	0	0	0
56	18	1	0	0	0	0
56	19	2	0	0	0	0
56	1A	946	0	0	0	0
56	1B	29	0	0	0	0
56	1D	21	0	0	0	0
56	1E	6	0	0	0	0
56	1F	9	0	0	0	0
56	1G	4	0	0	0	0
56	1H	2	0	0	0	0
56	1N	3	0	0	0	0
56	1O	1	0	0	0	0
56	1P	2	0	0	0	0
56	1Q	4	0	0	0	0
56	1R	4	0	0	0	0
56	1T	2	0	0	0	0
56	1U	5	0	0	0	0
56	1V	3	0	0	0	0
56	1W	3	0	0	0	0
56	1X	1	0	0	0	0
56	1Y	1	0	0	0	0
56	1Z	1	0	0	0	0
56	1a	261	0	0	0	0
56	1b	1	0	0	0	0
56	1d	4	0	0	0	0
56	1e	4	0	0	0	0
56	1f	1	0	0	0	0
56	1g	1	0	0	0	0
56	1i	1	0	0	0	0
56	1l	1	0	0	0	0
56	1n	1	0	0	0	0
56	1o	2	0	0	0	0
56	1r	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
56	1t	1	0	0	0	0
56	1x	12	0	0	0	0
56	20	1	0	0	0	0
56	21	1	0	0	0	0
56	23	1	0	0	0	0
56	28	2	0	0	0	0
56	2A	679	0	0	0	0
56	2B	17	0	0	0	0
56	2D	8	0	0	0	0
56	2E	7	0	0	0	0
56	2F	3	0	0	0	0
56	2G	2	0	0	0	0
56	2I	1	0	0	0	0
56	2N	1	0	0	0	0
56	2O	2	0	0	0	0
56	2P	1	0	0	0	0
56	2Q	2	0	0	0	0
56	2R	1	0	0	0	0
56	2T	4	0	0	0	0
56	2U	2	0	0	0	0
56	2V	3	0	0	0	0
56	2W	1	0	0	0	0
56	2X	1	0	0	0	0
56	2Y	1	0	0	0	0
56	2a	183	0	0	0	0
56	2e	1	0	0	0	0
56	2f	1	0	0	0	0
56	2j	1	0	0	0	0
56	2k	1	0	0	0	0
56	2l	1	0	0	0	0
56	2n	1	0	0	0	0
56	2p	1	0	0	0	0
56	2q	1	0	0	0	0
56	2t	1	0	0	0	0
56	2x	10	0	0	0	0
57	1A	1	0	0	0	0
57	2A	1	0	0	0	0
58	1A	8	0	14	1	0
58	1a	8	0	14	0	0
59	1B	12	0	12	1	0
60	14	1	0	0	0	0
60	15	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
60	16	1	0	0	0	0
60	19	1	0	0	0	0
60	1Y	1	0	0	0	0
60	1n	1	0	0	0	0
60	24	1	0	0	0	0
60	25	1	0	0	0	0
60	26	1	0	0	0	0
60	29	1	0	0	0	0
60	2Y	1	0	0	0	0
60	2n	1	0	0	0	0
61	1d	8	0	0	0	0
61	2d	8	0	0	0	0
62	2A	1	0	0	0	0
63	10	4	0	0	0	0
63	11	3	0	0	0	0
63	13	6	0	0	1	0
63	15	2	0	0	0	0
63	16	3	0	0	0	0
63	18	7	0	0	0	0
63	19	3	0	0	1	0
63	1A	1632	0	0	8	0
63	1B	50	0	0	0	0
63	1D	20	0	0	0	0
63	1E	17	0	0	0	0
63	1F	14	0	0	1	0
63	1G	5	0	0	0	0
63	1H	4	0	0	0	0
63	1N	7	0	0	0	0
63	1O	2	0	0	0	0
63	1P	18	0	0	0	0
63	1Q	5	0	0	0	0
63	1R	7	0	0	1	0
63	1T	4	0	0	0	0
63	1U	3	0	0	0	0
63	1V	3	0	0	0	0
63	1X	6	0	0	0	0
63	1Y	2	0	0	0	0
63	1a	369	0	0	1	0
63	1c	1	0	0	0	0
63	1d	6	0	0	0	0
63	1e	3	0	0	0	0
63	1f	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
63	1h	1	0	0	0	0
63	1l	3	0	0	0	0
63	1m	1	0	0	0	0
63	1n	1	0	0	0	0
63	1o	2	0	0	0	0
63	1p	1	0	0	0	0
63	1t	1	0	0	0	0
63	1x	2	0	0	0	0
63	20	2	0	0	0	0
63	21	2	0	0	0	0
63	23	2	0	0	0	0
63	25	1	0	0	0	0
63	26	2	0	0	0	0
63	28	5	0	0	0	0
63	2A	1221	0	0	6	0
63	2B	33	0	0	1	0
63	2D	13	0	0	0	0
63	2E	12	0	0	1	0
63	2F	4	0	0	0	0
63	2N	2	0	0	0	0
63	2O	4	0	0	0	0
63	2P	7	0	0	0	0
63	2Q	5	0	0	0	0
63	2R	2	0	0	0	0
63	2T	2	0	0	0	0
63	2U	3	0	0	0	0
63	2X	4	0	0	0	0
63	2Y	1	0	0	0	0
63	2a	305	0	0	6	0
63	2d	3	0	0	0	0
63	2e	1	0	0	0	0
63	2j	2	0	0	1	0
63	2l	1	0	0	0	0
63	2n	1	0	0	0	0
63	2p	1	0	0	0	0
63	2r	1	0	0	0	0
63	2t	1	0	0	0	0
63	2x	2	0	0	0	0
63	A	1	0	0	0	0
All	All	293672	0	194336	3566	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 (3566) 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:2564:OMU:C4	1:1A:2564:OMU:C5	1.78	1.59
1:2A:2552:OMU:C5	1:2A:2552:OMU:C4	1.78	1.58
1:1A:1405:A:N6	1:1A:1418:U:H3	1.34	1.23
32:2a:516:PSU:HN3	32:2a:533:A:N6	1.44	1.13
1:1A:2159:C:N4	1:1A:2176:G:H1	1.52	1.07
32:2a:1005:A:C5	32:2a:1024:G:N2	2.24	1.05
32:1a:516:PSU:HN3	32:1a:533:A:N6	1.55	1.03
2:2B:6:C:H42	2:2B:115:G:H1	1.01	1.00
32:1a:1005:A:C6	32:1a:1024:G:N2	2.29	1.00
13:1R:3:HIS:NE2	63:1R:303:HOH:O	1.96	0.98
33:1b:185:ILE:HG22	33:1b:199:TYR:HB2	1.46	0.97
53:1x:36:U:H3	55:B:114:A:H61	1.09	0.97
1:1A:1405:A:N1	1:1A:1418:U:O4	1.97	0.96
1:2A:1038:C:N4	1:2A:1117:G:H1	1.64	0.95
32:2a:516:PSU:O2	32:2a:533:A:N7	2.00	0.94
32:2a:1162:C:H42	32:2a:1174:G:H1	1.09	0.94
1:1A:2188:G:O6	1:1A:2194:U:C4	2.21	0.94
32:1a:1158:C:H5	32:1a:1181:G:H1	1.16	0.92
53:2x:36:U:H3	55:A:111:A:H61	0.97	0.92
1:2A:154(A):C:H42	1:2A:171:G:H1	1.16	0.91
53:2x:36:U:H3	55:A:111:A:N6	1.69	0.91
1:2A:1038:C:H42	1:2A:1117:G:H1	0.90	0.90
32:1a:1003:G:H2'	32:1a:1004:A:H4'	1.54	0.90
32:1a:404:U:O2	32:1a:498:U:O4	1.91	0.89
20:1Y:92:ASN:HB2	20:1Y:94:LYS:H	1.38	0.89
32:1a:516:PSU:O2	32:1a:533:A:N7	2.05	0.89
32:1a:1005:A:N6	32:1a:1024:G:N2	2.20	0.88
2:2B:8:U:H3	2:2B:113:G:H1	1.21	0.88
32:2a:1125:U:O4	32:2a:1280:A:N7	2.07	0.88
1:1A:303:C:H42	1:1A:385:G:H1	1.19	0.88
1:1A:2159:C:N3	1:1A:2176:G:N2	2.20	0.88
39:1h:64:LYS:HG2	39:1h:79:VAL:HG21	1.56	0.88
1:2A:1047:G:H21	1:2A:1111:A:H62	1.16	0.88
1:2A:2128:C:H42	1:2A:2160:G:H1	1.19	0.88
15:1T:55:ASN:H	15:1T:59:THR:HG22	1.39	0.87
53:2x:75:C:H3'	53:2x:76:A:H5''	1.58	0.86
1:2A:1264:G:OP1	27:25:19:ARG:NH2	2.10	0.85
32:2a:404:U:O2	32:2a:498:U:O4	1.93	0.85
5:1F:53:THR:HG22	5:1F:56:GLU:HG3	1.58	0.85
32:1a:1005:A:N6	32:1a:1024:G:C2	2.45	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1x:36:U:H3	55:B:114:A:N6	1.73	0.85
32:2a:677:U:H3	32:2a:713:G:H22	1.22	0.84
1:1A:2188:G:O6	1:1A:2194:U:O4	1.94	0.84
32:1a:1183:A:O2'	32:1a:1184:G:OP1	1.97	0.83
40:2i:86:VAL:HG11	40:2i:93:ARG:HH21	1.43	0.83
1:2A:2128:C:N4	1:2A:2160:G:H1	1.75	0.83
32:1a:407:G:H5''	35:1d:115:ARG:HG2	1.59	0.83
2:2B:6:C:N4	2:2B:115:G:H1	1.75	0.82
10:2O:48:PRO:HB3	32:2a:1422:G:H5''	1.61	0.82
5:1F:53:THR:HG23	5:1F:55:GLY:H	1.45	0.82
33:1b:17:PHE:HA	33:1b:44:LEU:HD11	1.61	0.82
36:2e:78:HIS:HE1	36:2e:143:ARG:H	1.26	0.82
22:10:11:ARG:O	22:10:14:ARG:NH2	2.14	0.81
4:2E:11:MET:HG2	4:2E:24:THR:HG22	1.61	0.81
1:1A:1873:G:O2'	3:1D:253:GLN:NE2	2.14	0.81
1:2A:1842:G:O2'	3:2D:253:GLN:NE2	2.14	0.80
32:2a:1005:A:N7	32:2a:1024:G:N2	2.29	0.80
46:2o:54:ARG:HG2	46:2o:58:MET:HE2	1.64	0.80
32:2a:1125:U:C4	32:2a:1280:A:N7	2.50	0.80
33:1b:15:VAL:HG22	33:1b:209:ARG:HB3	1.64	0.80
1:2A:1082:U:OP2	1:2A:1085:A:N6	2.15	0.80
21:2Z:2:GLU:HG2	21:2Z:56:VAL:HB	1.64	0.79
32:2a:975:A:H4'	32:2a:976:G:H5''	1.62	0.79
32:2a:1005:A:C6	32:2a:1024:G:N2	2.45	0.79
26:24:13:ARG:HH22	26:24:23:GLU:HG2	1.47	0.79
32:1a:78:G:N2	32:1a:91:C:N3	2.30	0.79
32:2a:36:C:N4	63:2a:5059:HOH:O	2.16	0.78
32:1a:992:U:H4'	32:1a:993:G:H5'	1.65	0.78
1:2A:854:G:H2'	1:2A:855:G:H8	1.49	0.78
1:1A:2297:C:OP2	28:16:6:ARG:NH1	2.16	0.78
1:1A:2133:C:OP2	1:1A:2167:C:N4	2.15	0.78
32:1a:1279:A:O2'	32:1a:1281:U:OP2	2.02	0.78
1:1A:2316:G:H22	1:1A:2324:U:H3	1.31	0.78
34:1c:58:GLU:HB3	41:1j:92:THR:HG21	1.64	0.78
1:2A:1482:G:H1	1:2A:1506:C:H42	1.32	0.77
19:1X:1:MET:HE1	24:12:26:ARG:HH21	1.48	0.77
32:1a:559:A:OP1	36:1e:126:ARG:NH2	2.17	0.77
1:1A:2155:G:H3'	1:1A:2179:G:H21	1.50	0.77
1:1A:1556:A:H2'	1:1A:1557:A:O4'	1.83	0.77
32:1a:975:A:H4'	32:1a:976:G:H5''	1.66	0.77
32:1a:1047:G:H5''	45:1n:4:LYS:HD3	1.65	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1310:G:OP1	27:15:19:ARG:NH2	2.16	0.77
32:2a:79:G:N2	32:2a:90:U:O2	2.17	0.77
21:1Z:69:THR:HG22	21:1Z:90:VAL:HA	1.67	0.76
32:2a:1189:C:OP1	41:2j:51:ARG:NH2	2.19	0.76
1:2A:2166:G:N2	1:2A:2172:U:O4	2.19	0.76
1:1A:9:U:N3	1:1A:2641:A:C2	2.53	0.76
39:2h:64:LYS:HG2	39:2h:79:VAL:HG21	1.66	0.76
4:1E:47:VAL:HG21	4:1E:86:PRO:HD2	1.66	0.75
10:1O:48:PRO:HB3	32:1a:1422:G:H5''	1.66	0.75
1:1A:555:G:N1	1:1A:2045:G:OP1	2.18	0.75
32:1a:143:A:H2	32:1a:220:G:H1	1.32	0.75
32:2a:1162:C:N4	32:2a:1174:G:H1	1.84	0.75
3:1D:69:ARG:NH2	3:1D:128:GLY:O	2.20	0.75
32:1a:160:A:H61	32:1a:347:G:H1'	1.52	0.75
8:2I:3:VAL:HG12	8:2I:38:LEU:HA	1.68	0.74
21:2Z:19:ARG:NH1	21:2Z:84:GLU:O	2.20	0.74
18:1W:65:LEU:HD12	18:1W:68:ARG:HE	1.52	0.74
21:1Z:202:GLU:HA	53:1x:53:G:O2'	1.88	0.74
32:1a:1441:G:H5''	32:1a:1442:G:H5'	1.69	0.74
1:2A:1798:U:H5'	3:2D:259:THR:HG22	1.69	0.74
1:2A:1087:G:H1	1:2A:1102:C:H42	1.34	0.74
1:2A:2206:G:H3'	1:2A:2207:G:C8	2.23	0.74
32:2a:1029:C:N4	32:2a:1030(A):G:O6	2.20	0.74
32:1a:1030(C):G:H2'	32:1a:1030(D):A:C8	2.22	0.73
1:2A:154(A):C:N4	1:2A:171:G:H1	1.86	0.73
1:2A:2206:G:H3'	1:2A:2207:G:H8	1.53	0.73
32:2a:1441:G:H5''	32:2a:1442:G:H5'	1.69	0.73
40:2i:53:VAL:O	40:2i:55:ALA:N	2.20	0.73
13:1R:67:LEU:HD13	13:1R:76:VAL:HG21	1.69	0.73
32:1a:1373:G:H5''	38:1g:36:LYS:HE2	1.70	0.73
52:2u:6:ARG:HG2	52:2u:15:ARG:HH12	1.54	0.73
6:2G:97:ASP:HA	6:2G:100:TRP:HD1	1.52	0.73
1:2A:1038:C:N3	1:2A:1117:G:N2	2.32	0.73
1:1A:1814:A:H5'	1:1A:2620:G:H4'	1.71	0.73
32:1a:656:C:O2'	46:1o:28:GLN:NE2	2.21	0.72
21:2Z:91:LEU:HD11	21:2Z:96:VAL:HG11	1.72	0.72
32:1a:343:U:H3	32:1a:346:G:H1	1.37	0.72
1:2A:631:A:OP1	11:2P:65:ARG:NH1	2.21	0.72
6:2G:114:ILE:HB	6:2G:117:PHE:HB2	1.70	0.72
44:2m:58:GLU:O	44:2m:62:ASN:ND2	2.22	0.72
50:1s:3:ARG:HH11	50:1s:10:PHE:HB2	1.54	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:1i:9:ARG:HB2	40:1i:104:ARG:HE	1.52	0.72
26:24:16:CYS:SG	26:24:17:GLY:N	2.62	0.72
32:2a:1411:C:H42	32:2a:1489:G:H1	1.37	0.72
1:1A:1829:U:H5'	3:1D:259:THR:HG22	1.70	0.72
25:23:5:LYS:HG3	25:23:36:VAL:HG22	1.72	0.72
39:1h:14:ARG:NH1	39:1h:83:ILE:O	2.22	0.72
10:2O:35:VAL:HG11	10:2O:103:ALA:HB3	1.71	0.72
32:1a:58:C:O2'	32:1a:388:G:N7	2.23	0.71
32:1a:277:C:OP1	48:1q:68:ARG:NH2	2.23	0.71
44:1m:90:LEU:HD23	44:1m:93:ARG:HH21	1.55	0.71
40:2i:9:ARG:HB2	40:2i:104:ARG:HE	1.55	0.71
1:1A:2188:G:C6	1:1A:2194:U:O4	2.43	0.71
7:1H:101:ARG:HG2	7:1H:117:PRO:HG2	1.72	0.71
41:1j:35:SER:HB3	41:1j:73:ASP:HB2	1.72	0.71
41:1j:49:VAL:HG23	45:1n:41:ARG:HB2	1.71	0.71
44:2m:80:ARG:HH22	50:2s:69:HIS:HE1	1.38	0.71
1:2A:1041:C:H42	1:2A:1114:G:H1	1.39	0.71
32:2a:407:G:H5''	35:2d:115:ARG:HG2	1.73	0.71
32:2a:427:U:OP1	35:2d:13:ARG:NH2	2.23	0.71
1:1A:929:G:H1	1:1A:940:C:H42	1.39	0.71
1:2A:2102:U:O2	1:2A:2187:G:O6	2.08	0.71
32:2a:501:C:OP1	43:2l:117:ARG:NH2	2.24	0.71
32:2a:1285:A:H4'	32:2a:1286:A:H5'	1.71	0.71
33:1b:87:ARG:HH11	33:1b:233:SER:HB3	1.56	0.71
1:2A:2469:A:H4'	12:2Q:56:ARG:HG2	1.73	0.71
3:2D:206:LEU:HD22	3:2D:211:ARG:HG2	1.70	0.71
34:2c:137:ALA:HA	34:2c:140:ARG:HE	1.56	0.71
1:2A:2140:C:H2'	1:2A:2141:G:H8	1.54	0.70
32:2a:1047:G:H5''	45:2n:4:LYS:HD3	1.71	0.70
9:2N:67:LEU:HD12	9:2N:87:LEU:HD13	1.73	0.70
21:2Z:28:MET:HE3	21:2Z:37:VAL:HG11	1.73	0.70
22:20:49:LYS:H	22:20:80:HIS:HD1	1.38	0.70
1:1A:303:C:N4	1:1A:385:G:H1	1.88	0.70
1:2A:2145:C:O2'	1:2A:2147:G:N2	2.25	0.70
26:24:58:ARG:HG3	50:2s:65:ASN:HA	1.71	0.70
26:24:59:PHE:HA	26:24:60:GLN:C	2.16	0.70
1:1A:2359:C:HO2'	28:16:21:TYR:HH	1.39	0.70
38:1g:113:GLU:HG2	38:1g:119:ARG:HG2	1.71	0.70
1:2A:984:A:H5''	1:2A:985:C:H5	1.57	0.70
11:1P:59:LEU:HD11	30:18:10:ALA:HB2	1.73	0.70
36:1e:137:GLU:OE2	36:1e:141:GLN:NE2	2.25	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:656:A:OP1	11:1P:65:ARG:NH1	2.25	0.69
1:1A:2457:G:OP1	5:1F:74:ARG:NH2	2.25	0.69
32:1a:143:A:N1	32:1a:220:G:O6	2.25	0.69
8:2I:4:ILE:HD11	8:2I:44:LEU:HD12	1.73	0.69
1:2A:1569:A:H5'	3:2D:61:LEU:HD21	1.73	0.69
41:2j:5:ARG:N	41:2j:99:LYS:O	2.24	0.69
41:2j:8:LEU:HB2	41:2j:70:ARG:HB2	1.74	0.69
48:1q:67:LYS:O	48:1q:69:LYS:N	2.25	0.69
21:2Z:69:THR:HG22	21:2Z:90:VAL:HA	1.74	0.69
1:2A:1047:G:N2	1:2A:1111:A:H62	1.90	0.69
1:2A:2296:U:OP2	14:2S:9:ARG:NH2	2.24	0.69
1:2A:2453:A:OP1	54:2y:3:LYS:NZ	2.22	0.69
32:2a:201:C:H42	32:2a:216:G:H1	1.39	0.69
32:1a:1103:C:OP1	33:1b:96:ARG:NH2	2.25	0.69
1:1A:2134:G:O6	1:1A:2191:A:N7	2.25	0.69
17:1V:40:LEU:HB2	17:1V:46:VAL:HG13	1.75	0.69
32:1a:1246:C:H42	32:1a:1291:G:H1	1.41	0.69
1:2A:857:C:H4'	22:20:23:VAL:HG21	1.74	0.69
18:2W:18:ARG:NH1	18:2W:76:VAL:O	2.25	0.69
32:2a:1075:C:H5''	33:2b:179:LYS:HE2	1.75	0.69
4:1E:28:ALA:HB3	4:1E:93:VAL:HG12	1.75	0.69
36:1e:37:ARG:HH12	36:1e:111:GLU:HG2	1.58	0.69
6:2G:101:ILE:HG22	6:2G:105:LYS:HE2	1.75	0.69
23:21:3:LYS:HB2	23:21:61:ARG:HH12	1.58	0.69
32:2a:406:G:H21	35:2d:119:GLN:HE22	1.41	0.69
53:2x:75:C:H3'	53:2x:76:A:C5'	2.21	0.69
1:2A:1266:G:O5'	18:2W:15:ARG:NH2	2.26	0.68
23:21:51:VAL:HG11	23:21:74:VAL:HG21	1.75	0.68
24:22:65:ASN:OD1	24:22:69:ARG:NH1	2.26	0.68
1:1A:1431:G:O2'	1:1A:1442:U:O2	2.10	0.68
15:1T:31:SER:OG	15:1T:85:LYS:NZ	2.24	0.68
26:14:16:CYS:SG	26:14:17:GLY:N	2.66	0.68
42:1k:99:GLN:HG2	42:1k:105:VAL:HG21	1.75	0.68
33:1b:223:ILE:HG22	33:1b:226:ARG:HH21	1.59	0.68
32:2a:1103:C:OP1	33:2b:96:ARG:NH2	2.26	0.68
40:2i:53:VAL:HG11	40:2i:92:TYR:HE1	1.57	0.68
8:1I:109:ILE:HG13	8:1I:130:TYR:CZ	2.28	0.68
32:1a:148:G:H1	32:1a:174:C:H42	1.40	0.68
36:2e:37:ARG:HH12	36:2e:111:GLU:HG2	1.59	0.68
1:1A:1093:G:H2'	1:1A:1156:G:H22	1.59	0.68
1:2A:2547:U:O2	10:2O:23:ARG:NH2	2.26	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:976:G:H5'	32:2a:1358:U:O2'	1.94	0.68
1:1A:273:G:H21	8:1I:50:ARG:HD3	1.59	0.68
33:1b:84:GLU:HB3	33:1b:219:VAL:HG21	1.74	0.68
32:1a:747:C:OP2	32:1a:748:C:N4	2.27	0.68
46:1o:54:ARG:HG2	46:1o:58:MET:HE2	1.76	0.68
1:2A:384:U:H2'	1:2A:385:C:H6	1.59	0.68
1:2A:1087:G:N2	1:2A:1102:C:N3	2.39	0.68
32:2a:64:G:H4'	32:2a:65:U:H3'	1.76	0.68
42:2k:99:GLN:HG2	42:2k:105:VAL:HG21	1.75	0.68
32:1a:404:U:O2	32:1a:498:U:C4	2.47	0.68
32:2a:343:U:O2	32:2a:346:G:O6	2.12	0.68
1:1A:1039:G:OP1	16:1U:50:ARG:NH2	2.27	0.67
1:1A:1094:A:OP2	1:1A:1155:C:N4	2.27	0.67
19:2X:43:VAL:HG21	19:2X:81:VAL:HG11	1.75	0.67
40:2i:121:ARG:NH1	40:2i:122:ALA:O	2.27	0.67
40:1i:50:LEU:HD13	40:1i:56:LEU:HA	1.75	0.67
1:2A:958:U:OP2	12:2Q:14:ARG:NH1	2.27	0.67
32:2a:673:G:H2'	32:2a:674:G:C8	2.29	0.67
32:2a:1286:A:H2'	32:2a:1287:A:H4'	1.76	0.67
10:2O:2:ILE:HD12	10:2O:6:THR:HG21	1.76	0.67
10:2O:97:ARG:HA	10:2O:117:LEU:HD22	1.77	0.67
32:1a:1492:A:H4'	32:1a:1493:A:C6	2.30	0.67
32:1a:1305:G:H22	32:1a:1331:G:H1'	1.59	0.67
32:1a:1402:4OC:HM22	32:1a:1403:C:H5'	1.76	0.67
1:1A:1221:G:N2	1:1A:1223:C:OP2	2.27	0.67
44:2m:20:THR:HG21	44:2m:27:LYS:HD2	1.76	0.67
38:1g:69:VAL:HG21	38:1g:104:LEU:HD13	1.77	0.67
46:1o:25:THR:HG21	46:1o:70:LEU:HB2	1.77	0.67
1:2A:2103:C:O2	1:2A:2186:G:N2	2.28	0.67
26:24:46:GLN:O	26:24:48:ARG:N	2.28	0.67
46:2o:25:THR:HG21	46:2o:70:LEU:HB2	1.76	0.66
7:2H:40:GLU:OE1	7:2H:61:HIS:NE2	2.27	0.66
32:1a:1346:A:OP1	40:1i:120:ARG:NH1	2.28	0.66
42:2k:82:VAL:HB	42:2k:108:ILE:HG12	1.78	0.66
1:1A:1219:A:H1'	1:1A:1220:U:H5'	1.78	0.66
1:2A:2445:G:OP1	5:2F:74:ARG:NH2	2.29	0.66
1:2A:2640:G:O3'	9:2N:74:ARG:NH2	2.20	0.66
32:2a:943:U:H1'	40:2i:124:GLN:HE22	1.60	0.66
34:2c:40:ARG:NH1	34:2c:55:VAL:O	2.28	0.66
16:1U:49:HIS:HA	16:1U:52:ARG:HG2	1.76	0.66
32:1a:406:G:H21	35:1d:119:GLN:HE22	1.41	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:2R:67:LEU:HD13	13:2R:76:VAL:HG21	1.77	0.66
32:2a:881:G:OP2	43:2l:12:ARG:NH2	2.29	0.66
34:2c:58:GLU:HB3	41:2j:92:THR:HG21	1.77	0.66
32:1a:727:G:N2	32:1a:730:G:OP2	2.26	0.66
32:1a:1003:G:C2'	32:1a:1004:A:H4'	2.25	0.66
40:1i:121:ARG:NH1	40:1i:122:ALA:O	2.28	0.66
32:1a:881:G:OP2	43:1l:12:ARG:NH2	2.28	0.66
8:2I:114:LEU:HD11	8:2I:128:LEU:HB3	1.76	0.66
11:1P:124:LYS:HE3	11:1P:146:VAL:HG21	1.78	0.66
47:1p:20:VAL:HG23	47:1p:35:LYS:HA	1.78	0.66
27:15:16:ARG:NH1	27:15:17:ASP:OD1	2.29	0.66
32:1a:166:G:H2'	32:1a:167:G:H8	1.61	0.66
32:1a:1305:G:N2	32:1a:1331:G:H1'	2.11	0.66
36:1e:18:ARG:HE	36:1e:20:GLN:HE22	1.40	0.66
32:2a:404:U:C2	32:2a:498:U:O4	2.49	0.66
40:2i:4:TYR:HB2	40:2i:19:LEU:HB2	1.78	0.66
41:2j:49:VAL:HG23	45:2n:41:ARG:HB2	1.77	0.66
44:2m:19:LEU:HD21	44:2m:56:LEU:HD21	1.78	0.66
1:1A:1312:G:O5'	18:1W:15:ARG:NH2	2.29	0.65
1:2A:309:G:N3	1:2A:329:G:O2'	2.29	0.65
1:2A:2134:A:N6	1:2A:2156:G:O2'	2.18	0.65
32:2a:1129:C:H2'	32:2a:1139:G:N7	2.11	0.65
32:1a:661:G:H1	32:1a:744:C:H42	1.43	0.65
32:2a:448:A:OP2	32:2a:485:G:N2	2.25	0.65
1:2A:2162:G:O3'	1:2A:2172:U:O2'	2.13	0.65
1:2A:2303:G:N2	1:2A:2313:C:O2	2.29	0.65
1:2A:468:G:N7	29:27:39:ARG:NH2	2.45	0.65
32:2a:79:G:H1	32:2a:90:U:H3	1.44	0.65
32:2a:343:U:C2	32:2a:346:G:O6	2.49	0.65
39:2h:14:ARG:NH1	39:2h:83:ILE:O	2.29	0.65
24:12:32:LEU:HD22	24:12:36:ARG:HH11	1.61	0.65
35:2d:13:ARG:HB2	35:2d:40:PRO:HD3	1.79	0.65
6:2G:145:THR:HG22	6:2G:148:MET:HE3	1.79	0.65
5:2F:135:LYS:HG2	5:2F:137:LYS:HG2	1.79	0.65
23:21:77:ALA:HA	23:21:80:LEU:HD13	1.79	0.65
32:1a:1227:A:OP2	44:1m:111:LYS:NZ	2.28	0.65
1:2A:2343:C:O2'	1:2A:2373:G:O2'	2.13	0.65
32:2a:404:U:O2	32:2a:498:U:C4	2.49	0.65
36:2e:100:VAL:HG22	36:2e:118:ILE:HG22	1.77	0.65
39:2h:28:ALA:HB3	39:2h:57:PRO:HB2	1.78	0.65
50:2s:20:LEU:HD23	50:2s:23:ASN:HD22	1.61	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:22:1:MET:SD	24:22:56:GLN:NE2	2.69	0.65
1:1A:2339:A:H2'	1:1A:2340:A:C8	2.31	0.64
32:1a:1005:A:H5'	32:1a:1038:C:H1'	1.79	0.64
32:1a:1189:C:OP1	41:1j:51:ARG:NH2	2.30	0.64
33:1b:187:LEU:HA	33:1b:201:ILE:HB	1.79	0.64
35:1d:107:ARG:HH22	35:1d:194:LEU:HG	1.62	0.64
1:2A:1062:G:H2'	1:2A:1063:G:H8	1.62	0.64
3:1D:221:VAL:HG23	3:1D:226:MET:HE2	1.77	0.64
32:1a:96:U:H2'	32:1a:97:G:H8	1.63	0.64
33:1b:69:LEU:HB3	33:1b:162:ILE:HG22	1.78	0.64
1:1A:2159:C:H42	1:1A:2176:G:H1	0.74	0.64
1:1A:2355:C:O2'	1:1A:2385:G:O2'	2.15	0.64
2:1B:13:A:N1	2:1B:69:G:O2'	2.27	0.64
32:1a:343:U:C2	32:1a:346:G:O6	2.50	0.64
1:2A:2103:C:N3	1:2A:2104:G:N2	2.45	0.64
1:1A:2324:U:H5'	6:1G:88:ILE:HD11	1.80	0.64
33:1b:16:HIS:HB3	33:1b:210:SER:HB2	1.78	0.64
1:2A:852:G:H2'	1:2A:853:G:H8	1.61	0.64
1:2A:1025:G:O2'	63:2A:4446:HOH:O	2.15	0.64
27:25:16:ARG:NH1	27:25:17:ASP:OD1	2.30	0.64
32:2a:1001:A:H2'	32:2a:1001(A):G:C8	2.32	0.64
41:2j:5:ARG:N	63:2j:8102:HOH:O	2.30	0.64
35:2d:163:GLU:HA	35:2d:166:LYS:HD3	1.78	0.64
26:14:54:GLY:O	26:14:56:VAL:HA	1.97	0.64
32:1a:452:A:H62	32:1a:480:U:H3	1.44	0.64
1:2A:1059:G:C2	1:2A:1060:U:O4	2.50	0.64
14:2S:49:VAL:HG21	14:2S:77:ALA:HA	1.79	0.64
1:1A:591:U:O2'	63:1A:4764:HOH:O	2.09	0.64
1:1A:1218:G:O2'	1:1A:1219:A:O5'	2.15	0.64
1:1A:2138:G:OP2	1:1A:2188:G:N2	2.31	0.64
33:2b:84:GLU:HB3	33:2b:219:VAL:HG21	1.80	0.64
25:13:3:ARG:HD3	25:13:60:GLU:HG3	1.79	0.64
39:1h:10:LEU:HD22	39:1h:83:ILE:HD11	1.80	0.64
32:1a:1030:C:N4	32:1a:1032:G:O6	2.30	0.64
39:1h:20:TYR:HE2	39:1h:75:ARG:HD2	1.62	0.64
44:1m:10:PRO:HG2	44:1m:21:TYR:CD2	2.33	0.64
47:1p:53:VAL:HG13	47:1p:79:VAL:HG12	1.80	0.64
1:2A:1365:A:O2'	23:21:11:ARG:NH1	2.31	0.64
32:1a:437:U:H5''	35:1d:155:LEU:HD11	1.80	0.64
40:1i:49:PRO:HD2	40:1i:81:ILE:HD11	1.80	0.64
1:2A:1073:A:H2'	1:2A:1074:G:C8	2.33	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2180:U:H2'	1:2A:2181:G:C8	2.33	0.64
1:1A:2228:G:O2'	1:1A:2229:A:OP1	2.16	0.63
2:1B:106:G:H5'	21:1Z:31:ARG:HB3	1.80	0.63
1:2A:2748:A:H5'	7:2H:4:ILE:HD12	1.80	0.63
2:2B:48:A:H4'	14:2S:95:HIS:HD2	1.63	0.63
32:2a:390:C:O3'	47:2p:28:ARG:NH2	2.31	0.63
32:2a:1360:A:OP2	45:2n:35:ARG:NH2	2.31	0.63
1:1A:1176:U:O2	4:1E:149:ARG:NH2	2.25	0.63
1:1A:1766:G:H8	1:1A:1770:A:H62	1.46	0.63
1:1A:2355:C:HO2'	1:1A:2385:G:HO2'	1.46	0.63
3:1D:76:PRO:HB2	3:1D:116:GLN:HE21	1.63	0.63
33:1b:82:ARG:NH1	33:1b:92:TYR:OH	2.31	0.63
1:2A:568:U:O2'	63:2A:4573:HOH:O	2.15	0.63
1:2A:1081:U:H3'	1:2A:1085:A:H61	1.62	0.63
2:1B:103:G:H21	21:1Z:73:GLN:HE22	1.44	0.63
32:1a:1135:U:H4'	32:1a:1136:U:H5	1.63	0.63
40:1i:17:VAL:HG21	40:1i:81:ILE:HG22	1.80	0.63
1:2A:2126:A:H4'	1:2A:2127:G:O5'	1.99	0.63
32:2a:582:U:OP1	46:2o:68:ARG:NH2	2.19	0.63
32:2a:769:G:H4'	32:2a:1513:A:H4'	1.81	0.63
3:1D:13:ARG:NH1	3:1D:16:MET:SD	2.72	0.63
10:2O:115:VAL:HG13	10:2O:121:VAL:HG21	1.79	0.63
36:2e:74:GLY:HA3	36:2e:116:THR:HG22	1.81	0.63
1:1A:2564:OMU:C4	1:1A:2564:OMU:C6	2.48	0.63
1:1A:2761:A:H5'	7:1H:4:ILE:HD12	1.81	0.63
1:2A:2805:G:H2'	1:2A:2807:G:C8	2.33	0.63
32:2a:1086:U:H3	32:2a:1099:G:H22	1.43	0.63
36:1e:50:GLU:HB2	36:1e:53:LEU:HD13	1.80	0.63
1:2A:323:G:HO2'	1:2A:1205:U:H3	1.43	0.63
1:2A:938:G:OP2	30:28:52:LYS:NZ	2.22	0.63
1:2A:2781:A:H5''	1:2A:2782:G:H5'	1.81	0.63
3:2D:76:PRO:HB2	3:2D:116:GLN:HE21	1.63	0.63
43:2l:70:ILE:HG12	43:2l:100:ILE:HD12	1.80	0.63
46:2o:87:ILE:HG22	46:2o:88:ARG:H	1.62	0.63
1:1A:234:G:O6	30:18:8:LYS:NZ	2.25	0.63
53:1x:21:A:H61	53:1x:46:G:H2'	1.62	0.63
12:2Q:42:ILE:HD12	12:2Q:97:VAL:HG21	1.80	0.63
32:2a:880:C:OP1	43:2l:8:ASN:ND2	2.30	0.63
32:2a:1162:C:N3	32:2a:1174:G:N2	2.37	0.63
1:2A:247:G:H4'	1:2A:386:G:C5	2.33	0.62
1:2A:301:G:OP2	20:2Y:84:ARG:NH2	2.31	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2130:U:H2'	1:2A:2158:A:H61	1.63	0.62
5:2F:154:VAL:HG22	5:2F:191:ARG:HB2	1.81	0.62
7:2H:17:VAL:HG13	7:2H:26:VAL:HG22	1.81	0.62
14:1S:30:ARG:HG3	14:1S:35:ILE:HD12	1.82	0.62
34:1c:131:ARG:HH21	36:1e:50:GLU:HG3	1.64	0.62
12:1Q:111:GLU:OE2	12:1Q:133:ARG:NH2	2.25	0.62
32:2a:1373:G:H5''	38:2g:36:LYS:HE2	1.82	0.62
1:1A:555:G:H4'	1:1A:556:C:OP1	1.99	0.62
19:2X:40:LYS:HG3	19:2X:51:VAL:HB	1.80	0.62
32:2a:406:G:H5'	35:2d:5:ILE:HD11	1.82	0.62
48:1q:6:LEU:HD23	48:1q:23:VAL:HG11	1.81	0.62
17:2V:62:LEU:HD23	17:2V:93:GLU:HG2	1.80	0.62
32:2a:403:C:N4	63:2a:5073:HOH:O	2.25	0.62
32:2a:546:G:OP1	35:2d:73:ARG:HG2	1.99	0.62
32:2a:559:A:OP1	36:2e:126:ARG:NH2	2.33	0.62
1:1A:902:G:O2'	22:10:27:GLU:OE2	2.18	0.62
32:1a:677:U:H3	32:1a:713:G:H22	1.47	0.62
39:1h:51:VAL:HG11	39:1h:60:ARG:HH12	1.65	0.62
36:2e:50:GLU:HB2	36:2e:53:LEU:HD13	1.82	0.62
32:1a:673:G:H2'	32:1a:674:G:C8	2.34	0.62
5:2F:11:VAL:HG22	5:2F:125:LEU:HB2	1.80	0.62
47:2p:53:VAL:HG13	47:2p:79:VAL:HG22	1.81	0.62
1:1A:181:C:O2'	1:1A:849:A:N3	2.32	0.62
33:1b:88:ALA:HB2	33:1b:219:VAL:HG13	1.82	0.62
32:1a:1309:G:OP1	44:1m:88:ARG:NH2	2.33	0.62
46:1o:28:GLN:HE21	46:1o:66:LEU:HD21	1.65	0.62
1:2A:1047:G:H2'	1:2A:1110:G:H22	1.64	0.62
1:2A:1081:U:H2'	1:2A:1082:U:H5''	1.82	0.62
2:1B:48:A:H4'	14:1S:95:HIS:HD2	1.65	0.61
14:2S:23:ARG:NH2	14:2S:84:GLN:OE1	2.33	0.61
33:2b:119:GLU:HG3	33:2b:153:ARG:HH22	1.64	0.61
38:1g:78:ARG:NH1	38:1g:154:TYR:O	2.33	0.61
1:2A:1057:A:H2'	1:2A:1058:G:H8	1.65	0.61
42:2k:22:HIS:HB3	42:2k:29:ILE:HB	1.81	0.61
32:1a:450:G:N2	32:1a:483:C:N3	2.46	0.61
1:2A:11:G:H2'	1:2A:12:U:H5'	1.80	0.61
3:2D:69:ARG:NH2	3:2D:128:GLY:O	2.28	0.61
5:2F:140:LEU:HD11	5:2F:170:LEU:HD11	1.81	0.61
32:2a:1030:C:H42	32:2a:1031:G:H1	1.48	0.61
33:2b:17:PHE:HA	33:2b:44:LEU:HD21	1.82	0.61
46:2o:4:THR:HG23	46:2o:7:GLU:H	1.66	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:1H:90:LYS:HD3	7:1H:159:GLU:HG2	1.81	0.61
32:1a:1007:C:N3	32:1a:1022:G:O6	2.34	0.61
53:1x:53:G:H2'	53:1x:54:5MU:C6	2.36	0.61
33:2b:93:VAL:HG21	33:2b:97:TRP:HD1	1.63	0.61
1:2A:2185:C:N4	1:2A:2186:G:O6	2.33	0.61
33:2b:178:ARG:HH12	39:2h:68:ARG:HH22	1.47	0.61
1:2A:2128:C:N3	1:2A:2160:G:N2	2.44	0.61
1:2A:1087:G:H1	1:2A:1102:C:N4	1.98	0.61
25:13:3:ARG:NH1	25:13:60:GLU:OE2	2.34	0.61
32:1a:501:C:OP1	43:1l:117:ARG:NH2	2.33	0.61
5:2F:21:ALA:HB3	5:2F:22:ALA:HA	1.83	0.61
6:2G:112:PRO:HG3	26:24:43:TYR:HE2	1.65	0.61
13:2R:56:LYS:NZ	13:2R:90:ARG:O	2.33	0.61
33:2b:178:ARG:HH22	39:2h:68:ARG:HH12	1.46	0.61
1:1A:297:C:H2'	1:1A:298:G:H8	1.66	0.61
11:1P:88:LEU:HD11	11:1P:114:ILE:HD12	1.83	0.61
32:1a:1302:U:OP2	44:1m:21:TYR:OH	2.13	0.61
1:2A:1652:A:OP1	13:2R:8:ARG:NH1	2.34	0.61
32:2a:992:U:H5''	32:2a:993:G:C5	2.36	0.61
32:1a:1086:U:H3	32:1a:1099:G:H22	1.47	0.61
33:1b:51:LEU:HD23	33:1b:201:ILE:HD12	1.83	0.61
33:2b:19:HIS:CG	33:2b:20:GLU:H	2.19	0.61
1:1A:1218:G:O2'	1:1A:1219:A:O4'	2.18	0.60
39:1h:86:ILE:HG21	39:1h:133:LEU:HD13	1.82	0.60
1:2A:994:C:OP1	16:2U:53:ARG:NH2	2.33	0.60
1:1A:1091:A:H5'	1:1A:1092:A:H5''	1.82	0.60
5:1F:165:ARG:HA	5:1F:168:ARG:HD3	1.83	0.60
6:1G:142:PRO:HB2	26:14:31:ILE:HG21	1.83	0.60
14:1S:23:ARG:NH2	14:1S:84:GLN:OE1	2.34	0.60
32:2a:411:A:OP2	35:2d:25:ARG:NH2	2.34	0.60
43:2l:53:ARG:HG3	43:2l:93:LEU:HD21	1.82	0.60
8:1I:92:VAL:HG13	8:1I:120:ILE:HB	1.83	0.60
33:1b:130:ARG:O	33:1b:135:GLN:NE2	2.34	0.60
49:2r:26:LEU:HD11	49:2r:42:ARG:HD3	1.82	0.60
44:2m:16:ASP:HB3	44:2m:34:LEU:HD11	1.84	0.60
1:1A:2156:A:O2'	1:1A:2181:G:N3	2.34	0.60
1:2A:852:G:H2'	1:2A:853:G:C8	2.36	0.60
1:2A:2206:G:H8	1:2A:2207:G:N7	1.99	0.60
21:2Z:52:SER:OG	21:2Z:53:ILE:N	2.32	0.60
37:2f:9:VAL:HB	37:2f:87:ARG:HB2	1.84	0.60
44:2m:80:ARG:HH22	50:2s:69:HIS:CE1	2.20	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2137:G:N3	1:1A:2139:A:N6	2.47	0.60
33:1b:101:MET:HA	33:1b:108:ILE:HG13	1.83	0.60
32:2a:954:G:H21	32:2a:1227:A:H62	1.49	0.60
32:1a:161:A:H2'	32:1a:162:A:H8	1.67	0.60
1:2A:1066:U:O2'	1:2A:1068:G:OP2	2.18	0.60
26:24:58:ARG:HH21	50:2s:68:GLY:H	1.48	0.60
1:1A:2149:G:H21	1:1A:2195:A:H1'	1.67	0.60
5:1F:185:ASP:OD1	5:1F:188:ARG:NH1	2.35	0.60
32:1a:1005:A:OP2	32:1a:1006:C:N4	2.34	0.60
1:2A:1045:A:H8	1:2A:1047:G:N3	1.99	0.60
32:2a:190:U:H2'	32:2a:191:G:H8	1.67	0.60
33:2b:63:MET:HG3	33:2b:225:ALA:HB1	1.84	0.60
1:1A:928:G:H1	1:1A:941:U:H3	1.49	0.60
2:1B:86:G:H1	2:1B:91:C:H42	1.49	0.60
20:1Y:102:CYS:SG	20:1Y:103:GLY:N	2.75	0.60
37:1f:97:PHE:HD2	49:1r:31:LEU:HD23	1.67	0.60
44:1m:3:ARG:HD2	44:1m:9:ILE:HG12	1.84	0.60
12:2Q:63:LYS:HD2	21:2Z:175:VAL:HG21	1.83	0.60
26:24:48:ARG:O	26:24:50:VAL:N	2.34	0.60
5:1F:185:ASP:HA	5:1F:188:ARG:HD3	1.84	0.59
7:1H:24:VAL:HG22	7:1H:35:VAL:HB	1.84	0.59
43:1l:70:ILE:HG12	43:1l:100:ILE:HD12	1.84	0.59
1:2A:1316:U:H2'	1:2A:1317:A:H8	1.67	0.59
25:13:3:ARG:HB2	25:13:60:GLU:HG3	1.84	0.59
36:1e:100:VAL:O	36:1e:107:ARG:NH2	2.34	0.59
32:2a:828:A:OP1	39:2h:21:LYS:NZ	2.33	0.59
34:2c:50:ALA:HB1	34:2c:70:VAL:HG21	1.83	0.59
10:1O:64:ARG:HG2	10:1O:83:ALA:HB3	1.85	0.59
32:1a:1207:2MG:H2'	32:1a:1208:C:C6	2.37	0.59
1:2A:1025:G:C4	1:2A:1135:C:H1'	2.37	0.59
18:2W:71:VAL:HA	18:2W:107:LEU:HD12	1.85	0.59
32:2a:202:U:H5''	32:2a:203:U:H5	1.67	0.59
32:2a:1135:U:H4'	32:2a:1136:U:H5	1.67	0.59
34:2c:179:ARG:NH1	34:2c:206:GLU:OE1	2.35	0.59
1:1A:831:A:H2'	1:1A:839:G:N7	2.17	0.59
32:2a:1305:G:N2	32:2a:1331:G:H1'	2.17	0.59
35:1d:129:ASN:HD21	35:1d:144:ASP:HA	1.68	0.59
43:1l:71:PRO:O	43:1l:102:ARG:NH1	2.33	0.59
4:2E:52:LEU:HB3	4:2E:53:PRO:HD2	1.84	0.59
30:28:6:THR:HG22	30:28:63:PRO:HD2	1.84	0.59
32:2a:661:G:H1	32:2a:744:C:H42	1.49	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:881:G:P	43:2l:12:ARG:HH22	2.25	0.59
32:2a:998:G:H1	32:2a:1043:C:H42	1.50	0.59
34:2c:6:HIS:HB3	45:2n:49:HIS:ND1	2.17	0.59
12:1Q:35:VAL:HG13	12:1Q:130:LYS:HB3	1.85	0.59
32:1a:272:C:H2'	32:1a:273:A:H8	1.67	0.59
32:1a:1504:G:OP1	32:1a:1507:A:H4'	2.03	0.59
33:2b:101:MET:HA	33:2b:108:ILE:HG13	1.84	0.59
34:2c:150:LYS:HG3	34:2c:169:ALA:HB2	1.84	0.59
1:1A:1495:G:O2'	1:1A:1575:A:N1	2.36	0.59
32:1a:450:G:OP1	47:1p:43:LYS:NZ	2.33	0.59
1:2A:2561:A:H2	10:2O:23:ARG:HH21	1.51	0.59
32:2a:933:G:O6	38:2g:3:ARG:NH2	2.35	0.59
1:1A:2348:A:H61	22:10:43:THR:HG22	1.67	0.59
1:2A:864:G:H1'	1:2A:914:C:H42	1.67	0.59
21:2Z:10:ARG:NH1	21:2Z:26:GLY:O	2.36	0.59
32:2a:1166:G:N2	32:2a:1170:A:OP2	2.34	0.59
1:1A:2658:C:OP2	1:1A:2745:G:O2'	2.13	0.59
32:1a:404:U:C2	32:1a:498:U:O4	2.55	0.59
1:2A:2849:U:O4	15:2T:23:ARG:NH2	2.35	0.59
5:2F:157:VAL:HB	5:2F:194:MET:HG2	1.84	0.59
32:2a:401:C:OP2	35:2d:73:ARG:NH2	2.36	0.59
32:2a:949:A:N7	44:2m:106:ASN:ND2	2.51	0.59
1:1A:2285:A:H2'	1:1A:2286:A:C8	2.38	0.59
32:1a:1010:G:N2	32:1a:1020:U:H1'	2.18	0.59
1:2A:2788:C:OP1	4:2E:61:ARG:NH2	2.35	0.59
35:2d:118:ARG:HH21	35:2d:136:PRO:HG2	1.68	0.59
1:1A:7:G:H2'	1:1A:8:A:O4'	2.03	0.58
1:1A:2597:U:H4'	1:1A:2598:C:OP1	2.02	0.58
32:1a:1314:C:N4	50:1s:2:PRO:O	2.36	0.58
39:1h:69:ARG:HG3	39:1h:76:PRO:HA	1.84	0.58
33:2b:77:ALA:HB2	33:2b:211:ILE:HD13	1.84	0.58
35:2d:62:GLN:OE1	35:2d:65:ARG:NH1	2.36	0.58
37:2f:13:ASN:ND2	37:2f:55:ASP:OD2	2.36	0.58
44:2m:80:ARG:NH2	50:2s:69:HIS:HE1	2.01	0.58
1:1A:238:C:O2	30:18:12:LYS:NZ	2.32	0.58
11:1P:126:VAL:HG12	11:1P:148:LEU:HG	1.86	0.58
32:1a:123:C:OP1	32:1a:311:C:O2'	2.20	0.58
33:1b:166:ASP:HB3	33:1b:169:LYS:HB3	1.85	0.58
42:1k:48:ILE:HD13	42:1k:63:LEU:HD12	1.85	0.58
1:2A:1412:A:H2'	1:2A:1413:G:C8	2.38	0.58
32:2a:1005:A:O5'	32:2a:1005:A:H8	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:1I:73:GLU:HG2	8:1I:139:GLN:HB2	1.85	0.58
36:1e:57:LYS:HG2	36:1e:61:TYR:CE2	2.38	0.58
37:1f:19:LEU:HD23	37:1f:23:LYS:HD2	1.84	0.58
1:2A:2748:A:O2'	7:2H:63:SER:O	2.20	0.58
32:2a:1151:A:O4'	41:2j:39:PRO:HB2	2.03	0.58
37:1f:1:MET:HE3	37:1f:66:GLU:HG2	1.84	0.58
42:1k:20:TYR:HB2	42:1k:31:THR:HG23	1.85	0.58
51:1t:46:GLU:HG3	51:1t:48:LYS:HD2	1.84	0.58
44:2m:10:PRO:HB2	44:2m:13:LYS:HB2	1.85	0.58
1:1A:2442:A:H2'	1:1A:2442:A:N3	2.17	0.58
11:1P:50:ARG:HD3	30:18:7:HIS:CD2	2.39	0.58
32:1a:1221:G:OP1	32:1a:1320:C:N4	2.34	0.58
32:1a:1244:C:H42	32:1a:1293:G:H1	1.51	0.58
5:2F:132:VAL:HG21	5:2F:163:VAL:HG22	1.84	0.58
33:2b:144:ARG:NH2	33:2b:148:TYR:OH	2.35	0.58
38:2g:140:ASP:HA	38:2g:143:ARG:HH12	1.68	0.58
1:1A:262:C:H42	1:1A:282:G:H1	1.52	0.58
2:1B:91:C:OP2	12:1Q:16:ARG:NH1	2.36	0.58
32:1a:516:PSU:HN3	32:1a:533:A:H62	0.73	0.58
38:1g:9:VAL:O	38:1g:11:GLN:NE2	2.36	0.58
41:1j:37:PRO:HA	41:1j:72:VAL:HG12	1.86	0.58
1:2A:299:A:N1	1:2A:322:A:O2'	2.35	0.58
1:2A:881:G:H1	1:2A:895:U:H3	1.51	0.58
18:2W:65:LEU:HD12	18:2W:68:ARG:HE	1.68	0.58
32:2a:67:C:H2'	32:2a:68:G:C8	2.38	0.58
4:2E:47:VAL:HG11	4:2E:86:PRO:HD2	1.85	0.58
6:2G:47:LYS:HG3	6:2G:48:GLU:H	1.68	0.58
1:1A:904:C:H4'	22:10:23:VAL:HG21	1.84	0.58
1:1A:2573:A:H2	10:1O:23:ARG:HH21	1.52	0.58
30:18:62:LEU:HB3	30:18:65:GLU:HG2	1.85	0.58
32:1a:790:A:OP1	53:1x:38:A:O2'	2.22	0.58
35:1d:155:LEU:O	35:1d:159:ARG:HG3	2.03	0.58
50:1s:50:ALA:HB1	50:1s:57:HIS:HB3	1.86	0.58
33:2b:15:VAL:O	33:2b:17:PHE:N	2.36	0.58
1:1A:1003:U:H5''	12:1Q:14:ARG:HD3	1.86	0.58
10:1O:68:GLU:OE1	10:1O:78:ARG:NH1	2.36	0.58
1:2A:1420:U:O2'	1:2A:1421:G:OP1	2.20	0.58
1:1A:1346:U:H4'	1:1A:1347:A:H5''	1.85	0.58
23:11:3:LYS:HG3	23:11:4:VAL:H	1.69	0.58
32:2a:1491:G:H5''	32:2a:1492:A:OP2	2.04	0.58
32:1a:757:U:O2'	32:1a:879:C:O2	2.21	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1094:U:OP1	1:2A:1096:A:N6	2.37	0.57
1:2A:2108:C:O2	1:2A:2182:G:N2	2.37	0.57
15:2T:60:THR:HG22	15:2T:77:PRO:HA	1.86	0.57
34:2c:35:GLU:OE2	34:2c:59:ARG:NH2	2.37	0.57
1:1A:1699:A:OP1	13:1R:8:ARG:NH1	2.37	0.57
21:1Z:19:ARG:NH1	21:1Z:84:GLU:O	2.37	0.57
26:14:62:ARG:C	26:14:64:GLY:HA2	2.29	0.57
32:1a:343:U:O2	32:1a:346:G:O6	2.21	0.57
1:2A:323:G:O2'	1:2A:1205:U:N3	2.26	0.57
15:2T:24:PRO:HA	15:2T:49:VAL:HG23	1.85	0.57
20:2Y:77:PRO:HD2	20:2Y:106:LEU:HD23	1.86	0.57
32:1a:461:A:O2'	32:1a:471:G:N7	2.30	0.57
1:2A:2232:U:P	23:21:40:ARG:HH12	2.28	0.57
1:2A:2635:C:O2'	4:2E:48:GLN:NE2	2.37	0.57
11:2P:50:ARG:HD3	30:28:7:HIS:CD2	2.39	0.57
17:2V:43:GLU:OE1	17:2V:43:GLU:N	2.36	0.57
1:1A:1087:C:H42	1:1A:1160:G:H1	1.50	0.57
19:1X:60:ARG:HH12	29:17:47:ARG:HH12	1.52	0.57
23:11:51:VAL:HG11	23:11:74:VAL:HG21	1.84	0.57
29:17:24:THR:HG23	29:17:27:GLY:H	1.69	0.57
33:1b:48:MET:HA	33:1b:51:LEU:HD12	1.85	0.57
40:1i:10:ARG:HH22	40:1i:107:ARG:HG3	1.68	0.57
1:2A:2186:G:N1	1:2A:2187:G:C6	2.72	0.57
2:2B:57:A:H1'	6:2G:29:TRP:HB2	1.87	0.57
7:2H:11:VAL:HG13	7:2H:15:VAL:HG22	1.85	0.57
8:2I:101:LEU:HD11	8:2I:140:LEU:HD11	1.85	0.57
33:2b:92:TYR:OH	33:2b:150:SER:OG	2.16	0.57
53:2x:53:G:H3'	53:2x:54:5MU:H73	1.86	0.57
6:1G:114:ILE:HB	6:1G:117:PHE:HB2	1.84	0.57
21:1Z:198:LYS:HE2	53:1x:63:G:H1'	1.85	0.57
32:1a:881:G:P	43:1l:12:ARG:HH22	2.26	0.57
44:1m:15:VAL:HG11	44:1m:48:LEU:HD21	1.85	0.57
1:2A:1059:G:C5	1:2A:1060:U:N3	2.73	0.57
1:1A:2402:U:P	30:18:35:GLN:HE22	2.27	0.57
3:1D:17:THR:O	3:1D:211:ARG:NH2	2.35	0.57
10:1O:98:VAL:HG13	10:1O:117:LEU:HB3	1.85	0.57
32:1a:618:C:N4	32:1a:621:A:N7	2.52	0.57
1:2A:970:C:HO2'	1:2A:984:A:HO2'	1.52	0.57
3:2D:108:PRO:HG2	3:2D:111:LEU:HB2	1.85	0.57
51:2t:57:ARG:HH12	51:2t:100:ILE:HB	1.70	0.57
6:1G:143:GLU:HA	26:14:28:LYS:HD2	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:1k:87:THR:O	42:1k:87:THR:OG1	2.17	0.57
51:1t:51:GLU:HA	51:1t:54:LYS:HE2	1.86	0.57
1:2A:577:G:O2'	1:2A:1254:A:OP1	2.21	0.57
1:2A:855:G:O2'	22:20:27:GLU:OE2	2.23	0.57
1:2A:2197:U:H1'	1:2A:2198:A:C8	2.39	0.57
21:2Z:33:LEU:HD11	21:2Z:90:VAL:HG21	1.86	0.57
32:2a:1183:A:O2'	32:2a:1184:G:OP1	2.16	0.57
39:2h:49:GLU:OE2	39:2h:62:TYR:OH	2.19	0.57
1:2A:848:G:H2'	1:2A:849:A:C8	2.40	0.57
1:2A:2646:C:OP2	1:2A:2732:G:O2'	2.21	0.57
19:1X:43:VAL:HG21	19:1X:81:VAL:HG11	1.87	0.57
26:14:57:GLU:HB2	26:14:58:ARG:HA	1.87	0.57
32:1a:750:G:O2'	46:1o:22:THR:O	2.14	0.57
44:1m:3:ARG:HG3	44:1m:4:ILE:H	1.70	0.57
32:2a:1279:A:O2'	32:2a:1281:U:OP2	2.15	0.57
33:2b:80:ILE:HD11	33:2b:212:GLN:HB2	1.87	0.57
1:1A:173:C:H2'	1:1A:174:U:C6	2.39	0.57
22:10:38:VAL:HB	22:10:59:LEU:HB2	1.87	0.57
32:1a:1070:U:H2'	32:1a:1071:C:H6	1.69	0.57
1:2A:1514:U:H2'	1:2A:1515:G:H8	1.70	0.57
4:2E:9:VAL:HB	15:2T:3:ARG:HG2	1.87	0.57
32:2a:974:A:OP2	45:2n:29:ARG:NH2	2.38	0.57
32:2a:1239:A:H62	32:2a:1299:A:H62	1.53	0.57
8:1I:8:PRO:HD3	8:1I:15:VAL:HB	1.87	0.56
12:1Q:42:ILE:HD12	12:1Q:97:VAL:HG21	1.87	0.56
21:1Z:202:GLU:OE2	53:1x:62:C:O2'	2.17	0.56
44:1m:78:ILE:HG22	44:1m:82:MET:HE2	1.87	0.56
1:2A:479:A:N3	1:2A:481:G:H5''	2.19	0.56
1:2A:827:U:O2'	1:2A:2068:U:C2	2.58	0.56
6:2G:41:GLN:HB3	6:2G:43:LEU:HD13	1.85	0.56
7:2H:89:ILE:O	7:2H:129:THR:HG23	2.05	0.56
20:2Y:5:MET:HE2	20:2Y:32:PRO:HA	1.88	0.56
23:21:50:ARG:HG2	23:21:59:THR:HG22	1.87	0.56
32:2a:1376:U:O4	38:2g:10:ARG:NH1	2.31	0.56
33:2b:91:PRO:HG3	33:2b:155:LEU:HD13	1.87	0.56
33:2b:128:GLU:OE1	33:2b:135:GLN:NE2	2.35	0.56
1:1A:1857:G:H4'	3:1D:242:ARG:HH21	1.70	0.56
1:1A:2152:U:O2'	1:1A:2155:G:O2'	2.20	0.56
12:1Q:30:GLY:HA2	12:1Q:107:ALA:HB2	1.86	0.56
14:1S:15:ARG:O	14:1S:19:LYS:HG2	2.05	0.56
32:1a:1148:U:H2'	32:1a:1149:C:O4'	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:1b:160:ASP:N	33:1b:160:ASP:OD1	2.38	0.56
1:2A:1063:G:H2'	1:2A:1065:U:H6	1.70	0.56
1:2A:2112:G:H2'	1:2A:2113:U:C6	2.40	0.56
6:2G:38:VAL:HG22	6:2G:93:THR:HG23	1.86	0.56
1:1A:1362:U:H2'	1:1A:1363:A:H8	1.70	0.56
3:1D:206:LEU:HD22	3:1D:211:ARG:HG2	1.87	0.56
10:1O:115:VAL:HG13	10:1O:121:VAL:HG21	1.88	0.56
20:1Y:28:LYS:HD2	20:1Y:40:GLU:HG3	1.86	0.56
32:1a:1014:A:C2	32:1a:1219:U:H1'	2.40	0.56
32:1a:1255:G:HO2'	32:1a:1258:G:HO2'	1.54	0.56
1:2A:1011:G:OP2	16:2U:66:ASN:ND2	2.37	0.56
1:2A:1063:G:H1	1:2A:1075:C:H42	1.54	0.56
1:2A:2839:G:H5'	13:2R:46:GLY:HA2	1.87	0.56
1:1A:323:A:H5''	20:1Y:86:ARG:HH21	1.69	0.56
39:1h:51:VAL:HG12	39:1h:52:ASP:H	1.69	0.56
1:2A:321:G:OP1	5:2F:135:LYS:NZ	2.38	0.56
1:2A:652(T):C:H2'	1:2A:652(U):G:C8	2.40	0.56
1:2A:1783:A:H5'	1:2A:2608:G:H4'	1.88	0.56
1:2A:2127:G:H2'	1:2A:2128:C:O4'	2.06	0.56
39:2h:112:LEU:HD11	39:2h:124:ALA:HB2	1.87	0.56
32:1a:316:G:OP2	32:1a:351:G:O2'	2.22	0.56
1:1A:10:G:N2	1:1A:2812:A:O2'	2.38	0.56
1:1A:1525:G:O2'	1:1A:1605:A:N7	2.37	0.56
7:1H:84:SER:OG	7:1H:132:ARG:NH1	2.39	0.56
12:1Q:51:ARG:HD3	12:1Q:66:ILE:HD11	1.87	0.56
32:1a:539:A:H2'	32:1a:540:G:C8	2.40	0.56
32:1a:632:A:H3'	32:1a:633:G:H8	1.71	0.56
33:1b:7:VAL:O	33:1b:217:ARG:NH2	2.39	0.56
1:2A:1075:C:H2'	1:2A:1076:C:H5'	1.88	0.56
11:2P:126:VAL:HG12	11:2P:148:LEU:HD23	1.88	0.56
32:2a:1221:G:OP1	32:2a:1320:C:N4	2.38	0.56
32:1a:165:C:H2'	32:1a:166:G:H8	1.70	0.56
1:2A:2529:G:O6	31:29:31:LYS:NZ	2.39	0.56
32:2a:653:A:OP1	39:2h:56:LYS:NZ	2.38	0.56
40:2i:17:VAL:HB	40:2i:63:ILE:HG12	1.88	0.56
1:1A:186:A:N6	1:1A:2442:A:O2'	2.38	0.56
32:1a:376:G:H4'	47:1p:5:ARG:NH1	2.21	0.56
45:1n:4:LYS:HA	45:1n:7:ILE:HG12	1.86	0.56
3:2D:108:PRO:HB3	3:2D:143:HIS:CE1	2.41	0.56
36:2e:81:GLU:HG2	36:2e:90:VAL:HG13	1.88	0.56
41:2j:38:ILE:HD11	41:2j:71:LEU:HD13	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1957:G:H1'	1:1A:1986:G:N2	2.20	0.56
31:19:14:CYS:HA	31:19:27:CYS:HB2	1.87	0.56
5:2F:150:GLY:HA2	5:2F:172:TRP:CE3	2.41	0.56
32:2a:811:C:N4	63:2a:4990:HOH:O	2.38	0.56
5:1F:155:LEU:HB2	5:1F:189:THR:HG21	1.88	0.55
15:1T:24:PRO:HA	15:1T:49:VAL:HG23	1.87	0.55
32:1a:1030(C):G:N7	32:1a:1031:G:N2	2.54	0.55
35:1d:15:GLU:OE2	35:1d:59:ARG:NH1	2.38	0.55
37:1f:20:ALA:HA	37:1f:23:LYS:HD3	1.87	0.55
14:2S:14:VAL:O	14:2S:18:ILE:HG12	2.06	0.55
20:2Y:8:LYS:HD3	20:2Y:97:ARG:NH2	2.21	0.55
26:24:59:PHE:HA	26:24:61:ARG:N	2.21	0.55
31:29:14:CYS:HA	31:29:27:CYS:HB2	1.89	0.55
32:2a:1027:C:O2	32:2a:1034:G:N1	2.39	0.55
4:1E:47:VAL:HG12	4:1E:49:LEU:HD13	1.88	0.55
9:1N:12:ARG:NH1	9:1N:50:ASP:OD2	2.39	0.55
30:18:14:VAL:HG23	30:18:24:ALA:HB2	1.87	0.55
1:2A:625:G:O6	11:2P:107:LYS:NZ	2.39	0.55
19:2X:1:MET:HE1	24:22:26:ARG:HH21	1.70	0.55
26:24:41:PRO:HG3	26:24:49:PHE:CE2	2.41	0.55
32:2a:143:A:H2	32:2a:220:G:H1	1.50	0.55
41:2j:16:LEU:HD23	41:2j:94:VAL:HG22	1.88	0.55
43:2l:71:PRO:O	43:2l:102:ARG:NH1	2.36	0.55
1:1A:2149:G:N2	1:1A:2195:A:H1'	2.22	0.55
20:1Y:92:ASN:N	20:1Y:93:GLY:HA2	2.20	0.55
32:1a:376:G:H5''	47:1p:5:ARG:HB2	1.88	0.55
39:2h:10:LEU:HD22	39:2h:83:ILE:HD11	1.87	0.55
32:1a:165:C:H2'	32:1a:166:G:C8	2.41	0.55
32:1a:166:G:H2'	32:1a:167:G:C8	2.39	0.55
32:1a:1157:A:H61	32:1a:1178:G:H21	1.54	0.55
32:2a:619:U:N3	35:2d:134:ASP:OD1	2.36	0.55
32:2a:920:U:H2'	32:2a:921:U:C6	2.42	0.55
32:2a:1256:A:OP2	34:2c:26:LYS:NZ	2.39	0.55
33:2b:97:TRP:HH2	33:2b:176:GLU:CD	2.14	0.55
1:1A:2148:A:H4'	1:1A:2149:G:O5'	2.06	0.55
21:1Z:144:LEU:HD11	21:1Z:150:LEU:HD22	1.87	0.55
48:1q:22:LEU:HD11	48:1q:39:SER:HB2	1.89	0.55
1:2A:652(E):G:O6	1:2A:652(S):C:N4	2.40	0.55
32:2a:564:C:O2'	39:2h:91:ARG:NH2	2.40	0.55
1:2A:1794:U:H2'	1:2A:1795:C:H6	1.72	0.55
1:1A:236:G:H4'	1:1A:413:G:C5	2.41	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:13:55:ARG:HD3	63:13:206:HOH:O	2.05	0.55
32:1a:396:G:O2'	32:1a:398:C:OP1	2.17	0.55
1:2A:2303:G:O2'	6:2G:132:ASN:HB2	2.07	0.55
5:2F:185:ASP:HA	5:2F:188:ARG:HD3	1.89	0.55
21:2Z:144:LEU:HD11	21:2Z:150:LEU:HD22	1.89	0.55
32:2a:1026:G:N3	32:2a:1026:G:H2'	2.22	0.55
33:2b:163:PHE:HD1	33:2b:185:ILE:HB	1.71	0.55
33:2b:187:LEU:HA	33:2b:201:ILE:HB	1.89	0.55
1:1A:691:G:N2	1:1A:700:A:H1'	2.22	0.55
1:1A:1199:C:OP1	16:1U:92:ARG:NH2	2.29	0.55
1:1A:1362:U:H2'	1:1A:1363:A:C8	2.42	0.55
1:1A:2340:A:H2'	1:1A:2341:G:C8	2.41	0.55
10:1O:64:ARG:HB2	10:1O:79:PHE:CG	2.42	0.55
18:1W:18:ARG:NH1	18:1W:76:VAL:O	2.40	0.55
37:1f:100:ASN:HD21	49:1r:23:LYS:HG2	1.72	0.55
1:2A:2472:G:H2'	1:2A:2475:C:H42	1.72	0.55
4:2E:135:HIS:NE2	63:2E:403:HOH:O	2.33	0.55
26:24:13:ARG:N	26:24:29:PRO:O	2.37	0.55
32:2a:1026:G:H3'	32:2a:1027:C:O4'	2.07	0.55
32:2a:1084:G:H5'	32:2a:1102:A:OP2	2.07	0.55
49:2r:32:ARG:HA	49:2r:69:THR:HG21	1.89	0.55
32:1a:1298:C:H4'	32:1a:1299:A:C4	2.42	0.55
33:1b:10:LEU:HD12	33:1b:48:MET:HE1	1.87	0.55
1:2A:2105:C:H2'	1:2A:2106:G:H8	1.72	0.55
1:2A:2305:A:H5''	6:2G:134:GLY:HA3	1.89	0.55
22:20:11:ARG:O	22:20:14:ARG:NH2	2.40	0.55
32:2a:1302:U:OP2	44:2m:21:TYR:OH	2.14	0.55
39:2h:6:ILE:HB	39:2h:85:ARG:NH1	2.22	0.55
1:2A:1482:G:H1	1:2A:1506:C:N4	2.02	0.55
32:2a:1051:C:H2'	32:2a:1052:U:C6	2.42	0.55
1:1A:2740:G:O2'	10:1O:70:LYS:NZ	2.39	0.54
32:1a:737:A:H2'	32:1a:738:C:C6	2.42	0.54
32:1a:976:G:H5'	32:1a:1358:U:O2'	2.07	0.54
45:1n:4:LYS:HG3	45:1n:7:ILE:HD11	1.88	0.54
1:2A:1073:A:H2'	1:2A:1074:G:H8	1.71	0.54
32:2a:624:C:H2'	32:2a:625:G:H8	1.71	0.54
32:2a:836:G:OP1	49:2r:61:LYS:NZ	2.40	0.54
32:2a:890:G:O2'	32:2a:906:G:O6	2.15	0.54
21:1Z:103:ARG:HD3	21:1Z:136:PHE:CD1	2.42	0.54
32:1a:532:A:N6	32:1a:1206:G:O2'	2.39	0.54
46:1o:55:GLY:HA2	46:1o:58:MET:HE3	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2319:G:N2	14:2S:3:ARG:HD3	2.21	0.54
33:2b:47:THR:HA	33:2b:202:PRO:HG2	1.87	0.54
36:2e:12:LEU:HD12	36:2e:128:PRO:HB2	1.89	0.54
1:1A:2450:U:O2'	1:1A:2452:C:OP1	2.16	0.54
2:1B:78:A:C2	2:1B:100:A:C4	2.96	0.54
32:1a:343:U:N3	32:1a:346:G:N1	2.53	0.54
1:2A:1316:U:H2'	1:2A:1317:A:C8	2.42	0.54
1:2A:2850:A:N7	1:2A:2868:A:O2'	2.38	0.54
23:21:64:ALA:HA	23:21:67:ILE:HG13	1.89	0.54
39:2h:84:ARG:NH1	39:2h:85:ARG:O	2.41	0.54
1:1A:1829:U:H5'	3:1D:259:THR:CG2	2.36	0.54
35:1d:3:ARG:HH12	35:1d:5:ILE:HG13	1.72	0.54
46:1o:70:LEU:HD11	46:1o:77:ARG:HB3	1.90	0.54
1:2A:1754:C:H5	15:2T:96:ARG:NH2	2.06	0.54
6:2G:109:VAL:HG11	6:2G:142:PRO:HB3	1.88	0.54
17:2V:40:LEU:HB2	17:2V:46:VAL:HG12	1.88	0.54
32:2a:1504:G:OP1	32:2a:1507:A:H4'	2.07	0.54
37:2f:20:ALA:HA	37:2f:23:LYS:HD3	1.90	0.54
48:2q:66:SER:O	48:2q:70:ARG:NH1	2.40	0.54
1:1A:1066:A:N1	1:1A:1186:U:O2'	2.31	0.54
32:1a:1442:G:H2'	32:1a:1442:G:N3	2.22	0.54
37:1f:69:GLU:O	37:1f:72:VAL:HG12	2.08	0.54
1:2A:1579:A:H2'	1:2A:1580:A:C8	2.43	0.54
1:2A:2420:C:H5'	28:26:54:ILE:HD11	1.90	0.54
1:2A:2577:A:H2'	1:2A:2614:A:N6	2.23	0.54
1:1A:1532:A:H2'	1:1A:1533:G:H8	1.72	0.54
1:1A:1952:G:O2'	1:1A:1990:G:O6	2.19	0.54
1:1A:2859:U:H4'	1:1A:2878:A:C2	2.43	0.54
2:1B:57:A:H1'	6:1G:29:TRP:HB2	1.89	0.54
7:1H:25:LYS:NZ	7:1H:32:GLU:OE1	2.35	0.54
38:1g:65:ALA:HB1	38:1g:127:ALA:HB3	1.90	0.54
32:2a:404:U:H2'	32:2a:405:U:C6	2.42	0.54
32:2a:1295:G:O2'	32:2a:1302:U:O4	2.21	0.54
32:2a:1465:C:H2'	32:2a:1466:C:O4'	2.08	0.54
7:1H:86:GLU:OE2	7:1H:132:ARG:NH2	2.41	0.54
32:1a:376:G:H4'	47:1p:5:ARG:HH11	1.73	0.54
32:1a:1108:G:H5'	34:1c:176:HIS:CD2	2.43	0.54
37:1f:44:GLY:HA2	37:1f:59:TYR:CZ	2.42	0.54
41:1j:11:PHE:HE1	41:1j:67:THR:HG22	1.72	0.54
50:1s:31:ILE:HD12	50:1s:49:ILE:HG12	1.89	0.54
1:2A:55:G:O2'	1:2A:127:A:N1	2.38	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:320:A:H4'	1:2A:322:A:N7	2.22	0.54
32:2a:542:G:P	35:2d:10:ARG:HH22	2.30	0.54
32:2a:1074:G:OP1	36:2e:64:ARG:NH1	2.27	0.54
36:2e:12:LEU:HB3	36:2e:31:LEU:HB2	1.88	0.54
38:2g:115:ARG:HH11	38:2g:118:VAL:HB	1.72	0.54
40:2i:21:PRO:HA	40:2i:59:PHE:HA	1.89	0.54
1:1A:2902:G:H4'	1:1A:2903:G:O5'	2.08	0.54
6:1G:150:ASP:OD1	6:1G:151:ALA:N	2.41	0.54
32:1a:67:C:H2'	32:1a:68:G:C8	2.43	0.54
33:1b:52:GLU:HG2	33:1b:56:ARG:HH12	1.73	0.54
1:2A:320:A:H4'	1:2A:322:A:C8	2.42	0.54
1:2A:1076:C:H4'	1:2A:1077:A:OP1	2.08	0.54
32:2a:922:G:H4'	36:2e:20:GLN:HA	1.90	0.54
32:2a:1376:U:H2'	32:2a:1377:A:C8	2.43	0.54
41:2j:11:PHE:HE1	41:2j:67:THR:HG22	1.73	0.54
1:1A:1899:A:H5'	1:1A:1900:G:OP2	2.07	0.54
1:1A:2298:A:H4'	1:1A:2299:A:O4'	2.08	0.54
8:1I:72:LEU:C	8:1I:74:ASN:H	2.16	0.54
32:1a:359:U:H2'	32:1a:360:A:C8	2.43	0.54
1:2A:2031:A:C6	1:2A:2498:C:H1'	2.43	0.54
1:2A:2156:G:O6	1:2A:2157:G:N2	2.38	0.54
32:2a:426:G:OP1	35:2d:38:TYR:OH	2.24	0.54
1:1A:1018:A:H8	1:1A:1018:A:OP1	1.91	0.54
6:1G:47:LYS:HG3	6:1G:48:GLU:H	1.73	0.54
15:1T:49:VAL:HG12	15:1T:63:VAL:HG22	1.88	0.54
19:1X:29:TRP:CE3	19:1X:78:LYS:HB3	2.43	0.54
26:14:57:GLU:HB2	26:14:58:ARG:HE	1.73	0.54
1:2A:1607:C:N4	1:2A:1622:G:OP2	2.40	0.54
1:2A:2112:G:H2'	1:2A:2113:U:H6	1.73	0.54
4:2E:9:VAL:HG22	4:2E:25:VAL:HB	1.89	0.54
5:2F:110:LEU:HD11	5:2F:181:LEU:HG	1.89	0.54
32:2a:667:G:O2'	46:2o:49:ASP:OD1	2.23	0.54
33:2b:18:GLY:HA2	33:2b:42:ILE:HG13	1.90	0.54
53:2x:61:C:H2'	53:2x:62:C:H6	1.73	0.54
1:1A:964:A:H5''	2:1B:98:G:O2'	2.08	0.53
1:1A:1185:C:O3'	9:1N:25:ARG:NH1	2.41	0.53
15:1T:53:ARG:O	15:1T:59:THR:HB	2.08	0.53
32:1a:1312:G:H5'	50:1s:5:LEU:HD12	1.90	0.53
48:1q:56:VAL:HB	48:1q:78:GLU:HB3	1.90	0.53
1:2A:1416:G:O2'	1:2A:1417:C:OP2	2.25	0.53
1:2A:2125:G:H22	1:2A:2172:U:H3'	1.72	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:2H:150:ALA:HA	7:2H:153:LYS:HG3	1.89	0.53
32:2a:424:G:H2'	32:2a:425:G:H8	1.73	0.53
1:1A:171:A:N3	1:1A:460:C:O2'	2.39	0.53
1:1A:275:C:H2'	1:1A:276:C:C6	2.43	0.53
1:1A:2476:C:H1'	63:1A:4823:HOH:O	2.07	0.53
6:1G:97:ASP:HA	6:1G:100:TRP:HD1	1.73	0.53
32:1a:501:C:H2'	32:1a:502:G:C8	2.43	0.53
40:1i:9:ARG:HG2	40:1i:14:VAL:HG13	1.90	0.53
5:2F:156:LEU:HD21	5:2F:163:VAL:HG12	1.90	0.53
8:2I:57:ARG:O	8:2I:61:ARG:HG2	2.08	0.53
30:28:33:ASN:HA	30:28:36:LYS:HD2	1.89	0.53
32:2a:108:G:C6	51:2t:15:ARG:HG2	2.43	0.53
32:2a:646:U:H2'	32:2a:647:C:C6	2.43	0.53
32:2a:1144:G:N2	32:2a:1146:A:H62	2.06	0.53
7:1H:3:ARG:HH22	7:1H:66:GLY:N	2.07	0.53
35:1d:128:VAL:HG12	35:1d:129:ASN:HD22	1.73	0.53
1:2A:1057:A:N1	1:2A:1081:U:O4	2.40	0.53
5:2F:161:GLU:O	5:2F:165:ARG:HG3	2.08	0.53
26:24:40:HIS:HB3	26:24:43:TYR:CD2	2.43	0.53
32:2a:1024:G:H2'	32:2a:1024:G:N3	2.24	0.53
32:2a:1275:A:H2'	32:2a:1276:G:O4'	2.08	0.53
33:2b:16:HIS:O	33:2b:18:GLY:N	2.38	0.53
1:1A:1098:C:H2'	1:1A:1099:C:O4'	2.08	0.53
1:1A:2144:U:H2'	1:1A:2145:G:C8	2.42	0.53
7:1H:27:LYS:HG2	7:1H:32:GLU:HG2	1.89	0.53
13:1R:59:ASP:OD1	13:1R:59:ASP:N	2.40	0.53
19:1X:44:GLU:HG3	19:1X:51:VAL:HG23	1.90	0.53
32:1a:1370:G:H4'	40:1i:12:GLU:HG3	1.90	0.53
13:2R:51:LEU:HD22	13:2R:66:VAL:HG13	1.91	0.53
32:2a:316:G:OP2	32:2a:351:G:O2'	2.26	0.53
35:2d:25:ARG:NH1	35:2d:30:LYS:O	2.42	0.53
7:1H:3:ARG:HE	7:1H:54:ARG:HH12	1.57	0.53
26:14:15:ILE:HD12	26:14:21:VAL:HG22	1.91	0.53
32:1a:1314:C:H2'	32:1a:1315:U:C6	2.44	0.53
33:1b:219:VAL:HA	33:1b:222:ILE:HD12	1.91	0.53
40:1i:8:GLY:O	40:1i:15:ALA:N	2.36	0.53
21:2Z:179:ASP:H	21:2Z:182:LYS:HE3	1.74	0.53
1:1A:405:C:N4	63:1A:5502:HOH:O	2.42	0.53
1:1A:560:C:O3'	16:1U:53:ARG:NH1	2.42	0.53
1:1A:2122:G:H1	1:1A:2211:U:H3	1.56	0.53
7:1H:41:MET:HE2	7:1H:65:HIS:HA	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:1P:100:LEU:HD12	11:1P:112:LEU:HD11	1.91	0.53
13:1R:33:ARG:NH2	27:15:57:VAL:O	2.32	0.53
32:1a:1157:A:H61	32:1a:1178:G:N2	2.05	0.53
32:1a:1207:2MG:H2'	32:1a:1208:C:H6	1.74	0.53
1:2A:807:U:OP2	11:2P:41:ARG:NH2	2.41	0.53
1:2A:2287:A:H61	1:2A:2344:U:H3	1.56	0.53
1:2A:2377:A:H2'	1:2A:2378:A:C8	2.43	0.53
32:2a:707:C:H2'	32:2a:708:C:C6	2.43	0.53
51:2t:16:HIS:O	51:2t:19:SER:OG	2.21	0.53
5:1F:110:LEU:HD12	5:1F:205:ARG:HD2	1.91	0.53
14:1S:25:ARG:NH1	14:1S:42:ASP:OD1	2.41	0.53
14:1S:27:SER:HA	14:1S:88:ASP:HB3	1.91	0.53
32:1a:1015:A:H2'	32:1a:1016:A:C8	2.44	0.53
32:1a:1218:C:H2'	32:1a:1219:U:C6	2.43	0.53
1:2A:2511:U:O4	1:2A:2575:C:N3	2.41	0.53
11:2P:97:PRO:HD3	11:2P:126:VAL:O	2.09	0.53
12:2Q:30:GLY:HA2	12:2Q:107:ALA:HB2	1.91	0.53
32:2a:1326:C:OP1	52:2u:12:LYS:NZ	2.40	0.53
34:2c:6:HIS:HD2	34:2c:8:ILE:H	1.54	0.53
41:2j:32:ALA:HB1	41:2j:33:GLN:HA	1.91	0.53
44:2m:82:MET:HE3	44:2m:92:HIS:HB3	1.91	0.53
47:2p:75:ARG:HG3	47:2p:80:PHE:HD2	1.74	0.53
1:1A:1653:C:N4	1:1A:1668:G:OP2	2.38	0.53
1:1A:2188:G:O6	1:1A:2194:U:C5	2.62	0.53
20:1Y:43:ASN:HB3	20:1Y:65:ALA:HB3	1.89	0.53
32:1a:539:A:H2'	32:1a:540:G:H8	1.73	0.53
47:1p:5:ARG:HH12	47:1p:28:ARG:HA	1.74	0.53
1:2A:1278:A:OP1	13:2R:36:THR:HG23	2.08	0.53
2:2B:95:C:N4	63:2B:3112:HOH:O	2.41	0.53
21:2Z:119:GLU:OE1	21:2Z:122:ARG:NH1	2.42	0.53
37:2f:99:ALA:HB2	49:2r:31:LEU:HD11	1.89	0.53
1:1A:39:C:O2	5:1F:46:ARG:NH2	2.41	0.53
1:1A:70:A:N7	19:1X:31:HIS:HE1	2.07	0.53
1:1A:2418:U:H2'	1:1A:2418:U:OP2	2.09	0.53
22:10:43:THR:OG1	22:10:46:LYS:HG2	2.08	0.53
22:10:70:GLN:HG2	22:10:80:HIS:HE2	1.74	0.53
32:1a:45:U:H2'	32:1a:46:G:C8	2.44	0.53
32:1a:1003:G:N2	32:1a:1004:A:N3	2.57	0.53
32:1a:1117:G:H4'	40:1i:104:ARG:NH1	2.24	0.53
1:2A:639:U:H2'	1:2A:640:C:C6	2.44	0.53
1:2A:1826:G:H4'	3:2D:242:ARG:CZ	2.39	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2184:G:C2	1:2A:2185:C:H1'	2.43	0.53
3:2D:75:ILE:HG21	3:2D:99:ASP:HB2	1.90	0.53
32:2a:300:A:O2'	32:2a:564:C:N3	2.38	0.53
1:1A:178:G:O6	1:1A:194:G:O2'	2.24	0.53
1:1A:664:U:H2'	1:1A:665:C:C6	2.44	0.53
1:1A:1836:U:O2	3:1D:50:THR:HB	2.09	0.53
1:1A:1895:U:OP1	1:1A:2422:G:O2'	2.26	0.53
1:1A:2801:C:OP1	4:1E:61:ARG:NH2	2.42	0.53
5:1F:110:LEU:HD21	5:1F:181:LEU:HG	1.91	0.53
21:1Z:198:LYS:HD3	21:1Z:202:GLU:HB2	1.90	0.53
39:1h:86:ILE:HG12	39:1h:135:CYS:HA	1.90	0.53
1:2A:2010:G:H5''	18:2W:42:ARG:HB2	1.90	0.53
4:2E:28:ALA:HB3	4:2E:93:VAL:HG12	1.90	0.53
32:2a:501:C:H2'	32:2a:502:G:C8	2.43	0.53
48:2q:19:VAL:HG23	48:2q:44:ALA:HB3	1.91	0.53
1:1A:714:U:O2	30:18:2:PRO:HD2	2.09	0.52
12:1Q:8:LYS:HA	21:1Z:197:ILE:HB	1.91	0.52
17:1V:43:GLU:OE1	17:1V:43:GLU:N	2.42	0.52
23:11:64:ALA:HA	23:11:67:ILE:HG13	1.91	0.52
27:15:41:PRO:O	27:15:44:THR:OG1	2.26	0.52
32:1a:96:U:H2'	32:1a:97:G:C8	2.42	0.52
32:1a:486:U:H2'	32:1a:487:A:H8	1.75	0.52
32:1a:1029:C:N4	32:1a:1030:C:H41	2.07	0.52
32:1a:1513:A:H2'	32:1a:1514:C:C6	2.44	0.52
13:2R:36:THR:HG22	13:2R:37:THR:H	1.74	0.52
32:2a:407:G:H2'	32:2a:408:A:C8	2.44	0.52
32:2a:737:A:H2'	32:2a:738:C:C6	2.44	0.52
32:2a:1292:U:P	38:2g:41:ARG:HH22	2.32	0.52
39:2h:26:VAL:HG22	39:2h:59:LEU:HB2	1.91	0.52
1:1A:2367:C:H1'	22:10:39:ARG:HH21	1.74	0.52
1:1A:2416:C:O3'	11:1P:77:ARG:NH2	2.42	0.52
32:1a:1003:G:H21	32:1a:1004:A:H1'	1.74	0.52
32:1a:1027:C:H2'	32:1a:1028:C:C6	2.44	0.52
33:1b:87:ARG:HH21	33:1b:219:VAL:HG12	1.74	0.52
41:1j:39:PRO:HA	41:1j:70:ARG:HD3	1.90	0.52
46:1o:39:LEU:HD13	46:1o:56:LEU:HB2	1.89	0.52
53:1x:53:G:H2'	53:1x:54:5MU:H6	1.74	0.52
2:2B:6:C:N3	2:2B:115:G:N2	2.44	0.52
32:2a:563:A:N6	63:2a:5035:HOH:O	2.42	0.52
32:2a:1411:C:N4	32:2a:1489:G:H1	2.04	0.52
1:1A:1100:A:H61	1:1A:1151:U:H3	1.58	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:950:U:H2'	32:1a:951:G:H8	1.75	0.52
1:2A:1710:C:H2'	1:2A:1711:C:H6	1.74	0.52
1:2A:1796:U:H2'	1:2A:1797:C:C6	2.44	0.52
1:2A:2360:A:H2'	1:2A:2361:A:O4'	2.09	0.52
17:2V:72:VAL:HG13	17:2V:85:LYS:HB3	1.92	0.52
32:2a:448:A:P	32:2a:485:G:H22	2.32	0.52
32:2a:1517:G:H3'	32:2a:1518:MA6:H8	1.90	0.52
38:2g:26:PHE:CE2	38:2g:30:ILE:HD11	2.45	0.52
39:2h:42:GLU:HG3	39:2h:109:ILE:HD13	1.90	0.52
1:1A:2156:A:OP2	1:1A:2178:G:N1	2.42	0.52
7:1H:11:VAL:HG21	7:1H:50:VAL:HG23	1.90	0.52
1:2A:876:C:H2'	1:2A:877:U:O4'	2.10	0.52
1:2A:2129:C:H2'	1:2A:2130:U:C2	2.44	0.52
6:2G:161:THR:HG22	6:2G:163:ALA:H	1.75	0.52
32:2a:123:C:OP1	32:2a:311:C:O2'	2.26	0.52
32:2a:728:A:H2'	32:2a:729:A:C8	2.43	0.52
32:2a:1022:G:H2'	32:2a:1023:G:C8	2.44	0.52
1:1A:1387:U:O4'	19:1X:57:LEU:HD23	2.10	0.52
1:1A:1900:G:H2'	1:1A:1901:C:C6	2.45	0.52
32:1a:1005:A:C5	32:1a:1024:G:N2	2.76	0.52
35:1d:60:GLU:OE1	35:1d:199:ASN:N	2.42	0.52
35:1d:119:GLN:HG3	35:1d:123:HIS:CE1	2.44	0.52
44:1m:49:THR:HG22	44:1m:51:ALA:H	1.74	0.52
3:2D:182:LEU:HB2	3:2D:272:ALA:HB3	1.92	0.52
10:2O:68:GLU:HB3	10:2O:78:ARG:HB2	1.90	0.52
17:2V:35:LEU:HB2	17:2V:57:VAL:HG13	1.90	0.52
32:2a:1028:C:H1'	32:2a:1034:G:H1'	1.91	0.52
1:1A:240:A:C5	1:1A:241:G:H1'	2.45	0.52
1:1A:1500:A:H5''	63:1A:5224:HOH:O	2.09	0.52
13:1R:96:ARG:HH12	13:1R:117:VAL:HG13	1.74	0.52
32:1a:957:U:H4'	50:1s:79:THR:HB	1.90	0.52
41:1j:8:LEU:HB2	41:1j:70:ARG:HB2	1.90	0.52
47:1p:75:ARG:HG3	47:1p:80:PHE:HB2	1.90	0.52
48:1q:81:ARG:HH21	48:1q:84:LEU:HD21	1.75	0.52
1:2A:1247:A:OP1	5:2F:95:ARG:NH2	2.31	0.52
1:2A:1250:G:H5''	63:2A:4844:HOH:O	2.08	0.52
1:2A:1514:U:H2'	1:2A:1515:G:C8	2.45	0.52
1:2A:2012:G:H4'	18:2W:96:ILE:HD13	1.92	0.52
1:2A:2067:G:O2'	1:2A:2069:G:H5'	2.09	0.52
1:2A:2125:G:O2'	1:2A:2173:A:N6	2.41	0.52
7:2H:3:ARG:HE	7:2H:54:ARG:HH12	1.58	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:300:A:H8	32:2a:300:A:O5'	1.93	0.52
49:2r:56:THR:HB	49:2r:58:LEU:HD13	1.92	0.52
1:1A:1425:A:H4'	1:1A:1426:G:OP2	2.08	0.52
6:1G:110:ALA:HB1	6:1G:140:ILE:HG22	1.92	0.52
36:1e:12:LEU:HB3	36:1e:31:LEU:HB2	1.91	0.52
1:2A:854:G:H2'	1:2A:855:G:C8	2.39	0.52
1:2A:2146:C:H4'	1:2A:2147:G:C8	2.45	0.52
1:2A:2659:G:O2'	7:2H:175:LYS:NZ	2.42	0.52
1:2A:2870:C:H2'	1:2A:2871:C:O4'	2.09	0.52
8:2I:65:ALA:O	8:2I:69:LYS:N	2.41	0.52
13:2R:55:ALA:HB2	13:2R:79:LEU:HD13	1.91	0.52
32:2a:520:A:N1	32:2a:536:C:H1'	2.25	0.52
32:2a:634:C:H2'	32:2a:635:G:H8	1.74	0.52
35:2d:128:VAL:HG12	35:2d:129:ASN:HD22	1.73	0.52
38:2g:20:ASP:HB3	38:2g:23:VAL:HB	1.90	0.52
36:1e:33:VAL:HG13	36:1e:112:LEU:HD12	1.92	0.52
40:1i:29:ASN:N	40:1i:63:ILE:O	2.40	0.52
49:1r:56:THR:HB	49:1r:58:LEU:HD13	1.92	0.52
53:1x:36:U:O2	55:B:114:A:N1	2.43	0.52
1:2A:581:C:H2'	1:2A:582:G:C8	2.45	0.52
1:2A:1405:U:H2'	1:2A:1406:U:C6	2.45	0.52
1:2A:2086:U:H2'	1:2A:2087:G:C8	2.44	0.52
1:2A:2638:G:P	4:2E:82:ARG:HH12	2.33	0.52
3:2D:79:VAL:HG21	3:2D:111:LEU:HD11	1.91	0.52
32:2a:45:U:H2'	32:2a:46:G:C8	2.44	0.52
33:2b:122:PHE:HA	33:2b:127:ILE:HG12	1.91	0.52
35:2d:102:ASP:HB2	35:2d:118:ARG:HG2	1.92	0.52
44:2m:33:ALA:O	44:2m:37:THR:OG1	2.25	0.52
2:1B:19:G:H1	2:1B:64:C:H42	1.57	0.52
9:1N:34:LEU:O	9:1N:49:GLY:HA3	2.10	0.52
32:1a:164:U:H2'	32:1a:165:C:C6	2.45	0.52
32:1a:1012:U:H2'	32:1a:1013:G:C8	2.44	0.52
32:1a:1316:G:H4'	45:1n:18:VAL:HG13	1.91	0.52
33:1b:127:ILE:HG22	33:1b:130:ARG:HG2	1.91	0.52
35:1d:121:VAL:O	35:1d:134:ASP:HA	2.10	0.52
1:2A:637:A:OP1	11:2P:133:SER:OG	2.23	0.52
1:2A:1919:A:N1	32:2a:1495:U:O2'	2.34	0.52
1:2A:2140:C:H2'	1:2A:2141:G:C8	2.41	0.52
11:2P:138:LEU:HD23	11:2P:145:PRO:HB3	1.90	0.52
32:2a:790:A:OP1	53:2x:38:A:O2'	2.26	0.52
32:2a:1404:5MC:O2	32:2a:1519:MA6:O2'	2.25	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1513:A:H2'	32:2a:1514:C:C6	2.45	0.52
36:2e:31:LEU:HD22	36:2e:43:LEU:HD11	1.92	0.52
1:1A:953:U:H4'	12:1Q:101:ARG:HH22	1.75	0.52
1:1A:1091:A:H1'	1:1A:1093:G:N3	2.23	0.52
1:1A:1432:C:H2'	1:1A:1433:C:C6	2.44	0.52
2:1B:66:A:H61	2:1B:108:U:H2'	1.75	0.52
7:1H:9:ILE:HD11	7:1H:69:ARG:HG2	1.92	0.52
11:1P:17:LYS:HE3	11:1P:27:HIS:CE1	2.45	0.52
32:1a:920:U:H2'	32:1a:921:U:C6	2.45	0.52
40:1i:46:ALA:HB2	40:1i:74:ILE:HG23	1.91	0.52
41:1j:81:THR:HA	41:1j:84:GLN:HE21	1.75	0.52
1:2A:1063:G:H2'	1:2A:1065:U:C6	2.45	0.52
6:2G:106:LEU:HD12	6:2G:110:ALA:HB3	1.92	0.52
13:2R:38:VAL:HG12	13:2R:42:LYS:HE3	1.92	0.52
18:2W:9:TYR:H	18:2W:102:HIS:CE1	2.27	0.52
32:2a:1182:G:H5'	32:2a:1184:G:H5'	1.92	0.52
32:2a:1218:C:H2'	32:2a:1219:U:C6	2.45	0.52
43:2l:110:VAL:HB	43:2l:113:ARG:HG2	1.92	0.52
1:1A:2389:A:H2'	1:1A:2390:A:C8	2.45	0.51
21:1Z:52:SER:OG	21:1Z:53:ILE:N	2.40	0.51
26:14:47:GLN:HG2	26:14:49:PHE:H	1.74	0.51
32:1a:263:A:OP2	51:1t:79:ARG:NH1	2.42	0.51
32:1a:1070:U:H2'	32:1a:1071:C:C6	2.45	0.51
32:1a:1346:A:N1	32:1a:1374:A:H5''	2.24	0.51
1:2A:271(E):U:H2'	1:2A:271(F):C:C6	2.45	0.51
1:2A:2079:U:O3'	23:21:35:THR:OG1	2.28	0.51
5:2F:184:TYR:CE2	5:2F:188:ARG:HD2	2.45	0.51
8:2I:77:LEU:HD11	8:2I:100:ALA:HB1	1.91	0.51
20:2Y:47:LYS:NZ	20:2Y:48:ALA:O	2.43	0.51
1:1A:843:C:H2'	1:1A:844:C:C6	2.45	0.51
3:1D:164:GLN:OE1	3:1D:176:ARG:NH2	2.43	0.51
7:1H:124:GLU:OE2	7:1H:132:ARG:HD2	2.09	0.51
32:1a:167:G:H2'	32:1a:168:G:H8	1.74	0.51
32:1a:982:U:H5''	45:1n:6:LEU:HD21	1.91	0.51
42:1k:82:VAL:HB	42:1k:108:ILE:HG12	1.92	0.51
44:1m:97:PRO:HA	44:1m:110:ARG:HG3	1.91	0.51
1:2A:172:C:H2'	1:2A:173:G:H8	1.75	0.51
1:2A:817:C:O2'	1:2A:839:U:H5''	2.10	0.51
1:2A:2224:G:OP1	3:2D:268:ARG:NE	2.43	0.51
1:2A:2291:U:H2'	1:2A:2292:C:C6	2.46	0.51
32:2a:96:U:H2'	32:2a:97:G:H8	1.74	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:2d:13:ARG:NH1	35:2d:38:TYR:O	2.42	0.51
53:2x:43:A:H2'	53:2x:44:A:C8	2.46	0.51
1:1A:1219:A:H4'	1:1A:1220:U:OP1	2.09	0.51
32:1a:1023:G:H2'	32:1a:1024:G:C8	2.45	0.51
1:2A:500:G:N1	1:2A:503:A:OP2	2.43	0.51
17:2V:60:GLU:OE1	17:2V:97:LYS:NZ	2.43	0.51
32:2a:153:C:H2'	32:2a:154:C:H6	1.75	0.51
40:2i:67:GLY:O	40:2i:73:GLN:NE2	2.38	0.51
1:1A:1263:C:H42	1:1A:1277:G:H1	1.57	0.51
1:1A:2331:G:N2	14:1S:3:ARG:HA	2.25	0.51
25:13:29:ARG:HG3	25:13:30:ARG:HG3	1.91	0.51
30:18:33:ASN:HA	30:18:36:LYS:HD2	1.93	0.51
32:1a:1187:G:H4'	40:1i:111:ARG:HH11	1.75	0.51
34:1c:42:LEU:O	34:1c:46:GLU:HG2	2.10	0.51
35:1d:79:PHE:CE1	35:1d:204:ILE:HD13	2.45	0.51
39:1h:42:GLU:HG3	39:1h:109:ILE:HD13	1.92	0.51
51:1t:11:SER:O	51:1t:14:LYS:HB3	2.10	0.51
1:2A:2172:U:H4'	1:2A:2173:A:OP2	2.10	0.51
7:2H:159:GLU:HG3	7:2H:169:VAL:HG11	1.91	0.51
32:2a:973:G:H3'	32:2a:974:A:H5''	1.91	0.51
32:2a:1435:G:H2'	32:2a:1436:U:C6	2.46	0.51
35:2d:79:PHE:HE1	35:2d:204:ILE:HD13	1.76	0.51
37:2f:89:MET:HE1	49:2r:72:ARG:HB3	1.92	0.51
1:1A:1834:A:O2'	3:1D:259:THR:HG21	2.09	0.51
32:1a:1246:C:N4	32:1a:1291:G:H1	2.08	0.51
46:1o:78:TYR:CZ	46:1o:82:ILE:HD13	2.44	0.51
53:1x:8:4SU:O5'	53:1x:8:4SU:H6	2.10	0.51
1:2A:526:A:O2'	1:2A:2043:C:O2	2.27	0.51
2:2B:49:C:H2'	2:2B:50:G:C8	2.46	0.51
6:1G:131:TYR:HB3	6:1G:159:VAL:HG13	1.92	0.51
32:1a:175:C:H2'	32:1a:176:C:C6	2.45	0.51
33:1b:54:THR:HG21	33:1b:201:ILE:HD11	1.92	0.51
35:1d:8:VAL:HG22	35:1d:21:LEU:HD13	1.93	0.51
35:1d:61:LYS:HD2	35:1d:207:TYR:OH	2.11	0.51
6:2G:150:ASP:OD1	6:2G:151:ALA:N	2.43	0.51
7:2H:86:GLU:OE2	7:2H:132:ARG:NH2	2.43	0.51
12:2Q:16:ARG:HG2	12:2Q:18:LYS:HD3	1.93	0.51
20:2Y:19:LYS:HE2	20:2Y:20:TYR:CE2	2.46	0.51
32:2a:297:G:N2	32:2a:300:A:OP2	2.42	0.51
42:2k:115:PRO:HB2	42:2k:117:ASN:C	2.36	0.51
47:2p:5:ARG:NH2	47:2p:28:ARG:HA	2.26	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1055:A:OP2	9:1N:37:LYS:NZ	2.32	0.51
15:1T:16:ARG:NH2	15:1T:83:ILE:O	2.42	0.51
32:1a:452:A:H4'	47:1p:72:ARG:NH1	2.26	0.51
32:1a:1003:G:N2	32:1a:1004:A:H1'	2.26	0.51
36:1e:100:VAL:HG22	36:1e:118:ILE:HG22	1.93	0.51
1:2A:2641:G:P	9:2N:74:ARG:HH22	2.32	0.51
3:2D:108:PRO:HB3	3:2D:143:HIS:HE1	1.76	0.51
4:2E:181:LEU:HD11	15:2T:6:LEU:HD23	1.93	0.51
10:2O:98:VAL:HG13	10:2O:117:LEU:HB3	1.93	0.51
12:2Q:111:GLU:O	12:2Q:115:MET:HG2	2.10	0.51
30:28:14:VAL:HG23	30:28:24:ALA:HB2	1.92	0.51
32:2a:1001:A:H2'	32:2a:1001(A):G:H8	1.74	0.51
1:1A:2454:C:H2'	1:1A:2455:C:H6	1.75	0.51
1:1A:2579:G:H2'	1:1A:2580:C:C6	2.46	0.51
3:1D:75:ILE:HG21	3:1D:99:ASP:HB2	1.91	0.51
15:1T:56:GLY:O	15:1T:59:THR:HG23	2.11	0.51
32:1a:36:C:O2'	32:1a:501:C:OP1	2.28	0.51
32:1a:542:G:H5'	35:1d:41:GLY:HA3	1.93	0.51
1:2A:121:G:H4'	1:2A:149:A:H5'	1.93	0.51
1:2A:807:U:O2'	1:2A:2060:A:N1	2.44	0.51
1:2A:1899:G:H2'	1:2A:1899:G:N3	2.26	0.51
6:2G:96:ARG:O	6:2G:99:MET:HB3	2.10	0.51
32:2a:955:U:O2	50:2s:83:HIS:NE2	2.34	0.51
47:2p:20:VAL:HG21	47:2p:32:TYR:CG	2.46	0.51
1:1A:1750:G:H2'	1:1A:1751:G:H8	1.74	0.51
21:1Z:19:ARG:HH11	21:1Z:84:GLU:HB2	1.76	0.51
25:13:37:LEU:HB3	25:13:43:ILE:HD13	1.92	0.51
32:1a:309:G:O2'	32:1a:607:A:N1	2.44	0.51
41:1j:26:ALA:HB1	41:1j:84:GLN:OE1	2.11	0.51
1:2A:422:A:H2'	1:2A:423:A:C8	2.46	0.51
1:2A:900:A:H2'	1:2A:901:A:O4'	2.10	0.51
2:2B:2:C:H2'	2:2B:3:C:H6	1.75	0.51
32:2a:737:A:H1'	37:2f:73:ASN:HD21	1.76	0.51
32:2a:1028:C:C2	32:2a:1033:G:N2	2.79	0.51
32:2a:1346:A:OP1	40:2i:120:ARG:NH1	2.43	0.51
42:2k:48:ILE:HD11	42:2k:64:ALA:HA	1.93	0.51
1:1A:517:A:H2'	1:1A:518:G:O4'	2.10	0.51
1:1A:2831:A:OP2	4:1E:110:GLY:N	2.39	0.51
1:2A:1803:A:O2'	3:2D:259:THR:HG21	2.11	0.51
2:2B:112:U:H2'	2:2B:113:G:H8	1.76	0.51
32:2a:1510:U:H2'	32:2a:1511:G:C8	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:2c:152:ILE:HG22	34:2c:167:TRP:HB2	1.93	0.51
1:1A:19:C:OP2	16:1U:30:LYS:NZ	2.44	0.50
1:1A:1560:U:H2'	1:1A:1561:C:C6	2.46	0.50
1:1A:2240:G:OP1	3:1D:261:LYS:NZ	2.36	0.50
1:1A:2376:C:H2'	1:1A:2377:G:O4'	2.11	0.50
32:1a:406:G:N2	35:1d:119:GLN:HE22	2.08	0.50
32:1a:769:G:H4'	32:1a:1513:A:H4'	1.92	0.50
32:1a:1510:U:H2'	32:1a:1511:G:C8	2.46	0.50
44:1m:58:GLU:O	44:1m:62:ASN:ND2	2.38	0.50
1:2A:26:G:H1'	1:2A:515:A:H61	1.76	0.50
1:2A:1062:G:H2'	1:2A:1063:G:C8	2.46	0.50
1:2A:2133:G:O2'	1:2A:2158:A:N6	2.44	0.50
1:2A:2321:G:O2'	1:2A:2322:A:OP1	2.28	0.50
32:2a:51:A:H61	32:2a:314:C:H1'	1.77	0.50
32:2a:164:U:H2'	32:2a:165:C:C6	2.47	0.50
33:2b:24:TRP:CD1	33:2b:24:TRP:H	2.29	0.50
43:2l:117:ARG:NH2	43:2l:124:LYS:HB2	2.26	0.50
1:1A:312:C:H2'	1:1A:313:A:H8	1.76	0.50
1:1A:794:U:O2	1:1A:2036:A:H1'	2.12	0.50
1:1A:2171:G:H2'	1:1A:2172:U:O4'	2.11	0.50
5:1F:13:SER:OG	5:1F:127:GLU:OE1	2.24	0.50
10:1O:120:GLU:OE1	15:1T:67:SER:OG	2.23	0.50
13:1R:12:ARG:O	13:1R:17:ARG:NH1	2.44	0.50
32:1a:265:G:O3'	48:1q:66:SER:HA	2.11	0.50
1:2A:277:C:H4'	1:2A:278:A:OP2	2.12	0.50
1:2A:579:G:H2'	1:2A:580:C:C6	2.46	0.50
1:2A:800:A:H8	1:2A:800:A:OP1	1.93	0.50
1:2A:1078:U:O2'	1:2A:1079:C:OP2	2.28	0.50
1:2A:1263:U:H1'	27:25:10:LYS:HG3	1.93	0.50
6:2G:145:THR:HG23	6:2G:148:MET:H	1.75	0.50
32:2a:96:U:H2'	32:2a:97:G:C8	2.46	0.50
50:2s:22:LEU:HB3	50:2s:27:GLU:HB3	1.93	0.50
50:2s:31:ILE:HB	50:2s:49:ILE:HG13	1.93	0.50
1:1A:211:A:H3'	1:1A:448:U:H5'	1.93	0.50
32:1a:452:A:N7	32:1a:480:U:O4	2.43	0.50
32:1a:1317:C:OP1	45:1n:17:LYS:HG2	2.11	0.50
50:1s:48:THR:HG22	50:1s:61:TYR:HA	1.94	0.50
1:2A:16:G:H2'	1:2A:17:G:H8	1.76	0.50
1:2A:1935:G:H1'	1:2A:1964:G:N2	2.27	0.50
12:2Q:60:ARG:NH2	21:2Z:181:GLU:OE2	2.44	0.50
34:2c:71:ALA:O	34:2c:73:PRO:HD3	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1e:33:VAL:HG21	36:1e:109:ILE:HA	1.93	0.50
42:1k:91:ARG:NH1	42:1k:110:ASP:OD2	2.45	0.50
1:2A:8:A:H2'	1:2A:9:U:C6	2.46	0.50
26:24:58:ARG:HD3	44:2m:80:ARG:HE	1.75	0.50
43:2l:53:ARG:NH2	43:2l:92:OTD:OD1	2.44	0.50
1:1A:542:C:OP1	27:15:16:ARG:NH2	2.44	0.50
1:1A:1557:A:H2'	1:1A:1558:G:O4'	2.11	0.50
1:1A:1588:G:H5''	1:1A:1589:A:OP2	2.12	0.50
1:1A:2573:A:H2	10:1O:23:ARG:NH2	2.09	0.50
1:1A:2879:G:H2'	1:1A:2880:C:O4'	2.12	0.50
16:1U:97:ASP:OD1	16:1U:101:ARG:NH1	2.45	0.50
32:1a:143:A:C2	32:1a:220:G:N1	2.68	0.50
32:1a:1143:G:H2'	32:1a:1144:G:C8	2.47	0.50
1:2A:1996:C:H4'	1:2A:1997:G:OP1	2.11	0.50
4:2E:116:VAL:HG13	4:2E:122:PHE:HB2	1.92	0.50
18:2W:78:GLU:OE2	18:2W:99:ARG:NH1	2.40	0.50
32:2a:1436:U:H2'	32:2a:1437:C:O4'	2.12	0.50
35:2d:175:SER:HB3	35:2d:186:LEU:HD11	1.92	0.50
46:2o:87:ILE:HG22	46:2o:88:ARG:N	2.27	0.50
1:1A:99:G:O3'	24:12:7:ARG:NH2	2.45	0.50
1:1A:1097:G:H2'	1:1A:1098:C:C6	2.47	0.50
3:1D:10:THR:OG1	3:1D:13:ARG:HG2	2.11	0.50
32:1a:950:U:H2'	32:1a:951:G:C8	2.47	0.50
32:1a:994:A:N1	32:1a:1047:G:H4'	2.26	0.50
1:2A:184:C:H2'	1:2A:185:U:C6	2.46	0.50
1:2A:1816:G:O6	3:2D:35:LYS:NZ	2.36	0.50
21:2Z:28:MET:HE1	21:2Z:61:LEU:HD11	1.92	0.50
32:2a:559:A:H4'	32:2a:560:U:H3'	1.94	0.50
32:2a:1010:G:H2'	32:2a:1011:G:C8	2.46	0.50
33:2b:166:ASP:HB3	33:2b:169:LYS:HB3	1.93	0.50
39:2h:109:ILE:HG13	39:2h:137:VAL:HG23	1.93	0.50
42:2k:115:PRO:C	42:2k:117:ASN:HA	2.35	0.50
42:2k:116:HIS:N	42:2k:117:ASN:HA	2.27	0.50
43:2l:117:ARG:HB3	43:2l:122:THR:O	2.12	0.50
46:2o:55:GLY:HA2	46:2o:58:MET:HE3	1.93	0.50
1:1A:207:A:C2	1:1A:224:U:H4'	2.46	0.50
1:1A:1346:U:H4'	1:1A:1347:A:C5'	2.41	0.50
32:1a:392:G:H2'	32:1a:393:A:H8	1.76	0.50
25:23:8:LEU:O	25:23:32:GLN:N	2.41	0.50
32:2a:1135:U:H2'	32:2a:1137:C:N3	2.27	0.50
38:2g:27:ILE:HD12	38:2g:40:ALA:HA	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2044:U:O2'	1:1A:2629:C:H5'	2.11	0.50
1:1A:2308:U:OP2	14:1S:9:ARG:NH2	2.45	0.50
6:1G:38:VAL:HG22	6:1G:93:THR:HG23	1.93	0.50
6:1G:107:LEU:HD11	6:1G:178:PHE:CE1	2.46	0.50
10:1O:35:VAL:HG11	10:1O:103:ALA:HB3	1.93	0.50
32:1a:161:A:H2'	32:1a:162:A:C8	2.47	0.50
32:1a:664:G:H22	32:1a:741:G:H1	1.60	0.50
32:1a:1435:G:H2'	32:1a:1436:U:C6	2.47	0.50
1:2A:116:C:H2'	1:2A:117:G:O4'	2.11	0.50
1:2A:271(Z):C:H1'	1:2A:272(C):G:H1'	1.94	0.50
1:1A:26:G:C6	1:1A:27:G:N1	2.80	0.50
2:1B:14:U:OP2	2:1B:70:C:O2'	2.23	0.50
2:1B:103:G:H21	21:1Z:73:GLN:NE2	2.10	0.50
32:1a:1326:C:OP1	52:1u:12:LYS:NZ	2.42	0.50
36:1e:31:LEU:HD22	36:1e:43:LEU:HD11	1.94	0.50
1:2A:19:C:H2'	1:2A:20:C:H6	1.77	0.50
1:2A:1503:U:H2'	1:2A:1504:C:C6	2.47	0.50
1:2A:2327:A:H2'	1:2A:2328:A:C8	2.47	0.50
1:2A:2816:C:O2	1:2A:2883:A:O2'	2.28	0.50
32:2a:503:C:OP2	43:2l:116:SER:HB3	2.11	0.50
32:2a:1285:A:H4'	32:2a:1286:A:C5'	2.40	0.50
32:2a:1442:G:H2'	32:2a:1442:G:N3	2.27	0.50
34:2c:3:ASN:OD1	34:2c:3:ASN:N	2.44	0.50
47:2p:20:VAL:HG23	47:2p:35:LYS:HA	1.93	0.50
1:1A:2101:U:O3'	23:11:35:THR:OG1	2.29	0.49
1:1A:2701:U:H4'	1:1A:2702:C:H5'	1.94	0.49
6:1G:179:PRO:HB2	26:14:42:PHE:HE2	1.76	0.49
32:1a:986:A:H1'	50:1s:54:GLY:O	2.12	0.49
32:1a:1256:A:OP1	34:1c:26:LYS:NZ	2.36	0.49
32:1a:1504:G:H4'	32:1a:1505:G:C4	2.47	0.49
44:1m:59:TYR:CZ	44:1m:63:THR:HG21	2.47	0.49
49:1r:32:ARG:HA	49:1r:69:THR:HG21	1.94	0.49
53:1x:19:G:H4'	53:1x:20:U:OP2	2.12	0.49
1:2A:271(D):G:H2'	1:2A:271(E):U:C6	2.47	0.49
3:2D:148:GLU:HB2	3:2D:151:LYS:HD2	1.94	0.49
32:2a:280:C:N3	48:2q:39:SER:OG	2.37	0.49
35:2d:191:ARG:NE	35:2d:200:GLU:OE2	2.45	0.49
1:1A:590:A:OP2	11:1P:29:LYS:NZ	2.35	0.49
1:1A:1458:A:H2'	1:1A:1459:G:C8	2.48	0.49
1:1A:2832:G:O2'	1:1A:2834:C:OP2	2.29	0.49
5:1F:161:GLU:O	5:1F:165:ARG:HG3	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:411:A:OP2	35:1d:25:ARG:NH2	2.44	0.49
34:1c:50:ALA:HB1	34:1c:70:VAL:HG21	1.94	0.49
39:1h:121:ASP:OD1	39:1h:121:ASP:N	2.44	0.49
23:21:83:GLU:OE1	23:21:83:GLU:N	2.45	0.49
32:2a:1125:U:O2'	32:2a:1126:U:O5'	2.29	0.49
33:2b:8:LYS:HD2	33:2b:48:MET:HG3	1.94	0.49
40:2i:25:LYS:O	40:2i:61:ALA:N	2.44	0.49
44:2m:3:ARG:HH12	44:2m:11:ARG:HE	1.58	0.49
52:2u:5:ASP:O	52:2u:11:GLY:HA3	2.12	0.49
1:1A:27:G:N2	1:1A:537:G:H1'	2.28	0.49
1:1A:906:G:O2'	1:1A:962:G:O6	2.25	0.49
1:1A:2359:C:H2'	1:1A:2360:U:C6	2.47	0.49
1:1A:2724:U:O2'	1:1A:2725:A:OP2	2.25	0.49
5:1F:154:VAL:HG22	5:1F:191:ARG:HB2	1.94	0.49
32:1a:41:G:H2'	32:1a:42:G:C8	2.48	0.49
32:1a:69:G:H1	32:1a:100:C:H42	1.61	0.49
32:1a:407:G:H2'	32:1a:408:A:C8	2.46	0.49
32:1a:632:A:H5'	32:1a:633:G:OP2	2.13	0.49
32:1a:1030(C):G:H2'	32:1a:1030(D):A:H8	1.74	0.49
33:1b:109:SER:HA	33:1b:112:VAL:HG13	1.94	0.49
1:2A:588:U:H2'	1:2A:589:C:C6	2.47	0.49
1:2A:1506:C:H2'	1:2A:1507:A:H5'	1.94	0.49
1:2A:1803:A:H4'	3:2D:259:THR:HG23	1.94	0.49
1:2A:2102:U:C2	1:2A:2187:G:O6	2.65	0.49
1:2A:2443:C:H2'	1:2A:2444:G:H8	1.77	0.49
26:24:57:GLU:CB	26:24:58:ARG:HD2	2.41	0.49
32:2a:153:C:H2'	32:2a:154:C:C6	2.47	0.49
32:2a:858:G:O6	32:2a:869:G:H3'	2.13	0.49
32:2a:918:A:H2'	32:2a:919:A:C8	2.46	0.49
1:1A:494:G:N7	29:17:39:ARG:NH2	2.59	0.49
1:1A:1821:C:H5''	1:1A:1822:A:OP1	2.13	0.49
1:1A:2156:A:N6	1:1A:2179:G:H4'	2.28	0.49
1:1A:2596:U:O2	54:1y:5:PRO:HG3	2.12	0.49
2:1B:48:A:H2'	2:1B:49:C:C6	2.48	0.49
7:1H:125:VAL:HG12	7:1H:127:GLU:O	2.12	0.49
8:1I:38:LEU:HB2	8:1I:40:THR:HG23	1.94	0.49
13:1R:53:HIS:ND1	13:1R:94:TYR:OH	2.29	0.49
32:1a:943:U:H1'	40:1i:124:GLN:HE22	1.77	0.49
41:1j:11:PHE:CE1	41:1j:67:THR:HG22	2.48	0.49
47:1p:20:VAL:HG21	47:1p:32:TYR:CG	2.48	0.49
1:2A:667:U:O2	30:28:2:PRO:HD2	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1084:A:H3'	1:2A:1085:A:H4'	1.95	0.49
1:2A:2115:G:H4'	1:2A:2167:U:H4'	1.93	0.49
14:2S:15:ARG:HD3	14:2S:25:ARG:HH21	1.77	0.49
32:2a:542:G:H2'	32:2a:543:C:H6	1.76	0.49
32:2a:1010:G:N2	32:2a:1020:U:H1'	2.27	0.49
35:2d:173:TRP:CD1	35:2d:189:PRO:HG3	2.47	0.49
1:1A:641:G:OP1	5:1F:40:GLN:NE2	2.32	0.49
1:1A:2377:G:O6	30:18:39:LYS:HE3	2.12	0.49
1:1A:2405:A:O2'	11:1P:60:MET:O	2.22	0.49
32:1a:857:C:H2'	32:1a:858:G:O4'	2.12	0.49
32:1a:1401:G:C2	32:1a:1402:4OC:H1'	2.47	0.49
1:2A:125:G:OP1	29:27:14:LYS:NZ	2.46	0.49
1:2A:250:G:OP2	30:28:13:ARG:NH1	2.42	0.49
1:2A:740:U:H2'	1:2A:741:G:C8	2.47	0.49
1:2A:2404:C:O3'	11:2P:77:ARG:NH2	2.45	0.49
18:2W:65:LEU:HD12	18:2W:68:ARG:NE	2.28	0.49
25:23:6:VAL:HG12	25:23:56:VAL:HG22	1.95	0.49
32:2a:1172:C:H2'	32:2a:1173:G:H8	1.77	0.49
32:2a:1320:C:H2'	32:2a:1321:C:O4'	2.12	0.49
33:2b:55:PHE:HD1	33:2b:221:LEU:HD22	1.76	0.49
35:2d:150:GLU:HA	35:2d:153:ARG:HG3	1.94	0.49
37:2f:97:PHE:HB2	49:2r:32:ARG:NH1	2.27	0.49
1:1A:1302:G:H5'	1:1A:1303:C:OP2	2.11	0.49
1:1A:1735:U:O2	1:1A:1747:A:H5'	2.13	0.49
35:1d:18:LYS:NZ	35:1d:31:CYS:SG	2.85	0.49
53:1x:23:C:H2'	53:1x:24:U:C6	2.47	0.49
1:2A:958:U:O2	2:2B:90:A:O2'	2.23	0.49
1:2A:2310:A:N1	6:2G:79:ASN:ND2	2.59	0.49
20:2Y:20:TYR:CE2	20:2Y:43:ASN:HA	2.48	0.49
32:2a:1288:A:H2'	32:2a:1289:A:C8	2.47	0.49
32:2a:1305:G:H22	32:2a:1331:G:H1'	1.77	0.49
33:2b:102:LEU:HD23	33:2b:182:ILE:HD12	1.94	0.49
1:1A:997:G:OP1	12:1Q:16:ARG:NH2	2.46	0.49
1:1A:1285:G:H2'	1:1A:1286:U:O4'	2.12	0.49
22:10:27:GLU:HB2	22:10:69:PHE:HD1	1.78	0.49
32:1a:652:U:O4	32:1a:752:G:O2'	2.29	0.49
1:2A:271(K):U:O2	8:2I:50:ARG:HD2	2.12	0.49
1:2A:1518:U:H2'	1:2A:1519:G:O4'	2.11	0.49
1:2A:1932:A:H2'	1:2A:1933:G:O4'	2.13	0.49
1:2A:2146:C:H4'	1:2A:2147:G:N9	2.28	0.49
1:2A:2304:G:N2	6:2G:156:ASP:OD2	2.43	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:2H:117:PRO:HG3	7:2H:123:PHE:CD2	2.47	0.49
10:2O:68:GLU:OE1	10:2O:78:ARG:NH1	2.45	0.49
11:2P:88:LEU:HA	11:2P:91:PHE:HD2	1.78	0.49
32:2a:382:A:H2'	32:2a:383:A:C8	2.48	0.49
33:2b:16:HIS:HB2	33:2b:204:ASN:CB	2.42	0.49
38:2g:22:LEU:HD23	38:2g:63:LYS:HG2	1.95	0.49
1:1A:509:A:H5''	20:1Y:50:ARG:HD3	1.95	0.49
1:1A:1150:C:H2'	1:1A:1151:U:C6	2.48	0.49
1:1A:1475:G:H2'	1:1A:1476:C:C6	2.48	0.49
6:1G:11:TYR:HA	6:1G:15:VAL:HB	1.94	0.49
21:1Z:28:MET:HE1	21:1Z:61:LEU:HD21	1.94	0.49
32:1a:148:G:H1	32:1a:174:C:N4	2.10	0.49
1:2A:459:U:H2'	1:2A:460:A:H8	1.77	0.49
1:2A:1092:C:H2'	1:2A:1092:C:O2	2.12	0.49
1:2A:1493:C:N4	1:2A:2206:G:O2'	2.46	0.49
1:2A:2870:C:H5''	13:2R:65:LEU:HD21	1.95	0.49
5:2F:21:ALA:CB	5:2F:22:ALA:HA	2.42	0.49
8:2I:75:LEU:HD11	8:2I:105:HIS:ND1	2.28	0.49
20:2Y:6:HIS:CD2	20:2Y:7:VAL:HG23	2.48	0.49
32:2a:489:C:H2'	32:2a:490:G:H8	1.77	0.49
32:2a:500:G:N2	32:2a:546:G:H1'	2.27	0.49
32:2a:539:A:H2'	32:2a:540:G:C8	2.48	0.49
32:2a:1118:C:H1'	32:2a:1179:A:C4	2.48	0.49
47:2p:19:ILE:HG22	47:2p:36:ILE:HG13	1.95	0.49
1:1A:602:G:H2'	1:1A:603:C:C6	2.48	0.49
5:1F:197:ASP:N	5:1F:197:ASP:OD1	2.46	0.49
19:1X:57:LEU:HD11	19:1X:78:LYS:HE2	1.93	0.49
25:13:8:LEU:HD13	25:13:31:LEU:HD23	1.93	0.49
32:1a:232:G:H1'	32:1a:262:A:N1	2.28	0.49
38:1g:111:ARG:NH1	38:1g:113:GLU:OE2	2.44	0.49
50:1s:3:ARG:NH1	50:1s:10:PHE:HB2	2.23	0.49
1:2A:301:G:H1'	1:2A:302:C:C6	2.48	0.49
1:2A:1420:U:HO2'	1:2A:1421:G:P	2.36	0.49
1:2A:1962:5MC:O2'	1:2A:1964:G:OP2	2.31	0.49
6:2G:38:VAL:HG13	6:2G:91:ARG:HD3	1.95	0.49
14:2S:34:HIS:ND1	14:2S:53:SER:OG	2.40	0.49
24:22:28:LYS:HD2	24:22:60:LEU:HD11	1.95	0.49
33:2b:71:VAL:HG23	33:2b:164:VAL:HG13	1.94	0.49
1:1A:2825:C:H5'	27:15:29:THR:HG21	1.95	0.49
7:1H:3:ARG:HH21	7:1H:65:HIS:HB3	1.78	0.49
8:1I:3:VAL:HG12	8:1I:38:LEU:HA	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:1S:14:VAL:O	14:1S:18:ILE:HG12	2.13	0.49
21:1Z:198:LYS:HB2	21:1Z:202:GLU:C	2.38	0.49
32:1a:1316:G:N2	32:1a:1318:A:H3'	2.28	0.49
34:1c:8:ILE:HG23	34:1c:16:ARG:HD3	1.95	0.49
1:2A:1495:A:H2'	1:2A:1496:A:C8	2.48	0.49
1:2A:2206:G:H5''	1:2A:2207:G:N7	2.28	0.49
1:2A:2295:C:OP1	14:2S:10:ARG:NH1	2.46	0.49
6:2G:144:ILE:HA	6:2G:148:MET:SD	2.53	0.49
32:2a:1348:U:H4'	40:2i:120:ARG:HD2	1.94	0.49
32:2a:1376:U:H2'	32:2a:1377:A:H8	1.78	0.49
33:2b:91:PRO:HD3	33:2b:154:LEU:HD12	1.95	0.49
39:2h:36:LEU:HD12	39:2h:59:LEU:HD13	1.95	0.49
1:1A:2639:G:O2'	1:1A:2794:A:N1	2.38	0.48
23:11:77:ALA:HA	23:11:80:LEU:HD13	1.95	0.48
33:1b:83:MET:SD	33:1b:234:PRO:HB2	2.52	0.48
34:1c:11:ARG:NH2	34:1c:177:THR:O	2.45	0.48
51:1t:57:ARG:HH12	51:1t:100:ILE:HD12	1.77	0.48
1:2A:277:C:H1'	1:2A:278:A:OP1	2.13	0.48
1:2A:390:A:H4'	1:2A:391:G:H5'	1.95	0.48
1:2A:910:A:C5	12:2Q:13:GLN:HG3	2.48	0.48
1:2A:2133:G:N3	1:2A:2157:G:H2'	2.28	0.48
1:2A:2170:A:H8	1:2A:2170:A:O5'	1.95	0.48
1:2A:2320:A:N3	1:2A:2320:A:H2'	2.26	0.48
6:2G:97:ASP:HA	6:2G:100:TRP:CD1	2.40	0.48
7:2H:26:VAL:HG12	7:2H:79:VAL:HG21	1.95	0.48
32:2a:437:U:O2'	35:2d:123:HIS:HD2	1.95	0.48
32:2a:1028:C:H2'	32:2a:1033:G:N2	2.28	0.48
35:2d:173:TRP:CZ3	35:2d:193:ASP:HB3	2.47	0.48
39:2h:41:ARG:NH2	39:2h:123:GLU:OE2	2.45	0.48
49:2r:58:LEU:HB3	49:2r:62:GLU:HG3	1.94	0.48
1:1A:273:G:N2	8:1I:50:ARG:HH21	2.10	0.48
1:1A:1874:C:H5'	3:1D:253:GLN:NE2	2.29	0.48
1:1A:2188:G:OP2	1:1A:2188:G:H8	1.96	0.48
32:1a:269:C:H2'	32:1a:270:A:C8	2.48	0.48
37:1f:9:VAL:HB	37:1f:87:ARG:HB2	1.94	0.48
51:1t:56:MET:HE3	51:1t:85:MET:HG2	1.95	0.48
1:2A:873:G:H1	1:2A:904:C:H42	1.60	0.48
1:2A:1798:U:OP2	3:2D:274:ARG:NH2	2.40	0.48
2:2B:91:C:OP2	12:2Q:16:ARG:NH1	2.46	0.48
21:2Z:93:ASP:HA	21:2Z:131:ARG:HH12	1.78	0.48
32:2a:51:A:N1	32:2a:314:C:O2'	2.44	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:719:C:N4	49:2r:71:LYS:HE2	2.28	0.48
32:2a:946:A:O2'	32:2a:1333:A:N3	2.45	0.48
1:1A:1303:C:H4'	5:1F:83:PHE:CD1	2.48	0.48
1:1A:1961:5MU:OP1	1:1A:2616:U:O2'	2.31	0.48
3:1D:231:HIS:CD2	3:1D:249:PRO:HG3	2.48	0.48
16:1U:28:ARG:NH1	16:1U:38:THR:OG1	2.43	0.48
17:1V:95:LEU:HD23	17:1V:97:LYS:HE3	1.95	0.48
29:17:47:ARG:HE	29:17:47:ARG:HB3	1.36	0.48
32:1a:167:G:H2'	32:1a:168:G:C8	2.47	0.48
1:2A:631:A:OP2	30:28:47:LYS:NZ	2.31	0.48
19:2X:53:LYS:HB3	19:2X:82:GLN:HB3	1.94	0.48
32:2a:1280:A:O2'	32:2a:1281:U:H5'	2.13	0.48
33:2b:184:VAL:N	33:2b:198:ASP:OD2	2.39	0.48
33:2b:195:ASP:O	39:2h:68:ARG:NH2	2.46	0.48
34:2c:7:PRO:HG3	34:2c:201:TYR:HE1	1.78	0.48
43:2l:28:LYS:N	43:2l:29:GLY:HA2	2.28	0.48
49:2r:25:THR:O	49:2r:25:THR:OG1	2.23	0.48
1:1A:174:U:H4'	1:1A:207:A:H4'	1.96	0.48
1:1A:331:G:H21	1:1A:354:A:H62	1.60	0.48
1:1A:1342:G:OP1	1:1A:2721:G:O2'	2.19	0.48
1:1A:2227:G:OP2	1:1A:2227:G:H4'	2.14	0.48
1:1A:2253:A:H2'	1:1A:2254:G:C8	2.48	0.48
2:1B:30:C:H2'	2:1B:31:C:H5'	1.96	0.48
5:1F:102:PRO:HB2	5:1F:105:VAL:HG23	1.95	0.48
32:1a:457:C:H2'	32:1a:458:C:C6	2.48	0.48
32:1a:575:G:O2'	32:1a:821:G:H5'	2.12	0.48
32:1a:1073:U:H2'	32:1a:1074:G:H8	1.78	0.48
34:1c:35:GLU:OE2	34:1c:59:ARG:NH2	2.46	0.48
1:2A:7:G:H2'	1:2A:8:A:O4'	2.14	0.48
1:2A:1722:A:H1'	1:2A:1739:U:H5	1.77	0.48
1:2A:2206:G:H5''	1:2A:2207:G:C8	2.48	0.48
1:2A:2712:U:H1'	1:2A:2712(A):A:C8	2.48	0.48
8:2I:114:LEU:HD21	8:2I:128:LEU:HD13	1.95	0.48
33:2b:127:ILE:C	33:2b:129:GLU:H	2.21	0.48
36:2e:72:GLN:O	36:2e:75:THR:HG22	2.14	0.48
44:2m:40:ASN:HB3	44:2m:43:THR:HG23	1.95	0.48
1:1A:360:C:O2'	20:1Y:35:TYR:OH	2.25	0.48
1:1A:485:U:OP2	29:17:39:ARG:NH1	2.45	0.48
1:1A:1940:A:O2'	1:1A:1942:OMC:N4	2.47	0.48
1:1A:1985:U:H4'	1:1A:1986:G:OP1	2.14	0.48
1:1A:2244:U:P	23:11:40:ARG:HH12	2.37	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2897:U:H2'	1:1A:2898:C:C6	2.48	0.48
9:1N:58:ASP:OD1	9:1N:58:ASP:N	2.46	0.48
10:1O:122:LEU:HD13	15:1T:72:VAL:HG11	1.95	0.48
32:1a:404:U:H2'	32:1a:405:U:C6	2.48	0.48
39:1h:20:TYR:CE2	39:1h:75:ARG:HD2	2.47	0.48
1:2A:1028:A:N6	1:2A:1125:G:H2'	2.29	0.48
32:2a:304:U:H2'	32:2a:305:G:C8	2.48	0.48
32:2a:501:C:H2'	32:2a:502:G:H8	1.77	0.48
32:2a:1333:A:H2'	32:2a:1334:G:O4'	2.13	0.48
40:2i:46:ALA:HB2	40:2i:74:ILE:HG23	1.95	0.48
40:2i:50:LEU:HD23	40:2i:85:LEU:HD11	1.96	0.48
53:2x:19:G:H4'	53:2x:20:U:OP2	2.12	0.48
1:1A:329:U:H2'	1:1A:330:U:C6	2.49	0.48
1:1A:1038:C:OP1	17:1V:74:LYS:NZ	2.38	0.48
1:1A:1566:U:H2'	1:1A:1567:G:O4'	2.13	0.48
19:1X:31:HIS:CD2	19:1X:33:LYS:H	2.31	0.48
32:1a:537:G:H5''	43:1l:113:ARG:NH1	2.28	0.48
1:2A:84:A:H5'	20:2Y:8:LYS:HB3	1.95	0.48
6:2G:131:TYR:HB3	6:2G:159:VAL:HG13	1.96	0.48
8:2I:6:LEU:HG	8:2I:36:ALA:HA	1.95	0.48
20:2Y:43:ASN:CG	20:2Y:65:ALA:HB3	2.38	0.48
21:2Z:31:ARG:HD3	21:2Z:32:HIS:NE2	2.29	0.48
32:2a:108:G:N1	51:2t:15:ARG:HG2	2.29	0.48
32:2a:1004:A:H2'	32:2a:1038:C:H1'	1.94	0.48
33:2b:58:ILE:HD11	33:2b:185:ILE:HG21	1.95	0.48
1:1A:1324:A:OP1	13:1R:36:THR:HG23	2.14	0.48
1:1A:2370:G:N1	63:1A:5143:HOH:O	2.18	0.48
32:1a:848:C:H2'	32:1a:849:C:C6	2.49	0.48
33:1b:198:ASP:OD1	39:1h:68:ARG:NH2	2.46	0.48
41:1j:5:ARG:HD3	41:1j:71:LEU:HD11	1.96	0.48
50:1s:27:GLU:CB	50:1s:28:LYS:HE2	2.43	0.48
1:2A:517:C:OP1	27:25:16:ARG:NH2	2.47	0.48
1:2A:792:G:N3	1:2A:2072:G:O2'	2.38	0.48
1:2A:2102:U:O2	1:2A:2187:G:C6	2.67	0.48
3:2D:124:PRO:HG2	3:2D:129:ASN:HD21	1.78	0.48
12:2Q:21:THR:HG21	12:2Q:101:ARG:HB2	1.95	0.48
1:1A:1361:C:O2'	1:1A:1438:A:N3	2.38	0.48
1:1A:1562:U:H2'	1:1A:1563:G:H8	1.79	0.48
2:1B:86:G:H1	2:1B:91:C:N4	2.11	0.48
5:1F:116:ASP:OD1	5:1F:119:ARG:NH2	2.43	0.48
8:1I:114:LEU:HD11	8:1I:128:LEU:HB3	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:946:A:H2'	32:1a:947:G:C8	2.48	0.48
32:1a:1288:A:H2'	32:1a:1289:A:C8	2.49	0.48
32:1a:1369:C:H2'	32:1a:1370:G:C8	2.47	0.48
35:1d:114:ARG:HA	35:1d:117:ALA:HB3	1.95	0.48
48:1q:67:LYS:C	48:1q:69:LYS:H	2.22	0.48
50:1s:63:THR:OG1	50:1s:65:ASN:OD1	2.32	0.48
1:2A:1041:C:N4	1:2A:1114:G:H1	2.07	0.48
1:2A:1614:A:C2	18:2W:93:ALA:HB2	2.49	0.48
1:2A:2127:G:N2	1:2A:2173:A:H1'	2.29	0.48
10:2O:49:ARG:NH1	32:2a:1422:G:O3'	2.43	0.48
37:2f:3:ARG:HB3	37:2f:93:SER:HB2	1.96	0.48
41:2j:51:ARG:NH1	45:2n:45:ARG:HH21	2.11	0.48
53:2x:61:C:H2'	53:2x:62:C:C6	2.49	0.48
1:1A:2108:U:H2'	1:1A:2109:G:C8	2.49	0.48
1:1A:2146:G:H2'	1:1A:2147:G:H5'	1.95	0.48
1:1A:2849:G:O2'	13:1R:49:ASP:OD2	2.30	0.48
9:1N:35:ARG:HH21	9:1N:42:TRP:HZ2	1.61	0.48
13:1R:72:ASP:OD2	13:1R:75:LEU:HB2	2.14	0.48
23:11:50:ARG:HG2	23:11:59:THR:HG22	1.96	0.48
32:1a:1132:C:H2'	32:1a:1133:G:H8	1.78	0.48
38:1g:32:ARG:HH22	38:1g:109:ASN:ND2	2.12	0.48
1:2A:565:C:N3	1:2A:576:U:O4	2.47	0.48
1:2A:1221(A):C:C2	1:2A:1229:G:C2	3.02	0.48
2:2B:90:A:N7	2:2B:91:C:H1'	2.29	0.48
4:2E:9:VAL:HG13	4:2E:25:VAL:O	2.13	0.48
32:2a:565:U:OP2	32:2a:566:G:O2'	2.29	0.48
32:2a:1402:4OC:HM22	32:2a:1403:C:H5'	1.96	0.48
45:2n:29:ARG:HD3	45:2n:40:CYS:SG	2.54	0.48
1:1A:320:C:H2'	1:1A:321:C:H6	1.77	0.48
1:1A:999:G:H5''	12:1Q:13:GLN:HB3	1.96	0.48
1:1A:1594:C:H2'	1:1A:1595:C:C6	2.49	0.48
1:1A:2692:C:OP2	4:1E:111:ARG:NH2	2.38	0.48
6:1G:161:THR:HG22	6:1G:163:ALA:H	1.79	0.48
20:1Y:92:ASN:HB2	20:1Y:94:LYS:N	2.18	0.48
32:1a:1298:C:H2'	38:1g:114:ARG:NH2	2.28	0.48
36:1e:148:VAL:O	36:1e:152:ARG:HG2	2.13	0.48
1:2A:443:A:H5''	1:2A:444:C:OP1	2.14	0.48
1:2A:1721:G:H8	1:2A:1741:A:H62	1.60	0.48
32:2a:272:C:H2'	32:2a:273:A:H8	1.78	0.48
32:2a:437:U:H5'	35:2d:155:LEU:HD21	1.95	0.48
32:2a:1062:U:H2'	32:2a:1063:C:C6	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:655:G:N2	1:1A:658:A:OP2	2.42	0.47
1:1A:1405:A:N1	1:1A:1418:U:C4	2.77	0.47
16:1U:29:SER:C	16:1U:30:LYS:HD2	2.39	0.47
20:1Y:56:PRO:C	20:1Y:58:GLY:H	2.22	0.47
32:1a:7:G:O2'	36:1e:120:THR:O	2.32	0.47
32:1a:243:A:H4'	32:1a:244:U:H5''	1.95	0.47
32:1a:603:U:H2'	32:1a:604:G:C8	2.49	0.47
32:1a:926:G:C6	32:1a:1505:G:C6	3.02	0.47
1:2A:1072:C:N4	1:2A:1093:G:H1	2.12	0.47
1:2A:2022:U:O2'	1:2A:2617:C:H5'	2.13	0.47
1:2A:2079:U:OP1	23:21:21:ARG:NH1	2.31	0.47
1:2A:2347:C:H2'	1:2A:2348:U:C6	2.49	0.47
4:2E:36:ARG:NH1	4:2E:85:ASN:OD1	2.46	0.47
32:2a:985:C:H2'	32:2a:986:A:C8	2.48	0.47
32:2a:1097:C:O2'	32:2a:1169:A:N3	2.39	0.47
32:2a:1503:A:N6	32:2a:1532:U:O2'	2.46	0.47
36:2e:40:ARG:HE	36:2e:68:GLU:HB3	1.79	0.47
38:2g:113:GLU:HG2	38:2g:119:ARG:HG2	1.95	0.47
38:2g:132:GLY:O	38:2g:136:LYS:HG2	2.14	0.47
49:2r:33:ASP:OD2	49:2r:36:ASN:HB2	2.13	0.47
50:2s:15:LEU:HD12	50:2s:18:LYS:HD2	1.95	0.47
52:2u:2:GLY:C	52:2u:4:GLY:H	2.22	0.47
1:1A:1175:A:O2'	1:1A:2527:C:O2	2.31	0.47
1:1A:2031:G:OP1	18:1W:41:LYS:NZ	2.35	0.47
28:16:6:ARG:NH1	28:16:26:ASN:HB2	2.28	0.47
32:1a:300:A:H8	32:1a:300:A:O5'	1.96	0.47
32:1a:565:U:OP2	32:1a:566:G:O2'	2.30	0.47
32:1a:1023:G:H2'	32:1a:1024:G:H8	1.79	0.47
32:1a:1278:U:H5'	32:1a:1279:A:O4'	2.14	0.47
1:2A:220:G:O2'	1:2A:233:A:N3	2.40	0.47
1:2A:918:A:H5''	2:2B:98:G:O2'	2.15	0.47
1:2A:2646:C:H2'	1:2A:2647:U:O4'	2.14	0.47
1:2A:2698:U:H2'	1:2A:2699:C:C6	2.49	0.47
11:2P:2:LYS:HE3	11:2P:4:SER:OG	2.13	0.47
20:2Y:102:CYS:SG	20:2Y:103:GLY:N	2.87	0.47
22:20:49:LYS:HG2	22:20:50:ASN:ND2	2.29	0.47
32:2a:45:U:H2'	32:2a:46:G:H8	1.79	0.47
32:2a:991:U:O2'	32:2a:992:U:OP2	2.25	0.47
1:1A:1211:U:H2'	1:1A:1212:C:C6	2.49	0.47
1:1A:1347:A:O2'	1:1A:1348:A:H3'	2.14	0.47
14:1S:59:LYS:NZ	14:1S:68:GLN:HE22	2.11	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:109:A:C6	32:1a:326:G:C6	3.02	0.47
32:1a:1391:U:H2'	32:1a:1392:G:C8	2.50	0.47
1:2A:885:C:H2'	1:2A:886:C:O4'	2.13	0.47
1:2A:1239:G:H2'	1:2A:1240:U:O4'	2.15	0.47
1:2A:2704:C:H2'	1:2A:2705:A:O4'	2.15	0.47
1:2A:2820:A:O2'	1:2A:2821:A:OP1	2.28	0.47
26:24:48:ARG:HD2	26:24:51:ASP:O	2.14	0.47
34:2c:47:LEU:HD13	34:2c:68:VAL:HG11	1.94	0.47
46:2o:68:ARG:O	46:2o:72:ARG:HG3	2.14	0.47
1:1A:388:A:H2'	1:1A:389:G:H8	1.80	0.47
5:1F:64:ILE:HG21	5:1F:78:ILE:HG23	1.96	0.47
5:1F:184:TYR:CE2	5:1F:188:ARG:HD2	2.49	0.47
7:1H:3:ARG:HH11	7:1H:4:ILE:H	1.61	0.47
7:1H:102:ALA:HA	7:1H:117:PRO:HD3	1.96	0.47
11:1P:17:LYS:HE3	11:1P:27:HIS:NE2	2.29	0.47
26:14:56:VAL:O	26:14:60:GLN:HB2	2.14	0.47
32:1a:1386:G:H2'	32:1a:1387:G:H8	1.80	0.47
33:1b:70:PHE:CD1	33:1b:163:PHE:HB3	2.49	0.47
33:1b:162:ILE:O	33:1b:185:ILE:HG12	2.13	0.47
39:1h:86:ILE:HG13	39:1h:133:LEU:HD22	1.97	0.47
1:2A:1268:A:H2'	1:2A:1269:A:O4'	2.15	0.47
1:2A:1300:U:H4'	1:2A:1301:A:H5'	1.95	0.47
1:2A:1667:G:O2'	1:2A:1991:U:O4	2.27	0.47
1:2A:2115:G:H22	1:2A:2119:A:H5'	1.80	0.47
1:2A:2115:G:H3'	1:2A:2116:G:C5'	2.42	0.47
1:2A:2171:A:H1'	1:2A:2172:U:C6	2.49	0.47
32:2a:35:G:H2'	32:2a:36:C:C6	2.48	0.47
32:2a:1125:U:H2'	32:2a:1127:G:N7	2.29	0.47
33:2b:80:ILE:HD13	33:2b:211:ILE:HB	1.96	0.47
1:1A:324:A:P	20:1Y:86:ARG:HH22	2.37	0.47
1:1A:895:G:H2'	1:1A:896:A:C8	2.48	0.47
1:1A:1400:A:H2'	1:1A:1401:G:O4'	2.15	0.47
1:1A:2023:A:H2'	1:1A:2024:G:C8	2.49	0.47
18:1W:86:LEU:HD22	18:1W:96:ILE:HD11	1.95	0.47
21:1Z:19:ARG:NH1	21:1Z:84:GLU:HB2	2.29	0.47
32:1a:661:G:H1	32:1a:744:C:N4	2.11	0.47
32:1a:1518:MA6:O5'	32:1a:1518:MA6:H8	2.15	0.47
44:1m:2:ALA:N	44:1m:8:GLU:OE1	2.47	0.47
1:2A:245:G:N7	30:28:8:LYS:NZ	2.62	0.47
1:2A:528:A:O2'	1:2A:529:A:H5'	2.15	0.47
1:2A:1223:G:N2	1:2A:1226:A:OP2	2.40	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1688:U:O2	1:2A:1700:A:H5'	2.15	0.47
32:2a:17:U:H2'	32:2a:18:C:C6	2.49	0.47
32:2a:143:A:N1	32:2a:220:G:O6	2.47	0.47
37:2f:69:GLU:CD	37:2f:69:GLU:H	2.21	0.47
41:2j:25:GLU:O	41:2j:29:ARG:HD3	2.14	0.47
43:2l:33:ARG:HD3	43:2l:62:SER:HB3	1.97	0.47
53:2x:36:U:O2	55:A:111:A:N1	2.47	0.47
1:1A:2147:G:O2'	1:1A:2195:A:N6	2.47	0.47
5:1F:117:ARG:HH12	11:1P:1:MET:N	2.13	0.47
11:1P:121:LYS:O	11:1P:123:LEU:N	2.48	0.47
20:1Y:7:VAL:HG21	20:1Y:72:VAL:HG12	1.96	0.47
32:1a:448:A:OP2	32:1a:485:G:N1	2.40	0.47
1:2A:184:C:H2'	1:2A:185:U:H6	1.80	0.47
1:2A:1279:G:H4'	13:2R:31:HIS:CD2	2.50	0.47
1:2A:1794:U:H2'	1:2A:1795:C:C6	2.48	0.47
1:2A:2133:G:C2	1:2A:2157:G:H2'	2.50	0.47
1:2A:2203:U:H2'	1:2A:2205:C:C6	2.50	0.47
4:2E:13:ARG:HG2	15:2T:58:ASN:HD21	1.78	0.47
33:2b:16:HIS:HB3	33:2b:210:SER:HB3	1.95	0.47
36:2e:78:HIS:CE1	36:2e:143:ARG:H	2.18	0.47
38:2g:113:GLU:CG	38:2g:119:ARG:HG2	2.45	0.47
40:2i:9:ARG:HB2	40:2i:104:ARG:NE	2.27	0.47
40:2i:28:VAL:HA	40:2i:63:ILE:O	2.14	0.47
44:2m:32:GLU:HB3	44:2m:64:TRP:HH2	1.79	0.47
1:1A:310:C:H2'	1:1A:311:C:C6	2.49	0.47
1:1A:1321:A:N1	1:1A:1341:C:O2'	2.45	0.47
1:1A:1388:A:O2'	1:1A:1390:G:OP2	2.31	0.47
1:1A:1532:A:H2'	1:1A:1533:G:C8	2.49	0.47
1:1A:2258:G:H2'	1:1A:2259:A:C8	2.49	0.47
1:1A:2661:U:H2'	1:1A:2662:U:C6	2.50	0.47
5:1F:9:ILE:HG21	5:1F:125:LEU:HD13	1.96	0.47
5:1F:126:VAL:HG11	5:1F:142:TRP:HZ2	1.80	0.47
7:1H:3:ARG:NH1	7:1H:4:ILE:H	2.12	0.47
10:1O:8:LEU:HB2	10:1O:19:ILE:HG13	1.95	0.47
11:1P:1:MET:HE2	11:1P:6:LEU:HD23	1.96	0.47
19:1X:40:LYS:HG3	19:1X:51:VAL:HB	1.96	0.47
32:1a:297:G:H4'	32:1a:557:G:H4'	1.97	0.47
32:1a:424:G:H2'	32:1a:425:G:H8	1.79	0.47
32:1a:486:U:H2'	32:1a:487:A:C8	2.50	0.47
32:1a:489:C:OP1	35:1d:132:ARG:NH2	2.46	0.47
32:1a:1026:G:H2'	32:1a:1026:G:N3	2.30	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:1b:24:TRP:CZ3	33:1b:26:PRO:HA	2.49	0.47
36:1e:77:PRO:HD2	36:1e:142:LEU:HD22	1.96	0.47
38:1g:32:ARG:HH22	38:1g:109:ASN:HD21	1.60	0.47
45:1n:23:ARG:NH1	45:1n:30:ALA:HB2	2.29	0.47
52:1u:3:LYS:HB3	52:1u:14:TRP:CD1	2.50	0.47
1:2A:11:G:C2'	1:2A:12:U:H5'	2.45	0.47
1:2A:275:G:H2'	1:2A:276:A:C8	2.49	0.47
1:2A:323:G:C8	5:2F:171:PRO:HG3	2.48	0.47
1:2A:1199:U:O2'	63:2A:3751:HOH:O	2.20	0.47
1:2A:1359:A:N3	1:2A:1359:A:H5'	2.30	0.47
1:2A:1508:A:H5'	1:2A:1509(A):A:C8	2.49	0.47
1:2A:2728:U:H5'	10:2O:70:LYS:NZ	2.29	0.47
1:2A:2808:U:H5''	1:2A:2891:G:O6	2.15	0.47
1:2A:2823:A:OP1	4:2E:113:PHE:HB2	2.14	0.47
9:2N:69:GLN:O	9:2N:71:ILE:HD12	2.15	0.47
12:2Q:39:PRO:HD3	12:2Q:99:PRO:HG3	1.97	0.47
19:2X:57:LEU:HD13	19:2X:78:LYS:HG3	1.96	0.47
29:27:12:ARG:NH2	29:27:44:PRO:HB3	2.29	0.47
32:2a:1038:C:H2'	32:2a:1039:C:C6	2.50	0.47
32:2a:1129:C:OP1	40:2i:16:ARG:NH1	2.48	0.47
32:2a:1498:UR3:OP2	55:A:111:A:O2'	2.30	0.47
45:2n:4:LYS:HA	45:2n:7:ILE:HG12	1.96	0.47
1:1A:768:C:H2'	1:1A:769:A:C8	2.50	0.47
1:1A:2747:A:H2'	1:1A:2748:G:O4'	2.15	0.47
7:1H:13:LYS:HB3	7:1H:13:LYS:HE2	1.65	0.47
8:1I:104:GLN:HE21	8:1I:105:HIS:CE1	2.33	0.47
12:1Q:57:HIS:HD2	12:1Q:117:ALA:HB2	1.79	0.47
25:13:6:VAL:HG12	25:13:54:VAL:HG21	1.97	0.47
32:1a:1172:C:H2'	32:1a:1173:G:H8	1.80	0.47
35:1d:173:TRP:CD1	35:1d:173:TRP:H	2.33	0.47
35:1d:173:TRP:CE3	35:1d:189:PRO:HG3	2.50	0.47
38:1g:62:PHE:HA	38:1g:124:LEU:HD22	1.97	0.47
1:2A:1292:U:H2'	1:2A:1293:C:C6	2.49	0.47
1:2A:1655:A:N6	1:2A:2005:A:O2'	2.48	0.47
1:2A:1709:U:H2'	1:2A:1710:C:C6	2.50	0.47
1:2A:1983:C:H4'	1:2A:2606:C:H4'	1.96	0.47
1:2A:2336:A:H61	22:20:43:THR:CG2	2.26	0.47
6:2G:7:LEU:HD23	6:2G:100:TRP:HE3	1.79	0.47
15:2T:125:ARG:NH1	32:2a:1443:G:H5'	2.30	0.47
32:2a:859:A:H2'	32:2a:860:A:O4'	2.13	0.47
34:2c:77:ILE:O	34:2c:83:ARG:N	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:2l:7:ILE:O	43:2l:11:VAL:HG23	2.15	0.47
53:2x:15:G:H2'	53:2x:59:A:N1	2.29	0.47
1:1A:1091:A:H1'	1:1A:1093:G:C2	2.49	0.47
1:1A:1554:A:H4'	1:1A:1556:A:C5	2.50	0.47
1:1A:1604:C:H5''	1:1A:1605:A:OP2	2.15	0.47
1:1A:2222:C:O2	1:1A:2238:C:N4	2.48	0.47
1:1A:2686:G:H5'	10:1O:26:LYS:HE3	1.97	0.47
17:1V:16:PRO:HD3	17:1V:99:ILE:HD11	1.97	0.47
20:1Y:5:MET:HE2	20:1Y:32:PRO:HA	1.96	0.47
32:1a:1412:C:H2'	32:1a:1413:A:C8	2.49	0.47
42:1k:20:TYR:CZ	42:1k:83:ILE:HD12	2.50	0.47
1:2A:774:A:H2'	1:2A:774:A:N3	2.30	0.47
1:2A:1761:C:H3'	1:2A:1762:A:H5''	1.96	0.47
1:2A:2128:C:H5'	1:2A:2129:C:OP2	2.15	0.47
2:2B:48:A:H4'	14:2S:95:HIS:CD2	2.47	0.47
7:2H:7:LEU:HB3	7:2H:69:ARG:HH21	1.80	0.47
8:2I:110:ASP:N	8:2I:130:TYR:OH	2.27	0.47
12:2Q:12:GLN:HE21	12:2Q:72:LYS:HG3	1.79	0.47
32:2a:1260:C:O5'	32:2a:1284:C:H4'	2.15	0.47
33:2b:96:ARG:HG2	33:2b:98:LEU:HD23	1.97	0.47
33:2b:185:ILE:HG23	33:2b:199:TYR:HB2	1.96	0.47
35:2d:76:ARG:HD2	35:2d:76:ARG:HA	1.69	0.47
37:2f:99:ALA:HB1	49:2r:23:LYS:HE3	1.95	0.47
40:2i:5:TYR:N	40:2i:87:GLN:OE1	2.34	0.47
48:2q:62:SER:OG	48:2q:72:ARG:NH1	2.48	0.47
1:1A:745:C:O2'	1:1A:781:A:N6	2.48	0.47
1:1A:1071:G:C4	1:1A:1180:C:H1'	2.50	0.47
1:1A:1904:C:H2'	1:1A:1905:G:O4'	2.15	0.47
6:1G:16:ARG:CZ	6:1G:31:VAL:HG21	2.45	0.47
32:1a:407:G:H2'	32:1a:408:A:H8	1.79	0.47
32:1a:520:A:N1	32:1a:536:C:H1'	2.30	0.47
32:1a:1201:A:H1'	32:1a:1202:G:OP2	2.14	0.47
32:1a:1429:C:H2'	32:1a:1430:C:C6	2.50	0.47
35:1d:76:ARG:HD3	35:1d:207:TYR:CE1	2.50	0.47
35:1d:108:LEU:HB3	35:1d:110:PHE:CE1	2.50	0.47
37:1f:99:ALA:HB2	49:1r:31:LEU:HD21	1.97	0.47
43:1l:60:LEU:HD21	43:1l:85:ILE:HD11	1.97	0.47
1:2A:298:G:H5''	1:2A:299:A:OP1	2.15	0.47
1:2A:641:C:O2'	1:2A:2350:C:OP1	2.31	0.47
1:2A:1474:C:H2'	1:2A:1475:G:C8	2.50	0.47
1:2A:1593:G:H2'	1:2A:1594:G:C8	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1639:U:H4'	1:2A:2699:C:H4'	1.97	0.47
8:2I:5:LEU:HD12	8:2I:36:ALA:HB2	1.97	0.47
32:2a:189(K):U:H2'	32:2a:189(L):G:C8	2.50	0.47
32:2a:376:G:OP2	47:2p:67:THR:HG21	2.15	0.47
32:2a:1095:U:P	32:2a:1108:G:H1	2.38	0.47
33:2b:52:GLU:HG2	33:2b:56:ARG:NH2	2.30	0.47
33:2b:158:LEU:HD12	33:2b:159:PRO:HD2	1.97	0.47
39:2h:19:VAL:HG23	39:2h:21:LYS:HG2	1.96	0.47
41:2j:11:PHE:CE1	41:2j:67:THR:HG22	2.49	0.47
53:2x:8:4SU:O5'	53:2x:8:4SU:H6	2.15	0.47
1:1A:626:A:H4'	1:1A:627:G:H5'	1.96	0.46
1:1A:1817:A:H1'	1:1A:1960:A:N6	2.30	0.46
1:1A:2569:G:H2'	1:1A:2570:C:C6	2.50	0.46
4:1E:175:VAL:O	4:1E:177:PRO:HD3	2.16	0.46
5:1F:178:PRO:HB2	5:1F:201:VAL:HG21	1.97	0.46
15:1T:60:THR:HG22	15:1T:77:PRO:HA	1.97	0.46
32:1a:371:G:O2'	32:1a:373:A:N7	2.48	0.46
32:1a:1252:A:H2'	32:1a:1253:G:O4'	2.15	0.46
32:1a:1356:G:H2'	32:1a:1357:A:C8	2.50	0.46
1:2A:196:A:N3	1:2A:196:A:H2'	2.30	0.46
1:2A:729:G:O2'	1:2A:763:G:H4'	2.15	0.46
1:2A:1359:A:H2'	1:2A:1360:A:H5'	1.98	0.46
1:2A:1641:A:H2'	1:2A:1642:G:O4'	2.15	0.46
1:2A:2371:G:H21	28:26:46:HIS:CE1	2.33	0.46
1:2A:2733:A:H2	4:2E:204:ALA:H	1.63	0.46
32:2a:437:U:O2	35:2d:119:GLN:NE2	2.47	0.46
40:2i:16:ARG:HH21	40:2i:18:PHE:HZ	1.61	0.46
1:1A:210:A:N1	1:1A:254:A:O2'	2.46	0.46
1:1A:848:G:O6	5:1F:53:THR:OG1	2.32	0.46
1:1A:1338:U:H2'	1:1A:1339:C:C6	2.50	0.46
13:1R:54:LEU:HD12	13:1R:54:LEU:HA	1.77	0.46
21:1Z:136:PHE:HE1	21:1Z:138:GLU:HG3	1.79	0.46
32:1a:601:C:H2'	32:1a:602:A:C8	2.50	0.46
32:1a:901:A:O5'	32:1a:901:A:H8	1.97	0.46
32:1a:1073:U:H2'	32:1a:1074:G:C8	2.50	0.46
1:2A:1608:A:H1'	1:2A:1610:A:OP2	2.14	0.46
4:2E:150:VAL:HG13	4:2E:154:LYS:HD2	1.98	0.46
44:2m:4:ILE:HD11	44:2m:60:VAL:HG11	1.96	0.46
1:1A:1934:A:O2'	32:1a:1494:G:O2'	2.27	0.46
1:1A:2602:A:H5''	3:1D:239:ARG:HG3	1.97	0.46
41:1j:34:VAL:HA	41:1j:74:ILE:HA	1.95	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2543:G:H2'	1:2A:2544:G:C8	2.50	0.46
9:2N:30:ILE:HG22	9:2N:34:LEU:HD22	1.98	0.46
10:2O:107:ARG:HH21	10:2O:115:VAL:HG11	1.79	0.46
18:2W:65:LEU:HB2	18:2W:68:ARG:HD2	1.98	0.46
32:2a:1068:G:N2	32:2a:1191:A:N3	2.59	0.46
33:2b:145:LEU:HB3	33:2b:149:LEU:HD12	1.96	0.46
33:2b:196:LEU:HD12	33:2b:196:LEU:HA	1.78	0.46
34:2c:19:GLU:C	34:2c:40:ARG:HH22	2.23	0.46
45:2n:22:THR:O	45:2n:33:VAL:HG21	2.15	0.46
1:1A:324:A:H2'	1:1A:358:C:H1'	1.98	0.46
1:1A:762:G:C2	46:1o:56:LEU:HD21	2.50	0.46
1:1A:1356:G:OP2	29:17:9:ARG:NE	2.42	0.46
1:1A:2135:U:H3	1:1A:2190:G:H4'	1.80	0.46
6:1G:144:ILE:HG23	6:1G:148:MET:HE2	1.97	0.46
7:1H:20:ALA:HB3	7:1H:23:ARG:HG2	1.97	0.46
32:1a:1051:C:H2'	32:1a:1052:U:C6	2.50	0.46
32:1a:1409:C:H2'	32:1a:1410:G:H8	1.80	0.46
39:1h:6:ILE:HB	39:1h:85:ARG:NH1	2.31	0.46
1:2A:411:G:OP2	1:2A:2406:U:O2'	2.32	0.46
1:2A:1047:G:H21	1:2A:1111:A:N6	1.97	0.46
2:2B:59:A:H2'	2:2B:60:C:O4'	2.15	0.46
32:2a:520:A:H2'	32:2a:521:G:O4'	2.15	0.46
32:2a:922:G:C6	32:2a:923:A:C6	3.03	0.46
33:2b:208:ILE:HA	33:2b:211:ILE:HD12	1.97	0.46
37:2f:69:GLU:O	37:2f:72:VAL:HG12	2.16	0.46
43:2l:113:ARG:NH2	43:2l:116:SER:OG	2.48	0.46
1:1A:1073:A:C2	1:1A:2500:A:H5'	2.50	0.46
1:1A:1314:A:H2'	1:1A:1315:A:O4'	2.16	0.46
1:1A:1700:G:H3'	13:1R:2:ARG:HD3	1.98	0.46
1:1A:1921:G:N3	1:1A:1921:G:H2'	2.31	0.46
1:1A:2181:G:H2'	1:1A:2182:G:H8	1.80	0.46
2:1B:103:G:N2	21:1Z:73:GLN:HE22	2.13	0.46
5:1F:30:PRO:HB3	11:1P:1:MET:HE1	1.97	0.46
32:1a:1232:U:H5''	40:1i:124:GLN:O	2.16	0.46
36:1e:11:ILE:HB	36:1e:31:LEU:HB3	1.97	0.46
42:1k:23:ALA:HB2	42:1k:28:THR:HG23	1.97	0.46
44:1m:45:VAL:HG13	44:1m:48:LEU:HD12	1.98	0.46
48:1q:53:LEU:HD23	48:1q:82:MET:HE1	1.97	0.46
1:2A:959:A:N3	1:2A:2457:U:O2'	2.42	0.46
1:2A:1045:A:H5'	1:2A:1047:G:OP1	2.15	0.46
1:2A:1056:G:O2'	1:2A:1086:A:H1'	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1218:C:H42	1:2A:1231:G:H1	1.63	0.46
1:2A:2118:U:O2'	1:2A:2119:A:H5''	2.15	0.46
1:2A:2273:A:H2'	1:2A:2274:A:C8	2.50	0.46
5:2F:129:PHE:CD2	5:2F:163:VAL:HG21	2.50	0.46
32:2a:719:C:O2'	49:2r:49:LYS:HB3	2.15	0.46
32:2a:1317:C:N4	45:2n:19:ARG:HH21	2.13	0.46
41:2j:35:SER:HB3	41:2j:73:ASP:H	1.81	0.46
1:1A:596:G:O2'	1:1A:597:C:H3'	2.15	0.46
1:1A:1248:G:H5'	11:1P:3:LEU:HD23	1.98	0.46
1:1A:1750:G:H2'	1:1A:1751:G:C8	2.50	0.46
5:1F:74:ARG:H	5:1F:74:ARG:HG3	1.53	0.46
16:1U:16:LYS:HB3	16:1U:16:LYS:HE2	1.74	0.46
21:1Z:31:ARG:NH1	21:1Z:94:GLU:OE2	2.49	0.46
32:1a:992:U:O2	32:1a:993:G:N2	2.48	0.46
39:1h:20:TYR:HA	39:1h:65:TYR:CZ	2.51	0.46
44:1m:13:LYS:HA	44:1m:44:ARG:HH11	1.81	0.46
51:1t:47:GLY:HA2	51:1t:48:LYS:HB2	1.98	0.46
1:2A:718:A:H8	1:2A:718:A:O5'	1.99	0.46
1:2A:1379:A:H4'	1:2A:1380:G:OP2	2.16	0.46
6:2G:108:ASN:N	6:2G:108:ASN:OD1	2.48	0.46
7:2H:124:GLU:HG3	7:2H:132:ARG:HB3	1.98	0.46
9:2N:20:GLY:HA2	9:2N:61:ARG:HG3	1.96	0.46
15:2T:53:ARG:O	15:2T:59:THR:HG23	2.15	0.46
19:2X:26:TYR:HB3	19:2X:92:LEU:HD22	1.97	0.46
23:21:3:LYS:HB3	23:21:4:VAL:H	1.53	0.46
32:2a:145:G:H1	32:2a:177:C:H42	1.63	0.46
32:2a:1012:U:H2'	32:2a:1013:G:C8	2.51	0.46
32:2a:1191:A:OP1	34:2c:4:LYS:HG3	2.15	0.46
37:2f:99:ALA:O	49:2r:28:GLU:HA	2.16	0.46
39:2h:20:TYR:HA	39:2h:65:TYR:CZ	2.51	0.46
45:2n:26:ARG:NH1	45:2n:46:GLU:OE1	2.47	0.46
50:2s:20:LEU:HD23	50:2s:23:ASN:ND2	2.31	0.46
1:1A:821:A:H2'	1:1A:821:A:N3	2.31	0.46
1:1A:2015:U:H4'	4:1E:128:SER:OG	2.16	0.46
6:1G:3:LEU:O	6:1G:8:LYS:NZ	2.36	0.46
11:1P:140:ALA:O	25:23:38:GLU:HG2	2.16	0.46
32:1a:542:G:P	35:1d:10:ARG:HH22	2.39	0.46
32:1a:839:U:H3'	32:1a:840:C:H6	1.81	0.46
32:1a:1222:G:H2'	32:1a:1223:C:O4'	2.15	0.46
1:2A:996:A:H4'	16:2U:91:ASP:OD2	2.15	0.46
1:2A:1056:G:H4'	1:2A:1086:A:H8	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1919:A:O3'	32:2a:1517:G:H1'	2.15	0.46
3:2D:61:LEU:HD13	3:2D:61:LEU:HA	1.85	0.46
6:2G:125:PHE:HB3	6:2G:166:ASP:CG	2.41	0.46
32:2a:565:U:H3'	32:2a:566:G:H2'	1.97	0.46
32:2a:657:G:H4'	46:2o:28:GLN:HG3	1.98	0.46
32:2a:691:G:H2'	32:2a:692:U:C6	2.51	0.46
32:2a:901:A:H8	32:2a:901:A:O5'	1.99	0.46
40:2i:49:PRO:HB3	40:2i:96:LEU:HD21	1.98	0.46
1:1A:142:G:H2'	1:1A:143:C:C6	2.51	0.46
1:1A:269:G:H2'	1:1A:270:C:C6	2.50	0.46
1:1A:2799:U:O2'	4:1E:62:PRO:O	2.25	0.46
4:1E:109:LYS:O	4:1E:111:ARG:NH1	2.49	0.46
4:1E:170:LEU:HB3	4:1E:184:VAL:CG2	2.46	0.46
8:1I:72:LEU:O	8:1I:74:ASN:N	2.43	0.46
19:1X:53:LYS:HB3	19:1X:82:GLN:HB3	1.98	0.46
32:1a:448:A:H2'	32:1a:449:C:C6	2.51	0.46
35:1d:109:GLY:HA3	35:1d:165:MET:SD	2.56	0.46
40:1i:21:PRO:HA	40:1i:59:PHE:HA	1.98	0.46
44:1m:10:PRO:HG2	44:1m:21:TYR:HD2	1.79	0.46
46:1o:84:LYS:HD2	46:1o:84:LYS:HA	1.78	0.46
1:2A:299:A:H5''	20:2Y:86:ARG:HH21	1.81	0.46
1:2A:403:U:H4'	1:2A:404:C:H5'	1.97	0.46
1:2A:527:C:H3'	63:2A:4002:HOH:O	2.15	0.46
1:2A:643:A:N1	1:2A:2369:A:O2'	2.39	0.46
1:2A:652(E):G:H2'	1:2A:652(F):G:C8	2.51	0.46
1:2A:716:A:C2	1:2A:717:G:H1'	2.51	0.46
1:2A:1507:A:O2'	1:2A:1508:A:O5'	2.28	0.46
1:2A:2287:A:O2'	1:2A:2288:A:H3'	2.16	0.46
6:2G:11:TYR:CZ	6:2G:16:ARG:HD3	2.50	0.46
10:2O:98:VAL:HG22	10:2O:118:ALA:HA	1.97	0.46
17:2V:24:LYS:HG3	17:2V:64:HIS:HD2	1.81	0.46
32:2a:328:C:H4'	32:2a:329:A:H5'	1.98	0.46
32:2a:692:U:O2'	32:2a:694:A:N7	2.32	0.46
32:2a:1132:C:H2'	32:2a:1133:G:H8	1.80	0.46
39:2h:38:ILE:HD12	39:2h:118:VAL:HG12	1.97	0.46
45:2n:23:ARG:NH1	45:2n:30:ALA:HB2	2.30	0.46
1:1A:864:C:O2'	1:1A:886:U:H5''	2.14	0.46
1:1A:2160:C:H2'	1:1A:2161:C:C5	2.51	0.46
8:1I:88:ILE:O	8:1I:121:LYS:NZ	2.48	0.46
28:16:23:THR:OG1	28:16:24:GLU:N	2.48	0.46
32:1a:262:A:C6	32:1a:263:A:C6	3.04	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:395:C:N4	63:1a:2218:HOH:O	2.34	0.46
32:1a:1118:C:H1'	32:1a:1179:A:C4	2.51	0.46
42:1k:45:GLY:O	42:1k:48:ILE:HG13	2.16	0.46
1:2A:192:C:O2'	1:2A:802:A:N3	2.47	0.46
1:2A:307:G:N1	1:2A:310:A:OP2	2.48	0.46
1:2A:1364:G:P	23:21:3:LYS:HG3	2.56	0.46
1:2A:2109:U:H1'	1:2A:2181:G:H22	1.80	0.46
1:2A:2803:C:H2'	1:2A:2804:C:H6	1.80	0.46
16:2U:104:GLN:NE2	16:2U:105:VAL:HG23	2.31	0.46
30:28:6:THR:HG23	30:28:64:TYR:HD2	1.81	0.46
32:2a:560:U:O5'	32:2a:560:U:H6	1.99	0.46
32:2a:964:A:N3	32:2a:969:A:O2'	2.45	0.46
32:2a:1060:C:H4'	41:2j:51:ARG:HB3	1.98	0.46
32:2a:1289:A:N1	32:2a:1371:G:O2'	2.36	0.46
1:1A:1704:C:H2'	1:1A:1705:C:C6	2.51	0.46
1:1A:2034:G:OP2	18:1W:16:LYS:NZ	2.49	0.46
1:1A:2062:C:H2'	1:1A:2063:U:O4'	2.16	0.46
7:1H:7:LEU:HD12	7:1H:8:PRO:HD2	1.98	0.46
13:1R:36:THR:HG22	13:1R:37:THR:H	1.80	0.46
32:1a:198:G:H2'	32:1a:199:G:H8	1.81	0.46
32:1a:524:G:H2'	32:1a:525:C:C6	2.51	0.46
32:1a:1060:C:H4'	41:1j:51:ARG:HB3	1.97	0.46
32:1a:1090:U:H3	32:1a:1095:U:H3	1.64	0.46
33:1b:192:SER:O	33:1b:194:PRO:HD3	2.16	0.46
34:1c:63:ASN:HB2	34:1c:98:ASN:HB2	1.98	0.46
35:1d:61:LYS:HD3	35:1d:206:PHE:CD2	2.51	0.46
38:1g:50:ILE:HG22	38:1g:125:MET:HG3	1.99	0.46
41:1j:6:ILE:HA	41:1j:97:GLU:O	2.16	0.46
51:1t:30:LYS:HA	51:1t:33:ILE:HD12	1.98	0.46
1:2A:1069:A:H2'	1:2A:1073:A:N7	2.31	0.46
1:2A:1429:G:H2'	1:2A:1430:C:C6	2.50	0.46
3:2D:125:ILE:HB	37:2f:81:ILE:HD11	1.98	0.46
5:2F:187:VAL:HG12	11:2P:3:LEU:HD12	1.98	0.46
8:2I:62:LYS:HE2	8:2I:133:HIS:NE2	2.31	0.46
32:2a:1164:G:H1	32:2a:1172:C:H42	1.64	0.46
32:2a:1330:U:H4'	44:2m:23:TYR:CZ	2.51	0.46
34:2c:32:LEU:HB3	34:2c:59:ARG:HH12	1.81	0.46
1:1A:310:C:H2'	1:1A:311:C:H6	1.80	0.45
1:1A:465:G:H2'	1:1A:466:G:C8	2.51	0.45
1:1A:694:G:N2	1:1A:697:C:H1'	2.31	0.45
2:1B:60:C:H2'	2:1B:61:G:H8	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:1V:21:ARG:HG2	17:1V:91:TYR:CD1	2.51	0.45
32:1a:130:A:O2'	32:1a:131:C:O5'	2.29	0.45
32:1a:1151:A:O4'	41:1j:39:PRO:HB2	2.16	0.45
33:1b:87:ARG:NH2	33:1b:220:ASP:OD1	2.32	0.45
38:1g:152:ALA:HB1	38:1g:155:ARG:HH12	1.80	0.45
46:1o:74:ASP:CG	46:1o:77:ARG:HB2	2.40	0.45
1:2A:384:U:H2'	1:2A:385:C:C6	2.44	0.45
1:2A:728:G:H4'	3:2D:13:ARG:HE	1.81	0.45
1:2A:1081:U:C2'	1:2A:1082:U:H5''	2.45	0.45
1:2A:1466:G:H2'	1:2A:1547:C:H41	1.79	0.45
1:2A:1799:G:N7	3:2D:179:SER:OG	2.42	0.45
1:2A:1823:G:OP1	3:2D:54:ARG:NH1	2.49	0.45
1:2A:2130:U:H2'	1:2A:2158:A:N1	2.32	0.45
1:2A:2756:U:H1'	1:2A:2757:A:H5''	1.98	0.45
7:2H:121:ILE:HG13	7:2H:144:VAL:HG21	1.98	0.45
13:2R:26:LYS:HE2	13:2R:70:LEU:O	2.16	0.45
27:25:41:PRO:O	27:25:44:THR:OG1	2.33	0.45
32:2a:56:U:H2'	32:2a:57:G:C8	2.52	0.45
32:2a:629:G:H2'	32:2a:630:G:O4'	2.16	0.45
32:2a:1220:G:N3	50:2s:54:GLY:HA2	2.31	0.45
32:2a:1372:U:H2'	32:2a:1373:G:O4'	2.15	0.45
34:2c:18:TRP:CD1	45:2n:54:PRO:HA	2.51	0.45
36:2e:37:ARG:NH1	36:2e:111:GLU:HG2	2.30	0.45
37:2f:15:ASP:O	37:2f:19:LEU:HB2	2.15	0.45
41:2j:47:PHE:CZ	45:2n:37:PHE:HE2	2.34	0.45
1:1A:77:A:H2'	1:1A:78:G:C8	2.52	0.45
1:1A:260:A:N6	1:1A:284:G:H1'	2.31	0.45
1:1A:1823:G:H5'	3:1D:205:VAL:HG13	1.99	0.45
6:1G:11:TYR:O	6:1G:16:ARG:N	2.40	0.45
21:1Z:19:ARG:HG3	21:1Z:25:PRO:HD3	1.99	0.45
35:1d:76:ARG:HA	35:1d:76:ARG:HD2	1.75	0.45
38:1g:18:TYR:CE1	38:1g:59:LEU:HB2	2.51	0.45
1:2A:300:A:N3	1:2A:319:C:H1'	2.30	0.45
1:2A:1091:G:H2'	1:2A:1091:G:N3	2.31	0.45
1:2A:1469:A:H2'	1:2A:1470:G:O4'	2.16	0.45
1:2A:2136:C:H5	1:2A:2137:C:H41	1.65	0.45
4:2E:59:VAL:HG21	4:2E:74:PRO:HB3	1.97	0.45
7:2H:23:ARG:HG3	7:2H:36:PRO:HA	1.97	0.45
9:2N:34:LEU:O	9:2N:49:GLY:HA3	2.16	0.45
10:2O:63:VAL:HG23	10:2O:64:ARG:HG3	1.98	0.45
18:2W:48:ALA:O	18:2W:52:GLU:HG2	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:868:C:H2'	32:2a:869:G:O4'	2.17	0.45
32:2a:1031:G:H2'	32:2a:1032:G:C8	2.51	0.45
32:2a:1130:A:H4'	40:2i:3:GLN:HE22	1.82	0.45
37:2f:97:PHE:HB2	49:2r:32:ARG:HH11	1.81	0.45
1:1A:1462:G:O2'	1:1A:1463:C:OP2	2.30	0.45
1:1A:1846:A:H8	1:1A:1846:A:OP1	1.99	0.45
1:1A:2855:G:H2'	1:1A:2856:G:C8	2.51	0.45
5:1F:172:TRP:CD1	5:1F:172:TRP:H	2.34	0.45
5:1F:188:ARG:NH2	63:1F:412:HOH:O	2.48	0.45
32:1a:815:A:N7	32:1a:1509:C:O2'	2.46	0.45
44:1m:45:VAL:HA	44:1m:48:LEU:HG	1.99	0.45
47:1p:28:ARG:HG2	47:1p:29:ASP:OD1	2.15	0.45
1:2A:779:U:OP1	3:2D:49:ILE:HG13	2.16	0.45
1:2A:797:C:H2'	1:2A:798:G:O4'	2.17	0.45
1:2A:1431:U:H2'	1:2A:1432:C:C6	2.51	0.45
1:2A:2687:U:H2'	1:2A:2688:U:O4'	2.16	0.45
19:2X:2:LYS:NZ	19:2X:38:GLU:OE2	2.31	0.45
32:2a:461:A:O2'	32:2a:471:G:N7	2.47	0.45
32:2a:1255:G:HO2'	32:2a:1258:G:HO2'	1.44	0.45
1:1A:1097:G:O2'	1:1A:1098:C:O5'	2.33	0.45
1:1A:1889:G:N2	1:1A:1905:G:H2'	2.31	0.45
1:1A:2053:A:C6	1:1A:2510:C:H1'	2.52	0.45
1:1A:2121:U:H3	1:1A:2212:G:H1	1.62	0.45
1:1A:2245:U:H2'	1:1A:2246:G:C8	2.52	0.45
1:1A:2303:U:H2'	1:1A:2304:C:C6	2.52	0.45
1:1A:2331:G:N2	14:1S:3:ARG:HD3	2.31	0.45
32:1a:300:A:O2'	32:1a:564:C:N3	2.37	0.45
33:1b:223:ILE:HG22	33:1b:226:ARG:NH2	2.30	0.45
36:1e:110:LEU:HD13	36:1e:118:ILE:HG21	1.97	0.45
41:1j:78:ASN:O	41:1j:80:LYS:N	2.49	0.45
1:2A:1636:C:H2'	1:2A:1637:A:C8	2.52	0.45
1:2A:2113:U:H2'	1:2A:2114:A:O4'	2.16	0.45
1:2A:2573:C:OP1	1:2A:2574:G:H5''	2.16	0.45
10:2O:122:LEU:HD13	15:2T:72:VAL:HG11	1.98	0.45
26:24:48:ARG:HG3	26:24:52:THR:HG23	1.98	0.45
32:2a:632:A:H5'	32:2a:633:G:OP2	2.16	0.45
32:2a:1058:G:N2	41:2j:53:PRO:HG3	2.31	0.45
32:2a:1250:A:C2	32:2a:1370:G:H1'	2.51	0.45
32:2a:1504:G:H4'	32:2a:1505:G:C4	2.52	0.45
33:2b:87:ARG:CZ	33:2b:233:SER:HB3	2.46	0.45
35:2d:13:ARG:HB3	35:2d:38:TYR:O	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:2d:153:ARG:NH1	35:2d:181:MET:SD	2.90	0.45
35:2d:173:TRP:CD1	35:2d:174:LEU:HG	2.52	0.45
38:2g:47:CYS:HA	38:2g:50:ILE:HG12	1.97	0.45
1:1A:1471:G:H2'	1:1A:1472:G:C8	2.52	0.45
12:1Q:2:LEU:HG	12:1Q:69:PHE:CE1	2.52	0.45
17:1V:14:VAL:HB	17:1V:96:ILE:HG13	1.99	0.45
20:1Y:19:LYS:HE2	20:1Y:20:TYR:CE2	2.51	0.45
32:1a:664:G:OP1	49:1r:64:ARG:NE	2.38	0.45
32:1a:1320:C:H2'	32:1a:1321:C:O4'	2.17	0.45
32:1a:1362:C:H2'	32:1a:1363:C:H5''	1.98	0.45
35:1d:158:ILE:HG13	35:1d:162:LEU:HD12	1.99	0.45
53:1x:21:A:N6	53:1x:46:G:H2'	2.31	0.45
1:2A:581:C:H2'	1:2A:582:G:H8	1.80	0.45
1:2A:674:G:O2'	5:2F:74:ARG:HD3	2.16	0.45
1:2A:2059:A:O2'	5:2F:69:HIS:HD2	2.00	0.45
1:2A:2167:U:H2'	1:2A:2168:G:C4	2.51	0.45
21:2Z:10:ARG:HD3	21:2Z:37:VAL:O	2.17	0.45
32:2a:60:A:N1	32:2a:107:G:O2'	2.40	0.45
32:2a:815:A:N7	32:2a:1509:C:O2'	2.46	0.45
1:1A:265:U:H2'	1:1A:266:C:C6	2.51	0.45
1:1A:394:C:H3'	63:1A:5451:HOH:O	2.17	0.45
1:1A:484:G:O2'	1:1A:495:G:O6	2.34	0.45
1:1A:1521:C:H2'	1:1A:1522:G:C8	2.51	0.45
1:1A:2332:A:H2'	1:1A:2332:A:N3	2.31	0.45
11:1P:39:LYS:HD2	11:1P:45:LEU:HD11	1.98	0.45
11:1P:82:GLY:HA2	11:1P:113:LYS:O	2.17	0.45
25:13:39:ASP:OD2	25:13:44:ARG:NH2	2.47	0.45
31:19:32:HIS:O	31:19:34:GLN:HG3	2.16	0.45
32:1a:1134:G:N3	32:1a:1134:G:H2'	2.31	0.45
33:1b:77:ALA:HA	33:1b:80:ILE:HG22	1.98	0.45
35:1d:173:TRP:CD2	35:1d:189:PRO:HG3	2.51	0.45
1:2A:1153:C:H2'	1:2A:1154:G:O4'	2.16	0.45
1:2A:1200:C:H5'	63:2A:3751:HOH:O	2.15	0.45
1:2A:1847:A:H3'	1:2A:1848:A:H5'	1.99	0.45
1:2A:2869:G:H2'	1:2A:2870:C:O4'	2.16	0.45
8:2I:116:LEU:HD11	8:2I:119:PRO:HA	1.99	0.45
28:26:23:THR:OG1	28:26:24:GLU:N	2.49	0.45
32:2a:243:A:H4'	32:2a:244:U:H5''	1.97	0.45
36:2e:31:LEU:HD23	36:2e:31:LEU:HA	1.80	0.45
38:2g:50:ILE:HD11	38:2g:58:PRO:HB3	1.99	0.45
40:2i:86:VAL:HG11	40:2i:93:ARG:NH2	2.22	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:2m:92:HIS:CE1	44:2m:98:VAL:HG21	2.51	0.45
1:1A:215:G:N2	1:1A:217:A:H62	2.15	0.45
1:1A:829:A:H5'	1:1A:830:A:N7	2.31	0.45
1:1A:2327:G:H2'	1:1A:2328:C:C6	2.51	0.45
1:1A:2490:A:H5'	31:19:31:LYS:HE2	1.99	0.45
8:1I:68:LEU:HD21	8:1I:109:ILE:HD11	1.98	0.45
14:1S:110:LEU:HD12	14:1S:110:LEU:HA	1.84	0.45
26:14:24:THR:OG1	26:14:25:TYR:N	2.50	0.45
32:1a:60:A:H4'	32:1a:61:G:H5'	1.98	0.45
33:1b:55:PHE:HA	33:1b:58:ILE:HD12	1.98	0.45
41:1j:33:GLN:O	41:1j:75:ILE:N	2.48	0.45
1:2A:728:G:H5''	3:2D:13:ARG:HH21	1.82	0.45
1:2A:903:C:H2'	1:2A:904:C:H6	1.81	0.45
14:2S:93:LYS:HE3	14:2S:95:HIS:HB2	1.97	0.45
23:21:83:GLU:HA	23:21:84:GLY:HA2	1.65	0.45
32:2a:736:C:H2'	32:2a:737:A:C8	2.52	0.45
32:2a:839:U:H3'	32:2a:840:C:C5	2.51	0.45
32:2a:1003:G:N3	32:2a:1003:G:H2'	2.31	0.45
32:2a:1427:U:H2'	32:2a:1428:A:C8	2.52	0.45
36:2e:145:LYS:HE2	36:2e:149:GLU:OE2	2.16	0.45
1:1A:765:A:H8	1:1A:765:A:O5'	1.99	0.45
1:1A:909:G:H2'	1:1A:910:A:O4'	2.17	0.45
1:1A:1941:A:N1	32:1a:1495:U:O2'	2.44	0.45
1:1A:2235:G:OP1	3:1D:172:TYR:OH	2.29	0.45
19:1X:12:VAL:HG22	19:1X:29:TRP:CE2	2.52	0.45
21:1Z:103:ARG:HD3	21:1Z:136:PHE:CG	2.52	0.45
21:1Z:128:VAL:HG21	21:1Z:161:VAL:HG12	1.98	0.45
32:1a:189(K):U:H2'	32:1a:189(L):G:C8	2.52	0.45
32:1a:392:G:H2'	32:1a:393:A:C8	2.52	0.45
32:1a:560:U:H4'	32:1a:561:U:O5'	2.16	0.45
32:1a:953:G:H5'	32:1a:965:A:H61	1.82	0.45
32:1a:983:A:H1'	32:1a:1049:U:O2	2.16	0.45
34:1c:29:TYR:OH	45:1n:54:PRO:O	2.33	0.45
35:1d:155:LEU:O	35:1d:158:ILE:HG23	2.17	0.45
36:1e:27:ARG:HE	36:1e:27:ARG:HB2	1.46	0.45
1:2A:212:G:H2'	1:2A:213:A:O4'	2.17	0.45
1:2A:322:A:OP2	5:2F:169:ASN:HB2	2.17	0.45
1:2A:1057:A:O2'	1:2A:1058:G:OP1	2.34	0.45
1:2A:2662:A:H8	1:2A:2662:A:O5'	1.99	0.45
8:2I:62:LYS:HB3	8:2I:133:HIS:CE1	2.52	0.45
9:2N:46:VAL:HG23	9:2N:48:MET:HG2	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:2O:17:ARG:HA	10:2O:17:ARG:HD3	1.83	0.45
10:2O:98:VAL:HG11	10:2O:114:ILE:HG23	1.97	0.45
26:24:24:THR:OG1	26:24:25:TYR:N	2.46	0.45
32:2a:149:A:H2'	32:2a:150:C:C6	2.52	0.45
32:2a:542:G:OP1	35:2d:10:ARG:NH2	2.32	0.45
32:2a:620:C:H2'	32:2a:621:A:O4'	2.17	0.45
32:2a:625:G:H4'	47:2p:16:HIS:CD2	2.51	0.45
1:1A:138:G:N3	1:1A:140:A:N6	2.57	0.45
1:1A:2255:U:H2'	1:1A:2256:U:C6	2.52	0.45
1:1A:2263:OMG:HM23	1:1A:2263:OMG:H1'	1.72	0.45
26:14:61:ARG:HG3	26:14:62:ARG:H	1.80	0.45
32:1a:565:U:H3'	32:1a:566:G:H2'	1.98	0.45
38:1g:26:PHE:CE2	38:1g:30:ILE:HD11	2.52	0.45
39:1h:13:ILE:O	39:1h:17:THR:HG23	2.17	0.45
42:1k:84:VAL:HG11	42:1k:91:ARG:HD2	1.98	0.45
1:2A:1028:A:N3	1:2A:2486:G:O2'	2.43	0.45
1:2A:1384:A:N3	1:2A:1405:U:H1'	2.32	0.45
1:2A:2410:G:C2	1:2A:2411:A:H1'	2.52	0.45
1:2A:2512:C:H4'	4:2E:122:PHE:CE2	2.52	0.45
1:2A:2848:G:H1'	1:2A:2867:G:N2	2.31	0.45
3:2D:124:PRO:HG2	3:2D:129:ASN:ND2	2.31	0.45
6:2G:126:ASP:HB3	6:2G:130:ASN:H	1.80	0.45
8:2I:14:ASP:O	8:2I:17:GLN:HB3	2.17	0.45
9:2N:42:TRP:HA	9:2N:48:MET:HE1	1.99	0.45
14:2S:27:SER:HA	14:2S:88:ASP:HB3	1.98	0.45
18:2W:35:ILE:HG23	27:25:28:PRO:HD2	1.98	0.45
32:2a:1142:G:H2'	32:2a:1143:G:O4'	2.17	0.45
33:2b:70:PHE:CD1	33:2b:163:PHE:HB3	2.52	0.45
33:2b:93:VAL:HG21	33:2b:97:TRP:CD1	2.48	0.45
1:1A:630:U:OP1	5:1F:102:PRO:HA	2.17	0.45
1:1A:1898:A:H2'	1:1A:1899:A:C8	2.52	0.45
7:1H:55:PRO:HG2	7:1H:61:HIS:ND1	2.31	0.45
15:1T:37:GLY:HA2	15:1T:38:ASN:HA	1.53	0.45
32:1a:674:G:H2'	32:1a:675:A:H8	1.82	0.45
36:1e:74:GLY:HA3	36:1e:116:THR:HG22	1.99	0.45
1:2A:26:G:C6	1:2A:27:G:N1	2.84	0.45
1:2A:311:A:C6	1:2A:328:U:C4	3.05	0.45
1:2A:607:U:OP1	5:2F:102:PRO:HA	2.17	0.45
1:2A:620:G:N3	1:2A:620:G:H5'	2.32	0.45
1:2A:851:U:H5'	25:23:49:LYS:HD2	1.99	0.45
1:2A:911:A:N6	12:2Q:11:LYS:O	2.48	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1843:C:H5'	3:2D:253:GLN:NE2	2.32	0.45
1:2A:2315:G:H2'	1:2A:2316:C:C6	2.52	0.45
1:2A:2405:G:H5'	11:2P:75:ILE:HD13	1.99	0.45
1:2A:2845:G:H2'	1:2A:2846:G:C8	2.51	0.45
3:2D:13:ARG:NH1	3:2D:16:MET:SD	2.90	0.45
8:2I:5:LEU:HD12	8:2I:5:LEU:HA	1.77	0.45
14:2S:26:LEU:HD22	14:2S:87:PHE:CD1	2.52	0.45
19:2X:11:PRO:HG2	19:2X:13:LEU:HD21	1.98	0.45
20:2Y:44:ILE:HD13	20:2Y:64:GLU:HG3	1.99	0.45
32:2a:792:A:H4'	32:2a:793:U:H5''	1.97	0.45
32:2a:1172:C:H2'	32:2a:1173:G:C8	2.52	0.45
38:2g:140:ASP:HA	38:2g:143:ARG:NH1	2.31	0.45
1:1A:535:C:H2'	1:1A:536:U:O4'	2.16	0.44
1:1A:842:C:H2'	1:1A:843:C:C6	2.52	0.44
1:1A:1405:A:H2'	1:1A:1406:A:H5'	1.98	0.44
1:1A:1464:G:O5'	1:1A:1464:G:H8	1.99	0.44
3:1D:142:VAL:HG23	3:1D:193:VAL:HA	1.98	0.44
4:1E:51:PHE:CD2	4:1E:52:LEU:HG	2.51	0.44
15:1T:51:ARG:HB3	15:1T:62:THR:HB	1.99	0.44
32:1a:17:U:H2'	32:1a:18:C:C6	2.52	0.44
32:1a:1227:A:C8	50:1s:83:HIS:HB3	2.52	0.44
33:1b:124:SER:HA	33:1b:125:PRO:HA	1.71	0.44
39:1h:14:ARG:O	39:1h:18:ARG:HG2	2.17	0.44
1:2A:1654:A:O2'	4:2E:113:PHE:O	2.29	0.44
1:2A:1722:A:H1'	1:2A:1739:U:C5	2.51	0.44
1:2A:2683:C:OP1	15:2T:53:ARG:NH2	2.49	0.44
2:2B:14:U:OP2	2:2B:70:C:O2'	2.31	0.44
2:2B:95:C:H2'	2:2B:96:U:C6	2.52	0.44
7:2H:26:VAL:O	7:2H:79:VAL:HG11	2.18	0.44
32:2a:642:A:N3	39:2h:113:SER:OG	2.35	0.44
32:2a:958:A:N6	50:2s:77:THR:O	2.50	0.44
35:2d:88:VAL:O	35:2d:92:VAL:HG23	2.17	0.44
1:1A:662:A:OP1	11:1P:133:SER:OG	2.34	0.44
1:1A:956:A:N1	1:1A:2289:G:H1'	2.32	0.44
1:1A:1053:C:H5''	9:1N:35:ARG:NH1	2.32	0.44
1:1A:1096:A:H2'	1:1A:1097:G:O4'	2.17	0.44
1:1A:1993:A:C4	3:1D:241:PRO:HD3	2.52	0.44
58:1A:3907:MPD:HM2	58:1A:3907:MPD:H4	1.77	0.44
32:1a:973:G:H3'	32:1a:974:A:H5''	1.98	0.44
32:1a:1004:A:C5	32:1a:1037:C:C2	3.05	0.44
33:1b:208:ILE:HA	33:1b:211:ILE:HD12	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:1c:6:HIS:HD2	34:1c:8:ILE:H	1.65	0.44
53:1x:75:C:H2'	53:1x:76:A:N7	2.33	0.44
1:2A:27:G:HO2'	1:2A:28:A:P	2.39	0.44
1:2A:1297:C:OP1	1:2A:2710:C:H4'	2.17	0.44
1:2A:2104:G:O6	1:2A:2185:C:H2'	2.17	0.44
1:2A:2849:U:H4'	1:2A:2868:A:C2	2.52	0.44
5:2F:120:GLU:HB3	5:2F:122:LYS:HG2	2.00	0.44
6:2G:86:MET:HA	6:2G:87:PRO:HD3	1.87	0.44
7:2H:33:LEU:HD21	7:2H:136:ILE:HG13	2.00	0.44
17:2V:98:GLU:OE2	17:2V:100:ARG:NH1	2.50	0.44
21:2Z:53:ILE:HG22	21:2Z:71:VAL:O	2.17	0.44
32:2a:1010:G:H2'	32:2a:1011:G:H8	1.82	0.44
32:2a:1232:U:H5''	40:2i:124:GLN:O	2.17	0.44
35:2d:10:ARG:HB2	35:2d:40:PRO:HG3	1.99	0.44
40:2i:89:ASN:O	40:2i:92:TYR:HB2	2.17	0.44
1:1A:559:U:H2'	1:1A:560:C:C6	2.52	0.44
1:1A:741:U:OP1	3:1D:59:LYS:NZ	2.40	0.44
1:1A:2144:U:H2'	1:1A:2145:G:H8	1.82	0.44
2:1B:77:U:O2'	2:1B:78:A:H5'	2.17	0.44
8:1I:40:THR:O	8:1I:44:LEU:HB2	2.18	0.44
16:1U:34:LYS:HD3	16:1U:34:LYS:HA	1.57	0.44
32:1a:110:C:H2'	32:1a:111:G:O4'	2.17	0.44
32:1a:114:U:H1'	32:1a:353:A:H1'	1.99	0.44
32:1a:266:G:H2'	32:1a:266:G:N3	2.31	0.44
32:1a:630:G:H2'	32:1a:631:G:C8	2.53	0.44
35:1d:53:ASP:HB3	35:1d:57:ARG:HH12	1.82	0.44
37:1f:45:LEU:HD12	37:1f:59:TYR:CD1	2.52	0.44
39:1h:12:ARG:NH1	39:1h:25:ASP:O	2.48	0.44
40:1i:7:THR:O	40:1i:83:ARG:NH1	2.50	0.44
1:2A:27:G:O2'	1:2A:28:A:OP2	2.28	0.44
1:2A:826:U:H2'	1:2A:828:U:O4'	2.18	0.44
1:2A:1067:A:H4'	1:2A:1068:G:OP2	2.17	0.44
1:2A:1754:C:H2'	1:2A:1755:A:O4'	2.17	0.44
4:2E:96:PHE:O	4:2E:175:VAL:HG11	2.16	0.44
5:2F:150:GLY:HA2	5:2F:172:TRP:CD2	2.52	0.44
7:2H:98:LEU:HD12	7:2H:103:LEU:HA	2.00	0.44
12:2Q:103:MET:HE1	12:2Q:125:LEU:HD13	2.00	0.44
19:2X:9:LEU:HA	24:22:36:ARG:HH21	1.82	0.44
33:2b:16:HIS:HB2	33:2b:204:ASN:HB3	2.00	0.44
38:2g:7:ALA:O	38:2g:8:GLU:HB2	2.17	0.44
47:2p:6:LEU:HB3	47:2p:17:TYR:HB3	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:254:A:N1	1:1A:454:U:O2'	2.49	0.44
1:1A:929:G:H1	1:1A:940:C:N4	2.10	0.44
1:1A:1231:G:H2'	1:1A:1232:G:O4'	2.17	0.44
1:1A:1562:U:H2'	1:1A:1563:G:C8	2.52	0.44
1:1A:1854:G:OP1	3:1D:54:ARG:NH1	2.50	0.44
1:1A:2123:G:H2'	1:1A:2124:U:O4'	2.16	0.44
1:1A:2559:U:O2	10:1O:23:ARG:NH2	2.39	0.44
8:1I:129:THR:HG22	8:1I:139:GLN:OE1	2.18	0.44
32:1a:35:G:O2'	43:1l:118:SER:O	2.28	0.44
32:1a:56:U:H2'	32:1a:57:G:C8	2.53	0.44
32:1a:100:C:H2'	32:1a:101:A:C8	2.52	0.44
32:1a:186:C:H2'	32:1a:187:C:C6	2.52	0.44
32:1a:973:G:OP1	41:1j:57:LYS:NZ	2.41	0.44
33:1b:184:VAL:N	33:1b:198:ASP:OD2	2.44	0.44
50:1s:31:ILE:HB	50:1s:49:ILE:HG23	2.00	0.44
1:2A:1328:G:H2'	1:2A:1330:C:C5	2.53	0.44
1:2A:2193:G:H2'	1:2A:2194:G:O4'	2.17	0.44
6:2G:113:ARG:HH22	6:2G:142:PRO:HA	1.82	0.44
12:2Q:110:THR:HG23	12:2Q:113:GLN:HB2	1.99	0.44
32:2a:25:C:H2'	32:2a:26:A:C8	2.52	0.44
32:2a:392:G:H2'	32:2a:393:A:C8	2.53	0.44
32:2a:1122:U:H2'	32:2a:1123:A:C8	2.53	0.44
32:2a:1157:A:H4'	32:2a:1158:C:O5'	2.18	0.44
42:2k:62:GLN:HG3	42:2k:97:ALA:HB2	2.00	0.44
1:1A:1100:A:P	1:1A:1100:A:O4'	2.75	0.44
1:1A:1690:G:H2'	1:1A:1691:C:O4'	2.17	0.44
1:1A:2096:U:H2'	1:1A:2097:U:C6	2.52	0.44
1:1A:2156:A:H62	1:1A:2179:G:H4'	1.83	0.44
1:1A:2390:A:C5	1:1A:2391:G:H1'	2.53	0.44
3:1D:175:LEU:HD12	3:1D:185:VAL:HG21	1.99	0.44
4:1E:119:ARG:HG2	4:1E:160:TYR:CG	2.53	0.44
6:1G:35:GLU:HB3	6:1G:160:VAL:HB	2.00	0.44
32:1a:10:A:H2'	32:1a:11:G:H8	1.82	0.44
32:1a:545:C:H5'	35:1d:72:GLU:CB	2.47	0.44
32:1a:1036:G:H2'	32:1a:1036:G:N3	2.33	0.44
32:1a:1038:C:H2'	32:1a:1039:C:C6	2.52	0.44
32:1a:1144:G:N2	32:1a:1146:A:H62	2.16	0.44
32:1a:1275:A:H2'	32:1a:1276:G:O4'	2.16	0.44
53:1x:53:G:O2'	53:1x:54:5MU:O5'	2.29	0.44
1:2A:271(L):U:H5'	8:2I:50:ARG:HH22	1.83	0.44
1:2A:2128:C:N4	1:2A:2160:G:N1	2.54	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2238:G:H2'	1:2A:2238:G:N3	2.32	0.44
14:2S:23:ARG:NH2	14:2S:84:GLN:HB3	2.33	0.44
32:2a:560:U:H4'	32:2a:561:U:O5'	2.17	0.44
37:2f:10:LEU:HD13	37:2f:61:LEU:HD13	1.99	0.44
38:2g:77:SER:OG	38:2g:86:GLN:NE2	2.50	0.44
1:1A:925:A:H2'	1:1A:926:G:H5'	1.98	0.44
5:1F:196:LEU:HD23	5:1F:196:LEU:HA	1.90	0.44
19:1X:68:ARG:HB3	19:1X:68:ARG:CZ	2.47	0.44
32:1a:45:U:H2'	32:1a:46:G:H8	1.82	0.44
32:1a:502:G:C2	32:1a:544:G:C2	3.06	0.44
32:1a:828:A:H2'	32:1a:829:G:O4'	2.18	0.44
32:1a:936:C:H2'	32:1a:937:A:O4'	2.17	0.44
37:1f:15:ASP:O	37:1f:19:LEU:HB2	2.18	0.44
38:1g:27:ILE:HD12	38:1g:40:ALA:HA	1.99	0.44
1:2A:1056:G:H4'	1:2A:1086:A:C8	2.52	0.44
1:2A:1786:A:H1'	1:2A:1938:A:N6	2.33	0.44
1:2A:2023:G:H5'	1:2A:2617:C:H4'	1.99	0.44
1:2A:2564:A:C2	1:2A:2647:U:H4'	2.53	0.44
19:2X:44:GLU:HG3	19:2X:51:VAL:HG23	1.99	0.44
21:2Z:94:GLU:H	21:2Z:94:GLU:HG3	1.56	0.44
32:2a:542:G:H2'	32:2a:543:C:C6	2.52	0.44
32:2a:612:C:O2	32:2a:629:G:N2	2.51	0.44
32:2a:719:C:H42	49:2r:71:LYS:HE2	1.82	0.44
32:2a:1226:C:H4'	50:2s:80:TYR:OH	2.16	0.44
32:2a:1452:C:H4'	32:2a:1457:G:C8	2.53	0.44
33:2b:82:ARG:HG3	33:2b:92:TYR:CZ	2.53	0.44
34:2c:21:ARG:NH2	34:2c:58:GLU:OE2	2.51	0.44
38:2g:115:ARG:H	38:2g:115:ARG:CZ	2.30	0.44
1:1A:155:C:H42	1:1A:160:G:H1	1.65	0.44
1:1A:549:U:H2'	1:1A:550:U:C6	2.53	0.44
1:1A:2745:G:H3'	1:1A:2746:A:O4'	2.17	0.44
2:1B:50:G:H5''	14:1S:61:ASN:ND2	2.33	0.44
32:1a:401:C:H2'	32:1a:402:G:C8	2.53	0.44
32:1a:406:G:H5'	35:1d:5:ILE:HD11	1.98	0.44
32:1a:1147:C:O2'	40:1i:16:ARG:NE	2.49	0.44
32:1a:1179:A:O3'	40:1i:103:THR:OG1	2.31	0.44
41:1j:31:GLY:HA2	41:1j:32:ALA:HA	1.48	0.44
1:2A:19:C:H2'	1:2A:20:C:C6	2.52	0.44
1:2A:1810:A:H8	1:2A:1810:A:O5'	2.01	0.44
1:2A:2405:G:O2'	1:2A:2411:A:N6	2.50	0.44
12:2Q:43:THR:HG22	12:2Q:94:VAL:HG12	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:2S:19:LYS:H	14:2S:19:LYS:HG2	1.61	0.44
17:2V:62:LEU:HD21	17:2V:95:LEU:HB2	2.00	0.44
19:2X:29:TRP:CE3	19:2X:78:LYS:HB3	2.52	0.44
21:2Z:5:LEU:HD13	21:2Z:47:VAL:HG21	1.99	0.44
23:21:88:LYS:O	23:21:92:LYS:HG3	2.16	0.44
26:24:12:ALA:HA	26:24:29:PRO:HA	2.00	0.44
30:28:62:LEU:HB3	30:28:65:GLU:HG2	1.99	0.44
32:2a:129(A):G:C6	32:2a:189(E):U:H4'	2.53	0.44
32:2a:661:G:H1	32:2a:744:C:N4	2.15	0.44
34:2c:181:ASN:ND2	34:2c:204:LEU:HD12	2.33	0.44
45:2n:27:CYS:SG	45:2n:29:ARG:HB2	2.58	0.44
1:1A:1263:C:N4	1:1A:1277:G:H1	2.15	0.44
1:1A:1491:A:H8	1:1A:1507:A:C4	2.36	0.44
1:1A:2699:U:H2'	1:1A:2700:U:O4'	2.16	0.44
4:1E:77:ILE:HG21	4:1E:195:LEU:HD11	2.00	0.44
5:1F:24:LEU:HB3	5:1F:115:ALA:HB2	1.98	0.44
6:1G:122:PRO:HG3	6:1G:180:PHE:HB3	2.00	0.44
13:1R:56:LYS:NZ	13:1R:90:ARG:O	2.50	0.44
21:1Z:128:VAL:HG22	21:1Z:132:ASN:HB3	1.99	0.44
26:14:48:ARG:O	26:14:50:VAL:N	2.51	0.44
32:1a:421:U:O2'	32:1a:423:G:N7	2.51	0.44
36:1e:12:LEU:HD12	36:1e:128:PRO:HB2	1.99	0.44
47:1p:19:ILE:HG23	47:1p:36:ILE:HG13	2.00	0.44
50:1s:50:ALA:HA	50:1s:58:VAL:O	2.18	0.44
53:1x:37:A:H2'	53:1x:38:A:O4'	2.17	0.44
1:2A:271(L):U:H4'	1:2A:271(M):G:H5'	1.99	0.44
1:2A:443:A:H1'	1:2A:1201:C:O4'	2.18	0.44
1:2A:1113:U:H2'	1:2A:1114:G:C8	2.53	0.44
1:2A:1336:A:H2'	1:2A:1337:G:C8	2.53	0.44
1:2A:2251:OMG:HM23	1:2A:2251:OMG:H1'	1.81	0.44
1:2A:2317:C:N4	1:2A:2318:G:O6	2.51	0.44
1:2A:2788:C:O2'	1:2A:2809:A:N3	2.49	0.44
4:2E:143:ASN:HD22	4:2E:147:PRO:CD	2.31	0.44
5:2F:165:ARG:HG2	5:2F:168:ARG:HH21	1.82	0.44
5:2F:172:TRP:H	5:2F:172:TRP:CD1	2.35	0.44
7:2H:144:VAL:O	7:2H:148:ILE:HG12	2.18	0.44
9:2N:97:ARG:HA	9:2N:100:GLU:HB2	2.00	0.44
14:2S:15:ARG:HD3	14:2S:25:ARG:NH2	2.33	0.44
16:2U:85:LYS:HB3	16:2U:116:ALA:HB1	2.00	0.44
21:2Z:76:LEU:HD12	21:2Z:83:PRO:HA	1.99	0.44
32:2a:269:C:H2'	32:2a:270:A:C8	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:2d:88:VAL:HG22	36:2e:96:PRO:HB2	1.99	0.44
36:2e:144:THR:H	36:2e:147:ASP:HB2	1.82	0.44
39:2h:25:ASP:HB3	39:2h:58:TYR:HD1	1.82	0.44
40:2i:4:TYR:CZ	40:2i:88:TYR:HD1	2.36	0.44
50:2s:20:LEU:HA	50:2s:23:ASN:ND2	2.33	0.44
52:2u:3:LYS:HD2	52:2u:14:TRP:CD1	2.53	0.44
1:1A:469:A:H1'	1:1A:1246:C:O4'	2.18	0.44
1:1A:1451:U:H2'	1:1A:1452:U:C6	2.52	0.44
1:1A:2187:G:O2'	1:1A:2188:G:H5'	2.18	0.44
6:1G:115:ARG:NH1	6:1G:137:GLU:OE2	2.51	0.44
15:1T:125:ARG:NH1	32:1a:1443:G:H5'	2.32	0.44
17:1V:60:GLU:OE1	17:1V:97:LYS:NZ	2.37	0.44
32:1a:601:C:H2'	32:1a:602:A:H8	1.82	0.44
33:1b:139:LYS:O	33:1b:143:GLU:HG3	2.17	0.44
43:1l:53:ARG:HG3	43:1l:93:LEU:HD21	1.99	0.44
44:1m:108:ARG:HD3	44:1m:108:ARG:HA	1.77	0.44
50:1s:52:TYR:HA	50:1s:56:GLN:O	2.18	0.44
51:1t:57:ARG:HD3	51:1t:101:GLY:O	2.18	0.44
1:2A:71:A:N7	19:2X:31:HIS:HE1	2.16	0.44
1:2A:483:A:H5''	20:2Y:50:ARG:HD3	1.98	0.44
1:2A:1450:G:H2'	1:2A:1450(A):C:H6	1.82	0.44
1:2A:1819:A:H4'	1:2A:1820:U:H5''	2.00	0.44
1:2A:2074:U:H2'	1:2A:2075:U:C6	2.53	0.44
1:2A:2648:C:H2'	1:2A:2649:U:C6	2.52	0.44
1:2A:2689:U:P	1:2A:2719:G:H22	2.40	0.44
7:2H:55:PRO:HG2	7:2H:61:HIS:ND1	2.32	0.44
14:2S:11:LYS:HE2	14:2S:91:PRO:HD3	2.00	0.44
28:26:9:LEU:HA	28:26:54:ILE:HB	2.00	0.44
32:2a:109:A:C6	32:2a:326:G:C6	3.06	0.44
32:2a:374:A:C6	32:2a:375:U:C4	3.06	0.44
32:2a:1014:A:C2	32:2a:1219:U:H1'	2.53	0.44
32:2a:1183:A:H8	32:2a:1183:A:H5''	1.82	0.44
32:2a:1412:C:H2'	32:2a:1413:A:C8	2.53	0.44
51:2t:14:LYS:HA	51:2t:17:ARG:CZ	2.48	0.44
1:1A:383:A:H2'	1:1A:384:G:O4'	2.17	0.43
1:1A:611:U:H2'	1:1A:612:C:C6	2.53	0.43
1:1A:950:C:H2'	1:1A:951:U:C6	2.52	0.43
1:1A:1068:G:N7	9:1N:66:LYS:HE2	2.33	0.43
1:1A:1309:U:C4	1:1A:1310:G:C6	3.06	0.43
1:1A:1386:U:OP1	19:1X:16:LYS:NZ	2.46	0.43
1:1A:1753:U:O2	1:1A:1788:U:H5'	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1834:A:H4'	3:1D:259:THR:HG23	1.99	0.43
1:1A:1857:G:H4'	3:1D:242:ARG:NH2	2.32	0.43
1:1A:2163:G:H3'	1:1A:2164:C:C6	2.54	0.43
1:1A:2474:U:H1'	1:1A:2503:U:O4	2.17	0.43
2:1B:31:C:O2'	2:1B:53:A:N1	2.48	0.43
4:1E:11:MET:HE2	4:1E:11:MET:HB3	1.88	0.43
14:1S:59:LYS:HB2	14:1S:60:GLY:H	1.51	0.43
19:1X:1:MET:HE1	24:12:26:ARG:NH2	2.25	0.43
25:13:46:ASN:O	25:13:50:VAL:HG22	2.17	0.43
32:1a:918:A:H2'	32:1a:919:A:C8	2.52	0.43
32:1a:971:G:N2	32:1a:1363(A):A:OP2	2.46	0.43
32:1a:977:A:H2'	32:1a:978:A:H5''	1.99	0.43
32:1a:1333:A:H2'	32:1a:1334:G:O4'	2.18	0.43
38:1g:79:ARG:NH1	38:1g:81:GLY:O	2.51	0.43
1:2A:242:G:O2'	1:2A:254:G:O6	2.31	0.43
1:2A:243:U:OP1	30:28:6:THR:OG1	2.28	0.43
1:2A:1839:G:C8	1:2A:1927:A:H1'	2.53	0.43
1:2A:1952:A:OP1	10:20:42:SER:OG	2.29	0.43
1:2A:1999:C:H4'	1:2A:2723:C:O2	2.18	0.43
1:2A:2364:C:H2'	1:2A:2365:G:O4'	2.17	0.43
3:2D:231:HIS:CD2	3:2D:249:PRO:HG3	2.52	0.43
6:2G:123:ASN:C	6:2G:125:PHE:H	2.26	0.43
7:2H:90:LYS:HD3	7:2H:159:GLU:HG2	1.99	0.43
16:2U:27:LEU:HA	16:2U:30:LYS:HB2	1.99	0.43
32:2a:128:G:H4'	48:2q:3:LYS:HG2	1.99	0.43
32:2a:292:G:C5	32:2a:293:G:H1'	2.52	0.43
32:2a:981:U:H5'	45:2n:21:TYR:CE2	2.52	0.43
1:1A:274:U:H5	8:1I:52:ARG:HD2	1.83	0.43
1:1A:834:U:H5''	1:1A:835:A:H5'	2.00	0.43
1:1A:1405:A:H61	1:1A:1418:U:H3	0.57	0.43
2:1B:53:A:H2'	2:1B:54:G:O4'	2.18	0.43
4:1E:115:GLY:O	4:1E:119:ARG:HB2	2.18	0.43
13:1R:63:ARG:O	13:1R:67:LEU:HB2	2.18	0.43
20:1Y:51:VAL:HG22	20:1Y:58:GLY:HA3	2.00	0.43
29:17:35:ARG:HG3	29:17:42:LEU:HD11	1.99	0.43
32:1a:715:A:H2'	32:1a:716:A:C8	2.53	0.43
33:1b:35:GLU:O	33:1b:39:ILE:N	2.51	0.43
34:1c:19:GLU:O	34:1c:40:ARG:NH2	2.51	0.43
1:2A:30:G:H2'	1:2A:31:C:C6	2.53	0.43
1:2A:864:G:H1'	1:2A:914:C:N4	2.31	0.43
1:2A:2130:U:H2'	1:2A:2158:A:N6	2.30	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2882:A:OP1	13:2R:96:ARG:NH1	2.51	0.43
2:2B:2:C:H2'	2:2B:3:C:C6	2.52	0.43
20:2Y:30:VAL:HG22	20:2Y:37:VAL:HG12	1.98	0.43
32:2a:352:C:H4'	32:2a:354:G:OP1	2.18	0.43
32:2a:600:C:H2'	32:2a:601:C:C6	2.54	0.43
32:2a:767:A:H2'	32:2a:768:A:O4'	2.19	0.43
32:2a:1239:A:H4'	32:2a:1240:U:H5''	2.00	0.43
32:2a:1305:G:H5'	52:2u:4:GLY:HA3	2.00	0.43
32:2a:1422:G:H2'	32:2a:1423:G:H8	1.83	0.43
37:2f:19:LEU:HD23	37:2f:23:LYS:HD2	2.00	0.43
1:1A:598:A:H4'	1:1A:2512:U:H4'	2.00	0.43
1:1A:1199:C:H2'	1:1A:1200:G:O4'	2.18	0.43
1:1A:1785:C:H5	15:1T:96:ARG:NH2	2.16	0.43
1:1A:2710:U:H2'	1:1A:2711:C:C6	2.52	0.43
3:1D:35:LYS:HB2	3:1D:36:PRO:HD2	2.00	0.43
3:1D:202:LYS:NZ	32:1a:774:G:OP1	2.51	0.43
4:1E:2:LYS:HB2	4:1E:95:ILE:HD12	2.00	0.43
32:1a:250:A:H4'	32:1a:251:G:O5'	2.19	0.43
32:1a:1323:G:H4'	32:1a:1363:C:C2	2.54	0.43
32:1a:1347:G:N2	32:1a:1373:G:H2'	2.34	0.43
33:1b:70:PHE:HD1	33:1b:163:PHE:HB3	1.83	0.43
35:1d:196:LEU:HD12	35:1d:196:LEU:H	1.83	0.43
51:1t:57:ARG:HH22	51:1t:100:ILE:HD12	1.83	0.43
1:2A:1012:U:H5	9:2N:28:THR:HG21	1.81	0.43
1:2A:1710:C:H2'	1:2A:1711:C:C6	2.52	0.43
4:2E:51:PHE:H	4:2E:75:VAL:CG1	2.31	0.43
20:2Y:56:PRO:C	20:2Y:58:GLY:H	2.27	0.43
32:2a:130:A:H5'	48:2q:63:ARG:HE	1.83	0.43
32:2a:149:A:H2'	32:2a:150:C:H6	1.83	0.43
32:2a:392:G:H2'	32:2a:393:A:H8	1.82	0.43
32:2a:573:A:N3	32:2a:883:C:O2'	2.50	0.43
32:2a:994:A:N7	32:2a:1216:G:H4'	2.32	0.43
35:2d:88:VAL:HG13	36:2e:97:GLY:HA2	2.00	0.43
39:2h:17:THR:HG22	39:2h:63:LEU:HG	2.00	0.43
48:2q:62:SER:OG	48:2q:72:ARG:HG3	2.17	0.43
1:1A:460:C:H2'	1:1A:461:U:C6	2.54	0.43
1:1A:936:C:O2'	1:1A:937:A:O5'	2.34	0.43
1:1A:2299:A:O2'	1:1A:2300:A:H3'	2.18	0.43
7:1H:164:TYR:HB2	7:1H:167:GLU:HB2	2.00	0.43
20:1Y:13:VAL:HG12	20:1Y:74:PRO:HA	2.00	0.43
20:1Y:87:LYS:HB3	20:1Y:95:LYS:HD2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:11:3:LYS:H	23:11:46:LEU:HD12	1.83	0.43
32:1a:684:A:H2'	32:1a:685:G:C8	2.52	0.43
32:1a:933:G:OP2	38:1g:3:ARG:HB2	2.18	0.43
32:1a:1220:G:N3	50:1s:54:GLY:HA2	2.34	0.43
33:1b:19:HIS:NE2	33:1b:206:ASP:OD2	2.47	0.43
43:1l:27:LEU:HD13	43:1l:27:LEU:HA	1.79	0.43
1:2A:30:G:C5	1:2A:31:C:C4	3.07	0.43
1:2A:373:U:H2'	1:2A:374:A:H8	1.84	0.43
1:2A:1235:G:C6	1:2A:1236:G:N1	2.86	0.43
1:2A:1449:A:O2'	1:2A:1529:G:N2	2.42	0.43
1:2A:1499:C:H2'	1:2A:1500:G:C8	2.54	0.43
1:2A:2148:G:C2	1:2A:2149:G:H1'	2.54	0.43
1:2A:2309:A:H2'	1:2A:2310:A:C8	2.52	0.43
3:2D:35:LYS:HB2	3:2D:36:PRO:HD2	2.01	0.43
7:2H:37:VAL:HG21	7:2H:72:ILE:HD11	2.00	0.43
12:2Q:65:PHE:HB2	12:2Q:105:GLU:HB2	2.00	0.43
17:2V:76:LYS:HB2	17:2V:81:TYR:HB3	2.00	0.43
32:2a:46:G:O2'	32:2a:365:U:H1'	2.17	0.43
32:2a:983:A:H2	32:2a:984:C:C6	2.36	0.43
32:2a:1004:A:N7	32:2a:1037:C:C2	2.85	0.43
32:2a:1256:A:N6	32:2a:1278:U:O2	2.51	0.43
34:2c:19:GLU:O	34:2c:40:ARG:NH2	2.45	0.43
37:2f:55:ASP:OD1	37:2f:57:GLN:HG2	2.19	0.43
40:2i:8:GLY:HA3	40:2i:76:ALA:O	2.18	0.43
45:2n:37:PHE:CE1	45:2n:53:LEU:HD13	2.54	0.43
47:2p:42:ARG:HB3	47:2p:44:THR:HG23	2.00	0.43
1:1A:933:C:H3'	1:1A:934:A:H5''	2.00	0.43
4:1E:9:VAL:HB	15:1T:3:ARG:HG2	1.98	0.43
4:1E:116:VAL:HG13	4:1E:122:PHE:HB2	1.99	0.43
6:1G:104:GLU:O	6:1G:108:ASN:ND2	2.30	0.43
32:1a:1072:G:N2	33:1b:107:THR:HG21	2.34	0.43
32:1a:1226:C:O2'	44:1m:103:THR:O	2.30	0.43
37:1f:97:PHE:N	49:1r:30:ASP:OD1	2.44	0.43
41:1j:17:ASP:OD1	41:1j:70:ARG:NE	2.51	0.43
44:1m:76:ALA:O	44:1m:80:ARG:HG2	2.18	0.43
1:2A:207:A:H2'	1:2A:208:C:O4'	2.18	0.43
1:2A:265:A:N6	1:2A:428:A:H1'	2.33	0.43
1:2A:272:G:N3	1:2A:272(B):G:H1'	2.33	0.43
1:2A:330:A:HO2'	1:2A:331:A:H8	1.63	0.43
1:2A:370:G:OP2	1:2A:370:G:H8	2.02	0.43
1:2A:981:A:N1	1:2A:2027:G:O2'	2.49	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1796:U:H2'	1:2A:1797:C:H6	1.81	0.43
2:2B:30:C:H2'	2:2B:31:C:H5'	1.99	0.43
3:2D:16:MET:HG3	3:2D:206:LEU:O	2.19	0.43
32:2a:1127:G:H5'	32:2a:1280:A:O2'	2.19	0.43
32:2a:1311:G:H2'	32:2a:1312:G:O4'	2.19	0.43
34:2c:22:TRP:CB	34:2c:59:ARG:HB2	2.49	0.43
35:2d:145:GLU:HA	35:2d:184:LYS:HG2	2.01	0.43
35:2d:196:LEU:H	35:2d:196:LEU:HD12	1.82	0.43
36:2e:122:GLU:O	36:2e:126:ARG:NH1	2.50	0.43
40:2i:85:LEU:HB3	40:2i:92:TYR:CE2	2.54	0.43
1:1A:231:G:O2'	1:1A:243:G:O6	2.32	0.43
1:1A:324:A:OP2	20:1Y:86:ARG:NH2	2.52	0.43
1:1A:982:U:H2'	1:1A:983:G:O4'	2.19	0.43
1:1A:2155:G:C2	1:1A:2179:G:H2'	2.53	0.43
1:1A:2346:G:H5'	14:1S:9:ARG:HG2	1.99	0.43
1:1A:2642:G:H2'	1:1A:2643:G:C8	2.54	0.43
2:1B:73:A:C4	2:1B:105:A:C2	3.07	0.43
4:1E:78:LEU:O	4:1E:79:ARG:NH1	2.51	0.43
17:1V:76:LYS:HB2	17:1V:81:TYR:HB3	2.00	0.43
21:1Z:9:TYR:OH	21:1Z:61:LEU:HD23	2.19	0.43
31:19:4:ARG:NH2	63:19:201:HOH:O	2.51	0.43
32:1a:1220:G:N2	50:1s:54:GLY:O	2.47	0.43
33:1b:45:GLN:HE21	33:1b:45:GLN:C	2.27	0.43
39:1h:11:THR:HG23	39:1h:14:ARG:HH21	1.83	0.43
50:1s:10:PHE:HE2	50:1s:37:ARG:HD3	1.83	0.43
1:2A:818:G:H4'	1:2A:838:C:O3'	2.18	0.43
1:2A:959:A:N6	1:2A:960:A:N1	2.67	0.43
1:2A:1799:G:O2'	3:2D:181:GLU:OE2	2.34	0.43
1:2A:1945:G:H2'	1:2A:1946:U:C6	2.54	0.43
1:2A:2689:U:H4'	1:2A:2690:C:H5'	2.00	0.43
15:2T:65:LYS:HE2	15:2T:67:SER:HB2	2.00	0.43
32:2a:526:C:OP2	43:2l:91:LYS:HE3	2.19	0.43
32:2a:560:U:H5'	32:2a:566:G:N2	2.34	0.43
33:2b:111:ARG:HH11	33:2b:111:ARG:HA	1.83	0.43
36:2e:18:ARG:NH1	36:2e:27:ARG:HH21	2.15	0.43
1:1A:572:A:O2'	1:1A:573:G:OP1	2.28	0.43
1:1A:1245:C:H1'	16:1U:2:PRO:HG3	2.00	0.43
1:1A:2060:G:H2'	1:1A:2061:C:O4'	2.19	0.43
1:1A:2798:C:OP1	4:1E:41:LYS:NZ	2.51	0.43
1:1A:2846:U:H2'	1:1A:2847:G:C8	2.54	0.43
1:1A:2864:G:H2'	1:1A:2865:C:C6	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:1D:145:VAL:HG12	3:1D:146:GLU:O	2.19	0.43
7:1H:3:ARG:NH2	7:1H:65:HIS:HB3	2.32	0.43
12:1Q:21:THR:HG21	12:1Q:101:ARG:HB2	2.01	0.43
14:1S:84:GLN:HA	14:1S:111:GLU:HB2	2.00	0.43
16:1U:52:ARG:HA	16:1U:55:ARG:HG3	1.99	0.43
20:1Y:9:LYS:HA	20:1Y:10:GLY:HA2	1.74	0.43
21:1Z:75:ASN:HB2	21:1Z:85:HIS:HB3	2.00	0.43
33:1b:19:HIS:CG	33:1b:20:GLU:N	2.86	0.43
39:1h:29:SER:HB3	39:1h:32:LYS:HG3	2.01	0.43
1:2A:2728:U:H5'	10:2O:70:LYS:HZ3	1.83	0.43
9:2N:4:TYR:HB2	16:2U:101:ARG:NH2	2.33	0.43
12:2Q:36:ALA:HB2	12:2Q:103:MET:SD	2.58	0.43
17:2V:31:ALA:O	17:2V:61:VAL:HG22	2.19	0.43
32:2a:376:G:O3'	47:2p:5:ARG:HD2	2.19	0.43
32:2a:487:A:H2'	32:2a:488:C:O4'	2.19	0.43
32:2a:1151:A:H5''	41:2j:41:PRO:HA	2.01	0.43
32:2a:1227:A:N3	50:2s:83:HIS:HB3	2.34	0.43
37:2f:100:ASN:ND2	49:2r:23:LYS:HE2	2.34	0.43
39:2h:6:ILE:O	39:2h:10:LEU:HG	2.18	0.43
1:1A:77:A:H2'	1:1A:78:G:H8	1.84	0.43
1:1A:589:U:H5''	11:1P:29:LYS:HE3	2.01	0.43
1:1A:1186:U:H4'	1:1A:1188:A:O4'	2.19	0.43
1:1A:2161:C:N4	1:1A:2174:G:H1	2.16	0.43
2:1B:29:A:H2'	2:1B:30:C:C6	2.54	0.43
6:1G:61:ALA:HB1	26:14:7:PRO:HG2	2.00	0.43
32:1a:102:G:O2'	32:1a:151:A:N3	2.49	0.43
32:1a:1111:A:N1	34:1c:177:THR:OG1	2.50	0.43
40:1i:8:GLY:HA3	40:1i:76:ALA:O	2.18	0.43
50:1s:40:ILE:HD12	50:1s:69:HIS:C	2.44	0.43
53:1x:21:A:H5'	53:1x:22:G:OP1	2.19	0.43
54:1y:11:ARG:HD3	54:1y:12:PRO:HD2	2.01	0.43
1:2A:80:G:H1	1:2A:106:C:H42	1.67	0.43
1:2A:107:C:H2'	1:2A:108:U:H6	1.84	0.43
1:2A:1973:G:H2'	1:2A:1974:C:C6	2.54	0.43
1:2A:2233:U:H2'	1:2A:2234:G:C8	2.54	0.43
3:2D:106:ILE:HD11	3:2D:144:ALA:HB2	2.00	0.43
3:2D:264:LYS:HA	3:2D:265:PRO:HD3	1.90	0.43
18:2W:86:LEU:HD22	18:2W:96:ILE:HD11	1.99	0.43
21:2Z:26:GLY:HA2	21:2Z:85:HIS:CD2	2.54	0.43
21:2Z:54:HIS:CG	21:2Z:101:PRO:HG3	2.54	0.43
32:2a:114:U:H1'	32:2a:353:A:H1'	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:745:C:H2'	32:2a:746:A:C8	2.54	0.43
32:2a:959:A:HO2'	32:2a:984:C:HO2'	1.59	0.43
34:2c:42:LEU:O	34:2c:46:GLU:HG2	2.18	0.43
35:2d:31:CYS:SG	35:2d:33:MET:N	2.92	0.43
39:2h:20:TYR:HE2	39:2h:75:ARG:HD2	1.83	0.43
48:2q:76:LEU:HD21	48:2q:79:SER:HB2	2.01	0.43
53:2x:20:U:H5''	53:2x:21:A:OP2	2.19	0.43
1:1A:1220:U:H1'	1:1A:1221:G:OP1	2.18	0.43
1:1A:1629:C:O2'	1:1A:1632:A:N3	2.48	0.43
1:1A:1736:A:H2'	1:1A:1737:A:C8	2.54	0.43
1:1A:2014:G:C2	1:1A:2019:G:C5	3.07	0.43
1:1A:2702:C:OP1	13:1R:17:ARG:NH2	2.46	0.43
1:1A:2713:C:H2'	1:1A:2714:U:H2'	1.99	0.43
1:1A:2859:U:OP2	15:1T:95:ARG:NH1	2.52	0.43
4:1E:9:VAL:HG22	4:1E:25:VAL:HB	1.99	0.43
6:1G:67:LYS:H	26:14:6:HIS:CE1	2.37	0.43
20:1Y:77:PRO:HD2	20:1Y:106:LEU:HD23	2.01	0.43
21:1Z:91:LEU:HD11	21:1Z:96:VAL:HG11	2.00	0.43
32:1a:445:G:H2'	32:1a:446:G:C8	2.54	0.43
32:1a:839:U:H1'	32:1a:840:C:OP1	2.19	0.43
32:1a:1124:G:N2	32:1a:1125:U:O4	2.51	0.43
32:1a:1346:A:H61	32:1a:1374:A:H3'	1.84	0.43
33:1b:53:ARG:HA	33:1b:56:ARG:HH11	1.83	0.43
41:1j:42:THR:HG23	41:1j:68:HIS:HA	2.01	0.43
1:2A:569:U:C4	1:2A:570:G:C6	3.07	0.43
1:2A:1131:G:O6	1:2A:2040:C:H1'	2.18	0.43
1:2A:2492:U:H2'	1:2A:2493:U:C6	2.54	0.43
1:2A:2567:G:H2'	1:2A:2568:C:C6	2.54	0.43
3:2D:94:LEU:HD23	3:2D:94:LEU:HA	1.89	0.43
6:2G:49:ASP:OD2	6:2G:49:ASP:N	2.52	0.43
6:2G:83:ARG:H	6:2G:86:MET:CE	2.31	0.43
16:2U:34:LYS:HA	16:2U:34:LYS:HD3	1.61	0.43
18:2W:46:PHE:O	18:2W:50:VAL:HG23	2.19	0.43
23:21:91:LYS:HA	23:21:94:LEU:HD12	2.00	0.43
32:2a:745:C:H1'	32:2a:836:G:O2'	2.18	0.43
32:2a:1068:G:H8	32:2a:1068:G:OP2	2.02	0.43
33:2b:70:PHE:HD1	33:2b:163:PHE:HB3	1.83	0.43
1:1A:23:G:OP1	1:1A:529:U:N3	2.51	0.43
1:1A:636:G:N2	1:1A:640:A:O2'	2.51	0.43
1:1A:1224:C:H2'	1:1A:1225:C:H6	1.84	0.43
1:1A:1586:G:H2'	1:1A:1587:U:O4'	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2161:C:H42	1:1A:2174:G:H1	1.67	0.43
6:1G:109:VAL:C	6:1G:112:PRO:HD2	2.43	0.43
8:1I:44:LEU:HD12	8:1I:44:LEU:HA	1.85	0.43
11:1P:138:LEU:HD23	11:1P:145:PRO:HB3	1.99	0.43
21:1Z:124:ILE:HD11	21:1Z:165:VAL:HG21	2.01	0.43
21:1Z:125:LEU:HG	21:1Z:164:ALA:HB3	2.01	0.43
32:1a:179:A:H2'	32:1a:180:U:C6	2.53	0.43
32:1a:458:C:H2'	32:1a:460:G:H8	1.84	0.43
32:1a:1031:G:H2'	32:1a:1032:G:H8	1.84	0.43
32:1a:1347:G:C8	40:1i:107:ARG:HB2	2.54	0.43
34:1c:148:GLY:HA3	34:1c:172:ARG:O	2.18	0.43
35:1d:23:GLY:HA3	35:1d:112:VAL:HB	2.01	0.43
35:1d:178:VAL:O	35:1d:180:GLY:N	2.47	0.43
1:2A:687:C:H2'	1:2A:688:U:O4'	2.18	0.43
1:2A:874:G:H2'	1:2A:875:G:O4'	2.18	0.43
1:2A:1005:C:H2'	1:2A:1006:C:C6	2.54	0.43
1:2A:1064:C:H3'	1:2A:1065:U:C5'	2.49	0.43
1:2A:1669:A:H5''	1:2A:2550:G:OP1	2.18	0.43
1:2A:2379:G:O2'	14:2S:17:ARG:NH1	2.45	0.43
1:2A:2405:G:O2'	1:2A:2406:U:OP1	2.36	0.43
3:2D:132:PRO:HD3	3:2D:190:TYR:CZ	2.53	0.43
8:2I:140:LEU:HD23	8:2I:140:LEU:HA	1.83	0.43
13:2R:87:TYR:OH	13:2R:116:LEU:HB3	2.18	0.43
15:2T:41:ARG:NH2	32:2a:346:G:OP1	2.36	0.43
17:2V:89:GLN:HA	17:2V:90:PRO:HD3	1.88	0.43
32:2a:620:C:H5''	63:2a:4928:HOH:O	2.18	0.43
32:2a:1015:A:H2'	32:2a:1016:A:C8	2.53	0.43
32:2a:1288:A:N1	32:2a:1371:G:H1'	2.34	0.43
42:2k:38:ASN:HA	42:2k:39:PRO:HD3	1.87	0.43
44:2m:10:PRO:HG2	44:2m:13:LYS:HD2	1.99	0.43
45:2n:24:CYS:HB3	45:2n:29:ARG:H	1.84	0.43
1:1A:823:G:N7	1:1A:840:A:O2'	2.46	0.42
1:1A:1639:G:H2'	1:1A:1640:G:C8	2.54	0.42
6:1G:107:LEU:HD11	6:1G:178:PHE:HE1	1.82	0.42
7:1H:154:PRO:HB3	7:1H:163:TYR:CE1	2.54	0.42
32:1a:262:A:H2'	32:1a:263:A:C8	2.54	0.42
32:1a:487:A:H2'	32:1a:488:C:O4'	2.19	0.42
32:1a:1034:G:H2'	32:1a:1035:A:O4'	2.19	0.42
32:1a:1239:A:H62	32:1a:1299:A:N6	2.16	0.42
32:1a:1394:A:N1	32:1a:1500:A:O2'	2.43	0.42
1:2A:576:U:H2'	1:2A:577:G:C8	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:610:G:H2'	1:2A:611:C:C6	2.54	0.42
1:2A:2689:U:OP2	1:2A:2719:G:N2	2.49	0.42
1:2A:2695:C:H2'	1:2A:2696:U:C6	2.54	0.42
4:2E:120:TRP:CD1	4:2E:155:LYS:HB3	2.54	0.42
4:2E:144:ARG:HB3	4:2E:145:LYS:H	1.49	0.42
7:2H:17:VAL:HG11	7:2H:50:VAL:HG21	2.01	0.42
15:2T:39:ARG:NH2	32:2a:345:C:OP2	2.51	0.42
20:2Y:87:LYS:HB3	20:2Y:95:LYS:HD2	2.01	0.42
31:29:10:ILE:HD12	31:29:32:HIS:HA	2.00	0.42
32:2a:517:G:N1	32:2a:533:A:OP2	2.40	0.42
32:2a:628:G:H2'	32:2a:629:G:C8	2.54	0.42
32:2a:1360:A:H8	32:2a:1360:A:OP1	2.02	0.42
37:2f:100:ASN:HD21	49:2r:23:LYS:HG2	1.84	0.42
48:2q:5:VAL:HA	48:2q:59:ILE:O	2.19	0.42
1:1A:766:C:H2'	1:1A:767:C:C6	2.55	0.42
1:1A:923:C:H2'	1:1A:924:U:O4'	2.19	0.42
1:1A:939:C:H2'	1:1A:940:C:C6	2.54	0.42
1:1A:2724:U:OP1	1:1A:2727:G:H4'	2.20	0.42
1:1A:2760:G:O6	1:1A:2768:C:H5''	2.18	0.42
20:1Y:53:PRO:O	20:1Y:56:PRO:HD3	2.20	0.42
24:12:1:MET:HE1	24:12:9:GLN:OE1	2.19	0.42
24:12:32:LEU:HD22	24:12:36:ARG:NH1	2.32	0.42
28:16:34:LEU:HB2	28:16:51:GLU:HB2	2.01	0.42
32:1a:1241:G:H2'	32:1a:1242:C:C6	2.54	0.42
33:1b:55:PHE:CE2	33:1b:218:ALA:HA	2.54	0.42
46:1o:16:ALA:HB1	46:1o:21:ASP:HB3	2.00	0.42
1:2A:143:G:H2'	1:2A:143(A):C:C6	2.53	0.42
1:2A:224:G:H2'	1:2A:225:A:O4'	2.19	0.42
1:2A:1160:G:C6	1:2A:1161:C:C4	3.06	0.42
1:2A:1450:G:H2'	1:2A:1450(A):C:C6	2.54	0.42
1:2A:2059:A:H2'	1:2A:2503:2MA:HM22	2.01	0.42
1:2A:2166:G:H2'	1:2A:2167:U:O4'	2.19	0.42
1:2A:2318:G:N2	14:2S:3:ARG:HE	2.17	0.42
3:2D:245:PRO:HA	3:2D:246:PRO:HD3	1.91	0.42
4:2E:50:GLY:O	4:2E:51:PHE:HB2	2.18	0.42
21:2Z:14:LYS:HA	21:2Z:15:PRO:HD3	1.88	0.42
38:2g:24:THR:O	38:2g:27:ILE:HB	2.19	0.42
1:1A:593:G:H2'	1:1A:2052:A:C5	2.53	0.42
1:1A:756:U:H2'	1:1A:757:G:C8	2.54	0.42
1:1A:762:G:H2'	1:1A:763:A:O4'	2.19	0.42
1:1A:956:A:H2'	1:1A:957:A:C8	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2856:G:H2'	1:1A:2857:U:O4'	2.20	0.42
2:1B:102:A:H2'	2:1B:103:G:O4'	2.19	0.42
5:1F:63:LYS:HA	5:1F:76:GLY:O	2.19	0.42
6:1G:148:MET:HE3	6:1G:148:MET:HB2	1.76	0.42
10:1O:12:ASP:CG	10:1O:14:THR:HG23	2.44	0.42
21:1Z:203:GLU:H	53:1x:53:G:H4'	1.83	0.42
32:1a:450:G:H1	32:1a:483:C:N4	2.17	0.42
32:1a:616:G:OP2	35:1d:141:ARG:NH2	2.53	0.42
32:1a:964:A:N3	32:1a:969:A:O2'	2.47	0.42
32:1a:1093:A:N3	32:1a:1109:C:O2'	2.45	0.42
34:1c:12:LEU:HD11	45:1n:51:GLY:HA2	2.01	0.42
35:1d:194:LEU:HD13	35:1d:195:ALA:H	1.85	0.42
36:1e:144:THR:H	36:1e:147:ASP:HB2	1.84	0.42
39:1h:51:VAL:HG11	39:1h:60:ARG:NH1	2.30	0.42
1:2A:305:U:H2'	1:2A:306:U:C6	2.54	0.42
1:2A:601:C:O2	1:2A:605:C:H4'	2.19	0.42
1:2A:857:C:OP2	22:20:77:ARG:NH2	2.52	0.42
1:2A:1085:A:H2'	1:2A:1086:A:C2	2.54	0.42
1:2A:2075:U:OP2	1:2A:2238:G:O2'	2.35	0.42
1:2A:2881:C:H2'	1:2A:2882:A:O4'	2.19	0.42
9:2N:103:VAL:HG11	9:2N:120:LEU:HD22	2.00	0.42
14:2S:49:VAL:HG12	14:2S:73:LEU:HD12	2.01	0.42
21:2Z:93:ASP:HB3	21:2Z:131:ARG:HH22	1.85	0.42
32:2a:841:U:C5	32:2a:848:C:H1'	2.53	0.42
32:2a:1005:A:N6	32:2a:1024:G:N2	2.66	0.42
32:2a:1151:A:O2'	32:2a:1152:A:O5'	2.36	0.42
34:2c:36:ASP:HA	34:2c:39:ILE:HD12	1.99	0.42
38:2g:65:ALA:HB1	38:2g:127:ALA:HB3	2.01	0.42
1:1A:485:U:H4'	29:17:40:TRP:CZ3	2.55	0.42
1:1A:1093:G:H2'	1:1A:1156:G:N2	2.31	0.42
1:1A:1686:U:H4'	1:1A:2711:C:H4'	2.01	0.42
1:1A:2432:C:H5'	28:16:54:ILE:HD11	2.01	0.42
4:1E:9:VAL:HG13	4:1E:25:VAL:O	2.20	0.42
19:1X:11:PRO:HG2	19:1X:13:LEU:HD21	2.01	0.42
32:1a:57:G:C5	32:1a:58:C:C4	3.08	0.42
32:1a:450:G:H1	32:1a:483:C:H42	1.65	0.42
32:1a:501:C:H2'	32:1a:502:G:H8	1.83	0.42
32:1a:574:A:HO2'	32:1a:882:C:HO2'	1.67	0.42
32:1a:646:U:H2'	32:1a:647:C:C6	2.54	0.42
32:1a:1286:A:H2'	32:1a:1287:A:H4'	2.00	0.42
34:1c:6:HIS:HB3	45:1n:49:HIS:ND1	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:1d:133:VAL:HG12	35:1d:135:LEU:H	1.84	0.42
43:1l:124:LYS:HA	43:1l:125:PRO:HD3	1.84	0.42
50:1s:3:ARG:HE	50:1s:7:LYS:HD3	1.85	0.42
1:2A:459:U:OP2	29:27:39:ARG:NH1	2.52	0.42
1:2A:2154:G:C6	1:2A:2155:G:C6	3.07	0.42
1:2A:2378:A:O5'	1:2A:2378:A:H8	2.02	0.42
6:2G:16:ARG:O	6:2G:20:ILE:HG13	2.20	0.42
13:2R:65:LEU:HD12	13:2R:65:LEU:HA	1.82	0.42
35:2d:112:VAL:HG13	35:2d:161:ASN:OD1	2.19	0.42
50:2s:50:ALA:HB1	50:2s:57:HIS:HB3	2.01	0.42
1:1A:933:C:H4'	1:1A:933:C:OP1	2.18	0.42
1:1A:1781:G:O2'	1:1A:2870:A:N1	2.50	0.42
1:1A:1857:G:H2'	1:1A:1858:C:O4'	2.19	0.42
1:1A:1897:C:H2'	1:1A:1898:A:O4'	2.19	0.42
1:1A:2203:G:H2'	1:1A:2204:G:C8	2.55	0.42
1:1A:2524:C:H2'	1:1A:2525:G:O4'	2.19	0.42
4:1E:27:LEU:HD12	4:1E:180:ASN:O	2.19	0.42
12:1Q:135:ASP:O	12:1Q:139:GLU:HG3	2.20	0.42
15:1T:109:GLU:O	15:1T:113:LYS:HG2	2.20	0.42
17:1V:28:GLU:HG3	17:1V:29:PRO:HD2	2.00	0.42
35:1d:53:ASP:O	35:1d:57:ARG:NH1	2.52	0.42
35:1d:178:VAL:HG12	35:1d:179:GLU:H	1.85	0.42
41:1j:19:SER:O	41:1j:23:ILE:HG12	2.19	0.42
1:2A:1127:A:N7	1:2A:2488:A:O2'	2.50	0.42
2:2B:77:U:OP1	21:2Z:19:ARG:NH2	2.53	0.42
9:2N:58:ASP:OD1	9:2N:58:ASP:N	2.47	0.42
19:2X:31:HIS:HA	19:2X:32:PRO:HD3	1.83	0.42
20:2Y:5:MET:HE3	20:2Y:30:VAL:HG13	2.02	0.42
22:20:43:THR:OG1	22:20:46:LYS:HG2	2.19	0.42
32:2a:433:C:H2'	32:2a:434:U:H6	1.85	0.42
32:2a:489:C:H2'	32:2a:490:G:C8	2.54	0.42
32:2a:1004:A:C2'	32:2a:1038:C:H1'	2.50	0.42
32:2a:1125:U:HO2'	32:2a:1126:U:H2'	1.85	0.42
32:2a:1286:A:N6	32:2a:1354:C:O3'	2.52	0.42
33:2b:53:ARG:HH12	33:2b:199:TYR:HA	1.84	0.42
33:2b:54:THR:O	33:2b:58:ILE:HG12	2.20	0.42
35:2d:79:PHE:CE1	35:2d:204:ILE:HD13	2.55	0.42
41:2j:16:LEU:HD12	41:2j:68:HIS:HB2	2.01	0.42
43:2l:66:VAL:HG11	43:2l:98:TYR:HE2	1.84	0.42
1:1A:518:G:H2'	1:1A:519:G:O4'	2.19	0.42
1:1A:766:C:H2'	1:1A:767:C:H6	1.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:826:U:OP1	3:1D:49:ILE:HG13	2.19	0.42
1:1A:1686:U:O2'	1:1A:1687:C:H5'	2.20	0.42
1:1A:1941:A:O3'	32:1a:1517:G:H1'	2.19	0.42
1:1A:2081:A:H2'	1:1A:2515:2MA:HM22	2.00	0.42
1:1A:2368:C:H2'	1:1A:2369:U:O4'	2.20	0.42
1:1A:2388:A:H2'	1:1A:2389:A:O4'	2.19	0.42
1:1A:2880:C:H2'	1:1A:2881:C:O4'	2.19	0.42
8:1I:38:LEU:HD22	8:1I:38:LEU:H	1.85	0.42
20:1Y:30:VAL:HG22	20:1Y:37:VAL:HG12	2.01	0.42
26:14:63:TYR:N	26:14:64:GLY:HA2	2.32	0.42
28:16:6:ARG:HH12	28:16:26:ASN:HB2	1.85	0.42
32:1a:600:C:H2'	32:1a:601:C:C6	2.54	0.42
32:1a:629:G:H2'	32:1a:630:G:O4'	2.19	0.42
32:1a:1498:UR3:OP2	55:B:114:A:O2'	2.36	0.42
33:1b:87:ARG:NH1	33:1b:233:SER:HB3	2.30	0.42
38:1g:113:GLU:HG3	38:1g:118:VAL:HG12	2.02	0.42
51:1t:58:LYS:HA	51:1t:58:LYS:HD2	1.71	0.42
53:1x:23:C:H2'	53:1x:24:U:H6	1.84	0.42
1:2A:321:G:H5'	5:2F:134:GLY:O	2.19	0.42
1:2A:495:G:H21	18:2W:61:ASN:HD21	1.68	0.42
1:2A:760:G:H2'	1:2A:761:A:O4'	2.19	0.42
1:2A:1062:G:H5'	1:2A:1070:A:H5'	2.00	0.42
4:2E:14:ILE:HB	15:2T:14:TYR:CZ	2.55	0.42
7:2H:74:ASN:O	7:2H:78:GLY:N	2.52	0.42
12:2Q:12:GLN:NE2	12:2Q:72:LYS:HG3	2.34	0.42
16:2U:83:LEU:HD21	16:2U:95:LEU:HD21	2.01	0.42
18:2W:82:LEU:HD22	18:2W:84:ARG:NH2	2.34	0.42
20:2Y:94:LYS:HA	20:2Y:94:LYS:HD3	1.92	0.42
21:2Z:9:TYR:OH	21:2Z:61:LEU:HD23	2.19	0.42
32:2a:439:A:C5	32:2a:441:A:H1'	2.55	0.42
32:2a:583:A:H2'	32:2a:584:G:O4'	2.19	0.42
33:2b:19:HIS:CG	33:2b:20:GLU:N	2.87	0.42
1:1A:397:G:OP2	1:1A:397:G:H8	2.02	0.42
1:1A:629:U:H4'	1:1A:705:C:H4'	2.00	0.42
1:1A:1481:G:H2'	1:1A:1482:G:O4'	2.20	0.42
1:1A:1710:C:HO2'	1:1A:1711:A:P	2.43	0.42
1:1A:1712:A:H4'	10:1O:67:LYS:HB2	2.00	0.42
1:1A:1715:A:H4'	1:1A:1716:A:O5'	2.19	0.42
1:1A:1992:A:H4'	1:1A:1993:A:OP1	2.20	0.42
14:1S:35:ILE:HG12	14:1S:101:LEU:HD12	2.02	0.42
15:1T:26:ASP:OD1	15:1T:120:ARG:NH2	2.37	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:1V:98:GLU:OE2	17:1V:100:ARG:NH1	2.42	0.42
32:1a:688:G:O2'	32:1a:704:A:N1	2.47	0.42
32:1a:1095:U:P	32:1a:1108:G:H1	2.42	0.42
32:1a:1302:U:C5	44:1m:17:VAL:HG21	2.55	0.42
34:1c:8:ILE:HD11	34:1c:184:TYR:HB3	2.00	0.42
35:1d:156:GLU:O	35:1d:160:GLN:HG2	2.20	0.42
53:1x:28:C:H42	53:1x:42:G:H1	1.68	0.42
1:2A:459:U:H2'	1:2A:460:A:C8	2.54	0.42
1:2A:864:G:C6	1:2A:865:C:N4	2.88	0.42
1:2A:1057:A:H2'	1:2A:1058:G:C8	2.51	0.42
1:2A:1739:U:O2'	1:2A:1740:G:H8	2.02	0.42
11:2P:101:VAL:HA	11:2P:106:LEU:O	2.20	0.42
32:2a:601:C:H2'	32:2a:602:A:C8	2.55	0.42
32:2a:977:A:H2'	32:2a:978:A:H5''	2.00	0.42
32:2a:1030(B):C:H41	32:2a:1030(C):G:H21	1.67	0.42
33:2b:76:GLN:H	33:2b:76:GLN:HG2	1.63	0.42
44:2m:73:GLU:O	44:2m:77:ASN:N	2.31	0.42
1:1A:1159:U:H2'	1:1A:1160:G:C8	2.54	0.42
1:1A:1710:C:O2'	1:1A:1711:A:O5'	2.32	0.42
2:1B:81:G:N7	59:1B:229:ARG:NH2	2.57	0.42
5:1F:95:ARG:HB3	5:1F:97:TYR:CE2	2.55	0.42
10:1O:64:ARG:HB2	10:1O:79:PHE:CD2	2.55	0.42
12:1Q:110:THR:HG23	12:1Q:113:GLN:OE1	2.20	0.42
24:12:7:ARG:O	24:12:11:GLU:HG3	2.20	0.42
32:1a:1179:A:H2'	32:1a:1180:A:O4'	2.19	0.42
34:1c:69:HIS:CD2	34:1c:104:GLN:HG2	2.55	0.42
38:1g:26:PHE:O	38:1g:30:ILE:HG13	2.20	0.42
51:1t:74:LYS:HE2	51:1t:74:LYS:HB3	1.86	0.42
1:2A:478:A:N1	1:2A:500:G:H4'	2.35	0.42
1:2A:678:C:H2'	1:2A:679:C:C6	2.55	0.42
1:2A:1128:A:O2'	1:2A:2490:G:OP1	2.30	0.42
1:2A:1227:G:OP1	16:2U:13:LYS:HE3	2.19	0.42
3:2D:5:LYS:HE3	3:2D:5:LYS:HB3	1.90	0.42
32:2a:105:G:C5	32:2a:106:C:C4	3.08	0.42
32:2a:277:C:H2'	32:2a:278:G:H8	1.85	0.42
32:2a:977:A:O2'	32:2a:981:U:N3	2.52	0.42
32:2a:1100:C:OP2	33:2b:96:ARG:HD3	2.20	0.42
46:2o:33:THR:HG21	46:2o:85:LEU:HD22	2.01	0.42
46:2o:39:LEU:HD23	46:2o:39:LEU:HA	1.90	0.42
1:1A:1159:U:H2'	1:1A:1160:G:H8	1.85	0.42
1:1A:2495:C:N3	12:1Q:124:LYS:NZ	2.62	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2576:A:C2	1:1A:2659:U:H4'	2.54	0.42
1:1A:2814:C:H2'	1:1A:2815:C:C6	2.55	0.42
21:1Z:14:LYS:HA	21:1Z:15:PRO:HD3	1.92	0.42
32:1a:76:C:H2'	32:1a:77:G:H8	1.85	0.42
32:1a:1372:U:OP1	40:1i:72:GLY:N	2.49	0.42
34:1c:26:LYS:HE3	34:1c:27:LYS:HE2	2.01	0.42
36:1e:92:LYS:HA	36:1e:93:PRO:HD3	1.91	0.42
1:2A:960:A:H5'	1:2A:2457:U:H4'	2.02	0.42
1:2A:1007:C:H5''	9:2N:35:ARG:NH1	2.35	0.42
1:2A:1186:G:C2	1:2A:1187:G:H1'	2.54	0.42
1:2A:1499:C:H2'	1:2A:1500:G:H8	1.85	0.42
1:2A:2059:A:H2'	1:2A:2503:2MA:CM2	2.50	0.42
1:2A:2134:A:H5''	1:2A:2156:G:N2	2.34	0.42
1:2A:2157:G:H3'	1:2A:2157:G:H8	1.85	0.42
1:2A:2494:G:C4	1:2A:2495:G:C8	3.08	0.42
2:2B:3:C:H2'	2:2B:4:C:C6	2.55	0.42
15:2T:81:PRO:HG2	15:2T:82:LEU:HD12	2.02	0.42
31:29:32:HIS:O	31:29:34:GLN:HG3	2.20	0.42
32:2a:130:A:H1'	32:2a:263:A:O2'	2.19	0.42
32:2a:718:G:H4'	42:2k:117:ASN:HD21	1.85	0.42
32:2a:1148:U:O4'	40:2i:16:ARG:HD2	2.19	0.42
32:2a:1318:A:O2'	50:2s:37:ARG:HD2	2.19	0.42
32:2a:1401:G:C2	32:2a:1402:4OC:H1'	2.54	0.42
34:2c:7:PRO:HG3	34:2c:201:TYR:CE1	2.54	0.42
53:2x:25:C:H2'	53:2x:26:G:O4'	2.20	0.42
1:1A:196:A:H2'	1:1A:197:C:O4'	2.19	0.42
1:1A:926:G:H2'	1:1A:927:G:O4'	2.19	0.42
1:1A:1404:G:O2'	1:1A:1405:A:H5''	2.20	0.42
1:1A:1765:U:H2'	1:1A:1766:G:O4'	2.20	0.42
1:1A:1926:G:O2'	1:1A:1950:A:N1	2.51	0.42
1:1A:2372:A:H2'	1:1A:2373:A:O4'	2.20	0.42
1:1A:2762:A:OP1	7:1H:3:ARG:NH1	2.53	0.42
7:1H:149:ARG:NH1	7:1H:167:GLU:OE2	2.53	0.42
32:1a:872:A:C4	32:1a:874:G:C8	3.08	0.42
32:1a:1004:A:O4'	32:1a:1025:U:N3	2.52	0.42
32:1a:1109:C:H2'	32:1a:1110:A:O4'	2.20	0.42
32:1a:1289:A:P	52:1u:10:ARG:HH22	2.43	0.42
33:1b:224:GLN:HA	33:1b:228:GLY:O	2.19	0.42
37:1f:70:ASP:OD1	37:1f:70:ASP:N	2.53	0.42
46:1o:3:ILE:H	46:1o:3:ILE:HG13	1.50	0.42
49:1r:73:ALA:HB3	49:1r:79:LEU:HD12	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1012:U:C5	9:2N:28:THR:HG21	2.55	0.42
1:2A:1130:U:O2	4:2E:149:ARG:NH2	2.48	0.42
1:2A:1637:A:H4'	1:2A:2711:A:O2'	2.20	0.42
1:2A:1889:A:N1	1:2A:2234:G:H1'	2.34	0.42
1:2A:2081:C:H2'	1:2A:2082:A:C8	2.55	0.42
7:2H:105:LEU:HD12	7:2H:105:LEU:HA	1.90	0.42
9:2N:4:TYR:CD2	16:2U:100:VAL:HG11	2.55	0.42
15:2T:49:VAL:HG12	15:2T:63:VAL:HG22	2.01	0.42
32:2a:621:A:H2'	32:2a:622:A:O4'	2.20	0.42
32:2a:722:A:H2'	32:2a:724:G:C8	2.54	0.42
32:2a:848:C:H2'	32:2a:849:C:C6	2.55	0.42
32:2a:947:G:O3'	44:2m:109:THR:OG1	2.38	0.42
37:2f:30:LEU:HD23	37:2f:75:LEU:HD11	2.02	0.42
44:2m:65:LYS:HB3	44:2m:69:GLU:CD	2.45	0.42
1:1A:142:G:H4'	19:1X:35:THR:HG21	2.02	0.41
1:1A:312:C:H2'	1:1A:313:A:C8	2.55	0.41
1:1A:1541:A:H2'	1:1A:1542:A:C8	2.54	0.41
1:1A:1560:U:H2'	1:1A:1561:C:H6	1.85	0.41
4:1E:144:ARG:HB3	4:1E:145:LYS:H	1.44	0.41
19:1X:47:PHE:O	19:1X:49:VAL:HG13	2.20	0.41
19:1X:60:ARG:HH22	29:17:47:ARG:NH1	2.17	0.41
20:1Y:8:LYS:HE2	20:1Y:97:ARG:NH2	2.34	0.41
23:11:53:VAL:HG22	23:11:74:VAL:HG13	2.02	0.41
32:1a:501:C:H1'	32:1a:549:C:H1'	2.02	0.41
32:1a:520:A:N6	32:1a:529:G:H1'	2.35	0.41
32:1a:767:A:H2'	32:1a:768:A:O4'	2.20	0.41
32:1a:1376:U:H2'	32:1a:1377:A:C8	2.54	0.41
33:1b:218:ALA:O	33:1b:222:ILE:HG13	2.20	0.41
42:1k:120:ARG:HA	42:1k:121:PRO:HD3	1.90	0.41
48:1q:75:ARG:NH1	48:1q:77:VAL:HG22	2.35	0.41
1:2A:1138:G:N3	9:2N:106:MET:HE2	2.35	0.41
1:2A:1336:A:H2'	1:2A:1337:G:H8	1.85	0.41
1:2A:1653:G:C6	13:2R:9:LYS:HB2	2.55	0.41
1:2A:1798:U:H5'	3:2D:259:THR:CG2	2.45	0.41
1:2A:2245:U:H5''	1:2A:2246:G:H5'	2.01	0.41
1:2A:2399:G:H2'	1:2A:2400:G:O4'	2.20	0.41
15:2T:27:THR:HB	15:2T:90:GLN:HB3	2.02	0.41
32:2a:10:A:H2'	32:2a:11:G:H8	1.85	0.41
32:2a:70:G:H1	32:2a:99:U:H3	1.66	0.41
32:2a:671:G:H2'	32:2a:672:U:O4'	2.20	0.41
32:2a:902:G:H2'	32:2a:903:G:H8	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1148:U:H2'	32:2a:1149:C:O4'	2.20	0.41
35:2d:61:LYS:HA	35:2d:203:VAL:HG22	2.02	0.41
1:1A:795:G:C8	18:1W:89:ALA:HB1	2.55	0.41
1:1A:1217:G:N3	1:1A:1217:G:H2'	2.35	0.41
1:1A:1501:U:O2'	1:1A:1502:G:N7	2.44	0.41
1:1A:2114:U:H4'	1:1A:2115:G:O5'	2.20	0.41
3:1D:61:LEU:HD12	3:1D:61:LEU:HA	1.90	0.41
4:1E:101:ARG:HG3	4:1E:169:ASN:HA	2.02	0.41
6:1G:86:MET:HA	6:1G:87:PRO:HD3	1.81	0.41
7:1H:3:ARG:HE	7:1H:54:ARG:NH1	2.18	0.41
10:1O:69:ILE:HD11	10:1O:105:GLU:CD	2.45	0.41
12:1Q:58:PHE:O	12:1Q:60:ARG:N	2.53	0.41
13:1R:51:LEU:HD22	13:1R:66:VAL:HG13	2.02	0.41
14:1S:66:ALA:HA	14:1S:69:VAL:HG13	2.02	0.41
15:1T:27:THR:HB	15:1T:89:VAL:HG22	2.02	0.41
25:13:5:LYS:HG3	25:13:36:VAL:HG22	2.01	0.41
32:1a:540:G:H2'	32:1a:541:G:O4'	2.19	0.41
32:1a:1323:G:H4'	32:1a:1363:C:N3	2.35	0.41
36:1e:6:PHE:HB2	36:1e:34:VAL:HG22	2.03	0.41
37:1f:35:ALA:HA	37:1f:67:MET:HB3	2.01	0.41
38:1g:100:ALA:O	38:1g:104:LEU:HB2	2.20	0.41
40:1i:107:ARG:H	40:1i:107:ARG:HG2	1.64	0.41
44:1m:39:ILE:HG23	44:1m:52:GLU:OE2	2.20	0.41
1:2A:78:A:H2'	1:2A:79:G:C8	2.55	0.41
1:2A:455:C:N3	1:2A:472:A:H2'	2.35	0.41
1:2A:652(A):A:N3	1:2A:652(A):A:H2'	2.35	0.41
1:2A:652(D):C:H2'	1:2A:652(E):G:O4'	2.20	0.41
1:2A:903:C:H2'	1:2A:904:C:C6	2.54	0.41
20:2Y:21:LYS:HE3	20:2Y:21:LYS:HB2	1.87	0.41
28:26:28:ARG:HE	28:26:28:ARG:HB2	1.59	0.41
32:2a:236:G:OP1	48:2q:40:LYS:NZ	2.45	0.41
32:2a:547:A:H5'	63:2a:5073:HOH:O	2.19	0.41
32:2a:940:C:H2'	32:2a:941:G:C8	2.55	0.41
32:2a:992:U:H4'	32:2a:993:G:O5'	2.19	0.41
32:2a:1103:C:P	33:2b:96:ARG:HH22	2.43	0.41
32:2a:1261:A:C6	32:2a:1262:C:C2	3.08	0.41
32:2a:1320:C:C1'	50:2s:73:GLU:HG2	2.49	0.41
33:2b:101:MET:HG2	33:2b:108:ILE:HG21	2.02	0.41
34:2c:30:ARG:HD2	45:2n:35:ARG:O	2.20	0.41
49:2r:45:SER:OG	49:2r:47:THR:HG22	2.20	0.41
1:1A:268:G:O2'	1:1A:269:G:H8	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:752:A:H2'	1:1A:753:A:O4'	2.20	0.41
1:1A:768:C:H2'	1:1A:769:A:H8	1.85	0.41
1:1A:874:U:O2'	1:1A:2090:U:C2	2.66	0.41
1:1A:901:G:H2'	1:1A:902:G:C8	2.56	0.41
1:1A:1093:G:O2'	1:1A:1094:A:H8	2.03	0.41
2:1B:2:C:H2'	2:1B:3:C:H6	1.84	0.41
2:1B:51:G:N7	14:1S:62:LYS:NZ	2.53	0.41
8:1I:107:VAL:HG12	8:1I:109:ILE:HD13	2.02	0.41
9:1N:110:GLY:O	9:1N:114:ARG:HB2	2.20	0.41
12:1Q:109:VAL:HG22	12:1Q:113:GLN:OE1	2.21	0.41
16:1U:17:ILE:HG23	16:1U:39:LEU:HD12	2.01	0.41
22:10:56:ASP:OD1	22:10:58:THR:OG1	2.34	0.41
32:1a:177:C:OP1	51:1t:65:LYS:NZ	2.45	0.41
32:1a:474:G:H2'	32:1a:475:G:H8	1.86	0.41
32:1a:685:G:O2'	32:1a:686:U:H5'	2.21	0.41
32:1a:1103:C:H2'	32:1a:1104:G:O4'	2.20	0.41
32:1a:1305:G:C2	32:1a:1331:G:N3	2.88	0.41
32:1a:1429:C:H2'	32:1a:1430:C:H6	1.84	0.41
32:1a:1436:U:H2'	32:1a:1437:C:O4'	2.20	0.41
44:1m:3:ARG:HG2	44:1m:8:GLU:HA	2.02	0.41
44:1m:60:VAL:HG12	44:1m:66:LEU:HD11	2.02	0.41
48:1q:45:HIS:CD2	48:1q:47:PRO:HG3	2.55	0.41
49:1r:76:LEU:HA	49:1r:76:LEU:HD12	1.86	0.41
1:2A:428:A:OP2	1:2A:428:A:H8	2.03	0.41
1:2A:582:G:H2'	1:2A:583:G:C8	2.55	0.41
1:2A:615:G:OP2	5:2F:43:LYS:HE3	2.20	0.41
1:2A:862:G:O2'	2:2B:78:A:N3	2.53	0.41
1:2A:1297:C:O2'	1:2A:1302:A:N1	2.53	0.41
1:2A:1614:A:P	1:2A:1614:A:H8	2.42	0.41
1:2A:2467:C:H4'	12:2Q:123:HIS:CD2	2.55	0.41
2:2B:31:C:H4'	6:2G:29:TRP:CH2	2.55	0.41
25:23:8:LEU:HG	25:23:31:LEU:HD22	2.01	0.41
25:23:52:HIS:CD2	25:23:53:LEU:HG	2.55	0.41
26:24:56:VAL:O	26:24:60:GLN:HB3	2.20	0.41
30:28:39:LYS:HA	30:28:42:ARG:NH1	2.35	0.41
32:2a:1073:U:H2'	32:2a:1074:G:H8	1.85	0.41
32:2a:1239:A:H62	32:2a:1299:A:N6	2.17	0.41
32:2a:1316:G:N2	32:2a:1318:A:H3'	2.35	0.41
35:2d:191:ARG:NH2	35:2d:200:GLU:OE1	2.53	0.41
37:2f:35:ALA:HA	37:2f:67:MET:HB3	2.03	0.41
40:2i:24:GLY:HA2	40:2i:59:PHE:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:716:G:H5''	1:1A:716:G:C8	2.56	0.41
1:1A:1087:C:N4	1:1A:1160:G:H1	2.17	0.41
1:1A:2291:G:H4'	21:1Z:199:LYS:O	2.20	0.41
5:1F:150:GLY:HA2	5:1F:172:TRP:CD2	2.55	0.41
7:1H:137:ASP:HB3	7:1H:140:LYS:HB3	2.03	0.41
13:1R:102:GLU:OE2	18:1W:37:ARG:NH2	2.48	0.41
21:1Z:145:GLU:O	21:1Z:148:ASP:N	2.42	0.41
32:1a:7:G:H5'	32:1a:298:A:O4'	2.19	0.41
32:1a:37:U:H2'	32:1a:38:G:O4'	2.20	0.41
32:1a:933:G:O6	38:1g:3:ARG:NH2	2.47	0.41
32:1a:1492:A:O5'	43:1l:47:LYS:HE3	2.20	0.41
33:1b:163:PHE:HA	33:1b:185:ILE:O	2.20	0.41
34:1c:28:GLN:O	34:1c:32:LEU:HG	2.21	0.41
34:1c:121:ALA:HB1	34:1c:189:ALA:HB2	2.02	0.41
43:1l:56:ALA:HB3	43:1l:100:ILE:HD11	2.02	0.41
46:1o:57:LEU:HD23	46:1o:57:LEU:HA	1.86	0.41
1:2A:372:G:O2'	1:2A:400:G:O6	2.38	0.41
1:2A:764:A:H5'	3:2D:210:GLY:HA2	2.02	0.41
1:2A:863:A:P	12:2Q:22:LYS:HG3	2.61	0.41
1:2A:1165:U:H2'	1:2A:1166:C:C6	2.55	0.41
1:2A:2160:G:OP2	1:2A:2160:G:H8	2.03	0.41
1:2A:2540:C:H2'	1:2A:2541:A:O4'	2.21	0.41
7:2H:27:LYS:HA	7:2H:32:GLU:HA	2.02	0.41
8:2I:1:MET:HE2	8:2I:38:LEU:HD11	2.02	0.41
8:2I:134:PRO:C	8:2I:136:VAL:H	2.28	0.41
13:2R:18:LEU:HD23	13:2R:18:LEU:HA	1.89	0.41
15:2T:11:GLU:O	15:2T:15:VAL:HG23	2.20	0.41
19:2X:12:VAL:HG22	19:2X:29:TRP:CE2	2.56	0.41
22:20:70:GLN:NE2	22:20:72:ARG:HD2	2.35	0.41
32:2a:9:G:OP2	36:2e:121:LYS:NZ	2.43	0.41
32:2a:499:A:H4'	32:2a:500:G:OP1	2.21	0.41
32:2a:946:A:H2'	32:2a:947:G:C8	2.55	0.41
32:2a:952:U:H4'	32:2a:964:A:N1	2.36	0.41
32:2a:1493:A:H5'	32:2a:1494:G:OP2	2.21	0.41
39:2h:86:ILE:HG13	39:2h:133:LEU:HD22	2.01	0.41
40:2i:3:GLN:HE21	40:2i:20:ARG:NE	2.19	0.41
40:2i:13:ALA:HB2	40:2i:68:GLY:HA3	2.02	0.41
40:2i:53:VAL:HG11	40:2i:92:TYR:CE1	2.46	0.41
41:2j:13:HIS:HA	41:2j:16:LEU:HB2	2.02	0.41
46:2o:57:LEU:HD23	46:2o:57:LEU:HA	1.89	0.41
53:2x:66:C:H2'	53:2x:67:C:C6	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1432:C:H2'	1:1A:1433:C:H6	1.84	0.41
1:1A:1682:G:C6	1:1A:1683:C:C4	3.07	0.41
1:1A:1893:G:H2'	1:1A:1894:G:H8	1.85	0.41
1:1A:2227:G:H5''	1:1A:2228:G:C5	2.56	0.41
3:1D:111:LEU:HD23	3:1D:111:LEU:HA	1.79	0.41
5:1F:33:LEU:HD12	5:1F:33:LEU:HA	1.85	0.41
8:1I:10:GLU:O	8:1I:10:GLU:HG2	2.21	0.41
9:1N:120:LEU:HG	9:1N:122:VAL:HG23	2.02	0.41
12:1Q:103:MET:HE1	12:1Q:125:LEU:HD13	2.01	0.41
26:14:56:VAL:HB	26:14:60:GLN:HG2	2.03	0.41
32:1a:339:C:H2'	32:1a:340:U:C6	2.55	0.41
32:1a:544:G:OP1	35:1d:59:ARG:NH2	2.53	0.41
32:1a:658:G:C6	32:1a:659:U:C4	3.09	0.41
32:1a:1326:C:H2'	32:1a:1327:C:C6	2.56	0.41
33:1b:122:PHE:HD1	33:1b:122:PHE:HA	1.67	0.41
36:1e:92:LYS:HB3	36:1e:119:LEU:HB2	2.02	0.41
1:2A:38:A:H2'	1:2A:39:C:C6	2.55	0.41
1:2A:466:A:P	29:27:34:ARG:HH21	2.43	0.41
1:2A:629:G:N3	1:2A:639:U:O2'	2.52	0.41
1:2A:839:U:H2'	1:2A:840:C:C6	2.55	0.41
1:2A:860:U:H2'	1:2A:861:A:H8	1.85	0.41
1:2A:1264:G:H2'	1:2A:2014:A:N6	2.36	0.41
1:2A:1275:A:N1	1:2A:1295:C:O2'	2.48	0.41
1:2A:1278:A:H2'	1:2A:1279:G:C8	2.55	0.41
1:2A:1287:A:H8	13:2R:104:ARG:HD3	1.84	0.41
1:2A:1412:A:H2'	1:2A:1413:G:H8	1.85	0.41
5:2F:29:ASN:H	5:2F:112:MET:HE3	1.86	0.41
12:2Q:63:LYS:HD3	12:2Q:65:PHE:CZ	2.55	0.41
31:29:27:CYS:SG	31:29:28:GLU:N	2.92	0.41
32:2a:937:A:N6	32:2a:1345:U:O4	2.47	0.41
32:2a:1125:U:O2'	32:2a:1126:U:H2'	2.20	0.41
33:2b:74:LYS:HD3	33:2b:76:GLN:HG3	2.01	0.41
36:2e:31:LEU:HD11	36:2e:129:ILE:HA	2.03	0.41
51:2t:90:GLN:HA	51:2t:93:GLU:HG2	2.03	0.41
1:1A:10:G:C4	1:1A:2641:A:C6	3.08	0.41
1:1A:509:A:O2'	20:1Y:49:VAL:O	2.28	0.41
1:1A:801:C:H2'	1:1A:802:C:C6	2.56	0.41
1:1A:1170:C:H2'	1:1A:1171:G:O4'	2.20	0.41
1:1A:2119:C:H2'	1:1A:2120:U:O4'	2.21	0.41
1:1A:2803:A:H2'	1:1A:2803:A:N3	2.35	0.41
3:1D:242:ARG:HD3	3:1D:246:PRO:HG3	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:1G:106:LEU:HA	6:1G:110:ALA:HB3	2.03	0.41
14:1S:34:HIS:ND1	14:1S:53:SER:OG	2.49	0.41
21:1Z:99:TYR:HB3	21:1Z:123:ASP:OD2	2.21	0.41
26:14:67:TYR:HE1	50:1s:41:VAL:HG21	1.86	0.41
32:1a:108:G:N1	51:1t:15:ARG:HG2	2.35	0.41
32:1a:872:A:C5	32:1a:874:G:C8	3.09	0.41
32:1a:1187:G:H4'	40:1i:111:ARG:NH1	2.36	0.41
33:1b:74:LYS:NZ	33:1b:206:ASP:OD1	2.51	0.41
39:1h:36:LEU:HD23	39:1h:36:LEU:HA	1.81	0.41
40:1i:89:ASN:O	40:1i:92:TYR:HB2	2.21	0.41
42:1k:18:ARG:HB2	42:1k:33:THR:OG1	2.20	0.41
50:1s:12:ASP:OD2	50:1s:37:ARG:HD2	2.21	0.41
1:2A:357:A:H2'	1:2A:358:U:C6	2.55	0.41
1:2A:1349:A:H61	1:2A:1598:C:N4	2.19	0.41
1:2A:2637:U:H5''	4:2E:82:ARG:NH1	2.35	0.41
11:2P:39:LYS:HB2	11:2P:45:LEU:HD21	2.01	0.41
12:2Q:111:GLU:OE2	12:2Q:133:ARG:NH2	2.38	0.41
14:2S:15:ARG:O	14:2S:19:LYS:HG2	2.20	0.41
17:2V:29:PRO:HA	17:2V:61:VAL:HG23	2.01	0.41
32:2a:406:G:N2	35:2d:119:GLN:HE22	2.11	0.41
32:2a:1086:U:H2'	32:2a:1087:G:O4'	2.20	0.41
32:2a:1108:G:H5'	34:2c:176:HIS:CD2	2.56	0.41
32:2a:1179:A:H2'	32:2a:1180:A:O4'	2.20	0.41
32:2a:1278:U:H5'	32:2a:1279:A:O4'	2.20	0.41
34:2c:108:ASN:HA	34:2c:109:PRO:HD3	1.89	0.41
37:2f:2:ARG:NH2	46:2o:2:PRO:HD2	2.35	0.41
44:2m:13:LYS:HE3	44:2m:21:TYR:OH	2.21	0.41
1:1A:868:A:H2'	1:1A:991:G:H5''	2.02	0.41
1:1A:1597:C:OP1	1:1A:1765:U:O2'	2.32	0.41
1:1A:1688:A:H2'	1:1A:1689:G:O4'	2.21	0.41
1:1A:2568:C:H2'	1:1A:2569:G:O4'	2.21	0.41
1:1A:2659:U:H2'	1:1A:2660:C:C6	2.55	0.41
2:1B:33:G:C2	2:1B:50:G:C2	3.08	0.41
3:1D:69:ARG:C	3:1D:71:ASP:H	2.29	0.41
6:1G:107:LEU:HD21	6:1G:178:PHE:CD1	2.56	0.41
9:1N:69:GLN:O	9:1N:71:ILE:HD12	2.21	0.41
10:1O:64:ARG:HD3	10:1O:79:PHE:CD1	2.56	0.41
20:1Y:15:VAL:HG21	20:1Y:42:VAL:HG11	2.01	0.41
24:12:52:ASP:O	24:12:56:GLN:HG3	2.20	0.41
26:14:67:TYR:CD2	26:14:67:TYR:N	2.89	0.41
32:1a:129(A):G:C6	32:1a:189(E):U:H4'	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:352:C:H4'	32:1a:354:G:OP1	2.21	0.41
32:1a:691:G:H1'	32:1a:696:A:N6	2.36	0.41
32:1a:1288:A:H2'	32:1a:1289:A:H8	1.85	0.41
32:1a:1360:A:OP2	45:1n:35:ARG:NH2	2.54	0.41
35:1d:73:ARG:HD2	35:1d:73:ARG:HA	1.91	0.41
48:1q:52:LYS:HE2	48:1q:52:LYS:HB3	1.77	0.41
1:2A:603:A:H4'	1:2A:604:G:H5'	2.02	0.41
1:2A:644:A:H4'	1:2A:645:C:H5	1.85	0.41
1:2A:1504:C:H2'	1:2A:1505:C:C6	2.55	0.41
1:2A:2379:G:H4'	14:2S:21:THR:HG21	2.02	0.41
1:2A:2390:U:P	30:28:35:GLN:HE22	2.43	0.41
1:2A:2512:C:H2'	1:2A:2513:G:O4'	2.21	0.41
9:2N:28:THR:HG22	9:2N:29:LYS:N	2.36	0.41
9:2N:108:PRO:O	9:2N:113:GLY:HA3	2.21	0.41
30:28:37:SER:O	30:28:41:ILE:HG12	2.20	0.41
32:2a:130:A:O2'	32:2a:131:C:O5'	2.24	0.41
32:2a:263:A:H2'	32:2a:264:U:C6	2.56	0.41
32:2a:437:U:H1'	35:2d:119:GLN:NE2	2.34	0.41
32:2a:454:C:N4	32:2a:479:C:N3	2.69	0.41
32:2a:590:C:H2'	32:2a:591:U:H6	1.86	0.41
32:2a:1269:A:H2	32:2a:1312:G:N3	2.19	0.41
33:2b:16:HIS:CG	33:2b:17:PHE:N	2.88	0.41
36:2e:92:LYS:HA	36:2e:93:PRO:HD3	1.91	0.41
44:2m:67:GLU:HB3	44:2m:68:GLY:H	1.62	0.41
45:2n:22:THR:HB	45:2n:33:VAL:HG11	2.02	0.41
1:1A:9:U:C2	1:1A:2641:A:N1	2.89	0.41
1:1A:637:U:H5'	1:1A:640:A:N6	2.36	0.41
1:1A:752:A:C2	1:1A:774:A:H1'	2.56	0.41
1:1A:1247:C:N4	1:1A:1248:G:C6	2.88	0.41
1:1A:1281:G:C6	1:1A:1282:G:N1	2.89	0.41
1:1A:1771:G:H8	1:1A:1771:G:O5'	2.03	0.41
1:1A:1954:A:H2'	1:1A:1955:G:O4'	2.21	0.41
1:1A:2050:U:H2'	1:1A:2051:G:O4'	2.21	0.41
1:1A:2231:G:H2'	1:1A:2232:G:H8	1.86	0.41
1:1A:2383:G:H21	28:16:46:HIS:HE1	1.69	0.41
24:12:1:MET:HE3	24:12:6:VAL:HA	2.03	0.41
26:14:50:VAL:HG21	44:1m:64:TRP:C	2.46	0.41
32:1a:1016:A:H2'	32:1a:1017:G:O4'	2.20	0.41
32:1a:1027:C:H2'	32:1a:1028:C:C5	2.55	0.41
32:1a:1131:G:H8	32:1a:1131:G:O5'	2.04	0.41
32:1a:1206:G:C6	32:1a:1207:2MG:C5	3.09	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:1b:24:TRP:H	33:1b:24:TRP:CD1	2.39	0.41
33:1b:47:THR:HA	33:1b:202:PRO:HG2	2.03	0.41
33:1b:96:ARG:HG2	33:1b:98:LEU:HD23	2.02	0.41
33:1b:101:MET:HG2	33:1b:108:ILE:HG21	2.03	0.41
39:1h:51:VAL:HG21	39:1h:60:ARG:HH11	1.85	0.41
40:1i:127:LYS:HB2	40:1i:127:LYS:HE2	1.81	0.41
41:1j:62:HIS:HB3	45:1n:59:ALA:HB3	2.02	0.41
1:2A:278:A:OP2	1:2A:278:A:H8	2.04	0.41
1:2A:459:U:H5''	29:27:40:TRP:CD2	2.56	0.41
1:2A:568:U:H5'	1:2A:945:A:N6	2.36	0.41
1:2A:2168:G:O2'	1:2A:2170:A:N7	2.50	0.41
1:2A:2839:G:H5'	13:2R:46:GLY:CA	2.51	0.41
6:2G:11:TYR:HB2	6:2G:176:LEU:HD21	2.03	0.41
6:2G:151:ALA:O	6:2G:153:ARG:NH1	2.54	0.41
7:2H:55:PRO:HG2	7:2H:61:HIS:CE1	2.56	0.41
11:2P:98:GLU:H	11:2P:98:GLU:CD	2.28	0.41
22:20:27:GLU:HB2	22:20:69:PHE:HD1	1.85	0.41
26:24:45:GLY:C	26:24:47:GLN:H	2.28	0.41
32:2a:425:G:O3'	35:2d:45:GLN:NE2	2.54	0.41
32:2a:575:G:O2'	32:2a:821:G:H5'	2.20	0.41
34:2c:180:ALA:HA	34:2c:206:GLU:HB3	2.03	0.41
35:2d:122:ARG:HD2	35:2d:122:ARG:HA	1.77	0.41
35:2d:173:TRP:NE1	35:2d:189:PRO:HG3	2.35	0.41
41:2j:33:GLN:HB2	41:2j:75:ILE:H	1.85	0.41
53:2x:37:A:H2'	53:2x:38:A:O4'	2.21	0.41
1:1A:339:G:H2'	1:1A:340:C:C6	2.55	0.41
1:1A:609:A:O2'	1:1A:718:C:O2'	2.37	0.41
1:1A:619:G:H2'	1:1A:620:U:O4'	2.20	0.41
1:1A:659:C:H2'	1:1A:660:C:C6	2.56	0.41
1:1A:747:G:H2'	1:1A:748:G:O4'	2.21	0.41
1:1A:956:A:C5	12:1Q:13:GLN:HG3	2.56	0.41
1:1A:1098:C:H42	1:1A:1153:G:H1	1.68	0.41
1:1A:1220:U:O2'	1:1A:1221:G:O5'	2.31	0.41
1:1A:1565:G:C6	1:1A:1566:U:C4	3.08	0.41
1:1A:1747:A:H5'	1:1A:1747:A:H8	1.86	0.41
1:1A:2136:A:O2'	1:1A:2190:G:OP1	2.39	0.41
1:1A:2734:A:O2'	1:1A:2884:C:H5'	2.20	0.41
2:1B:91:C:P	12:1Q:16:ARG:HH11	2.43	0.41
2:1B:96:U:H2'	2:1B:97:G:C8	2.55	0.41
7:1H:71:LEU:HD12	7:1H:71:LEU:HA	1.86	0.41
17:1V:25:LEU:O	17:1V:64:HIS:HE1	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:13:3:ARG:HD3	25:13:60:GLU:CG	2.49	0.41
32:1a:61:G:OP2	51:1t:10:LEU:HD22	2.20	0.41
32:1a:410:G:H5''	35:1d:30:LYS:NZ	2.35	0.41
32:1a:458:C:H2'	32:1a:460:G:C8	2.56	0.41
32:1a:728:A:H2'	32:1a:729:A:C8	2.56	0.41
32:1a:836:G:OP1	49:1r:61:LYS:NZ	2.36	0.41
32:1a:1068:G:OP2	32:1a:1068:G:H8	2.04	0.41
32:1a:1158:C:H5	32:1a:1181:G:N1	1.99	0.41
32:1a:1285:A:H1'	32:1a:1286:A:OP2	2.21	0.41
32:1a:1315:U:C4	32:1a:1316:G:C6	3.09	0.41
32:1a:1445:C:O2'	32:1a:1447:A:N6	2.41	0.41
32:1a:1519:MA6:O5'	32:1a:1519:MA6:H8	2.21	0.41
35:1d:107:ARG:HD3	35:1d:107:ARG:HA	1.88	0.41
38:1g:48:LYS:O	38:1g:52:GLU:HG2	2.21	0.41
38:1g:152:ALA:O	38:1g:155:ARG:NH1	2.54	0.41
39:1h:77:GLU:HG2	39:1h:78:GLN:N	2.36	0.41
40:1i:92:TYR:HD1	40:1i:92:TYR:HA	1.77	0.41
41:1j:16:LEU:HD22	41:1j:68:HIS:HB2	2.03	0.41
43:1l:42:THR:OG1	43:1l:52:LEU:HD22	2.21	0.41
44:1m:4:ILE:HA	44:1m:5:ALA:HA	1.57	0.41
44:1m:39:ILE:HG12	44:1m:52:GLU:HG2	2.02	0.41
47:1p:21:VAL:HG22	47:1p:33:ILE:HD12	2.02	0.41
53:1x:25:C:H2'	53:1x:26:G:O4'	2.21	0.41
53:1x:43:A:H2'	53:1x:44:A:C8	2.56	0.41
1:2A:98:G:H5''	24:22:3:LEU:HG	2.03	0.41
1:2A:483:A:O4'	20:2Y:48:ALA:HB1	2.20	0.41
1:2A:483:A:O2'	20:2Y:49:VAL:O	2.29	0.41
1:2A:557:U:H2'	1:2A:558:G:C8	2.56	0.41
1:2A:1203:G:H2'	1:2A:1241:A:N6	2.35	0.41
1:2A:1282:U:H2'	1:2A:1283:G:O4'	2.21	0.41
1:2A:2537:U:H2'	1:2A:2538:C:C6	2.56	0.41
1:2A:2555:U:H5''	1:2A:2556:C:OP2	2.20	0.41
1:2A:2745:C:C4	1:2A:2746:U:C4	3.09	0.41
4:2E:51:PHE:H	4:2E:75:VAL:HG11	1.86	0.41
4:2E:175:VAL:O	4:2E:177:PRO:HD3	2.21	0.41
5:2F:46:ARG:HB3	5:2F:48:THR:HG23	2.03	0.41
13:2R:38:VAL:HG22	13:2R:112:ALA:HB2	2.02	0.41
26:24:13:ARG:NH2	26:24:23:GLU:HG2	2.26	0.41
26:24:59:PHE:HE2	50:2s:64:GLU:HB2	1.86	0.41
30:28:63:PRO:HG2	30:28:64:TYR:CD2	2.55	0.41
32:2a:4:U:C4	39:2h:105:ARG:HD3	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:193:C:H2'	32:2a:194:C:C6	2.56	0.41
32:2a:253:U:H2'	32:2a:254:G:H8	1.85	0.41
32:2a:643:C:H2'	32:2a:644:G:H8	1.85	0.41
32:2a:953:G:H5'	32:2a:965:A:H61	1.86	0.41
32:2a:1004:A:N7	32:2a:1037:C:H2'	2.36	0.41
32:2a:1090:U:H2'	32:2a:1091:U:C6	2.55	0.41
32:2a:1216:G:OP1	45:2n:2:ALA:HA	2.21	0.41
32:2a:1221:G:H1'	50:2s:54:GLY:HA3	2.02	0.41
34:2c:8:ILE:HG23	34:2c:16:ARG:HD3	2.03	0.41
35:2d:57:ARG:NH2	36:2e:107:ARG:HD3	2.35	0.41
35:2d:171:GLY:HA2	35:2d:172:PRO:HD3	1.82	0.41
38:2g:116:ALA:O	38:2g:120:ILE:HG12	2.20	0.41
41:2j:62:HIS:HB3	45:2n:59:ALA:HB3	2.03	0.41
47:2p:3:LYS:HE3	47:2p:3:LYS:HB3	1.91	0.41
47:2p:8:ARG:HB3	47:2p:28:ARG:NH1	2.36	0.41
49:2r:38:GLU:O	49:2r:41:LYS:HG2	2.21	0.41
1:1A:230:A:H5''	63:1A:4740:HOH:O	2.19	0.41
1:1A:636:G:O2'	1:1A:640:A:N1	2.46	0.41
1:1A:901:G:H2'	1:1A:902:G:H8	1.86	0.41
1:1A:1730:C:H2'	1:1A:1731:C:C6	2.55	0.41
1:1A:2081:A:H2'	1:1A:2515:2MA:CM2	2.51	0.41
1:1A:2202:U:H2'	1:1A:2203:G:O4'	2.21	0.41
3:1D:5:LYS:HB3	3:1D:5:LYS:HE3	1.85	0.41
10:1O:34:THR:OG1	10:1O:35:VAL:N	2.53	0.41
12:1Q:31:ASP:HA	12:1Q:134:ARG:NH1	2.36	0.41
14:1S:61:ASN:O	14:1S:65:VAL:HG23	2.21	0.41
24:12:1:MET:SD	24:12:56:GLN:NE2	2.94	0.41
26:14:61:ARG:HD3	50:1s:67:VAL:HG11	2.02	0.41
32:1a:272:C:H2'	32:1a:273:A:C8	2.51	0.41
33:1b:53:ARG:HH12	33:1b:199:TYR:HA	1.86	0.41
47:1p:60:LEU:HD12	47:1p:60:LEU:HA	1.97	0.41
1:2A:71:A:H5''	1:2A:73:A:C8	2.56	0.41
1:2A:82:G:N1	1:2A:103:A:OP2	2.45	0.41
1:2A:588:U:H1'	5:2F:90:PHE:HB3	2.03	0.41
1:2A:919:G:N2	1:2A:2269:A:OP2	2.54	0.41
1:2A:1203:G:C6	1:2A:1204:A:N6	2.89	0.41
1:2A:1638:C:O2	1:2A:2698:U:O2'	2.35	0.41
1:2A:2466:C:C2	1:2A:2485:G:C2	3.08	0.41
2:2B:6:C:H2'	2:2B:7:G:O4'	2.21	0.41
3:2D:206:LEU:HD23	3:2D:206:LEU:HA	1.90	0.41
4:2E:31:CYS:HA	4:2E:32:PRO:HD2	1.96	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:2I:3:VAL:HA	8:2I:39:ALA:H	1.86	0.41
10:2O:63:VAL:HB	10:2O:102:VAL:HG12	2.02	0.41
16:2U:32:PHE:HZ	16:2U:36:ARG:HH21	1.68	0.41
23:21:98:LEU:HD23	23:21:98:LEU:HA	1.96	0.41
32:2a:250:A:H4'	32:2a:251:G:O5'	2.21	0.41
32:2a:253:U:H2'	32:2a:254:G:C8	2.56	0.41
32:2a:1069:C:O2'	32:2a:1192:C:O2	2.28	0.41
32:2a:1125:U:C5	32:2a:1280:A:C8	3.09	0.41
32:2a:1261:A:H61	32:2a:1274:G:H1'	1.87	0.41
32:2a:1320:C:N4	50:2s:36:ARG:HB2	2.36	0.41
33:2b:59:GLU:HB2	33:2b:221:LEU:HD21	2.03	0.41
35:2d:61:LYS:HD2	35:2d:207:TYR:OH	2.21	0.41
1:1A:783:C:H5''	63:1A:4849:HOH:O	2.19	0.40
1:1A:1074:A:N6	1:1A:1171:G:H2'	2.36	0.40
1:1A:2018:C:H4'	1:1A:2019:G:OP1	2.20	0.40
1:1A:2407:C:O2'	23:11:30:VAL:O	2.39	0.40
4:1E:119:ARG:HG2	4:1E:160:TYR:CD2	2.56	0.40
5:1F:65:TRP:CZ2	5:1F:75:HIS:HD2	2.39	0.40
7:1H:11:VAL:HA	7:1H:12:PRO:HD2	1.95	0.40
8:1I:130:TYR:C	8:1I:131:LYS:HG2	2.45	0.40
32:1a:957:U:OP1	50:1s:81:ARG:NH1	2.54	0.40
32:1a:993:G:H2'	32:1a:993:G:N3	2.36	0.40
32:1a:1024:G:H2'	32:1a:1024:G:N3	2.36	0.40
32:1a:1131:G:H2'	32:1a:1132:C:C6	2.56	0.40
42:1k:23:ALA:HA	42:1k:28:THR:HA	2.03	0.40
44:1m:37:THR:O	44:1m:55:ARG:NH1	2.49	0.40
1:2A:230:U:H2'	1:2A:231:C:C6	2.57	0.40
1:2A:285:C:H2'	1:2A:286:C:C6	2.55	0.40
1:2A:2081:C:H2'	1:2A:2082:A:H8	1.86	0.40
1:2A:2443:C:OP1	5:2F:68:LYS:HD3	2.20	0.40
2:2B:106:G:H5'	21:2Z:31:ARG:HB3	2.04	0.40
10:2O:64:ARG:HD3	10:2O:101:PRO:O	2.21	0.40
11:2P:121:LYS:O	11:2P:123:LEU:N	2.54	0.40
32:2a:21:G:H2'	32:2a:22:G:C8	2.56	0.40
32:2a:422:C:H4'	32:2a:423:G:C4	2.56	0.40
32:2a:792:A:H4'	32:2a:793:U:C5'	2.51	0.40
32:2a:977:A:O2'	32:2a:979:C:OP2	2.29	0.40
32:2a:1125:U:C5	32:2a:1280:A:N7	2.88	0.40
32:2a:1233:G:H2'	32:2a:1234:C:C6	2.56	0.40
32:2a:1516:G:H2'	32:2a:1518:MA6:OP2	2.21	0.40
32:2a:1530:G:OP1	32:2a:1530:G:H4'	2.20	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:2b:37:ASN:HB2	33:2b:39:ILE:HD12	2.02	0.40
34:2c:10:PHE:HA	45:2n:58:LYS:HD3	2.03	0.40
36:2e:100:VAL:O	36:2e:107:ARG:NH2	2.52	0.40
1:1A:347:G:C8	5:1F:171:PRO:HG3	2.56	0.40
1:1A:1830:G:O2'	3:1D:181:GLU:OE2	2.22	0.40
1:1A:2190:G:H8	1:1A:2190:G:O5'	2.04	0.40
1:1A:2391:G:O2'	14:1S:17:ARG:NH1	2.39	0.40
6:1G:61:ALA:O	26:14:7:PRO:HG2	2.21	0.40
14:1S:19:LYS:HE2	14:1S:25:ARG:NH1	2.37	0.40
17:1V:35:LEU:HA	17:1V:36:PRO:HD3	1.97	0.40
32:1a:110:C:O2'	47:1p:25:ARG:O	2.35	0.40
35:1d:127:THR:OG1	35:1d:128:VAL:N	2.54	0.40
45:1n:45:ARG:O	45:1n:49:HIS:HD2	2.04	0.40
51:1t:89:ARG:O	51:1t:93:GLU:HG2	2.21	0.40
53:1x:14:A:C2	53:1x:15:G:H1'	2.55	0.40
1:2A:907:U:O2'	12:2Q:101:ARG:NH2	2.53	0.40
1:2A:1466:G:H2'	1:2A:1547:C:N4	2.36	0.40
1:2A:2443:C:H2'	1:2A:2444:G:C8	2.55	0.40
1:2A:2711:A:OP1	1:2A:2712:U:H3'	2.21	0.40
2:2B:103:G:H21	21:2Z:73:GLN:HE22	1.67	0.40
18:2W:82:LEU:HD22	18:2W:84:ARG:HH22	1.86	0.40
24:22:53:LEU:HD23	24:22:53:LEU:HA	1.91	0.40
32:2a:110:C:H2'	32:2a:111:G:O4'	2.22	0.40
32:2a:407:G:H2'	32:2a:408:A:H8	1.86	0.40
32:2a:418:C:H1'	32:2a:540:G:O2'	2.21	0.40
33:2b:88:ALA:HB2	33:2b:219:VAL:HG13	2.02	0.40
34:2c:180:ALA:HB1	34:2c:203:PHE:CE1	2.56	0.40
41:2j:54:PHE:O	41:2j:56:HIS:ND1	2.54	0.40
44:2m:108:ARG:HA	44:2m:108:ARG:HD3	1.90	0.40
1:1A:635:C:H2'	1:1A:636:G:O4'	2.21	0.40
1:1A:818:G:OP1	29:17:10:ARG:NH1	2.52	0.40
1:1A:1841:A:H2'	1:1A:1842:G:O4'	2.21	0.40
1:1A:2227:G:H2'	1:1A:2228:G:C2	2.57	0.40
1:1A:2304:C:OP1	14:1S:17:ARG:NH2	2.40	0.40
32:1a:198:G:H2'	32:1a:199:G:C8	2.57	0.40
32:1a:713:G:H2'	32:1a:714:G:C8	2.55	0.40
32:1a:792:A:O2'	32:1a:794:A:N7	2.44	0.40
33:1b:10:LEU:HA	33:1b:48:MET:HE1	2.04	0.40
34:1c:71:ALA:HA	34:1c:106:VAL:HB	2.04	0.40
38:1g:75:VAL:HG13	38:1g:145:ALA:HA	2.02	0.40
39:1h:120:THR:HG23	39:1h:123:GLU:OE1	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:1i:3:GLN:HE21	40:1i:20:ARG:CZ	2.35	0.40
51:1t:61:SER:O	51:1t:65:LYS:HG3	2.22	0.40
1:2A:361:G:O2'	1:2A:362:U:H5'	2.22	0.40
1:2A:833:U:O2	11:2P:55:ARG:NH1	2.50	0.40
1:2A:923:C:H2'	1:2A:924:C:C6	2.56	0.40
1:2A:1021:A:H3'	1:2A:1021:A:N3	2.37	0.40
1:2A:1125:G:H5'	31:29:37:GLY:HA2	2.04	0.40
1:2A:1824:G:N3	3:2D:254:THR:OG1	2.54	0.40
1:2A:2776:A:H4'	1:2A:2777:G:H5''	2.04	0.40
10:2O:18:LYS:HB2	10:2O:45:GLU:HB3	2.03	0.40
15:2T:99:LEU:HD22	15:2T:101:PHE:HE2	1.86	0.40
32:2a:922:G:H1'	36:2e:19:MET:HB2	2.03	0.40
32:2a:1027:C:O2	32:2a:1034:G:C6	2.74	0.40
32:2a:1107:C:C4	32:2a:1108:G:C8	3.09	0.40
32:2a:1142:G:H3'	32:2a:1143:G:H8	1.86	0.40
32:2a:1301:U:O2'	32:2a:1302:U:H5'	2.21	0.40
33:2b:8:LYS:HG3	33:2b:9:GLU:H	1.86	0.40
42:2k:110:ASP:HB3	49:2r:85:LEU:HB3	2.03	0.40
47:2p:43:LYS:HA	47:2p:48:TRP:HB3	2.04	0.40
1:1A:1551:C:H2'	1:1A:1552:C:C6	2.57	0.40
1:1A:1890:A:N6	1:1A:1905:G:O2'	2.55	0.40
1:1A:2342:G:H2'	1:1A:2343:G:O4'	2.21	0.40
1:1A:2724:U:O2'	1:1A:2726:A:H5'	2.22	0.40
1:1A:2784:C:H2'	1:1A:2785:C:C6	2.57	0.40
2:1B:32:C:C2	2:1B:51:G:N2	2.89	0.40
2:1B:54:G:H2'	2:1B:55:U:H6	1.86	0.40
15:1T:107:ASP:O	15:1T:111:ARG:HG3	2.22	0.40
32:1a:671:G:H2'	32:1a:672:U:O4'	2.21	0.40
32:1a:721:G:H4'	32:1a:722:A:O4'	2.21	0.40
32:1a:1347:G:H8	40:1i:107:ARG:HB2	1.86	0.40
1:2A:58:G:O2'	1:2A:73:A:N1	2.46	0.40
1:2A:304:G:H2'	1:2A:305:U:C6	2.57	0.40
1:2A:784:A:O4'	3:2D:227:ASN:ND2	2.54	0.40
1:2A:1513:C:H2'	1:2A:1514:U:C6	2.56	0.40
1:2A:1991:U:H2'	1:2A:1992:G:H5''	2.03	0.40
1:2A:2371:G:N3	28:26:46:HIS:HE1	2.19	0.40
1:2A:2661:G:H2'	1:2A:2662:A:C8	2.56	0.40
21:2Z:26:GLY:HA3	21:2Z:86:VAL:HG23	2.02	0.40
32:2a:1077:G:N2	32:2a:1080:A:OP2	2.46	0.40
32:2a:1157:A:C6	32:2a:1180:A:C5	3.10	0.40
32:2a:1278:U:H5''	32:2a:1279:A:H5'	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:2d:196:LEU:O	35:2d:198:VAL:N	2.51	0.40
41:2j:61:GLU:OE2	45:2n:58:LYS:NZ	2.45	0.40
46:2o:87:ILE:CG2	46:2o:88:ARG:H	2.32	0.40
1:1A:233:A:C2	1:1A:244:A:C4	3.10	0.40
1:1A:1725:G:N3	1:1A:1725:G:H5''	2.36	0.40
1:1A:1735:U:H1'	1:1A:1748:A:C6	2.57	0.40
1:1A:1925:G:OP1	3:1D:241:PRO:HB2	2.21	0.40
1:1A:1959:A:O2'	1:1A:1961:5MU:OP2	2.39	0.40
1:1A:2786:C:H2'	1:1A:2787:C:H6	1.86	0.40
3:1D:127:VAL:HA	3:1D:193:VAL:HG22	2.03	0.40
3:1D:182:LEU:HB2	3:1D:272:ALA:HB3	2.04	0.40
8:1I:81:VAL:O	8:1I:147:GLN:N	2.53	0.40
24:12:22:GLU:HG3	24:12:64:LEU:HD11	2.03	0.40
32:1a:627:G:H2'	32:1a:628:G:H8	1.86	0.40
32:1a:901:A:C5	32:1a:902:G:H1'	2.57	0.40
36:1e:150:ARG:HE	36:1e:150:ARG:HB2	1.73	0.40
42:1k:97:ALA:O	42:1k:101:SER:HB3	2.21	0.40
1:2A:217:G:H2'	1:2A:218:A:O4'	2.21	0.40
1:2A:275:G:C6	1:2A:276:A:C6	3.09	0.40
1:2A:954:G:O2'	1:2A:2274:A:N1	2.40	0.40
1:2A:1421:G:C2	1:2A:1422:G:C8	3.09	0.40
1:2A:2462:U:H1'	1:2A:2491:U:O4	2.22	0.40
2:2B:7:G:H3'	2:2B:8:U:H5''	2.03	0.40
3:2D:69:ARG:C	3:2D:71:ASP:H	2.30	0.40
7:2H:11:VAL:HA	7:2H:12:PRO:HD2	1.98	0.40
7:2H:13:LYS:HA	7:2H:14:GLY:HA2	1.64	0.40
18:2W:13:SER:HA	18:2W:14:PRO:HD3	1.93	0.40
20:2Y:7:VAL:HG21	20:2Y:72:VAL:HG12	2.02	0.40
23:21:25:LYS:HG3	23:21:31:GLY:HA2	2.03	0.40
32:2a:37:U:O2'	32:2a:500:G:H4'	2.22	0.40
32:2a:524:G:H2'	32:2a:525:C:C6	2.57	0.40
32:2a:1151:A:O2'	32:2a:1152:A:H8	2.04	0.40
32:2a:1256:A:N6	32:2a:1278:U:H1'	2.36	0.40
32:2a:1516:G:N2	32:2a:1519:MA6:OP2	2.54	0.40
35:2d:9:CYS:O	35:2d:13:ARG:HG3	2.21	0.40
36:2e:93:PRO:HG2	39:2h:105:ARG:HG3	2.04	0.40
38:2g:89:MET:SD	38:2g:155:ARG:HB2	2.61	0.40
38:2g:114:ARG:HB2	38:2g:115:ARG:NH2	2.37	0.40
39:2h:25:ASP:HB3	39:2h:58:TYR:CD1	2.57	0.40
41:2j:6:ILE:HD13	41:2j:6:ILE:HA	1.94	0.40
44:2m:15:VAL:HG12	44:2m:45:VAL:HG22	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	1D	273/275 (99%)	259 (95%)	14 (5%)	0	100	100
3	2D	273/275 (99%)	259 (95%)	14 (5%)	0	100	100
4	1E	202/204 (99%)	195 (96%)	6 (3%)	1 (0%)	24	57
4	2E	202/204 (99%)	193 (96%)	8 (4%)	1 (0%)	24	57
5	1F	201/203 (99%)	193 (96%)	7 (4%)	1 (0%)	24	57
5	2F	201/203 (99%)	195 (97%)	4 (2%)	2 (1%)	12	41
6	1G	179/181 (99%)	167 (93%)	10 (6%)	2 (1%)	11	39
6	2G	179/181 (99%)	163 (91%)	13 (7%)	3 (2%)	7	30
7	1H	172/174 (99%)	162 (94%)	10 (6%)	0	100	100
7	2H	171/174 (98%)	162 (95%)	9 (5%)	0	100	100
8	1I	145/147 (99%)	132 (91%)	9 (6%)	4 (3%)	4	20
8	2I	144/147 (98%)	134 (93%)	9 (6%)	1 (1%)	18	49
9	1N	138/140 (99%)	135 (98%)	3 (2%)	0	100	100
9	2N	138/140 (99%)	135 (98%)	3 (2%)	0	100	100
10	1O	120/122 (98%)	114 (95%)	6 (5%)	0	100	100
10	2O	120/122 (98%)	114 (95%)	6 (5%)	0	100	100
11	1P	147/149 (99%)	138 (94%)	8 (5%)	1 (1%)	18	49
11	2P	147/149 (99%)	139 (95%)	7 (5%)	1 (1%)	18	49
12	1Q	139/141 (99%)	130 (94%)	9 (6%)	0	100	100
12	2Q	139/141 (99%)	130 (94%)	9 (6%)	0	100	100
13	1R	116/118 (98%)	109 (94%)	7 (6%)	0	100	100
13	2R	116/118 (98%)	109 (94%)	7 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
14	1S	108/110 (98%)	100 (93%)	7 (6%)	1 (1%)	14	44
14	2S	108/110 (98%)	102 (94%)	6 (6%)	0	100	100
15	1T	129/131 (98%)	123 (95%)	6 (5%)	0	100	100
15	2T	129/131 (98%)	126 (98%)	3 (2%)	0	100	100
16	1U	114/116 (98%)	114 (100%)	0	0	100	100
16	2U	114/116 (98%)	114 (100%)	0	0	100	100
17	1V	99/101 (98%)	93 (94%)	5 (5%)	1 (1%)	12	41
17	2V	99/101 (98%)	93 (94%)	5 (5%)	1 (1%)	12	41
18	1W	110/112 (98%)	107 (97%)	3 (3%)	0	100	100
18	2W	110/112 (98%)	107 (97%)	3 (3%)	0	100	100
19	1X	93/95 (98%)	91 (98%)	1 (1%)	1 (1%)	11	39
19	2X	93/95 (98%)	90 (97%)	2 (2%)	1 (1%)	11	39
20	1Y	105/107 (98%)	98 (93%)	7 (7%)	0	100	100
20	2Y	105/107 (98%)	100 (95%)	5 (5%)	0	100	100
21	1Z	201/203 (99%)	187 (93%)	14 (7%)	0	100	100
21	2Z	199/203 (98%)	183 (92%)	16 (8%)	0	100	100
22	10	75/77 (97%)	73 (97%)	2 (3%)	0	100	100
22	20	75/77 (97%)	72 (96%)	3 (4%)	0	100	100
23	11	95/97 (98%)	94 (99%)	1 (1%)	0	100	100
23	21	95/97 (98%)	92 (97%)	3 (3%)	0	100	100
24	12	68/70 (97%)	67 (98%)	1 (2%)	0	100	100
24	22	68/70 (97%)	67 (98%)	1 (2%)	0	100	100
25	13	57/59 (97%)	56 (98%)	1 (2%)	0	100	100
25	23	57/59 (97%)	55 (96%)	2 (4%)	0	100	100
26	14	67/69 (97%)	52 (78%)	12 (18%)	3 (4%)	2	12
26	24	67/69 (97%)	51 (76%)	12 (18%)	4 (6%)	1	7
27	15	57/59 (97%)	55 (96%)	2 (4%)	0	100	100
27	25	57/59 (97%)	54 (95%)	3 (5%)	0	100	100
28	16	51/53 (96%)	48 (94%)	3 (6%)	0	100	100
28	26	51/53 (96%)	48 (94%)	3 (6%)	0	100	100
29	17	46/48 (96%)	44 (96%)	2 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
29	27	46/48 (96%)	45 (98%)	1 (2%)	0	100	100
30	18	62/64 (97%)	60 (97%)	2 (3%)	0	100	100
30	28	62/64 (97%)	61 (98%)	1 (2%)	0	100	100
31	19	35/37 (95%)	35 (100%)	0	0	100	100
31	29	35/37 (95%)	35 (100%)	0	0	100	100
33	1b	229/231 (99%)	199 (87%)	21 (9%)	9 (4%)	2	14
33	2b	229/231 (99%)	200 (87%)	23 (10%)	6 (3%)	4	21
34	1c	204/206 (99%)	194 (95%)	10 (5%)	0	100	100
34	2c	204/206 (99%)	191 (94%)	11 (5%)	2 (1%)	12	41
35	1d	206/208 (99%)	193 (94%)	11 (5%)	2 (1%)	12	41
35	2d	206/208 (99%)	196 (95%)	8 (4%)	2 (1%)	12	41
36	1e	146/148 (99%)	141 (97%)	5 (3%)	0	100	100
36	2e	146/148 (99%)	141 (97%)	5 (3%)	0	100	100
37	1f	98/100 (98%)	95 (97%)	3 (3%)	0	100	100
37	2f	98/100 (98%)	94 (96%)	4 (4%)	0	100	100
38	1g	153/155 (99%)	146 (95%)	7 (5%)	0	100	100
38	2g	153/155 (99%)	143 (94%)	8 (5%)	2 (1%)	9	35
39	1h	135/137 (98%)	129 (96%)	6 (4%)	0	100	100
39	2h	135/137 (98%)	130 (96%)	5 (4%)	0	100	100
40	1i	125/127 (98%)	115 (92%)	9 (7%)	1 (1%)	16	47
40	2i	124/127 (98%)	111 (90%)	11 (9%)	2 (2%)	7	30
41	1j	95/97 (98%)	82 (86%)	9 (10%)	4 (4%)	2	13
41	2j	94/97 (97%)	84 (89%)	9 (10%)	1 (1%)	11	39
42	1k	112/114 (98%)	105 (94%)	6 (5%)	1 (1%)	14	44
42	2k	112/114 (98%)	107 (96%)	5 (4%)	0	100	100
43	1l	119/122 (98%)	112 (94%)	7 (6%)	0	100	100
43	2l	119/122 (98%)	110 (92%)	9 (8%)	0	100	100
44	1m	114/116 (98%)	106 (93%)	7 (6%)	1 (1%)	14	44
44	2m	112/116 (97%)	105 (94%)	5 (4%)	2 (2%)	6	28
45	1n	58/60 (97%)	56 (97%)	2 (3%)	0	100	100
45	2n	58/60 (97%)	55 (95%)	3 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
46	1o	86/88 (98%)	84 (98%)	1 (1%)	1 (1%)	10	37
46	2o	86/88 (98%)	81 (94%)	3 (4%)	2 (2%)	5	23
47	1p	80/82 (98%)	75 (94%)	5 (6%)	0	100	100
47	2p	80/82 (98%)	74 (92%)	6 (8%)	0	100	100
48	1q	97/99 (98%)	92 (95%)	4 (4%)	1 (1%)	12	41
48	2q	97/99 (98%)	93 (96%)	4 (4%)	0	100	100
49	1r	66/68 (97%)	65 (98%)	1 (2%)	0	100	100
49	2r	66/68 (97%)	65 (98%)	1 (2%)	0	100	100
50	1s	81/83 (98%)	75 (93%)	6 (7%)	0	100	100
50	2s	81/83 (98%)	75 (93%)	6 (7%)	0	100	100
51	1t	94/98 (96%)	90 (96%)	1 (1%)	3 (3%)	3	18
51	2t	96/98 (98%)	90 (94%)	3 (3%)	3 (3%)	3	18
52	1u	21/23 (91%)	19 (90%)	2 (10%)	0	100	100
52	2u	21/23 (91%)	19 (90%)	1 (5%)	1 (5%)	2	11
54	1y	10/19 (53%)	9 (90%)	1 (10%)	0	100	100
54	2y	10/19 (53%)	9 (90%)	1 (10%)	0	100	100
All	All	11460/11686 (98%)	10814 (94%)	571 (5%)	75 (1%)	18	49

All (75) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	1F	130	ALA
8	1I	105	HIS
26	14	49	PHE
35	1d	171	GLY
40	1i	127	LYS
41	1j	77	PRO
41	1j	79	ARG
44	1m	67	GLU
48	1q	68	ARG
5	2F	21	ALA
5	2F	130	ALA
6	2G	50	ALA
19	2X	94	GLY
26	24	49	PHE
33	2b	8	LYS

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Mol	Chain	Res	Type
33	2b	16	HIS
33	2b	17	PHE
38	2g	8	GLU
40	2i	44	VAL
40	2i	54	ASP
44	2m	67	GLU
8	1I	11	ASN
19	1X	94	GLY
26	14	45	GLY
33	1b	17	PHE
33	1b	126	GLU
42	1k	118	GLY
4	2E	51	PHE
6	2G	43	LEU
34	2c	107	GLN
35	2d	171	GLY
38	2g	7	ALA
6	1G	43	LEU
8	1I	73	GLU
14	1S	59	LYS
33	1b	20	GLU
35	1d	129	ASN
41	1j	78	ASN
26	24	47	GLN
26	24	60	GLN
46	2o	88	ARG
51	2t	100	ILE
51	2t	102	GLY
4	1E	52	LEU
8	1I	85	GLU
33	1b	8	LYS
51	1t	95	ALA
8	2I	85	GLU
33	2b	125	PRO
34	2c	108	ASN
35	2d	129	ASN
41	2j	78	ASN
46	2o	23	GLY
51	2t	95	ALA
11	1P	122	PRO
33	1b	125	PRO
11	2P	122	PRO

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Mol	Chain	Res	Type
17	2V	79	VAL
33	2b	123	ALA
52	2u	3	LYS
6	1G	47	LYS
26	14	55	ARG
33	1b	21	ARG
46	1o	23	GLY
6	2G	47	LYS
44	2m	5	ALA
41	1j	31	GLY
17	1V	79	VAL
33	1b	124	SER
33	1b	127	ILE
26	24	45	GLY
33	2b	232	PRO
51	1t	100	ILE
33	1b	232	PRO
51	1t	98	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	1D	214/217 (99%)	199 (93%)	15 (7%)	14	41
3	2D	215/217 (99%)	201 (94%)	14 (6%)	15	44
4	1E	164/165 (99%)	150 (92%)	14 (8%)	10	35
4	2E	164/165 (99%)	152 (93%)	12 (7%)	13	40
5	1F	160/161 (99%)	145 (91%)	15 (9%)	8	31
5	2F	159/161 (99%)	144 (91%)	15 (9%)	8	31
6	1G	144/155 (93%)	130 (90%)	14 (10%)	8	30
6	2G	142/155 (92%)	132 (93%)	10 (7%)	14	41
7	1H	144/145 (99%)	136 (94%)	8 (6%)	19	49
7	2H	143/145 (99%)	135 (94%)	8 (6%)	19	49

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	1I	111/123 (90%)	101 (91%)	10 (9%)	9	33
8	2I	108/123 (88%)	99 (92%)	9 (8%)	10	35
9	1N	119/119 (100%)	111 (93%)	8 (7%)	15	43
9	2N	118/119 (99%)	111 (94%)	7 (6%)	18	48
10	1O	100/100 (100%)	96 (96%)	4 (4%)	28	60
10	2O	100/100 (100%)	95 (95%)	5 (5%)	22	53
11	1P	115/116 (99%)	106 (92%)	9 (8%)	11	38
11	2P	115/116 (99%)	111 (96%)	4 (4%)	32	62
12	1Q	111/111 (100%)	104 (94%)	7 (6%)	16	45
12	2Q	111/111 (100%)	104 (94%)	7 (6%)	16	45
13	1R	101/101 (100%)	89 (88%)	12 (12%)	5	21
13	2R	101/101 (100%)	88 (87%)	13 (13%)	4	18
14	1S	87/87 (100%)	83 (95%)	4 (5%)	24	55
14	2S	85/87 (98%)	81 (95%)	4 (5%)	23	55
15	1T	115/115 (100%)	108 (94%)	7 (6%)	17	46
15	2T	113/115 (98%)	109 (96%)	4 (4%)	32	62
16	1U	93/93 (100%)	88 (95%)	5 (5%)	20	50
16	2U	93/93 (100%)	87 (94%)	6 (6%)	15	44
17	1V	81/82 (99%)	73 (90%)	8 (10%)	7	29
17	2V	80/82 (98%)	72 (90%)	8 (10%)	7	29
18	1W	90/91 (99%)	83 (92%)	7 (8%)	11	38
18	2W	90/91 (99%)	85 (94%)	5 (6%)	19	49
19	1X	77/77 (100%)	76 (99%)	1 (1%)	61	77
19	2X	77/77 (100%)	74 (96%)	3 (4%)	28	60
20	1Y	86/88 (98%)	81 (94%)	5 (6%)	18	48
20	2Y	86/88 (98%)	83 (96%)	3 (4%)	32	62
21	1Z	169/176 (96%)	156 (92%)	13 (8%)	12	38
21	2Z	165/176 (94%)	152 (92%)	13 (8%)	11	37
22	10	61/62 (98%)	57 (93%)	4 (7%)	15	43
22	20	61/62 (98%)	59 (97%)	2 (3%)	33	63
23	11	79/82 (96%)	77 (98%)	2 (2%)	42	69

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	21	81/82 (99%)	78 (96%)	3 (4%)	30	61
24	12	65/66 (98%)	64 (98%)	1 (2%)	57	75
24	22	66/66 (100%)	64 (97%)	2 (3%)	36	65
25	13	51/51 (100%)	47 (92%)	4 (8%)	11	38
25	23	50/51 (98%)	47 (94%)	3 (6%)	17	47
26	14	58/62 (94%)	52 (90%)	6 (10%)	7	27
26	24	54/62 (87%)	51 (94%)	3 (6%)	19	49
27	15	51/51 (100%)	49 (96%)	2 (4%)	28	60
27	25	50/51 (98%)	49 (98%)	1 (2%)	48	72
28	16	51/51 (100%)	48 (94%)	3 (6%)	18	48
28	26	50/51 (98%)	48 (96%)	2 (4%)	28	60
29	17	41/41 (100%)	38 (93%)	3 (7%)	13	40
29	27	41/41 (100%)	40 (98%)	1 (2%)	43	69
30	18	54/54 (100%)	51 (94%)	3 (6%)	19	49
30	28	54/54 (100%)	52 (96%)	2 (4%)	30	61
31	19	34/34 (100%)	33 (97%)	1 (3%)	37	66
31	29	34/34 (100%)	34 (100%)	0	100	100
33	1b	191/199 (96%)	169 (88%)	22 (12%)	5	23
33	2b	187/199 (94%)	171 (91%)	16 (9%)	10	34
34	1c	144/160 (90%)	137 (95%)	7 (5%)	22	53
34	2c	140/160 (88%)	130 (93%)	10 (7%)	13	41
35	1d	171/180 (95%)	160 (94%)	11 (6%)	16	44
35	2d	172/180 (96%)	165 (96%)	7 (4%)	27	59
36	1e	114/114 (100%)	110 (96%)	4 (4%)	32	62
36	2e	114/114 (100%)	110 (96%)	4 (4%)	32	62
37	1f	85/90 (94%)	83 (98%)	2 (2%)	43	69
37	2f	85/90 (94%)	84 (99%)	1 (1%)	63	78
38	1g	120/126 (95%)	115 (96%)	5 (4%)	26	58
38	2g	119/126 (94%)	112 (94%)	7 (6%)	18	48
39	1h	116/118 (98%)	111 (96%)	5 (4%)	26	57
39	2h	114/118 (97%)	105 (92%)	9 (8%)	11	37

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
40	1i	91/98 (93%)	84 (92%)	7 (8%)	12	38
40	2i	88/98 (90%)	82 (93%)	6 (7%)	14	42
41	1j	68/87 (78%)	64 (94%)	4 (6%)	18	48
41	2j	68/87 (78%)	66 (97%)	2 (3%)	37	66
42	1k	83/86 (96%)	80 (96%)	3 (4%)	31	62
42	2k	83/86 (96%)	78 (94%)	5 (6%)	17	47
43	1l	96/102 (94%)	92 (96%)	4 (4%)	26	58
43	2l	96/102 (94%)	91 (95%)	5 (5%)	21	51
44	1m	90/94 (96%)	82 (91%)	8 (9%)	9	33
44	2m	87/94 (93%)	78 (90%)	9 (10%)	7	27
45	1n	49/49 (100%)	46 (94%)	3 (6%)	17	46
45	2n	49/49 (100%)	48 (98%)	1 (2%)	48	72
46	1o	78/79 (99%)	76 (97%)	2 (3%)	40	68
46	2o	78/79 (99%)	74 (95%)	4 (5%)	21	52
47	1p	69/71 (97%)	61 (88%)	8 (12%)	5	22
47	2p	68/71 (96%)	61 (90%)	7 (10%)	7	27
48	1q	94/94 (100%)	92 (98%)	2 (2%)	47	71
48	2q	94/94 (100%)	92 (98%)	2 (2%)	47	71
49	1r	59/59 (100%)	58 (98%)	1 (2%)	53	74
49	2r	59/59 (100%)	56 (95%)	3 (5%)	21	52
50	1s	68/72 (94%)	64 (94%)	4 (6%)	18	48
50	2s	67/72 (93%)	62 (92%)	5 (8%)	12	39
51	1t	71/76 (93%)	69 (97%)	2 (3%)	38	66
51	2t	70/76 (92%)	68 (97%)	2 (3%)	37	66
52	1u	18/18 (100%)	18 (100%)	0	100	100
52	2u	18/18 (100%)	18 (100%)	0	100	100
54	1y	12/19 (63%)	12 (100%)	0	100	100
54	2y	12/19 (63%)	12 (100%)	0	100	100
All	All	9387/9734 (96%)	8814 (94%)	573 (6%)	17	46

All (573) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	1D	61	LEU
3	1D	69	ARG
3	1D	78	LYS
3	1D	94	LEU
3	1D	103	ARG
3	1D	106	ILE
3	1D	111	LEU
3	1D	113	VAL
3	1D	138	VAL
3	1D	141	VAL
3	1D	193	VAL
3	1D	211	ARG
3	1D	217	ARG
3	1D	229	VAL
3	1D	242	ARG
4	1E	7	VAL
4	1E	9	VAL
4	1E	21	VAL
4	1E	33	VAL
4	1E	49	LEU
4	1E	73	GLU
4	1E	75	VAL
4	1E	77	ILE
4	1E	78	LEU
4	1E	116	VAL
4	1E	119	ARG
4	1E	144	ARG
4	1E	175	VAL
4	1E	178	GLU
5	1F	12	LEU
5	1F	18	ARG
5	1F	33	LEU
5	1F	53	THR
5	1F	57	VAL
5	1F	74	ARG
5	1F	88	VAL
5	1F	95	ARG
5	1F	110	LEU
5	1F	132	VAL
5	1F	170	LEU
5	1F	183	VAL
5	1F	192	LEU
5	1F	197	ASP

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Mol	Chain	Res	Type
5	1F	201	VAL
6	1G	5	VAL
6	1G	7	LEU
6	1G	21	ARG
6	1G	28	VAL
6	1G	43	LEU
6	1G	45	GLU
6	1G	52	ILE
6	1G	53	LEU
6	1G	82	LEU
6	1G	133	LEU
6	1G	148	MET
6	1G	159	VAL
6	1G	165	THR
6	1G	167	GLU
7	1H	13	LYS
7	1H	15	VAL
7	1H	45	VAL
7	1H	49	VAL
7	1H	71	LEU
7	1H	84	SER
7	1H	105	LEU
7	1H	125	VAL
8	1I	5	LEU
8	1I	10	GLU
8	1I	12	LEU
8	1I	38	LEU
8	1I	44	LEU
8	1I	64	GLU
8	1I	78	THR
8	1I	92	VAL
8	1I	109	ILE
8	1I	140	LEU
9	1N	5	VAL
9	1N	33	LEU
9	1N	62	VAL
9	1N	67	LEU
9	1N	71	ILE
9	1N	87	LEU
9	1N	97	ARG
9	1N	99	LEU
10	1O	10	VAL

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Mol	Chain	Res	Type
10	1O	24	VAL
10	1O	69	ILE
10	1O	98	VAL
11	1P	2	LYS
11	1P	3	LEU
11	1P	59	LEU
11	1P	83	VAL
11	1P	98	GLU
11	1P	99	LEU
11	1P	112	LEU
11	1P	125	VAL
11	1P	147	LEU
12	1Q	2	LEU
12	1Q	21	THR
12	1Q	55	VAL
12	1Q	75	THR
12	1Q	109	VAL
12	1Q	110	THR
12	1Q	112	GLU
13	1R	6	SER
13	1R	29	LEU
13	1R	33	ARG
13	1R	36	THR
13	1R	44	LEU
13	1R	54	LEU
13	1R	65	LEU
13	1R	67	LEU
13	1R	75	LEU
13	1R	96	ARG
13	1R	100	LEU
13	1R	111	LEU
14	1S	13	ARG
14	1S	14	VAL
14	1S	59	LYS
14	1S	69	VAL
15	1T	13	ARG
15	1T	17	THR
15	1T	28	VAL
15	1T	34	VAL
15	1T	59	THR
15	1T	89	VAL
15	1T	108	ARG

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Mol	Chain	Res	Type
16	1U	8	VAL
16	1U	52	ARG
16	1U	74	LEU
16	1U	83	LEU
16	1U	104	GLN
17	1V	46	VAL
17	1V	51	VAL
17	1V	52	VAL
17	1V	61	VAL
17	1V	62	LEU
17	1V	72	VAL
17	1V	79	VAL
17	1V	82	ARG
18	1W	11	ARG
18	1W	17	VAL
18	1W	19	LEU
18	1W	23	LEU
18	1W	60	ASN
18	1W	100	THR
18	1W	107	LEU
19	1X	66	LEU
20	1Y	43	ASN
20	1Y	72	VAL
20	1Y	85	VAL
20	1Y	90	LEU
20	1Y	99	CYS
21	1Z	11	GLU
21	1Z	18	LEU
21	1Z	42	VAL
21	1Z	46	LYS
21	1Z	72	ARG
21	1Z	86	VAL
21	1Z	91	LEU
21	1Z	94	GLU
21	1Z	126	VAL
21	1Z	150	LEU
21	1Z	182	LYS
21	1Z	202	GLU
21	1Z	203	GLU
22	10	10	THR
22	10	11	ARG
22	10	39	ARG

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Mol	Chain	Res	Type
22	10	59	LEU
23	11	23	LYS
23	11	95	LEU
24	12	3	LEU
25	13	6	VAL
25	13	8	LEU
25	13	31	LEU
25	13	54	VAL
26	14	13	ARG
26	14	23	GLU
26	14	49	PHE
26	14	50	VAL
26	14	60	GLN
26	14	67	TYR
27	15	6	VAL
27	15	29	THR
28	16	6	ARG
28	16	14	THR
28	16	48	VAL
29	17	1	MET
29	17	10	ARG
29	17	43	THR
30	18	6	THR
30	18	14	VAL
30	18	34	TRP
31	19	17	ILE
33	1b	15	VAL
33	1b	19	HIS
33	1b	45	GLN
33	1b	67	THR
33	1b	68	ILE
33	1b	71	VAL
33	1b	73	THR
33	1b	81	VAL
33	1b	106	LYS
33	1b	111	ARG
33	1b	112	VAL
33	1b	122	PHE
33	1b	126	GLU
33	1b	128	GLU
33	1b	158	LEU
33	1b	160	ASP

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Mol	Chain	Res	Type
33	1b	172	ILE
33	1b	178	ARG
33	1b	185	ILE
33	1b	200	ILE
33	1b	221	LEU
33	1b	224	GLN
34	1c	3	ASN
34	1c	15	THR
34	1c	36	ASP
34	1c	64	VAL
34	1c	161	GLU
34	1c	188	LEU
34	1c	206	GLU
35	1d	8	VAL
35	1d	59	ARG
35	1d	127	THR
35	1d	135	LEU
35	1d	141	ARG
35	1d	158	ILE
35	1d	178	VAL
35	1d	184	LYS
35	1d	188	LEU
35	1d	194	LEU
35	1d	196	LEU
36	1e	41	VAL
36	1e	69	VAL
36	1e	79	GLU
36	1e	120	THR
37	1f	40	VAL
37	1f	92	LYS
38	1g	10	ARG
38	1g	11	GLN
38	1g	23	VAL
38	1g	75	VAL
38	1g	90	GLU
39	1h	26	VAL
39	1h	51	VAL
39	1h	52	ASP
39	1h	63	LEU
39	1h	95	VAL
40	1i	2	GLU
40	1i	17	VAL

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Mol	Chain	Res	Type
40	1i	27	THR
40	1i	51	ARG
40	1i	87	GLN
40	1i	92	TYR
40	1i	108	VAL
41	1j	22	LYS
41	1j	49	VAL
41	1j	92	THR
41	1j	100	THR
42	1k	87	THR
42	1k	114	VAL
42	1k	117	ASN
43	1l	27	LEU
43	1l	33	ARG
43	1l	66	VAL
43	1l	83	VAL
44	1m	3	ARG
44	1m	4	ILE
44	1m	8	GLU
44	1m	19	LEU
44	1m	56	LEU
44	1m	102	ARG
44	1m	109	THR
44	1m	117	VAL
45	1n	3	ARG
45	1n	18	VAL
45	1n	33	VAL
46	1o	3	ILE
46	1o	39	LEU
47	1p	2	VAL
47	1p	8	ARG
47	1p	11	SER
47	1p	19	ILE
47	1p	28	ARG
47	1p	42	ARG
47	1p	45	THR
47	1p	67	THR
48	1q	16	GLN
48	1q	93	GLN
49	1r	76	LEU
50	1s	4	SER
50	1s	5	LEU

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Mol	Chain	Res	Type
50	1s	37	ARG
50	1s	41	VAL
51	1t	84	LEU
51	1t	100	ILE
3	2D	61	LEU
3	2D	69	ARG
3	2D	94	LEU
3	2D	103	ARG
3	2D	111	LEU
3	2D	113	VAL
3	2D	138	VAL
3	2D	141	VAL
3	2D	173	VAL
3	2D	193	VAL
3	2D	211	ARG
3	2D	221	VAL
3	2D	229	VAL
3	2D	242	ARG
4	2E	9	VAL
4	2E	21	VAL
4	2E	33	VAL
4	2E	75	VAL
4	2E	77	ILE
4	2E	89	ASP
4	2E	116	VAL
4	2E	134	ILE
4	2E	144	ARG
4	2E	154	LYS
4	2E	175	VAL
4	2E	184	VAL
5	2F	18	ARG
5	2F	24	LEU
5	2F	27	GLU
5	2F	33	LEU
5	2F	53	THR
5	2F	57	VAL
5	2F	74	ARG
5	2F	88	VAL
5	2F	132	VAL
5	2F	158	THR
5	2F	170	LEU
5	2F	183	VAL

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Mol	Chain	Res	Type
5	2F	192	LEU
5	2F	197	ASP
5	2F	201	VAL
6	2G	3	LEU
6	2G	5	VAL
6	2G	28	VAL
6	2G	49	ASP
6	2G	53	LEU
6	2G	91	ARG
6	2G	108	ASN
6	2G	133	LEU
6	2G	159	VAL
6	2G	165	THR
7	2H	13	LYS
7	2H	15	VAL
7	2H	18	GLU
7	2H	49	VAL
7	2H	71	LEU
7	2H	105	LEU
7	2H	124	GLU
7	2H	171	LEU
8	2I	5	LEU
8	2I	47	LEU
8	2I	66	GLU
8	2I	75	LEU
8	2I	92	VAL
8	2I	116	LEU
8	2I	123	LEU
8	2I	140	LEU
8	2I	144	VAL
9	2N	28	THR
9	2N	33	LEU
9	2N	34	LEU
9	2N	62	VAL
9	2N	71	ILE
9	2N	87	LEU
9	2N	99	LEU
10	2O	10	VAL
10	2O	24	VAL
10	2O	53	LYS
10	2O	69	ILE
10	2O	98	VAL

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Mol	Chain	Res	Type
11	2P	59	LEU
11	2P	83	VAL
11	2P	112	LEU
11	2P	125	VAL
12	2Q	16	ARG
12	2Q	21	THR
12	2Q	55	VAL
12	2Q	75	THR
12	2Q	109	VAL
12	2Q	110	THR
12	2Q	112	GLU
13	2R	6	SER
13	2R	18	LEU
13	2R	36	THR
13	2R	44	LEU
13	2R	65	LEU
13	2R	67	LEU
13	2R	71	GLN
13	2R	75	LEU
13	2R	79	LEU
13	2R	86	ARG
13	2R	96	ARG
13	2R	100	LEU
13	2R	111	LEU
14	2S	13	ARG
14	2S	14	VAL
14	2S	44	LYS
14	2S	75	GLU
15	2T	16	ARG
15	2T	28	VAL
15	2T	74	ARG
15	2T	89	VAL
16	2U	8	VAL
16	2U	60	LEU
16	2U	74	LEU
16	2U	95	LEU
16	2U	112	ARG
16	2U	117	GLN
17	2V	7	THR
17	2V	51	VAL
17	2V	52	VAL
17	2V	57	VAL

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Mol	Chain	Res	Type
17	2V	62	LEU
17	2V	72	VAL
17	2V	79	VAL
17	2V	82	ARG
18	2W	11	ARG
18	2W	15	ARG
18	2W	17	VAL
18	2W	100	THR
18	2W	107	LEU
19	2X	8	ILE
19	2X	57	LEU
19	2X	66	LEU
20	2Y	72	VAL
20	2Y	85	VAL
20	2Y	99	CYS
21	2Z	31	ARG
21	2Z	42	VAL
21	2Z	53	ILE
21	2Z	76	LEU
21	2Z	86	VAL
21	2Z	93	ASP
21	2Z	94	GLU
21	2Z	126	VAL
21	2Z	136	PHE
21	2Z	150	LEU
21	2Z	161	VAL
21	2Z	190	GLU
21	2Z	193	GLU
22	20	10	THR
22	20	39	ARG
23	21	75	GLU
23	21	85	LEU
23	21	95	LEU
24	22	32	LEU
24	22	70	GLN
25	23	6	VAL
25	23	23	LEU
25	23	31	LEU
26	24	50	VAL
26	24	53	GLU
26	24	67	TYR
27	25	6	VAL

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Mol	Chain	Res	Type
28	26	14	THR
28	26	48	VAL
29	27	43	THR
30	28	14	VAL
30	28	34	TRP
33	2b	67	THR
33	2b	68	ILE
33	2b	73	THR
33	2b	127	ILE
33	2b	128	GLU
33	2b	135	GLN
33	2b	136	VAL
33	2b	139	LYS
33	2b	154	LEU
33	2b	185	ILE
33	2b	191	ASP
33	2b	196	LEU
33	2b	200	ILE
33	2b	217	ARG
33	2b	224	GLN
33	2b	230	VAL
34	2c	3	ASN
34	2c	20	SER
34	2c	52	LEU
34	2c	70	VAL
34	2c	77	ILE
34	2c	115	LEU
34	2c	128	PHE
34	2c	152	ILE
34	2c	166	GLU
34	2c	188	LEU
35	2d	8	VAL
35	2d	31	CYS
35	2d	34	GLU
35	2d	76	ARG
35	2d	135	LEU
35	2d	141	ARG
35	2d	194	LEU
36	2e	40	ARG
36	2e	41	VAL
36	2e	69	VAL
36	2e	72	GLN

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Mol	Chain	Res	Type
37	2f	40	VAL
38	2g	9	VAL
38	2g	51	GLN
38	2g	53	LYS
38	2g	75	VAL
38	2g	104	LEU
38	2g	113	GLU
38	2g	115	ARG
39	2h	26	VAL
39	2h	52	ASP
39	2h	63	LEU
39	2h	91	ARG
39	2h	97	VAL
39	2h	98	LYS
39	2h	112	LEU
39	2h	135	CYS
39	2h	137	VAL
40	2i	14	VAL
40	2i	17	VAL
40	2i	53	VAL
40	2i	92	TYR
40	2i	93	ARG
40	2i	108	VAL
41	2j	29	ARG
41	2j	69	ASN
42	2k	14	VAL
42	2k	103	LEU
42	2k	106	LYS
42	2k	109	VAL
42	2k	114	VAL
43	2l	27	LEU
43	2l	33	ARG
43	2l	47	LYS
43	2l	66	VAL
43	2l	83	VAL
44	2m	4	ILE
44	2m	8	GLU
44	2m	19	LEU
44	2m	60	VAL
44	2m	65	LYS
44	2m	88	ARG
44	2m	94	ARG

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Mol	Chain	Res	Type
44	2m	102	ARG
44	2m	109	THR
45	2n	18	VAL
46	2o	5	LYS
46	2o	10	LYS
46	2o	28	GLN
46	2o	83	GLU
47	2p	2	VAL
47	2p	5	ARG
47	2p	42	ARG
47	2p	60	LEU
47	2p	67	THR
47	2p	69	THR
47	2p	76	GLN
48	2q	50	LYS
48	2q	74	LEU
49	2r	25	THR
49	2r	54	ARG
49	2r	55	ARG
50	2s	13	ASP
50	2s	16	LEU
50	2s	27	GLU
50	2s	41	VAL
50	2s	81	ARG
51	2t	84	LEU
51	2t	99	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (143) such sidechains are listed below:

Mol	Chain	Res	Type
3	1D	116	GLN
3	1D	143	HIS
3	1D	166	GLN
3	1D	201	HIS
3	1D	253	GLN
4	1E	48	GLN
4	1E	143	ASN
4	1E	180	ASN
5	1F	8	GLN
5	1F	69	HIS
5	1F	75	HIS
5	1F	133	ASN

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Mol	Chain	Res	Type
5	1F	203	GLN
6	1G	26	GLN
6	1G	41	GLN
6	1G	79	ASN
8	1I	54	GLN
8	1I	104	GLN
9	1N	8	GLN
9	1N	133	GLN
10	1O	5	GLN
11	1P	35	HIS
12	1Q	123	HIS
13	1R	13	HIS
13	1R	50	HIS
13	1R	71	GLN
14	1S	68	GLN
14	1S	95	HIS
15	1T	58	ASN
16	1U	104	GLN
19	1X	31	HIS
19	1X	82	GLN
20	1Y	6	HIS
20	1Y	43	ASN
20	1Y	92	ASN
21	1Z	32	HIS
21	1Z	55	HIS
21	1Z	73	GLN
23	11	19	GLN
24	12	70	GLN
25	13	32	GLN
28	16	49	HIS
30	18	35	GLN
33	1b	212	GLN
34	1c	6	HIS
34	1c	69	HIS
34	1c	181	ASN
35	1d	77	ASN
35	1d	119	GLN
35	1d	123	HIS
35	1d	129	ASN
35	1d	160	GLN
36	1e	20	GLN
37	1f	100	ASN

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Mol	Chain	Res	Type
38	1g	13	GLN
38	1g	28	ASN
38	1g	56	GLN
38	1g	86	GLN
38	1g	109	ASN
39	1h	82	HIS
40	1i	3	GLN
40	1i	58	HIS
41	1j	56	HIS
41	1j	62	HIS
41	1j	68	HIS
42	1k	22	HIS
42	1k	93	GLN
42	1k	116	HIS
46	1o	28	GLN
48	1q	26	GLN
50	1s	14	HIS
50	1s	47	HIS
50	1s	56	GLN
50	1s	57	HIS
3	2D	87	ASN
3	2D	116	GLN
3	2D	253	GLN
5	2F	69	HIS
5	2F	75	HIS
5	2F	203	GLN
6	2G	41	GLN
7	2H	111	HIS
8	2I	43	ASN
9	2N	94	HIS
9	2N	133	GLN
10	2O	5	GLN
10	2O	90	GLN
12	2Q	12	GLN
12	2Q	123	HIS
13	2R	13	HIS
14	2S	95	HIS
15	2T	58	ASN
16	2U	94	ASN
18	2W	61	ASN
19	2X	31	HIS
19	2X	82	GLN

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Mol	Chain	Res	Type
21	2Z	54	HIS
21	2Z	55	HIS
21	2Z	73	GLN
21	2Z	151	HIS
22	20	70	GLN
25	23	32	GLN
26	24	46	GLN
30	28	35	GLN
30	28	43	GLN
31	29	20	HIS
33	2b	110	GLN
34	2c	6	HIS
34	2c	31	HIS
34	2c	102	ASN
34	2c	181	ASN
35	2d	77	ASN
35	2d	116	GLN
35	2d	119	GLN
35	2d	123	HIS
35	2d	129	ASN
35	2d	161	ASN
35	2d	201	GLN
36	2e	20	GLN
36	2e	78	HIS
37	2f	94	GLN
37	2f	100	ASN
38	2g	11	GLN
38	2g	28	ASN
38	2g	86	GLN
38	2g	106	GLN
38	2g	148	ASN
40	2i	3	GLN
40	2i	31	GLN
40	2i	124	GLN
41	2j	13	HIS
41	2j	21	GLN
41	2j	69	ASN
42	2k	93	GLN
43	2l	80	HIS
44	2m	92	HIS
47	2p	76	GLN
48	2q	16	GLN

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Mol	Chain	Res	Type
48	2q	26	GLN
49	2r	63	GLN
50	2s	23	ASN
50	2s	57	HIS
50	2s	69	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1A	2816/2915 (96%)	427 (15%)	31 (1%)
1	2A	2860/2915 (98%)	485 (16%)	28 (0%)
2	1B	119/120 (99%)	10 (8%)	0
2	2B	119/120 (99%)	12 (10%)	0
32	1a	1497/1521 (98%)	257 (17%)	0
32	2a	1501/1521 (98%)	252 (16%)	0
53	1x	75/76 (98%)	7 (9%)	0
53	2x	75/76 (98%)	8 (10%)	0
55	A	2/27 (7%)	0	0
55	B	2/27 (7%)	0	0
All	All	9066/9318 (97%)	1458 (16%)	59 (0%)

All (1458) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1A	12	U
1	1A	15	G
1	1A	34	C
1	1A	45	C
1	1A	54	G
1	1A	60	G
1	1A	63	A
1	1A	70	A
1	1A	73	A
1	1A	74	G
1	1A	116	A
1	1A	117	A
1	1A	118	U
1	1A	121	G
1	1A	123	G
1	1A	170	A
1	1A	171	A

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Mol	Chain	Res	Type
1	1A	185	A
1	1A	188	A
1	1A	194	G
1	1A	203	G
1	1A	204	G
1	1A	205	A
1	1A	206	G
1	1A	211	A
1	1A	218	A
1	1A	222	A
1	1A	237	G
1	1A	269	G
1	1A	271	U
1	1A	272	U
1	1A	273	G
1	1A	274	U
1	1A	275	C
1	1A	288	U
1	1A	289	G
1	1A	296	U
1	1A	299	G
1	1A	303	C
1	1A	335	A
1	1A	348	A
1	1A	354	A
1	1A	376	G
1	1A	387	G
1	1A	397	G
1	1A	398	A
1	1A	399	G
1	1A	413	G
1	1A	423	G
1	1A	432	U
1	1A	438	G
1	1A	439	A
1	1A	448	U
1	1A	455	A
1	1A	474	U
1	1A	480	A
1	1A	481	C
1	1A	483	A
1	1A	507	G

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Mol	Chain	Res	Type
1	1A	510	C
1	1A	530	A
1	1A	534	C
1	1A	554	A
1	1A	555	G
1	1A	556	C
1	1A	557	A
1	1A	558	G
1	1A	569	G
1	1A	573	G
1	1A	586	G
1	1A	596	G
1	1A	598	A
1	1A	626	A
1	1A	627	G
1	1A	630	U
1	1A	638	U
1	1A	639	G
1	1A	641	G
1	1A	642	G
1	1A	652	A
1	1A	662	A
1	1A	670	C
1	1A	692	C
1	1A	693	G
1	1A	694	G
1	1A	697	C
1	1A	698	G
1	1A	716	G
1	1A	733	G
1	1A	764	G
1	1A	777	C
1	1A	787	U
1	1A	800	C
1	1A	809	U
1	1A	812	G
1	1A	822	G
1	1A	823	G
1	1A	829	A
1	1A	831	A
1	1A	832	G
1	1A	837	C

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Mol	Chain	Res	Type
1	1A	839	G
1	1A	847	A
1	1A	852	G
1	1A	858	U
1	1A	859	C
1	1A	874	U
1	1A	875	U
1	1A	906	G
1	1A	913	A
1	1A	926	G
1	1A	927	G
1	1A	931	C
1	1A	932	C
1	1A	933	C
1	1A	935	C
1	1A	936	C
1	1A	937	A
1	1A	938	G
1	1A	942	A
1	1A	956	A
1	1A	977	G
1	1A	990	A
1	1A	991	G
1	1A	998	A
1	1A	1003	U
1	1A	1004	A
1	1A	1006	C
1	1A	1019	G
1	1A	1020	C
1	1A	1029	A
1	1A	1036	A
1	1A	1042	A
1	1A	1051	C
1	1A	1058	U
1	1A	1059	C
1	1A	1067	A
1	1A	1072	U
1	1A	1079	U
1	1A	1088	G
1	1A	1092	A
1	1A	1093	G
1	1A	1094	A

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Mol	Chain	Res	Type
1	1A	1098	C
1	1A	1099	C
1	1A	1100	A
1	1A	1152	G
1	1A	1155	C
1	1A	1156	G
1	1A	1158	G
1	1A	1162	C
1	1A	1174	A
1	1A	1175	A
1	1A	1176	U
1	1A	1180	C
1	1A	1181	G
1	1A	1184	G
1	1A	1186	U
1	1A	1195	G
1	1A	1201	A
1	1A	1202	A
1	1A	1217	G
1	1A	1218	G
1	1A	1219	A
1	1A	1220	U
1	1A	1221	G
1	1A	1222	A
1	1A	1223	C
1	1A	1234	A
1	1A	1255	A
1	1A	1256	U
1	1A	1263	C
1	1A	1290	G
1	1A	1299	A
1	1A	1302	G
1	1A	1314	A
1	1A	1317	G
1	1A	1318	A
1	1A	1321	A
1	1A	1335	C
1	1A	1346	U
1	1A	1347	A
1	1A	1359	U
1	1A	1367	A
1	1A	1378	G

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Mol	Chain	Res	Type
1	1A	1391	C
1	1A	1398	U
1	1A	1405	A
1	1A	1406	A
1	1A	1411	A
1	1A	1414	G
1	1A	1416	C
1	1A	1425	A
1	1A	1430	A
1	1A	1431	G
1	1A	1432	C
1	1A	1441	A
1	1A	1462	G
1	1A	1463	C
1	1A	1466	U
1	1A	1467	G
1	1A	1474	C
1	1A	1483	C
1	1A	1491	A
1	1A	1492	C
1	1A	1497	G
1	1A	1500	A
1	1A	1506	G
1	1A	1514	C
1	1A	1518	A
1	1A	1529	G
1	1A	1539	C
1	1A	1542	A
1	1A	1554	A
1	1A	1555	C
1	1A	1556	A
1	1A	1589	A
1	1A	1605	A
1	1A	1613	A
1	1A	1616	A
1	1A	1625	U
1	1A	1626	A
1	1A	1631	C
1	1A	1632	A
1	1A	1654	A
1	1A	1655	A
1	1A	1656	A

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Mol	Chain	Res	Type
1	1A	1662	A
1	1A	1686	U
1	1A	1695	C
1	1A	1701	A
1	1A	1711	A
1	1A	1721	G
1	1A	1743	G
1	1A	1747	A
1	1A	1748	A
1	1A	1766	G
1	1A	1767	A
1	1A	1768	U
1	1A	1769	G
1	1A	1787	G
1	1A	1794	G
1	1A	1795	G
1	1A	1804	A
1	1A	1805	C
1	1A	1811	A
1	1A	1813	C
1	1A	1822	A
1	1A	1831	C
1	1A	1832	G
1	1A	1847	G
1	1A	1859	G
1	1A	1870	G
1	1A	1878	A
1	1A	1879	A
1	1A	1896	G
1	1A	1899	A
1	1A	1900	G
1	1A	1911	A
1	1A	1922	A
1	1A	1928	G
1	1A	1935	A
1	1A	1936	C
1	1A	1937	5MU
1	1A	1942	OMC
1	1A	1951	G
1	1A	1952	G
1	1A	1959	A
1	1A	1960	A

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Mol	Chain	Res	Type
1	1A	1977	U
1	1A	1985	U
1	1A	1989	C
1	1A	1992	A
1	1A	1993	A
1	1A	1994	A
1	1A	2014	G
1	1A	2015	U
1	1A	2019	G
1	1A	2045	G
1	1A	2049	G
1	1A	2053	A
1	1A	2054	G
1	1A	2055	A
1	1A	2061	C
1	1A	2065	C
1	1A	2077	C
1	1A	2078	G
1	1A	2082	A
1	1A	2083	G
1	1A	2084	A
1	1A	2091	G
1	1A	2121	U
1	1A	2124	U
1	1A	2125	C
1	1A	2126	G
1	1A	2129	C
1	1A	2130	C
1	1A	2132	G
1	1A	2137	G
1	1A	2138	G
1	1A	2139	A
1	1A	2141	A
1	1A	2142	G
1	1A	2144	U
1	1A	2147	G
1	1A	2148	A
1	1A	2149	G
1	1A	2150	C
1	1A	2152	U
1	1A	2153	G
1	1A	2155	G

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Mol	Chain	Res	Type
1	1A	2158	C
1	1A	2159	C
1	1A	2160	C
1	1A	2168	C
1	1A	2174	G
1	1A	2180	A
1	1A	2181	G
1	1A	2184	G
1	1A	2187	G
1	1A	2188	G
1	1A	2191	A
1	1A	2192	A
1	1A	2202	U
1	1A	2205	C
1	1A	2206	G
1	1A	2208	G
1	1A	2209	G
1	1A	2212	G
1	1A	2214	G
1	1A	2220	A
1	1A	2226	C
1	1A	2227	G
1	1A	2228	G
1	1A	2229	A
1	1A	2231	G
1	1A	2237	A
1	1A	2246	G
1	1A	2250	G
1	1A	2251	G
1	1A	2280	A
1	1A	2281	A
1	1A	2290	A
1	1A	2295	C
1	1A	2299	A
1	1A	2301	G
1	1A	2306	C
1	1A	2317	A
1	1A	2324	U
1	1A	2332	A
1	1A	2333	G
1	1A	2337	G
1	1A	2348	A

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Mol	Chain	Res	Type
1	1A	2359	C
1	1A	2362	C
1	1A	2395	G
1	1A	2397	C
1	1A	2412	G
1	1A	2418	U
1	1A	2426	G
1	1A	2434	A
1	1A	2437	A
1	1A	2441	G
1	1A	2442	A
1	1A	2446	A
1	1A	2447	A
1	1A	2451	A
1	1A	2453	C
1	1A	2457	G
1	1A	2460	A
1	1A	2480	G
1	1A	2481	A
1	1A	2488	A
1	1A	2514	G
1	1A	2517	G
1	1A	2518	U
1	1A	2530	A
1	1A	2532	C
1	1A	2541	G
1	1A	2547	G
1	1A	2561	G
1	1A	2562	G
1	1A	2566	U
1	1A	2578	A
1	1A	2579	G
1	1A	2586	G
1	1A	2594	G
1	1A	2597	U
1	1A	2598	C
1	1A	2614	A
1	1A	2621	U
1	1A	2623	U
1	1A	2624	C
1	1A	2641	A
1	1A	2642	G

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Mol	Chain	Res	Type
1	1A	2666	A
1	1A	2674	A
1	1A	2701	U
1	1A	2702	C
1	1A	2703	C
1	1A	2714	U
1	1A	2715	C
1	1A	2725	A
1	1A	2726	A
1	1A	2727	G
1	1A	2739	U
1	1A	2746	A
1	1A	2771	A
1	1A	2778	A
1	1A	2779	G
1	1A	2780	C
1	1A	2791	A
1	1A	2793	G
1	1A	2803	A
1	1A	2804	C
1	1A	2813	G
1	1A	2828	G
1	1A	2830	A
1	1A	2831	A
1	1A	2843	G
1	1A	2845	A
1	1A	2882	G
1	1A	2884	C
1	1A	2885	C
1	1A	2890	C
1	1A	2901	A
1	1A	2903	G
2	1B	2	C
2	1B	7	G
2	1B	13	A
2	1B	47	C
2	1B	56	G
2	1B	57	A
2	1B	73	A
2	1B	84	C
2	1B	106	G
2	1B	110	G

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Mol	Chain	Res	Type
32	1a	9	G
32	1a	22	G
32	1a	32	A
32	1a	39	G
32	1a	48	C
32	1a	50	A
32	1a	51	A
32	1a	61	G
32	1a	78	G
32	1a	79	G
32	1a	96	U
32	1a	101	A
32	1a	116	A
32	1a	121	C
32	1a	131	C
32	1a	144	G
32	1a	151	A
32	1a	159	G
32	1a	163	C
32	1a	173	U
32	1a	174	C
32	1a	182	U
32	1a	189(E)	U
32	1a	189(F)	U
32	1a	195	A
32	1a	197	A
32	1a	201	C
32	1a	202	U
32	1a	203	U
32	1a	204	U
32	1a	216	G
32	1a	218	C
32	1a	220	G
32	1a	247	G
32	1a	251	G
32	1a	258	G
32	1a	266	G
32	1a	267	C
32	1a	289	G
32	1a	298	A
32	1a	321	A
32	1a	328	C

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Mol	Chain	Res	Type
32	1a	332	G
32	1a	348	G
32	1a	351	G
32	1a	352	C
32	1a	353	A
32	1a	354	G
32	1a	367	U
32	1a	372	C
32	1a	373	A
32	1a	381	C
32	1a	384	G
32	1a	388	G
32	1a	397	A
32	1a	398	C
32	1a	406	G
32	1a	412	A
32	1a	413	G
32	1a	422	C
32	1a	423	G
32	1a	424	G
32	1a	429	U
32	1a	439	A
32	1a	442	C
32	1a	452	A
32	1a	458	C
32	1a	461	A
32	1a	470	C
32	1a	477	A
32	1a	482	A
32	1a	485	G
32	1a	496	A
32	1a	498	U
32	1a	505	G
32	1a	509	A
32	1a	510	A
32	1a	511	C
32	1a	518	C
32	1a	521	G
32	1a	527	G7M
32	1a	532	A
32	1a	533	A
32	1a	547	A

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Mol	Chain	Res	Type
32	1a	550	G
32	1a	558	G
32	1a	559	A
32	1a	560	U
32	1a	561	U
32	1a	562	C
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	618	C
32	1a	619	U
32	1a	630	G
32	1a	631	G
32	1a	632	A
32	1a	633	G
32	1a	653	A
32	1a	661	G
32	1a	665	A
32	1a	680	C
32	1a	687	A
32	1a	688	G
32	1a	723	U
32	1a	731	G
32	1a	735	C
32	1a	746	A
32	1a	753	A
32	1a	755	G
32	1a	777	A
32	1a	792	A
32	1a	793	U
32	1a	794	A
32	1a	796	C
32	1a	817	C
32	1a	821	G
32	1a	828	A
32	1a	829	G
32	1a	838	G
32	1a	840	C
32	1a	841	U

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Mol	Chain	Res	Type
32	1a	848	C
32	1a	851	G
32	1a	859	A
32	1a	872	A
32	1a	873	A
32	1a	902	G
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	972	C
32	1a	974	A
32	1a	975	A
32	1a	976	G
32	1a	977	A
32	1a	992	U
32	1a	993	G
32	1a	994	A
32	1a	998	G
32	1a	999	C
32	1a	1001(A)	G
32	1a	1004	A
32	1a	1005	A
32	1a	1006	C
32	1a	1009	G
32	1a	1020	U
32	1a	1022	G
32	1a	1023	G
32	1a	1024	G
32	1a	1025	U
32	1a	1026	G
32	1a	1027	C
32	1a	1028	C
32	1a	1029	C
32	1a	1030	C
32	1a	1030(A)	G
32	1a	1030(C)	G

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Mol	Chain	Res	Type
32	1a	1032	G
32	1a	1033	G
32	1a	1037	C
32	1a	1039	C
32	1a	1040	U
32	1a	1043	C
32	1a	1044	A
32	1a	1045	C
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	1094	G
32	1a	1101	A
32	1a	1118	C
32	1a	1122	U
32	1a	1125	U
32	1a	1130	A
32	1a	1132	C
32	1a	1134	G
32	1a	1136	U
32	1a	1137	C
32	1a	1139	G
32	1a	1151	A
32	1a	1152	A
32	1a	1159	U
32	1a	1168	A
32	1a	1183	A
32	1a	1184	G
32	1a	1193	G
32	1a	1196	U
32	1a	1197	G
32	1a	1202	G
32	1a	1208	C
32	1a	1213	A
32	1a	1224	G
32	1a	1227	A
32	1a	1238	A
32	1a	1240	U

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Mol	Chain	Res	Type
32	1a	1250	A
32	1a	1256	A
32	1a	1257	U
32	1a	1258	G
32	1a	1260	C
32	1a	1270	C
32	1a	1278	U
32	1a	1280	A
32	1a	1281	U
32	1a	1282	C
32	1a	1286	A
32	1a	1287	A
32	1a	1299	A
32	1a	1300	G
32	1a	1302	U
32	1a	1305	G
32	1a	1312	G
32	1a	1315	U
32	1a	1317	C
32	1a	1319	A
32	1a	1320	C
32	1a	1338	G
32	1a	1340	A
32	1a	1347	G
32	1a	1353	G
32	1a	1363	C
32	1a	1370	G
32	1a	1397	C
32	1a	1402	4OC
32	1a	1419	G
32	1a	1442	G
32	1a	1442(A)	G
32	1a	1447	A
32	1a	1456	G
32	1a	1487	G
32	1a	1492	A
32	1a	1493	A
32	1a	1499	A
32	1a	1503	A
32	1a	1504	G
32	1a	1505	G
32	1a	1506	U

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Mol	Chain	Res	Type
32	1a	1517	G
32	1a	1519	MA6
32	1a	1520	G
32	1a	1529	G
32	1a	1530	G
53	1x	9	G
53	1x	20	U
53	1x	21	A
53	1x	42	G
53	1x	50	U
53	1x	54	5MU
53	1x	68	C
1	2A	10	G
1	2A	11	G
1	2A	12	U
1	2A	15	G
1	2A	45	C
1	2A	61	G
1	2A	71	A
1	2A	74	A
1	2A	75	G
1	2A	84	A
1	2A	95	G
1	2A	118	A
1	2A	120	U
1	2A	131	G
1	2A	141	A
1	2A	157	U
1	2A	173	G
1	2A	181	A
1	2A	182	A
1	2A	196	A
1	2A	199	A
1	2A	205	G
1	2A	211	A
1	2A	215	G
1	2A	216	A
1	2A	221	A
1	2A	222	A
1	2A	228	A
1	2A	229	A
1	2A	230	U

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Mol	Chain	Res	Type
1	2A	248	G
1	2A	249	C
1	2A	271(K)	U
1	2A	271(L)	U
1	2A	271(M)	G
1	2A	271(N)	U
1	2A	271(O)	C
1	2A	272(B)	G
1	2A	277	C
1	2A	278	A
1	2A	292	C
1	2A	311	A
1	2A	324	A
1	2A	327	G
1	2A	329	G
1	2A	330	A
1	2A	345	A
1	2A	352	G
1	2A	354	G
1	2A	362	U
1	2A	363	G
1	2A	370	G
1	2A	372	G
1	2A	386	G
1	2A	396	G
1	2A	399	G
1	2A	405	U
1	2A	407	G
1	2A	411	G
1	2A	412	A
1	2A	428	A
1	2A	443	A
1	2A	444	C
1	2A	454	A
1	2A	455	C
1	2A	457	A
1	2A	464	U
1	2A	470	A
1	2A	479	A
1	2A	481	G
1	2A	504	U
1	2A	505	A

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Mol	Chain	Res	Type
1	2A	509	C
1	2A	530	G
1	2A	531	C
1	2A	532	A
1	2A	533	G
1	2A	545	G
1	2A	556	G
1	2A	563	G
1	2A	568	U
1	2A	573	G
1	2A	575	A
1	2A	603	A
1	2A	604	G
1	2A	607	U
1	2A	614(B)	G
1	2A	614(C)	A
1	2A	615	G
1	2A	616	G
1	2A	627	A
1	2A	637	A
1	2A	645	C
1	2A	646	A
1	2A	652(B)	A
1	2A	652(C)	G
1	2A	652(F)	G
1	2A	652(T)	C
1	2A	652(U)	G
1	2A	669	G
1	2A	686	G
1	2A	717	G
1	2A	726	G
1	2A	730	C
1	2A	740	U
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	790	C
1	2A	792	G

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Mol	Chain	Res	Type
1	2A	793	A
1	2A	794	G
1	2A	802	A
1	2A	805	G
1	2A	812	C
1	2A	827	U
1	2A	828	U
1	2A	832	G
1	2A	848	G
1	2A	857	C
1	2A	859	G
1	2A	869	G
1	2A	874	G
1	2A	883	G
1	2A	886	C
1	2A	887	A
1	2A	888	C
1	2A	889	C
1	2A	890	A
1	2A	893	C
1	2A	896	A
1	2A	899	A
1	2A	900	A
1	2A	901	A
1	2A	910	A
1	2A	917	A
1	2A	932	G
1	2A	936	C
1	2A	938	G
1	2A	941	A
1	2A	944	G
1	2A	945	A
1	2A	946	G
1	2A	953	A
1	2A	958	U
1	2A	961	C
1	2A	974	G
1	2A	975	C
1	2A	980	A
1	2A	983	A
1	2A	996	A
1	2A	997	G

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Mol	Chain	Res	Type
1	2A	1006	C
1	2A	1012	U
1	2A	1013	C
1	2A	1022	G
1	2A	1026	U
1	2A	1033	U
1	2A	1038	C
1	2A	1043	C
1	2A	1045	A
1	2A	1046	A
1	2A	1047	G
1	2A	1052	C
1	2A	1053	C
1	2A	1054	A
1	2A	1058	G
1	2A	1060	U
1	2A	1064	C
1	2A	1065	U
1	2A	1066	U
1	2A	1067	A
1	2A	1068	G
1	2A	1070	A
1	2A	1071	G
1	2A	1072	C
1	2A	1073	A
1	2A	1074	G
1	2A	1076	C
1	2A	1077	A
1	2A	1078	U
1	2A	1079	C
1	2A	1082	U
1	2A	1083	U
1	2A	1084	A
1	2A	1085	A
1	2A	1086	A
1	2A	1087	G
1	2A	1088	A
1	2A	1090	U
1	2A	1091	G
1	2A	1092	C
1	2A	1093	G
1	2A	1094	U

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Mol	Chain	Res	Type
1	2A	1096	A
1	2A	1109	C
1	2A	1110	G
1	2A	1112	G
1	2A	1130	U
1	2A	1135	C
1	2A	1136	G
1	2A	1170	G
1	2A	1171	G
1	2A	1211	U
1	2A	1220	A
1	2A	1229	G
1	2A	1236	G
1	2A	1237	A
1	2A	1244	G
1	2A	1253	A
1	2A	1256	G
1	2A	1268	A
1	2A	1271	G
1	2A	1272	A
1	2A	1273	U
1	2A	1284	A
1	2A	1300	U
1	2A	1301	A
1	2A	1313	U
1	2A	1314	C
1	2A	1342	A
1	2A	1352	U
1	2A	1359	A
1	2A	1360	A
1	2A	1365	A
1	2A	1368	G
1	2A	1373	A
1	2A	1376	C
1	2A	1384	A
1	2A	1385	G
1	2A	1386	C
1	2A	1416	G
1	2A	1417	C
1	2A	1420	U
1	2A	1421	G
1	2A	1428	C

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Mol	Chain	Res	Type
1	2A	1437	C
1	2A	1445	A
1	2A	1459	G
1	2A	1460	A
1	2A	1467	C
1	2A	1471	A
1	2A	1482	G
1	2A	1493	C
1	2A	1494	A
1	2A	1497	U
1	2A	1508	A
1	2A	1509	C
1	2A	1509(A)	A
1	2A	1525	G
1	2A	1542	A
1	2A	1543	C
1	2A	1547	C
1	2A	1558	A
1	2A	1559	G
1	2A	1566	A
1	2A	1569	A
1	2A	1578	U
1	2A	1580	A
1	2A	1584	C
1	2A	1586	A
1	2A	1602	U
1	2A	1603	A
1	2A	1608	A
1	2A	1609	A
1	2A	1639	U
1	2A	1648	C
1	2A	1664	A
1	2A	1674	G
1	2A	1675	C
1	2A	1700	A
1	2A	1701	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

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Mol	Chain	Res	Type
1	2A	1764	G
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	1820	U
1	2A	1828	G
1	2A	1835	G
1	2A	1847	A
1	2A	1861	G
1	2A	1877	A
1	2A	1878	G
1	2A	1889	A
1	2A	1900	A
1	2A	1906	G
1	2A	1914	C
1	2A	1929	G
1	2A	1930	G
1	2A	1936	A
1	2A	1937	A
1	2A	1947	C
1	2A	1955	U
1	2A	1962	5MC
1	2A	1963	U
1	2A	1967	C
1	2A	1970	A
1	2A	1971	A
1	2A	1972	A
1	2A	1992	G
1	2A	1993	U
1	2A	1997	G
1	2A	2004	G
1	2A	2023	G
1	2A	2031	A
1	2A	2033	A
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	2070	G
1	2A	2076	U
1	2A	2093	G
1	2A	2101	G
1	2A	2103	C
1	2A	2104	G
1	2A	2105	C
1	2A	2107	C
1	2A	2108	C
1	2A	2109	U
1	2A	2111	C
1	2A	2112	G
1	2A	2116	G
1	2A	2117	A
1	2A	2118	U
1	2A	2119	A
1	2A	2121	G
1	2A	2123	G
1	2A	2124	G
1	2A	2126	A
1	2A	2127	G
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	2136	C
1	2A	2137	C
1	2A	2138	C
1	2A	2141	G
1	2A	2142	C
1	2A	2145	C
1	2A	2146	C
1	2A	2148	G
1	2A	2151	G
1	2A	2159	G
1	2A	2162	G

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Mol	Chain	Res	Type
1	2A	2163	C
1	2A	2164	C
1	2A	2172	U
1	2A	2173	A
1	2A	2180	U
1	2A	2186	G
1	2A	2187	G
1	2A	2189	U
1	2A	2191	G
1	2A	2192	G
1	2A	2198	A
1	2A	2206	G
1	2A	2207	G
1	2A	2208	A
1	2A	2225	A
1	2A	2235	G
1	2A	2239	G
1	2A	2268	A
1	2A	2269	A
1	2A	2273	A
1	2A	2275	C
1	2A	2279	G
1	2A	2283	C
1	2A	2287	A
1	2A	2289	G
1	2A	2297	C
1	2A	2305	A
1	2A	2308	G
1	2A	2311	A
1	2A	2312	U
1	2A	2316	C
1	2A	2320	A
1	2A	2321	G
1	2A	2322	A
1	2A	2325	G
1	2A	2334	G
1	2A	2336	A
1	2A	2340	G
1	2A	2343	C
1	2A	2347	C
1	2A	2350	C
1	2A	2379	G

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Mol	Chain	Res	Type
1	2A	2383	G
1	2A	2385	C
1	2A	2406	U
1	2A	2410	G
1	2A	2414	G
1	2A	2422	A
1	2A	2423	U
1	2A	2425	A
1	2A	2427	C
1	2A	2429	G
1	2A	2430	A
1	2A	2435	A
1	2A	2439	A
1	2A	2441	C
1	2A	2445	G
1	2A	2448	A
1	2A	2474	C
1	2A	2476	A
1	2A	2478	A
1	2A	2502	G
1	2A	2505	G
1	2A	2506	U
1	2A	2518	A
1	2A	2520	C
1	2A	2529	G
1	2A	2549	G
1	2A	2553	G
1	2A	2554	U
1	2A	2555	U
1	2A	2566	A
1	2A	2567	G
1	2A	2572	A
1	2A	2574	G
1	2A	2576	G
1	2A	2577	A
1	2A	2582	G
1	2A	2585	U
1	2A	2602	A
1	2A	2611	U
1	2A	2612	C
1	2A	2620	C
1	2A	2629	A

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Mol	Chain	Res	Type
1	2A	2630	G
1	2A	2654	A
1	2A	2663	G
1	2A	2682	U
1	2A	2689	U
1	2A	2690	C
1	2A	2691	C
1	2A	2702	U
1	2A	2703	C
1	2A	2712(A)	A
1	2A	2713	A
1	2A	2714	G
1	2A	2718	G
1	2A	2726	U
1	2A	2733	A
1	2A	2748	A
1	2A	2757	A
1	2A	2758	A
1	2A	2764	A
1	2A	2765	A
1	2A	2769	C
1	2A	2778	A
1	2A	2802	G
1	2A	2818	G
1	2A	2820	A
1	2A	2821	A
1	2A	2823	A
1	2A	2833	G
1	2A	2866	U
1	2A	2872	G
1	2A	2880	C
1	2A	2892	A
1	2A	2894	G
1	2A	2896	C
1	2A	2897	U
2	2B	2	C
2	2B	7	G
2	2B	8	U
2	2B	13	A
2	2B	15	A
2	2B	33	G
2	2B	42	C

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Mol	Chain	Res	Type
2	2B	56	G
2	2B	73	A
2	2B	84	C
2	2B	106	G
2	2B	110	G
32	2a	5	U
32	2a	9	G
32	2a	10	A
32	2a	22	G
32	2a	32	A
32	2a	39	G
32	2a	48	C
32	2a	50	A
32	2a	51	A
32	2a	66	G
32	2a	89	C
32	2a	96	U
32	2a	101	A
32	2a	116	A
32	2a	121	C
32	2a	131	C
32	2a	144	G
32	2a	151	A
32	2a	163	C
32	2a	173	U
32	2a	174	C
32	2a	182	U
32	2a	189(E)	U
32	2a	189(F)	U
32	2a	195	A
32	2a	197	A
32	2a	201	C
32	2a	202	U
32	2a	203	U
32	2a	204	U
32	2a	216	G
32	2a	218	C
32	2a	220	G
32	2a	247	G
32	2a	251	G
32	2a	258	G
32	2a	266	G

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Mol	Chain	Res	Type
32	2a	267	C
32	2a	289	G
32	2a	298	A
32	2a	321	A
32	2a	328	C
32	2a	332	G
32	2a	348	G
32	2a	351	G
32	2a	352	C
32	2a	353	A
32	2a	354	G
32	2a	367	U
32	2a	372	C
32	2a	373	A
32	2a	381	C
32	2a	384	G
32	2a	388	G
32	2a	397	A
32	2a	398	C
32	2a	406	G
32	2a	412	A
32	2a	413	G
32	2a	422	C
32	2a	423	G
32	2a	424	G
32	2a	429	U
32	2a	439	A
32	2a	442	C
32	2a	452	A
32	2a	458	C
32	2a	461	A
32	2a	470	C
32	2a	477	A
32	2a	482	A
32	2a	485	G
32	2a	496	A
32	2a	498	U
32	2a	505	G
32	2a	509	A
32	2a	510	A
32	2a	511	C
32	2a	518	C

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Mol	Chain	Res	Type
32	2a	521	G
32	2a	527	G7M
32	2a	532	A
32	2a	533	A
32	2a	547	A
32	2a	550	G
32	2a	558	G
32	2a	559	A
32	2a	560	U
32	2a	561	U
32	2a	562	C
32	2a	572	A
32	2a	573	A
32	2a	576	G
32	2a	592	G
32	2a	596	C
32	2a	618	C
32	2a	619	U
32	2a	630	G
32	2a	631	G
32	2a	632	A
32	2a	633	G
32	2a	653	A
32	2a	661	G
32	2a	665	A
32	2a	687	A
32	2a	688	G
32	2a	723	U
32	2a	731	G
32	2a	746	A
32	2a	753	A
32	2a	755	G
32	2a	766	A
32	2a	777	A
32	2a	792	A
32	2a	793	U
32	2a	794	A
32	2a	796	C
32	2a	817	C
32	2a	821	G
32	2a	828	A
32	2a	829	G

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Mol	Chain	Res	Type
32	2a	838	G
32	2a	840	C
32	2a	841	U
32	2a	848	C
32	2a	851	G
32	2a	859	A
32	2a	872	A
32	2a	873	A
32	2a	902	G
32	2a	914	A
32	2a	926	G
32	2a	927	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	992	U
32	2a	993	G
32	2a	994	A
32	2a	1005	A
32	2a	1009	G
32	2a	1022	G
32	2a	1023	G
32	2a	1024	G
32	2a	1025	U
32	2a	1026	G
32	2a	1027	C
32	2a	1028	C
32	2a	1030(A)	G
32	2a	1030(B)	C
32	2a	1030(C)	G
32	2a	1032	G
32	2a	1033	G
32	2a	1034	G

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Mol	Chain	Res	Type
32	2a	1039	C
32	2a	1040	U
32	2a	1044	A
32	2a	1045	C
32	2a	1053	G
32	2a	1054	C
32	2a	1065	U
32	2a	1066	C
32	2a	1068	G
32	2a	1081	G
32	2a	1086	U
32	2a	1094	G
32	2a	1095	U
32	2a	1101	A
32	2a	1117	G
32	2a	1118	C
32	2a	1122	U
32	2a	1125	U
32	2a	1129	C
32	2a	1130	A
32	2a	1132	C
32	2a	1136	U
32	2a	1137	C
32	2a	1138	G
32	2a	1139	G
32	2a	1140	C
32	2a	1147	C
32	2a	1151	A
32	2a	1152	A
32	2a	1158	C
32	2a	1159	U
32	2a	1168	A
32	2a	1183	A
32	2a	1184	G
32	2a	1193	G
32	2a	1196	U
32	2a	1197	G
32	2a	1211	U
32	2a	1212	U
32	2a	1213	A
32	2a	1224	G
32	2a	1227	A

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Mol	Chain	Res	Type
32	2a	1238	A
32	2a	1240	U
32	2a	1250	A
32	2a	1256	A
32	2a	1257	U
32	2a	1258	G
32	2a	1260	C
32	2a	1270	C
32	2a	1278	U
32	2a	1279	A
32	2a	1280	A
32	2a	1281	U
32	2a	1282	C
32	2a	1286	A
32	2a	1287	A
32	2a	1299	A
32	2a	1300	G
32	2a	1305	G
32	2a	1312	G
32	2a	1315	U
32	2a	1317	C
32	2a	1319	A
32	2a	1320	C
32	2a	1340	A
32	2a	1347	G
32	2a	1353	G
32	2a	1363	C
32	2a	1370	G
32	2a	1397	C
32	2a	1402	4OC
32	2a	1419	G
32	2a	1442	G
32	2a	1442(A)	G
32	2a	1447	A
32	2a	1456	G
32	2a	1487	G
32	2a	1492	A
32	2a	1493	A
32	2a	1499	A
32	2a	1503	A
32	2a	1504	G
32	2a	1505	G

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Mol	Chain	Res	Type
32	2a	1506	U
32	2a	1517	G
32	2a	1520	G
32	2a	1529	G
32	2a	1530	G
53	2x	9	G
53	2x	20	U
53	2x	21	A
53	2x	42	G
53	2x	50	U
53	2x	68	C
53	2x	69	C
53	2x	76	A

All (59) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1A	78	G
1	1A	115	G
1	1A	185	A
1	1A	302	A
1	1A	509	A
1	1A	532	A
1	1A	831	A
1	1A	874	U
1	1A	913	A
1	1A	941	U
1	1A	1003	U
1	1A	1065	U
1	1A	1067	A
1	1A	1093	G
1	1A	1097	G
1	1A	1099	C
1	1A	1201	A
1	1A	1219	A
1	1A	1220	U
1	1A	1221	G
1	1A	1255	A
1	1A	1299	A
1	1A	1346	U
1	1A	1700	G
1	1A	1710	C

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Mol	Chain	Res	Type
1	1A	2300	A
1	1A	2434	A
1	1A	2442	A
1	1A	2597	U
1	1A	2701	U
1	1A	2902	G
1	2A	9	U
1	2A	195	A
1	2A	266	G
1	2A	271(M)	G
1	2A	277	C
1	2A	532	A
1	2A	652(E)	G
1	2A	752	A
1	2A	840	C
1	2A	856	C
1	2A	900	A
1	2A	1053	C
1	2A	1057	A
1	2A	1065	U
1	2A	1067	A
1	2A	1073	A
1	2A	1076	C
1	2A	1210	A
1	2A	1420	U
1	2A	1442	G
1	2A	1491	G
1	2A	1992	G
1	2A	2126	A
1	2A	2171	A
1	2A	2172	U
1	2A	2321	G
1	2A	2689	U
1	2A	2756	U

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

56 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	5MC	1a	1407	32	19,22,23	1.06	1 (5%)	26,32,35	1.20	4 (15%)
32	5MC	1a	1400	32	19,22,23	1.09	2 (10%)	26,32,35	1.32	3 (11%)
53	4SU	1x	8	53	18,21,22	1.24	2 (11%)	25,30,33	0.80	1 (4%)
1	PSU	2A	2605	1	18,21,22	1.40	3 (16%)	21,30,33	1.78	4 (19%)
1	PSU	2A	1911	1	18,21,22	1.36	3 (16%)	21,30,33	1.69	5 (23%)
32	MA6	2a	1518	32	23,26,27	1.07	2 (8%)	33,38,41	4.52	14 (42%)
1	PSU	1A	1933	1	18,21,22	1.33	3 (16%)	21,30,33	1.62	6 (28%)
32	5MC	2a	1400	32	19,22,23	1.03	1 (5%)	26,32,35	1.32	4 (15%)
32	5MC	2a	1407	32	19,22,23	0.97	2 (10%)	26,32,35	1.23	4 (15%)
32	5MC	2a	967	32	19,22,23	0.96	2 (10%)	26,32,35	1.31	4 (15%)
32	MA6	1a	1518	32	23,26,27	1.07	3 (13%)	33,38,41	4.24	14 (42%)
53	5MU	2x	54	53	19,22,23	0.97	2 (10%)	27,32,35	1.11	2 (7%)
53	5MC	2x	32	53	19,22,23	1.06	2 (10%)	26,32,35	1.30	4 (15%)
1	2MA	1A	2515	56,1	22,25,26	2.74	8 (36%)	32,37,40	3.12	10 (31%)
1	PSU	1A	1939	56,1	18,21,22	1.18	3 (16%)	21,30,33	1.57	5 (23%)
32	M2G	1a	966	32	24,27,28	2.13	5 (20%)	33,40,43	1.61	7 (21%)
53	5MC	1x	32	53	19,22,23	1.05	3 (15%)	26,32,35	1.26	4 (15%)
1	5MU	1A	1961	1	19,22,23	0.79	1 (5%)	27,32,35	1.21	3 (11%)
53	PSU	1x	55	53	18,21,22	1.46	3 (16%)	21,30,33	1.69	3 (14%)
53	4SU	2x	8	53,56	18,21,22	1.25	2 (11%)	25,30,33	0.87	2 (8%)
43	0TD	2l	92	43	8,9,10	3.07	3 (37%)	6,11,13	2.47	3 (50%)
1	5MC	1A	1984	1	19,22,23	1.05	2 (10%)	26,32,35	1.33	4 (15%)
32	G7M	1a	527	56,32	23,26,27	2.79	8 (34%)	34,39,42	1.61	7 (20%)
32	5MC	1a	1404	32	19,22,23	0.91	0	26,32,35	1.23	4 (15%)
1	5MU	2A	1939	1	19,22,23	0.80	1 (5%)	27,32,35	1.16	2 (7%)
32	5MC	2a	1404	32	19,22,23	0.96	1 (5%)	26,32,35	1.22	5 (19%)
1	OMC	1A	1942	56,1	19,22,23	2.45	7 (36%)	25,31,34	0.92	1 (4%)
1	5MC	2A	1962	56,1	19,22,23	1.01	1 (5%)	26,32,35	1.32	4 (15%)
32	G7M	2a	527	56,32	23,26,27	2.79	8 (34%)	34,39,42	1.62	9 (26%)
32	2MG	1a	1207	56,32	23,26,27	2.22	6 (26%)	33,38,41	2.39	14 (42%)
43	0TD	1l	92	43	8,9,10	2.77	3 (37%)	6,11,13	3.05	4 (66%)
32	2MG	2a	1207	32	23,26,27	2.14	5 (21%)	33,38,41	2.23	12 (36%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
32	UR3	2a	1498	32	19,22,23	1.99	3 (15%)	26,32,35	1.67	4 (15%)
32	M2G	2a	966	32	24,27,28	2.19	5 (20%)	33,40,43	1.67	7 (21%)
1	5MU	1A	1937	1	19,22,23	1.32	2 (10%)	27,32,35	1.49	5 (18%)
32	5MC	1a	967	32	19,22,23	1.09	2 (10%)	26,32,35	1.21	4 (15%)
32	4OC	2a	1402	32	20,23,24	2.64	8 (40%)	25,32,35	0.99	1 (4%)
32	PSU	1a	516	32	18,21,22	1.40	3 (16%)	21,30,33	2.09	5 (23%)
32	PSU	2a	516	32	18,21,22	1.39	2 (11%)	21,30,33	2.24	7 (33%)
1	5MC	2A	1942	1	19,22,23	0.99	1 (5%)	26,32,35	1.23	4 (15%)
32	MA6	2a	1519	32	23,26,27	1.07	2 (8%)	33,38,41	4.36	14 (42%)
32	MA6	1a	1519	32	23,26,27	1.07	2 (8%)	33,38,41	4.42	14 (42%)
1	OMC	2A	1920	1	19,22,23	2.50	7 (36%)	25,31,34	0.89	1 (4%)
1	OMU	2A	2552	56,1	19,22,23	6.85	10 (52%)	25,31,34	2.57	7 (28%)
1	2MA	2A	2503	56,1	22,25,26	2.71	7 (31%)	32,37,40	3.28	11 (34%)
1	5MC	1A	1964	1	19,22,23	1.03	1 (5%)	26,32,35	1.31	4 (15%)
1	5MU	2A	1915	1	19,22,23	1.22	2 (10%)	27,32,35	1.32	3 (11%)
1	PSU	1A	2617	1	18,21,22	1.18	3 (16%)	21,30,33	1.71	2 (9%)
32	UR3	1a	1498	32	19,22,23	2.00	4 (21%)	26,32,35	1.60	4 (15%)
1	OMG	1A	2263	53,56,1	23,26,27	1.75	4 (17%)	32,38,41	2.25	10 (31%)
53	PSU	2x	55	53	18,21,22	1.56	3 (16%)	21,30,33	1.79	5 (23%)
1	OMU	1A	2564	1	19,22,23	6.85	10 (52%)	25,31,34	2.75	8 (32%)
53	5MU	1x	54	53	19,22,23	1.09	2 (10%)	27,32,35	1.14	2 (7%)
1	OMG	2A	2251	53,56,1	23,26,27	1.72	2 (8%)	32,38,41	2.23	11 (34%)
1	PSU	2A	1917	1	18,21,22	1.31	3 (16%)	21,30,33	1.73	5 (23%)
32	4OC	1a	1402	32	20,23,24	2.63	8 (40%)	25,32,35	0.84	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
32	5MC	1a	1407	32	-	0/7/25/26	0/2/2/2
32	5MC	1a	1400	32	-	2/7/25/26	0/2/2/2
53	4SU	1x	8	53	-	0/7/25/26	0/2/2/2
1	PSU	2A	2605	1	-	0/7/25/26	0/2/2/2
1	PSU	2A	1911	1	-	0/7/25/26	0/2/2/2
32	MA6	2a	1518	32	-	0/11/29/30	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	PSU	1A	1933	1	-	0/7/25/26	0/2/2/2
32	5MC	2a	1400	32	-	1/7/25/26	0/2/2/2
32	5MC	2a	1407	32	-	0/7/25/26	0/2/2/2
32	5MC	2a	967	32	-	0/7/25/26	0/2/2/2
32	MA6	1a	1518	32	-	0/11/29/30	0/3/3/3
53	5MU	2x	54	53	-	0/7/25/26	0/2/2/2
53	5MC	2x	32	53	-	0/7/25/26	0/2/2/2
1	2MA	1A	2515	56,1	-	2/7/25/26	0/3/3/3
1	PSU	1A	1939	56,1	-	1/7/25/26	0/2/2/2
32	M2G	1a	966	32	-	1/11/29/30	0/3/3/3
53	5MC	1x	32	53	-	0/7/25/26	0/2/2/2
1	5MU	1A	1961	1	-	0/7/25/26	0/2/2/2
53	PSU	1x	55	53	-	0/7/25/26	0/2/2/2
53	4SU	2x	8	53,56	-	0/7/25/26	0/2/2/2
43	0TD	2l	92	43	-	2/7/12/14	-
1	5MC	1A	1984	1	-	0/7/25/26	0/2/2/2
32	G7M	1a	527	56,32	-	3/7/25/26	0/3/3/3
32	5MC	1a	1404	32	-	0/7/25/26	0/2/2/2
1	5MU	2A	1939	1	-	0/7/25/26	0/2/2/2
32	5MC	2a	1404	32	-	0/7/25/26	0/2/2/2
1	OMC	1A	1942	56,1	-	3/9/27/28	0/2/2/2
1	5MC	2A	1962	56,1	-	2/7/25/26	0/2/2/2
32	G7M	2a	527	56,32	-	2/7/25/26	0/3/3/3
32	2MG	1a	1207	56,32	-	2/9/27/28	0/3/3/3
43	0TD	1l	92	43	-	2/7/12/14	-
32	2MG	2a	1207	32	-	0/9/27/28	0/3/3/3
32	UR3	2a	1498	32	-	0/7/25/26	0/2/2/2
32	M2G	2a	966	32	-	0/11/29/30	0/3/3/3
1	5MU	1A	1937	1	-	4/7/25/26	0/2/2/2
32	5MC	1a	967	32	-	1/7/25/26	0/2/2/2
32	4OC	2a	1402	32	-	5/9/29/30	0/2/2/2
32	PSU	1a	516	32	-	1/7/25/26	0/2/2/2
32	PSU	2a	516	32	-	1/7/25/26	0/2/2/2
1	5MC	2A	1942	1	-	0/7/25/26	0/2/2/2
32	MA6	2a	1519	32	-	4/11/29/30	0/3/3/3
32	MA6	1a	1519	32	-	4/11/29/30	0/3/3/3
1	OMC	2A	1920	1	-	0/9/27/28	0/2/2/2
1	OMU	2A	2552	56,1	-	0/9/27/28	0/2/2/2
1	2MA	2A	2503	56,1	-	3/7/25/26	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	5MC	1A	1964	1	-	0/7/25/26	0/2/2/2
1	5MU	2A	1915	1	-	2/7/25/26	0/2/2/2
1	PSU	1A	2617	1	-	0/7/25/26	0/2/2/2
32	UR3	1a	1498	32	-	1/7/25/26	0/2/2/2
1	OMG	1A	2263	53,56,1	-	1/9/27/28	0/3/3/3
53	PSU	2x	55	53	-	0/7/25/26	0/2/2/2
1	OMU	1A	2564	1	-	1/9/27/28	0/2/2/2
53	5MU	1x	54	53	-	2/7/25/26	0/2/2/2
1	OMG	2A	2251	53,56,1	-	0/9/27/28	0/3/3/3
1	PSU	2A	1917	1	-	0/7/25/26	0/2/2/2
32	4OC	1a	1402	32	-	2/9/29/30	0/2/2/2

All (194) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1A	2564	OMU	C5-C4	15.99	1.78	1.43
1	2A	2552	OMU	C5-C4	15.94	1.78	1.43
1	1A	2564	OMU	C4-N3	-15.53	1.12	1.38
1	2A	2552	OMU	C4-N3	-15.22	1.12	1.38
1	1A	2564	OMU	C6-C5	-10.27	1.11	1.35
1	2A	2552	OMU	C6-C5	-10.22	1.11	1.35
1	1A	2564	OMU	C3'-C2'	-9.12	1.33	1.53
1	2A	2552	OMU	C3'-C2'	-8.83	1.33	1.53
1	2A	2552	OMU	C6-N1	8.79	1.59	1.38
32	2a	527	G7M	C8-N7	8.63	1.47	1.33
1	1A	2564	OMU	C6-N1	8.46	1.58	1.38
32	1a	527	G7M	C8-N7	8.44	1.47	1.33
1	1A	2515	2MA	C4-N3	7.90	1.44	1.34
1	2A	2503	2MA	C4-N3	7.72	1.44	1.34
1	2A	2552	OMU	O4'-C1'	6.67	1.57	1.42
43	2l	92	0TD	CB-CA	-6.65	1.52	1.54
1	1A	2564	OMU	O4'-C1'	6.49	1.57	1.42
1	2A	2552	OMU	O4'-C4'	-6.30	1.31	1.45
1	1A	2564	OMU	O4'-C4'	-5.80	1.32	1.45
1	2A	1920	OMC	C4-N4	5.74	1.47	1.33
32	1a	1402	4OC	C4-N4	5.68	1.47	1.36
1	1A	1942	OMC	C4-N4	5.66	1.47	1.33
32	2a	1402	4OC	C4-N4	5.64	1.47	1.36
32	2a	966	M2G	C4-N3	5.55	1.47	1.34
32	1a	1207	2MG	C2-N3	5.42	1.42	1.32
43	1l	92	0TD	CB-SB	-5.41	1.76	1.82
1	1A	2564	OMU	C1'-N1	-5.41	1.32	1.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	2A	2503	2MA	C2-N3	5.32	1.43	1.34
32	2a	1207	2MG	C2-N3	5.29	1.42	1.32
32	2a	966	M2G	C2-N2	5.29	1.44	1.35
32	2a	966	M2G	C2-N3	5.26	1.45	1.32
32	1a	966	M2G	C4-N3	5.23	1.46	1.34
1	2A	2552	OMU	C1'-N1	-5.22	1.32	1.47
32	2a	1498	UR3	C6-C5	5.14	1.47	1.35
1	1A	2515	2MA	C2-N1	5.12	1.42	1.34
32	1a	1498	UR3	C6-C5	5.11	1.46	1.35
32	1a	966	M2G	C2-N2	5.10	1.44	1.35
32	1a	966	M2G	C2-N3	5.09	1.44	1.32
1	2A	2251	OMG	C4-N3	5.05	1.45	1.34
32	1a	1207	2MG	C2-N1	5.04	1.44	1.36
1	2A	2503	2MA	C2-N1	5.03	1.42	1.34
1	1A	2515	2MA	C2-N3	4.99	1.42	1.34
1	1A	2263	OMG	C4-N3	4.95	1.45	1.34
32	1a	527	G7M	C4-N3	4.94	1.45	1.34
32	1a	1498	UR3	C2-N1	4.92	1.45	1.38
32	2a	527	G7M	C4-N3	4.87	1.45	1.34
1	2A	1920	OMC	C6-C5	4.80	1.46	1.35
32	2a	1402	4OC	C6-C5	4.79	1.46	1.35
32	1a	527	G7M	C8-N9	4.79	1.48	1.35
32	2a	527	G7M	C8-N9	4.76	1.48	1.35
32	1a	527	G7M	C2-N3	4.72	1.44	1.33
1	1A	1942	OMC	C2-N3	4.69	1.45	1.36
1	1A	1937	5MU	C2-N1	4.68	1.45	1.38
32	1a	1402	4OC	C6-C5	4.67	1.45	1.35
32	2a	1207	2MG	C2-N1	4.66	1.44	1.36
32	1a	1402	4OC	C4-N3	4.66	1.40	1.32
32	1a	1402	4OC	C2-N3	4.62	1.45	1.36
1	2A	1920	OMC	C2-N3	4.60	1.45	1.36
32	2a	1498	UR3	C2-N1	4.59	1.44	1.38
32	1a	1207	2MG	C4-N3	4.56	1.44	1.34
1	1A	2263	OMG	C2-N3	4.55	1.44	1.33
32	2a	1207	2MG	C4-N3	4.53	1.44	1.34
32	1a	1207	2MG	C2-N2	4.51	1.42	1.33
1	1A	1942	OMC	C6-C5	4.50	1.45	1.35
32	2a	527	G7M	C2-N3	4.49	1.44	1.33
53	2x	55	PSU	C2-N1	4.49	1.42	1.36
32	2a	1402	4OC	C2-N3	4.46	1.45	1.36
1	2A	2251	OMG	C2-N3	4.42	1.43	1.33
32	2a	1207	2MG	C2-N2	4.39	1.42	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
53	1x	55	PSU	C2-N1	4.30	1.42	1.36
1	1A	2515	2MA	C6-N1	4.30	1.40	1.35
53	1x	8	4SU	C4-S4	-4.22	1.61	1.68
1	1A	2564	OMU	C3'-C4'	4.15	1.63	1.53
32	2a	516	PSU	C2-N1	4.14	1.42	1.36
1	2A	2552	OMU	C3'-C4'	4.12	1.63	1.53
43	2l	92	0TD	CB-SB	-4.11	1.78	1.82
1	2A	2503	2MA	C6-N1	4.11	1.40	1.35
32	2a	1402	4OC	C4-N3	4.10	1.39	1.32
43	1l	92	0TD	CB-CA	-4.06	1.53	1.54
32	1a	516	PSU	C2-N1	4.03	1.41	1.36
1	2A	1917	PSU	C2-N1	3.96	1.41	1.36
1	2A	1915	5MU	C2-N1	3.93	1.44	1.38
32	2a	1498	UR3	C2-N3	3.90	1.46	1.39
1	2A	1911	PSU	C2-N1	3.87	1.41	1.36
1	1A	1942	OMC	C2-N1	3.80	1.48	1.40
1	2A	1920	OMC	C2-N1	3.79	1.48	1.40
32	1a	1498	UR3	C2-N3	3.77	1.46	1.39
32	2a	1402	4OC	C5-C4	3.76	1.49	1.41
1	2A	2605	PSU	C2-N1	3.76	1.41	1.36
32	1a	1402	4OC	C5-C4	3.69	1.49	1.41
32	2a	1402	4OC	C2-N1	3.62	1.47	1.40
1	1A	1933	PSU	C2-N1	3.47	1.41	1.36
1	2A	2503	2MA	C5-C6	3.30	1.50	1.41
32	2a	1518	MA6	C6-N6	3.29	1.45	1.36
32	2a	527	G7M	C2-N2	3.27	1.41	1.34
32	1a	527	G7M	C2-N2	3.26	1.41	1.34
32	1a	1402	4OC	C2-N1	3.23	1.46	1.40
32	1a	966	M2G	C2-N1	3.16	1.43	1.36
1	1A	2515	2MA	C5-C6	3.15	1.49	1.41
53	2x	55	PSU	C4-N3	3.10	1.44	1.38
32	2a	966	M2G	C2-N1	3.08	1.43	1.36
32	1a	1400	5MC	C2-N1	3.06	1.46	1.40
53	2x	32	5MC	C2-N1	3.06	1.46	1.40
53	1x	54	5MU	C2-N1	3.03	1.43	1.38
32	1a	1518	MA6	C6-N6	3.03	1.45	1.36
32	2a	1402	4OC	O2-C2	-3.02	1.18	1.23
32	2a	1519	MA6	C6-N6	3.02	1.45	1.36
1	1A	1942	OMC	C4-N3	3.01	1.40	1.34
32	1a	1519	MA6	C6-N6	2.96	1.45	1.36
32	1a	527	G7M	C5-C6	2.94	1.51	1.43
32	1a	1402	4OC	O2-C2	-2.94	1.18	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1A	1939	PSU	C2-N1	2.94	1.40	1.36
53	2x	8	4SU	C2-N3	2.93	1.43	1.38
1	2A	2605	PSU	C4-N3	2.92	1.44	1.38
32	2a	1402	4OC	CM4-N4	-2.91	1.40	1.45
1	2A	1920	OMC	O2-C2	-2.90	1.18	1.23
32	2a	527	G7M	C5-C6	2.89	1.51	1.43
53	2x	8	4SU	C4-S4	-2.88	1.63	1.68
1	2A	1920	OMC	C4-N3	2.87	1.40	1.34
32	1a	1407	5MC	C2-N1	2.83	1.46	1.40
1	1A	1933	PSU	C4-N3	2.82	1.44	1.38
1	1A	1942	OMC	O2-C2	-2.77	1.18	1.23
1	2A	1920	OMC	C5-C4	2.77	1.49	1.42
32	2a	527	G7M	C2-N1	2.77	1.44	1.37
32	1a	967	5MC	C2-N1	2.76	1.45	1.40
32	1a	527	G7M	C2-N1	2.75	1.44	1.37
32	2a	516	PSU	O4'-C1'	-2.75	1.40	1.43
1	1A	2617	PSU	C2-N1	2.72	1.40	1.36
32	2a	1400	5MC	C2-N1	2.67	1.45	1.40
1	2A	2552	OMU	O2'-C2'	2.66	1.49	1.42
53	1x	55	PSU	C4-N3	2.63	1.43	1.38
32	1a	516	PSU	O4'-C1'	-2.60	1.40	1.43
53	2x	54	5MU	C2-N1	2.60	1.42	1.38
53	2x	55	PSU	C6-N1	2.60	1.40	1.36
1	2A	1915	5MU	C2-N3	2.59	1.42	1.38
32	2a	527	G7M	C5-N7	2.58	1.42	1.39
53	1x	55	PSU	C6-N1	2.55	1.40	1.36
32	1a	1402	4OC	CM4-N4	-2.52	1.41	1.45
1	1A	2515	2MA	C8-N7	2.52	1.36	1.31
53	1x	54	5MU	C2-N3	2.49	1.42	1.38
1	2A	2605	PSU	C6-N1	2.49	1.40	1.36
1	1A	1942	OMC	C5-C4	2.48	1.48	1.42
53	1x	8	4SU	C2-N3	2.44	1.42	1.38
1	2A	2503	2MA	C8-N7	2.44	1.36	1.31
1	1A	1964	5MC	C5-C4	-2.44	1.42	1.44
32	1a	527	G7M	C5-N7	2.43	1.42	1.39
1	1A	1939	PSU	C4-N3	2.41	1.43	1.38
1	1A	1937	5MU	C2-N3	2.40	1.42	1.38
1	1A	2564	OMU	O2'-C2'	2.39	1.48	1.42
32	2a	967	5MC	C2-N1	2.39	1.45	1.40
53	2x	54	5MU	C2-N3	2.33	1.42	1.38
1	2A	1911	PSU	C4-N3	2.32	1.43	1.38
1	1A	2515	2MA	C4-N9	-2.32	1.32	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1A	2263	OMG	C2-N2	2.32	1.39	1.34
32	1a	516	PSU	C6-N1	2.30	1.40	1.36
1	2A	1911	PSU	C6-N1	2.30	1.40	1.36
53	1x	32	5MC	C2-N1	2.29	1.44	1.40
32	2a	1207	2MG	CM2-N2	-2.28	1.41	1.45
1	2A	1942	5MC	C2-N1	2.28	1.44	1.40
1	1A	2617	PSU	C4-N3	2.27	1.43	1.38
53	1x	32	5MC	C6-C5	2.24	1.38	1.34
1	1A	1933	PSU	C6-N1	2.24	1.40	1.36
1	2A	1917	PSU	C6-N1	2.24	1.40	1.36
1	2A	1962	5MC	C2-N1	2.23	1.44	1.40
1	1A	2617	PSU	C6-N1	2.23	1.39	1.36
43	1l	92	0TD	CA-N	-2.22	1.41	1.47
32	1a	1518	MA6	C5-C4	-2.21	1.35	1.39
1	2A	1917	PSU	C4-N3	2.20	1.43	1.38
1	1A	1984	5MC	C5-C4	-2.17	1.42	1.44
1	2A	1939	5MU	C2-N3	2.16	1.41	1.38
1	1A	2515	2MA	C5-C4	-2.16	1.35	1.39
1	1A	1984	5MC	C2-N1	2.16	1.44	1.40
32	1a	1207	2MG	CM2-N2	-2.15	1.41	1.45
53	1x	32	5MC	C2-N3	2.13	1.40	1.36
1	1A	1939	PSU	C6-N1	2.13	1.39	1.36
43	2l	92	0TD	CA-N	-2.12	1.41	1.47
32	1a	966	M2G	C5-C6	2.11	1.52	1.44
32	1a	1518	MA6	C5-C6	-2.11	1.36	1.41
32	1a	967	5MC	C2-N3	2.10	1.40	1.36
32	2a	1407	5MC	C2-N1	2.09	1.44	1.40
1	2A	2503	2MA	C5-C4	-2.08	1.35	1.39
32	1a	1519	MA6	C5-C4	-2.08	1.35	1.39
1	1A	1961	5MU	C2-N3	2.08	1.41	1.38
32	2a	1407	5MC	C6-C5	2.07	1.38	1.34
32	1a	1207	2MG	C5-N7	-2.05	1.35	1.39
53	2x	32	5MC	C6-C5	2.05	1.38	1.34
1	1A	2263	OMG	C2-N1	2.05	1.42	1.37
32	2a	966	M2G	C5-C6	2.04	1.52	1.44
32	2a	967	5MC	C2-N3	2.03	1.40	1.36
32	2a	1404	5MC	C2-N1	2.03	1.44	1.40
32	2a	1519	MA6	C5-C4	-2.03	1.35	1.39
32	1a	1400	5MC	C2-N3	2.01	1.40	1.36
32	1a	1498	UR3	C3U-N3	-2.01	1.43	1.47
32	2a	1518	MA6	C5-C4	-2.01	1.35	1.39

All (310) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	2a	1518	MA6	N1-C6-N6	-17.74	95.24	116.86
32	1a	1519	MA6	N1-C6-N6	-17.09	96.03	116.86
32	2a	1519	MA6	N1-C6-N6	-16.90	96.26	116.86
32	1a	1518	MA6	N1-C6-N6	-16.20	97.12	116.86
32	2a	1518	MA6	C5-C6-N6	12.79	145.57	125.33
32	1a	1519	MA6	C5-C6-N6	12.25	144.73	125.33
32	2a	1519	MA6	C5-C6-N6	11.95	144.25	125.33
32	1a	1518	MA6	C5-C6-N6	11.65	143.77	125.33
1	2A	2503	2MA	C1'-N9-C8	-11.38	101.83	127.09
1	1A	2515	2MA	C1'-N9-C8	-10.60	103.56	127.09
1	2A	2503	2MA	C4-N9-C1'	9.00	147.69	126.63
1	1A	2515	2MA	C4-N9-C1'	8.27	145.97	126.63
1	2A	2552	OMU	C5-C4-N3	7.97	125.97	114.80
1	1A	2564	OMU	C5-C4-N3	7.78	125.71	114.80
32	2a	516	PSU	C6-C5-C4	7.25	123.06	118.17
32	1a	516	PSU	C6-C5-C4	6.71	122.70	118.17
1	1A	2564	OMU	C4-N3-C2	-6.70	118.30	126.61
32	2a	1207	2MG	C2-N3-C4	6.34	119.93	112.00
32	1a	1207	2MG	C2-N3-C4	6.30	119.88	112.00
1	2A	2552	OMU	C4-N3-C2	-6.14	118.99	126.61
1	2A	2605	PSU	C6-C5-C4	5.86	122.13	118.17
32	2a	1498	UR3	C4-N3-C2	-5.79	119.92	124.58
1	2A	2503	2MA	N9-C8-N7	-5.66	105.91	113.94
32	2a	1519	MA6	C5-C4-N3	-5.60	119.01	126.72
32	1a	1519	MA6	C5-C4-N3	-5.59	119.02	126.72
1	1A	2515	2MA	N9-C8-N7	-5.58	106.02	113.94
32	1a	1519	MA6	C4-C5-C6	5.48	121.58	115.91
53	2x	55	PSU	C6-C5-C4	5.48	121.87	118.17
32	2a	1518	MA6	N1-C2-N3	-5.48	120.29	128.58
1	2A	2251	OMG	C1'-N9-C8	-5.47	111.18	126.73
32	2a	1519	MA6	N1-C2-N3	-5.45	120.34	128.58
32	1a	1519	MA6	N1-C2-N3	-5.42	120.38	128.58
32	1a	1498	UR3	C4-N3-C2	-5.41	120.22	124.58
53	1x	55	PSU	C6-C5-C4	5.36	121.79	118.17
1	1A	2617	PSU	C6-C5-C4	5.33	121.77	118.17
32	1a	1518	MA6	N1-C2-N3	-5.28	120.59	128.58
32	2a	1519	MA6	C4-C5-C6	5.27	121.36	115.91
1	1A	2263	OMG	C1'-N9-C8	-5.27	111.77	126.73
32	1a	1518	MA6	C4-C5-C6	5.26	121.35	115.91
32	2a	1518	MA6	C5-C4-N3	-5.25	119.48	126.72
1	2A	1917	PSU	C6-C5-C4	5.17	121.66	118.17
32	1a	1518	MA6	C5-C4-N3	-5.16	119.62	126.72
32	2a	966	M2G	C5-C4-N3	-5.13	120.22	128.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	1a	1207	2MG	C5-C4-N3	-5.06	120.33	128.39
1	1A	2263	OMG	C5-C4-N3	-5.01	120.42	128.39
32	2a	1207	2MG	C5-C4-N3	-5.00	120.43	128.39
1	2A	2503	2MA	C5-C4-N3	-4.96	121.95	127.18
32	1a	966	M2G	C5-C4-N3	-4.95	120.52	128.39
1	2A	2251	OMG	C5-C4-N3	-4.88	120.63	128.39
32	2a	1518	MA6	C4-C5-C6	4.84	120.91	115.91
1	2A	1911	PSU	C6-C5-C4	4.81	121.42	118.17
1	1A	2564	OMU	N3-C2-N1	4.79	121.12	114.89
32	2a	1518	MA6	C4-N9-C1'	-4.65	115.77	126.63
1	1A	2263	OMG	C2-N3-C4	4.56	120.15	112.30
1	2A	2503	2MA	C4-N9-C8	4.51	110.48	105.74
1	1A	2515	2MA	C4-N9-C8	4.50	110.47	105.74
32	1a	1518	MA6	C4-N9-C1'	-4.44	116.26	126.63
32	2a	527	G7M	C2-N3-C4	4.42	119.92	112.30
32	1a	527	G7M	C2-N3-C4	4.34	119.78	112.30
1	1A	2515	2MA	C5-C4-N3	-4.32	122.63	127.18
43	2l	92	0TD	CSB-SB-CB	4.32	110.13	102.36
1	1A	1933	PSU	C6-C5-C4	4.27	121.06	118.17
1	2A	2251	OMG	C1'-N9-C4	4.23	138.98	126.49
32	1a	1518	MA6	N9-C8-N7	-4.19	107.99	113.94
1	1A	2263	OMG	C1'-N9-C4	4.19	138.85	126.49
43	1l	92	0TD	OD2-CG-CB	4.15	122.10	113.15
32	2a	1519	MA6	C4-N9-C1'	-4.13	116.97	126.63
32	1a	1519	MA6	N9-C8-N7	-4.12	108.09	113.94
43	1l	92	0TD	CSB-SB-CB	4.11	109.75	102.36
32	2a	1518	MA6	N9-C8-N7	-4.10	108.12	113.94
32	2a	1518	MA6	C1'-N9-C8	4.09	136.17	127.09
1	2A	2251	OMG	C2-N3-C4	4.06	119.30	112.30
32	1a	1519	MA6	C4-N9-C1'	-4.04	117.17	126.63
32	2a	1519	MA6	N3-C4-N9	4.03	134.02	127.17
32	2a	1519	MA6	N9-C8-N7	-4.02	108.23	113.94
32	2a	966	M2G	C2-N3-C4	4.00	119.90	112.51
32	1a	1207	2MG	C1'-N9-C4	-3.94	114.85	126.49
32	1a	1519	MA6	N3-C4-N9	3.93	133.85	127.17
32	1a	527	G7M	C5-C4-N3	-3.88	120.81	128.15
32	1a	1518	MA6	N3-C4-N9	3.86	133.73	127.17
1	1A	1939	PSU	C6-C5-C4	3.85	120.77	118.17
32	1a	966	M2G	C2-N3-C4	3.84	119.61	112.51
1	2A	2552	OMU	N3-C2-N1	3.78	119.82	114.89
32	1a	1207	2MG	N1-C2-N2	3.77	120.41	116.56
32	1a	1207	2MG	C2-N1-C6	-3.76	120.01	124.55

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	2a	1207	2MG	C1'-N9-C4	-3.76	115.38	126.49
32	2a	1400	5MC	C5-C4-N3	3.76	125.61	121.75
32	1a	1400	5MC	C5-C4-N3	3.73	125.58	121.75
1	1A	1964	5MC	C5-C4-N3	3.73	125.58	121.75
32	1a	1207	2MG	C1'-N9-C8	3.69	137.21	126.73
32	1a	527	G7M	C5-C6-N1	3.68	119.45	111.84
1	1A	1984	5MC	C5-C4-N3	3.67	125.51	121.75
53	2x	32	5MC	C5-C4-N3	3.66	125.51	121.75
32	2a	527	G7M	C5-C6-N1	3.65	119.39	111.84
32	2a	1498	UR3	C5-C4-N3	3.63	119.82	115.04
1	2A	2251	OMG	N9-C8-N7	-3.61	106.70	113.40
32	2a	527	G7M	C5-C4-N3	-3.58	121.39	128.15
32	1a	1518	MA6	C1'-N9-C8	3.56	134.99	127.09
32	2a	1207	2MG	C1'-N9-C8	3.53	136.76	126.73
32	2a	1207	2MG	N1-C2-N2	3.52	120.15	116.56
32	2a	967	5MC	C5-C4-N3	3.52	125.36	121.75
32	2a	516	PSU	N1-C2-N3	3.50	118.86	115.17
32	2a	1518	MA6	C2-N1-C6	3.50	120.38	111.83
1	2A	1962	5MC	C5-C4-N3	3.46	125.30	121.75
1	1A	2263	OMG	N9-C8-N7	-3.46	106.99	113.40
32	2a	1207	2MG	C2-N1-C6	-3.45	120.38	124.55
32	1a	967	5MC	C5-C4-N3	3.45	125.30	121.75
1	1A	2515	2MA	CM2-C2-N1	3.44	122.28	117.13
32	2a	1519	MA6	C1'-N9-C8	3.44	134.74	127.09
32	1a	1518	MA6	C2-N1-C6	3.43	120.22	111.83
32	1a	1519	MA6	C2-N1-C6	3.42	120.19	111.83
1	2A	2552	OMU	O4-C4-C5	-3.42	119.27	125.16
43	1l	92	0TD	CB-CA-N	-3.40	102.22	109.10
32	1a	516	PSU	N1-C2-N3	3.37	118.73	115.17
32	2a	1518	MA6	N3-C4-N9	3.37	132.89	127.17
1	1A	1961	5MU	C6-C5-C4	3.36	120.79	118.02
32	1a	1498	UR3	C5-C4-N3	3.36	119.47	115.04
32	2a	1519	MA6	C2-N1-C6	3.36	120.03	111.83
1	2A	1962	5MC	C5-C6-N1	-3.35	119.68	123.31
32	1a	1519	MA6	C1'-N9-C8	3.35	134.52	127.09
53	1x	54	5MU	C6-C5-C4	3.31	120.75	118.02
1	1A	2564	OMU	O4-C4-C5	-3.27	119.53	125.16
32	2a	1519	MA6	C2-N3-C4	3.26	119.79	111.83
1	2A	1915	5MU	C6-C5-C4	3.26	120.70	118.02
1	1A	1961	5MU	C4-N3-C2	-3.25	123.08	127.34
32	2a	1518	MA6	C2-N3-C4	3.25	119.76	111.83
1	2A	1939	5MU	C6-C5-C4	3.21	120.67	118.02

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	2a	1407	5MC	C5-C4-N3	3.21	125.05	121.75
1	1A	1964	5MC	C5-C6-N1	-3.20	119.84	123.31
1	1A	2263	OMG	C2-N1-C6	-3.20	119.32	125.11
32	2a	1400	5MC	C5-C6-N1	-3.19	119.85	123.31
1	2A	2251	OMG	N9-C4-N3	3.19	132.33	125.95
32	1a	1407	5MC	C5-C4-N3	3.19	125.02	121.75
1	1A	1984	5MC	C5-C6-N1	-3.18	119.86	123.31
32	1a	1519	MA6	C2-N3-C4	3.18	119.60	111.83
53	2x	32	5MC	C5-C6-N1	-3.17	119.87	123.31
1	2A	2251	OMG	C2-N1-C6	-3.17	119.36	125.11
1	2A	1942	5MC	C5-C4-N3	3.16	125.00	121.75
32	2a	966	M2G	N9-C4-N3	3.15	132.26	125.95
1	1A	1937	5MU	C4-N3-C2	-3.15	123.21	127.34
53	1x	32	5MC	C5-C6-N1	-3.13	119.91	123.31
1	2A	2503	2MA	N3-C4-N9	3.12	130.95	126.99
1	2A	2552	OMU	O4-C4-N3	-3.11	114.76	119.27
1	1A	2564	OMU	O4-C4-N3	-3.11	114.76	119.27
1	2A	1942	5MC	C5-C6-N1	-3.11	119.94	123.31
1	2A	2503	2MA	C5-N7-C8	3.10	108.33	103.45
1	1A	2515	2MA	N6-C6-N1	3.08	121.19	117.03
1	1A	2263	OMG	N9-C4-N3	3.08	132.11	125.95
32	2a	966	M2G	N9-C8-N7	-3.07	107.71	113.40
1	2A	1939	5MU	C4-N3-C2	-3.06	123.33	127.34
1	1A	1937	5MU	C6-C5-C4	3.05	120.54	118.02
1	2A	2552	OMU	C6-C5-C4	-3.04	115.64	119.53
32	2a	967	5MC	C5-C6-N1	-3.02	120.04	123.31
1	2A	1915	5MU	C4-N3-C2	-3.01	123.39	127.34
1	1A	2564	OMU	O2-C2-N1	-3.01	118.88	122.80
53	1x	32	5MC	C5-C4-N3	3.01	124.84	121.75
32	2a	1404	5MC	C5-C4-N3	3.01	124.84	121.75
1	2A	1962	5MC	C4-N3-C2	-2.99	116.65	120.81
32	1a	966	M2G	N9-C8-N7	-2.99	107.86	113.40
32	2a	1518	MA6	C5-N7-C8	2.98	108.14	103.45
32	1a	1518	MA6	C2-N3-C4	2.98	119.12	111.83
32	1a	1404	5MC	C5-C4-N3	2.98	124.81	121.75
1	1A	2515	2MA	N3-C2-N1	-2.98	120.51	125.77
32	2a	1407	5MC	C5-C6-N1	-2.98	120.08	123.31
1	1A	1933	PSU	O2-C2-N1	-2.97	119.72	122.79
32	1a	1207	2MG	N9-C8-N7	-2.95	107.92	113.40
53	2x	54	5MU	C6-C5-C4	2.94	120.44	118.02
53	2x	54	5MU	C4-N3-C2	-2.93	123.50	127.34
53	1x	8	4SU	C4-N3-C2	-2.92	124.51	127.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1A	1984	5MC	C4-N3-C2	-2.92	116.75	120.81
32	1a	1519	MA6	C5-N7-C8	2.92	108.04	103.45
1	1A	1939	PSU	O2-C2-N1	-2.92	119.78	122.79
43	2l	92	0TD	OD2-CG-CB	2.91	119.45	113.15
32	1a	1400	5MC	C5-C6-N1	-2.90	120.17	123.31
32	1a	1404	5MC	C5-C6-N1	-2.89	120.17	123.31
1	1A	1937	5MU	C1'-N1-C2	2.89	122.79	117.59
32	1a	527	G7M	O6-C6-C5	-2.88	121.57	128.01
32	2a	527	G7M	O6-C6-C5	-2.88	121.58	128.01
32	1a	1518	MA6	C4-N9-C8	2.87	108.75	105.74
1	1A	2515	2MA	C5-N7-C8	2.85	107.93	103.45
32	2a	1207	2MG	N9-C8-N7	-2.85	108.12	113.40
1	1A	1964	5MC	C4-N3-C2	-2.85	116.86	120.81
32	2a	1404	5MC	C5-C6-N1	-2.83	120.24	123.31
32	2a	1519	MA6	C5-N7-C8	2.83	107.89	103.45
32	2a	967	5MC	C4-N3-C2	-2.83	116.89	120.81
53	1x	32	5MC	C4-N3-C2	-2.82	116.89	120.81
32	1a	967	5MC	C5-C6-N1	-2.82	120.25	123.31
1	2A	2503	2MA	N3-C2-N1	-2.79	120.85	125.77
1	1A	2263	OMG	C5-C6-N1	2.78	120.32	113.25
32	1a	1207	2MG	N9-C4-N3	2.76	131.46	125.95
32	1a	966	M2G	N9-C4-N3	2.75	131.45	125.95
32	1a	1404	5MC	C4-N3-C2	-2.75	116.99	120.81
53	1x	54	5MU	C4-N3-C2	-2.74	123.75	127.34
1	2A	2503	2MA	N6-C6-N1	2.72	120.70	117.03
1	1A	2564	OMU	C6-C5-C4	-2.71	116.07	119.53
32	2a	1207	2MG	N9-C4-N3	2.71	131.37	125.95
32	2a	1400	5MC	C4-N3-C2	-2.70	117.06	120.81
32	2a	1402	4OC	O2-C2-N3	-2.70	118.08	122.33
1	2A	1942	5MC	C4-N3-C2	-2.70	117.06	120.81
1	2A	1911	PSU	O2-C2-N1	-2.69	120.01	122.79
32	2a	516	PSU	C6-N1-C2	-2.69	120.19	122.69
32	2a	1404	5MC	C4-N3-C2	-2.66	117.11	120.81
1	2A	1917	PSU	O2-C2-N1	-2.66	120.05	122.79
32	1a	1518	MA6	C5-N7-C8	2.65	107.62	103.45
1	2A	2552	OMU	O2-C2-N1	-2.65	119.35	122.80
32	2a	527	G7M	N9-C8-N7	-2.65	106.05	112.48
32	1a	1400	5MC	C4-N3-C2	-2.64	117.14	120.81
1	2A	2503	2MA	CM2-C2-N1	2.64	121.08	117.13
53	2x	32	5MC	C4-N3-C2	-2.61	117.18	120.81
32	2a	966	M2G	C5-C6-N1	2.61	119.90	113.25
53	2x	8	4SU	C6-C5-C4	2.60	122.21	119.95

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	2A	2251	OMG	C5-C6-N1	2.59	119.84	113.25
53	2x	55	PSU	O2-C2-N1	-2.59	120.12	122.79
53	2x	8	4SU	C4-N3-C2	-2.58	124.84	127.31
1	2A	2251	OMG	O6-C6-C5	-2.57	119.74	126.53
1	1A	1937	5MU	C1'-N1-C6	-2.56	116.93	121.15
32	2a	966	M2G	O6-C6-C5	-2.54	119.82	126.53
32	1a	967	5MC	C4-N3-C2	-2.54	117.29	120.81
32	1a	1498	UR3	C6-N1-C2	-2.53	119.73	121.80
1	1A	2617	PSU	O2-C2-N1	-2.53	120.18	122.79
43	1l	92	0TD	OD2-CG-OD1	-2.51	118.39	124.08
1	2A	2605	PSU	O2-C2-N1	-2.49	120.22	122.79
1	1A	2515	2MA	N3-C4-N9	2.49	130.15	126.99
53	1x	55	PSU	O2-C2-N1	-2.48	120.23	122.79
32	2a	1407	5MC	C4-N3-C2	-2.48	117.37	120.81
32	1a	966	M2G	C5-C6-N1	2.47	119.54	113.25
32	1a	516	PSU	C4-N3-C2	-2.45	122.99	126.37
1	1A	2263	OMG	O6-C6-C5	-2.45	120.06	126.53
32	1a	527	G7M	N9-C8-N7	-2.44	106.57	112.48
53	2x	32	5MC	N4-C4-N3	-2.43	114.10	118.51
32	1a	1519	MA6	C4-N9-C8	2.43	108.29	105.74
32	1a	1207	2MG	C5-C6-N1	2.42	119.41	113.25
1	1A	1939	PSU	O4-C4-N3	-2.42	115.57	120.11
32	1a	1407	5MC	C5-C6-N1	-2.40	120.70	123.31
32	2a	1519	MA6	C4-N9-C8	2.40	108.26	105.74
32	2a	516	PSU	C4-N3-C2	-2.39	123.08	126.37
32	1a	527	G7M	C2-N1-C6	-2.38	120.80	125.11
32	1a	1518	MA6	C6-C5-N7	-2.37	129.66	133.43
1	1A	1933	PSU	N1-C2-N3	2.36	117.66	115.17
32	2a	1207	2MG	C5-C6-N1	2.36	119.25	113.25
32	1a	966	M2G	O6-C6-C5	-2.35	120.34	126.53
1	2A	2251	OMG	C8-N7-C5	2.34	108.43	104.26
32	2a	967	5MC	N4-C4-N3	-2.34	114.28	118.51
1	1A	2564	OMU	C2'-C1'-N1	-2.33	109.81	114.24
1	2A	1920	OMC	O2-C2-N3	-2.32	118.67	122.33
32	1a	1407	5MC	N4-C4-N3	-2.32	114.31	118.51
32	1a	516	PSU	C6-N1-C2	-2.32	120.54	122.69
32	1a	1407	5MC	C4-N3-C2	-2.32	117.59	120.81
1	1A	2263	OMG	C8-N7-C5	2.32	108.39	104.26
1	2A	1911	PSU	O4-C4-N3	-2.31	115.77	120.11
1	2A	1911	PSU	N1-C2-N3	2.30	117.59	115.17
32	1a	1207	2MG	C8-N7-C5	2.30	108.35	104.26
1	2A	1917	PSU	N1-C2-N3	2.24	117.53	115.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	2A	1917	PSU	O4-C4-N3	-2.24	115.90	120.11
32	1a	1207	2MG	O3'-C3'-C2'	2.24	118.99	111.82
32	1a	1498	UR3	C1'-N1-C2	2.23	120.69	117.04
32	2a	527	G7M	C5-C4-N9	2.22	110.61	105.88
32	2a	516	PSU	O4'-C1'-C2'	2.22	108.22	105.15
32	2a	1518	MA6	C4-C5-N7	-2.21	108.05	110.58
53	1x	32	5MC	N4-C4-N3	-2.21	114.51	118.51
32	2a	1518	MA6	C4-N9-C8	2.20	108.05	105.74
32	2a	1498	UR3	C1'-N1-C2	2.20	120.65	117.04
53	2x	55	PSU	C4-N3-C2	-2.20	123.34	126.37
32	2a	1400	5MC	N4-C4-N3	-2.19	114.53	118.51
32	1a	1207	2MG	O6-C6-C5	-2.19	120.76	126.53
32	2a	1404	5MC	N4-C4-N3	-2.19	114.55	118.51
32	1a	516	PSU	O2-C2-N1	-2.18	120.54	122.79
32	2a	1407	5MC	N4-C4-N3	-2.18	114.57	118.51
1	1A	1933	PSU	O4-C4-N3	-2.18	116.02	120.11
32	1a	1519	MA6	C6-C5-N7	-2.18	129.96	133.43
53	2x	55	PSU	N1-C2-N3	2.17	117.46	115.17
32	1a	1404	5MC	N4-C4-N3	-2.17	114.57	118.51
32	2a	527	G7M	C2-N1-C6	-2.17	121.18	125.11
1	1A	1939	PSU	O4-C4-C5	2.16	129.37	124.01
32	2a	1519	MA6	C6-C5-N7	-2.15	130.00	133.43
32	2a	1207	2MG	C8-N7-C5	2.15	108.09	104.26
1	1A	1939	PSU	N1-C2-N3	2.15	117.43	115.17
32	2a	1498	UR3	C6-N1-C2	-2.14	120.05	121.80
1	1A	1942	OMC	O2-C2-N3	-2.14	118.96	122.33
1	2A	1911	PSU	O4-C4-C5	2.14	129.32	124.01
53	1x	55	PSU	C4-N3-C2	-2.14	123.42	126.37
1	1A	1964	5MC	N4-C4-N3	-2.14	114.64	118.51
32	1a	1207	2MG	CM2-N2-C2	-2.13	119.07	123.65
1	2A	1917	PSU	C4-N3-C2	-2.13	123.44	126.37
32	2a	1404	5MC	CM5-C5-C6	-2.12	119.98	122.85
32	2a	516	PSU	O4-C4-N3	-2.12	116.12	120.11
53	2x	55	PSU	O4-C4-N3	-2.12	116.13	120.11
32	1a	527	G7M	C5-C4-N9	2.11	110.39	105.88
32	2a	1207	2MG	N1-C2-N3	-2.11	120.12	123.68
32	2a	527	G7M	N1-C2-N3	-2.11	119.46	123.32
32	2a	527	G7M	N2-C2-N1	2.10	121.20	116.76
32	2a	966	M2G	C8-N7-C5	2.10	108.00	104.26
32	2a	516	PSU	O2-C2-N1	-2.10	120.63	122.79
1	2A	2503	2MA	C4-C5-N7	-2.09	108.19	110.58
32	2a	1207	2MG	O6-C6-C5	-2.09	121.03	126.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	1a	966	M2G	C8-N7-C5	2.08	107.97	104.26
1	2A	1962	5MC	N4-C4-N3	-2.08	114.74	118.51
1	2A	2605	PSU	C4-N3-C2	-2.08	123.50	126.37
1	2A	1942	5MC	N4-C4-N3	-2.07	114.76	118.51
1	1A	1933	PSU	C4-N3-C2	-2.06	123.53	126.37
1	1A	1984	5MC	N4-C4-N3	-2.06	114.78	118.51
1	2A	1915	5MU	C1'-N1-C2	2.06	121.29	117.59
32	1a	1207	2MG	N1-C2-N3	-2.05	120.22	123.68
1	2A	2605	PSU	N1-C2-N3	2.05	117.33	115.17
43	2l	92	0TD	OD2-CG-OD1	-2.04	119.45	124.08
1	2A	2251	OMG	C8-N9-C4	2.03	109.84	106.03
32	1a	967	5MC	N4-C4-N3	-2.03	114.83	118.51
1	1A	1933	PSU	O4-C4-C5	2.02	129.03	124.01
1	1A	1937	5MU	C5M-C5-C6	-2.01	120.13	122.85
1	1A	1961	5MU	C5-C6-N1	-2.00	121.14	123.31

There are no chirality outliers.

All (55) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	1A	1937	5MU	O4'-C1'-N1-C2
1	1A	1937	5MU	O4'-C1'-N1-C6
1	1A	1937	5MU	O4'-C4'-C5'-O5'
1	1A	2263	OMG	C1'-C2'-O2'-CM2
32	1a	1402	4OC	O4'-C4'-C5'-O5'
32	1a	1519	MA6	O4'-C4'-C5'-O5'
53	1x	54	5MU	O4'-C4'-C5'-O5'
1	2A	1915	5MU	O4'-C1'-N1-C2
1	2A	1915	5MU	O4'-C1'-N1-C6
1	2A	1962	5MC	O4'-C4'-C5'-O5'
32	2a	1402	4OC	O4'-C4'-C5'-O5'
32	2a	1402	4OC	C3'-C4'-C5'-O5'
32	2a	1519	MA6	O4'-C4'-C5'-O5'
32	1a	1402	4OC	C3'-C4'-C5'-O5'
53	1x	54	5MU	C3'-C4'-C5'-O5'
32	1a	1400	5MC	O4'-C4'-C5'-O5'
32	2a	527	G7M	C3'-C4'-C5'-O5'
1	2A	1962	5MC	C3'-C4'-C5'-O5'
32	2a	1519	MA6	C3'-C4'-C5'-O5'
1	1A	1937	5MU	C3'-C4'-C5'-O5'
32	1a	527	G7M	C3'-C4'-C5'-O5'
32	1a	1519	MA6	C3'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
32	2a	527	G7M	O4'-C4'-C5'-O5'
32	2a	1519	MA6	C5-C6-N6-C10
1	2A	2503	2MA	O4'-C4'-C5'-O5'
32	1a	1400	5MC	C3'-C4'-C5'-O5'
1	2A	2503	2MA	C3'-C4'-C5'-O5'
32	1a	1207	2MG	O4'-C4'-C5'-O5'
32	1a	527	G7M	O4'-C4'-C5'-O5'
32	1a	1207	2MG	C3'-C4'-C5'-O5'
43	1l	92	0TD	CG-CB-SB-CSB
43	2l	92	0TD	CG-CB-SB-CSB
1	1A	1942	OMC	C3'-C4'-C5'-O5'
1	1A	1942	OMC	O4'-C4'-C5'-O5'
43	2l	92	0TD	SB-CB-CG-OD1
1	1A	2515	2MA	O4'-C4'-C5'-O5'
32	2a	1402	4OC	C3'-C2'-O2'-CM2
32	1a	1519	MA6	C5-C6-N6-C9
32	1a	527	G7M	C4'-C5'-O5'-P
1	2A	2503	2MA	C4'-C5'-O5'-P
1	1A	2564	OMU	C3'-C2'-O2'-CM2
32	2a	1519	MA6	C4'-C5'-O5'-P
32	1a	516	PSU	O4'-C4'-C5'-O5'
32	2a	1400	5MC	O4'-C4'-C5'-O5'
43	1l	92	0TD	SB-CB-CG-OD2
32	1a	967	5MC	O4'-C4'-C5'-O5'
32	2a	516	PSU	O4'-C4'-C5'-O5'
32	2a	1402	4OC	C2'-C1'-N1-C6
32	1a	1498	UR3	O4'-C4'-C5'-O5'
1	1A	1939	PSU	O4'-C4'-C5'-O5'
1	1A	2515	2MA	C3'-C4'-C5'-O5'
32	2a	1402	4OC	C2'-C1'-N1-C2
32	1a	1519	MA6	C4'-C5'-O5'-P
1	1A	1942	OMC	C2'-C1'-N1-C2
32	1a	966	M2G	C3'-C4'-C5'-O5'

There are no ring outliers.

26 monomers are involved in 40 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
53	1x	8	4SU	1	0
32	2a	1518	MA6	2	0
32	1a	1518	MA6	1	0
53	2x	54	5MU	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	1A	2515	2MA	2	0
1	1A	1961	5MU	2	0
53	2x	8	4SU	1	0
43	2l	92	0TD	1	0
32	2a	1404	5MC	1	0
1	1A	1942	OMC	1	0
1	2A	1962	5MC	1	0
32	1a	1207	2MG	3	0
32	2a	1498	UR3	1	0
32	2a	1402	4OC	2	0
32	1a	516	PSU	3	0
32	2a	516	PSU	2	0
32	2a	1519	MA6	2	0
32	1a	1519	MA6	1	0
1	2A	2552	OMU	1	0
1	2A	2503	2MA	2	0
32	1a	1498	UR3	1	0
1	1A	2263	OMG	1	0
1	1A	2564	OMU	2	0
53	1x	54	5MU	3	0
1	2A	2251	OMG	1	0
32	1a	1402	4OC	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2322 ligands modelled in this entry, 2315 are monoatomic and 2 are unknown - leaving 5 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
61	SF4	1d	501	35	0,12,12	-	-	-		
61	SF4	2d	501	35	0,12,12	-	-	-		
59	ARG	1B	229	-	10,11,11	0.74	1 (10%)	9,13,13	1.00	1 (11%)
58	MPD	1a	1860	-	7,7,7	0.42	0	9,10,10	0.36	0
58	MPD	1A	3907	-	7,7,7	0.36	0	9,10,10	0.26	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
61	SF4	1d	501	35	-	-	0/6/5/5
61	SF4	2d	501	35	-	-	0/6/5/5
59	ARG	1B	229	-	-	2/11/11/11	-
58	MPD	1a	1860	-	-	4/5/5/5	-
58	MPD	1A	3907	-	-	1/5/5/5	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
59	1B	229	ARG	OXT-C	-2.12	1.23	1.30

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
59	1B	229	ARG	OXT-C-O	-2.91	117.49	124.08

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
58	1a	1860	MPD	C2-C3-C4-O4
58	1a	1860	MPD	C2-C3-C4-C5
59	1B	229	ARG	NE-CD-CG-CB
58	1A	3907	MPD	O2-C2-C3-C4
58	1a	1860	MPD	C1-C2-C3-C4
59	1B	229	ARG	CG-CD-NE-CZ

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Mol	Chain	Res	Type	Atoms
58	1a	1860	MPD	CM-C2-C3-C4

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
59	1B	229	ARG	1	0
58	1A	3907	MPD	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	1A	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	1A	1151:U	O3'	1152:G	P	3.02

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	2813/2915 (96%)	-0.28	97 (3%) 48 28	23, 42, 82, 95	0
1	2A	2858/2915 (98%)	-0.12	115 (4%) 42 23	40, 59, 86, 96	0
2	1B	120/120 (100%)	-0.41	0 100 100	38, 57, 63, 76	0
2	2B	120/120 (100%)	0.29	0 100 100	62, 75, 81, 82	0
3	1D	275/275 (100%)	0.09	1 (0%) 88 76	30, 44, 54, 67	0
3	2D	275/275 (100%)	0.23	5 (1%) 67 47	43, 55, 62, 69	0
4	1E	204/204 (100%)	0.04	1 (0%) 87 73	28, 47, 60, 69	0
4	2E	204/204 (100%)	0.20	4 (1%) 65 44	43, 59, 67, 75	0
5	1F	203/203 (100%)	0.07	0 100 100	26, 48, 66, 73	0
5	2F	203/203 (100%)	0.11	1 (0%) 87 73	44, 65, 72, 79	0
6	1G	181/181 (100%)	0.10	2 (1%) 78 59	55, 64, 72, 80	0
6	2G	181/181 (100%)	0.68	9 (4%) 34 18	71, 75, 79, 85	0
7	1H	174/174 (100%)	0.08	3 (1%) 69 48	43, 54, 62, 65	0
7	2H	173/174 (99%)	0.46	5 (2%) 53 32	66, 75, 79, 85	0
8	1I	147/147 (100%)	0.03	2 (1%) 73 53	51, 67, 74, 76	0
8	2I	146/147 (99%)	0.15	0 100 100	59, 75, 79, 82	0
9	1N	140/140 (100%)	0.06	0 100 100	35, 45, 61, 67	0
9	2N	140/140 (100%)	0.14	0 100 100	52, 63, 71, 78	0
10	1O	122/122 (100%)	0.12	2 (1%) 70 49	38, 47, 58, 62	0
10	2O	122/122 (100%)	0.11	0 100 100	50, 57, 64, 69	0
11	1P	149/149 (100%)	-0.03	1 (0%) 84 68	28, 50, 61, 73	0
11	2P	149/149 (100%)	0.29	4 (2%) 56 35	46, 67, 75, 78	0
12	1Q	141/141 (100%)	0.24	3 (2%) 63 42	36, 49, 56, 63	0
12	2Q	141/141 (100%)	0.24	2 (1%) 73 53	51, 64, 69, 75	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
13	1R	118/118 (100%)	0.15	2 (1%) 69 48	35, 42, 53, 65	0
13	2R	118/118 (100%)	0.17	1 (0%) 82 65	48, 56, 62, 69	0
14	1S	110/110 (100%)	0.00	0 100 100	45, 53, 60, 64	0
14	2S	110/110 (100%)	0.78	7 (6%) 25 14	65, 71, 74, 76	0
15	1T	131/131 (100%)	0.04	3 (2%) 61 39	42, 51, 67, 74	0
15	2T	131/131 (100%)	0.07	1 (0%) 82 65	55, 60, 70, 75	0
16	1U	116/116 (100%)	0.07	1 (0%) 81 63	30, 40, 52, 58	0
16	2U	116/116 (100%)	0.26	1 (0%) 81 63	50, 60, 69, 74	0
17	1V	101/101 (100%)	-0.21	0 100 100	27, 49, 59, 64	0
17	2V	101/101 (100%)	0.06	0 100 100	48, 67, 73, 76	0
18	1W	112/112 (100%)	-0.08	0 100 100	31, 38, 54, 71	0
18	2W	112/112 (100%)	0.15	0 100 100	46, 54, 64, 71	0
19	1X	95/95 (100%)	0.19	1 (1%) 78 59	34, 44, 60, 67	0
19	2X	95/95 (100%)	0.54	3 (3%) 50 30	53, 61, 68, 69	0
20	1Y	107/107 (100%)	0.19	1 (0%) 81 63	46, 53, 65, 68	0
20	2Y	107/107 (100%)	0.53	6 (5%) 30 16	62, 68, 73, 83	0
21	1Z	203/203 (100%)	0.49	15 (7%) 20 11	50, 61, 72, 81	0
21	2Z	201/203 (99%)	0.55	12 (5%) 27 15	66, 73, 79, 82	0
22	10	77/77 (100%)	0.25	2 (2%) 57 36	37, 45, 53, 57	0
22	20	77/77 (100%)	0.44	3 (3%) 43 24	57, 63, 68, 70	0
23	11	97/97 (100%)	0.18	2 (2%) 63 42	32, 48, 65, 71	0
23	21	97/97 (100%)	0.28	1 (1%) 79 61	47, 59, 70, 74	0
24	12	70/70 (100%)	0.18	3 (4%) 40 22	44, 52, 58, 71	0
24	22	70/70 (100%)	0.50	3 (4%) 40 22	61, 67, 72, 74	0
25	13	59/59 (100%)	0.10	0 100 100	36, 45, 62, 70	0
25	23	59/59 (100%)	0.04	0 100 100	57, 62, 69, 72	0
26	14	69/69 (100%)	0.31	1 (1%) 73 53	62, 73, 82, 84	0
26	24	69/69 (100%)	0.97	6 (8%) 16 9	75, 80, 84, 85	0
27	15	59/59 (100%)	-0.03	1 (1%) 69 48	28, 45, 57, 63	0
27	25	59/59 (100%)	0.06	1 (1%) 69 48	46, 57, 68, 73	0
28	16	53/53 (100%)	-0.21	0 100 100	45, 50, 58, 60	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
28	26	53/53 (100%)	0.10	1 (1%) 66 45	59, 63, 67, 72	0
29	17	48/48 (100%)	0.31	5 (10%) 11 6	30, 33, 52, 56	0
29	27	48/48 (100%)	0.33	3 (6%) 26 14	43, 48, 61, 69	0
30	18	64/64 (100%)	0.19	1 (1%) 70 49	35, 41, 46, 48	0
30	28	64/64 (100%)	0.54	1 (1%) 70 49	52, 57, 62, 64	0
31	19	37/37 (100%)	0.35	2 (5%) 31 17	40, 48, 58, 62	0
31	29	37/37 (100%)	0.87	3 (8%) 18 10	62, 66, 70, 71	0
32	1a	1488/1521 (97%)	0.16	30 (2%) 65 44	45, 72, 87, 97	0
32	2a	1492/1521 (98%)	0.20	46 (3%) 51 30	52, 73, 88, 95	0
33	1b	231/231 (100%)	0.45	4 (1%) 69 48	69, 75, 81, 84	0
33	2b	231/231 (100%)	0.60	8 (3%) 47 27	72, 77, 82, 84	0
34	1c	206/206 (100%)	0.53	7 (3%) 48 28	70, 76, 79, 81	0
34	2c	206/206 (100%)	0.72	9 (4%) 39 21	73, 78, 81, 84	0
35	1d	208/208 (100%)	0.60	9 (4%) 40 22	65, 74, 78, 81	0
35	2d	208/208 (100%)	0.45	3 (1%) 73 53	64, 70, 75, 78	0
36	1e	148/148 (100%)	0.19	2 (1%) 73 53	61, 68, 73, 82	0
36	2e	148/148 (100%)	0.33	3 (2%) 65 44	65, 71, 76, 83	0
37	1f	100/100 (100%)	0.27	2 (2%) 65 44	63, 70, 73, 76	0
37	2f	100/100 (100%)	0.40	1 (1%) 79 61	67, 71, 75, 77	0
38	1g	155/155 (100%)	0.43	9 (5%) 29 16	67, 72, 80, 85	0
38	2g	155/155 (100%)	0.56	6 (3%) 43 24	74, 77, 80, 86	0
39	1h	137/137 (100%)	0.35	3 (2%) 62 41	64, 68, 72, 76	0
39	2h	137/137 (100%)	0.39	4 (2%) 53 32	67, 71, 74, 75	0
40	1i	127/127 (100%)	1.01	18 (14%) 6 3	69, 78, 81, 83	0
40	2i	126/127 (99%)	1.54	38 (30%) 1 1	72, 80, 83, 85	0
41	1j	97/97 (100%)	1.13	13 (13%) 7 4	71, 78, 80, 83	0
41	2j	96/97 (98%)	1.47	27 (28%) 1 1	74, 80, 83, 85	0
42	1k	114/114 (100%)	0.14	1 (0%) 81 63	56, 68, 72, 74	0
42	2k	114/114 (100%)	0.24	3 (2%) 57 36	63, 72, 75, 79	0
43	1l	121/122 (99%)	0.47	7 (5%) 29 16	58, 66, 70, 74	0
43	2l	121/122 (99%)	0.38	6 (4%) 34 18	60, 65, 70, 74	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
44	1m	116/116 (100%)	0.54	5 (4%) 40 22	64, 74, 78, 80	0
44	2m	114/116 (98%)	1.08	15 (13%) 7 4	73, 79, 82, 82	0
45	1n	60/60 (100%)	1.05	8 (13%) 7 4	71, 74, 77, 79	0
45	2n	60/60 (100%)	1.36	15 (25%) 2 1	74, 78, 81, 82	0
46	1o	88/88 (100%)	0.25	1 (1%) 78 59	57, 66, 73, 76	0
46	2o	88/88 (100%)	0.35	0 100 100	63, 69, 74, 76	0
47	1p	82/82 (100%)	0.99	6 (7%) 21 11	67, 73, 77, 79	0
47	2p	82/82 (100%)	0.68	4 (4%) 35 18	63, 69, 74, 76	0
48	1q	99/99 (100%)	0.45	1 (1%) 79 61	62, 66, 72, 73	0
48	2q	99/99 (100%)	0.33	1 (1%) 79 61	63, 69, 73, 75	0
49	1r	68/68 (100%)	0.19	1 (1%) 72 52	64, 69, 75, 77	0
49	2r	68/68 (100%)	0.14	0 100 100	68, 71, 76, 77	0
50	1s	83/83 (100%)	0.86	7 (8%) 17 9	70, 76, 79, 81	0
50	2s	83/83 (100%)	1.20	12 (14%) 6 3	71, 80, 82, 83	0
51	1t	96/98 (97%)	0.76	13 (13%) 7 4	65, 70, 75, 78	0
51	2t	98/98 (100%)	0.62	5 (5%) 33 18	62, 68, 75, 75	0
52	1u	23/23 (100%)	1.75	11 (47%) 0 0	70, 73, 76, 77	0
52	2u	23/23 (100%)	1.86	9 (39%) 1 0	76, 77, 79, 80	0
53	1x	72/76 (94%)	-0.40	0 100 100	41, 66, 76, 80	0
53	2x	72/76 (94%)	-0.09	1 (1%) 73 53	56, 73, 81, 90	0
54	1y	12/19 (63%)	0.84	1 (8%) 17 9	37, 48, 57, 59	0
54	2y	12/19 (63%)	1.44	4 (33%) 1 0	52, 59, 62, 69	0
55	A	3/27 (11%)	0.70	0 100 100	70, 70, 71, 74	0
55	B	3/27 (11%)	0.59	0 100 100	64, 64, 65, 69	0
All	All	20701/21004 (98%)	0.18	729 (3%) 47 27	23, 65, 82, 97	0

All (729) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
21	1Z	200	GLY	10.5
22	10	8	GLY	8.3
21	1Z	203	GLU	8.2
21	1Z	197	ILE	8.1
21	1Z	193	GLU	7.9

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Mol	Chain	Res	Type	RSRZ
21	1Z	198	LYS	7.6
1	1A	2154	U	7.3
1	2A	2125	G	6.8
1	2A	2173	A	6.4
40	2i	126	SER	6.4
32	2a	1030(A)	G	6.3
23	21	2	SER	6.3
21	1Z	192	ALA	6.2
21	1Z	199	LYS	6.0
1	1A	2145	G	6.0
21	1Z	196	VAL	5.8
21	1Z	194	PRO	5.8
45	2n	2	ALA	5.7
1	2A	2147	G	5.7
1	2A	2162	G	5.6
21	2Z	196	VAL	5.6
1	2A	2174	C	5.3
32	2a	1030(B)	C	5.3
21	1Z	195	GLU	5.2
1	2A	2110	G	5.1
1	2A	2109	U	5.0
29	17	48	LYS	5.0
1	2A	2146	C	5.0
1	1A	2152	U	5.0
1	2A	2148	G	4.9
50	2s	2	PRO	4.8
21	1Z	202	GLU	4.8
23	11	2	SER	4.8
1	2A	2124	G	4.8
1	2A	1082	U	4.7
1	1A	2169	G	4.7
45	1n	2	ALA	4.7
1	1A	2183	C	4.7
32	1a	1286	A	4.7
1	1A	2193	A	4.7
32	2a	1036	G	4.6
1	1A	2816	G	4.6
21	2Z	195	GLU	4.6
1	1A	2139	A	4.5
1	2A	2144	U	4.4
1	2A	2127	G	4.4
40	1i	106	ALA	4.4

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Mol	Chain	Res	Type	RSRZ
20	1Y	1	MET	4.4
1	2A	2108	C	4.3
1	2A	2128	C	4.3
51	1t	18	GLN	4.3
50	1s	4	SER	4.3
32	2a	1034	G	4.3
1	2A	1085	A	4.3
1	2A	2169	A	4.3
1	2A	2133	G	4.2
1	2A	2134	A	4.2
1	2A	1067	A	4.2
1	1A	2175	G	4.2
52	2u	14	TRP	4.2
21	2Z	193	GLU	4.1
1	1A	2194	U	4.1
1	2A	1083	U	4.1
1	2A	2130	U	4.1
40	1i	126	SER	4.1
32	1a	1034	G	4.1
32	2a	1026	G	4.1
1	1A	2129	C	4.1
3	2D	153	ALA	4.1
52	2u	11	GLY	4.1
40	2i	7	THR	4.0
1	1A	2188	G	4.0
1	2A	1076	C	4.0
32	1a	1036	G	4.0
22	20	8	GLY	4.0
1	1A	2138	G	4.0
1	1A	2195	A	4.0
3	2D	38	LYS	4.0
1	2A	2897	U	3.9
7	1H	2	SER	3.9
1	2A	2176	A	3.9
32	2a	1027	C	3.9
40	2i	14	VAL	3.9
4	2E	163	GLU	3.9
21	2Z	191	VAL	3.8
1	2A	1536	C	3.8
1	2A	2159	G	3.8
34	2c	175	LEU	3.8
1	2A	2896	C	3.8

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Mol	Chain	Res	Type	RSRZ
51	2t	6	PRO	3.8
44	2m	7	VAL	3.8
1	2A	2118	U	3.8
40	2i	2	GLU	3.8
1	1A	2190	G	3.8
45	2n	18	VAL	3.7
40	1i	128	ARG	3.7
31	29	37	GLY	3.7
43	1l	28	LYS	3.7
1	1A	2149	G	3.7
1	1A	2187	G	3.7
1	2A	652(B)	A	3.7
1	1A	2173	G	3.6
1	2A	1046	A	3.6
1	2A	1084	A	3.6
1	1A	935	C	3.6
1	2A	2129	C	3.6
40	2i	15	ALA	3.6
1	2A	1026	U	3.6
1	1A	2165	C	3.6
1	2A	1064	C	3.6
24	22	1	MET	3.6
1	1A	2905	C	3.6
1	1A	1221	G	3.5
1	1A	1555	C	3.5
43	1l	89	ARG	3.5
1	2A	2126	A	3.5
54	2y	12	PRO	3.5
1	1A	2182	G	3.5
1	2A	2145	C	3.5
32	1a	1037	C	3.5
1	1A	2141	A	3.5
1	1A	2151	C	3.5
1	2A	1091	G	3.5
1	2A	1095	A	3.5
47	2p	82	GLN	3.5
37	1f	55	ASP	3.5
1	1A	2163	G	3.5
1	1A	2164	C	3.4
1	2A	2175	C	3.4
44	2m	102	ARG	3.4
32	2a	1286	A	3.4

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Mol	Chain	Res	Type	RSRZ
1	1A	1099	C	3.4
1	1A	2189	U	3.4
33	1b	214	ILE	3.4
1	1A	2142	G	3.4
50	2s	71	LEU	3.4
44	1m	102	ARG	3.4
34	1c	2	GLY	3.4
21	2Z	197	ILE	3.4
1	1A	2130	C	3.4
1	2A	2123	G	3.4
40	2i	74	ILE	3.4
1	1A	2815	C	3.3
1	2A	2172	U	3.3
1	2A	2151	G	3.3
1	2A	2154	G	3.3
1	2A	2150	U	3.3
1	2A	2179	C	3.3
51	1t	17	ARG	3.3
34	2c	3	ASN	3.3
50	2s	67	VAL	3.3
1	1A	2134	G	3.3
41	2j	75	ILE	3.3
52	2u	13	ILE	3.3
1	2A	2119	A	3.3
1	1A	2186	C	3.3
1	1A	2814	C	3.3
1	1A	639	G	3.3
1	1A	2128	G	3.3
1	1A	2137	G	3.3
32	1a	1035	A	3.3
52	1u	4	GLY	3.3
45	1n	18	VAL	3.2
50	2s	9	VAL	3.2
41	2j	6	ILE	3.2
1	1A	2181	G	3.2
1	1A	2180	A	3.2
40	2i	5	TYR	3.2
26	24	56	VAL	3.2
40	2i	105	ASP	3.2
41	2j	76	ASN	3.2
1	2A	2168	G	3.2
44	2m	87	TYR	3.2

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Mol	Chain	Res	Type	RSRZ
1	1A	2906	U	3.2
1	2A	1066	U	3.2
1	2A	2160	G	3.2
21	2Z	200	GLY	3.2
50	2s	84	GLY	3.2
34	1c	206	GLU	3.2
6	2G	20	ILE	3.2
50	1s	39	THR	3.2
32	1a	1001	A	3.1
32	1a	1030(B)	C	3.1
24	12	70	GLN	3.1
21	1Z	201	LYS	3.1
29	27	48	LYS	3.1
45	2n	20	ALA	3.1
1	1A	2166	U	3.1
32	2a	1035	A	3.1
1	2A	2143	C	3.1
32	2a	1030	C	3.1
45	1n	17	LYS	3.1
30	28	25	MET	3.1
50	2s	76	PRO	3.1
1	2A	2139	C	3.0
38	1g	7	ALA	3.0
41	2j	32	ALA	3.0
38	1g	156	TRP	3.0
1	2A	229	A	3.0
1	1A	2184	G	3.0
1	2A	1087	G	3.0
1	2A	2153	G	3.0
41	2j	58	ASP	3.0
52	1u	18	TYR	3.0
13	1R	45	ARG	3.0
34	2c	2	GLY	3.0
41	2j	44	VAL	3.0
1	2A	1104	C	3.0
34	2c	5	ILE	3.0
40	2i	63	ILE	3.0
39	1h	4	ASP	3.0
41	2j	72	VAL	3.0
1	1A	2156	A	3.0
1	1A	696	C	3.0
38	2g	38	LEU	2.9

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Mol	Chain	Res	Type	RSRZ
1	1A	2147	G	2.9
1	2A	2131	G	2.9
1	2A	2319	G	2.9
32	1a	344	A	2.9
1	1A	2196	C	2.9
32	1a	1029	C	2.9
32	2a	1116	C	2.9
21	2Z	199	LYS	2.9
11	2P	109	GLY	2.9
40	2i	117	HIS	2.9
32	1a	1028	C	2.9
1	1A	2131	U	2.9
1	1A	2144	U	2.9
50	2s	35	SER	2.9
47	1p	3	LYS	2.9
1	1A	2153	G	2.9
1	2A	2120	G	2.9
32	1a	1026	G	2.9
32	2a	1032	G	2.9
1	1A	2136	A	2.9
1	2A	2107	C	2.9
1	2A	2161	C	2.9
44	1m	87	TYR	2.9
8	1I	117	GLU	2.9
46	1o	6	GLU	2.9
32	2a	1117	G	2.9
36	1e	118	ILE	2.9
32	2a	1028	C	2.8
54	1y	12	PRO	2.8
40	2i	9	ARG	2.8
20	2Y	1	MET	2.8
41	1j	75	ILE	2.8
41	2j	65	LEU	2.8
40	2i	13	ALA	2.8
1	2A	2155	G	2.8
41	1j	55	LYS	2.8
26	24	9	LEU	2.8
41	1j	10	GLY	2.8
40	2i	125	TYR	2.8
32	1a	1000	U	2.8
1	2A	34	C	2.8
3	2D	28	GLU	2.8

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Mol	Chain	Res	Type	RSRZ
41	1j	98	ILE	2.8
47	2p	19	ILE	2.8
51	1t	103	GLY	2.8
52	2u	15	ARG	2.8
1	1A	2160	C	2.8
1	2A	888	C	2.8
1	2A	1079	C	2.8
1	2A	1089	G	2.8
1	2A	2157	G	2.8
33	2b	134	GLU	2.8
1	2A	2158	A	2.7
44	2m	74	VAL	2.7
54	2y	1	VAL	2.7
32	2a	1037	C	2.7
35	2d	71	SER	2.7
41	2j	59	SER	2.7
48	1q	7	THR	2.7
42	1k	42	TRP	2.7
1	2A	2152	G	2.7
32	1a	1002	G	2.7
40	2i	113	LYS	2.7
41	2j	62	HIS	2.7
35	1d	135	LEU	2.7
47	1p	17	TYR	2.7
21	2Z	192	ALA	2.7
38	1g	117	ALA	2.7
40	2i	108	VAL	2.7
1	2A	2121	G	2.7
20	2Y	38	ILE	2.7
1	2A	1069	A	2.7
1	2A	2892	A	2.7
53	2x	76	A	2.7
21	1Z	191	VAL	2.7
41	2j	56	HIS	2.7
1	2A	2138	C	2.7
12	2Q	104	PHE	2.7
21	2Z	198	LYS	2.7
21	2Z	201	LYS	2.7
41	2j	61	GLU	2.7
50	2s	73	GLU	2.7
51	2t	103	GLY	2.7
1	1A	2174	G	2.7

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Mol	Chain	Res	Type	RSRZ
1	2A	652(F)	G	2.7
40	2i	46	ALA	2.7
21	1Z	99	TYR	2.7
1	1A	2148	A	2.6
40	2i	123	PRO	2.6
35	2d	115	ARG	2.6
52	1u	15	ARG	2.6
1	1A	933	C	2.6
32	1a	1030	C	2.6
41	2j	100	THR	2.6
22	20	9	SER	2.6
39	1h	2	LEU	2.6
1	1A	2155	G	2.6
1	1A	12	U	2.6
3	2D	150	LYS	2.6
29	17	1	MET	2.6
33	2b	133	LYS	2.6
1	1A	2191	A	2.6
1	2A	1103	A	2.6
32	2a	975	A	2.6
45	1n	30	ALA	2.6
1	1A	34	C	2.6
43	2l	17	LYS	2.6
54	2y	9	ARG	2.6
50	1s	13	ASP	2.6
1	2A	2122	U	2.6
29	27	45	ALA	2.6
47	1p	69	THR	2.6
33	1b	201	ILE	2.6
26	14	59	PHE	2.6
40	2i	33	PHE	2.6
50	2s	74	PHE	2.6
1	2A	2111	C	2.6
1	2A	2142	C	2.6
1	2A	2178	C	2.6
36	1e	20	GLN	2.6
44	2m	100	GLY	2.6
52	1u	2	GLY	2.6
6	1G	35	GLU	2.6
33	1b	12	GLU	2.6
45	2n	44	LEU	2.6
38	1g	2	ALA	2.6

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Mol	Chain	Res	Type	RSRZ
1	2A	2167	U	2.6
40	2i	10	ARG	2.6
54	2y	11	ARG	2.6
32	2a	1001(A)	G	2.6
19	2X	46	ALA	2.6
35	1d	133	VAL	2.6
44	2m	88	ARG	2.6
43	2l	99	HIS	2.5
43	1l	5	PRO	2.5
1	1A	2146	G	2.5
1	2A	2802	G	2.5
32	2a	1030(C)	G	2.5
33	2b	7	VAL	2.5
41	2j	69	ASN	2.5
45	2n	15	LYS	2.5
51	1t	9	ASN	2.5
51	1t	65	LYS	2.5
52	2u	6	ARG	2.5
1	2A	2170	A	2.5
45	2n	7	ILE	2.5
1	1A	2185	C	2.5
1	2A	2803	C	2.5
40	1i	33	PHE	2.5
19	1X	92	LEU	2.5
51	1t	70	SER	2.5
35	1d	153	ARG	2.5
31	19	29	ASN	2.5
41	2j	63	PHE	2.5
32	2a	1190	G	2.5
7	2H	112	PRO	2.5
33	2b	72	GLY	2.5
52	1u	6	ARG	2.5
24	22	52	ASP	2.5
41	2j	41	PRO	2.5
48	2q	100	LYS	2.5
51	1t	10	LEU	2.5
1	2A	6	A	2.5
1	2A	2117	A	2.5
7	2H	113	VAL	2.5
34	2c	207	VAL	2.5
38	2g	9	VAL	2.5
1	2A	2112	G	2.5

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Mol	Chain	Res	Type	RSRZ
1	1A	697	C	2.5
41	2j	78	ASN	2.5
43	2l	32	PHE	2.5
40	1i	7	THR	2.5
29	17	47	ARG	2.5
43	1l	91	LYS	2.5
41	1j	72	VAL	2.5
40	2i	76	ALA	2.4
1	1A	218	A	2.4
20	2Y	5	MET	2.4
45	1n	16	PHE	2.4
6	2G	74	LYS	2.4
31	19	12	ASP	2.4
45	2n	17	LYS	2.4
52	2u	3	LYS	2.4
1	2A	1075	C	2.4
32	1a	1001(A)	G	2.4
32	1a	1030(A)	G	2.4
32	2a	1249	C	2.4
44	2m	81	LEU	2.4
49	1r	78	LEU	2.4
21	2Z	116	VAL	2.4
45	2n	59	ALA	2.4
50	1s	40	ILE	2.4
50	2s	31	ILE	2.4
33	2b	101	MET	2.4
37	2f	89	MET	2.4
40	2i	11	LYS	2.4
1	1A	2198	A	2.4
1	1A	2641	A	2.4
6	2G	31	VAL	2.4
40	1i	14	VAL	2.4
1	2A	2136	C	2.4
40	1i	13	ALA	2.4
1	1A	2126	G	2.4
1	2A	1044	G	2.4
29	27	22	MET	2.4
22	10	74	ARG	2.4
24	12	11	GLU	2.4
27	15	59	GLU	2.4
35	1d	122	ARG	2.4
40	2i	118	LYS	2.4

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Mol	Chain	Res	Type	RSRZ
41	2j	49	VAL	2.4
42	2k	36	ASP	2.4
35	1d	4	TYR	2.4
40	2i	6	GLY	2.4
15	1T	130	ALA	2.4
29	17	45	ALA	2.4
1	1A	2157	A	2.4
1	2A	887	A	2.4
1	2A	1073	A	2.4
44	2m	4	ILE	2.4
11	1P	68	GLN	2.4
10	1O	23	ARG	2.4
26	24	28	LYS	2.4
39	2h	30	ARG	2.4
1	2A	2132	U	2.4
32	1a	1533	C	2.4
1	2A	2894	G	2.4
32	2a	1031	G	2.4
41	1j	31	GLY	2.4
40	1i	15	ALA	2.4
45	1n	5	ALA	2.4
1	1A	700	A	2.4
1	2A	1088	A	2.4
32	2a	1363(A)	A	2.4
26	24	66	SER	2.4
6	1G	2	PRO	2.4
12	1Q	21	THR	2.3
32	1a	345	C	2.3
40	2i	64	THR	2.3
52	1u	16	GLY	2.3
14	2S	93	LYS	2.3
15	1T	126	ALA	2.3
28	26	54	ILE	2.3
40	2i	119	ALA	2.3
40	2i	127	LYS	2.3
41	1j	56	HIS	2.3
52	1u	21	TYR	2.3
4	2E	168	MET	2.3
1	1A	2132	G	2.3
32	2a	1310	G	2.3
51	2t	13	LEU	2.3
40	2i	109	VAL	2.3

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Mol	Chain	Res	Type	RSRZ
1	1A	2192	A	2.3
1	2A	2135	A	2.3
40	1i	70	LYS	2.3
41	2j	55	LYS	2.3
47	1p	5	ARG	2.3
6	2G	50	ALA	2.3
1	1A	1072	U	2.3
21	1Z	1	MET	2.3
1	1A	2168	C	2.3
19	2X	28	PHE	2.3
1	1A	2813	G	2.3
1	1A	2902	G	2.3
32	1a	1030(C)	G	2.3
32	2a	1124	G	2.3
12	1Q	85	LYS	2.3
43	1l	126	LYS	2.3
43	2l	23	LYS	2.3
33	2b	190	THR	2.3
40	2i	43	ALA	2.3
44	2m	105	THR	2.3
45	2n	60	SER	2.3
37	1f	48	LEU	2.3
32	2a	1183	A	2.3
1	1A	2140	U	2.3
32	2a	1148	U	2.3
45	2n	8	GLU	2.3
1	2A	2789	C	2.3
32	1a	1317	C	2.3
41	2j	34	VAL	2.3
41	1j	42	THR	2.3
1	1A	2170	G	2.3
1	1A	2806	G	2.3
1	2A	2116	G	2.3
22	20	45	PHE	2.3
32	2a	1042	G	2.3
14	2S	61	ASN	2.3
16	1U	117	GLN	2.3
1	1A	934	A	2.3
1	2A	1057	A	2.3
38	1g	4	ARG	2.3
40	2i	104	ARG	2.3
32	2a	1065	U	2.3

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Mol	Chain	Res	Type	RSRZ
52	1u	23	PRO	2.3
38	2g	7	ALA	2.3
1	1A	1098	C	2.3
1	2A	2137	C	2.3
32	2a	1114	C	2.3
6	2G	76	SER	2.3
41	1j	47	PHE	2.3
36	2e	20	GLN	2.3
43	2l	46	LYS	2.3
38	1g	118	VAL	2.3
1	1A	2171	G	2.2
1	2A	1533	G	2.2
45	1n	7	ILE	2.2
21	2Z	194	PRO	2.2
14	2S	54	LEU	2.2
32	2a	1531	A	2.2
34	1c	52	LEU	2.2
39	2h	112	LEU	2.2
44	2m	116	THR	2.2
47	1p	67	THR	2.2
36	2e	87	SER	2.2
41	2j	7	LYS	2.2
41	2j	57	LYS	2.2
45	1n	15	LYS	2.2
51	1t	29	LYS	2.2
32	1a	1027	C	2.2
34	1c	207	VAL	2.2
47	1p	82	GLN	2.2
8	1I	10	GLU	2.2
40	1i	35	GLU	2.2
33	1b	237	ALA	2.2
34	2c	7	PRO	2.2
44	2m	97	PRO	2.2
40	1i	40	LEU	2.2
51	2t	67	ALA	2.2
1	1A	10	G	2.2
1	1A	2179	G	2.2
1	2A	2149	G	2.2
40	1i	117	HIS	2.2
35	1d	168	ARG	2.2
40	2i	66	ARG	2.2
41	2j	5	ARG	2.2

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Mol	Chain	Res	Type	RSRZ
1	2A	1070	A	2.2
34	1c	130	VAL	2.2
1	1A	932	C	2.2
1	1A	2167	C	2.2
32	1a	163	C	2.2
32	2a	972	C	2.2
6	2G	53	LEU	2.2
20	2Y	66	PRO	2.2
39	2h	2	LEU	2.2
41	1j	71	LEU	2.2
40	1i	66	ARG	2.2
38	1g	9	VAL	2.2
44	2m	54	VAL	2.2
1	1A	554	A	2.2
1	1A	2177	G	2.2
1	2A	1096	A	2.2
32	1a	158	G	2.2
32	1a	1032	G	2.2
32	2a	1001	A	2.2
38	2g	16	LEU	2.2
45	2n	39	LEU	2.2
4	2E	204	ALA	2.2
31	29	21	GLY	2.2
33	2b	237	ALA	2.2
34	2c	129	ALA	2.2
47	2p	1	MET	2.2
35	1d	2	GLY	2.2
14	2S	59	LYS	2.2
39	1h	88	LYS	2.2
52	1u	9	ARG	2.2
52	2u	17	THR	2.2
26	24	67	TYR	2.2
40	2i	65	VAL	2.2
7	1H	139	GLN	2.2
40	2i	81	ILE	2.2
4	2E	195	LEU	2.2
3	1D	153	ALA	2.2
6	2G	46	ALA	2.2
15	1T	131	ALA	2.2
34	1c	169	ALA	2.2
36	2e	86	ALA	2.2
39	2h	99	GLU	2.2

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Mol	Chain	Res	Type	RSRZ
40	1i	127	LYS	2.2
1	1A	9	U	2.2
1	2A	1065	U	2.2
11	2P	65	ARG	2.2
38	1g	5	ARG	2.2
40	1i	75	ASP	2.2
1	1A	6	A	2.2
32	2a	1250	A	2.2
1	2A	2165	G	2.2
32	1a	1031	G	2.2
32	2a	1202	G	2.2
32	2a	1353	G	2.2
43	1l	99	HIS	2.2
40	1i	41	VAL	2.1
41	2j	42	THR	2.1
42	2k	109	VAL	2.1
43	1l	18	VAL	2.1
43	2l	64	TYR	2.1
1	1A	936	C	2.1
1	2A	1092	C	2.1
32	2a	1113	C	2.1
10	1O	91	LEU	2.1
26	24	26	SER	2.1
6	2G	35	GLU	2.1
35	2d	73	ARG	2.1
50	1s	84	GLY	2.1
44	2m	60	VAL	2.1
50	2s	77	THR	2.1
52	1u	17	THR	2.1
34	2c	178	LEU	2.1
38	1g	35	LYS	2.1
45	2n	58	LYS	2.1
15	2T	94	ALA	2.1
24	12	69	ARG	2.1
34	2c	163	ALA	2.1
45	2n	3	ARG	2.1
51	1t	69	GLY	2.1
52	2u	2	GLY	2.1
1	1A	2197	C	2.1
1	1A	2807	C	2.1
4	1E	89	ASP	2.1
45	2n	25	VAL	2.1

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Mol	Chain	Res	Type	RSRZ
32	1a	1257	U	2.1
32	2a	1364	U	2.1
40	1i	11	LYS	2.1
40	2i	78	LYS	2.1
40	2i	103	THR	2.1
51	1t	62	LEU	2.1
7	2H	102	ALA	2.1
50	1s	56	GLN	2.1
1	2A	2320	A	2.1
1	2A	2805	G	2.1
14	2S	28	VAL	2.1
32	2a	1002	G	2.1
32	2a	1363	C	2.1
12	2Q	22	LYS	2.1
51	2t	7	LYS	2.1
34	1c	5	ILE	2.1
40	2i	102	LEU	2.1
41	1j	8	LEU	2.1
41	1j	74	ILE	2.1
30	18	46	ARG	2.1
51	1t	79	ARG	2.1
41	2j	27	ALA	2.1
44	2m	107	ALA	2.1
1	1A	2172	U	2.1
11	2P	38	GLN	2.1
32	1a	202	U	2.1
35	1d	167	GLY	2.1
40	2i	68	GLY	2.1
24	22	5	GLU	2.1
40	2i	49	PRO	2.1
51	1t	11	SER	2.1
31	29	16	VAL	2.1
44	1m	117	VAL	2.1
1	2A	2171	A	2.1
32	1a	1041	A	2.1
51	1t	14	LYS	2.1
6	2G	34	LEU	2.1
7	2H	111	HIS	2.1
35	1d	3	ARG	2.1
40	2i	77	ILE	2.1
52	2u	5	ASP	2.1
50	2s	79	THR	2.1

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Mol	Chain	Res	Type	RSRZ
1	1A	155	C	2.1
32	2a	1029	C	2.1
32	2a	1354	C	2.1
1	1A	11	G	2.1
1	2A	1093	G	2.1
1	2A	2141	G	2.1
1	2A	2166	G	2.1
32	2a	1224	G	2.1
44	1m	100	GLY	2.1
44	1m	101	GLN	2.1
7	1H	58	GLU	2.1
1	1A	2135	U	2.0
20	2Y	34	LYS	2.0
3	2D	52	ARG	2.0
19	2X	92	LEU	2.0
29	17	41	ARG	2.0
41	2j	60	ARG	2.0
42	2k	126	ARG	2.0
5	2F	75	HIS	2.0
13	2R	69	ASP	2.0
45	2n	5	ALA	2.0
7	2H	82	GLY	2.0
11	2P	68	GLN	2.0
33	2b	70	PHE	2.0
41	2j	64	GLU	2.0
1	2A	2177	C	2.0
27	25	60	VAL	2.0
32	1a	218	C	2.0
32	1a	1038	C	2.0
32	2a	1149	C	2.0
32	2a	1260	C	2.0
1	2A	2156	G	2.0
23	11	95	LEU	2.0
52	1u	24	ARG	2.0
14	2S	5	THR	2.0
47	2p	69	THR	2.0
12	1Q	33	GLY	2.0
14	2S	62	LYS	2.0
16	2U	51	LYS	2.0
44	2m	113	PRO	2.0
1	2A	1086	A	2.0
32	2a	978	A	2.0

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Mol	Chain	Res	Type	RSRZ
13	1R	68	ARG	2.0
20	2Y	37	VAL	2.0
38	2g	80	VAL	2.0
40	1i	16	ARG	2.0
50	1s	29	ARG	2.0
38	2g	12	LEU	2.0
41	1j	40	LEU	2.0
1	1A	2150	C	2.0
32	2a	1277	C	2.0
32	2a	1533	C	2.0

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

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
53	PSU	2x	55	20/21	0.65	0.13	74,74,76,76	0
32	PSU	2a	516	20/21	0.79	0.12	73,74,78,78	0
32	PSU	1a	516	20/21	0.80	0.12	69,72,73,73	0
1	5MU	1A	1937	21/22	0.82	0.12	69,72,80,81	0
1	5MU	2A	1915	21/22	0.85	0.10	78,80,84,87	0
32	G7M	2a	527	24/25	0.87	0.13	69,70,71,72	0
53	5MU	2x	54	21/22	0.87	0.10	73,74,76,77	0
53	PSU	1x	55	20/21	0.87	0.09	66,67,69,69	0
43	0TD	1l	92	10/11	0.88	0.13	66,66,67,69	0
53	4SU	2x	8	20/21	0.88	0.09	72,75,76,77	0
53	5MC	1x	32	21/22	0.89	0.12	65,66,69,69	0
53	5MC	2x	32	21/22	0.89	0.11	70,71,72,73	0
53	5MU	1x	54	21/22	0.89	0.09	67,69,72,75	0
1	PSU	1A	1939	20/21	0.89	0.09	62,65,68,69	0
32	4OC	2a	1402	22/23	0.90	0.10	64,66,67,69	0
43	0TD	2l	92	10/11	0.90	0.12	65,65,66,67	0
32	2MG	1a	1207	24/25	0.90	0.09	72,75,78,79	0
53	4SU	1x	8	20/21	0.90	0.09	66,68,68,69	0
32	5MC	2a	967	21/22	0.90	0.13	70,71,74,77	0
32	2MG	2a	1207	24/25	0.90	0.09	75,77,78,79	0
1	PSU	2A	1917	20/21	0.91	0.09	67,70,73,74	0
1	PSU	1A	1933	20/21	0.92	0.09	58,61,63,64	0
32	M2G	2a	966	25/26	0.92	0.11	68,70,72,73	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
32	M2G	1a	966	25/26	0.92	0.12	66,67,69,70	0
1	2MA	2A	2503	23/24	0.92	0.14	41,43,46,48	0
1	PSU	2A	1911	20/21	0.92	0.08	67,68,69,69	0
32	G7M	1a	527	24/25	0.93	0.11	66,67,68,68	0
32	5MC	1a	1407	21/22	0.93	0.11	52,56,59,60	0
32	5MC	2a	1407	21/22	0.93	0.10	58,63,64,65	0
32	5MC	1a	967	21/22	0.93	0.11	67,68,69,70	0
32	5MC	1a	1404	21/22	0.94	0.10	57,59,61,61	0
32	5MC	2a	1400	21/22	0.94	0.09	67,69,71,71	0
1	OMC	1A	1942	21/22	0.94	0.12	54,57,58,59	0
32	5MC	1a	1400	21/22	0.94	0.09	62,64,65,65	0
32	UR3	2a	1498	21/22	0.94	0.09	60,61,63,64	0
32	4OC	1a	1402	22/23	0.95	0.09	60,61,62,62	0
32	5MC	2a	1404	21/22	0.95	0.08	59,60,62,62	0
1	OMC	2A	1920	21/22	0.95	0.08	62,64,66,66	0
1	5MC	1A	1964	21/22	0.95	0.09	40,43,44,45	0
32	MA6	2a	1518	24/25	0.95	0.10	60,61,62,62	0
1	OMU	1A	2564	21/22	0.96	0.09	35,37,38,39	0
1	5MU	1A	1961	21/22	0.96	0.10	37,39,40,40	0
32	UR3	1a	1498	21/22	0.96	0.09	56,57,60,61	0
32	MA6	2a	1519	24/25	0.96	0.09	58,59,60,60	0
32	MA6	1a	1518	24/25	0.96	0.10	53,54,56,57	0
1	5MC	2A	1942	21/22	0.96	0.06	55,56,57,57	0
1	OMG	2A	2251	24/25	0.96	0.09	45,46,50,51	0
32	MA6	1a	1519	24/25	0.96	0.10	51,55,55,56	0
1	PSU	2A	2605	20/21	0.96	0.09	42,45,45,45	0
1	5MC	1A	1984	21/22	0.97	0.09	42,43,46,49	0
1	PSU	1A	2617	20/21	0.97	0.11	36,37,38,39	0
1	OMU	2A	2552	21/22	0.97	0.08	45,46,48,48	0
1	OMG	1A	2263	24/25	0.97	0.08	31,33,36,36	0
1	5MU	2A	1939	21/22	0.97	0.08	46,49,50,50	0
1	2MA	1A	2515	23/24	0.97	0.09	24,26,28,30	0
1	5MC	2A	1962	21/22	0.97	0.10	53,54,57,58	0

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
56	MG	1a	1765	1/1	0.32	0.27	80,80,80,80	0
56	MG	2A	3108	1/1	0.40	0.19	72,72,72,72	0
56	MG	1A	3658	1/1	0.45	0.21	50,50,50,50	0
56	MG	2a	1666	1/1	0.45	0.25	84,84,84,84	0
56	MG	1a	1764	1/1	0.46	0.17	70,70,70,70	0
56	MG	1a	1827	1/1	0.46	0.29	77,77,77,77	0
56	MG	2A	3292	1/1	0.51	0.19	60,60,60,60	0
56	MG	2a	1639	1/1	0.52	0.47	68,68,68,68	0
56	MG	2a	1684	1/1	0.52	0.26	66,66,66,66	0
56	MG	2x	105	1/1	0.52	0.25	75,75,75,75	0
56	MG	2A	3600	1/1	0.53	0.13	80,80,80,80	0
56	MG	1a	1843	1/1	0.53	0.29	62,62,62,62	0
56	MG	2A	3078	1/1	0.53	0.15	67,67,67,67	0
56	MG	1a	1754	1/1	0.53	0.36	68,68,68,68	0
56	MG	1a	1667	1/1	0.53	0.49	83,83,83,83	0
56	MG	2A	3428	1/1	0.54	0.21	57,57,57,57	0
56	MG	1H	8001	1/1	0.56	0.33	61,61,61,61	0
56	MG	1B	215	1/1	0.57	0.18	71,71,71,71	0
56	MG	1A	3538	1/1	0.57	0.16	56,56,56,56	0
56	MG	1a	1641	1/1	0.57	0.20	75,75,75,75	0
56	MG	2A	3650	1/1	0.58	0.13	70,70,70,70	0
56	MG	2a	1668	1/1	0.58	0.19	60,60,60,60	0
56	MG	1a	1678	1/1	0.59	0.28	74,74,74,74	0
56	MG	1A	3584	1/1	0.59	0.29	61,61,61,61	0
56	MG	2A	3124	1/1	0.59	0.32	63,63,63,63	0
56	MG	1A	3583	1/1	0.59	0.09	65,65,65,65	0
56	MG	2A	3220	1/1	0.60	0.36	51,51,51,51	0
56	MG	2j	8001	1/1	0.61	0.13	79,79,79,79	0
56	MG	1a	1795	1/1	0.61	0.26	76,76,76,76	0
56	MG	2a	1715	1/1	0.62	0.13	75,75,75,75	0
56	MG	1A	3277	1/1	0.62	0.08	70,70,70,70	0
56	MG	2A	3249	1/1	0.62	0.17	76,76,76,76	0
56	MG	2a	1606	1/1	0.63	0.44	59,59,59,59	0
56	MG	2a	1608	1/1	0.63	0.70	69,69,69,69	0
56	MG	1a	1713	1/1	0.63	0.47	72,72,72,72	0
56	MG	1B	209	1/1	0.64	0.28	61,61,61,61	0
56	MG	2a	1641	1/1	0.64	0.26	76,76,76,76	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2a	1659	1/1	0.64	0.28	77,77,77,77	0
56	MG	1A	3258	1/1	0.64	0.19	71,71,71,71	0
56	MG	1x	111	1/1	0.64	0.35	72,72,72,72	0
56	MG	1a	1657	1/1	0.64	0.28	71,71,71,71	0
56	MG	2a	1701	1/1	0.64	0.39	61,61,61,61	0
56	MG	1a	1767	1/1	0.64	0.14	72,72,72,72	0
56	MG	1a	1732	1/1	0.64	0.65	74,74,74,74	0
56	MG	1a	1803	1/1	0.64	0.33	63,63,63,63	0
56	MG	1a	1659	1/1	0.65	0.37	64,64,64,64	0
56	MG	1e	202	1/1	0.65	0.26	64,64,64,64	0
56	MG	1A	3545	1/1	0.65	0.11	54,54,54,54	0
56	MG	1A	3607	1/1	0.65	0.15	45,45,45,45	0
56	MG	2A	3171	1/1	0.66	0.24	69,69,69,69	0
56	MG	1A	3873	1/1	0.66	0.17	55,55,55,55	0
56	MG	2a	1671	1/1	0.66	0.38	71,71,71,71	0
56	MG	2A	3099	1/1	0.66	0.31	57,57,57,57	0
56	MG	1a	1819	1/1	0.66	0.19	69,69,69,69	0
56	MG	2a	1702	1/1	0.66	0.13	62,62,62,62	0
56	MG	2A	3349	1/1	0.66	0.14	55,55,55,55	0
56	MG	1A	3598	1/1	0.66	0.14	55,55,55,55	0
56	MG	2n	101	1/1	0.66	0.23	77,77,77,77	0
56	MG	2A	3452	1/1	0.66	0.10	66,66,66,66	0
56	MG	2B	3002	1/1	0.67	0.18	72,72,72,72	0
56	MG	2a	1646	1/1	0.67	0.33	66,66,66,66	0
56	MG	2a	1649	1/1	0.67	0.25	68,68,68,68	0
56	MG	2A	3322	1/1	0.67	0.19	71,71,71,71	0
56	MG	2a	1754	1/1	0.67	0.11	69,69,69,69	0
56	MG	1A	3203	1/1	0.67	0.17	65,65,65,65	0
56	MG	2a	1638	1/1	0.67	0.21	71,71,71,71	0
56	MG	2A	3158	1/1	0.67	0.17	78,78,78,78	0
56	MG	1a	1685	1/1	0.68	0.35	67,67,67,67	0
56	MG	1a	1737	1/1	0.68	0.15	74,74,74,74	0
56	MG	2G	201	1/1	0.68	0.12	72,72,72,72	0
56	MG	2a	1714	1/1	0.68	0.26	62,62,62,62	0
56	MG	1A	3613	1/1	0.68	0.24	68,68,68,68	0
56	MG	2A	3121	1/1	0.68	0.26	68,68,68,68	0
56	MG	2a	1756	1/1	0.68	0.21	73,73,73,73	0
56	MG	2a	1766	1/1	0.68	0.17	70,70,70,70	0
56	MG	2a	1618	1/1	0.68	0.20	80,80,80,80	0
56	MG	2a	1635	1/1	0.68	0.26	73,73,73,73	0
56	MG	1a	1823	1/1	0.68	0.16	54,54,54,54	0
56	MG	2A	3183	1/1	0.69	0.36	54,54,54,54	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3116	1/1	0.69	0.13	40,40,40,40	0
56	MG	2a	1643	1/1	0.69	0.15	67,67,67,67	0
56	MG	1A	3914	1/1	0.69	0.17	57,57,57,57	0
56	MG	1a	1804	1/1	0.69	0.15	67,67,67,67	0
56	MG	1a	1604	1/1	0.69	0.29	72,72,72,72	0
56	MG	2A	3157	1/1	0.69	0.22	47,47,47,47	0
56	MG	2A	3022	1/1	0.69	0.26	59,59,59,59	0
56	MG	1A	3612	1/1	0.69	0.13	65,65,65,65	0
56	MG	2A	3466	1/1	0.69	0.17	57,57,57,57	0
56	MG	2A	3206	1/1	0.70	0.17	57,57,57,57	0
56	MG	2a	1703	1/1	0.70	0.33	77,77,77,77	0
56	MG	1a	1766	1/1	0.70	0.27	72,72,72,72	0
56	MG	1a	1682	1/1	0.70	0.10	55,55,55,55	0
56	MG	2a	1720	1/1	0.70	0.20	57,57,57,57	0
56	MG	2A	3289	1/1	0.70	0.14	55,55,55,55	0
56	MG	1A	3340	1/1	0.70	0.22	53,53,53,53	0
56	MG	1a	1862	1/1	0.70	0.28	70,70,70,70	0
56	MG	2a	1675	1/1	0.70	0.47	69,69,69,69	0
56	MG	2B	3013	1/1	0.70	0.10	72,72,72,72	0
56	MG	2A	3191	1/1	0.70	0.19	50,50,50,50	0
56	MG	1a	1674	1/1	0.71	0.23	74,74,74,74	0
56	MG	2a	1677	1/1	0.71	0.27	76,76,76,76	0
56	MG	2A	3051	1/1	0.71	0.28	49,49,49,49	0
56	MG	1A	3488	1/1	0.71	0.16	46,46,46,46	0
56	MG	2a	1636	1/1	0.71	0.17	81,81,81,81	0
56	MG	2A	3431	1/1	0.71	0.17	61,61,61,61	0
56	MG	2A	3187	1/1	0.71	0.25	57,57,57,57	0
56	MG	1A	3392	1/1	0.71	0.26	57,57,57,57	0
56	MG	2A	3482	1/1	0.71	0.17	74,74,74,74	0
56	MG	1B	216	1/1	0.71	0.13	49,49,49,49	0
56	MG	1d	502	1/1	0.71	0.15	68,68,68,68	0
56	MG	2A	3226	1/1	0.71	0.30	56,56,56,56	0
56	MG	2A	3123	1/1	0.71	0.23	69,69,69,69	0
56	MG	1a	1693	1/1	0.71	0.15	75,75,75,75	0
56	MG	1a	1711	1/1	0.71	0.15	77,77,77,77	0
56	MG	1a	1849	1/1	0.72	0.20	62,62,62,62	0
56	MG	2a	1693	1/1	0.72	0.36	63,63,63,63	0
56	MG	2A	3258	1/1	0.72	0.20	58,58,58,58	0
56	MG	2A	3264	1/1	0.72	0.12	49,49,49,49	0
56	MG	2A	3272	1/1	0.72	0.18	54,54,54,54	0
56	MG	2A	3126	1/1	0.72	0.25	57,57,57,57	0
56	MG	1A	3275	1/1	0.72	0.20	70,70,70,70	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2A	3299	1/1	0.72	0.24	66,66,66,66	0
56	MG	1a	1706	1/1	0.72	0.34	66,66,66,66	0
56	MG	1A	3905	1/1	0.72	0.20	54,54,54,54	0
56	MG	2A	3368	1/1	0.72	0.18	55,55,55,55	0
56	MG	2A	3404	1/1	0.72	0.20	55,55,55,55	0
56	MG	2A	3410	1/1	0.72	0.18	63,63,63,63	0
56	MG	2A	3175	1/1	0.72	0.16	58,58,58,58	0
56	MG	2A	3097	1/1	0.73	0.35	62,62,62,62	0
56	MG	1a	1739	1/1	0.73	0.34	65,65,65,65	0
56	MG	1A	3741	1/1	0.73	0.14	31,31,31,31	0
56	MG	1A	3246	1/1	0.73	0.38	59,59,59,59	0
56	MG	1n	101	1/1	0.73	0.32	71,71,71,71	0
56	MG	1A	3171	1/1	0.73	0.27	42,42,42,42	0
56	MG	1B	226	1/1	0.73	0.12	48,48,48,48	0
56	MG	2A	3418	1/1	0.73	0.16	65,65,65,65	0
56	MG	2A	3231	1/1	0.73	0.14	64,64,64,64	0
56	MG	1a	1733	1/1	0.73	0.25	65,65,65,65	0
56	MG	2A	3061	1/1	0.73	0.28	61,61,61,61	0
56	MG	2A	3159	1/1	0.73	0.18	53,53,53,53	0
56	MG	2A	3168	1/1	0.73	0.09	52,52,52,52	0
56	MG	2a	1644	1/1	0.73	0.33	69,69,69,69	0
56	MG	2A	3504	1/1	0.73	0.08	64,64,64,64	0
56	MG	2a	1647	1/1	0.73	0.26	73,73,73,73	0
56	MG	2A	3518	1/1	0.73	0.15	63,63,63,63	0
56	MG	2l	201	1/1	0.73	0.18	71,71,71,71	0
56	MG	1A	3693	1/1	0.73	0.13	34,34,34,34	0
56	MG	2p	101	1/1	0.73	0.41	58,58,58,58	0
56	MG	2a	1663	1/1	0.73	0.29	65,65,65,65	0
58	MPD	1a	1860	8/8	0.73	0.20	65,70,76,77	0
56	MG	2A	3041	1/1	0.74	0.23	63,63,63,63	0
56	MG	2A	3203	1/1	0.74	0.19	71,71,71,71	0
56	MG	1a	1619	1/1	0.74	0.25	74,74,74,74	0
56	MG	2a	1609	1/1	0.74	0.28	67,67,67,67	0
56	MG	2a	1721	1/1	0.74	0.17	71,71,71,71	0
56	MG	2A	3055	1/1	0.74	0.23	62,62,62,62	0
56	MG	2A	3314	1/1	0.74	0.21	65,65,65,65	0
56	MG	1o	101	1/1	0.74	0.37	66,66,66,66	0
56	MG	2A	3336	1/1	0.74	0.14	78,78,78,78	0
56	MG	1A	3460	1/1	0.74	0.12	44,44,44,44	0
56	MG	2A	3080	1/1	0.74	0.31	61,61,61,61	0
56	MG	2A	3374	1/1	0.74	0.12	74,74,74,74	0
56	MG	1A	3624	1/1	0.74	0.08	62,62,62,62	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2A	3188	1/1	0.74	0.36	55,55,55,55	0
62	K	2A	3665	1/1	0.74	0.22	60,60,60,60	0
56	MG	1A	3751	1/1	0.75	0.18	43,43,43,43	0
56	MG	2A	3069	1/1	0.75	0.22	41,41,41,41	0
56	MG	1a	1637	1/1	0.75	0.32	52,52,52,52	0
56	MG	2A	3519	1/1	0.75	0.19	44,44,44,44	0
56	MG	2a	1673	1/1	0.75	0.24	65,65,65,65	0
56	MG	1b	3001	1/1	0.75	0.20	73,73,73,73	0
56	MG	1a	1724	1/1	0.75	0.30	78,78,78,78	0
56	MG	2A	3312	1/1	0.75	0.18	69,69,69,69	0
56	MG	1a	1725	1/1	0.75	0.30	59,59,59,59	0
56	MG	1A	3146	1/1	0.75	0.31	52,52,52,52	0
56	MG	2A	3334	1/1	0.75	0.12	61,61,61,61	0
56	MG	2x	109	1/1	0.75	0.21	69,69,69,69	0
56	MG	2A	3263	1/1	0.75	0.12	52,52,52,52	0
56	MG	2A	3475	1/1	0.75	0.13	48,48,48,48	0
56	MG	2A	3488	1/1	0.76	0.22	74,74,74,74	0
56	MG	1a	1698	1/1	0.76	0.19	72,72,72,72	0
56	MG	1a	1859	1/1	0.76	0.17	62,62,62,62	0
56	MG	1a	1651	1/1	0.76	0.21	52,52,52,52	0
56	MG	2A	3526	1/1	0.76	0.14	60,60,60,60	0
56	MG	2a	1670	1/1	0.76	0.23	58,58,58,58	0
56	MG	2A	3563	1/1	0.76	0.18	45,45,45,45	0
56	MG	1A	3236	1/1	0.76	0.18	47,47,47,47	0
56	MG	1Q	203	1/1	0.76	0.19	47,47,47,47	0
56	MG	2A	3204	1/1	0.76	0.19	56,56,56,56	0
56	MG	2B	3004	1/1	0.76	0.21	64,64,64,64	0
56	MG	2A	3337	1/1	0.76	0.16	60,60,60,60	0
56	MG	2D	302	1/1	0.76	0.44	48,48,48,48	0
56	MG	1A	3243	1/1	0.76	0.11	55,55,55,55	0
56	MG	1f	8001	1/1	0.76	0.12	63,63,63,63	0
56	MG	1l	201	1/1	0.76	0.08	63,63,63,63	0
56	MG	2A	3398	1/1	0.76	0.11	64,64,64,64	0
56	MG	2a	1610	1/1	0.76	0.16	72,72,72,72	0
56	MG	1A	3795	1/1	0.76	0.18	39,39,39,39	0
56	MG	2a	1621	1/1	0.76	0.22	60,60,60,60	0
56	MG	1a	1627	1/1	0.76	0.29	57,57,57,57	0
56	MG	1a	1814	1/1	0.76	0.26	64,64,64,64	0
56	MG	2A	3419	1/1	0.76	0.35	44,44,44,44	0
56	MG	1a	1635	1/1	0.76	0.35	75,75,75,75	0
56	MG	2a	1640	1/1	0.76	0.42	71,71,71,71	0
56	MG	1A	3412	1/1	0.76	0.13	28,28,28,28	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2t	3001	1/1	0.76	0.40	66,66,66,66	0
56	MG	2x	101	1/1	0.76	0.20	70,70,70,70	0
56	MG	1a	1687	1/1	0.76	0.25	71,71,71,71	0
56	MG	2A	3273	1/1	0.76	0.15	61,61,61,61	0
56	MG	1a	1831	1/1	0.76	0.13	69,69,69,69	0
56	MG	1A	3123	1/1	0.76	0.13	41,41,41,41	0
56	MG	2A	3181	1/1	0.77	0.32	57,57,57,57	0
56	MG	1B	208	1/1	0.77	0.14	54,54,54,54	0
56	MG	1D	307	1/1	0.77	0.17	45,45,45,45	0
56	MG	1a	1773	1/1	0.77	0.39	82,82,82,82	0
56	MG	2A	3190	1/1	0.77	0.18	52,52,52,52	0
56	MG	1a	1777	1/1	0.77	0.11	74,74,74,74	0
56	MG	1a	1631	1/1	0.77	0.38	72,72,72,72	0
56	MG	1A	3591	1/1	0.77	0.28	54,54,54,54	0
56	MG	2A	3060	1/1	0.77	0.22	48,48,48,48	0
56	MG	1A	3025	1/1	0.77	0.28	55,55,55,55	0
56	MG	1A	3930	1/1	0.77	0.37	32,32,32,32	0
56	MG	2a	1614	1/1	0.77	0.28	65,65,65,65	0
56	MG	2A	3160	1/1	0.77	0.15	63,63,63,63	0
56	MG	2A	3237	1/1	0.77	0.31	58,58,58,58	0
56	MG	2a	1630	1/1	0.77	0.46	76,76,76,76	0
56	MG	2x	104	1/1	0.77	0.17	72,72,72,72	0
56	MG	1a	1756	1/1	0.77	0.19	58,58,58,58	0
56	MG	1a	1644	1/1	0.77	0.22	62,62,62,62	0
56	MG	2A	3539	1/1	0.77	0.18	57,57,57,57	0
56	MG	1a	1683	1/1	0.77	0.27	67,67,67,67	0
56	MG	1D	304	1/1	0.78	0.17	49,49,49,49	0
56	MG	1a	1634	1/1	0.78	0.19	63,63,63,63	0
56	MG	1A	3361	1/1	0.78	0.21	47,47,47,47	0
56	MG	1F	304	1/1	0.78	0.28	32,32,32,32	0
56	MG	1a	1752	1/1	0.78	0.21	67,67,67,67	0
56	MG	2a	1676	1/1	0.78	0.20	68,68,68,68	0
56	MG	1r	3001	1/1	0.78	0.31	70,70,70,70	0
56	MG	2A	3411	1/1	0.78	0.20	58,58,58,58	0
56	MG	1A	3511	1/1	0.78	0.20	47,47,47,47	0
56	MG	2a	1698	1/1	0.78	0.23	77,77,77,77	0
56	MG	2A	3009	1/1	0.78	0.21	59,59,59,59	0
56	MG	1A	3868	1/1	0.78	0.15	56,56,56,56	0
56	MG	1a	1759	1/1	0.78	0.18	69,69,69,69	0
56	MG	2A	3445	1/1	0.78	0.13	61,61,61,61	0
56	MG	1a	1603	1/1	0.78	0.26	64,64,64,64	0
56	MG	2A	3052	1/1	0.78	0.27	62,62,62,62	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2a	1633	1/1	0.78	0.14	54,54,54,54	0
56	MG	2a	1745	1/1	0.78	0.08	71,71,71,71	0
56	MG	1A	3711	1/1	0.78	0.09	45,45,45,45	0
56	MG	2A	3479	1/1	0.78	0.22	49,49,49,49	0
56	MG	1a	1858	1/1	0.78	0.24	62,62,62,62	0
56	MG	2a	1774	1/1	0.78	0.19	68,68,68,68	0
56	MG	2a	1776	1/1	0.78	0.13	65,65,65,65	0
56	MG	2A	3176	1/1	0.78	0.14	52,52,52,52	0
56	MG	1a	1606	1/1	0.78	0.26	62,62,62,62	0
56	MG	1A	3740	1/1	0.78	0.12	47,47,47,47	0
56	MG	1a	1668	1/1	0.78	0.27	70,70,70,70	0
56	MG	1A	3143	1/1	0.78	0.17	63,63,63,63	0
56	MG	2A	3081	1/1	0.78	0.47	62,62,62,62	0
56	MG	2A	3088	1/1	0.78	0.35	60,60,60,60	0
56	MG	2A	3581	1/1	0.78	0.21	67,67,67,67	0
56	MG	2A	3201	1/1	0.78	0.21	53,53,53,53	0
56	MG	2A	3621	1/1	0.78	0.11	76,76,76,76	0
56	MG	2A	3644	1/1	0.78	0.18	56,56,56,56	0
56	MG	2a	1603	1/1	0.79	0.13	60,60,60,60	0
56	MG	1a	1625	1/1	0.79	0.18	71,71,71,71	0
56	MG	1a	1852	1/1	0.79	0.26	63,63,63,63	0
56	MG	2A	3459	1/1	0.79	0.11	56,56,56,56	0
56	MG	2a	1689	1/1	0.79	0.12	75,75,75,75	0
56	MG	1a	1728	1/1	0.79	0.34	75,75,75,75	0
56	MG	1a	1729	1/1	0.79	0.20	52,52,52,52	0
56	MG	1A	3622	1/1	0.79	0.14	56,56,56,56	0
56	MG	1a	1785	1/1	0.79	0.33	71,71,71,71	0
56	MG	1a	1789	1/1	0.79	0.22	74,74,74,74	0
56	MG	2a	1632	1/1	0.79	0.28	60,60,60,60	0
56	MG	1a	1646	1/1	0.79	0.27	72,72,72,72	0
56	MG	1a	1647	1/1	0.79	0.40	66,66,66,66	0
56	MG	1A	3822	1/1	0.79	0.20	37,37,37,37	0
56	MG	1a	1806	1/1	0.79	0.30	68,68,68,68	0
56	MG	2A	3112	1/1	0.79	0.30	56,56,56,56	0
56	MG	2A	3116	1/1	0.79	0.33	73,73,73,73	0
56	MG	2A	3565	1/1	0.79	0.14	48,48,48,48	0
56	MG	1a	1809	1/1	0.79	0.13	62,62,62,62	0
56	MG	1A	3510	1/1	0.79	0.10	52,52,52,52	0
56	MG	1a	1613	1/1	0.79	0.12	75,75,75,75	0
56	MG	2A	3628	1/1	0.79	0.17	58,58,58,58	0
56	MG	2A	3405	1/1	0.79	0.12	66,66,66,66	0
56	MG	1B	213	1/1	0.79	0.14	49,49,49,49	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2a	1660	1/1	0.79	0.20	81,81,81,81	0
56	MG	2A	3142	1/1	0.79	0.23	61,61,61,61	0
56	MG	1a	1639	1/1	0.79	0.30	61,61,61,61	0
56	MG	2B	3007	1/1	0.79	0.21	63,63,63,63	0
56	MG	1a	1670	1/1	0.79	0.20	59,59,59,59	0
56	MG	1a	1640	1/1	0.79	0.22	71,71,71,71	0
56	MG	1a	1845	1/1	0.79	0.28	61,61,61,61	0
56	MG	1A	3662	1/1	0.80	0.13	39,39,39,39	0
56	MG	1a	1632	1/1	0.80	0.19	63,63,63,63	0
56	MG	1A	3208	1/1	0.80	0.11	45,45,45,45	0
56	MG	2A	3057	1/1	0.80	0.22	53,53,53,53	0
56	MG	1a	1793	1/1	0.80	0.15	71,71,71,71	0
56	MG	1A	3579	1/1	0.80	0.35	37,37,37,37	0
56	MG	1a	1652	1/1	0.80	0.21	55,55,55,55	0
56	MG	2A	3308	1/1	0.80	0.11	51,51,51,51	0
56	MG	2A	3441	1/1	0.80	0.18	65,65,65,65	0
56	MG	2B	3001	1/1	0.80	0.13	71,71,71,71	0
56	MG	2A	3140	1/1	0.80	0.31	65,65,65,65	0
56	MG	1a	1616	1/1	0.80	0.12	73,73,73,73	0
56	MG	1t	3001	1/1	0.80	0.39	69,69,69,69	0
56	MG	2A	3462	1/1	0.80	0.21	66,66,66,66	0
56	MG	2A	3328	1/1	0.80	0.15	71,71,71,71	0
56	MG	2a	1654	1/1	0.80	0.32	62,62,62,62	0
56	MG	2D	308	1/1	0.80	0.14	47,47,47,47	0
56	MG	1A	3606	1/1	0.80	0.12	40,40,40,40	0
56	MG	2G	202	1/1	0.80	0.19	74,74,74,74	0
56	MG	1a	1689	1/1	0.80	0.32	69,69,69,69	0
56	MG	2A	3089	1/1	0.80	0.34	69,69,69,69	0
56	MG	2A	3162	1/1	0.80	0.35	57,57,57,57	0
56	MG	2A	3357	1/1	0.80	0.16	51,51,51,51	0
56	MG	2A	3092	1/1	0.80	0.31	61,61,61,61	0
56	MG	2a	1674	1/1	0.80	0.12	64,64,64,64	0
56	MG	1A	3834	1/1	0.80	0.12	47,47,47,47	0
56	MG	1A	3947	1/1	0.80	0.19	56,56,56,56	0
56	MG	2a	1620	1/1	0.80	0.48	56,56,56,56	0
56	MG	2A	3083	1/1	0.81	0.22	76,76,76,76	0
56	MG	2A	3455	1/1	0.81	0.11	53,53,53,53	0
56	MG	2A	3457	1/1	0.81	0.09	63,63,63,63	0
56	MG	2a	1601	1/1	0.81	0.24	58,58,58,58	0
56	MG	2A	3085	1/1	0.81	0.23	62,62,62,62	0
56	MG	1a	1786	1/1	0.81	0.14	65,65,65,65	0
56	MG	1x	110	1/1	0.81	0.12	58,58,58,58	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3523	1/1	0.81	0.25	57,57,57,57	0
56	MG	1A	3802	1/1	0.81	0.09	54,54,54,54	0
56	MG	2a	1612	1/1	0.81	0.25	66,66,66,66	0
56	MG	2A	3014	1/1	0.81	0.33	76,76,76,76	0
56	MG	1A	3300	1/1	0.81	0.19	45,45,45,45	0
56	MG	2A	3031	1/1	0.81	0.24	56,56,56,56	0
56	MG	2A	3039	1/1	0.81	0.27	56,56,56,56	0
56	MG	2a	1624	1/1	0.81	0.43	64,64,64,64	0
56	MG	1a	1761	1/1	0.81	0.25	68,68,68,68	0
56	MG	2a	1719	1/1	0.81	0.21	63,63,63,63	0
56	MG	2A	3205	1/1	0.81	0.29	51,51,51,51	0
56	MG	2A	3045	1/1	0.81	0.10	56,56,56,56	0
56	MG	2A	3207	1/1	0.81	0.33	68,68,68,68	0
56	MG	1A	3717	1/1	0.81	0.15	57,57,57,57	0
56	MG	1A	3216	1/1	0.81	0.79	34,34,34,34	0
56	MG	1a	1808	1/1	0.81	0.14	66,66,66,66	0
56	MG	1a	1664	1/1	0.81	0.15	71,71,71,71	0
56	MG	1F	309	1/1	0.81	0.12	43,43,43,43	0
56	MG	1a	1817	1/1	0.81	0.19	72,72,72,72	0
56	MG	2A	3065	1/1	0.81	0.36	47,47,47,47	0
56	MG	2A	3651	1/1	0.81	0.13	65,65,65,65	0
56	MG	2A	3658	1/1	0.81	0.11	49,49,49,49	0
56	MG	2A	3679	1/1	0.81	0.13	53,53,53,53	0
56	MG	2A	3420	1/1	0.81	0.09	64,64,64,64	0
56	MG	1G	3004	1/1	0.81	0.15	59,59,59,59	0
56	MG	1A	3272	1/1	0.81	0.11	52,52,52,52	0
56	MG	2A	3439	1/1	0.81	0.39	70,70,70,70	0
56	MG	1a	1783	1/1	0.81	0.12	63,63,63,63	0
56	MG	1A	3690	1/1	0.81	0.11	42,42,42,42	0
56	MG	1A	3220	1/1	0.82	0.18	28,28,28,28	0
56	MG	1A	3416	1/1	0.82	0.10	44,44,44,44	0
56	MG	2A	3233	1/1	0.82	0.13	49,49,49,49	0
56	MG	2A	3091	1/1	0.82	0.28	54,54,54,54	0
56	MG	1A	3692	1/1	0.82	0.15	58,58,58,58	0
56	MG	1a	1774	1/1	0.82	0.23	70,70,70,70	0
56	MG	1a	1696	1/1	0.82	0.29	58,58,58,58	0
56	MG	2a	1708	1/1	0.82	0.18	56,56,56,56	0
56	MG	1a	1820	1/1	0.82	0.22	63,63,63,63	0
56	MG	1A	3166	1/1	0.82	0.33	36,36,36,36	0
56	MG	2A	3520	1/1	0.82	0.17	46,46,46,46	0
56	MG	2U	202	1/1	0.82	0.29	59,59,59,59	0
56	MG	1a	1703	1/1	0.82	0.14	72,72,72,72	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2A	3119	1/1	0.82	0.18	49,49,49,49	0
56	MG	2a	1604	1/1	0.82	0.12	72,72,72,72	0
56	MG	2a	1657	1/1	0.82	0.23	69,69,69,69	0
56	MG	2a	1763	1/1	0.82	0.16	82,82,82,82	0
56	MG	2a	1658	1/1	0.82	0.33	58,58,58,58	0
56	MG	2A	3555	1/1	0.82	0.09	59,59,59,59	0
56	MG	1B	206	1/1	0.82	0.21	49,49,49,49	0
56	MG	2a	1778	1/1	0.82	0.17	77,77,77,77	0
56	MG	2a	1662	1/1	0.82	0.42	77,77,77,77	0
56	MG	1a	1840	1/1	0.82	0.20	67,67,67,67	0
56	MG	1A	3705	1/1	0.82	0.15	45,45,45,45	0
56	MG	1A	3555	1/1	0.82	0.21	38,38,38,38	0
56	MG	2A	3130	1/1	0.82	0.17	62,62,62,62	0
56	MG	1A	3855	1/1	0.82	0.27	42,42,42,42	0
56	MG	2a	1619	1/1	0.82	0.20	65,65,65,65	0
56	MG	1a	1762	1/1	0.82	0.13	71,71,71,71	0
56	MG	2x	107	1/1	0.82	0.17	69,69,69,69	0
56	MG	2A	3156	1/1	0.82	0.34	58,58,58,58	0
56	MG	1A	3559	1/1	0.82	0.09	39,39,39,39	0
56	MG	1A	3567	1/1	0.82	0.11	52,52,52,52	0
56	MG	1A	3586	1/1	0.83	0.15	36,36,36,36	0
56	MG	2A	3636	1/1	0.83	0.11	52,52,52,52	0
56	MG	2A	3169	1/1	0.83	0.26	50,50,50,50	0
56	MG	1A	3703	1/1	0.83	0.18	43,43,43,43	0
56	MG	2A	3172	1/1	0.83	0.16	68,68,68,68	0
56	MG	1A	3078	1/1	0.83	0.24	45,45,45,45	0
56	MG	2A	3068	1/1	0.83	0.11	51,51,51,51	0
56	MG	2a	1664	1/1	0.83	0.37	65,65,65,65	0
56	MG	2a	1665	1/1	0.83	0.20	81,81,81,81	0
56	MG	1A	3922	1/1	0.83	0.38	31,31,31,31	0
56	MG	1a	1781	1/1	0.83	0.15	58,58,58,58	0
56	MG	1a	1782	1/1	0.83	0.28	58,58,58,58	0
56	MG	1A	3927	1/1	0.83	0.13	50,50,50,50	0
56	MG	1A	3229	1/1	0.83	0.14	32,32,32,32	0
56	MG	1A	3316	1/1	0.83	0.16	45,45,45,45	0
56	MG	2A	3195	1/1	0.83	0.29	43,43,43,43	0
56	MG	2E	305	1/1	0.83	0.26	45,45,45,45	0
56	MG	1a	1660	1/1	0.83	0.14	68,68,68,68	0
56	MG	2a	1683	1/1	0.83	0.15	71,71,71,71	0
56	MG	1A	3317	1/1	0.83	0.10	45,45,45,45	0
56	MG	1A	3469	1/1	0.83	0.11	39,39,39,39	0
56	MG	2A	3437	1/1	0.83	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
56	MG	1a	1801	1/1	0.83	0.08	85,85,85,85	0
56	MG	2a	1699	1/1	0.83	0.15	59,59,59,59	0
56	MG	1A	3474	1/1	0.83	0.10	56,56,56,56	0
56	MG	1a	1736	1/1	0.83	0.11	73,73,73,73	0
56	MG	1x	106	1/1	0.83	0.29	62,62,62,62	0
56	MG	1A	3179	1/1	0.83	0.14	57,57,57,57	0
56	MG	2A	3115	1/1	0.83	0.14	46,46,46,46	0
56	MG	1A	3576	1/1	0.83	0.09	43,43,43,43	0
56	MG	1A	3816	1/1	0.83	0.19	42,42,42,42	0
56	MG	1a	1633	1/1	0.83	0.29	51,51,51,51	0
56	MG	1B	224	1/1	0.83	0.19	54,54,54,54	0
56	MG	2A	3476	1/1	0.83	0.13	57,57,57,57	0
56	MG	2a	1751	1/1	0.83	0.11	77,77,77,77	0
56	MG	2A	3027	1/1	0.83	0.25	42,42,42,42	0
56	MG	2A	3125	1/1	0.83	0.38	68,68,68,68	0
56	MG	1a	1758	1/1	0.83	0.11	70,70,70,70	0
56	MG	2a	1631	1/1	0.83	0.38	64,64,64,64	0
56	MG	2A	3038	1/1	0.83	0.25	49,49,49,49	0
56	MG	2A	3275	1/1	0.83	0.20	55,55,55,55	0
56	MG	2a	1634	1/1	0.83	0.22	69,69,69,69	0
56	MG	1a	1684	1/1	0.83	0.55	56,56,56,56	0
56	MG	2A	3040	1/1	0.83	0.30	42,42,42,42	0
56	MG	2A	3148	1/1	0.83	0.26	66,66,66,66	0
56	MG	1A	3490	1/1	0.83	0.14	44,44,44,44	0
56	MG	2q	201	1/1	0.83	0.20	62,62,62,62	0
56	MG	1A	3507	1/1	0.83	0.16	52,52,52,52	0
56	MG	1a	1828	1/1	0.83	0.13	60,60,60,60	0
56	MG	1A	3187	1/1	0.83	0.18	41,41,41,41	0
56	MG	2A	3579	1/1	0.83	0.13	50,50,50,50	0
56	MG	1A	3585	1/1	0.83	0.07	39,39,39,39	0
56	MG	2A	3331	1/1	0.83	0.10	57,57,57,57	0
56	MG	1A	3870	1/1	0.83	0.11	35,35,35,35	0
56	MG	2a	1650	1/1	0.83	0.35	61,61,61,61	0
56	MG	2A	3677	1/1	0.84	0.12	57,57,57,57	0
56	MG	1A	3345	1/1	0.84	0.11	45,45,45,45	0
56	MG	1A	3729	1/1	0.84	0.14	32,32,32,32	0
56	MG	2A	3218	1/1	0.84	0.25	55,55,55,55	0
56	MG	2B	3003	1/1	0.84	0.17	68,68,68,68	0
56	MG	1a	1630	1/1	0.84	0.19	64,64,64,64	0
56	MG	2B	3006	1/1	0.84	0.25	69,69,69,69	0
56	MG	2A	3222	1/1	0.84	0.11	57,57,57,57	0
56	MG	2B	3009	1/1	0.84	0.14	66,66,66,66	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2B	3012	1/1	0.84	0.09	64,64,64,64	0
56	MG	2A	3047	1/1	0.84	0.23	56,56,56,56	0
56	MG	2A	3434	1/1	0.84	0.14	58,58,58,58	0
56	MG	2a	1672	1/1	0.84	0.41	52,52,52,52	0
56	MG	1A	3629	1/1	0.84	0.15	64,64,64,64	0
56	MG	1A	3654	1/1	0.84	0.19	49,49,49,49	0
56	MG	2E	307	1/1	0.84	0.18	52,52,52,52	0
56	MG	1D	309	1/1	0.84	0.26	42,42,42,42	0
56	MG	2A	3240	1/1	0.84	0.28	60,60,60,60	0
56	MG	1A	3437	1/1	0.84	0.16	26,26,26,26	0
56	MG	2A	3144	1/1	0.84	0.10	49,49,49,49	0
56	MG	1F	308	1/1	0.84	0.27	56,56,56,56	0
56	MG	1A	3926	1/1	0.84	0.10	45,45,45,45	0
56	MG	2a	1605	1/1	0.84	0.12	73,73,73,73	0
56	MG	1a	1740	1/1	0.84	0.16	70,70,70,70	0
56	MG	2A	3463	1/1	0.84	0.15	52,52,52,52	0
56	MG	1a	1744	1/1	0.84	0.13	62,62,62,62	0
56	MG	2A	3470	1/1	0.84	0.14	57,57,57,57	0
56	MG	1A	3781	1/1	0.84	0.08	66,66,66,66	0
56	MG	2a	1713	1/1	0.84	0.08	67,67,67,67	0
56	MG	2a	1613	1/1	0.84	0.33	61,61,61,61	0
56	MG	1A	3010	1/1	0.84	0.26	45,45,45,45	0
56	MG	2A	3079	1/1	0.84	0.25	51,51,51,51	0
56	MG	1A	3560	1/1	0.84	0.10	35,35,35,35	0
56	MG	1A	3198	1/1	0.84	0.32	60,60,60,60	0
56	MG	1x	101	1/1	0.84	0.23	69,69,69,69	0
56	MG	1a	1691	1/1	0.84	0.11	67,67,67,67	0
56	MG	2a	1626	1/1	0.84	0.35	61,61,61,61	0
56	MG	2A	3086	1/1	0.84	0.27	58,58,58,58	0
56	MG	2A	3323	1/1	0.84	0.32	50,50,50,50	0
56	MG	1A	3520	1/1	0.84	0.19	40,40,40,40	0
56	MG	1a	1694	1/1	0.84	0.16	64,64,64,64	0
56	MG	1A	3401	1/1	0.84	0.12	56,56,56,56	0
56	MG	2A	3184	1/1	0.84	0.39	59,59,59,59	0
56	MG	2e	201	1/1	0.84	0.30	57,57,57,57	0
56	MG	1A	3842	1/1	0.84	0.10	47,47,47,47	0
56	MG	1A	3535	1/1	0.84	0.14	34,34,34,34	0
56	MG	2A	3023	1/1	0.84	0.18	53,53,53,53	0
56	MG	2A	3361	1/1	0.84	0.20	60,60,60,60	0
56	MG	2A	3107	1/1	0.84	0.15	66,66,66,66	0
56	MG	1a	1653	1/1	0.84	0.34	56,56,56,56	0
56	MG	2A	3383	1/1	0.84	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
56	MG	1a	1771	1/1	0.84	0.10	71,71,71,71	0
56	MG	2A	3649	1/1	0.84	0.25	57,57,57,57	0
56	MG	2x	106	1/1	0.84	0.16	63,63,63,63	0
56	MG	2a	1648	1/1	0.84	0.12	70,70,70,70	0
56	MG	2x	108	1/1	0.84	0.52	57,57,57,57	0
56	MG	2A	3033	1/1	0.84	0.20	58,58,58,58	0
56	MG	1a	1617	1/1	0.84	0.13	69,69,69,69	0
56	MG	1A	3059	1/1	0.84	0.32	60,60,60,60	0
56	MG	1a	1638	1/1	0.85	0.17	68,68,68,68	0
56	MG	2a	1669	1/1	0.85	0.15	63,63,63,63	0
56	MG	1a	1671	1/1	0.85	0.25	57,57,57,57	0
56	MG	1a	1614	1/1	0.85	0.24	51,51,51,51	0
56	MG	1a	1769	1/1	0.85	0.10	68,68,68,68	0
56	MG	2A	3067	1/1	0.85	0.29	42,42,42,42	0
56	MG	2A	3548	1/1	0.85	0.13	46,46,46,46	0
56	MG	1A	3725	1/1	0.85	0.14	46,46,46,46	0
56	MG	2A	3384	1/1	0.85	0.16	48,48,48,48	0
56	MG	2A	3133	1/1	0.85	0.15	52,52,52,52	0
56	MG	2a	1682	1/1	0.85	0.30	58,58,58,58	0
56	MG	1A	3878	1/1	0.85	0.14	51,51,51,51	0
56	MG	2A	3074	1/1	0.85	0.17	48,48,48,48	0
56	MG	2A	3228	1/1	0.85	0.29	46,46,46,46	0
56	MG	1a	1824	1/1	0.85	0.31	54,54,54,54	0
56	MG	2A	3413	1/1	0.85	0.30	62,62,62,62	0
56	MG	2a	1625	1/1	0.85	0.29	72,72,72,72	0
56	MG	2A	3147	1/1	0.85	0.17	54,54,54,54	0
56	MG	1A	3890	1/1	0.85	0.10	32,32,32,32	0
56	MG	1a	1621	1/1	0.85	0.14	71,71,71,71	0
56	MG	1a	1624	1/1	0.85	0.23	51,51,51,51	0
56	MG	1A	3727	1/1	0.85	0.10	67,67,67,67	0
56	MG	1A	3314	1/1	0.85	0.15	32,32,32,32	0
56	MG	1a	1742	1/1	0.85	0.20	71,71,71,71	0
56	MG	2a	1717	1/1	0.85	0.21	67,67,67,67	0
56	MG	2A	3270	1/1	0.85	0.14	50,50,50,50	0
56	MG	1A	3098	1/1	0.85	0.10	51,51,51,51	0
56	MG	1A	3234	1/1	0.85	0.08	41,41,41,41	0
56	MG	2a	1723	1/1	0.85	0.17	62,62,62,62	0
56	MG	2A	3090	1/1	0.85	0.16	58,58,58,58	0
56	MG	1a	1855	1/1	0.85	0.29	52,52,52,52	0
56	MG	2a	1642	1/1	0.85	0.28	75,75,75,75	0
56	MG	1a	1658	1/1	0.85	0.36	67,67,67,67	0
56	MG	2a	1761	1/1	0.85	0.19	63,63,63,63	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1V	201	1/1	0.85	0.13	45,45,45,45	0
56	MG	2A	3098	1/1	0.85	0.34	59,59,59,59	0
56	MG	2B	3010	1/1	0.85	0.17	69,69,69,69	0
56	MG	1a	1799	1/1	0.85	0.08	66,66,66,66	0
56	MG	2A	3465	1/1	0.85	0.21	57,57,57,57	0
56	MG	2a	1782	1/1	0.85	0.13	63,63,63,63	0
56	MG	2B	3015	1/1	0.85	0.07	76,76,76,76	0
56	MG	2a	1651	1/1	0.85	0.50	62,62,62,62	0
56	MG	2a	1652	1/1	0.85	0.39	58,58,58,58	0
56	MG	2B	3016	1/1	0.85	0.08	71,71,71,71	0
56	MG	2a	1655	1/1	0.85	0.11	68,68,68,68	0
56	MG	2a	1656	1/1	0.85	0.19	68,68,68,68	0
56	MG	2A	3100	1/1	0.85	0.32	60,60,60,60	0
56	MG	1A	3224	1/1	0.85	0.23	46,46,46,46	0
56	MG	2x	103	1/1	0.85	0.18	73,73,73,73	0
56	MG	2A	3046	1/1	0.85	0.31	61,61,61,61	0
56	MG	2A	3111	1/1	0.85	0.19	48,48,48,48	0
56	MG	2a	1661	1/1	0.85	0.20	65,65,65,65	0
56	MG	1a	1661	1/1	0.85	0.14	66,66,66,66	0
56	MG	1B	228	1/1	0.85	0.10	67,67,67,67	0
56	MG	1A	3587	1/1	0.85	0.12	45,45,45,45	0
56	MG	1A	3259	1/1	0.85	0.15	71,71,71,71	0
56	MG	2A	3517	1/1	0.85	0.07	60,60,60,60	0
56	MG	1A	3749	1/1	0.86	0.14	45,45,45,45	0
56	MG	2A	3199	1/1	0.86	0.23	56,56,56,56	0
56	MG	1Z	8001	1/1	0.86	0.10	60,60,60,60	0
56	MG	2a	1637	1/1	0.86	0.25	60,60,60,60	0
56	MG	10	101	1/1	0.86	0.12	48,48,48,48	0
56	MG	2A	3072	1/1	0.86	0.17	54,54,54,54	0
56	MG	15	104	1/1	0.86	0.15	63,63,63,63	0
56	MG	1a	1830	1/1	0.86	0.08	68,68,68,68	0
56	MG	1A	3678	1/1	0.86	0.13	44,44,44,44	0
56	MG	1A	3763	1/1	0.86	0.09	33,33,33,33	0
56	MG	1a	1841	1/1	0.86	0.16	67,67,67,67	0
56	MG	2A	3493	1/1	0.86	0.09	61,61,61,61	0
56	MG	1A	3269	1/1	0.86	0.22	41,41,41,41	0
56	MG	2A	3223	1/1	0.86	0.35	60,60,60,60	0
56	MG	1a	1609	1/1	0.86	0.12	68,68,68,68	0
56	MG	1A	3601	1/1	0.86	0.18	31,31,31,31	0
56	MG	2A	3087	1/1	0.86	0.09	51,51,51,51	0
56	MG	1a	1757	1/1	0.86	0.23	55,55,55,55	0
56	MG	2A	3528	1/1	0.86	0.33	51,51,51,51	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1a	1854	1/1	0.86	0.11	72,72,72,72	0
56	MG	2A	3239	1/1	0.86	0.12	63,63,63,63	0
56	MG	1B	202	1/1	0.86	0.27	61,61,61,61	0
56	MG	2A	3557	1/1	0.86	0.11	51,51,51,51	0
56	MG	2A	3559	1/1	0.86	0.12	47,47,47,47	0
56	MG	1B	205	1/1	0.86	0.18	57,57,57,57	0
56	MG	1a	1760	1/1	0.86	0.37	65,65,65,65	0
56	MG	2A	3571	1/1	0.86	0.15	57,57,57,57	0
56	MG	1A	3797	1/1	0.86	0.12	45,45,45,45	0
56	MG	1a	1672	1/1	0.86	0.11	61,61,61,61	0
56	MG	1a	1763	1/1	0.86	0.21	82,82,82,82	0
56	MG	2A	3602	1/1	0.86	0.17	47,47,47,47	0
56	MG	1A	3180	1/1	0.86	0.12	51,51,51,51	0
56	MG	1e	204	1/1	0.86	0.12	63,63,63,63	0
56	MG	1A	3811	1/1	0.86	0.13	30,30,30,30	0
56	MG	1a	1679	1/1	0.86	0.18	81,81,81,81	0
56	MG	1A	3479	1/1	0.86	0.16	33,33,33,33	0
56	MG	2A	3114	1/1	0.86	0.15	50,50,50,50	0
56	MG	1a	1768	1/1	0.86	0.11	68,68,68,68	0
56	MG	2A	3654	1/1	0.86	0.23	50,50,50,50	0
56	MG	2A	3309	1/1	0.86	0.17	61,61,61,61	0
56	MG	2A	3661	1/1	0.86	0.18	62,62,62,62	0
56	MG	2a	1678	1/1	0.86	0.22	64,64,64,64	0
56	MG	2A	3663	1/1	0.86	0.16	55,55,55,55	0
56	MG	1o	102	1/1	0.86	0.10	49,49,49,49	0
56	MG	1A	3273	1/1	0.86	0.08	41,41,41,41	0
56	MG	2A	3316	1/1	0.86	0.11	67,67,67,67	0
56	MG	1a	1770	1/1	0.86	0.40	65,65,65,65	0
56	MG	2a	1697	1/1	0.86	0.17	65,65,65,65	0
56	MG	1A	3182	1/1	0.86	0.27	60,60,60,60	0
56	MG	1B	219	1/1	0.86	0.09	42,42,42,42	0
56	MG	1A	3712	1/1	0.86	0.11	48,48,48,48	0
56	MG	1A	3854	1/1	0.86	0.21	59,59,59,59	0
56	MG	2A	3127	1/1	0.86	0.20	61,61,61,61	0
56	MG	2a	1704	1/1	0.86	0.14	70,70,70,70	0
56	MG	2A	3002	1/1	0.86	0.28	59,59,59,59	0
56	MG	2a	1712	1/1	0.86	0.17	66,66,66,66	0
56	MG	2A	3348	1/1	0.86	0.11	41,41,41,41	0
56	MG	1B	227	1/1	0.86	0.10	51,51,51,51	0
56	MG	2A	3353	1/1	0.86	0.25	53,53,53,53	0
56	MG	2A	3010	1/1	0.86	0.13	43,43,43,43	0
56	MG	1A	3716	1/1	0.86	0.18	60,60,60,60	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3491	1/1	0.86	0.12	35,35,35,35	0
56	MG	1a	1695	1/1	0.86	0.20	67,67,67,67	0
56	MG	2A	3024	1/1	0.86	0.21	45,45,45,45	0
56	MG	2A	3154	1/1	0.86	0.12	48,48,48,48	0
56	MG	2A	3387	1/1	0.86	0.11	69,69,69,69	0
56	MG	2Q	201	1/1	0.86	0.25	59,59,59,59	0
56	MG	2T	3004	1/1	0.86	0.07	50,50,50,50	0
56	MG	2A	3393	1/1	0.86	0.24	54,54,54,54	0
56	MG	2A	3397	1/1	0.86	0.09	48,48,48,48	0
56	MG	1a	1636	1/1	0.86	0.54	60,60,60,60	0
56	MG	2A	3028	1/1	0.86	0.07	51,51,51,51	0
56	MG	1a	1697	1/1	0.86	0.15	55,55,55,55	0
56	MG	1A	3548	1/1	0.86	0.10	47,47,47,47	0
56	MG	2A	3036	1/1	0.86	0.20	65,65,65,65	0
56	MG	1A	3872	1/1	0.86	0.11	58,58,58,58	0
56	MG	1D	316	1/1	0.86	0.13	34,34,34,34	0
56	MG	1A	3550	1/1	0.86	0.13	51,51,51,51	0
56	MG	1A	3154	1/1	0.86	0.19	45,45,45,45	0
56	MG	2A	3426	1/1	0.86	0.20	60,60,60,60	0
56	MG	2a	1616	1/1	0.86	0.14	57,57,57,57	0
56	MG	1a	1718	1/1	0.86	0.10	73,73,73,73	0
56	MG	1a	1723	1/1	0.86	0.07	69,69,69,69	0
56	MG	1A	3075	1/1	0.86	0.12	37,37,37,37	0
56	MG	1a	1645	1/1	0.86	0.39	59,59,59,59	0
56	MG	1a	1813	1/1	0.86	0.10	72,72,72,72	0
56	MG	1A	3593	1/1	0.86	0.12	52,52,52,52	0
56	MG	2A	3185	1/1	0.86	0.36	56,56,56,56	0
56	MG	1A	3911	1/1	0.86	0.09	28,28,28,28	0
56	MG	1a	1818	1/1	0.86	0.23	73,73,73,73	0
56	MG	1a	1649	1/1	0.86	0.13	70,70,70,70	0
56	MG	1A	3745	1/1	0.86	0.17	49,49,49,49	0
56	MG	1A	3399	1/1	0.87	0.11	49,49,49,49	0
56	MG	2A	3509	1/1	0.87	0.11	59,59,59,59	0
56	MG	1D	319	1/1	0.87	0.08	66,66,66,66	0
56	MG	2A	3021	1/1	0.87	0.24	67,67,67,67	0
56	MG	2A	3246	1/1	0.87	0.13	54,54,54,54	0
56	MG	2A	3248	1/1	0.87	0.11	51,51,51,51	0
56	MG	2A	3522	1/1	0.87	0.13	50,50,50,50	0
56	MG	1D	321	1/1	0.87	0.15	46,46,46,46	0
56	MG	1A	3527	1/1	0.87	0.18	49,49,49,49	0
56	MG	2A	3118	1/1	0.87	0.12	47,47,47,47	0
56	MG	1A	3142	1/1	0.87	0.12	34,34,34,34	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2A	3025	1/1	0.87	0.20	56,56,56,56	0
56	MG	1A	3881	1/1	0.87	0.15	53,53,53,53	0
56	MG	1A	3061	1/1	0.87	0.20	43,43,43,43	0
56	MG	2a	1653	1/1	0.87	0.45	67,67,67,67	0
56	MG	2A	3029	1/1	0.87	0.15	50,50,50,50	0
56	MG	1a	1816	1/1	0.87	0.11	57,57,57,57	0
56	MG	2A	3570	1/1	0.87	0.13	43,43,43,43	0
56	MG	1A	3893	1/1	0.87	0.76	39,39,39,39	0
56	MG	2A	3575	1/1	0.87	0.12	65,65,65,65	0
56	MG	1A	3230	1/1	0.87	0.16	36,36,36,36	0
56	MG	1A	3737	1/1	0.87	0.21	31,31,31,31	0
56	MG	2A	3584	1/1	0.87	0.14	64,64,64,64	0
56	MG	2A	3134	1/1	0.87	0.15	68,68,68,68	0
56	MG	2A	3135	1/1	0.87	0.47	43,43,43,43	0
56	MG	1a	1743	1/1	0.87	0.20	73,73,73,73	0
56	MG	1A	3064	1/1	0.87	0.19	46,46,46,46	0
56	MG	1a	1746	1/1	0.87	0.16	69,69,69,69	0
56	MG	2A	3043	1/1	0.87	0.31	61,61,61,61	0
56	MG	1A	3455	1/1	0.87	0.13	37,37,37,37	0
56	MG	10	107	1/1	0.87	0.13	54,54,54,54	0
56	MG	2A	3332	1/1	0.87	0.19	43,43,43,43	0
56	MG	1A	3552	1/1	0.87	0.19	32,32,32,32	0
56	MG	1a	1602	1/1	0.87	0.12	82,82,82,82	0
56	MG	1A	3623	1/1	0.87	0.22	53,53,53,53	0
56	MG	2A	3054	1/1	0.87	0.58	66,66,66,66	0
56	MG	1A	3928	1/1	0.87	0.34	35,35,35,35	0
56	MG	1a	1842	1/1	0.87	0.16	62,62,62,62	0
56	MG	2A	3355	1/1	0.87	0.19	53,53,53,53	0
56	MG	2A	3167	1/1	0.87	0.17	66,66,66,66	0
56	MG	1A	3069	1/1	0.87	0.57	30,30,30,30	0
56	MG	1A	3934	1/1	0.87	0.13	44,44,44,44	0
56	MG	2B	3005	1/1	0.87	0.27	77,77,77,77	0
56	MG	1A	3944	1/1	0.87	0.16	31,31,31,31	0
56	MG	2a	1695	1/1	0.87	0.24	58,58,58,58	0
56	MG	2A	3379	1/1	0.87	0.12	55,55,55,55	0
56	MG	2B	3008	1/1	0.87	0.25	64,64,64,64	0
56	MG	1A	3753	1/1	0.87	0.12	51,51,51,51	0
56	MG	2A	3173	1/1	0.87	0.16	56,56,56,56	0
56	MG	2A	3174	1/1	0.87	0.28	55,55,55,55	0
56	MG	1A	3948	1/1	0.87	0.29	44,44,44,44	0
56	MG	1A	3165	1/1	0.87	0.14	36,36,36,36	0
56	MG	2A	3177	1/1	0.87	0.22	54,54,54,54	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2A	3180	1/1	0.87	0.18	65,65,65,65	0
56	MG	1A	3764	1/1	0.87	0.20	47,47,47,47	0
56	MG	1a	1620	1/1	0.87	0.14	60,60,60,60	0
56	MG	1A	3244	1/1	0.87	0.07	31,31,31,31	0
56	MG	1A	3121	1/1	0.87	0.25	68,68,68,68	0
56	MG	1A	3250	1/1	0.87	0.10	48,48,48,48	0
56	MG	2O	202	1/1	0.87	0.11	63,63,63,63	0
56	MG	1A	3665	1/1	0.87	0.10	46,46,46,46	0
56	MG	2A	3082	1/1	0.87	0.09	47,47,47,47	0
56	MG	1a	1629	1/1	0.87	0.19	54,54,54,54	0
56	MG	1A	3329	1/1	0.87	0.16	49,49,49,49	0
56	MG	2A	3196	1/1	0.87	0.20	52,52,52,52	0
56	MG	1a	1776	1/1	0.87	0.08	80,80,80,80	0
56	MG	1A	3581	1/1	0.87	0.15	29,29,29,29	0
56	MG	2A	3202	1/1	0.87	0.18	52,52,52,52	0
56	MG	2A	3440	1/1	0.87	0.08	55,55,55,55	0
56	MG	1A	3331	1/1	0.87	0.13	40,40,40,40	0
56	MG	2A	3442	1/1	0.87	0.18	64,64,64,64	0
56	MG	1B	223	1/1	0.87	0.12	43,43,43,43	0
56	MG	1A	3494	1/1	0.87	0.10	42,42,42,42	0
56	MG	1A	3256	1/1	0.87	0.36	48,48,48,48	0
56	MG	1A	3849	1/1	0.87	0.08	60,60,60,60	0
56	MG	2A	3209	1/1	0.87	0.22	61,61,61,61	0
56	MG	2A	3213	1/1	0.87	0.21	53,53,53,53	0
56	MG	2A	3216	1/1	0.87	0.13	52,52,52,52	0
56	MG	2A	3094	1/1	0.87	0.09	55,55,55,55	0
56	MG	2A	3096	1/1	0.87	0.24	62,62,62,62	0
56	MG	1x	104	1/1	0.87	0.21	69,69,69,69	0
56	MG	1A	3056	1/1	0.87	0.24	55,55,55,55	0
56	MG	1A	3130	1/1	0.87	0.39	31,31,31,31	0
56	MG	2A	3477	1/1	0.87	0.08	50,50,50,50	0
56	MG	1D	306	1/1	0.87	0.21	35,35,35,35	0
56	MG	1A	3260	1/1	0.87	0.27	42,42,42,42	0
56	MG	1A	3714	1/1	0.87	0.18	52,52,52,52	0
56	MG	2A	3234	1/1	0.87	0.13	55,55,55,55	0
58	MPD	1A	3907	8/8	0.87	0.34	51,53,55,56	0
56	MG	2A	3499	1/1	0.87	0.15	41,41,41,41	0
56	MG	2A	3502	1/1	0.87	0.10	70,70,70,70	0
56	MG	1A	3942	1/1	0.88	0.15	55,55,55,55	0
56	MG	1a	1669	1/1	0.88	0.37	57,57,57,57	0
56	MG	1a	1851	1/1	0.88	0.09	78,78,78,78	0
56	MG	1A	3070	1/1	0.88	0.09	31,31,31,31	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1a	1607	1/1	0.88	0.38	60,60,60,60	0
56	MG	1A	3759	1/1	0.88	0.09	53,53,53,53	0
56	MG	1a	1856	1/1	0.88	0.23	62,62,62,62	0
56	MG	1a	1612	1/1	0.88	0.21	56,56,56,56	0
56	MG	1A	3108	1/1	0.88	0.18	40,40,40,40	0
56	MG	1A	3294	1/1	0.88	0.13	42,42,42,42	0
56	MG	1a	1681	1/1	0.88	0.24	56,56,56,56	0
56	MG	2A	3364	1/1	0.88	0.13	58,58,58,58	0
56	MG	1a	1615	1/1	0.88	0.17	71,71,71,71	0
56	MG	2A	3372	1/1	0.88	0.14	58,58,58,58	0
56	MG	2A	3641	1/1	0.88	0.11	61,61,61,61	0
56	MG	1d	503	1/1	0.88	0.11	70,70,70,70	0
56	MG	1e	201	1/1	0.88	0.45	68,68,68,68	0
56	MG	2A	3381	1/1	0.88	0.16	53,53,53,53	0
56	MG	1A	3424	1/1	0.88	0.19	51,51,51,51	0
56	MG	1e	203	1/1	0.88	0.15	63,63,63,63	0
56	MG	1A	3792	1/1	0.88	0.12	34,34,34,34	0
56	MG	2A	3389	1/1	0.88	0.17	49,49,49,49	0
56	MG	2A	3662	1/1	0.88	0.18	63,63,63,63	0
56	MG	1A	3223	1/1	0.88	0.12	46,46,46,46	0
56	MG	2A	3396	1/1	0.88	0.26	58,58,58,58	0
56	MG	1A	3308	1/1	0.88	0.15	58,58,58,58	0
56	MG	1A	3255	1/1	0.88	0.18	30,30,30,30	0
56	MG	1A	3467	1/1	0.88	0.11	48,48,48,48	0
56	MG	1A	3671	1/1	0.88	0.10	62,62,62,62	0
56	MG	1A	3821	1/1	0.88	0.18	37,37,37,37	0
56	MG	2A	3093	1/1	0.88	0.17	61,61,61,61	0
56	MG	1A	3557	1/1	0.88	0.15	42,42,42,42	0
56	MG	1A	3679	1/1	0.88	0.19	32,32,32,32	0
56	MG	1x	103	1/1	0.88	0.32	63,63,63,63	0
56	MG	2a	1680	1/1	0.88	0.54	58,58,58,58	0
56	MG	1A	3034	1/1	0.88	0.28	45,45,45,45	0
56	MG	2A	3422	1/1	0.88	0.16	54,54,54,54	0
56	MG	1A	3228	1/1	0.88	0.23	40,40,40,40	0
56	MG	2A	3427	1/1	0.88	0.08	63,63,63,63	0
56	MG	1x	109	1/1	0.88	0.25	63,63,63,63	0
56	MG	1A	3477	1/1	0.88	0.21	49,49,49,49	0
56	MG	2a	1696	1/1	0.88	0.35	63,63,63,63	0
56	MG	1a	1792	1/1	0.88	0.10	68,68,68,68	0
56	MG	2A	3219	1/1	0.88	0.16	45,45,45,45	0
56	MG	2A	3001	1/1	0.88	0.28	60,60,60,60	0
56	MG	1A	3119	1/1	0.88	0.23	30,30,30,30	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2F	302	1/1	0.88	0.13	47,47,47,47	0
56	MG	2A	3008	1/1	0.88	0.15	45,45,45,45	0
56	MG	1a	1708	1/1	0.88	0.08	64,64,64,64	0
56	MG	2A	3227	1/1	0.88	0.17	58,58,58,58	0
56	MG	1A	3482	1/1	0.88	0.13	28,28,28,28	0
56	MG	2A	3230	1/1	0.88	0.26	55,55,55,55	0
56	MG	1a	1712	1/1	0.88	0.19	70,70,70,70	0
56	MG	2W	201	1/1	0.88	0.15	62,62,62,62	0
56	MG	1A	3710	1/1	0.88	0.15	30,30,30,30	0
56	MG	1A	3486	1/1	0.88	0.20	46,46,46,46	0
56	MG	1D	313	1/1	0.88	0.11	41,41,41,41	0
56	MG	1A	3487	1/1	0.88	0.09	51,51,51,51	0
56	MG	1A	3713	1/1	0.88	0.38	59,59,59,59	0
56	MG	2a	1743	1/1	0.88	0.15	60,60,60,60	0
56	MG	2A	3243	1/1	0.88	0.24	50,50,50,50	0
56	MG	2A	3472	1/1	0.88	0.08	68,68,68,68	0
56	MG	1a	1812	1/1	0.88	0.22	67,67,67,67	0
56	MG	1A	3032	1/1	0.88	0.13	35,35,35,35	0
56	MG	2A	3128	1/1	0.88	0.27	51,51,51,51	0
56	MG	1A	3263	1/1	0.88	0.23	36,36,36,36	0
56	MG	2a	1615	1/1	0.88	0.18	63,63,63,63	0
56	MG	1A	3080	1/1	0.88	0.42	33,33,33,33	0
56	MG	2A	3483	1/1	0.88	0.18	51,51,51,51	0
56	MG	1A	3270	1/1	0.88	0.06	49,49,49,49	0
56	MG	1A	3504	1/1	0.88	0.07	44,44,44,44	0
56	MG	2A	3139	1/1	0.88	0.32	57,57,57,57	0
56	MG	2A	3037	1/1	0.88	0.20	66,66,66,66	0
56	MG	2k	201	1/1	0.88	0.19	64,64,64,64	0
56	MG	2A	3274	1/1	0.88	0.13	54,54,54,54	0
56	MG	1A	3366	1/1	0.88	0.20	44,44,44,44	0
56	MG	2a	1628	1/1	0.88	0.25	58,58,58,58	0
56	MG	1N	201	1/1	0.88	0.41	41,41,41,41	0
56	MG	1A	3917	1/1	0.88	0.14	40,40,40,40	0
56	MG	1A	3920	1/1	0.88	0.19	47,47,47,47	0
56	MG	1a	1655	1/1	0.88	0.34	51,51,51,51	0
56	MG	1A	3371	1/1	0.88	0.12	30,30,30,30	0
56	MG	1A	3383	1/1	0.88	0.09	33,33,33,33	0
56	MG	10	105	1/1	0.88	0.09	49,49,49,49	0
56	MG	2A	3531	1/1	0.88	0.23	65,65,65,65	0
56	MG	2A	3533	1/1	0.88	0.09	60,60,60,60	0
56	MG	1A	3204	1/1	0.88	0.18	45,45,45,45	0
56	MG	1A	3522	1/1	0.88	0.15	39,39,39,39	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3088	1/1	0.88	0.33	32,32,32,32	0
56	MG	1A	3526	1/1	0.88	0.10	36,36,36,36	0
56	MG	1A	3282	1/1	0.89	0.13	67,67,67,67	0
56	MG	1a	1802	1/1	0.89	0.10	71,71,71,71	0
56	MG	2A	3131	1/1	0.89	0.29	63,63,63,63	0
56	MG	1A	3426	1/1	0.89	0.13	32,32,32,32	0
56	MG	2A	3283	1/1	0.89	0.07	56,56,56,56	0
56	MG	2A	3285	1/1	0.89	0.12	49,49,49,49	0
56	MG	1B	201	1/1	0.89	0.16	53,53,53,53	0
56	MG	2A	3521	1/1	0.89	0.14	49,49,49,49	0
56	MG	1A	3614	1/1	0.89	0.10	42,42,42,42	0
56	MG	1a	1807	1/1	0.89	0.21	56,56,56,56	0
56	MG	2A	3301	1/1	0.89	0.09	52,52,52,52	0
56	MG	2A	3305	1/1	0.89	0.20	57,57,57,57	0
56	MG	1A	3117	1/1	0.89	0.23	45,45,45,45	0
56	MG	1A	3760	1/1	0.89	0.09	58,58,58,58	0
56	MG	2A	3311	1/1	0.89	0.15	45,45,45,45	0
56	MG	2A	3143	1/1	0.89	0.18	56,56,56,56	0
56	MG	1A	3005	1/1	0.89	0.18	40,40,40,40	0
56	MG	2A	3558	1/1	0.89	0.15	50,50,50,50	0
56	MG	2A	3146	1/1	0.89	0.32	55,55,55,55	0
56	MG	1A	3012	1/1	0.89	0.17	35,35,35,35	0
56	MG	2A	3035	1/1	0.89	0.21	70,70,70,70	0
56	MG	2A	3326	1/1	0.89	0.15	55,55,55,55	0
56	MG	1A	3778	1/1	0.89	0.10	53,53,53,53	0
56	MG	2A	3573	1/1	0.89	0.16	59,59,59,59	0
56	MG	1A	3181	1/1	0.89	0.07	45,45,45,45	0
56	MG	2A	3577	1/1	0.89	0.09	48,48,48,48	0
56	MG	2A	3578	1/1	0.89	0.14	51,51,51,51	0
56	MG	1A	3632	1/1	0.89	0.10	34,34,34,34	0
56	MG	1A	3793	1/1	0.89	0.08	37,37,37,37	0
56	MG	2A	3335	1/1	0.89	0.14	63,63,63,63	0
56	MG	1A	3636	1/1	0.89	0.10	42,42,42,42	0
56	MG	1A	3640	1/1	0.89	0.21	43,43,43,43	0
56	MG	1A	3084	1/1	0.89	0.14	49,49,49,49	0
56	MG	1A	3472	1/1	0.89	0.11	42,42,42,42	0
56	MG	1a	1826	1/1	0.89	0.19	68,68,68,68	0
56	MG	1A	3659	1/1	0.89	0.16	38,38,38,38	0
56	MG	1D	302	1/1	0.89	0.48	34,34,34,34	0
56	MG	1A	3818	1/1	0.89	0.12	29,29,29,29	0
56	MG	1A	3554	1/1	0.89	0.23	45,45,45,45	0
56	MG	1a	1832	1/1	0.89	0.15	73,73,73,73	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1a	1642	1/1	0.89	0.33	68,68,68,68	0
56	MG	1A	3249	1/1	0.89	0.11	48,48,48,48	0
56	MG	1A	3826	1/1	0.89	0.10	47,47,47,47	0
56	MG	1D	311	1/1	0.89	0.23	47,47,47,47	0
56	MG	1A	3323	1/1	0.89	0.14	42,42,42,42	0
56	MG	2a	1681	1/1	0.89	0.25	69,69,69,69	0
56	MG	2A	3672	1/1	0.89	0.18	64,64,64,64	0
56	MG	2A	3674	1/1	0.89	0.38	50,50,50,50	0
56	MG	1a	1648	1/1	0.89	0.21	57,57,57,57	0
56	MG	2a	1687	1/1	0.89	0.13	62,62,62,62	0
56	MG	2A	3386	1/1	0.89	0.28	48,48,48,48	0
56	MG	2a	1690	1/1	0.89	0.17	65,65,65,65	0
56	MG	1a	1745	1/1	0.89	0.15	54,54,54,54	0
56	MG	2A	3071	1/1	0.89	0.25	65,65,65,65	0
56	MG	1A	3325	1/1	0.89	0.18	42,42,42,42	0
56	MG	1A	3086	1/1	0.89	0.14	52,52,52,52	0
56	MG	1A	3684	1/1	0.89	0.07	50,50,50,50	0
56	MG	1a	1755	1/1	0.89	0.20	68,68,68,68	0
56	MG	2A	3194	1/1	0.89	0.09	54,54,54,54	0
56	MG	1A	3190	1/1	0.89	0.12	44,44,44,44	0
56	MG	1A	3569	1/1	0.89	0.11	30,30,30,30	0
56	MG	1a	1656	1/1	0.89	0.14	73,73,73,73	0
56	MG	1A	3574	1/1	0.89	0.11	32,32,32,32	0
56	MG	2a	1709	1/1	0.89	0.16	63,63,63,63	0
56	MG	1A	3134	1/1	0.89	0.21	38,38,38,38	0
56	MG	1A	3015	1/1	0.89	0.15	37,37,37,37	0
56	MG	1A	3707	1/1	0.89	0.13	52,52,52,52	0
56	MG	2A	3421	1/1	0.89	0.11	61,61,61,61	0
56	MG	1Q	201	1/1	0.89	0.16	41,41,41,41	0
56	MG	1A	3089	1/1	0.89	0.09	41,41,41,41	0
56	MG	1a	1665	1/1	0.89	0.22	55,55,55,55	0
56	MG	1U	204	1/1	0.89	0.32	35,35,35,35	0
56	MG	2F	303	1/1	0.89	0.14	50,50,50,50	0
56	MG	2A	3430	1/1	0.89	0.06	56,56,56,56	0
56	MG	1A	3021	1/1	0.89	0.25	36,36,36,36	0
56	MG	1A	3149	1/1	0.89	0.34	35,35,35,35	0
56	MG	2a	1752	1/1	0.89	0.13	64,64,64,64	0
56	MG	1A	3500	1/1	0.89	0.13	39,39,39,39	0
56	MG	1A	3910	1/1	0.89	0.26	39,39,39,39	0
56	MG	1A	3373	1/1	0.89	0.11	60,60,60,60	0
56	MG	1A	3104	1/1	0.89	0.36	32,32,32,32	0
56	MG	1A	3155	1/1	0.89	0.17	32,32,32,32	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3721	1/1	0.89	0.13	53,53,53,53	0
56	MG	2A	3448	1/1	0.89	0.11	47,47,47,47	0
56	MG	2A	3102	1/1	0.89	0.24	48,48,48,48	0
56	MG	2A	3454	1/1	0.89	0.10	60,60,60,60	0
56	MG	1a	1680	1/1	0.89	0.12	45,45,45,45	0
56	MG	1A	3158	1/1	0.89	0.10	42,42,42,42	0
56	MG	1x	108	1/1	0.89	0.29	65,65,65,65	0
56	MG	1A	3515	1/1	0.89	0.09	46,46,46,46	0
56	MG	1A	3600	1/1	0.89	0.10	38,38,38,38	0
56	MG	1A	3072	1/1	0.89	0.12	43,43,43,43	0
56	MG	1A	3022	1/1	0.89	0.08	43,43,43,43	0
56	MG	1A	3932	1/1	0.89	0.17	51,51,51,51	0
56	MG	2A	3005	1/1	0.89	0.15	53,53,53,53	0
56	MG	2A	3120	1/1	0.89	0.20	60,60,60,60	0
56	MG	2A	3006	1/1	0.89	0.28	52,52,52,52	0
56	MG	2A	3007	1/1	0.89	0.18	51,51,51,51	0
56	MG	2A	3250	1/1	0.89	0.13	48,48,48,48	0
56	MG	2A	3251	1/1	0.89	0.23	53,53,53,53	0
56	MG	1A	3168	1/1	0.89	0.16	39,39,39,39	0
56	MG	1A	3609	1/1	0.89	0.09	43,43,43,43	0
57	UNX	2A	3667	1/1	0.89	0.35	45,45,45,45	0
56	MG	2A	3489	1/1	0.89	0.22	55,55,55,55	0
56	MG	1a	1692	1/1	0.89	0.15	70,70,70,70	0
56	MG	1A	3746	1/1	0.89	0.10	40,40,40,40	0
56	MG	1A	3445	1/1	0.90	0.09	42,42,42,42	0
56	MG	1A	3935	1/1	0.90	0.16	38,38,38,38	0
56	MG	2A	3352	1/1	0.90	0.11	49,49,49,49	0
56	MG	1A	3936	1/1	0.90	0.14	32,32,32,32	0
56	MG	1A	3036	1/1	0.90	0.10	58,58,58,58	0
56	MG	2A	3564	1/1	0.90	0.08	68,68,68,68	0
56	MG	1A	3301	1/1	0.90	0.09	40,40,40,40	0
56	MG	2A	3358	1/1	0.90	0.10	43,43,43,43	0
56	MG	1a	1779	1/1	0.90	0.07	66,66,66,66	0
56	MG	1A	3551	1/1	0.90	0.42	54,54,54,54	0
56	MG	1A	3779	1/1	0.90	0.08	46,46,46,46	0
56	MG	2A	3370	1/1	0.90	0.14	62,62,62,62	0
56	MG	1A	3657	1/1	0.90	0.10	41,41,41,41	0
56	MG	1a	1688	1/1	0.90	0.32	58,58,58,58	0
56	MG	1A	3782	1/1	0.90	0.13	44,44,44,44	0
56	MG	1A	3040	1/1	0.90	0.20	49,49,49,49	0
56	MG	1A	3241	1/1	0.90	0.22	30,30,30,30	0
56	MG	1A	3183	1/1	0.90	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
56	MG	2A	3614	1/1	0.90	0.10	64,64,64,64	0
56	MG	1a	1794	1/1	0.90	0.35	69,69,69,69	0
56	MG	1A	3122	1/1	0.90	0.11	37,37,37,37	0
56	MG	2A	3212	1/1	0.90	0.27	53,53,53,53	0
56	MG	2A	3105	1/1	0.90	0.18	42,42,42,42	0
56	MG	2A	3394	1/1	0.90	0.07	62,62,62,62	0
56	MG	1A	3189	1/1	0.90	0.35	43,43,43,43	0
56	MG	2A	3217	1/1	0.90	0.21	53,53,53,53	0
56	MG	1A	3247	1/1	0.90	0.14	36,36,36,36	0
56	MG	2A	3399	1/1	0.90	0.14	53,53,53,53	0
56	MG	1A	3041	1/1	0.90	0.19	46,46,46,46	0
56	MG	2A	3659	1/1	0.90	0.07	60,60,60,60	0
56	MG	1A	3681	1/1	0.90	0.07	47,47,47,47	0
56	MG	2A	3113	1/1	0.90	0.19	59,59,59,59	0
56	MG	1a	1700	1/1	0.90	0.12	50,50,50,50	0
56	MG	2A	3666	1/1	0.90	0.14	54,54,54,54	0
56	MG	2A	3668	1/1	0.90	0.13	62,62,62,62	0
56	MG	2A	3224	1/1	0.90	0.43	46,46,46,46	0
56	MG	2A	3416	1/1	0.90	0.16	62,62,62,62	0
56	MG	2A	3676	1/1	0.90	0.10	54,54,54,54	0
56	MG	2A	3225	1/1	0.90	0.18	57,57,57,57	0
56	MG	1A	3484	1/1	0.90	0.21	43,43,43,43	0
56	MG	2A	3011	1/1	0.90	0.17	59,59,59,59	0
56	MG	2A	3013	1/1	0.90	0.09	57,57,57,57	0
56	MG	1A	3160	1/1	0.90	0.12	40,40,40,40	0
56	MG	1A	3201	1/1	0.90	0.19	25,25,25,25	0
56	MG	1A	3106	1/1	0.90	0.13	39,39,39,39	0
56	MG	1A	3580	1/1	0.90	0.18	48,48,48,48	0
56	MG	2A	3235	1/1	0.90	0.28	49,49,49,49	0
56	MG	1A	3043	1/1	0.90	0.31	29,29,29,29	0
56	MG	1A	3851	1/1	0.90	0.08	63,63,63,63	0
56	MG	1A	3363	1/1	0.90	0.14	54,54,54,54	0
56	MG	2B	3011	1/1	0.90	0.11	78,78,78,78	0
56	MG	1A	3138	1/1	0.90	0.05	50,50,50,50	0
56	MG	1D	308	1/1	0.90	0.08	42,42,42,42	0
56	MG	1A	3496	1/1	0.90	0.13	40,40,40,40	0
56	MG	1A	3170	1/1	0.90	0.24	42,42,42,42	0
56	MG	1A	3218	1/1	0.90	0.15	35,35,35,35	0
56	MG	1A	3506	1/1	0.90	0.07	44,44,44,44	0
56	MG	1D	317	1/1	0.90	0.30	35,35,35,35	0
56	MG	2A	3260	1/1	0.90	0.13	63,63,63,63	0
56	MG	1A	3876	1/1	0.90	0.18	32,32,32,32	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3115	1/1	0.90	0.21	41,41,41,41	0
56	MG	2A	3458	1/1	0.90	0.17	42,42,42,42	0
56	MG	2a	1716	1/1	0.90	0.25	72,72,72,72	0
56	MG	2A	3266	1/1	0.90	0.10	50,50,50,50	0
56	MG	1A	3508	1/1	0.90	0.13	53,53,53,53	0
56	MG	1A	3882	1/1	0.90	0.16	57,57,57,57	0
56	MG	1A	3388	1/1	0.90	0.10	42,42,42,42	0
56	MG	1G	3002	1/1	0.90	0.11	57,57,57,57	0
56	MG	1a	1654	1/1	0.90	0.16	71,71,71,71	0
56	MG	2A	3279	1/1	0.90	0.17	60,60,60,60	0
56	MG	2a	1602	1/1	0.90	0.12	64,64,64,64	0
56	MG	2A	3280	1/1	0.90	0.09	42,42,42,42	0
56	MG	1A	3221	1/1	0.90	0.38	29,29,29,29	0
56	MG	1a	1751	1/1	0.90	0.15	69,69,69,69	0
56	MG	2a	1759	1/1	0.90	0.08	78,78,78,78	0
56	MG	1A	3222	1/1	0.90	0.09	62,62,62,62	0
56	MG	1H	8002	1/1	0.90	0.16	44,44,44,44	0
56	MG	2a	1764	1/1	0.90	0.09	66,66,66,66	0
56	MG	1A	3174	1/1	0.90	0.11	56,56,56,56	0
56	MG	2A	3484	1/1	0.90	0.09	53,53,53,53	0
56	MG	2A	3486	1/1	0.90	0.28	54,54,54,54	0
56	MG	1A	3274	1/1	0.90	0.09	41,41,41,41	0
56	MG	1A	3413	1/1	0.90	0.15	24,24,24,24	0
56	MG	1T	202	1/1	0.90	0.07	51,51,51,51	0
56	MG	2A	3494	1/1	0.90	0.14	60,60,60,60	0
56	MG	1a	1663	1/1	0.90	0.15	74,74,74,74	0
56	MG	1A	3175	1/1	0.90	0.26	57,57,57,57	0
56	MG	1A	3743	1/1	0.90	0.09	41,41,41,41	0
56	MG	1A	3921	1/1	0.90	0.12	55,55,55,55	0
56	MG	1A	3176	1/1	0.90	0.43	33,33,33,33	0
56	MG	1A	3925	1/1	0.90	0.16	42,42,42,42	0
56	MG	1A	3616	1/1	0.90	0.07	67,67,67,67	0
56	MG	2x	102	1/1	0.90	0.13	73,73,73,73	0
56	MG	2a	1627	1/1	0.90	0.23	58,58,58,58	0
56	MG	2A	3076	1/1	0.90	0.42	49,49,49,49	0
56	MG	2A	3077	1/1	0.90	0.12	56,56,56,56	0
56	MG	1A	3529	1/1	0.90	0.14	44,44,44,44	0
56	MG	1A	3035	1/1	0.90	0.10	33,33,33,33	0
56	MG	1A	3057	1/1	0.90	0.22	32,32,32,32	0
56	MG	1a	1675	1/1	0.90	0.14	46,46,46,46	0
56	MG	2x	110	1/1	0.90	0.20	70,70,70,70	0
56	MG	1A	3544	1/1	0.90	0.08	59,59,59,59	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1g	3001	1/1	0.90	0.24	62,62,62,62	0
56	MG	2A	3340	1/1	0.90	0.17	50,50,50,50	0
56	MG	2A	3551	1/1	0.90	0.12	48,48,48,48	0
56	MG	2A	3254	1/1	0.91	0.24	42,42,42,42	0
56	MG	2a	1611	1/1	0.91	0.15	59,59,59,59	0
56	MG	2A	3256	1/1	0.91	0.17	56,56,56,56	0
56	MG	1A	3326	1/1	0.91	0.12	48,48,48,48	0
56	MG	1E	302	1/1	0.91	0.26	30,30,30,30	0
56	MG	1a	1666	1/1	0.91	0.19	65,65,65,65	0
56	MG	1A	3257	1/1	0.91	0.18	55,55,55,55	0
56	MG	1F	305	1/1	0.91	0.18	28,28,28,28	0
56	MG	1A	3689	1/1	0.91	0.12	37,37,37,37	0
56	MG	1A	3124	1/1	0.91	0.17	40,40,40,40	0
56	MG	2A	3129	1/1	0.91	0.26	49,49,49,49	0
56	MG	1A	3156	1/1	0.91	0.23	41,41,41,41	0
56	MG	2A	3017	1/1	0.91	0.36	48,48,48,48	0
56	MG	2A	3490	1/1	0.91	0.17	42,42,42,42	0
56	MG	2A	3492	1/1	0.91	0.13	45,45,45,45	0
56	MG	2A	3132	1/1	0.91	0.15	49,49,49,49	0
56	MG	2a	1629	1/1	0.91	0.09	78,78,78,78	0
56	MG	2A	3020	1/1	0.91	0.16	49,49,49,49	0
56	MG	1A	3871	1/1	0.91	0.12	43,43,43,43	0
56	MG	2A	3501	1/1	0.91	0.07	60,60,60,60	0
56	MG	1A	3341	1/1	0.91	0.09	35,35,35,35	0
56	MG	1A	3701	1/1	0.91	0.12	47,47,47,47	0
56	MG	2A	3506	1/1	0.91	0.15	61,61,61,61	0
56	MG	1A	3128	1/1	0.91	0.21	43,43,43,43	0
56	MG	1A	3877	1/1	0.91	0.09	35,35,35,35	0
56	MG	2A	3026	1/1	0.91	0.17	41,41,41,41	0
56	MG	1A	3091	1/1	0.91	0.23	23,23,23,23	0
56	MG	1A	3267	1/1	0.91	0.24	52,52,52,52	0
56	MG	1A	3489	1/1	0.91	0.12	32,32,32,32	0
56	MG	1A	3268	1/1	0.91	0.21	40,40,40,40	0
56	MG	2A	3152	1/1	0.91	0.27	51,51,51,51	0
56	MG	2A	3032	1/1	0.91	0.29	63,63,63,63	0
56	MG	2A	3529	1/1	0.91	0.13	59,59,59,59	0
56	MG	1V	203	1/1	0.91	0.06	62,62,62,62	0
56	MG	1A	3225	1/1	0.91	0.48	38,38,38,38	0
56	MG	1A	3895	1/1	0.91	0.12	35,35,35,35	0
56	MG	2A	3544	1/1	0.91	0.08	61,61,61,61	0
56	MG	1A	3904	1/1	0.91	0.07	53,53,53,53	0
56	MG	1A	3227	1/1	0.91	0.09	39,39,39,39	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2A	3161	1/1	0.91	0.14	47,47,47,47	0
56	MG	13	102	1/1	0.91	0.16	53,53,53,53	0
56	MG	2A	3166	1/1	0.91	0.28	49,49,49,49	0
56	MG	1A	3908	1/1	0.91	0.09	41,41,41,41	0
56	MG	1A	3379	1/1	0.91	0.15	43,43,43,43	0
56	MG	1A	3497	1/1	0.91	0.31	45,45,45,45	0
56	MG	1A	3039	1/1	0.91	0.28	53,53,53,53	0
56	MG	2A	3344	1/1	0.91	0.22	61,61,61,61	0
56	MG	1A	3188	1/1	0.91	0.08	42,42,42,42	0
56	MG	1A	3594	1/1	0.91	0.10	48,48,48,48	0
56	MG	2A	3351	1/1	0.91	0.09	53,53,53,53	0
56	MG	2A	3576	1/1	0.91	0.08	70,70,70,70	0
56	MG	2A	3050	1/1	0.91	0.11	56,56,56,56	0
56	MG	1A	3596	1/1	0.91	0.08	41,41,41,41	0
56	MG	2A	3354	1/1	0.91	0.08	59,59,59,59	0
56	MG	1a	1699	1/1	0.91	0.16	68,68,68,68	0
56	MG	1A	3118	1/1	0.91	0.33	39,39,39,39	0
56	MG	1A	3730	1/1	0.91	0.32	40,40,40,40	0
56	MG	1A	3393	1/1	0.91	0.10	31,31,31,31	0
56	MG	2A	3606	1/1	0.91	0.08	47,47,47,47	0
56	MG	2A	3363	1/1	0.91	0.09	44,44,44,44	0
56	MG	1A	3396	1/1	0.91	0.16	41,41,41,41	0
56	MG	2A	3624	1/1	0.91	0.09	48,48,48,48	0
56	MG	2A	3626	1/1	0.91	0.10	49,49,49,49	0
56	MG	1A	3605	1/1	0.91	0.08	47,47,47,47	0
56	MG	2a	1679	1/1	0.91	0.37	62,62,62,62	0
56	MG	2A	3630	1/1	0.91	0.22	50,50,50,50	0
56	MG	1A	3233	1/1	0.91	0.26	50,50,50,50	0
56	MG	2A	3640	1/1	0.91	0.19	59,59,59,59	0
56	MG	2A	3186	1/1	0.91	0.31	59,59,59,59	0
56	MG	1A	3400	1/1	0.91	0.14	61,61,61,61	0
56	MG	2A	3375	1/1	0.91	0.20	50,50,50,50	0
56	MG	1a	1839	1/1	0.91	0.10	63,63,63,63	0
56	MG	1A	3167	1/1	0.91	0.20	50,50,50,50	0
56	MG	2A	3652	1/1	0.91	0.27	41,41,41,41	0
56	MG	2A	3653	1/1	0.91	0.29	52,52,52,52	0
56	MG	1A	3410	1/1	0.91	0.07	50,50,50,50	0
56	MG	1A	3085	1/1	0.91	0.27	42,42,42,42	0
56	MG	1A	3285	1/1	0.91	0.13	37,37,37,37	0
56	MG	1A	3943	1/1	0.91	0.12	47,47,47,47	0
56	MG	2A	3198	1/1	0.91	0.32	59,59,59,59	0
56	MG	2A	3390	1/1	0.91	0.11	49,49,49,49	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1a	1628	1/1	0.91	0.38	63,63,63,63	0
56	MG	1A	3291	1/1	0.91	0.19	26,26,26,26	0
56	MG	1A	3946	1/1	0.91	0.21	29,29,29,29	0
56	MG	2A	3673	1/1	0.91	0.13	51,51,51,51	0
56	MG	1A	3619	1/1	0.91	0.18	32,32,32,32	0
56	MG	1A	3200	1/1	0.91	0.07	46,46,46,46	0
56	MG	1A	3120	1/1	0.91	0.08	55,55,55,55	0
56	MG	2A	3678	1/1	0.91	0.11	53,53,53,53	0
56	MG	1A	3769	1/1	0.91	0.05	67,67,67,67	0
56	MG	1A	3532	1/1	0.91	0.08	40,40,40,40	0
56	MG	2A	3409	1/1	0.91	0.12	56,56,56,56	0
56	MG	1A	3626	1/1	0.91	0.11	51,51,51,51	0
56	MG	2A	3210	1/1	0.91	0.20	42,42,42,42	0
56	MG	2A	3211	1/1	0.91	0.17	60,60,60,60	0
56	MG	2a	1724	1/1	0.91	0.07	74,74,74,74	0
56	MG	1A	3435	1/1	0.91	0.14	35,35,35,35	0
56	MG	1A	3630	1/1	0.91	0.10	37,37,37,37	0
56	MG	2A	3214	1/1	0.91	0.37	49,49,49,49	0
56	MG	1A	3790	1/1	0.91	0.09	32,32,32,32	0
56	MG	1a	1749	1/1	0.91	0.09	59,59,59,59	0
56	MG	1A	3042	1/1	0.91	0.30	21,21,21,21	0
56	MG	2a	1757	1/1	0.91	0.10	69,69,69,69	0
56	MG	2A	3425	1/1	0.91	0.09	48,48,48,48	0
56	MG	1A	3147	1/1	0.91	0.45	36,36,36,36	0
56	MG	1A	3451	1/1	0.91	0.10	38,38,38,38	0
56	MG	1A	3796	1/1	0.91	0.21	37,37,37,37	0
56	MG	1A	3641	1/1	0.91	0.11	40,40,40,40	0
56	MG	2D	303	1/1	0.91	0.09	58,58,58,58	0
56	MG	2D	306	1/1	0.91	0.11	54,54,54,54	0
56	MG	1B	225	1/1	0.91	0.16	55,55,55,55	0
56	MG	1A	3645	1/1	0.91	0.16	37,37,37,37	0
56	MG	2A	3436	1/1	0.91	0.12	41,41,41,41	0
56	MG	2f	3001	1/1	0.91	0.14	67,67,67,67	0
56	MG	2F	301	1/1	0.91	0.11	45,45,45,45	0
56	MG	1A	3058	1/1	0.91	0.16	52,52,52,52	0
56	MG	1A	3215	1/1	0.91	0.19	48,48,48,48	0
56	MG	2A	3101	1/1	0.91	0.26	47,47,47,47	0
56	MG	1A	3466	1/1	0.91	0.23	29,29,29,29	0
56	MG	2I	3001	1/1	0.91	0.13	74,74,74,74	0
56	MG	1A	3153	1/1	0.91	0.23	49,49,49,49	0
56	MG	1A	3177	1/1	0.91	0.11	35,35,35,35	0
56	MG	1A	3470	1/1	0.91	0.06	37,37,37,37	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2A	3110	1/1	0.91	0.32	53,53,53,53	0
56	MG	1A	3556	1/1	0.91	0.27	39,39,39,39	0
56	MG	23	101	1/1	0.91	0.11	58,58,58,58	0
56	MG	28	102	1/1	0.91	0.14	49,49,49,49	0
56	MG	1A	3836	1/1	0.91	0.09	42,42,42,42	0
56	MG	1A	3838	1/1	0.91	0.11	45,45,45,45	0
56	MG	1A	3027	1/1	0.91	0.44	39,39,39,39	0
56	MG	1D	315	1/1	0.91	0.22	49,49,49,49	0
56	MG	1A	3843	1/1	0.91	0.11	29,29,29,29	0
56	MG	1A	3846	1/1	0.91	0.10	31,31,31,31	0
56	MG	1a	1662	1/1	0.91	0.09	70,70,70,70	0
56	MG	1A	3558	1/1	0.91	0.21	31,31,31,31	0
56	MG	1a	1650	1/1	0.92	0.29	51,51,51,51	0
56	MG	1A	3875	1/1	0.92	0.11	28,28,28,28	0
56	MG	1D	312	1/1	0.92	0.10	48,48,48,48	0
56	MG	2A	3491	1/1	0.92	0.22	58,58,58,58	0
56	MG	2A	3276	1/1	0.92	0.11	47,47,47,47	0
56	MG	1A	3360	1/1	0.92	0.10	44,44,44,44	0
56	MG	1A	3205	1/1	0.92	0.07	30,30,30,30	0
56	MG	2A	3496	1/1	0.92	0.08	45,45,45,45	0
56	MG	1A	3539	1/1	0.92	0.21	53,53,53,53	0
56	MG	2a	1622	1/1	0.92	0.40	56,56,56,56	0
56	MG	1A	3540	1/1	0.92	0.16	42,42,42,42	0
56	MG	2A	3136	1/1	0.92	0.12	54,54,54,54	0
56	MG	1A	3542	1/1	0.92	0.09	49,49,49,49	0
56	MG	1A	3883	1/1	0.92	0.28	47,47,47,47	0
56	MG	2A	3508	1/1	0.92	0.15	50,50,50,50	0
56	MG	2A	3015	1/1	0.92	0.19	51,51,51,51	0
56	MG	2A	3514	1/1	0.92	0.07	63,63,63,63	0
56	MG	1A	3888	1/1	0.92	0.48	32,32,32,32	0
56	MG	2A	3019	1/1	0.92	0.07	51,51,51,51	0
56	MG	1E	303	1/1	0.92	0.43	33,33,33,33	0
56	MG	1E	304	1/1	0.92	0.08	50,50,50,50	0
56	MG	1a	1778	1/1	0.92	0.09	63,63,63,63	0
56	MG	2A	3149	1/1	0.92	0.15	44,44,44,44	0
56	MG	2A	3525	1/1	0.92	0.08	55,55,55,55	0
56	MG	1E	305	1/1	0.92	0.19	31,31,31,31	0
56	MG	2A	3317	1/1	0.92	0.08	54,54,54,54	0
56	MG	2A	3321	1/1	0.92	0.13	48,48,48,48	0
56	MG	2A	3530	1/1	0.92	0.09	56,56,56,56	0
56	MG	2A	3153	1/1	0.92	0.16	51,51,51,51	0
56	MG	1A	3739	1/1	0.92	0.11	28,28,28,28	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3033	1/1	0.92	0.18	45,45,45,45	0
56	MG	1F	306	1/1	0.92	0.24	31,31,31,31	0
56	MG	1A	3365	1/1	0.92	0.08	43,43,43,43	0
56	MG	1A	3902	1/1	0.92	0.22	35,35,35,35	0
56	MG	1a	1787	1/1	0.92	0.08	65,65,65,65	0
56	MG	1A	3178	1/1	0.92	0.19	37,37,37,37	0
56	MG	1A	3107	1/1	0.92	0.10	32,32,32,32	0
56	MG	2A	3163	1/1	0.92	0.38	48,48,48,48	0
56	MG	1A	3082	1/1	0.92	0.15	59,59,59,59	0
56	MG	2A	3342	1/1	0.92	0.24	61,61,61,61	0
56	MG	1A	3909	1/1	0.92	0.18	43,43,43,43	0
56	MG	1A	3378	1/1	0.92	0.10	40,40,40,40	0
56	MG	1a	1796	1/1	0.92	0.11	68,68,68,68	0
56	MG	1a	1798	1/1	0.92	0.07	71,71,71,71	0
56	MG	1N	202	1/1	0.92	0.07	46,46,46,46	0
56	MG	1A	3631	1/1	0.92	0.12	43,43,43,43	0
56	MG	1A	3478	1/1	0.92	0.07	41,41,41,41	0
56	MG	2A	3042	1/1	0.92	0.13	57,57,57,57	0
56	MG	2A	3356	1/1	0.92	0.16	55,55,55,55	0
56	MG	2A	3580	1/1	0.92	0.19	52,52,52,52	0
56	MG	1A	3633	1/1	0.92	0.14	31,31,31,31	0
56	MG	2A	3044	1/1	0.92	0.25	61,61,61,61	0
56	MG	2a	1667	1/1	0.92	0.17	66,66,66,66	0
56	MG	2A	3179	1/1	0.92	0.13	52,52,52,52	0
56	MG	1U	203	1/1	0.92	0.26	36,36,36,36	0
56	MG	1A	3919	1/1	0.92	0.18	41,41,41,41	0
56	MG	2A	3365	1/1	0.92	0.14	48,48,48,48	0
56	MG	1A	3019	1/1	0.92	0.36	27,27,27,27	0
56	MG	2A	3623	1/1	0.92	0.09	51,51,51,51	0
56	MG	1A	3639	1/1	0.92	0.22	45,45,45,45	0
56	MG	1A	3293	1/1	0.92	0.11	35,35,35,35	0
56	MG	1a	1810	1/1	0.92	0.22	74,74,74,74	0
56	MG	1A	3924	1/1	0.92	0.13	51,51,51,51	0
56	MG	10	102	1/1	0.92	0.15	43,43,43,43	0
56	MG	1A	3768	1/1	0.92	0.16	27,27,27,27	0
56	MG	2A	3382	1/1	0.92	0.22	56,56,56,56	0
56	MG	1A	3385	1/1	0.92	0.13	53,53,53,53	0
56	MG	2A	3192	1/1	0.92	0.08	50,50,50,50	0
56	MG	2A	3193	1/1	0.92	0.33	66,66,66,66	0
56	MG	1A	3386	1/1	0.92	0.12	32,32,32,32	0
56	MG	1A	3161	1/1	0.92	0.13	35,35,35,35	0
56	MG	2a	1688	1/1	0.92	0.07	58,58,58,58	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	17	102	1/1	0.92	0.08	35,35,35,35	0
56	MG	2A	3391	1/1	0.92	0.09	48,48,48,48	0
56	MG	1a	1601	1/1	0.92	0.16	50,50,50,50	0
56	MG	1A	3929	1/1	0.92	0.29	31,31,31,31	0
56	MG	2A	3395	1/1	0.92	0.15	58,58,58,58	0
56	MG	1A	3389	1/1	0.92	0.10	44,44,44,44	0
56	MG	1A	3931	1/1	0.92	0.17	42,42,42,42	0
56	MG	1A	3295	1/1	0.92	0.17	50,50,50,50	0
56	MG	1A	3164	1/1	0.92	0.38	29,29,29,29	0
56	MG	1A	3791	1/1	0.92	0.11	60,60,60,60	0
56	MG	1A	3661	1/1	0.92	0.10	40,40,40,40	0
56	MG	1A	3939	1/1	0.92	0.18	32,32,32,32	0
56	MG	2A	3208	1/1	0.92	0.18	50,50,50,50	0
56	MG	1A	3941	1/1	0.92	0.07	49,49,49,49	0
56	MG	2a	1711	1/1	0.92	0.49	77,77,77,77	0
56	MG	1a	1710	1/1	0.92	0.16	58,58,58,58	0
56	MG	1A	3186	1/1	0.92	0.12	34,34,34,34	0
56	MG	1A	3023	1/1	0.92	0.16	35,35,35,35	0
56	MG	1A	3666	1/1	0.92	0.14	37,37,37,37	0
56	MG	1A	3141	1/1	0.92	0.08	43,43,43,43	0
56	MG	1A	3676	1/1	0.92	0.17	34,34,34,34	0
56	MG	1A	3048	1/1	0.92	0.33	40,40,40,40	0
56	MG	1a	1622	1/1	0.92	0.22	65,65,65,65	0
56	MG	1a	1727	1/1	0.92	0.12	51,51,51,51	0
56	MG	1a	1623	1/1	0.92	0.09	65,65,65,65	0
56	MG	1A	3815	1/1	0.92	0.09	27,27,27,27	0
56	MG	2a	1730	1/1	0.92	0.09	66,66,66,66	0
56	MG	1a	1731	1/1	0.92	0.16	63,63,63,63	0
56	MG	1A	3403	1/1	0.92	0.10	35,35,35,35	0
56	MG	1B	203	1/1	0.92	0.18	55,55,55,55	0
56	MG	1a	1734	1/1	0.92	0.10	54,54,54,54	0
56	MG	1A	3261	1/1	0.92	0.22	52,52,52,52	0
56	MG	1A	3262	1/1	0.92	0.20	42,42,42,42	0
56	MG	1d	504	1/1	0.92	0.07	82,82,82,82	0
56	MG	1A	3685	1/1	0.92	0.15	42,42,42,42	0
56	MG	2D	305	1/1	0.92	0.13	46,46,46,46	0
56	MG	1A	3053	1/1	0.92	0.43	34,34,34,34	0
56	MG	1A	3414	1/1	0.92	0.11	63,63,63,63	0
56	MG	1A	3191	1/1	0.92	0.19	40,40,40,40	0
56	MG	2a	1772	1/1	0.92	0.15	62,62,62,62	0
56	MG	1A	3589	1/1	0.92	0.15	46,46,46,46	0
56	MG	1A	3420	1/1	0.92	0.06	43,43,43,43	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3028	1/1	0.92	0.08	39,39,39,39	0
56	MG	1A	3030	1/1	0.92	0.10	28,28,28,28	0
56	MG	2a	1783	1/1	0.92	0.16	67,67,67,67	0
56	MG	1a	1750	1/1	0.92	0.11	63,63,63,63	0
56	MG	1A	3431	1/1	0.92	0.09	29,29,29,29	0
56	MG	1A	3597	1/1	0.92	0.15	34,34,34,34	0
56	MG	1a	1753	1/1	0.92	0.19	50,50,50,50	0
56	MG	1A	3333	1/1	0.92	0.09	45,45,45,45	0
56	MG	2R	8001	1/1	0.92	0.16	50,50,50,50	0
56	MG	1A	3337	1/1	0.92	0.11	36,36,36,36	0
56	MG	2A	3467	1/1	0.92	0.08	62,62,62,62	0
56	MG	1A	3860	1/1	0.92	0.16	35,35,35,35	0
56	MG	20	8001	1/1	0.92	0.12	60,60,60,60	0
56	MG	2I	101	1/1	0.92	0.07	54,54,54,54	0
56	MG	2A	3471	1/1	0.92	0.13	48,48,48,48	0
56	MG	1a	1643	1/1	0.92	0.07	65,65,65,65	0
56	MG	2A	3473	1/1	0.92	0.06	57,57,57,57	0
56	MG	1A	3096	1/1	0.92	0.16	33,33,33,33	0
56	MG	2A	3262	1/1	0.92	0.22	49,49,49,49	0
56	MG	1A	3528	1/1	0.92	0.20	45,45,45,45	0
56	MG	1A	3076	1/1	0.92	0.43	37,37,37,37	0
56	MG	2A	3481	1/1	0.92	0.11	59,59,59,59	0
57	UNX	1A	3906	1/1	0.92	0.32	38,38,38,38	0
56	MG	1A	3024	1/1	0.92	0.35	34,34,34,34	0
56	MG	1A	3534	1/1	0.92	0.07	36,36,36,36	0
56	MG	2A	3271	1/1	0.92	0.10	60,60,60,60	0
59	ARG	1B	229	12/12	0.92	0.14	41,46,51,52	0
56	MG	1D	310	1/1	0.92	0.10	36,36,36,36	0
56	MG	2A	3137	1/1	0.93	0.25	49,49,49,49	0
56	MG	2A	3609	1/1	0.93	0.06	58,58,58,58	0
56	MG	1a	1833	1/1	0.93	0.06	73,73,73,73	0
56	MG	2A	3414	1/1	0.93	0.10	53,53,53,53	0
56	MG	1A	3083	1/1	0.93	0.09	34,34,34,34	0
56	MG	1A	3137	1/1	0.93	0.13	32,32,32,32	0
56	MG	1A	3495	1/1	0.93	0.08	37,37,37,37	0
56	MG	1A	3252	1/1	0.93	0.40	41,41,41,41	0
56	MG	1A	3561	1/1	0.93	0.08	54,54,54,54	0
56	MG	2A	3631	1/1	0.93	0.07	57,57,57,57	0
56	MG	2A	3259	1/1	0.93	0.23	59,59,59,59	0
56	MG	2A	3639	1/1	0.93	0.09	57,57,57,57	0
56	MG	1A	3563	1/1	0.93	0.18	23,23,23,23	0
56	MG	1A	3254	1/1	0.93	0.10	52,52,52,52	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1a	1850	1/1	0.93	0.10	72,72,72,72	0
56	MG	2A	3150	1/1	0.93	0.28	46,46,46,46	0
56	MG	1A	3362	1/1	0.93	0.07	41,41,41,41	0
56	MG	15	101	1/1	0.93	0.20	32,32,32,32	0
56	MG	2A	3432	1/1	0.93	0.06	49,49,49,49	0
56	MG	1A	3571	1/1	0.93	0.08	45,45,45,45	0
56	MG	2A	3053	1/1	0.93	0.32	58,58,58,58	0
56	MG	1A	3097	1/1	0.93	0.32	34,34,34,34	0
56	MG	19	101	1/1	0.93	0.24	48,48,48,48	0
56	MG	1A	3649	1/1	0.93	0.11	36,36,36,36	0
56	MG	2A	3058	1/1	0.93	0.13	31,31,31,31	0
56	MG	1B	214	1/1	0.93	0.18	44,44,44,44	0
56	MG	2A	3664	1/1	0.93	0.08	55,55,55,55	0
56	MG	1A	3747	1/1	0.93	0.07	40,40,40,40	0
56	MG	2A	3282	1/1	0.93	0.11	49,49,49,49	0
56	MG	2A	3062	1/1	0.93	0.29	44,44,44,44	0
56	MG	2A	3063	1/1	0.93	0.08	53,53,53,53	0
56	MG	2A	3286	1/1	0.93	0.13	51,51,51,51	0
56	MG	1A	3195	1/1	0.93	0.13	41,41,41,41	0
56	MG	1a	1605	1/1	0.93	0.09	67,67,67,67	0
56	MG	1a	1676	1/1	0.93	0.28	54,54,54,54	0
56	MG	2A	3170	1/1	0.93	0.14	52,52,52,52	0
56	MG	1B	217	1/1	0.93	0.08	59,59,59,59	0
56	MG	2A	3464	1/1	0.93	0.14	65,65,65,65	0
56	MG	2A	3070	1/1	0.93	0.12	49,49,49,49	0
56	MG	1A	3006	1/1	0.93	0.16	34,34,34,34	0
56	MG	1a	1608	1/1	0.93	0.12	78,78,78,78	0
56	MG	1B	220	1/1	0.93	0.14	44,44,44,44	0
56	MG	2A	3075	1/1	0.93	0.11	42,42,42,42	0
56	MG	2A	3315	1/1	0.93	0.10	48,48,48,48	0
56	MG	1A	3752	1/1	0.93	0.07	50,50,50,50	0
56	MG	1A	3296	1/1	0.93	0.07	45,45,45,45	0
56	MG	2a	1691	1/1	0.93	0.18	60,60,60,60	0
56	MG	2A	3318	1/1	0.93	0.10	50,50,50,50	0
56	MG	2A	3320	1/1	0.93	0.07	56,56,56,56	0
56	MG	2A	3478	1/1	0.93	0.10	50,50,50,50	0
56	MG	1A	3060	1/1	0.93	0.18	33,33,33,33	0
56	MG	1A	3375	1/1	0.93	0.06	56,56,56,56	0
56	MG	1A	3885	1/1	0.93	0.22	30,30,30,30	0
56	MG	2a	1700	1/1	0.93	0.08	65,65,65,65	0
56	MG	2A	3324	1/1	0.93	0.22	51,51,51,51	0
56	MG	1A	3887	1/1	0.93	0.10	36,36,36,36	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3376	1/1	0.93	0.10	29,29,29,29	0
56	MG	1A	3519	1/1	0.93	0.09	56,56,56,56	0
56	MG	2a	1707	1/1	0.93	0.15	68,68,68,68	0
56	MG	1A	3892	1/1	0.93	0.26	31,31,31,31	0
56	MG	1a	1784	1/1	0.93	0.12	60,60,60,60	0
56	MG	1x	102	1/1	0.93	0.20	64,64,64,64	0
56	MG	1A	3765	1/1	0.93	0.08	54,54,54,54	0
56	MG	1A	3377	1/1	0.93	0.09	34,34,34,34	0
56	MG	2A	3338	1/1	0.93	0.22	40,40,40,40	0
56	MG	2A	3495	1/1	0.93	0.08	65,65,65,65	0
56	MG	1x	105	1/1	0.93	0.15	64,64,64,64	0
56	MG	1A	3670	1/1	0.93	0.15	46,46,46,46	0
56	MG	2A	3500	1/1	0.93	0.11	51,51,51,51	0
56	MG	2Q	202	1/1	0.93	0.15	61,61,61,61	0
56	MG	1x	107	1/1	0.93	0.16	56,56,56,56	0
56	MG	2A	3346	1/1	0.93	0.13	60,60,60,60	0
56	MG	1A	3773	1/1	0.93	0.08	44,44,44,44	0
56	MG	2V	202	1/1	0.93	0.15	53,53,53,53	0
56	MG	2a	1732	1/1	0.93	0.05	74,74,74,74	0
56	MG	2a	1734	1/1	0.93	0.08	69,69,69,69	0
56	MG	1a	1626	1/1	0.93	0.13	60,60,60,60	0
56	MG	2A	3095	1/1	0.93	0.22	47,47,47,47	0
56	MG	2a	1747	1/1	0.93	0.08	66,66,66,66	0
56	MG	1A	3457	1/1	0.93	0.08	28,28,28,28	0
56	MG	1A	3672	1/1	0.93	0.12	45,45,45,45	0
56	MG	1A	3226	1/1	0.93	0.37	36,36,36,36	0
56	MG	1A	3463	1/1	0.93	0.09	31,31,31,31	0
56	MG	2A	3003	1/1	0.93	0.10	54,54,54,54	0
56	MG	1A	3465	1/1	0.93	0.06	50,50,50,50	0
56	MG	1A	3026	1/1	0.93	0.27	32,32,32,32	0
56	MG	1A	3380	1/1	0.93	0.19	44,44,44,44	0
56	MG	1A	3017	1/1	0.93	0.22	25,25,25,25	0
56	MG	1A	3533	1/1	0.93	0.07	51,51,51,51	0
56	MG	2a	1769	1/1	0.93	0.09	73,73,73,73	0
56	MG	2a	1770	1/1	0.93	0.06	68,68,68,68	0
56	MG	1A	3008	1/1	0.93	0.20	47,47,47,47	0
56	MG	1a	1805	1/1	0.93	0.13	70,70,70,70	0
56	MG	1A	3112	1/1	0.93	0.17	37,37,37,37	0
56	MG	2a	1777	1/1	0.93	0.12	66,66,66,66	0
56	MG	1A	3473	1/1	0.93	0.16	39,39,39,39	0
56	MG	2A	3532	1/1	0.93	0.10	50,50,50,50	0
56	MG	1F	303	1/1	0.93	0.29	38,38,38,38	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3809	1/1	0.93	0.06	40,40,40,40	0
56	MG	1A	3321	1/1	0.93	0.16	26,26,26,26	0
56	MG	2A	3117	1/1	0.93	0.18	55,55,55,55	0
56	MG	1A	3207	1/1	0.93	0.21	35,35,35,35	0
56	MG	1A	3391	1/1	0.93	0.09	50,50,50,50	0
56	MG	1A	3185	1/1	0.93	0.10	42,42,42,42	0
56	MG	1A	3820	1/1	0.93	0.11	33,33,33,33	0
56	MG	1A	3480	1/1	0.93	0.07	35,35,35,35	0
56	MG	1A	3209	1/1	0.93	0.37	40,40,40,40	0
56	MG	1A	3824	1/1	0.93	0.12	51,51,51,51	0
56	MG	1A	3211	1/1	0.93	0.64	30,30,30,30	0
56	MG	2A	3568	1/1	0.93	0.12	56,56,56,56	0
56	MG	2A	3392	1/1	0.93	0.12	52,52,52,52	0
56	MG	1a	1821	1/1	0.93	0.07	76,76,76,76	0
56	MG	1A	3832	1/1	0.93	0.11	45,45,45,45	0
56	MG	2A	3030	1/1	0.93	0.20	51,51,51,51	0
56	MG	1A	3330	1/1	0.93	0.20	33,33,33,33	0
56	MG	1A	3213	1/1	0.93	0.39	37,37,37,37	0
56	MG	2A	3236	1/1	0.93	0.17	50,50,50,50	0
56	MG	1R	201	1/1	0.93	0.19	35,35,35,35	0
56	MG	2A	3400	1/1	0.93	0.17	54,54,54,54	0
56	MG	1R	203	1/1	0.93	0.10	39,39,39,39	0
56	MG	1A	3020	1/1	0.93	0.28	36,36,36,36	0
56	MG	1A	3093	1/1	0.93	0.18	50,50,50,50	0
56	MG	1A	3133	1/1	0.93	0.17	35,35,35,35	0
56	MG	1A	3564	1/1	0.94	0.09	35,35,35,35	0
56	MG	1A	3566	1/1	0.94	0.10	41,41,41,41	0
56	MG	1A	3813	1/1	0.94	0.07	35,35,35,35	0
56	MG	1A	3669	1/1	0.94	0.06	64,64,64,64	0
56	MG	2A	3281	1/1	0.94	0.10	52,52,52,52	0
56	MG	1A	3310	1/1	0.94	0.08	30,30,30,30	0
56	MG	1A	3063	1/1	0.94	0.09	37,37,37,37	0
56	MG	1B	210	1/1	0.94	0.06	57,57,57,57	0
56	MG	1A	3136	1/1	0.94	0.07	33,33,33,33	0
56	MG	1A	3095	1/1	0.94	0.26	44,44,44,44	0
56	MG	2a	1617	1/1	0.94	0.16	51,51,51,51	0
56	MG	1A	3575	1/1	0.94	0.12	55,55,55,55	0
56	MG	2A	3293	1/1	0.94	0.07	63,63,63,63	0
56	MG	1A	3823	1/1	0.94	0.09	59,59,59,59	0
56	MG	1A	3318	1/1	0.94	0.08	25,25,25,25	0
56	MG	2A	3304	1/1	0.94	0.14	53,53,53,53	0
56	MG	1A	3319	1/1	0.94	0.07	43,43,43,43	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3831	1/1	0.94	0.07	58,58,58,58	0
56	MG	1A	3682	1/1	0.94	0.08	41,41,41,41	0
56	MG	1A	3833	1/1	0.94	0.06	59,59,59,59	0
56	MG	1A	3038	1/1	0.94	0.20	39,39,39,39	0
56	MG	2A	3145	1/1	0.94	0.35	53,53,53,53	0
56	MG	1A	3322	1/1	0.94	0.06	68,68,68,68	0
56	MG	1A	3837	1/1	0.94	0.08	46,46,46,46	0
56	MG	1A	3687	1/1	0.94	0.15	46,46,46,46	0
56	MG	1B	230	1/1	0.94	0.08	55,55,55,55	0
56	MG	1A	3839	1/1	0.94	0.18	41,41,41,41	0
56	MG	1a	1775	1/1	0.94	0.14	66,66,66,66	0
56	MG	1A	3688	1/1	0.94	0.16	40,40,40,40	0
56	MG	1A	3582	1/1	0.94	0.30	39,39,39,39	0
56	MG	1A	3845	1/1	0.94	0.07	32,32,32,32	0
56	MG	1A	3402	1/1	0.94	0.07	36,36,36,36	0
56	MG	1A	3847	1/1	0.94	0.07	46,46,46,46	0
56	MG	1A	3003	1/1	0.94	0.14	40,40,40,40	0
56	MG	1A	3324	1/1	0.94	0.08	34,34,34,34	0
56	MG	2A	3333	1/1	0.94	0.13	58,58,58,58	0
56	MG	1A	3700	1/1	0.94	0.07	35,35,35,35	0
56	MG	2a	1645	1/1	0.94	0.15	68,68,68,68	0
56	MG	1A	3046	1/1	0.94	0.23	37,37,37,37	0
56	MG	2A	3534	1/1	0.94	0.19	50,50,50,50	0
56	MG	1A	3859	1/1	0.94	0.06	35,35,35,35	0
56	MG	1A	3702	1/1	0.94	0.10	37,37,37,37	0
56	MG	2A	3034	1/1	0.94	0.21	49,49,49,49	0
56	MG	1a	1788	1/1	0.94	0.07	67,67,67,67	0
56	MG	1A	3864	1/1	0.94	0.10	42,42,42,42	0
56	MG	1a	1790	1/1	0.94	0.08	59,59,59,59	0
56	MG	1D	318	1/1	0.94	0.18	51,51,51,51	0
56	MG	1A	3100	1/1	0.94	0.15	28,28,28,28	0
56	MG	1A	3704	1/1	0.94	0.12	36,36,36,36	0
56	MG	2A	3350	1/1	0.94	0.13	65,65,65,65	0
56	MG	1A	3327	1/1	0.94	0.06	46,46,46,46	0
56	MG	2A	3566	1/1	0.94	0.11	62,62,62,62	0
56	MG	1A	3194	1/1	0.94	0.09	40,40,40,40	0
56	MG	2A	3569	1/1	0.94	0.13	66,66,66,66	0
56	MG	1A	3514	1/1	0.94	0.07	42,42,42,42	0
56	MG	1A	3874	1/1	0.94	0.10	47,47,47,47	0
56	MG	2A	3572	1/1	0.94	0.11	61,61,61,61	0
56	MG	2A	3178	1/1	0.94	0.11	49,49,49,49	0
56	MG	1A	3265	1/1	0.94	0.16	32,32,32,32	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3169	1/1	0.94	0.32	37,37,37,37	0
56	MG	1A	3145	1/1	0.94	0.26	38,38,38,38	0
56	MG	2A	3359	1/1	0.94	0.09	47,47,47,47	0
56	MG	2A	3182	1/1	0.94	0.28	57,57,57,57	0
56	MG	2A	3362	1/1	0.94	0.10	46,46,46,46	0
56	MG	2A	3048	1/1	0.94	0.36	51,51,51,51	0
56	MG	2A	3049	1/1	0.94	0.09	62,62,62,62	0
56	MG	2A	3599	1/1	0.94	0.07	59,59,59,59	0
56	MG	1A	3429	1/1	0.94	0.12	34,34,34,34	0
56	MG	2A	3366	1/1	0.94	0.08	44,44,44,44	0
56	MG	2A	3604	1/1	0.94	0.10	49,49,49,49	0
56	MG	2A	3367	1/1	0.94	0.09	59,59,59,59	0
56	MG	1F	307	1/1	0.94	0.19	36,36,36,36	0
56	MG	1A	3199	1/1	0.94	0.26	37,37,37,37	0
56	MG	1A	3525	1/1	0.94	0.12	31,31,31,31	0
56	MG	2A	3189	1/1	0.94	0.09	49,49,49,49	0
56	MG	1G	3001	1/1	0.94	0.07	69,69,69,69	0
56	MG	1A	3231	1/1	0.94	0.11	36,36,36,36	0
56	MG	1A	3271	1/1	0.94	0.10	42,42,42,42	0
56	MG	1A	3886	1/1	0.94	0.11	38,38,38,38	0
56	MG	1A	3726	1/1	0.94	0.05	51,51,51,51	0
56	MG	1A	3342	1/1	0.94	0.14	33,33,33,33	0
56	MG	1a	1815	1/1	0.94	0.11	57,57,57,57	0
56	MG	2A	3197	1/1	0.94	0.25	50,50,50,50	0
56	MG	1A	3728	1/1	0.94	0.06	38,38,38,38	0
56	MG	1A	3071	1/1	0.94	0.19	32,32,32,32	0
56	MG	1A	3611	1/1	0.94	0.09	50,50,50,50	0
56	MG	1A	3894	1/1	0.94	0.07	53,53,53,53	0
56	MG	1A	3530	1/1	0.94	0.18	43,43,43,43	0
56	MG	1A	3897	1/1	0.94	0.22	34,34,34,34	0
56	MG	1A	3531	1/1	0.94	0.09	52,52,52,52	0
56	MG	1A	3357	1/1	0.94	0.13	29,29,29,29	0
56	MG	2A	3656	1/1	0.94	0.12	50,50,50,50	0
56	MG	1U	205	1/1	0.94	0.13	40,40,40,40	0
56	MG	2a	1705	1/1	0.94	0.06	62,62,62,62	0
56	MG	1A	3359	1/1	0.94	0.08	34,34,34,34	0
56	MG	1A	3618	1/1	0.94	0.18	30,30,30,30	0
56	MG	1A	3458	1/1	0.94	0.11	69,69,69,69	0
56	MG	2A	3403	1/1	0.94	0.13	60,60,60,60	0
56	MG	1A	3172	1/1	0.94	0.21	37,37,37,37	0
56	MG	1A	3173	1/1	0.94	0.13	40,40,40,40	0
56	MG	2A	3406	1/1	0.94	0.10	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	10	104	1/1	0.94	0.10	47,47,47,47	0
56	MG	1A	3464	1/1	0.94	0.10	26,26,26,26	0
56	MG	1A	3915	1/1	0.94	0.15	29,29,29,29	0
56	MG	2a	1718	1/1	0.94	0.06	62,62,62,62	0
56	MG	2A	3675	1/1	0.94	0.07	59,59,59,59	0
56	MG	1a	1701	1/1	0.94	0.07	53,53,53,53	0
56	MG	11	101	1/1	0.94	0.07	34,34,34,34	0
56	MG	11	103	1/1	0.94	0.14	41,41,41,41	0
56	MG	2A	3417	1/1	0.94	0.08	62,62,62,62	0
56	MG	2a	1727	1/1	0.94	0.09	64,64,64,64	0
56	MG	1A	3750	1/1	0.94	0.06	44,44,44,44	0
56	MG	1A	3239	1/1	0.94	0.09	41,41,41,41	0
56	MG	2a	1733	1/1	0.94	0.10	75,75,75,75	0
56	MG	1A	3001	1/1	0.94	0.25	42,42,42,42	0
56	MG	2a	1738	1/1	0.94	0.07	58,58,58,58	0
56	MG	2a	1742	1/1	0.94	0.12	70,70,70,70	0
56	MG	1A	3279	1/1	0.94	0.07	49,49,49,49	0
56	MG	1A	3051	1/1	0.94	0.30	32,32,32,32	0
56	MG	1a	1715	1/1	0.94	0.17	59,59,59,59	0
56	MG	19	103	1/1	0.94	0.07	51,51,51,51	0
56	MG	1a	1720	1/1	0.94	0.18	52,52,52,52	0
56	MG	2A	3229	1/1	0.94	0.28	45,45,45,45	0
56	MG	1A	3283	1/1	0.94	0.12	32,32,32,32	0
56	MG	1A	3549	1/1	0.94	0.17	32,32,32,32	0
56	MG	1a	1861	1/1	0.94	0.07	72,72,72,72	0
56	MG	1A	3471	1/1	0.94	0.07	33,33,33,33	0
56	MG	2A	3435	1/1	0.94	0.06	54,54,54,54	0
56	MG	1A	3638	1/1	0.94	0.09	44,44,44,44	0
56	MG	1A	3150	1/1	0.94	0.39	32,32,32,32	0
56	MG	2a	1767	1/1	0.94	0.14	63,63,63,63	0
56	MG	1A	3286	1/1	0.94	0.10	27,27,27,27	0
56	MG	2A	3238	1/1	0.94	0.21	55,55,55,55	0
56	MG	2a	1771	1/1	0.94	0.05	79,79,79,79	0
56	MG	1a	1730	1/1	0.94	0.05	55,55,55,55	0
56	MG	2D	307	1/1	0.94	0.24	46,46,46,46	0
56	MG	2A	3103	1/1	0.94	0.06	63,63,63,63	0
56	MG	2E	304	1/1	0.94	0.17	47,47,47,47	0
56	MG	2A	3443	1/1	0.94	0.13	53,53,53,53	0
56	MG	2a	1780	1/1	0.94	0.06	70,70,70,70	0
56	MG	2A	3241	1/1	0.94	0.14	45,45,45,45	0
56	MG	2A	3242	1/1	0.94	0.09	55,55,55,55	0
56	MG	2A	3451	1/1	0.94	0.06	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2A	3104	1/1	0.94	0.12	48,48,48,48	0
56	MG	1A	3287	1/1	0.94	0.21	41,41,41,41	0
56	MG	1A	3777	1/1	0.94	0.13	39,39,39,39	0
56	MG	1A	3644	1/1	0.94	0.17	38,38,38,38	0
56	MG	2A	3109	1/1	0.94	0.20	54,54,54,54	0
56	MG	1A	3245	1/1	0.94	0.09	44,44,44,44	0
56	MG	1A	3646	1/1	0.94	0.09	37,37,37,37	0
56	MG	1A	3152	1/1	0.94	0.36	36,36,36,36	0
56	MG	2T	3001	1/1	0.94	0.15	54,54,54,54	0
56	MG	1A	3029	1/1	0.94	0.06	30,30,30,30	0
56	MG	2U	201	1/1	0.94	0.08	52,52,52,52	0
56	MG	1A	3656	1/1	0.94	0.08	41,41,41,41	0
56	MG	1A	3109	1/1	0.94	0.30	40,40,40,40	0
56	MG	2V	203	1/1	0.94	0.18	61,61,61,61	0
56	MG	1A	3129	1/1	0.94	0.22	30,30,30,30	0
56	MG	1A	3111	1/1	0.94	0.15	30,30,30,30	0
56	MG	1A	3945	1/1	0.94	0.33	38,38,38,38	0
56	MG	2A	3265	1/1	0.94	0.07	60,60,60,60	0
56	MG	1A	3062	1/1	0.94	0.22	41,41,41,41	0
56	MG	1a	1747	1/1	0.94	0.10	56,56,56,56	0
56	MG	1a	1748	1/1	0.94	0.07	74,74,74,74	0
56	MG	1A	3159	1/1	0.94	0.37	38,38,38,38	0
56	MG	1A	3664	1/1	0.94	0.07	44,44,44,44	0
56	MG	1A	3807	1/1	0.94	0.09	60,60,60,60	0
56	MG	2A	3595	1/1	0.95	0.07	66,66,66,66	0
56	MG	2A	3596	1/1	0.95	0.06	56,56,56,56	0
56	MG	1A	3568	1/1	0.95	0.08	44,44,44,44	0
56	MG	1A	3219	1/1	0.95	0.08	34,34,34,34	0
56	MG	1F	301	1/1	0.95	0.05	44,44,44,44	0
56	MG	2A	3267	1/1	0.95	0.07	49,49,49,49	0
56	MG	1F	302	1/1	0.95	0.14	31,31,31,31	0
56	MG	1a	1836	1/1	0.95	0.07	61,61,61,61	0
56	MG	1A	3708	1/1	0.95	0.14	35,35,35,35	0
56	MG	2A	3617	1/1	0.95	0.07	49,49,49,49	0
56	MG	1A	3918	1/1	0.95	0.06	27,27,27,27	0
56	MG	1A	3709	1/1	0.95	0.08	37,37,37,37	0
56	MG	1A	3266	1/1	0.95	0.34	31,31,31,31	0
56	MG	1A	3299	1/1	0.95	0.08	47,47,47,47	0
56	MG	2A	3278	1/1	0.95	0.16	61,61,61,61	0
56	MG	2A	3056	1/1	0.95	0.26	41,41,41,41	0
56	MG	1A	3151	1/1	0.95	0.13	31,31,31,31	0
56	MG	2A	3634	1/1	0.95	0.08	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3524	1/1	0.95	0.07	55,55,55,55	0
56	MG	2A	3165	1/1	0.95	0.28	47,47,47,47	0
56	MG	2A	3059	1/1	0.95	0.16	46,46,46,46	0
56	MG	2A	3284	1/1	0.95	0.07	44,44,44,44	0
56	MG	1A	3343	1/1	0.95	0.09	25,25,25,25	0
56	MG	2A	3646	1/1	0.95	0.06	66,66,66,66	0
56	MG	1A	3090	1/1	0.95	0.20	29,29,29,29	0
56	MG	1G	3003	1/1	0.95	0.17	60,60,60,60	0
56	MG	2A	3291	1/1	0.95	0.07	52,52,52,52	0
56	MG	1A	3643	1/1	0.95	0.10	37,37,37,37	0
56	MG	1A	3305	1/1	0.95	0.21	47,47,47,47	0
56	MG	2A	3066	1/1	0.95	0.17	59,59,59,59	0
56	MG	2A	3300	1/1	0.95	0.24	42,42,42,42	0
56	MG	2A	3446	1/1	0.95	0.06	60,60,60,60	0
56	MG	2A	3447	1/1	0.95	0.16	42,42,42,42	0
56	MG	1A	3047	1/1	0.95	0.37	44,44,44,44	0
56	MG	2A	3302	1/1	0.95	0.08	51,51,51,51	0
56	MG	1A	3099	1/1	0.95	0.74	34,34,34,34	0
56	MG	2A	3453	1/1	0.95	0.08	47,47,47,47	0
56	MG	1A	3408	1/1	0.95	0.13	42,42,42,42	0
56	MG	2A	3306	1/1	0.95	0.08	59,59,59,59	0
56	MG	1O	8001	1/1	0.95	0.06	44,44,44,44	0
56	MG	1A	3652	1/1	0.95	0.16	40,40,40,40	0
56	MG	1A	3933	1/1	0.95	0.23	49,49,49,49	0
56	MG	2A	3073	1/1	0.95	0.12	50,50,50,50	0
56	MG	1A	3184	1/1	0.95	0.05	37,37,37,37	0
56	MG	1A	3092	1/1	0.95	0.09	33,33,33,33	0
56	MG	1A	3733	1/1	0.95	0.07	29,29,29,29	0
56	MG	1d	505	1/1	0.95	0.12	77,77,77,77	0
56	MG	1U	201	1/1	0.95	0.21	37,37,37,37	0
56	MG	2A	3468	1/1	0.95	0.05	69,69,69,69	0
56	MG	2A	3469	1/1	0.95	0.07	51,51,51,51	0
56	MG	1A	3735	1/1	0.95	0.07	55,55,55,55	0
56	MG	1A	3251	1/1	0.95	0.06	47,47,47,47	0
56	MG	1A	3113	1/1	0.95	0.26	35,35,35,35	0
56	MG	1A	3253	1/1	0.95	0.09	40,40,40,40	0
56	MG	1A	3418	1/1	0.95	0.07	52,52,52,52	0
56	MG	2A	3084	1/1	0.95	0.16	42,42,42,42	0
56	MG	1i	3001	1/1	0.95	0.17	68,68,68,68	0
56	MG	1Y	502	1/1	0.95	0.13	56,56,56,56	0
56	MG	1A	3848	1/1	0.95	0.09	54,54,54,54	0
56	MG	1A	3320	1/1	0.95	0.09	26,26,26,26	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3663	1/1	0.95	0.08	48,48,48,48	0
56	MG	10	103	1/1	0.95	0.06	42,42,42,42	0
56	MG	1A	3423	1/1	0.95	0.06	57,57,57,57	0
56	MG	1A	3372	1/1	0.95	0.06	28,28,28,28	0
56	MG	2D	304	1/1	0.95	0.63	44,44,44,44	0
56	MG	2A	3487	1/1	0.95	0.07	56,56,56,56	0
56	MG	1a	1673	1/1	0.95	0.28	53,53,53,53	0
56	MG	2A	3339	1/1	0.95	0.05	65,65,65,65	0
56	MG	1A	3857	1/1	0.95	0.11	44,44,44,44	0
56	MG	2E	301	1/1	0.95	0.27	45,45,45,45	0
56	MG	2E	302	1/1	0.95	0.10	52,52,52,52	0
56	MG	1A	3858	1/1	0.95	0.14	38,38,38,38	0
56	MG	1A	3114	1/1	0.95	0.16	34,34,34,34	0
56	MG	1A	3428	1/1	0.95	0.10	24,24,24,24	0
56	MG	1B	207	1/1	0.95	0.24	45,45,45,45	0
56	MG	1a	1780	1/1	0.95	0.06	71,71,71,71	0
56	MG	1A	3861	1/1	0.95	0.06	50,50,50,50	0
56	MG	17	101	1/1	0.95	0.06	36,36,36,36	0
56	MG	1A	3546	1/1	0.95	0.06	41,41,41,41	0
56	MG	1x	112	1/1	0.95	0.07	65,65,65,65	0
56	MG	2O	201	1/1	0.95	0.10	54,54,54,54	0
56	MG	1A	3603	1/1	0.95	0.09	48,48,48,48	0
56	MG	1A	3126	1/1	0.95	0.15	32,32,32,32	0
56	MG	2A	3106	1/1	0.95	0.18	49,49,49,49	0
56	MG	1A	3755	1/1	0.95	0.07	45,45,45,45	0
56	MG	1a	1686	1/1	0.95	0.18	67,67,67,67	0
56	MG	2a	1744	1/1	0.95	0.10	62,62,62,62	0
56	MG	2A	3511	1/1	0.95	0.07	64,64,64,64	0
56	MG	1A	3673	1/1	0.95	0.17	44,44,44,44	0
56	MG	2A	3360	1/1	0.95	0.17	62,62,62,62	0
56	MG	2V	201	1/1	0.95	0.06	64,64,64,64	0
56	MG	1A	3674	1/1	0.95	0.06	39,39,39,39	0
56	MG	1A	3762	1/1	0.95	0.07	45,45,45,45	0
56	MG	1a	1690	1/1	0.95	0.15	55,55,55,55	0
56	MG	2A	3221	1/1	0.95	0.21	51,51,51,51	0
56	MG	1A	3675	1/1	0.95	0.10	36,36,36,36	0
56	MG	1A	3101	1/1	0.95	0.24	32,32,32,32	0
56	MG	1A	3432	1/1	0.95	0.12	34,34,34,34	0
56	MG	1A	3767	1/1	0.95	0.17	43,43,43,43	0
56	MG	1A	3880	1/1	0.95	0.06	35,35,35,35	0
56	MG	1a	1610	1/1	0.95	0.07	71,71,71,71	0
56	MG	1a	1800	1/1	0.95	0.05	66,66,66,66	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1a	1611	1/1	0.95	0.20	49,49,49,49	0
56	MG	1A	3608	1/1	0.95	0.09	36,36,36,36	0
56	MG	2A	3380	1/1	0.95	0.07	59,59,59,59	0
56	MG	1A	3434	1/1	0.95	0.07	38,38,38,38	0
56	MG	2A	3541	1/1	0.95	0.07	49,49,49,49	0
56	MG	1A	3770	1/1	0.95	0.05	50,50,50,50	0
56	MG	1A	3045	1/1	0.95	0.28	40,40,40,40	0
56	MG	2a	1781	1/1	0.95	0.48	50,50,50,50	0
56	MG	1A	3776	1/1	0.95	0.08	40,40,40,40	0
56	MG	2A	3385	1/1	0.95	0.09	53,53,53,53	0
56	MG	1A	3212	1/1	0.95	0.38	30,30,30,30	0
56	MG	1a	1707	1/1	0.95	0.11	47,47,47,47	0
56	MG	1A	3501	1/1	0.95	0.06	43,43,43,43	0
56	MG	2A	3561	1/1	0.95	0.07	58,58,58,58	0
56	MG	1a	1709	1/1	0.95	0.10	56,56,56,56	0
56	MG	1a	1811	1/1	0.95	0.07	73,73,73,73	0
56	MG	1A	3502	1/1	0.95	0.11	43,43,43,43	0
56	MG	1A	3891	1/1	0.95	0.15	38,38,38,38	0
56	MG	2a	1623	1/1	0.95	0.33	49,49,49,49	0
56	MG	1A	3049	1/1	0.95	0.11	28,28,28,28	0
56	MG	1A	3131	1/1	0.95	0.20	35,35,35,35	0
56	MG	2A	3247	1/1	0.95	0.11	52,52,52,52	0
56	MG	1A	3328	1/1	0.95	0.19	49,49,49,49	0
56	MG	1A	3691	1/1	0.95	0.10	48,48,48,48	0
56	MG	1A	3288	1/1	0.95	0.07	25,25,25,25	0
56	MG	1A	3900	1/1	0.95	0.09	33,33,33,33	0
56	MG	1A	3079	1/1	0.95	0.08	39,39,39,39	0
56	MG	1A	3696	1/1	0.95	0.09	40,40,40,40	0
56	MG	1A	3217	1/1	0.95	0.42	33,33,33,33	0
56	MG	1A	3513	1/1	0.95	0.08	49,49,49,49	0
56	MG	1A	3627	1/1	0.95	0.08	40,40,40,40	0
56	MG	1A	3461	1/1	0.95	0.08	30,30,30,30	0
56	MG	1A	3196	1/1	0.95	0.06	41,41,41,41	0
56	MG	2A	3586	1/1	0.95	0.08	68,68,68,68	0
60	ZN	24	501	1/1	0.95	0.25	94,94,94,94	0
56	MG	2A	3594	1/1	0.95	0.07	82,82,82,82	0
56	MG	1A	3065	1/1	0.96	0.14	37,37,37,37	0
56	MG	1A	3068	1/1	0.96	0.15	40,40,40,40	0
56	MG	1A	3509	1/1	0.96	0.10	39,39,39,39	0
56	MG	2A	3155	1/1	0.96	0.07	46,46,46,46	0
56	MG	2A	3592	1/1	0.96	0.12	47,47,47,47	0
56	MG	1A	3315	1/1	0.96	0.10	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3016	1/1	0.96	0.35	30,30,30,30	0
56	MG	1A	3787	1/1	0.96	0.06	31,31,31,31	0
56	MG	1a	1834	1/1	0.96	0.07	57,57,57,57	0
56	MG	1A	3788	1/1	0.96	0.08	55,55,55,55	0
56	MG	2A	3601	1/1	0.96	0.10	54,54,54,54	0
56	MG	1a	1838	1/1	0.96	0.05	69,69,69,69	0
56	MG	2A	3603	1/1	0.96	0.09	46,46,46,46	0
56	MG	2A	3423	1/1	0.96	0.05	56,56,56,56	0
56	MG	1A	3278	1/1	0.96	0.08	28,28,28,28	0
56	MG	2A	3608	1/1	0.96	0.09	62,62,62,62	0
56	MG	1A	3896	1/1	0.96	0.13	31,31,31,31	0
56	MG	1A	3697	1/1	0.96	0.17	37,37,37,37	0
56	MG	2A	3615	1/1	0.96	0.06	63,63,63,63	0
56	MG	1A	3898	1/1	0.96	0.13	43,43,43,43	0
56	MG	1A	3899	1/1	0.96	0.14	41,41,41,41	0
56	MG	1a	1741	1/1	0.96	0.07	63,63,63,63	0
56	MG	1a	1846	1/1	0.96	0.05	48,48,48,48	0
56	MG	2A	3433	1/1	0.96	0.09	52,52,52,52	0
56	MG	2A	3287	1/1	0.96	0.06	60,60,60,60	0
56	MG	2A	3629	1/1	0.96	0.05	57,57,57,57	0
56	MG	2A	3288	1/1	0.96	0.11	41,41,41,41	0
56	MG	1A	3699	1/1	0.96	0.11	32,32,32,32	0
56	MG	1A	3102	1/1	0.96	0.11	31,31,31,31	0
56	MG	1A	3903	1/1	0.96	0.08	53,53,53,53	0
56	MG	1A	3407	1/1	0.96	0.08	47,47,47,47	0
56	MG	2A	3294	1/1	0.96	0.07	50,50,50,50	0
56	MG	2A	3296	1/1	0.96	0.14	42,42,42,42	0
56	MG	2A	3643	1/1	0.96	0.07	54,54,54,54	0
56	MG	1A	3516	1/1	0.96	0.06	38,38,38,38	0
56	MG	2A	3645	1/1	0.96	0.12	50,50,50,50	0
56	MG	1A	3517	1/1	0.96	0.10	33,33,33,33	0
56	MG	2A	3648	1/1	0.96	0.07	64,64,64,64	0
56	MG	1A	3518	1/1	0.96	0.07	37,37,37,37	0
56	MG	1A	3570	1/1	0.96	0.20	42,42,42,42	0
56	MG	1A	3706	1/1	0.96	0.10	36,36,36,36	0
56	MG	1A	3810	1/1	0.96	0.22	28,28,28,28	0
56	MG	1A	3054	1/1	0.96	0.06	30,30,30,30	0
56	MG	1A	3637	1/1	0.96	0.08	33,33,33,33	0
56	MG	2A	3655	1/1	0.96	0.06	46,46,46,46	0
56	MG	1A	3814	1/1	0.96	0.07	42,42,42,42	0
56	MG	1A	3572	1/1	0.96	0.09	35,35,35,35	0
56	MG	1A	3573	1/1	0.96	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
56	MG	2A	3660	1/1	0.96	0.30	47,47,47,47	0
56	MG	2A	3313	1/1	0.96	0.06	44,44,44,44	0
56	MG	1A	3817	1/1	0.96	0.09	32,32,32,32	0
56	MG	2A	3461	1/1	0.96	0.08	53,53,53,53	0
56	MG	1A	3105	1/1	0.96	0.31	42,42,42,42	0
56	MG	1A	3923	1/1	0.96	0.09	36,36,36,36	0
56	MG	1A	3521	1/1	0.96	0.05	44,44,44,44	0
56	MG	2A	3671	1/1	0.96	0.09	44,44,44,44	0
56	MG	2a	1685	1/1	0.96	0.05	68,68,68,68	0
56	MG	1A	3642	1/1	0.96	0.09	32,32,32,32	0
56	MG	2A	3319	1/1	0.96	0.07	51,51,51,51	0
56	MG	1A	3135	1/1	0.96	0.15	33,33,33,33	0
56	MG	1A	3237	1/1	0.96	0.16	38,38,38,38	0
56	MG	1A	3238	1/1	0.96	0.04	65,65,65,65	0
56	MG	1A	3055	1/1	0.96	0.08	37,37,37,37	0
56	MG	1R	204	1/1	0.96	0.10	39,39,39,39	0
56	MG	1T	201	1/1	0.96	0.12	52,52,52,52	0
56	MG	2A	3681	1/1	0.96	0.09	54,54,54,54	0
56	MG	1A	3648	1/1	0.96	0.09	37,37,37,37	0
56	MG	2A	3474	1/1	0.96	0.07	47,47,47,47	0
56	MG	1A	3417	1/1	0.96	0.08	34,34,34,34	0
56	MG	1U	202	1/1	0.96	0.25	42,42,42,42	0
56	MG	1A	3374	1/1	0.96	0.06	31,31,31,31	0
56	MG	2A	3200	1/1	0.96	0.29	52,52,52,52	0
56	MG	1a	1772	1/1	0.96	0.08	68,68,68,68	0
56	MG	1A	3094	1/1	0.96	0.09	36,36,36,36	0
56	MG	1A	3157	1/1	0.96	0.04	33,33,33,33	0
56	MG	1A	3004	1/1	0.96	0.07	37,37,37,37	0
56	MG	1A	3732	1/1	0.96	0.07	46,46,46,46	0
56	MG	1W	3001	1/1	0.96	0.24	38,38,38,38	0
56	MG	1W	3002	1/1	0.96	0.24	41,41,41,41	0
56	MG	1A	3018	1/1	0.96	0.13	33,33,33,33	0
56	MG	1A	3841	1/1	0.96	0.07	45,45,45,45	0
56	MG	2D	301	1/1	0.96	0.07	49,49,49,49	0
56	MG	1A	3734	1/1	0.96	0.06	49,49,49,49	0
56	MG	1A	3110	1/1	0.96	0.08	35,35,35,35	0
56	MG	1A	3660	1/1	0.96	0.11	38,38,38,38	0
56	MG	1A	3738	1/1	0.96	0.35	36,36,36,36	0
56	MG	1A	3297	1/1	0.96	0.17	37,37,37,37	0
56	MG	2A	3004	1/1	0.96	0.13	52,52,52,52	0
56	MG	1A	3592	1/1	0.96	0.06	43,43,43,43	0
56	MG	1A	3382	1/1	0.96	0.08	30,30,30,30	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2a	1726	1/1	0.96	0.08	70,70,70,70	0
56	MG	1A	3850	1/1	0.96	0.07	44,44,44,44	0
56	MG	2E	303	1/1	0.96	0.07	51,51,51,51	0
56	MG	1A	3011	1/1	0.96	0.14	37,37,37,37	0
56	MG	1A	3852	1/1	0.96	0.10	47,47,47,47	0
56	MG	1a	1791	1/1	0.96	0.13	74,74,74,74	0
56	MG	2a	1737	1/1	0.96	0.05	74,74,74,74	0
56	MG	2A	3505	1/1	0.96	0.07	59,59,59,59	0
56	MG	2a	1740	1/1	0.96	0.06	73,73,73,73	0
56	MG	1B	204	1/1	0.96	0.08	56,56,56,56	0
56	MG	2A	3012	1/1	0.96	0.06	45,45,45,45	0
56	MG	1A	3744	1/1	0.96	0.08	46,46,46,46	0
56	MG	1A	3433	1/1	0.96	0.11	48,48,48,48	0
56	MG	2A	3512	1/1	0.96	0.09	45,45,45,45	0
56	MG	2a	1750	1/1	0.96	0.05	76,76,76,76	0
56	MG	2N	8001	1/1	0.96	0.04	55,55,55,55	0
56	MG	1A	3163	1/1	0.96	0.07	33,33,33,33	0
56	MG	2a	1753	1/1	0.96	0.07	58,58,58,58	0
56	MG	2A	3515	1/1	0.96	0.06	62,62,62,62	0
56	MG	2a	1755	1/1	0.96	0.07	72,72,72,72	0
56	MG	2P	3401	1/1	0.96	0.11	55,55,55,55	0
56	MG	1A	3667	1/1	0.96	0.12	37,37,37,37	0
56	MG	2A	3018	1/1	0.96	0.09	48,48,48,48	0
56	MG	1A	3668	1/1	0.96	0.18	51,51,51,51	0
56	MG	2A	3122	1/1	0.96	0.25	44,44,44,44	0
56	MG	2T	3002	1/1	0.96	0.05	58,58,58,58	0
56	MG	2T	3003	1/1	0.96	0.07	56,56,56,56	0
56	MG	1A	3335	1/1	0.96	0.07	44,44,44,44	0
56	MG	2a	1768	1/1	0.96	0.13	69,69,69,69	0
56	MG	1A	3493	1/1	0.96	0.08	29,29,29,29	0
56	MG	2A	3524	1/1	0.96	0.06	42,42,42,42	0
56	MG	1A	3144	1/1	0.96	0.09	36,36,36,36	0
56	MG	1A	3866	1/1	0.96	0.14	36,36,36,36	0
56	MG	2A	3377	1/1	0.96	0.08	49,49,49,49	0
56	MG	2a	1775	1/1	0.96	0.07	65,65,65,65	0
56	MG	2A	3378	1/1	0.96	0.09	50,50,50,50	0
56	MG	1A	3602	1/1	0.96	0.10	48,48,48,48	0
56	MG	1A	3439	1/1	0.96	0.09	31,31,31,31	0
56	MG	1A	3757	1/1	0.96	0.07	38,38,38,38	0
56	MG	28	101	1/1	0.96	0.11	62,62,62,62	0
56	MG	1A	3443	1/1	0.96	0.06	35,35,35,35	0
56	MG	1B	221	1/1	0.96	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
56	MG	1A	3547	1/1	0.96	0.06	38,38,38,38	0
56	MG	1A	3077	1/1	0.96	0.18	41,41,41,41	0
56	MG	2A	3245	1/1	0.96	0.06	56,56,56,56	0
56	MG	1A	3677	1/1	0.96	0.11	40,40,40,40	0
56	MG	2A	3388	1/1	0.96	0.08	48,48,48,48	0
56	MG	1A	3499	1/1	0.96	0.22	43,43,43,43	0
56	MG	1A	3446	1/1	0.96	0.08	46,46,46,46	0
56	MG	1A	3766	1/1	0.96	0.21	42,42,42,42	0
56	MG	2A	3138	1/1	0.96	0.14	42,42,42,42	0
56	MG	1A	3879	1/1	0.96	0.05	66,66,66,66	0
56	MG	2A	3252	1/1	0.96	0.08	41,41,41,41	0
56	MG	1a	1618	1/1	0.96	0.06	73,73,73,73	0
56	MG	2A	3255	1/1	0.96	0.09	69,69,69,69	0
56	MG	1A	3450	1/1	0.96	0.08	35,35,35,35	0
56	MG	2A	3567	1/1	0.96	0.07	69,69,69,69	0
56	MG	1D	303	1/1	0.96	0.12	41,41,41,41	0
56	MG	1A	3306	1/1	0.96	0.07	40,40,40,40	0
56	MG	1A	3307	1/1	0.96	0.09	34,34,34,34	0
56	MG	2A	3261	1/1	0.96	0.06	52,52,52,52	0
56	MG	1a	1722	1/1	0.96	0.15	67,67,67,67	0
56	MG	1A	3505	1/1	0.96	0.10	50,50,50,50	0
56	MG	1A	3127	1/1	0.96	0.27	28,28,28,28	0
56	MG	2A	3407	1/1	0.96	0.07	59,59,59,59	0
56	MG	2A	3408	1/1	0.96	0.06	66,66,66,66	0
56	MG	1A	3617	1/1	0.96	0.04	60,60,60,60	0
61	SF4	1d	501	8/8	0.96	0.06	72,75,79,82	0
56	MG	1a	1726	1/1	0.96	0.06	60,60,60,60	0
56	MG	2A	3638	1/1	0.97	0.06	58,58,58,58	0
56	MG	1A	3453	1/1	0.97	0.06	46,46,46,46	0
56	MG	1A	3232	1/1	0.97	0.10	56,56,56,56	0
56	MG	1A	3456	1/1	0.97	0.06	36,36,36,36	0
56	MG	2A	3642	1/1	0.97	0.15	51,51,51,51	0
56	MG	1A	3276	1/1	0.97	0.12	49,49,49,49	0
56	MG	1A	3073	1/1	0.97	0.20	32,32,32,32	0
56	MG	1A	3719	1/1	0.97	0.10	42,42,42,42	0
56	MG	1a	1825	1/1	0.97	0.06	66,66,66,66	0
56	MG	2A	3647	1/1	0.97	0.06	60,60,60,60	0
56	MG	2A	3232	1/1	0.97	0.14	50,50,50,50	0
56	MG	1A	3459	1/1	0.97	0.06	46,46,46,46	0
56	MG	1A	3723	1/1	0.97	0.06	51,51,51,51	0
56	MG	1A	3647	1/1	0.97	0.08	28,28,28,28	0
56	MG	1a	1829	1/1	0.97	0.09	55,55,55,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3578	1/1	0.97	0.11	36,36,36,36	0
56	MG	1A	3394	1/1	0.97	0.07	33,33,33,33	0
56	MG	2A	3480	1/1	0.97	0.07	49,49,49,49	0
56	MG	1A	3825	1/1	0.97	0.07	46,46,46,46	0
56	MG	2A	3657	1/1	0.97	0.22	49,49,49,49	0
56	MG	1A	3650	1/1	0.97	0.05	40,40,40,40	0
56	MG	1A	3829	1/1	0.97	0.07	40,40,40,40	0
56	MG	1A	3395	1/1	0.97	0.07	43,43,43,43	0
56	MG	2A	3485	1/1	0.97	0.09	53,53,53,53	0
56	MG	1A	3653	1/1	0.97	0.05	47,47,47,47	0
56	MG	1A	3002	1/1	0.97	0.04	44,44,44,44	0
56	MG	1A	3347	1/1	0.97	0.07	30,30,30,30	0
56	MG	1A	3835	1/1	0.97	0.07	59,59,59,59	0
56	MG	1A	3350	1/1	0.97	0.10	32,32,32,32	0
56	MG	2A	3670	1/1	0.97	0.10	50,50,50,50	0
56	MG	1A	3355	1/1	0.97	0.07	31,31,31,31	0
56	MG	2A	3369	1/1	0.97	0.12	45,45,45,45	0
56	MG	1A	3736	1/1	0.97	0.07	37,37,37,37	0
56	MG	2A	3371	1/1	0.97	0.04	50,50,50,50	0
56	MG	1A	3356	1/1	0.97	0.06	26,26,26,26	0
56	MG	2A	3373	1/1	0.97	0.05	45,45,45,45	0
56	MG	2A	3497	1/1	0.97	0.10	51,51,51,51	0
56	MG	2A	3151	1/1	0.97	0.18	41,41,41,41	0
56	MG	1a	1848	1/1	0.97	0.07	69,69,69,69	0
56	MG	1A	3313	1/1	0.97	0.06	35,35,35,35	0
56	MG	1Q	202	1/1	0.97	0.08	35,35,35,35	0
56	MG	2a	1686	1/1	0.97	0.04	69,69,69,69	0
56	MG	2A	3503	1/1	0.97	0.05	62,62,62,62	0
56	MG	2A	3257	1/1	0.97	0.07	46,46,46,46	0
56	MG	1A	3132	1/1	0.97	0.16	39,39,39,39	0
56	MG	1Q	204	1/1	0.97	0.10	44,44,44,44	0
56	MG	1A	3588	1/1	0.97	0.08	33,33,33,33	0
56	MG	1A	3844	1/1	0.97	0.09	32,32,32,32	0
56	MG	1A	3280	1/1	0.97	0.07	35,35,35,35	0
56	MG	1A	3937	1/1	0.97	0.24	32,32,32,32	0
56	MG	2A	3513	1/1	0.97	0.11	52,52,52,52	0
56	MG	1A	3938	1/1	0.97	0.17	33,33,33,33	0
56	MG	2A	3064	1/1	0.97	0.11	46,46,46,46	0
56	MG	2A	3516	1/1	0.97	0.08	57,57,57,57	0
56	MG	1A	3590	1/1	0.97	0.07	47,47,47,47	0
56	MG	2A	3164	1/1	0.97	0.10	46,46,46,46	0
56	MG	2B	3017	1/1	0.97	0.06	66,66,66,66	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2A	3269	1/1	0.97	0.13	43,43,43,43	0
56	MG	1A	3940	1/1	0.97	0.06	42,42,42,42	0
56	MG	2a	1706	1/1	0.97	0.10	56,56,56,56	0
56	MG	1A	3281	1/1	0.97	0.08	35,35,35,35	0
56	MG	1A	3067	1/1	0.97	0.09	35,35,35,35	0
56	MG	1A	3007	1/1	0.97	0.09	50,50,50,50	0
56	MG	1A	3475	1/1	0.97	0.03	32,32,32,32	0
56	MG	1A	3364	1/1	0.97	0.05	39,39,39,39	0
56	MG	1A	3415	1/1	0.97	0.05	55,55,55,55	0
56	MG	2A	3277	1/1	0.97	0.15	67,67,67,67	0
56	MG	1A	3148	1/1	0.97	0.14	32,32,32,32	0
56	MG	1A	3087	1/1	0.97	0.25	38,38,38,38	0
56	MG	1A	3536	1/1	0.97	0.15	35,35,35,35	0
56	MG	1A	3481	1/1	0.97	0.10	54,54,54,54	0
56	MG	1A	3756	1/1	0.97	0.06	39,39,39,39	0
56	MG	2A	3536	1/1	0.97	0.09	57,57,57,57	0
56	MG	1A	3368	1/1	0.97	0.05	58,58,58,58	0
56	MG	2a	1722	1/1	0.97	0.05	66,66,66,66	0
56	MG	2A	3540	1/1	0.97	0.06	47,47,47,47	0
56	MG	1A	3483	1/1	0.97	0.06	39,39,39,39	0
56	MG	1A	3541	1/1	0.97	0.08	35,35,35,35	0
56	MG	2A	3547	1/1	0.97	0.07	55,55,55,55	0
56	MG	2a	1729	1/1	0.97	0.12	64,64,64,64	0
56	MG	1A	3370	1/1	0.97	0.06	35,35,35,35	0
56	MG	2A	3550	1/1	0.97	0.05	43,43,43,43	0
56	MG	1a	1677	1/1	0.97	0.07	49,49,49,49	0
56	MG	1A	3242	1/1	0.97	0.07	29,29,29,29	0
56	MG	2a	1735	1/1	0.97	0.12	74,74,74,74	0
56	MG	2a	1736	1/1	0.97	0.07	66,66,66,66	0
56	MG	1A	3162	1/1	0.97	0.06	36,36,36,36	0
56	MG	13	101	1/1	0.97	0.12	38,38,38,38	0
56	MG	2A	3415	1/1	0.97	0.08	52,52,52,52	0
56	MG	2a	1741	1/1	0.97	0.12	68,68,68,68	0
56	MG	1A	3206	1/1	0.97	0.06	35,35,35,35	0
56	MG	2A	3562	1/1	0.97	0.06	43,43,43,43	0
56	MG	1A	3683	1/1	0.97	0.05	46,46,46,46	0
56	MG	15	103	1/1	0.97	0.10	39,39,39,39	0
56	MG	1A	3125	1/1	0.97	0.04	29,29,29,29	0
56	MG	2A	3298	1/1	0.97	0.08	46,46,46,46	0
56	MG	1A	3013	1/1	0.97	0.18	29,29,29,29	0
56	MG	1A	3686	1/1	0.97	0.19	49,49,49,49	0
56	MG	1A	3430	1/1	0.97	0.06	32,32,32,32	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2A	3424	1/1	0.97	0.06	63,63,63,63	0
56	MG	2X	101	1/1	0.97	0.09	61,61,61,61	0
56	MG	1A	3492	1/1	0.97	0.06	45,45,45,45	0
56	MG	2A	3303	1/1	0.97	0.07	44,44,44,44	0
56	MG	2a	1758	1/1	0.97	0.10	66,66,66,66	0
56	MG	1A	3775	1/1	0.97	0.05	36,36,36,36	0
56	MG	2a	1760	1/1	0.97	0.05	65,65,65,65	0
56	MG	1A	3014	1/1	0.97	0.16	41,41,41,41	0
56	MG	2a	1762	1/1	0.97	0.04	79,79,79,79	0
56	MG	2A	3429	1/1	0.97	0.06	58,58,58,58	0
56	MG	1A	3248	1/1	0.97	0.05	37,37,37,37	0
56	MG	2A	3307	1/1	0.97	0.04	48,48,48,48	0
56	MG	1A	3553	1/1	0.97	0.07	58,58,58,58	0
56	MG	1A	3620	1/1	0.97	0.06	48,48,48,48	0
56	MG	1A	3210	1/1	0.97	0.06	33,33,33,33	0
56	MG	2A	3583	1/1	0.97	0.07	68,68,68,68	0
56	MG	2a	1607	1/1	0.97	0.07	70,70,70,70	0
56	MG	1A	3884	1/1	0.97	0.06	44,44,44,44	0
56	MG	1A	3193	1/1	0.97	0.16	33,33,33,33	0
56	MG	2A	3587	1/1	0.97	0.05	70,70,70,70	0
56	MG	1A	3786	1/1	0.97	0.08	38,38,38,38	0
56	MG	2A	3438	1/1	0.97	0.05	56,56,56,56	0
56	MG	1D	301	1/1	0.97	0.10	35,35,35,35	0
56	MG	2a	1779	1/1	0.97	0.08	67,67,67,67	0
56	MG	1A	3031	1/1	0.97	0.28	32,32,32,32	0
56	MG	2A	3598	1/1	0.97	0.04	54,54,54,54	0
56	MG	1A	3625	1/1	0.97	0.10	36,36,36,36	0
56	MG	1A	3889	1/1	0.97	0.24	35,35,35,35	0
56	MG	1a	1702	1/1	0.97	0.10	51,51,51,51	0
56	MG	1A	3436	1/1	0.97	0.07	33,33,33,33	0
56	MG	1a	1704	1/1	0.97	0.04	63,63,63,63	0
56	MG	1A	3037	1/1	0.97	0.34	38,38,38,38	0
56	MG	1A	3302	1/1	0.97	0.05	36,36,36,36	0
56	MG	2A	3607	1/1	0.97	0.06	66,66,66,66	0
56	MG	2A	3449	1/1	0.97	0.11	42,42,42,42	0
56	MG	2A	3016	1/1	0.97	0.13	50,50,50,50	0
56	MG	2A	3611	1/1	0.97	0.04	57,57,57,57	0
56	MG	1A	3442	1/1	0.97	0.05	61,61,61,61	0
56	MG	1A	3503	1/1	0.97	0.07	38,38,38,38	0
56	MG	1A	3384	1/1	0.97	0.07	30,30,30,30	0
56	MG	2A	3619	1/1	0.97	0.05	55,55,55,55	0
56	MG	1A	3444	1/1	0.97	0.07	31,31,31,31	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2A	3456	1/1	0.97	0.10	63,63,63,63	0
56	MG	1A	3798	1/1	0.97	0.07	37,37,37,37	0
56	MG	2A	3625	1/1	0.97	0.05	65,65,65,65	0
56	MG	1A	3303	1/1	0.97	0.10	32,32,32,32	0
56	MG	2A	3627	1/1	0.97	0.04	46,46,46,46	0
56	MG	1A	3304	1/1	0.97	0.08	47,47,47,47	0
56	MG	1a	1717	1/1	0.97	0.09	67,67,67,67	0
56	MG	1A	3448	1/1	0.97	0.15	30,30,30,30	0
56	MG	1A	3338	1/1	0.97	0.12	31,31,31,31	0
56	MG	1A	3214	1/1	0.97	0.14	30,30,30,30	0
60	ZN	14	501	1/1	0.97	0.19	89,89,89,89	0
56	MG	2A	3635	1/1	0.97	0.05	48,48,48,48	0
56	MG	1D	320	1/1	0.97	0.06	46,46,46,46	0
61	SF4	2d	501	8/8	0.97	0.04	70,73,77,79	0
56	MG	2A	3637	1/1	0.97	0.08	60,60,60,60	0
56	MG	1a	1735	1/1	0.98	0.04	62,62,62,62	0
56	MG	1A	3698	1/1	0.98	0.04	30,30,30,30	0
56	MG	2A	3591	1/1	0.98	0.11	68,68,68,68	0
56	MG	1A	3901	1/1	0.98	0.16	51,51,51,51	0
56	MG	1A	3192	1/1	0.98	0.09	32,32,32,32	0
56	MG	1A	3103	1/1	0.98	0.09	48,48,48,48	0
56	MG	2a	1692	1/1	0.98	0.04	62,62,62,62	0
56	MG	1A	3409	1/1	0.98	0.05	38,38,38,38	0
56	MG	2A	3376	1/1	0.98	0.04	50,50,50,50	0
56	MG	1a	1822	1/1	0.98	0.04	60,60,60,60	0
56	MG	1A	3651	1/1	0.98	0.11	74,74,74,74	0
56	MG	1A	3604	1/1	0.98	0.05	54,54,54,54	0
56	MG	10	106	1/1	0.98	0.06	46,46,46,46	0
56	MG	1A	3240	1/1	0.98	0.07	41,41,41,41	0
56	MG	1A	3485	1/1	0.98	0.09	47,47,47,47	0
56	MG	11	102	1/1	0.98	0.03	41,41,41,41	0
56	MG	1A	3655	1/1	0.98	0.07	49,49,49,49	0
56	MG	1A	3447	1/1	0.98	0.09	34,34,34,34	0
56	MG	1D	305	1/1	0.98	0.10	34,34,34,34	0
56	MG	13	103	1/1	0.98	0.11	42,42,42,42	0
56	MG	2A	3613	1/1	0.98	0.06	56,56,56,56	0
56	MG	1A	3344	1/1	0.98	0.05	31,31,31,31	0
56	MG	1A	3916	1/1	0.98	0.13	42,42,42,42	0
56	MG	2a	1710	1/1	0.98	0.03	73,73,73,73	0
56	MG	2A	3616	1/1	0.98	0.13	73,73,73,73	0
56	MG	1A	3449	1/1	0.98	0.06	53,53,53,53	0
56	MG	2Y	201	1/1	0.98	0.13	60,60,60,60	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2A	3290	1/1	0.98	0.04	55,55,55,55	0
56	MG	2A	3620	1/1	0.98	0.04	44,44,44,44	0
56	MG	1A	3610	1/1	0.98	0.09	45,45,45,45	0
56	MG	2A	3622	1/1	0.98	0.04	67,67,67,67	0
56	MG	1A	3772	1/1	0.98	0.08	45,45,45,45	0
56	MG	18	101	1/1	0.98	0.08	49,49,49,49	0
56	MG	1A	3139	1/1	0.98	0.07	33,33,33,33	0
56	MG	1A	3774	1/1	0.98	0.06	45,45,45,45	0
56	MG	2A	3297	1/1	0.98	0.11	43,43,43,43	0
56	MG	1A	3140	1/1	0.98	0.05	31,31,31,31	0
56	MG	1A	3452	1/1	0.98	0.04	40,40,40,40	0
56	MG	1A	3349	1/1	0.98	0.05	26,26,26,26	0
56	MG	2A	3401	1/1	0.98	0.06	56,56,56,56	0
56	MG	2a	1728	1/1	0.98	0.09	70,70,70,70	0
56	MG	1a	1847	1/1	0.98	0.06	72,72,72,72	0
56	MG	1A	3853	1/1	0.98	0.05	43,43,43,43	0
56	MG	1A	3615	1/1	0.98	0.07	59,59,59,59	0
56	MG	1A	3454	1/1	0.98	0.06	36,36,36,36	0
56	MG	1A	3284	1/1	0.98	0.07	39,39,39,39	0
56	MG	2A	3507	1/1	0.98	0.11	72,72,72,72	0
56	MG	1A	3352	1/1	0.98	0.07	40,40,40,40	0
56	MG	2A	3215	1/1	0.98	0.07	47,47,47,47	0
56	MG	1a	1853	1/1	0.98	0.05	66,66,66,66	0
56	MG	1A	3722	1/1	0.98	0.11	36,36,36,36	0
56	MG	2A	3412	1/1	0.98	0.04	47,47,47,47	0
56	MG	1A	3074	1/1	0.98	0.11	32,32,32,32	0
56	MG	1A	3066	1/1	0.98	0.18	13,13,13,13	0
56	MG	1a	1857	1/1	0.98	0.04	64,64,64,64	0
56	MG	1A	3498	1/1	0.98	0.07	56,56,56,56	0
56	MG	2a	1746	1/1	0.98	0.04	71,71,71,71	0
56	MG	1E	306	1/1	0.98	0.07	47,47,47,47	0
56	MG	2a	1748	1/1	0.98	0.05	60,60,60,60	0
56	MG	2a	1749	1/1	0.98	0.07	59,59,59,59	0
56	MG	1A	3537	1/1	0.98	0.07	32,32,32,32	0
56	MG	1A	3422	1/1	0.98	0.08	40,40,40,40	0
56	MG	1A	3869	1/1	0.98	0.07	46,46,46,46	0
56	MG	1A	3081	1/1	0.98	0.46	39,39,39,39	0
56	MG	2A	3523	1/1	0.98	0.04	57,57,57,57	0
56	MG	2A	3141	1/1	0.98	0.08	57,57,57,57	0
56	MG	1A	3358	1/1	0.98	0.06	30,30,30,30	0
56	MG	1A	3731	1/1	0.98	0.09	32,32,32,32	0
56	MG	1A	3425	1/1	0.98	0.09	44,44,44,44	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3009	1/1	0.98	0.14	27,27,27,27	0
56	MG	1A	3289	1/1	0.98	0.07	32,32,32,32	0
56	MG	1A	3806	1/1	0.98	0.14	60,60,60,60	0
56	MG	1A	3309	1/1	0.98	0.05	36,36,36,36	0
56	MG	1A	3290	1/1	0.98	0.05	34,34,34,34	0
56	MG	1A	3311	1/1	0.98	0.04	28,28,28,28	0
56	MG	1A	3634	1/1	0.98	0.07	34,34,34,34	0
56	MG	2A	3537	1/1	0.98	0.06	60,60,60,60	0
56	MG	2A	3669	1/1	0.98	0.05	47,47,47,47	0
56	MG	1A	3812	1/1	0.98	0.06	37,37,37,37	0
56	MG	1a	1705	1/1	0.98	0.10	51,51,51,51	0
56	MG	1A	3635	1/1	0.98	0.05	35,35,35,35	0
56	MG	2A	3542	1/1	0.98	0.04	56,56,56,56	0
56	MG	1A	3332	1/1	0.98	0.07	48,48,48,48	0
56	MG	2A	3545	1/1	0.98	0.07	57,57,57,57	0
56	MG	1N	203	1/1	0.98	0.10	59,59,59,59	0
56	MG	1A	3052	1/1	0.98	0.08	28,28,28,28	0
56	MG	2A	3549	1/1	0.98	0.10	53,53,53,53	0
56	MG	2A	3244	1/1	0.98	0.04	58,58,58,58	0
56	MG	2A	3343	1/1	0.98	0.07	58,58,58,58	0
56	MG	2A	3553	1/1	0.98	0.14	63,63,63,63	0
56	MG	2A	3554	1/1	0.98	0.10	63,63,63,63	0
56	MG	1P	202	1/1	0.98	0.04	55,55,55,55	0
56	MG	2A	3556	1/1	0.98	0.11	47,47,47,47	0
56	MG	1A	3742	1/1	0.98	0.11	33,33,33,33	0
56	MG	2A	3347	1/1	0.98	0.07	42,42,42,42	0
56	MG	1A	3235	1/1	0.98	0.09	32,32,32,32	0
56	MG	1A	3367	1/1	0.98	0.08	33,33,33,33	0
56	MG	1a	1797	1/1	0.98	0.10	76,76,76,76	0
56	MG	1A	3819	1/1	0.98	0.12	53,53,53,53	0
56	MG	1A	3202	1/1	0.98	0.12	29,29,29,29	0
56	MG	2A	3450	1/1	0.98	0.06	50,50,50,50	0
56	MG	1A	3050	1/1	0.98	0.14	36,36,36,36	0
56	MG	2B	3014	1/1	0.98	0.03	64,64,64,64	0
56	MG	2A	3253	1/1	0.98	0.05	53,53,53,53	0
56	MG	1a	1719	1/1	0.98	0.09	71,71,71,71	0
56	MG	1A	3595	1/1	0.98	0.13	49,49,49,49	0
56	MG	1B	211	1/1	0.98	0.05	41,41,41,41	0
56	MG	1A	3438	1/1	0.98	0.07	46,46,46,46	0
56	MG	1A	3339	1/1	0.98	0.06	43,43,43,43	0
56	MG	1A	3441	1/1	0.98	0.07	40,40,40,40	0
56	MG	2A	3574	1/1	0.98	0.07	60,60,60,60	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3694	1/1	0.98	0.05	39,39,39,39	0
56	MG	1A	3828	1/1	0.98	0.08	43,43,43,43	0
56	MG	1B	218	1/1	0.98	0.04	39,39,39,39	0
56	MG	1A	3599	1/1	0.98	0.04	35,35,35,35	0
56	MG	1V	202	1/1	0.98	0.04	46,46,46,46	0
56	MG	1A	3754	1/1	0.98	0.08	41,41,41,41	0
56	MG	1A	3264	1/1	0.98	0.06	34,34,34,34	0
60	ZN	29	501	1/1	0.98	0.03	67,67,67,67	0
60	ZN	2n	102	1/1	0.98	0.06	84,84,84,84	0
56	MG	1B	222	1/1	0.98	0.07	49,49,49,49	0
56	MG	2E	306	1/1	0.98	0.05	46,46,46,46	0
56	MG	1W	3003	1/1	0.98	0.17	33,33,33,33	0
56	MG	1a	1844	1/1	0.99	0.04	68,68,68,68	0
56	MG	1A	3761	1/1	0.99	0.04	45,45,45,45	0
56	MG	1A	3348	1/1	0.99	0.03	32,32,32,32	0
56	MG	1A	3197	1/1	0.99	0.06	29,29,29,29	0
56	MG	1D	314	1/1	0.99	0.05	33,33,33,33	0
56	MG	2A	3310	1/1	0.99	0.07	48,48,48,48	0
56	MG	1A	3577	1/1	0.99	0.06	28,28,28,28	0
56	MG	1A	3336	1/1	0.99	0.07	41,41,41,41	0
56	MG	2A	3560	1/1	0.99	0.04	54,54,54,54	0
56	MG	1a	1714	1/1	0.99	0.04	53,53,53,53	0
56	MG	1A	3427	1/1	0.99	0.05	53,53,53,53	0
56	MG	1a	1716	1/1	0.99	0.05	49,49,49,49	0
56	MG	1A	3695	1/1	0.99	0.05	38,38,38,38	0
56	MG	1A	3405	1/1	0.99	0.05	26,26,26,26	0
56	MG	1A	3406	1/1	0.99	0.03	34,34,34,34	0
56	MG	2a	1725	1/1	0.99	0.04	63,63,63,63	0
56	MG	1A	3387	1/1	0.99	0.07	34,34,34,34	0
56	MG	1a	1721	1/1	0.99	0.04	55,55,55,55	0
56	MG	1A	3771	1/1	0.99	0.10	33,33,33,33	0
56	MG	1A	3351	1/1	0.99	0.06	29,29,29,29	0
56	MG	2A	3402	1/1	0.99	0.04	52,52,52,52	0
56	MG	2a	1731	1/1	0.99	0.04	69,69,69,69	0
56	MG	1A	3298	1/1	0.99	0.09	28,28,28,28	0
56	MG	1A	3390	1/1	0.99	0.07	35,35,35,35	0
56	MG	1A	3353	1/1	0.99	0.04	43,43,43,43	0
56	MG	2A	3327	1/1	0.99	0.04	58,58,58,58	0
56	MG	1A	3827	1/1	0.99	0.04	47,47,47,47	0
56	MG	2A	3329	1/1	0.99	0.03	50,50,50,50	0
56	MG	2A	3680	1/1	0.99	0.04	65,65,65,65	0
56	MG	2a	1739	1/1	0.99	0.04	57,57,57,57	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2A	3330	1/1	0.99	0.04	48,48,48,48	0
56	MG	1A	3354	1/1	0.99	0.10	31,31,31,31	0
56	MG	1A	3292	1/1	0.99	0.04	45,45,45,45	0
56	MG	1A	3830	1/1	0.99	0.10	33,33,33,33	0
56	MG	2A	3582	1/1	0.99	0.10	60,60,60,60	0
56	MG	1A	3312	1/1	0.99	0.06	27,27,27,27	0
56	MG	1A	3562	1/1	0.99	0.07	45,45,45,45	0
56	MG	2A	3585	1/1	0.99	0.13	59,59,59,59	0
56	MG	1A	3780	1/1	0.99	0.04	44,44,44,44	0
56	MG	1A	3346	1/1	0.99	0.07	43,43,43,43	0
56	MG	2A	3588	1/1	0.99	0.03	47,47,47,47	0
56	MG	2A	3590	1/1	0.99	0.04	47,47,47,47	0
56	MG	2A	3498	1/1	0.99	0.04	42,42,42,42	0
56	MG	1A	3512	1/1	0.99	0.07	54,54,54,54	0
56	MG	2A	3593	1/1	0.99	0.03	48,48,48,48	0
56	MG	1A	3783	1/1	0.99	0.04	51,51,51,51	0
56	MG	1A	3785	1/1	0.99	0.04	36,36,36,36	0
56	MG	2A	3341	1/1	0.99	0.10	55,55,55,55	0
56	MG	2A	3597	1/1	0.99	0.07	52,52,52,52	0
56	MG	1a	1738	1/1	0.99	0.05	57,57,57,57	0
56	MG	1A	3381	1/1	0.99	0.08	38,38,38,38	0
56	MG	1A	3621	1/1	0.99	0.06	53,53,53,53	0
56	MG	2A	3345	1/1	0.99	0.11	64,64,64,64	0
56	MG	1A	3840	1/1	0.99	0.04	39,39,39,39	0
56	MG	2A	3268	1/1	0.99	0.03	45,45,45,45	0
56	MG	2a	1765	1/1	0.99	0.09	66,66,66,66	0
56	MG	1A	3680	1/1	0.99	0.03	30,30,30,30	0
56	MG	2A	3605	1/1	0.99	0.03	49,49,49,49	0
56	MG	2A	3510	1/1	0.99	0.13	67,67,67,67	0
56	MG	1A	3789	1/1	0.99	0.06	41,41,41,41	0
56	MG	1B	212	1/1	0.99	0.03	40,40,40,40	0
56	MG	1A	3440	1/1	0.99	0.08	23,23,23,23	0
56	MG	2A	3610	1/1	0.99	0.06	62,62,62,62	0
56	MG	2a	1773	1/1	0.99	0.06	63,63,63,63	0
56	MG	1A	3748	1/1	0.99	0.03	49,49,49,49	0
56	MG	2A	3612	1/1	0.99	0.04	51,51,51,51	0
56	MG	1P	201	1/1	0.99	0.06	34,34,34,34	0
56	MG	1A	3397	1/1	0.99	0.05	34,34,34,34	0
56	MG	1A	3419	1/1	0.99	0.02	42,42,42,42	0
56	MG	1A	3794	1/1	0.99	0.06	44,44,44,44	0
56	MG	1A	3715	1/1	0.99	0.10	69,69,69,69	0
56	MG	2A	3618	1/1	0.99	0.06	42,42,42,42	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3398	1/1	0.99	0.05	33,33,33,33	0
56	MG	1A	3468	1/1	0.99	0.03	47,47,47,47	0
56	MG	1R	202	1/1	0.99	0.05	38,38,38,38	0
56	MG	1A	3718	1/1	0.99	0.06	72,72,72,72	0
56	MG	1A	3799	1/1	0.99	0.04	32,32,32,32	0
56	MG	1A	3912	1/1	0.99	0.06	54,54,54,54	0
56	MG	1A	3913	1/1	0.99	0.04	32,32,32,32	0
56	MG	2A	3527	1/1	0.99	0.11	60,60,60,60	0
56	MG	1A	3800	1/1	0.99	0.07	51,51,51,51	0
56	MG	1A	3801	1/1	0.99	0.03	51,51,51,51	0
56	MG	1A	3421	1/1	0.99	0.05	55,55,55,55	0
56	MG	1A	3856	1/1	0.99	0.04	46,46,46,46	0
56	MG	1A	3803	1/1	0.99	0.07	53,53,53,53	0
56	MG	2A	3632	1/1	0.99	0.04	55,55,55,55	0
56	MG	1A	3805	1/1	0.99	0.06	31,31,31,31	0
56	MG	1A	3628	1/1	0.99	0.09	43,43,43,43	0
56	MG	2A	3535	1/1	0.99	0.08	52,52,52,52	0
56	MG	2a	1694	1/1	0.99	0.04	63,63,63,63	0
56	MG	1A	3369	1/1	0.99	0.05	43,43,43,43	0
56	MG	1A	3808	1/1	0.99	0.11	55,55,55,55	0
56	MG	2A	3538	1/1	0.99	0.10	56,56,56,56	0
56	MG	2A	3295	1/1	0.99	0.06	52,52,52,52	0
56	MG	1a	1835	1/1	0.99	0.05	64,64,64,64	0
56	MG	1A	3862	1/1	0.99	0.06	31,31,31,31	0
56	MG	1a	1837	1/1	0.99	0.07	57,57,57,57	0
56	MG	2A	3543	1/1	0.99	0.06	45,45,45,45	0
60	ZN	1Y	501	1/1	0.99	0.03	63,63,63,63	0
56	MG	1A	3758	1/1	0.99	0.03	31,31,31,31	0
60	ZN	1n	102	1/1	0.99	0.04	76,76,76,76	0
60	ZN	2Y	202	1/1	0.99	0.03	77,77,77,77	0
56	MG	1X	101	1/1	0.99	0.07	39,39,39,39	0
60	ZN	26	101	1/1	0.99	0.03	67,67,67,67	0
56	MG	2A	3546	1/1	0.99	0.03	56,56,56,56	0
56	MG	1A	3865	1/1	0.99	0.06	44,44,44,44	0
56	MG	1A	3044	1/1	0.99	0.03	26,26,26,26	0
56	MG	1A	3867	1/1	0.99	0.12	52,52,52,52	0
56	MG	1A	3724	1/1	0.99	0.15	44,44,44,44	0
56	MG	2A	3552	1/1	1.00	0.02	47,47,47,47	0
56	MG	1A	3462	1/1	1.00	0.04	30,30,30,30	0
56	MG	1A	3411	1/1	1.00	0.04	62,62,62,62	0
56	MG	1A	3565	1/1	1.00	0.05	31,31,31,31	0
56	MG	1A	3784	1/1	1.00	0.03	39,39,39,39	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2A	3589	1/1	1.00	0.04	47,47,47,47	0
56	MG	1A	3863	1/1	1.00	0.05	29,29,29,29	0
56	MG	1A	3720	1/1	1.00	0.03	34,34,34,34	0
56	MG	1E	301	1/1	1.00	0.06	34,34,34,34	0
60	ZN	15	102	1/1	1.00	0.01	54,54,54,54	0
60	ZN	16	101	1/1	1.00	0.03	49,49,49,49	0
60	ZN	19	102	1/1	1.00	0.03	52,52,52,52	0
56	MG	1A	3804	1/1	1.00	0.04	37,37,37,37	0
56	MG	1A	3476	1/1	1.00	0.02	38,38,38,38	0
56	MG	2A	3325	1/1	1.00	0.02	50,50,50,50	0
60	ZN	25	101	1/1	1.00	0.03	65,65,65,65	0
56	MG	1A	3334	1/1	1.00	0.07	33,33,33,33	0
56	MG	2A	3444	1/1	1.00	0.02	46,46,46,46	0
56	MG	1A	3543	1/1	1.00	0.03	36,36,36,36	0
56	MG	2A	3633	1/1	1.00	0.02	48,48,48,48	0
56	MG	2A	3460	1/1	1.00	0.02	46,46,46,46	0
56	MG	1A	3404	1/1	1.00	0.03	32,32,32,32	0

6.5 Other polymers [i](#)

There are no such residues in this entry.