



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 30, 2026 – 02:24 PM UTC

PDB ID : 6CFK / pdb_00006cfk
Title : Crystal structure of the *Thermus thermophilus* 70S ribosome in complex with D-histidyl-CAM and bound to protein Y (YfiA) at 2.7Å resolution
Authors : Tereshchenkov, A.G.; Dobosz-Bartoszek, M.; Osterman, I.A.; Marks, J.; Sergeeva, V.A.; Kasatsky, P.; Komarova, E.S.; Stavrianidi, A.N.; Rodin, I.A.; Konevega, A.L.; Sergiev, P.V.; Sumbatyan, N.V.; Mankin, A.S.; Bogdanov, A.A.; Polikanov, Y.S.
Deposited on : 2018-02-15
Resolution : 2.70 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

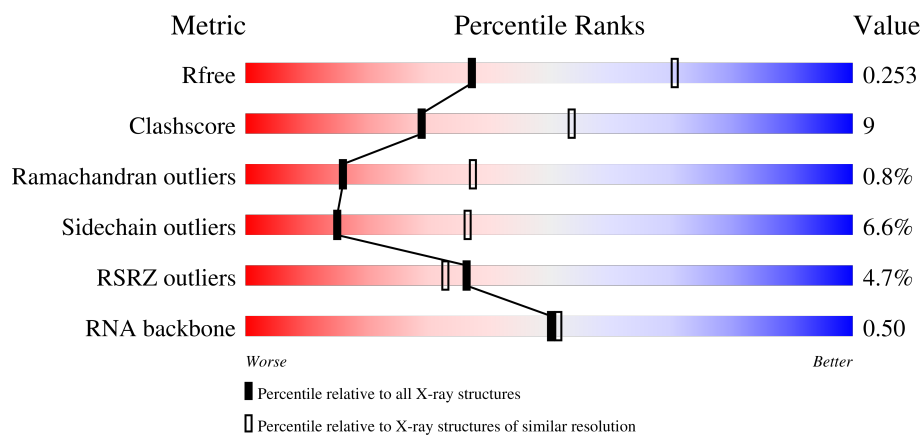
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	3538 (2.70-2.70)
Clashscore	190562	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)
RSRZ outliers	180081	3538 (2.70-2.70)
RNA backbone	3983	1044 (2.90-2.50)

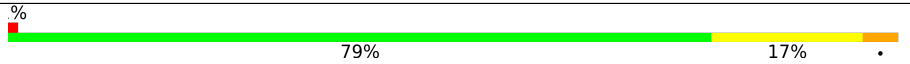
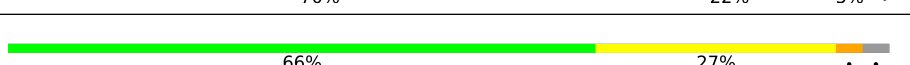
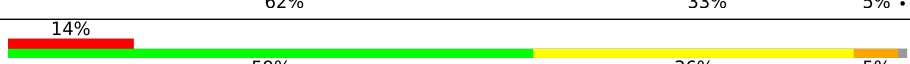
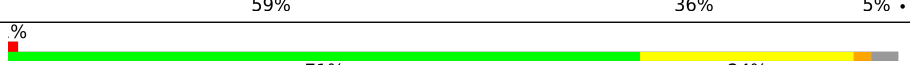
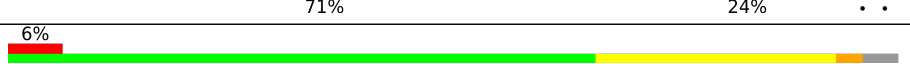
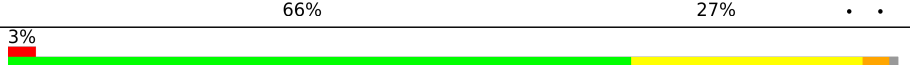
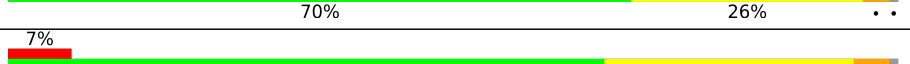
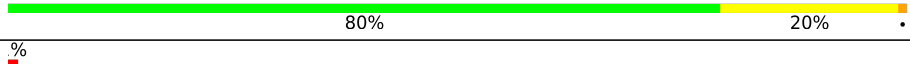
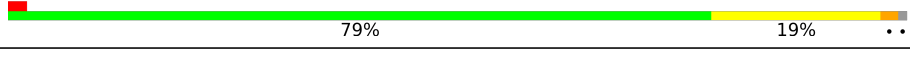
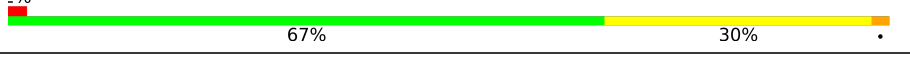
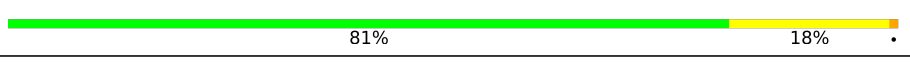
The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	1A	2915	4% 65% 28% 6%
1	2A	2915	5% 58% 33% 8%

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Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
 Validation Pipeline (wwPDB-VP) : 2.49

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Mol	Chain	Length	Quality of chain
2	1B	121	
2	2B	121	
3	1D	276	
3	2D	276	
4	1E	206	
4	2E	206	
5	1F	210	
5	2F	210	
6	1G	182	
6	2G	182	
7	1H	180	
7	2H	180	
8	1I	148	
8	2I	148	
9	1N	140	
9	2N	140	
10	1O	122	
10	2O	122	
11	1P	150	
11	2P	150	
12	1Q	141	
12	2Q	141	
13	1R	118	
13	2R	118	
14	1S	112	

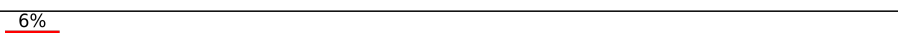
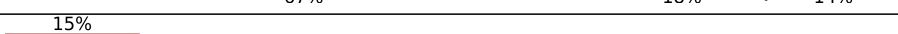
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Mol	Chain	Length	Quality of chain
14	2S	112	
15	1T	146	
15	2T	146	
16	1U	118	
16	2U	118	
17	1V	101	
17	2V	101	
18	1W	113	
18	2W	113	
19	1X	96	
19	2X	96	
20	1Y	110	
20	2Y	110	
21	1Z	206	
21	2Z	206	
22	10	85	
22	20	85	
23	11	98	
23	21	98	
24	12	72	
24	22	72	
25	13	60	
25	23	60	
26	14	71	
26	24	71	

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Mol	Chain	Length	Quality of chain
27	15	60	
27	25	60	
28	16	54	
28	26	54	
29	17	49	
29	27	49	
30	18	65	
30	28	65	
31	19	37	
31	29	37	
32	1a	1521	
32	2a	1521	
33	1b	256	
33	2b	256	
34	1c	239	
34	2c	239	
35	1d	209	
35	2d	209	
36	1e	162	
36	2e	162	
37	1f	101	
37	2f	101	
38	1g	156	
38	2g	156	
39	1h	138	

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Mol	Chain	Length	Quality of chain
39	2h	138	
40	1i	128	
40	2i	128	
41	1j	105	
41	2j	105	
42	1k	129	
42	2k	129	
43	1l	132	
43	2l	132	
44	1m	126	
44	2m	126	
45	1n	61	
45	2n	61	
46	1o	89	
46	2o	89	
47	1p	88	
47	2p	88	
48	1q	105	
48	2q	105	
49	1r	88	
49	2r	88	
50	1s	93	
50	2s	93	
51	1t	106	
51	2t	106	

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Mol	Chain	Length	Quality of chain
52	1u	27	
52	2u	27	
53	1y	113	
53	2y	113	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
54	MG	2A	3215	-	-	-	X

2 Entry composition

There are 61 unique types of molecules in this entry. The entry contains 295438 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called 23S Ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	1A	2872	Total	C	N	O	P	0	0	0
			61869	27540	11574	19884	2871			
1	2A	2867	Total	C	N	O	P	0	0	0
			61758	27491	11552	19850	2865			

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 54 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
54	1A	1024	Total	Mg	0	0
			1024	1024		
54	1B	29	Total	Mg	0	0
			29	29		
54	1D	13	Total	Mg	0	0
			13	13		
54	1E	7	Total	Mg	0	0
			7	7		
54	1F	13	Total	Mg	0	0
			13	13		
54	1G	4	Total	Mg	0	0
			4	4		
54	1H	2	Total	Mg	0	0
			2	2		
54	1N	3	Total	Mg	0	0
			3	3		
54	1O	2	Total	Mg	0	0
			2	2		
54	1P	3	Total	Mg	0	0
			3	3		
54	1Q	4	Total	Mg	0	0
			4	4		
54	1R	3	Total	Mg	0	0
			3	3		
54	1S	1	Total	Mg	0	0
			1	1		
54	1T	3	Total	Mg	0	0
			3	3		
54	1U	2	Total	Mg	0	0
			2	2		
54	1V	3	Total	Mg	0	0
			3	3		
54	1W	2	Total	Mg	0	0
			2	2		
54	1X	2	Total	Mg	0	0
			2	2		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
54	1Z	1	Total 1	Mg 1	0	0
54	10	6	Total 6	Mg 6	0	0
54	11	3	Total 3	Mg 3	0	0
54	13	2	Total 2	Mg 2	0	0
54	14	1	Total 1	Mg 1	0	0
54	15	3	Total 3	Mg 3	0	0
54	17	2	Total 2	Mg 2	0	0
54	18	1	Total 1	Mg 1	0	0
54	19	2	Total 2	Mg 2	0	0
54	1a	255	Total 255	Mg 255	0	0
54	1b	1	Total 1	Mg 1	0	0
54	1d	6	Total 6	Mg 6	0	0
54	1e	2	Total 2	Mg 2	0	0
54	1f	2	Total 2	Mg 2	0	0
54	1g	3	Total 3	Mg 3	0	0
54	1h	2	Total 2	Mg 2	0	0
54	1i	1	Total 1	Mg 1	0	0
54	1l	2	Total 2	Mg 2	0	0
54	1n	1	Total 1	Mg 1	0	0
54	1o	1	Total 1	Mg 1	0	0
54	1t	1	Total 1	Mg 1	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
54	1y	4	Total 4 Mg 4	0	0
54	2A	721	Total 721 Mg 721	0	0
54	2B	19	Total 19 Mg 19	0	0
54	2D	8	Total 8 Mg 8	0	0
54	2E	6	Total 6 Mg 6	0	0
54	2F	3	Total 3 Mg 3	0	0
54	2G	3	Total 3 Mg 3	0	0
54	2I	1	Total 1 Mg 1	0	0
54	2N	1	Total 1 Mg 1	0	0
54	2O	1	Total 1 Mg 1	0	0
54	2P	2	Total 2 Mg 2	0	0
54	2Q	2	Total 2 Mg 2	0	0
54	2R	1	Total 1 Mg 1	0	0
54	2T	4	Total 4 Mg 4	0	0
54	2V	1	Total 1 Mg 1	0	0
54	2W	2	Total 2 Mg 2	0	0
54	2X	1	Total 1 Mg 1	0	0
54	20	1	Total 1 Mg 1	0	0
54	21	1	Total 1 Mg 1	0	0
54	25	1	Total 1 Mg 1	0	0
54	28	3	Total 3 Mg 3	0	0

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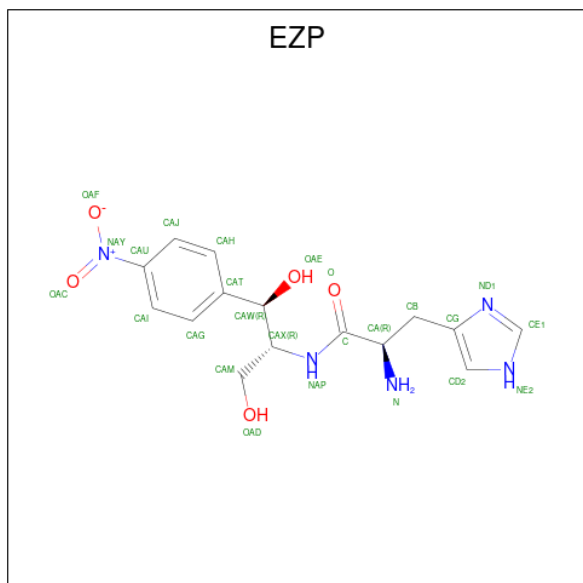
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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
54	2a	151	Total Mg 151 151	0	0
54	2e	1	Total Mg 1 1	0	0
54	2f	1	Total Mg 1 1	0	0
54	2j	1	Total Mg 1 1	0	0
54	2p	1	Total Mg 1 1	0	0
54	2q	1	Total Mg 1 1	0	0
54	2r	1	Total Mg 1 1	0	0
54	2t	1	Total Mg 1 1	0	0

- Molecule 55 is POTASSIUM ION (CCD ID: K) (formula: K).

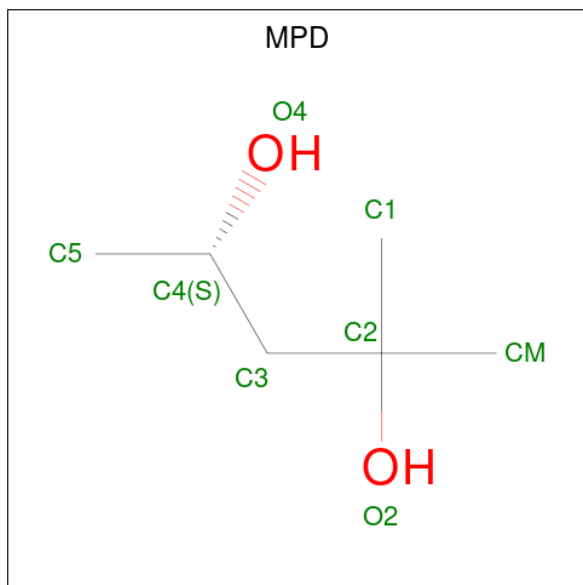
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
55	1A	1	Total K 1 1	0	0
55	2A	1	Total K 1 1	0	0

- Molecule 56 is N-[(1R,2R)-1,3-dihydroxy-1-(4-nitrophenyl)propan-2-yl]-D-histidinamide (CCD ID: EZP) (formula: C₁₅H₁₉N₅O₅).



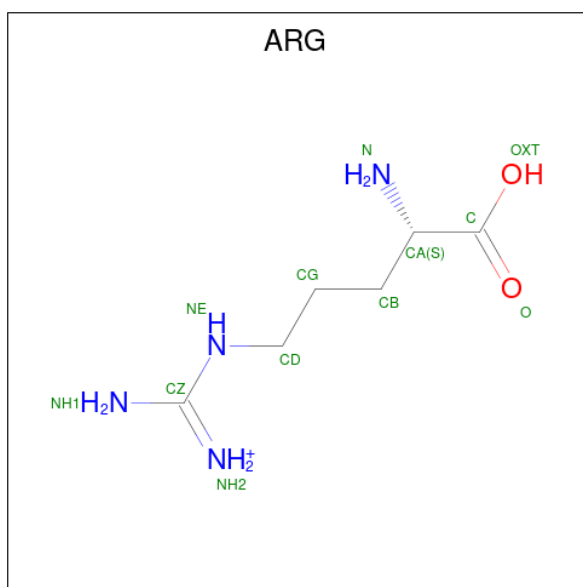
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
56	1A	1	Total	C	N	O	0	0
			25	15	5	5		
56	2A	1	Total	C	N	O	0	0
			25	15	5	5		

- Molecule 57 is (4S)-2-METHYL-2,4-PENTANEDIOL (CCD ID: MPD) (formula: C₆H₁₄O₂).



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

- Molecule 58 is ARGinine (CCD ID: ARG) (formula: C₆H₁₅N₄O₂).



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

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

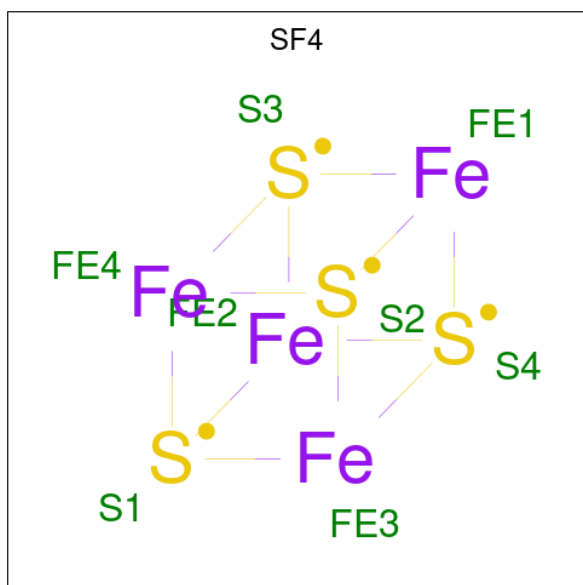
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
59	1Y	1	Total	Zn	0	0
			1	1		
59	14	1	Total	Zn	0	0
			1	1		
59	15	1	Total	Zn	0	0
			1	1		
59	16	1	Total	Zn	0	0
			1	1		
59	19	1	Total	Zn	0	0
			1	1		
59	1n	1	Total	Zn	0	0
			1	1		
59	2Y	1	Total	Zn	0	0
			1	1		
59	24	1	Total	Zn	0	0
			1	1		
59	25	1	Total	Zn	0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

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

- Molecule 60 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe_4S_4).



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

- Molecule 61 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
61	1A	2980	Total	O	0	0
			2980	2980		
61	1B	105	Total	O	0	0
			105	105		
61	1D	116	Total	O	0	0
			116	116		
61	1E	76	Total	O	0	0
			76	76		
61	1F	63	Total	O	0	0
			63	63		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
61	1G	22	Total 22	O 22	0	0
61	1H	16	Total 16	O 16	0	0
61	1I	7	Total 7	O 7	0	0
61	1N	50	Total 50	O 50	0	0
61	1O	22	Total 22	O 22	0	0
61	1P	58	Total 58	O 58	0	0
61	1Q	42	Total 42	O 42	0	0
61	1R	37	Total 37	O 37	0	0
61	1S	13	Total 13	O 13	0	0
61	1T	42	Total 42	O 42	0	0
61	1U	45	Total 45	O 45	0	0
61	1V	37	Total 37	O 37	0	0
61	1W	24	Total 24	O 24	0	0
61	1X	24	Total 24	O 24	0	0
61	1Y	15	Total 15	O 15	0	0
61	1Z	14	Total 14	O 14	0	0
61	10	22	Total 22	O 22	0	0
61	11	28	Total 28	O 28	0	0
61	12	14	Total 14	O 14	0	0
61	13	22	Total 22	O 22	0	0
61	14	2	Total 2	O 2	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
61	15	26	Total 26	O 26	0	0
61	16	17	Total 17	O 17	0	0
61	17	14	Total 14	O 14	0	0
61	18	30	Total 30	O 30	0	0
61	19	8	Total 8	O 8	0	0
61	1a	261	Total 261	O 261	0	0
61	1b	1	Total 1	O 1	0	0
61	1d	9	Total 9	O 9	0	0
61	1e	6	Total 6	O 6	0	0
61	1f	3	Total 3	O 3	0	0
61	1h	1	Total 1	O 1	0	0
61	1i	1	Total 1	O 1	0	0
61	1j	1	Total 1	O 1	0	0
61	1k	1	Total 1	O 1	0	0
61	1l	4	Total 4	O 4	0	0
61	1n	1	Total 1	O 1	0	0
61	1o	5	Total 5	O 5	0	0
61	1p	3	Total 3	O 3	0	0
61	1y	5	Total 5	O 5	0	0
61	2A	1686	Total 1686	O 1686	0	0
61	2B	65	Total 65	O 65	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
61	2D	52	Total 52	O 52	0	0
61	2E	25	Total 25	O 25	0	0
61	2F	21	Total 21	O 21	0	0
61	2G	7	Total 7	O 7	0	0
61	2H	4	Total 4	O 4	0	0
61	2I	4	Total 4	O 4	0	0
61	2N	6	Total 6	O 6	0	0
61	2O	22	Total 22	O 22	0	0
61	2P	23	Total 23	O 23	0	0
61	2Q	30	Total 30	O 30	0	0
61	2R	21	Total 21	O 21	0	0
61	2S	8	Total 8	O 8	0	0
61	2T	10	Total 10	O 10	0	0
61	2U	14	Total 14	O 14	0	0
61	2V	9	Total 9	O 9	0	0
61	2W	21	Total 21	O 21	0	0
61	2X	9	Total 9	O 9	0	0
61	2Y	3	Total 3	O 3	0	0
61	2Z	15	Total 15	O 15	0	0
61	20	13	Total 13	O 13	0	0
61	21	24	Total 24	O 24	0	0

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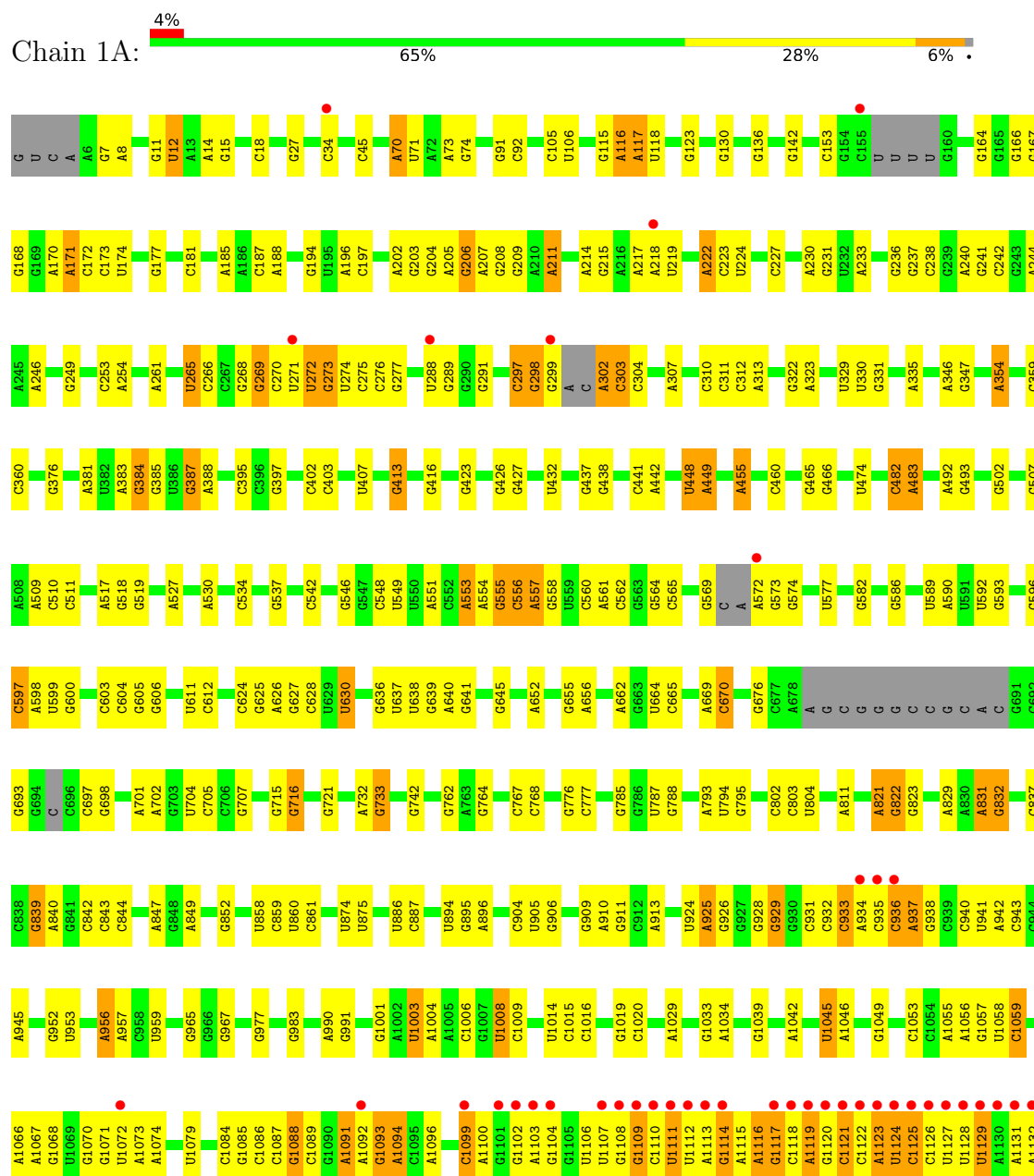
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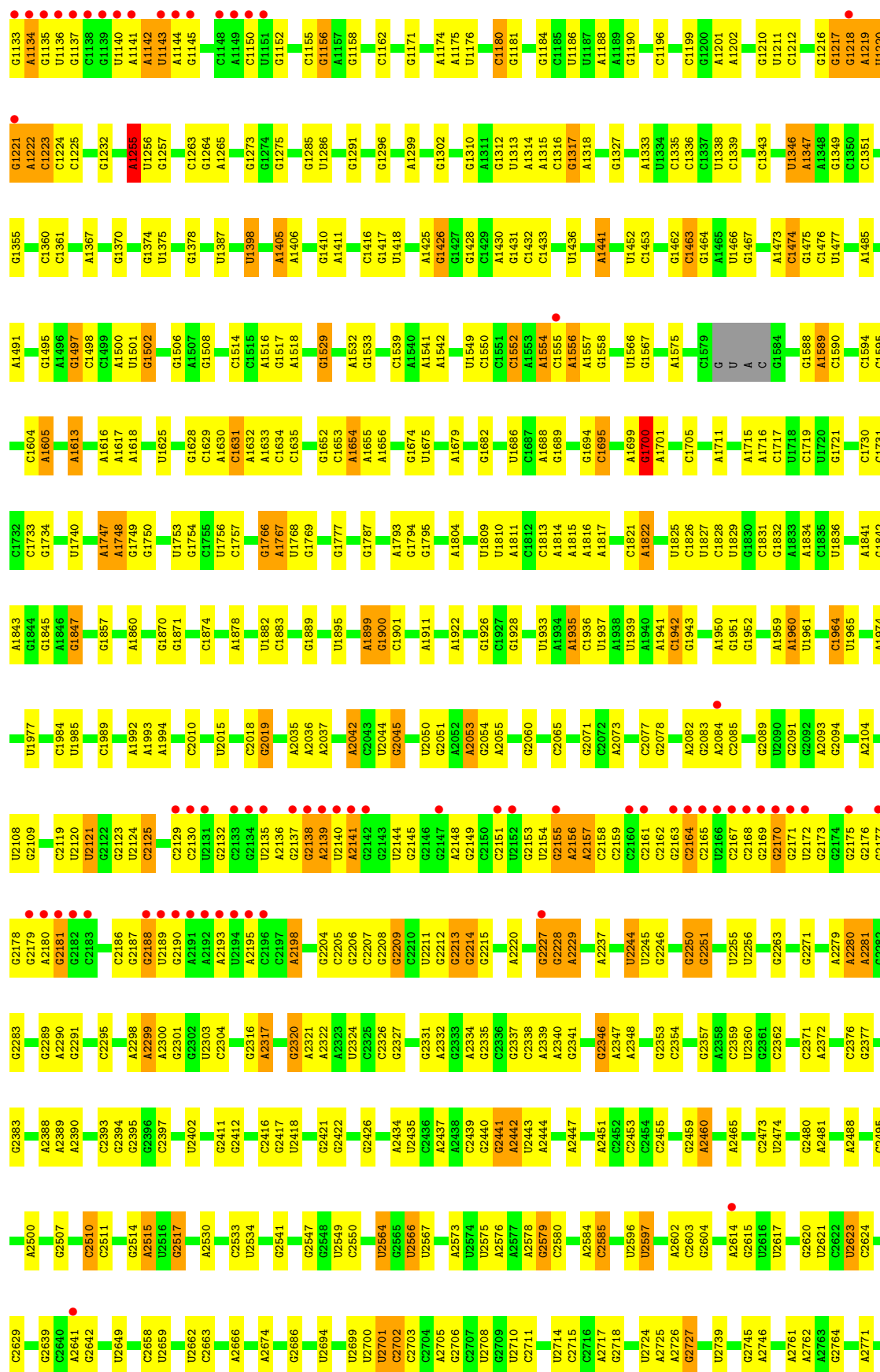
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
61	22	5	Total 5	O 5	0	0
61	23	3	Total 3	O 3	0	0
61	24	2	Total 2	O 2	0	0
61	25	9	Total 9	O 9	0	0
61	26	6	Total 6	O 6	0	0
61	27	7	Total 7	O 7	0	0
61	28	15	Total 15	O 15	0	0
61	29	2	Total 2	O 2	0	0
61	2a	100	Total 100	O 100	0	0
61	2d	6	Total 6	O 6	0	0
61	2e	1	Total 1	O 1	0	0
61	2f	1	Total 1	O 1	0	0
61	2j	2	Total 2	O 2	0	0
61	2l	1	Total 1	O 1	0	0
61	2m	1	Total 1	O 1	0	0
61	2o	2	Total 2	O 2	0	0
61	2p	1	Total 1	O 1	0	0
61	2q	1	Total 1	O 1	0	0
61	2r	4	Total 4	O 4	0	0
61	2y	1	Total 1	O 1	0	0

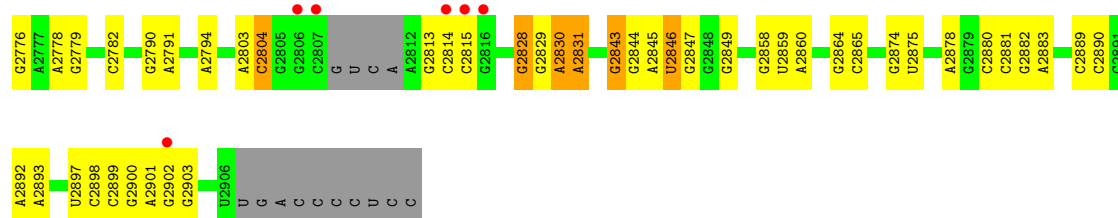
3 Residue-property plots [i](#)

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

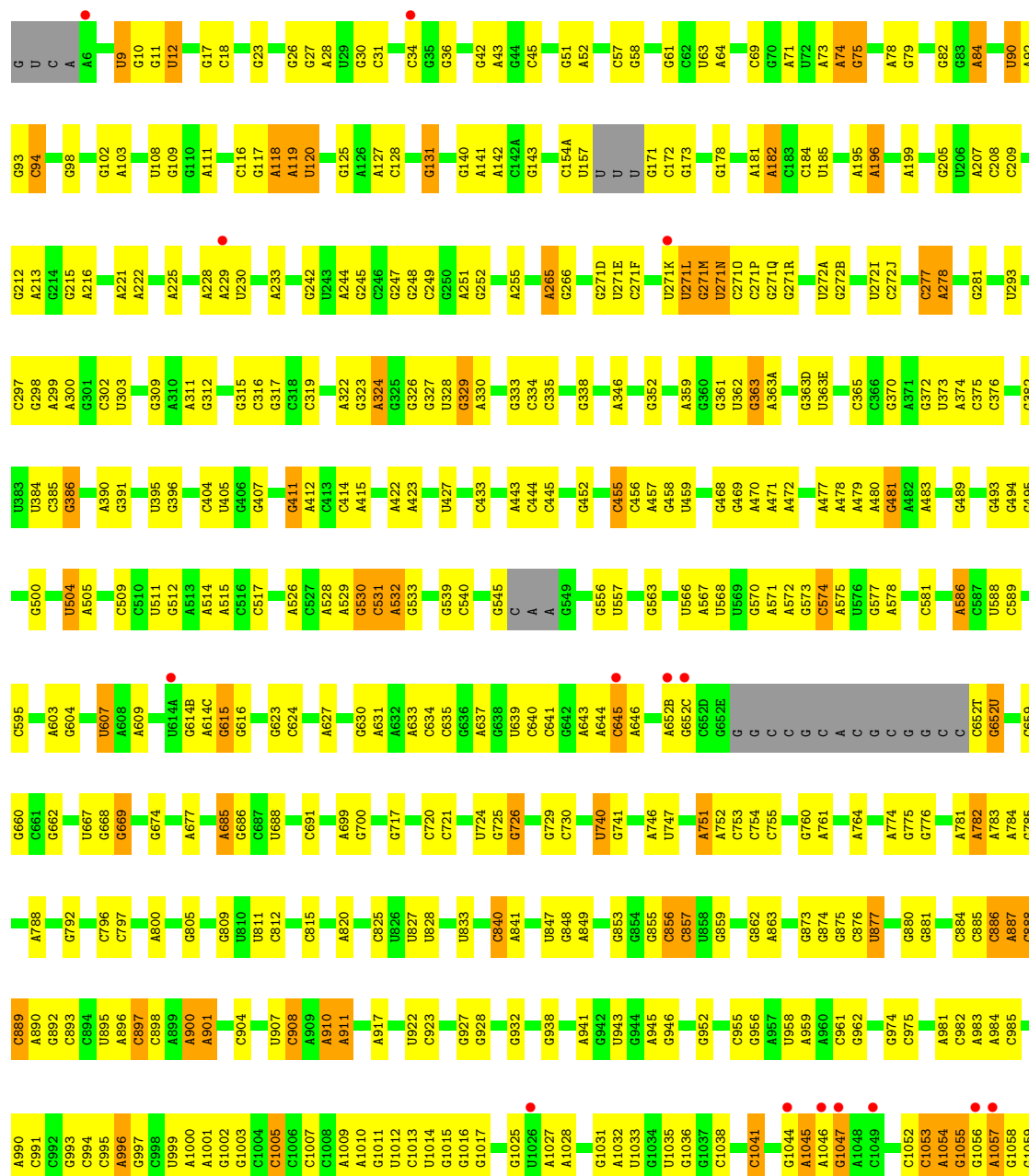
• Molecule 1: 23S Ribosomal RNA



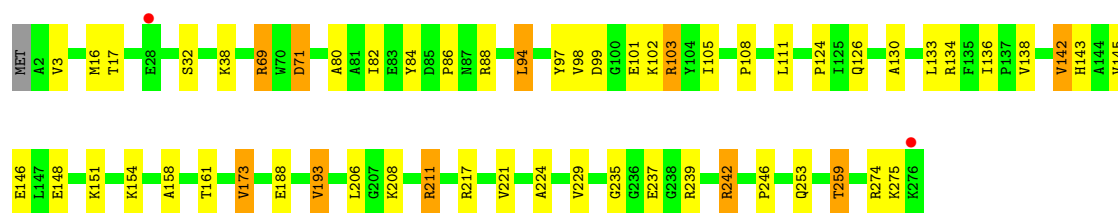




• Molecule 1: 23S Ribosomal RNA

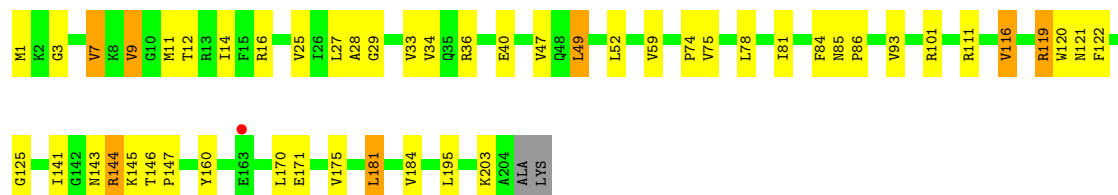


C2364	A2287	A2117	G2027	A1900	C1781	C1858	G1538	C1446	G1324	A1126	U1060
G2365	A2288	U2118	G2027	A1901	C1782	A1664	G1539	G1447	C1327	A1129	G1062
A2366	G2289	U2180	A2030	C1902	A1783	A1665	G1540	G1448	G1328	U1130	G1063
G2375	C2292	G2181	A2030	G1906	A1784	A1666	G1541	A1449	G1131	C1135	C1064
A2376	C2295	G2182	G2032	G1910	A1785	G1667	A1542	C1450A	U1341	C1136	U1065
A2377	U2296	G2183	A2033	U1911	A1786	A1668	C1543	G1450A	A1342	C1137	U1066
A2378	G2297	G2184	G2036	U1912	A1791	A1669	C1547	G1455	U1240	U1141	A1067
G2379	C2297	C2185	G2037	A1912	G1792	C1674	C1550	G1459	A1241	U1142	G1068
A2380	G2298	A2126	G2038	A1913	U1793	C1675	C1557	G1467	A1246	U1143	A1069
G2383	G2299	G2187	G2039	C1914	U1794	G1676	C1558	C1467	G1356	A1144	A1070
G2384	C2300	C2128	C2040	U1915	C1795	U1680	A1559	A1467	U1246	U1145	G1071
C2385	G2302	U2189	G2040	A1916	U1796	U1681	A1560	A1471	A1253	A1142A	C1072
A2388	G2303	G2190	C2043	U1917	C1797	C1686	G1566	A1482	U1255	C1153	A1073
G2389	G2304	G2191	G2043	C1920	U1798	G1687	A1567	G1482	C1257	G1154	G1074
A2390	C2305	G2192	A2051	G1921	U1799	U1688	A1568	A1486	G1260	A1155	C1075
G2391	G2306	A2198	G2055	G1929	C1800	G1696	A1569	A1487	G1261	U1185	C1076
C2397	G2308	G2136	G2056	G1930	A1801	G1697	C1577	G1488	G1264	U1186	U1078
A2398	A2309	G2137	G2060	G1937	A1802	A1700	U1578	A1489	U1187	U1167	C1079
G2400	A2310	C2138	A2061	A1938	G1807	A1701	C1579	A1490	A1272	G1168	C1080
U2401	G2311	C2139	G2062	U1939	U1816	A1702	A1580	G1491	U1273	U1081	U1082
C2402	G2312	G2140	A2062	U1939	A1815	G1703	G1581	G1492	A1274	G1169	U1083
U2406	G2313	G2141	G2069	C1942	G1816	G1707	C1582	C1493	A1278	G1170	A1084
G2407	A2225	C2142	G2070	C1942	U1818	C1708	A1583	A1494	G1271	G1171	A1085
G2410	G2237	U2144	G2070	U1946	U1818	C1709	C1584	A1495	A1272	G	A1086
C2411	G2238	C2145	U2074	C1947	G1826	U1709	A1586	A1496	U1273	A	G1087
G2414	G2239	C2146	U2075	C1947	C1827	C1710	C1587	A1497	G1385	U	U1088
C2417	A2225	G2147	U2079	A1952	G1828	U1720	C1589	C1498	A1278	C	G1089
U2418	G2243	C2148	U2079	A1953	A1829	G1721	U1590	U1503	A1392	A	U1090
A2419	U2444	U2150	U2086	G1954	C1830	A1722	C1591	C1504	G1281	C1178	G1091
G2420	C2248	G2151	G2087	U1955	G1831	G1739	G1595	C1506	U1292	C1179	C1092
C2421	G2251	G2152	U2092	C1962	C1832	U1740	A1596	A1507	A1287	C1180	G1093
A2422	G2252	G2153	G2093	U1963	G1835	A1741	A1597	A1508	U1288	C1181	U1094
A2423	G2253	G2154	G2094	C1967	G1839	G1746	C1598	C1509	G1186	A1096	A1095
C2424	G2254	G2155	G2095	C1967	U1842	U1748	C1599	A1509A	G1187	U1097	A1096
A2425	C2260	G2156	U2096	A1970	G1847	A1749	C1607	A1509B	U1188	A1098	A1097
G2429	C2261	A2158	U2099	A1971	A1847	G1750	A1608	G1510	U1189	G1100	G1099
A2430	U2262	G2159	G2100	A1972	A1848	C1754	A1610	U1514	G1195	C1102	U1101
U2431	A2267	C2160	G2101	U1991	G1858	A1755	A1614	G1515	U1300	A1103	C1104
A2435	A2268	C2161	U2102	U1993	U1854	G1756	U1629	U1518	A1302	U1105	U1105
G2439	G2270	C2162	C2103	C1996	U1876	G1762	A1631A	G1525	A1308	A1210	C1109
C2440	G2271	G2163	G2104	G1997	A1877	A1763	A1631A	G1526	U1211	U1211	G1110
C2441	U2272	G2164	C2105	G1997	A1878	G1764	U1639	G1527	G1212	A1111	A1111
G2445	A2273	U2167	G2106	G1997	G1877	C1771	C1640	A1528A	C1314	G1219	U1113
A2448	C2274	G2168	C2107	A2001	G1878	U1772	G1647	G1529	C1315	U1316	G1114
G2454	C2275	A2170	C2108	G2002	C1881	A1773	C1648	U1533	U1317	C1221	G1115
C2459	G2280	U2171	C2109	A2014	C1882	G1776	U1654	U	G1442	C1221A	G1116
G2460	U2172	A2172	C2110	A2014	C1882	U1777	A1654	A	C1320	G1223	G1117
C2464	C2283	U2173	U2113	A2020	A1889	U1778	U1654	C1536	A1321	G1224	G1122
U2465	C2284	C2174	A2114	G2021	A1890	U1779	U1654	C1537	A1445	G1225	G1123
G2466	A2286	A2176	G2116	G2023	G1899	A1780	C1657	U1537	A1445A	C1226	G1125



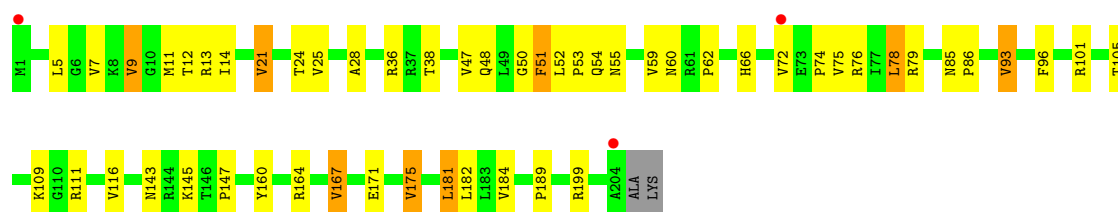
• Molecule 4: 50S ribosomal protein L3

Chain 1E: 75% 21% ..



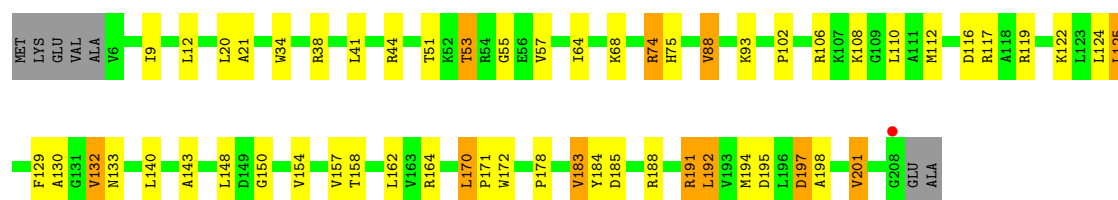
• Molecule 4: 50S ribosomal protein L3

Chain 2E: 73% 22% ..



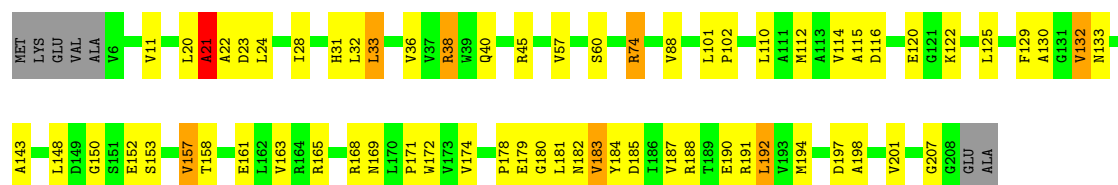
• Molecule 5: 50S ribosomal protein L4

Chain 1F: 70% 22% 5% .

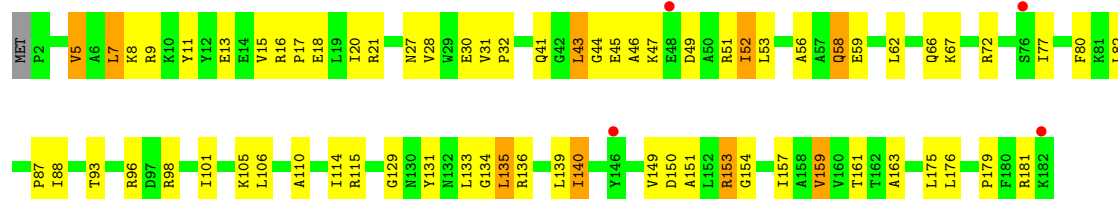


• Molecule 5: 50S ribosomal protein L4

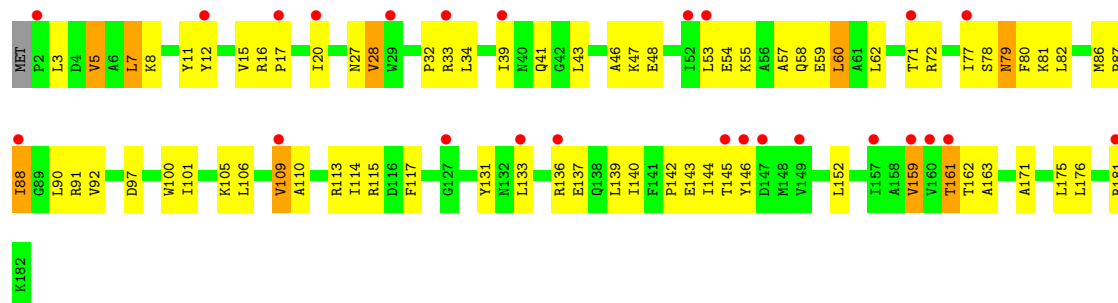
Chain 2F: 66% 27% ..



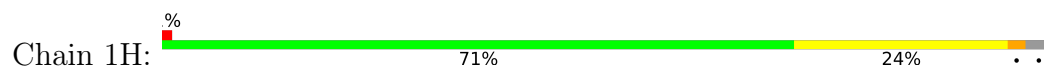
• Molecule 6: 50S ribosomal protein L5



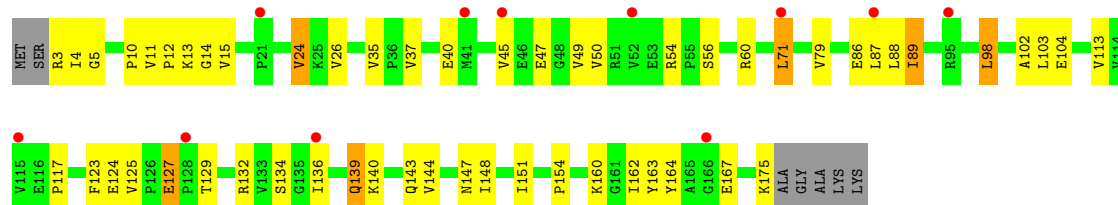
• Molecule 6: 50S ribosomal protein L5



• Molecule 7: 50S ribosomal protein L6

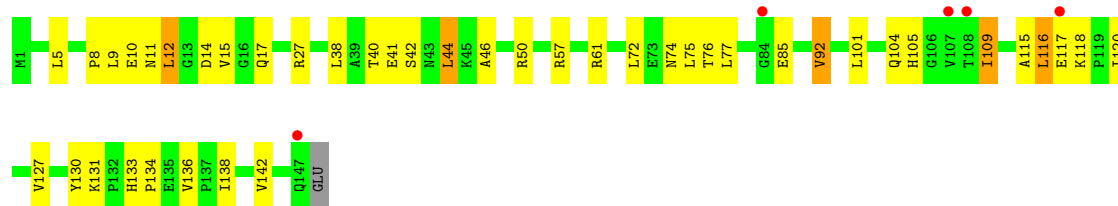


• Molecule 7: 50S ribosomal protein L6

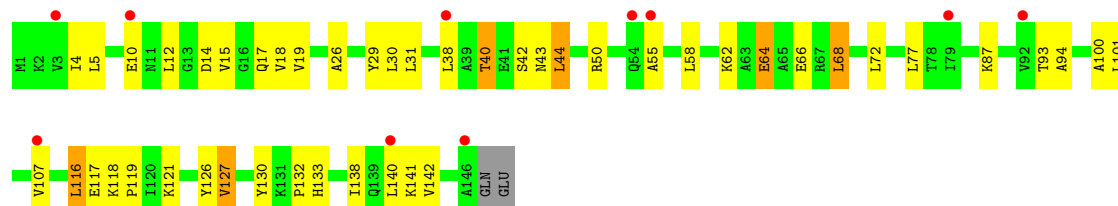


• Molecule 8: 50S ribosomal protein L9

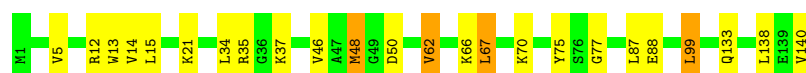
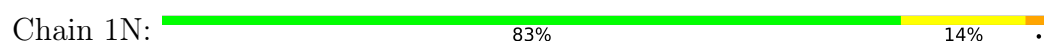




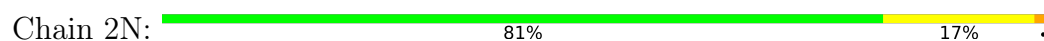
• Molecule 8: 50S ribosomal protein L9



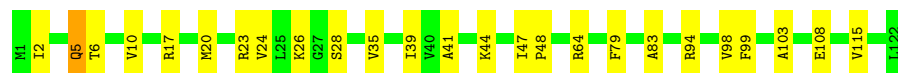
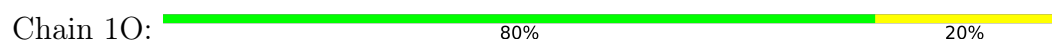
• Molecule 9: 50S ribosomal protein L13



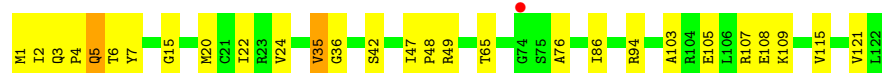
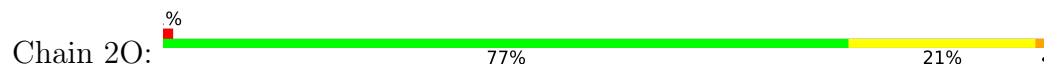
• Molecule 9: 50S ribosomal protein L13



• Molecule 10: 50S ribosomal protein L14

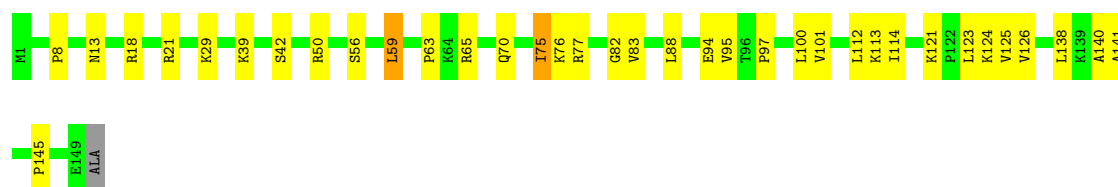


• Molecule 10: 50S ribosomal protein L14

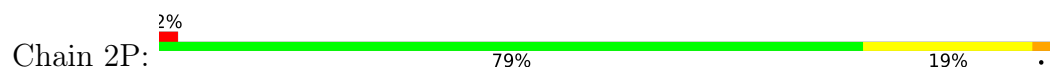


• Molecule 11: 50S ribosomal protein L15

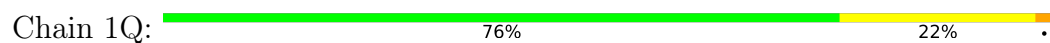




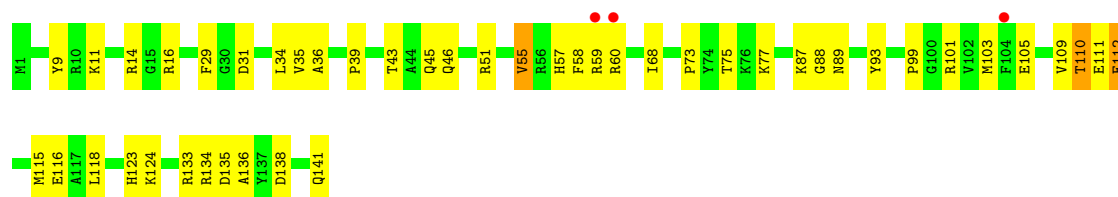
- Molecule 11: 50S ribosomal protein L15



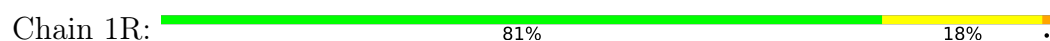
- Molecule 12: 50S ribosomal protein L16



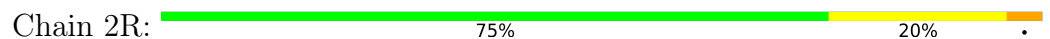
- Molecule 12: 50S ribosomal protein L16



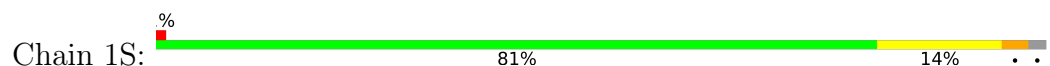
- Molecule 13: 50S ribosomal protein L17



- Molecule 13: 50S ribosomal protein L17

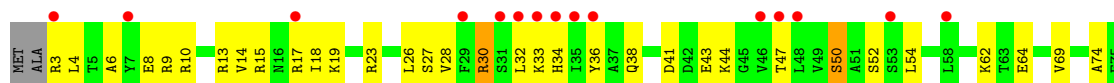


- Molecule 14: 50S ribosomal protein L18

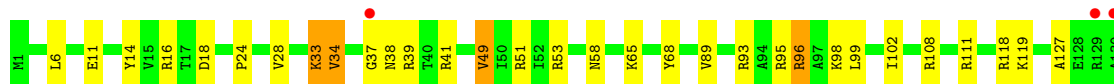




- Molecule 14: 50S ribosomal protein L18



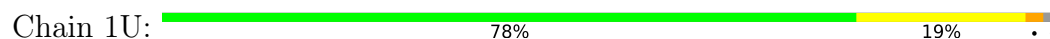
- Molecule 15: 50S ribosomal protein L19



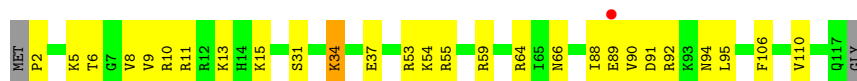
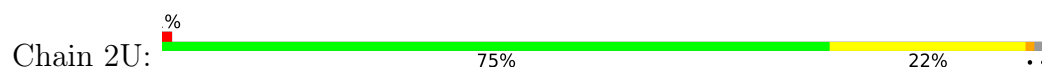
- Molecule 15: 50S ribosomal protein L19



- Molecule 16: 50S ribosomal protein L20



- Molecule 16: 50S ribosomal protein L20



- Molecule 17: 50S ribosomal protein L21

Chain 1V:  76% 22% .



- Molecule 17: 50S ribosomal protein L21

Chain 2V:  72% 24% ..



- Molecule 18: 50S ribosomal protein L22

Chain 1W:  81% 16% ..



- Molecule 18: 50S ribosomal protein L22

Chain 2W:  78% 18% ..



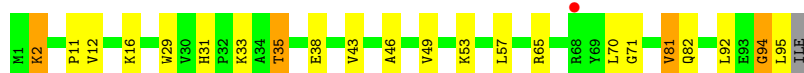
- Molecule 19: 50S ribosomal protein L23

Chain 1X:  73% 22% ..



- Molecule 19: 50S ribosomal protein L23

Chain 2X:  76% 19% ..



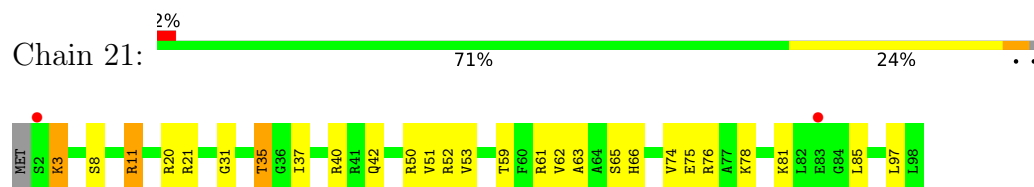
- Molecule 20: 50S ribosomal protein L24

Chain 1Y:  72% 22% ..

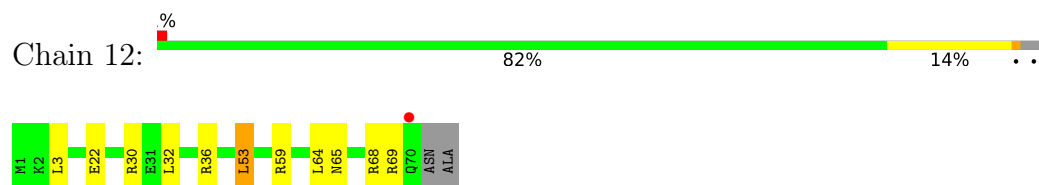


-
- Heatmap showing the distribution of 20 amino acids across 20 different conditions. The amino acids are listed on the y-axis: MET, S2, K3, P12, R21, G22, K23, G29, V30, T35, R40, R50, V51, R52, G55, T59, P67, P68, K69, V70, Y71, V74, K81, K92, L95, and L98. The conditions are represented by colored bars for each amino acid. MET has a red dot above it. The colors range from yellow to dark red, indicating different levels of distribution.

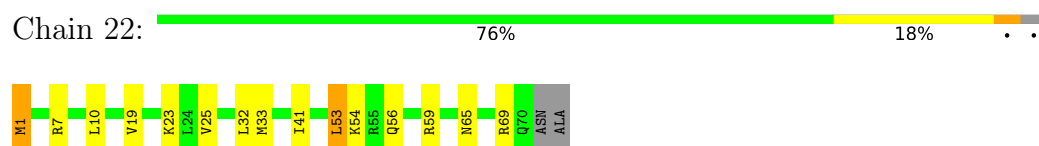
- Molecule 23: 50S ribosomal protein L28



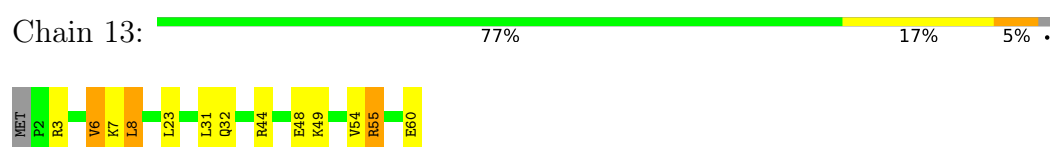
- Molecule 24: 50S ribosomal protein L29



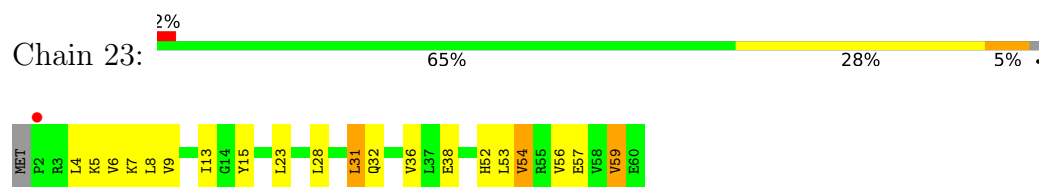
- Molecule 24: 50S ribosomal protein L29



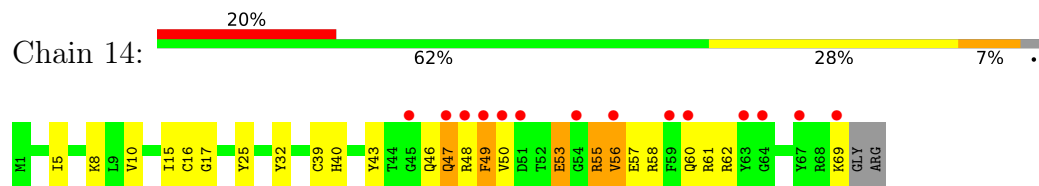
- Molecule 25: 50S ribosomal protein L30



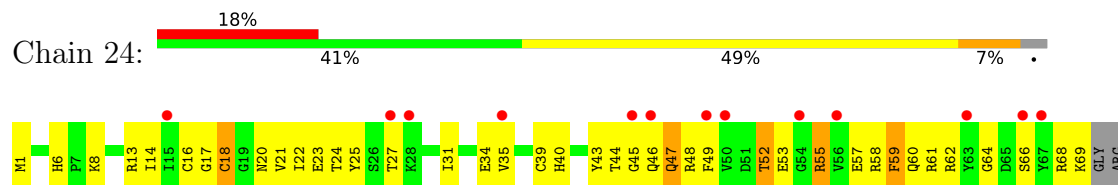
- Molecule 25: 50S ribosomal protein L30



- Molecule 26: 50S ribosomal protein L31



- Molecule 26: 50S ribosomal protein L31



- Molecule 27: 50S ribosomal protein L32

Chain 15:  68% 27% ..



- Molecule 27: 50S ribosomal protein L32

Chain 25:  82% 15% ..



- Molecule 28: 50S ribosomal protein L33

Chain 16:  63% 31% ..



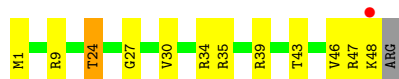
- Molecule 28: 50S ribosomal protein L33

Chain 26:  72% 22% ..



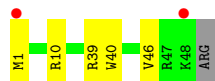
- Molecule 29: 50S ribosomal protein L34

Chain 17:  73% 22% ..



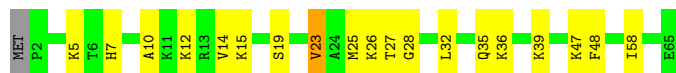
- Molecule 29: 50S ribosomal protein L34

Chain 27:  88% 10% ..

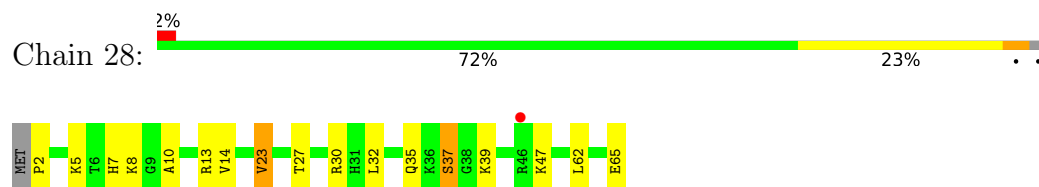


- Molecule 30: 50S ribosomal protein L35

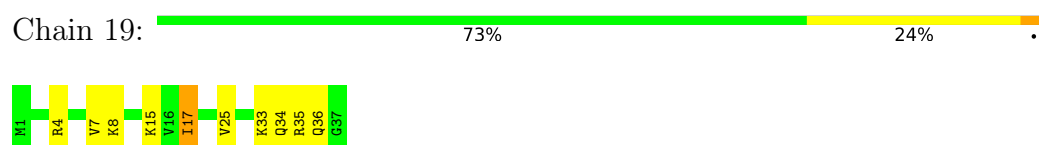
Chain 18:  69% 28% ..



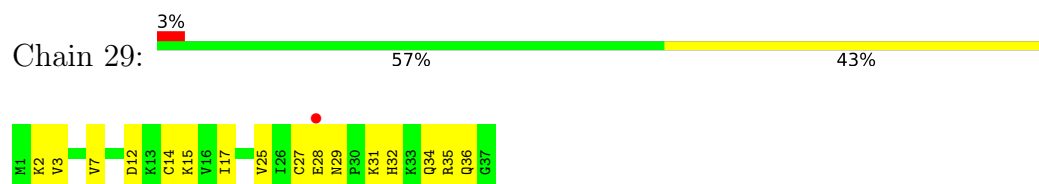
- Molecule 30: 50S ribosomal protein L35



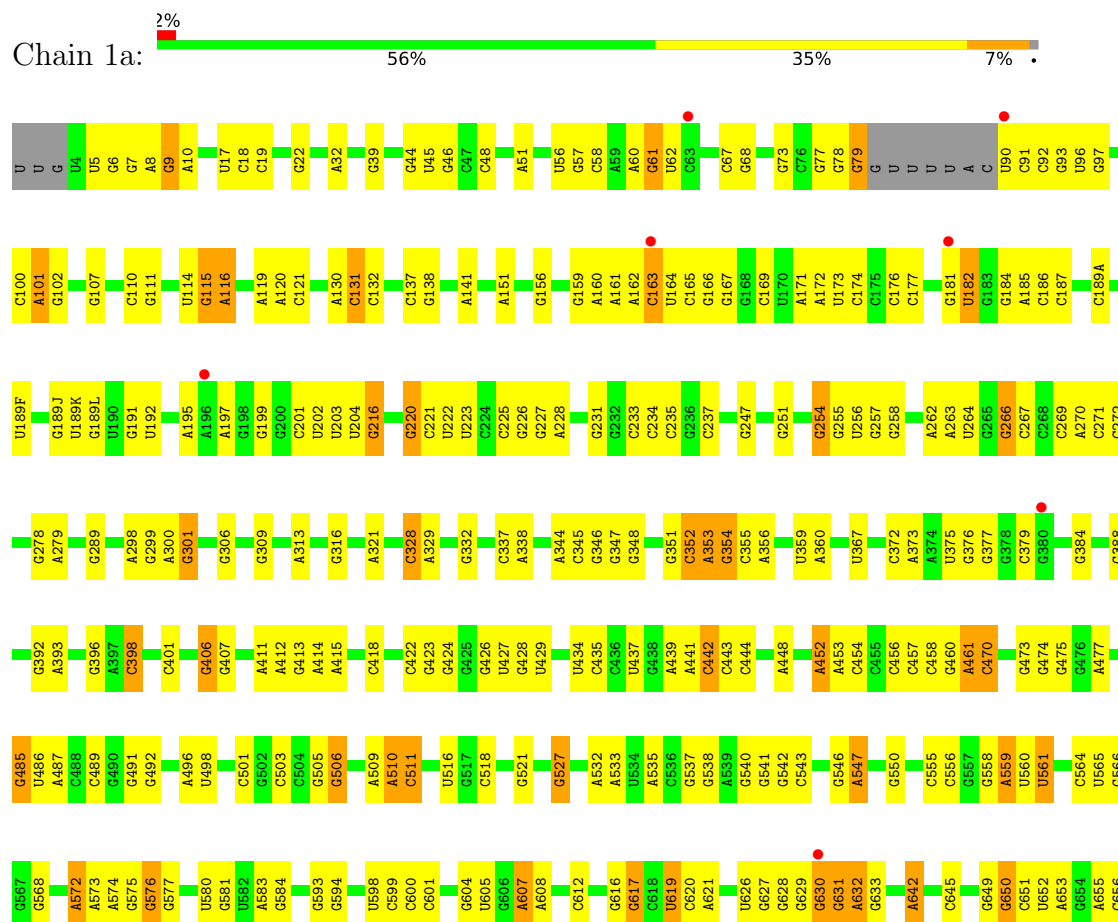
- Molecule 31: 50S ribosomal protein L36

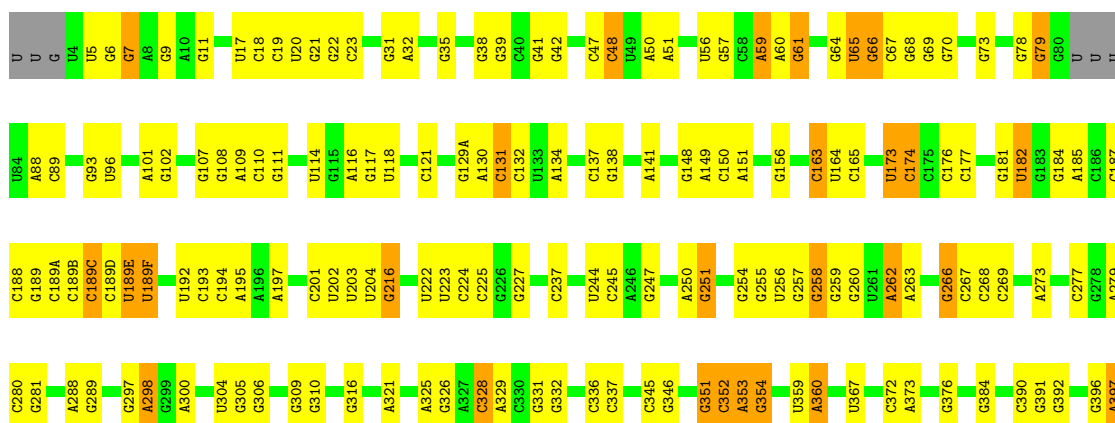


- Molecule 31: 50S ribosomal protein L36

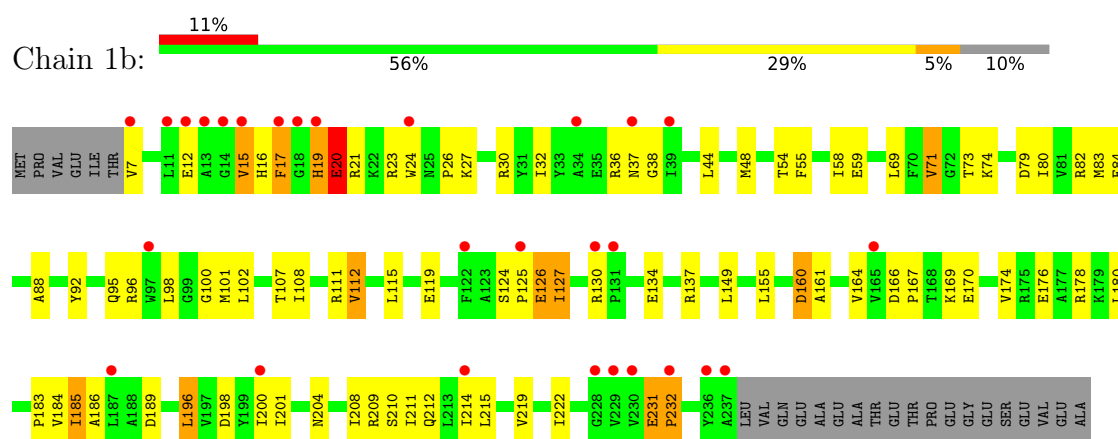


- Molecule 32: 16S Ribosomal RNA

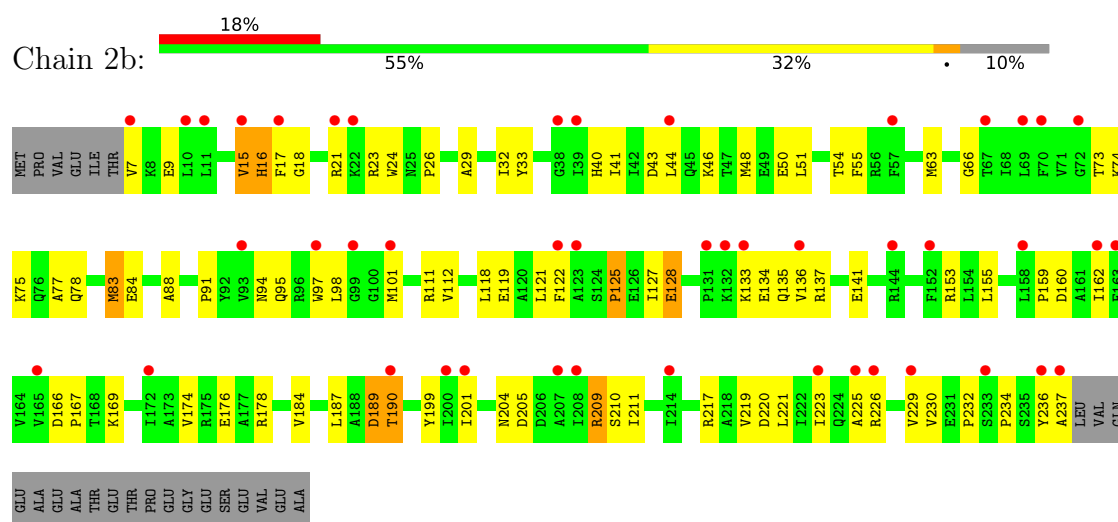




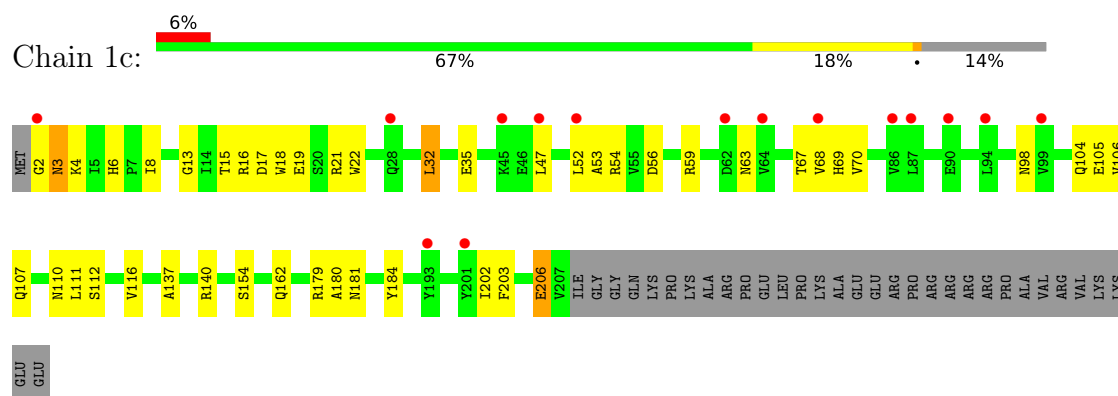
- Molecule 33: 30S ribosomal protein S2



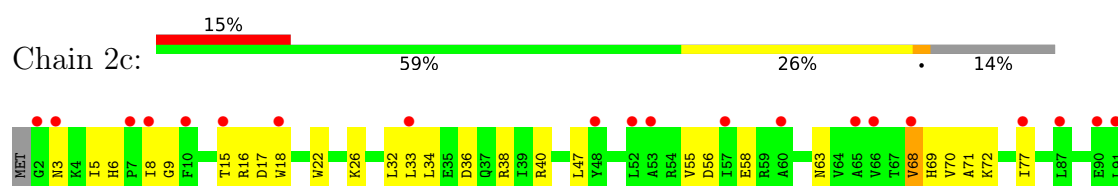
- Molecule 33: 30S ribosomal protein S2

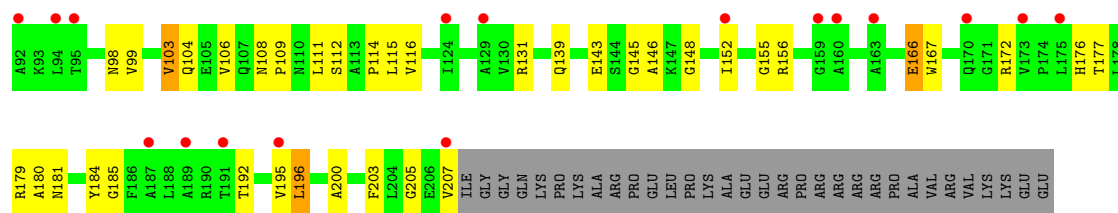


- Molecule 34: 30S ribosomal protein S3

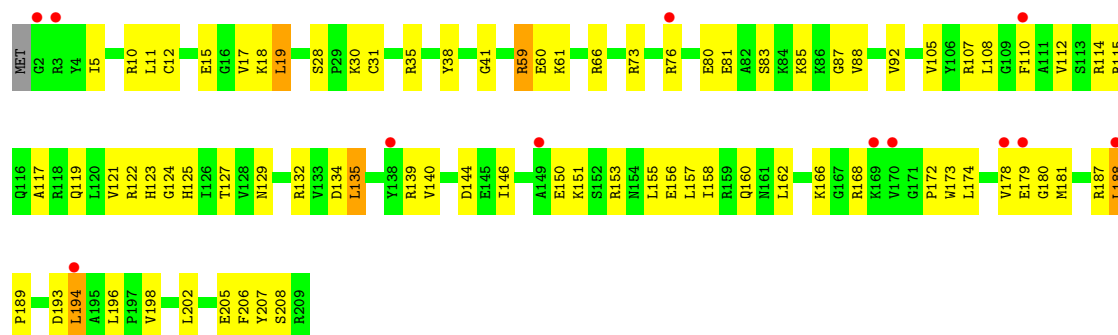


- Molecule 34: 30S ribosomal protein S3

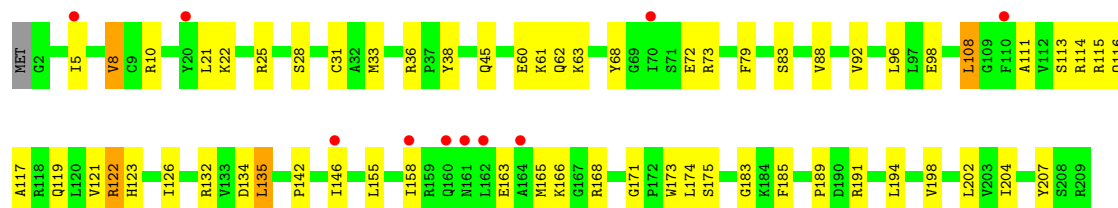




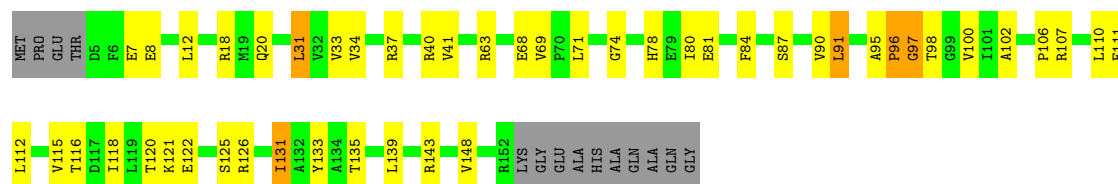
• Molecule 35: 30S ribosomal protein S4



• Molecule 35: 30S ribosomal protein S4

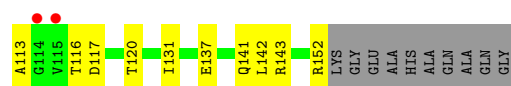


• Molecule 36: 30S ribosomal protein S5

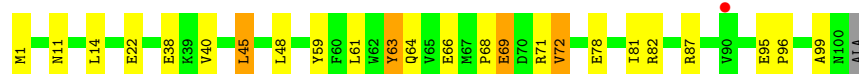
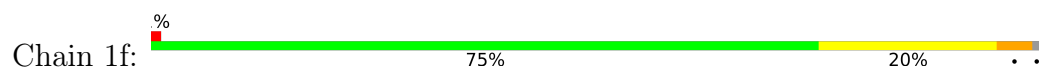


• Molecule 36: 30S ribosomal protein S5

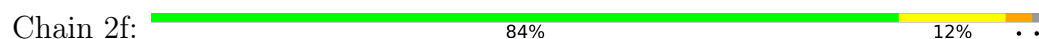




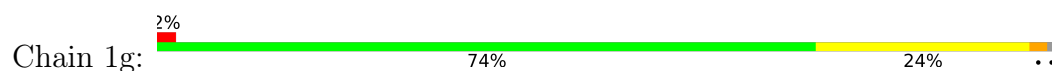
- Molecule 37: 30S ribosomal protein S6



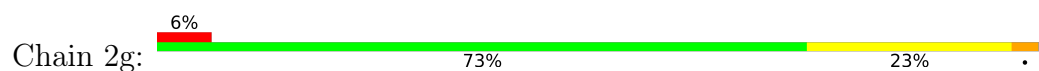
- Molecule 37: 30S ribosomal protein S6



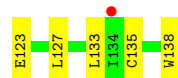
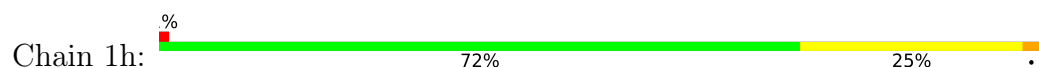
- Molecule 38: 30S ribosomal protein S7



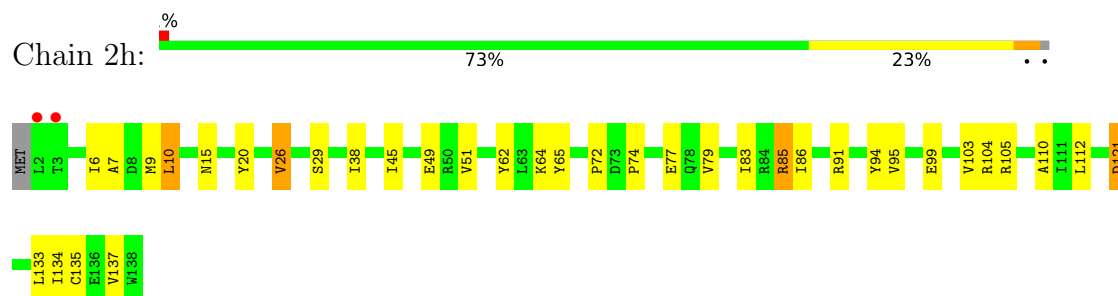
- Molecule 38: 30S ribosomal protein S7



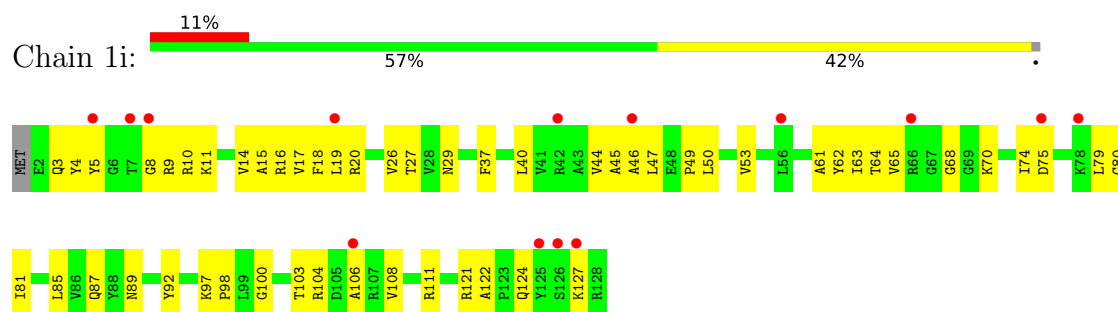
- Molecule 39: 30S ribosomal protein S8



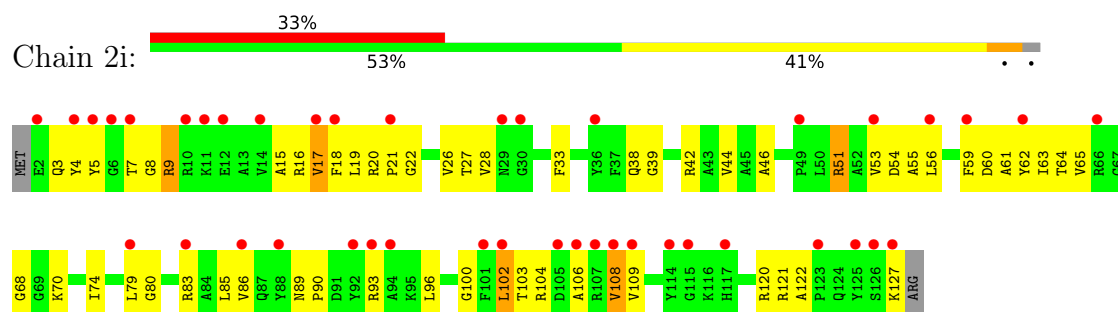
- Molecule 39: 30S ribosomal protein S8



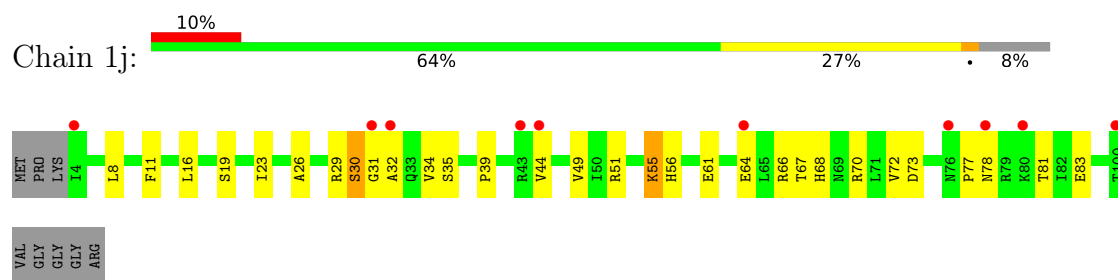
- Molecule 40: 30S ribosomal protein S9



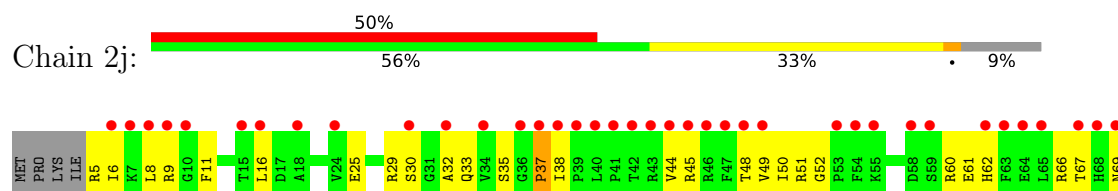
- Molecule 40: 30S ribosomal protein S9

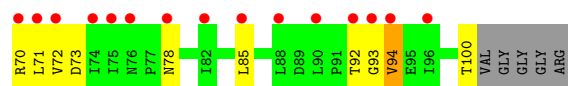


- Molecule 41: 30S ribosomal protein S10

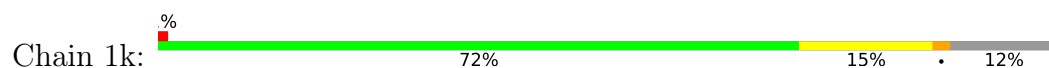


- Molecule 41: 30S ribosomal protein S10





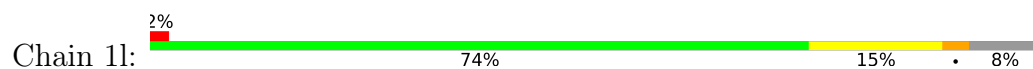
- Molecule 42: 30S ribosomal protein S11



- Molecule 42: 30S ribosomal protein S11



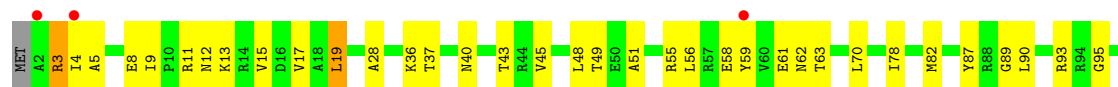
- Molecule 43: 30S ribosomal protein S12



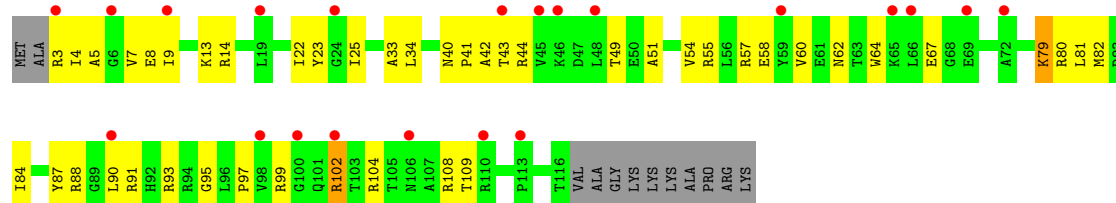
- Molecule 43: 30S ribosomal protein S12



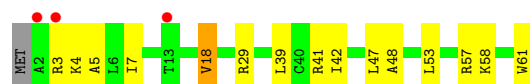
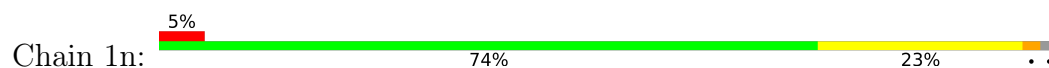
- Molecule 44: 30S ribosomal protein S13



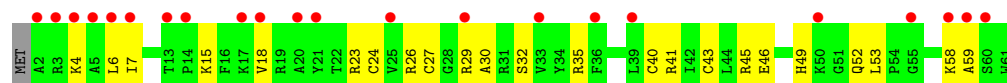
- Molecule 44: 30S ribosomal protein S13



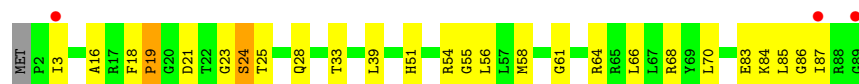
- Molecule 45: 30S ribosomal protein S14 type Z



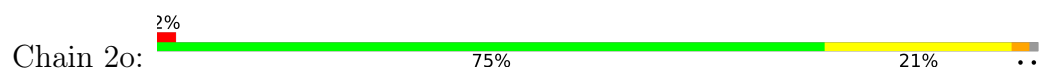
- Molecule 45: 30S ribosomal protein S14 type Z



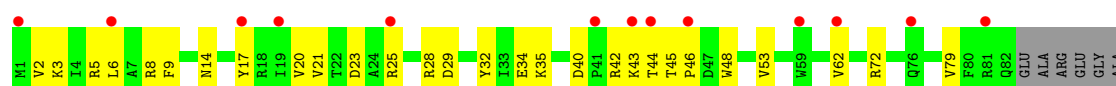
- Molecule 46: 30S ribosomal protein S15



- Molecule 46: 30S ribosomal protein S15

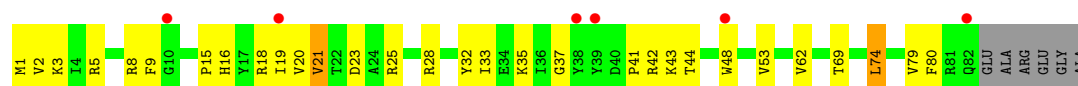


- Molecule 47: 30S ribosomal protein S16

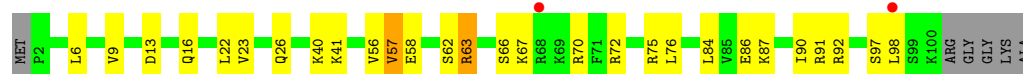


- Molecule 47: 30S ribosomal protein S16

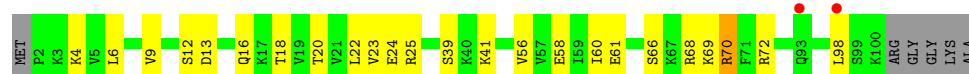




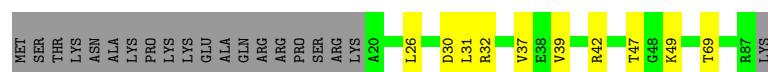
- Molecule 48: 30S ribosomal protein S17



- Molecule 48: 30S ribosomal protein S17



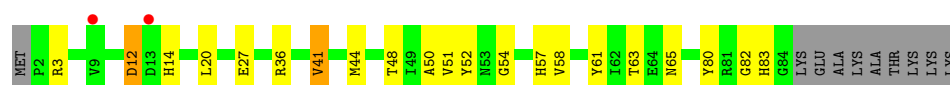
- Molecule 49: 30S ribosomal protein S18



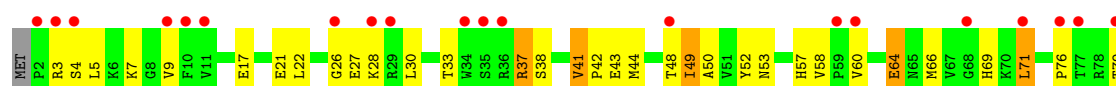
- Molecule 49: 30S ribosomal protein S18

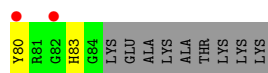


- Molecule 50: 30S ribosomal protein S19



- Molecule 50: 30S ribosomal protein S19

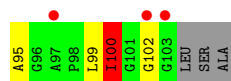
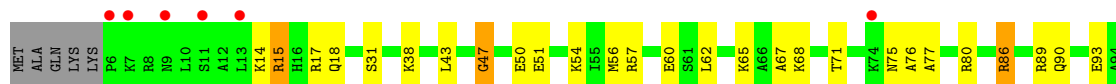




- Molecule 51: 30S ribosomal protein S20



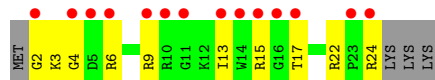
- Molecule 51: 30S ribosomal protein S20



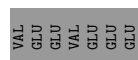
- Molecule 52: 30S ribosomal protein Thx



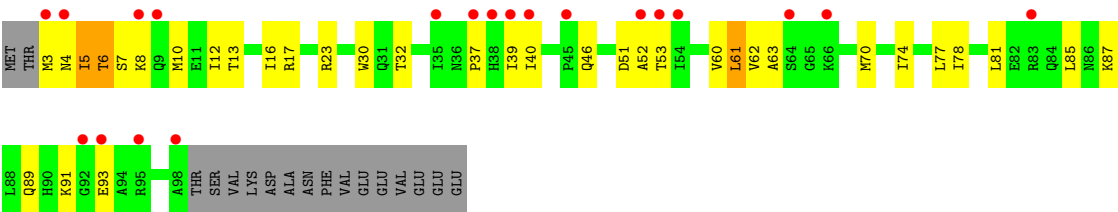
- Molecule 52: 30S ribosomal protein Thx



- Molecule 53: Ribosome-associated inhibitor A



- Molecule 53: Ribosome-associated inhibitor A



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	210.09Å 449.12Å 621.91Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	121.92 – 2.70 121.92 – 2.70	Depositor EDS
% Data completeness (in resolution range)	99.2 (121.92-2.70) 99.2 (121.92-2.70)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.24 (at 2.69Å)	Xtriage
Refinement program	PHENIX 1.8.2	Depositor
R, R_{free}	0.206 , 0.253 0.207 , 0.253	Depositor DCC
R_{free} test set	79057 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å ²)	52.6	Xtriage
Anisotropy	0.142	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 49.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.43$, $\langle L^2 \rangle = 0.25$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	295438	wwPDB-VP
Average B, all atoms (Å ²)	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.62% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 2MG, 7MG, MPD, 2MA, 2MU, UR3, M2G, K, 5MU, 4OC, 5MC, 0TD, MA6, EZP, OMG, MG, SF4, ZN, PSU

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	1A	0.29	0/69029	0.47	2/107746 (0.0%)
1	2A	0.23	0/68901	0.43	2/107544 (0.0%)
2	1B	0.24	0/2876	0.43	0/4486
2	2B	0.20	0/2878	0.38	0/4490
3	1D	0.29	0/2181	0.53	0/2940
3	2D	0.25	0/2186	0.52	2/2944 (0.1%)
4	1E	0.29	0/1592	0.52	0/2149
4	2E	0.24	0/1592	0.51	0/2149
5	1F	0.27	0/1619	0.50	0/2193
5	2F	0.22	0/1615	0.48	2/2188 (0.1%)
6	1G	0.22	0/1451	0.47	1/1961 (0.1%)
6	2G	0.23	0/1449	0.47	0/1957
7	1H	0.23	0/1356	0.45	0/1834
7	2H	0.20	0/1350	0.43	0/1826
8	1I	0.23	0/1109	0.47	0/1512
8	2I	0.19	0/1091	0.40	0/1490
9	1N	0.29	0/1148	0.48	0/1547
9	2N	0.20	0/1144	0.43	0/1543
10	1O	0.27	0/943	0.50	0/1269
10	2O	0.22	0/943	0.47	0/1269
11	1P	0.29	0/1152	0.52	0/1533
11	2P	0.23	0/1152	0.48	0/1533
12	1Q	0.28	0/1143	0.50	0/1527
12	2Q	0.21	0/1143	0.44	0/1527
13	1R	0.29	0/982	0.51	0/1312
13	2R	0.26	0/982	0.53	0/1312
14	1S	0.23	0/887	0.50	0/1180
14	2S	0.23	0/880	0.48	0/1172
15	1T	0.26	0/1105	0.52	0/1477
15	2T	0.23	0/1097	0.48	0/1468
16	1U	0.31	0/977	0.48	0/1301

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
16	2U	0.22	0/977	0.41	0/1301
17	1V	0.28	0/786	0.51	0/1053
17	2V	0.22	0/782	0.43	0/1049
18	1W	0.27	0/897	0.46	0/1205
18	2W	0.24	0/897	0.46	0/1205
19	1X	0.29	0/764	0.52	0/1025
19	2X	0.22	0/764	0.48	0/1025
20	1Y	0.28	0/823	0.64	2/1099 (0.2%)
20	2Y	0.21	0/823	0.44	0/1100
21	1Z	0.22	0/1620	0.45	0/2200
21	2Z	0.21	0/1590	0.45	1/2162 (0.0%)
22	10	0.27	0/616	0.52	0/821
22	20	0.27	0/616	0.47	0/821
23	11	0.28	0/761	0.47	0/1013
23	21	0.25	0/766	0.45	0/1018
24	12	0.23	0/590	0.46	0/781
24	22	0.22	0/594	0.50	1/785 (0.1%)
25	13	0.27	0/474	0.49	0/635
25	23	0.21	0/469	0.41	0/630
26	14	0.29	0/559	0.61	0/754
26	24	0.28	0/549	0.65	1/741 (0.1%)
27	15	0.30	0/473	0.55	0/639
27	25	0.26	0/469	0.48	0/635
28	16	0.27	0/460	0.51	0/613
28	26	0.24	0/456	0.43	0/608
29	17	0.34	0/426	0.59	0/561
29	27	0.26	0/426	0.51	0/561
30	18	0.30	0/525	0.50	0/691
30	28	0.23	0/525	0.45	0/691
31	19	0.31	0/310	0.50	0/407
31	29	0.23	0/310	0.43	0/407
32	1a	0.21	0/35795	0.40	0/55864
32	2a	0.20	0/35890	0.40	1/56012 (0.0%)
33	1b	0.24	0/1876	0.49	2/2533 (0.1%)
33	2b	0.27	0/1860	0.53	2/2518 (0.1%)
34	1c	0.21	0/1582	0.43	0/2137
34	2c	0.24	0/1566	0.45	0/2119
35	1d	0.22	0/1695	0.47	0/2274
35	2d	0.22	0/1698	0.47	0/2277
36	1e	0.23	0/1149	0.47	0/1548
36	2e	0.23	0/1149	0.50	1/1548 (0.1%)
37	1f	0.22	0/827	0.45	0/1120
37	2f	0.21	0/829	0.45	0/1123

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
38	1g	0.19	0/1254	0.43	0/1683
38	2g	0.20	0/1248	0.39	0/1676
39	1h	0.20	0/1118	0.43	0/1506
39	2h	0.21	0/1108	0.44	0/1494
40	1i	0.18	0/1005	0.46	0/1351
40	2i	0.23	0/985	0.48	0/1329
41	1j	0.27	0/732	0.46	0/993
41	2j	0.23	0/723	0.45	0/984
42	1k	0.22	0/849	0.44	0/1150
42	2k	0.24	0/848	0.54	1/1149 (0.1%)
43	1l	0.20	0/937	0.44	0/1260
43	2l	0.22	0/937	0.49	1/1260 (0.1%)
44	1m	0.20	0/924	0.44	0/1242
44	2m	0.28	0/905	0.59	1/1217 (0.1%)
45	1n	0.22	0/501	0.43	0/664
45	2n	0.23	0/501	0.43	0/664
46	1o	0.21	0/739	0.46	0/985
46	2o	0.19	0/739	0.43	0/985
47	1p	0.23	0/697	0.52	0/939
47	2p	0.23	0/693	0.47	0/935
48	1q	0.22	0/836	0.45	0/1117
48	2q	0.19	0/836	0.40	0/1117
49	1r	0.21	0/560	0.43	0/746
49	2r	0.19	0/560	0.42	0/746
50	1s	0.21	0/663	0.46	0/895
50	2s	0.19	0/660	0.42	0/893
51	1t	0.21	0/734	0.49	1/969 (0.1%)
51	2t	0.20	0/736	0.44	0/976
52	1u	0.16	0/203	0.42	0/266
52	2u	0.27	0/203	0.56	0/266
53	1y	0.28	0/776	0.41	0/1048
53	2y	0.18	0/761	0.38	0/1030
All	All	0.24	0/309937	0.44	24/463223 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
19	1X	0	1
26	24	0	1

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

There are no bond length outliers.

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	2m	5	ALA	CB-CA-C	-10.07	103.53	117.23
20	1Y	102	CYS	CA-C-O	8.42	122.83	117.94
24	22	41	ILE	N-CA-C	-7.54	105.20	112.29
3	2D	98	VAL	N-CA-C	-7.14	103.71	113.00
1	2A	1992	G	C2'-C3'-O3'	6.69	119.54	109.50
36	2e	48	ALA	N-CA-C	6.23	113.83	108.22
21	2Z	141	VAL	N-CA-C	-6.16	106.50	112.29
33	2b	232	PRO	CA-C-N	6.03	138.47	120.69
33	2b	232	PRO	C-N-CA	6.03	138.47	120.69
42	2k	116	HIS	N-CA-C	5.93	119.75	111.56
3	2D	275	LYS	N-CA-C	-5.75	99.57	108.42
51	1t	101	GLY	N-CA-C	5.60	119.27	111.10
32	2a	266	G	C2'-C3'-O3'	5.54	117.81	109.50
1	1A	1255	A	C4'-C3'-O3'	5.51	117.66	109.40
26	24	59	PHE	N-CA-C	5.46	117.00	107.49
43	2l	28	LYS	N-CA-C	5.39	117.76	111.02
6	1G	96	ARG	CB-CA-C	-5.33	110.42	116.54
5	2F	21	ALA	CA-C-N	5.24	131.13	121.70
5	2F	21	ALA	C-N-CA	5.24	131.13	121.70
20	1Y	102	CYS	CB-CA-C	-5.21	109.56	117.07
33	1b	19	HIS	CA-C-N	5.21	131.49	121.54
33	1b	19	HIS	C-N-CA	5.21	131.49	121.54
1	1A	1700	G	C2'-C3'-O3'	5.12	117.19	109.50
1	2A	1992	G	P-O3'-C3'	5.05	127.78	120.20

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
19	1X	93	GLU	Peptide
33	1b	127	ILE	Peptide
33	1b	231	GLU	Peptide
26	24	18	CYS	Peptide

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1A	61869	0	31201	585	0
1	2A	61758	0	31149	725	0
2	1B	2572	0	1305	17	0
2	2B	2573	0	1306	34	0
3	1D	2131	0	2207	48	0
3	2D	2136	0	2218	36	0
4	1E	1559	0	1618	33	0
4	2E	1559	0	1618	39	0
5	1F	1584	0	1625	35	0
5	2F	1580	0	1619	45	0
6	1G	1426	0	1445	42	0
6	2G	1424	0	1441	50	0
7	1H	1330	0	1407	26	0
7	2H	1324	0	1402	40	0
8	1I	1094	0	1127	35	0
8	2I	1076	0	1094	29	0
9	1N	1121	0	1195	18	0
9	2N	1117	0	1184	16	0
10	1O	933	0	996	15	0
10	2O	933	0	996	19	0
11	1P	1135	0	1212	30	0
11	2P	1135	0	1212	22	0
12	1Q	1122	0	1179	25	0
12	2Q	1122	0	1179	28	0
13	1R	968	0	1033	12	0
13	2R	968	0	1033	18	0
14	1S	877	0	938	16	0
14	2S	870	0	923	36	0
15	1T	1091	0	1151	23	0
15	2T	1083	0	1136	27	0
16	1U	959	0	1019	17	0
16	2U	959	0	1019	23	0
17	1V	775	0	841	12	0
17	2V	771	0	830	21	0
18	1W	886	0	940	11	0
18	2W	886	0	940	14	0
19	1X	750	0	814	16	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	2X	750	0	814	12	0
20	1Y	810	0	892	18	0
20	2Y	810	0	887	24	0
21	1Z	1587	0	1598	23	0
21	2Z	1557	0	1564	36	0
22	10	608	0	622	10	0
22	20	608	0	622	12	0
23	11	754	0	823	14	0
23	21	759	0	837	20	0
24	12	588	0	643	10	0
24	22	592	0	654	9	0
25	13	469	0	518	11	0
25	23	464	0	514	16	0
26	14	546	0	522	17	0
26	24	536	0	514	32	0
27	15	459	0	476	11	0
27	25	455	0	465	9	0
28	16	453	0	473	11	0
28	26	449	0	469	10	0
29	17	418	0	467	10	0
29	27	418	0	467	4	0
30	18	517	0	582	16	0
30	28	517	0	582	12	0
31	19	307	0	335	8	0
31	29	307	0	335	10	0
32	1a	32246	0	16296	430	0
32	2a	32331	0	16339	509	0
33	1b	1842	0	1862	50	0
33	2b	1825	0	1828	57	0
34	1c	1558	0	1557	32	0
34	2c	1542	0	1517	48	0
35	1d	1665	0	1687	62	0
35	2d	1668	0	1703	48	0
36	1e	1133	0	1191	35	0
36	2e	1133	0	1191	26	0
37	1f	814	0	808	15	0
37	2f	816	0	808	11	0
38	1g	1235	0	1249	27	0
38	2g	1229	0	1238	26	0
39	1h	1098	0	1143	27	0
39	2h	1088	0	1126	25	0
40	1i	986	0	990	41	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
40	2i	966	0	953	47	0
41	1j	719	0	672	20	0
41	2j	710	0	661	29	0
42	1k	834	0	838	10	0
42	2k	833	0	836	12	0
43	1l	932	0	981	18	0
43	2l	932	0	981	17	0
44	1m	914	0	954	23	0
44	2m	895	0	920	33	0
45	1n	492	0	529	13	0
45	2n	492	0	529	24	0
46	1o	728	0	760	21	0
46	2o	728	0	760	15	0
47	1p	681	0	697	20	0
47	2p	677	0	686	23	0
48	1q	823	0	891	25	0
48	2q	823	0	891	17	0
49	1r	555	0	618	6	0
49	2r	555	0	618	14	0
50	1s	648	0	658	17	0
50	2s	645	0	635	34	0
51	1t	732	0	809	20	0
51	2t	733	0	795	20	0
52	1u	199	0	208	6	0
52	2u	199	0	208	7	0
53	1y	764	0	786	16	0
53	2y	749	0	757	29	0
54	10	6	0	0	0	0
54	11	3	0	0	0	0
54	13	2	0	0	0	0
54	14	1	0	0	0	0
54	15	3	0	0	0	0
54	17	2	0	0	0	0
54	18	1	0	0	0	0
54	19	2	0	0	0	0
54	1A	1024	0	0	0	0
54	1B	29	0	0	0	0
54	1D	13	0	0	0	0
54	1E	7	0	0	0	0
54	1F	13	0	0	0	0
54	1G	4	0	0	0	0
54	1H	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
54	1N	3	0	0	0	0
54	1O	2	0	0	0	0
54	1P	3	0	0	0	0
54	1Q	4	0	0	0	0
54	1R	3	0	0	0	0
54	1S	1	0	0	0	0
54	1T	3	0	0	0	0
54	1U	2	0	0	0	0
54	1V	3	0	0	0	0
54	1W	2	0	0	0	0
54	1X	2	0	0	0	0
54	1Z	1	0	0	0	0
54	1a	255	0	0	0	0
54	1b	1	0	0	0	0
54	1d	6	0	0	0	0
54	1e	2	0	0	0	0
54	1f	2	0	0	0	0
54	1g	3	0	0	0	0
54	1h	2	0	0	0	0
54	1i	1	0	0	0	0
54	1l	2	0	0	0	0
54	1n	1	0	0	0	0
54	1o	1	0	0	0	0
54	1t	1	0	0	0	0
54	1y	4	0	0	0	0
54	20	1	0	0	0	0
54	21	1	0	0	0	0
54	25	1	0	0	0	0
54	28	3	0	0	0	0
54	2A	721	0	0	0	0
54	2B	19	0	0	0	0
54	2D	8	0	0	0	0
54	2E	6	0	0	0	0
54	2F	3	0	0	0	0
54	2G	3	0	0	0	0
54	2I	1	0	0	0	0
54	2N	1	0	0	0	0
54	2O	1	0	0	0	0
54	2P	2	0	0	0	0
54	2Q	2	0	0	0	0
54	2R	1	0	0	0	0
54	2T	4	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
54	2V	1	0	0	0	0
54	2W	2	0	0	0	0
54	2X	1	0	0	0	0
54	2a	151	0	0	0	0
54	2e	1	0	0	0	0
54	2f	1	0	0	0	0
54	2j	1	0	0	0	0
54	2p	1	0	0	0	0
54	2q	1	0	0	0	0
54	2r	1	0	0	0	0
54	2t	1	0	0	0	0
55	1A	1	0	0	0	0
55	2A	1	0	0	0	0
56	1A	25	0	0	0	0
56	2A	25	0	0	0	0
57	18	8	0	14	1	0
57	1A	8	0	14	0	0
57	1T	8	0	14	1	0
57	1a	8	0	14	2	0
57	2A	16	0	28	2	0
57	2B	8	0	14	0	0
58	1B	12	0	12	3	0
58	1F	12	0	12	3	0
59	14	1	0	0	0	0
59	15	1	0	0	0	0
59	16	1	0	0	0	0
59	19	1	0	0	0	0
59	1Y	1	0	0	0	0
59	1n	1	0	0	0	0
59	24	1	0	0	0	0
59	25	1	0	0	0	0
59	26	1	0	0	0	0
59	29	1	0	0	0	0
59	2Y	1	0	0	0	0
59	2n	1	0	0	0	0
60	1d	8	0	0	0	0
60	2d	8	0	0	1	0
61	10	22	0	0	0	0
61	11	28	0	0	0	0
61	12	14	0	0	2	0
61	13	22	0	0	2	0
61	14	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
61	15	26	0	0	0	0
61	16	17	0	0	1	0
61	17	14	0	0	2	0
61	18	30	0	0	0	0
61	19	8	0	0	1	0
61	1A	2980	0	0	97	0
61	1B	105	0	0	3	0
61	1D	116	0	0	6	0
61	1E	76	0	0	4	0
61	1F	63	0	0	5	0
61	1G	22	0	0	0	0
61	1H	16	0	0	0	0
61	1I	7	0	0	1	0
61	1N	50	0	0	0	0
61	1O	22	0	0	0	0
61	1P	58	0	0	4	0
61	1Q	42	0	0	4	0
61	1R	37	0	0	0	0
61	1S	13	0	0	1	0
61	1T	42	0	0	3	0
61	1U	45	0	0	4	0
61	1V	37	0	0	1	0
61	1W	24	0	0	0	0
61	1X	24	0	0	1	0
61	1Y	15	0	0	1	0
61	1Z	14	0	0	0	0
61	1a	261	0	0	16	0
61	1b	1	0	0	0	0
61	1d	9	0	0	2	0
61	1e	6	0	0	1	0
61	1f	3	0	0	0	0
61	1h	1	0	0	0	0
61	1i	1	0	0	0	0
61	1j	1	0	0	0	0
61	1k	1	0	0	0	0
61	1l	4	0	0	0	0
61	1n	1	0	0	1	0
61	1o	5	0	0	1	0
61	1p	3	0	0	0	0
61	1y	5	0	0	0	0
61	20	13	0	0	2	0
61	21	24	0	0	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
61	22	5	0	0	0	0
61	23	3	0	0	1	0
61	24	2	0	0	0	0
61	25	9	0	0	1	0
61	26	6	0	0	1	0
61	27	7	0	0	0	0
61	28	15	0	0	1	0
61	29	2	0	0	0	0
61	2A	1686	0	0	85	0
61	2B	65	0	0	6	0
61	2D	52	0	0	2	0
61	2E	25	0	0	1	0
61	2F	21	0	0	3	0
61	2G	7	0	0	0	0
61	2H	4	0	0	0	0
61	2I	4	0	0	0	0
61	2N	6	0	0	0	0
61	2O	22	0	0	0	0
61	2P	23	0	0	0	0
61	2Q	30	0	0	0	0
61	2R	21	0	0	1	0
61	2S	8	0	0	2	0
61	2T	10	0	0	0	0
61	2U	14	0	0	2	0
61	2V	9	0	0	0	0
61	2W	21	0	0	0	0
61	2X	9	0	0	0	0
61	2Y	3	0	0	0	0
61	2Z	15	0	0	3	0
61	2a	100	0	0	6	0
61	2d	6	0	0	1	0
61	2e	1	0	0	0	0
61	2f	1	0	0	0	0
61	2j	2	0	0	1	0
61	2l	1	0	0	0	0
61	2m	1	0	0	0	0
61	2o	2	0	0	0	0
61	2p	1	0	0	0	0
61	2q	1	0	0	0	0
61	2r	4	0	0	1	0
61	2y	1	0	0	0	0
All	All	295438	0	194513	4034	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 9.

All (4034) 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:1128:U:H3	1:1A:1132:A:N6	1.36	1.23
1:1A:2159:C:N4	1:1A:2176:G:H1	1.50	1.09
32:1a:78:G:H1	32:1a:91:C:N4	1.57	1.02
1:2A:2139:C:N4	1:2A:2152:G:H1	1.56	1.01
1:1A:2331:G:H22	14:1S:3:ARG:HD3	1.23	1.01
32:2a:1003:G:H2'	32:2a:1004:A:H4'	1.45	0.97
32:1a:407:G:H5''	35:1d:115:ARG:HG2	1.47	0.94
1:1A:1128:U:O4	1:1A:1132:A:N1	1.99	0.94
32:2a:999:C:N4	32:2a:1042:G:H1	1.64	0.94
32:2a:1030:C:N3	32:2a:1031:G:N2	2.15	0.94
32:2a:1256:A:H61	32:2a:1278:U:H1'	1.34	0.93
1:2A:2107:C:H42	1:2A:2182:G:H1	0.99	0.92
32:2a:999:C:H42	32:2a:1042:G:H1	0.93	0.92
32:2a:1030:C:N4	32:2a:1031:G:N1	2.18	0.92
1:2A:1041:C:H42	1:2A:1114:G:H1	1.18	0.91
29:17:24:THR:HG22	29:17:27:GLY:H	1.32	0.91
32:1a:1441:G:H5''	32:1a:1442:G:H5'	1.53	0.91
1:2A:2319:G:H22	14:2S:3:ARG:HD3	1.34	0.90
10:1O:35:VAL:HG11	10:1O:103:ALA:HB3	1.54	0.89
32:2a:1030:C:H42	32:2a:1031:G:H1	0.92	0.89
1:2A:2107:C:N4	1:2A:2182:G:H1	1.69	0.89
1:1A:1829:U:H5'	3:1D:259:THR:HG22	1.55	0.88
32:2a:1224:G:H4'	44:2m:102:ARG:HH12	1.36	0.88
32:2a:1030:C:N4	32:2a:1031:G:H1	1.71	0.88
32:1a:559:A:OP1	36:1e:126:ARG:NH2	2.06	0.88
1:2A:1842:G:O2'	3:2D:253:GLN:NE2	2.08	0.87
32:2a:1011:G:H1	32:2a:1018:C:H42	1.19	0.86
1:1A:2159:C:H42	1:1A:2176:G:H1	0.87	0.86
20:1Y:92:ASN:HB2	20:1Y:94:LYS:H	1.39	0.85
10:2O:48:PRO:HB3	32:2a:1422:G:H5''	1.55	0.85
32:1a:73:G:H1	32:1a:96:U:H3	1.20	0.85
1:1A:2159:C:N3	1:1A:2176:G:N2	2.23	0.85
1:1A:1128:U:H3	1:1A:1132:A:H61	0.85	0.85
1:1A:2125:C:H42	1:1A:2208:G:H1	1.21	0.84
6:1G:161:THR:HG22	6:1G:163:ALA:H	1.39	0.84
1:2A:2099:U:H3	1:2A:2190:G:H1	1.15	0.84
1:1A:542:C:OP1	27:15:16:ARG:NH2	2.10	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1162:C:H42	32:2a:1174:G:H1	1.27	0.83
32:1a:975:A:H4'	32:1a:976:G:H5''	1.60	0.83
32:2a:677:U:H3	32:2a:713:G:H22	1.27	0.82
1:1A:2138:G:H1	1:1A:2187:G:H22	1.26	0.82
4:1E:47:VAL:HG21	4:1E:86:PRO:HD2	1.62	0.82
11:1P:100:LEU:HD12	11:1P:112:LEU:HD11	1.61	0.81
32:2a:1011:G:H1	32:2a:1018:C:N4	1.78	0.81
32:2a:1410:G:N2	32:2a:1490:C:O2	2.11	0.81
1:2A:1084:A:H3'	1:2A:1085:A:H4'	1.63	0.81
1:2A:2136:C:N4	1:2A:2155:G:H1	1.77	0.81
44:2m:54:VAL:HA	44:2m:57:ARG:HB3	1.63	0.80
51:2t:57:ARG:HH22	51:2t:100:ILE:HD12	1.46	0.80
1:2A:2365:G:N7	30:28:39:LYS:NZ	2.30	0.80
4:2E:47:VAL:HG11	4:2E:86:PRO:HD2	1.63	0.79
32:2a:437:U:H5''	35:2d:155:LEU:HD11	1.64	0.79
1:2A:2602:A:H1'	1:2A:2603:G:H5''	1.62	0.79
1:1A:242:C:OP1	61:1A:4117:HOH:O	1.99	0.79
33:2b:166:ASP:HB3	33:2b:169:LYS:HB3	1.64	0.79
2:1B:81:G:N7	58:1B:228:ARG:NH2	2.30	0.79
1:2A:788:A:N6	61:2A:3845:HOH:O	2.16	0.79
1:2A:2136:C:C2	1:2A:2155:G:N2	2.51	0.79
3:1D:17:THR:O	3:1D:211:ARG:NH2	2.16	0.79
1:1A:11:G:H2'	1:1A:12:U:H5''	1.65	0.79
32:1a:664:G:H22	32:1a:741:G:H1	1.32	0.78
33:2b:88:ALA:O	33:2b:226:ARG:NH1	2.17	0.78
1:2A:2748:A:H5'	7:2H:4:ILE:HD12	1.65	0.78
32:2a:1376:U:H2'	32:2a:1377:A:H8	1.49	0.78
1:1A:1131:A:O2'	1:1A:1150:C:O2'	2.02	0.77
25:13:8:LEU:HD13	25:13:31:LEU:HD23	1.66	0.77
40:1i:50:LEU:HD23	40:1i:85:LEU:HD11	1.65	0.77
1:2A:2139:C:H42	1:2A:2152:G:H1	0.81	0.77
32:1a:78:G:H1	32:1a:91:C:H42	0.81	0.77
11:2P:59:LEU:HD11	30:28:10:ALA:HB2	1.66	0.77
1:2A:2805:G:H2'	1:2A:2807:G:C8	2.20	0.77
1:1A:427:G:N7	61:1A:4153:HOH:O	2.16	0.77
32:1a:78:G:N2	32:1a:91:C:N3	2.31	0.77
40:2i:53:VAL:O	40:2i:55:ALA:N	2.16	0.77
1:1A:2125:C:N4	1:1A:2208:G:H1	1.82	0.77
2:1B:23:G:O6	61:1B:3101:HOH:O	2.02	0.77
11:1P:59:LEU:HD11	30:18:10:ALA:HB2	1.63	0.77
46:2o:54:ARG:HG2	46:2o:58:MET:HE2	1.67	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:17:34:ARG:HE	29:17:39:ARG:HG3	1.50	0.77
32:2a:999:C:N3	32:2a:1042:G:N2	2.31	0.77
1:1A:1128:U:N3	1:1A:1132:A:N6	2.20	0.76
39:2h:64:LYS:HG2	39:2h:79:VAL:HG21	1.68	0.76
32:1a:501:C:OP1	43:1l:117:ARG:NH2	2.17	0.76
32:2a:559:A:H4'	32:2a:560:U:H3'	1.67	0.76
32:2a:1031:G:H2'	32:2a:1032:G:C8	2.21	0.76
32:1a:1025:U:C2	32:1a:1036:G:O6	2.39	0.76
32:1a:1027:C:N3	32:1a:1034:G:C6	2.53	0.76
7:2H:164:TYR:HB2	7:2H:167:GLU:HB2	1.68	0.76
35:1d:172:PRO:HB2	35:1d:187:ARG:HH21	1.49	0.75
1:1A:1378:G:OP1	61:1A:4118:HOH:O	2.03	0.75
3:1D:242:ARG:HG3	3:1D:242:ARG:HH11	1.50	0.75
47:2p:15:PRO:HD2	47:2p:42:ARG:HD2	1.68	0.75
1:2A:2379:G:OP1	14:2S:23:ARG:NH2	2.14	0.75
22:20:10:THR:HG22	22:20:12:ASN:H	1.50	0.75
32:2a:975:A:H4'	32:2a:976:G:H5''	1.69	0.75
1:1A:787:U:OP2	61:1A:4119:HOH:O	2.05	0.74
1:2A:1057:A:N6	1:2A:1087:G:OP1	2.20	0.74
49:2r:32:ARG:HA	49:2r:69:THR:HG21	1.68	0.74
1:1A:1045:U:OP2	61:1A:4120:HOH:O	2.05	0.74
32:1a:1003:G:N2	32:1a:1004:A:N3	2.35	0.74
1:2A:994:C:OP1	16:2U:53:ARG:NH2	2.19	0.74
40:1i:17:VAL:HG21	40:1i:81:ILE:HG22	1.68	0.74
32:1a:506:G:OP1	61:1a:3305:HOH:O	2.05	0.74
16:2U:89:GLU:HG2	17:2V:50:PRO:HB3	1.69	0.74
1:1A:2138:G:OP2	1:1A:2188:G:N2	2.20	0.74
3:1D:88:ARG:NH1	61:1D:402:HOH:O	2.20	0.74
1:2A:11:G:H2'	1:2A:12:U:H5'	1.68	0.74
32:2a:1244:C:H42	32:2a:1293:G:H1	1.35	0.74
36:2e:102:ALA:HB1	36:2e:106:PRO:HG2	1.69	0.74
4:1E:28:ALA:HB3	4:1E:93:VAL:HG12	1.69	0.74
5:1F:197:ASP:OD1	5:1F:197:ASP:N	2.19	0.74
46:1o:54:ARG:HG2	46:1o:58:MET:HE2	1.69	0.74
1:2A:751:A:H5'	18:2W:90:ARG:HA	1.70	0.74
24:22:32:LEU:HD11	24:22:54:LYS:HG3	1.69	0.74
32:2a:426:G:OP1	35:2d:38:TYR:OH	2.04	0.74
32:2a:1360:A:OP2	45:2n:35:ARG:NH2	2.21	0.74
1:2A:323:G:HO2'	1:2A:1205:U:H3	1.34	0.74
61:2A:3804:HOH:O	13:2R:3:HIS:NE2	2.21	0.74
3:2D:206:LEU:HD22	3:2D:211:ARG:HG2	1.68	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:1p:53:VAL:HG13	47:1p:79:VAL:HG22	1.67	0.73
1:2A:958:U:OP2	12:2Q:14:ARG:NH1	2.21	0.73
35:1d:140:VAL:HG11	35:1d:146:ILE:HD11	1.70	0.73
1:2A:2128:C:H42	1:2A:2160:G:H1	1.36	0.73
1:2A:2141:G:O6	1:2A:2150:U:O2	2.06	0.73
33:2b:54:THR:HG23	33:2b:199:TYR:HB3	1.70	0.73
1:2A:2206:G:H3'	1:2A:2207:G:H8	1.54	0.73
1:2A:2116:G:OP1	1:2A:2117:A:N6	2.22	0.73
2:2B:49:C:OP1	61:2B:3101:HOH:O	2.05	0.73
36:2e:74:GLY:HA3	36:2e:116:THR:HG22	1.69	0.73
28:16:6:ARG:NE	28:16:24:GLU:OE1	2.19	0.73
42:2k:99:GLN:HG2	42:2k:105:VAL:HG21	1.71	0.73
32:1a:201:C:H42	32:1a:216:G:H1	1.35	0.73
1:2A:2139:C:N3	1:2A:2152:G:N2	2.32	0.73
1:2A:143:G:H4'	19:2X:35:THR:HG21	1.71	0.73
50:2s:3:ARG:HH11	50:2s:7:LYS:HB3	1.54	0.73
32:1a:1286:A:H2'	32:1a:1287:A:H4'	1.71	0.72
1:2A:1798:U:H5'	3:2D:259:THR:HG22	1.70	0.72
25:13:6:VAL:HG12	25:13:54:VAL:HG11	1.71	0.72
32:1a:1103:C:OP1	33:1b:96:ARG:NH2	2.22	0.72
1:2A:1782:C:OP1	61:2A:3815:HOH:O	2.07	0.72
3:2D:134:ARG:NH1	3:2D:188:GLU:OE2	2.21	0.72
32:2a:1179:A:OP2	40:2i:93:ARG:NH2	2.19	0.72
32:1a:376:G:H5''	47:1p:5:ARG:HD2	1.72	0.72
1:1A:597:C:N3	4:1E:145:LYS:NZ	2.37	0.72
1:1A:2702:C:OP1	13:1R:17:ARG:NH2	2.23	0.72
32:1a:1500:A:OP1	61:1a:3306:HOH:O	2.07	0.72
50:2s:22:LEU:HD13	50:2s:28:LYS:H	1.54	0.72
1:1A:493:G:OP2	29:17:34:ARG:HD3	1.88	0.72
1:1A:1093:G:H2'	1:1A:1156:G:H22	1.52	0.72
1:1A:1436:U:O2	1:1A:1441:A:N6	2.19	0.72
21:2Z:19:ARG:NH1	21:2Z:84:GLU:O	2.22	0.72
1:1A:1815:A:OP2	61:1A:4119:HOH:O	2.07	0.72
51:2t:50:GLU:HB2	51:2t:99:LEU:HD22	1.72	0.71
1:1A:395:C:OP2	61:1A:4121:HOH:O	2.07	0.71
1:1A:397:G:OP2	61:1A:4123:HOH:O	2.08	0.71
32:2a:1162:C:N4	32:2a:1174:G:H1	1.87	0.71
5:1F:53:THR:HG22	5:1F:55:GLY:H	1.56	0.71
1:1A:656:A:OP1	11:1P:65:ARG:NH1	2.22	0.71
1:1A:715:G:N7	61:1A:4191:HOH:O	2.24	0.71
32:1a:1025:U:O2	32:1a:1036:G:O6	2.09	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:656:C:O2'	46:2o:28:GLN:NE2	2.24	0.71
32:2a:1070:U:H2'	32:2a:1071:C:H6	1.53	0.71
34:2c:70:VAL:HG22	34:2c:72:LYS:H	1.56	0.71
1:1A:2658:C:OP2	1:1A:2745:G:O2'	2.08	0.71
32:2a:35:G:O2'	43:2l:118:SER:O	2.08	0.71
1:1A:2831:A:OP2	61:1A:4115:HOH:O	2.06	0.71
1:2A:2248:C:OP2	61:2A:3817:HOH:O	2.08	0.71
32:2a:1286:A:C8	32:2a:1287:A:H4'	2.25	0.71
9:1N:21:LYS:NZ	9:1N:140:VAL:OXT	2.24	0.71
32:2a:977:A:N6	32:2a:1224:G:OP1	2.23	0.71
32:2a:1051:C:H42	32:2a:1207:2MG:HN1	1.38	0.71
8:1I:92:VAL:HG13	8:1I:120:ILE:HB	1.71	0.71
41:1j:49:VAL:HG23	45:1n:41:ARG:HB2	1.71	0.71
1:2A:1257:C:OP2	61:2A:3816:HOH:O	2.08	0.71
50:2s:53:ASN:ND2	50:2s:76:PRO:O	2.23	0.71
1:2A:2122:U:H3	1:2A:2176:A:H61	1.39	0.71
1:2A:2425:A:N7	61:2A:3882:HOH:O	2.23	0.71
1:1A:1034:A:OP1	61:1A:4122:HOH:O	2.07	0.70
32:1a:1086:U:H3	32:1a:1099:G:H22	1.36	0.70
51:1t:10:LEU:HB3	51:1t:12:ALA:H	1.54	0.70
1:1A:1343:C:OP1	61:1A:4124:HOH:O	2.08	0.70
19:1X:35:THR:HG22	19:1X:38:GLU:H	1.56	0.70
1:1A:449:A:OP2	61:1A:4123:HOH:O	2.08	0.70
13:2R:97:VAL:HG22	13:2R:114:VAL:HG22	1.72	0.70
21:2Z:144:LEU:HD21	21:2Z:150:LEU:HD13	1.72	0.70
40:2i:121:ARG:NH1	40:2i:122:ALA:O	2.24	0.70
44:1m:58:GLU:O	44:1m:62:ASN:ND2	2.23	0.70
4:2E:48:GLN:HE21	4:2E:78:LEU:HG	1.57	0.70
40:2i:7:THR:OG1	40:2i:83:ARG:NH1	2.24	0.70
1:2A:277:C:O2'	1:2A:278:A:OP1	2.10	0.70
32:2a:1164:G:H1	32:2a:1172:C:H42	1.37	0.70
50:1s:50:ALA:HB1	50:1s:57:HIS:HB3	1.72	0.70
1:2A:2036:C:O2'	61:2A:3818:HOH:O	2.10	0.70
40:2i:8:GLY:HA2	40:2i:79:LEU:HD23	1.73	0.70
1:2A:955:C:OP1	12:2Q:87:LYS:NZ	2.22	0.70
1:2A:2206:G:H3'	1:2A:2207:G:C8	2.26	0.70
1:1A:2042:A:OP2	61:1A:4126:HOH:O	2.09	0.70
48:1q:6:LEU:HD23	48:1q:23:VAL:HG11	1.73	0.70
44:2m:58:GLU:O	44:2m:62:ASN:ND2	2.23	0.70
1:2A:1566:A:OP1	3:2D:211:ARG:NH1	2.25	0.70
1:2A:2126:A:H4'	1:2A:2127:G:O5'	1.91	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:2l:32:PHE:HB3	43:2l:84:LEU:HD11	1.73	0.70
7:1H:21:PRO:O	7:1H:23:ARG:NH1	2.25	0.69
1:1A:2708:U:O3'	61:1A:4129:HOH:O	2.11	0.69
53:1y:49:VAL:HG22	53:1y:66:LYS:HG2	1.73	0.69
1:1A:2073:A:OP2	61:1A:4128:HOH:O	2.10	0.69
1:2A:2296:U:OP2	14:2S:9:ARG:NH2	2.25	0.69
33:2b:75:LYS:HA	33:2b:78:GLN:HB2	1.75	0.69
32:1a:612:C:O2	32:1a:629:G:N2	2.25	0.69
1:2A:956:G:H5''	12:2Q:77:LYS:HD2	1.75	0.69
3:2D:71:ASP:OD2	3:2D:103:ARG:NH2	2.23	0.69
33:1b:100:GLY:N	33:1b:176:GLU:OE2	2.25	0.69
32:2a:953:G:N7	44:2m:104:ARG:NH2	2.40	0.69
1:1A:788:G:OP2	61:1A:4127:HOH:O	2.10	0.69
32:1a:964:A:OP1	61:1a:3307:HOH:O	2.11	0.69
40:1i:46:ALA:HB2	40:1i:74:ILE:HG23	1.74	0.69
1:2A:154(A):C:H42	1:2A:171:G:H1	1.39	0.69
1:2A:2156:G:N7	1:2A:2157:G:N2	2.41	0.69
1:2A:2483:C:N3	12:2Q:124:LYS:NZ	2.40	0.69
6:2G:97:ASP:HA	6:2G:100:TRP:HD1	1.56	0.69
10:2O:35:VAL:HG11	10:2O:103:ALA:HB3	1.73	0.69
32:2a:1129:C:N4	32:2a:1143:G:H1	1.91	0.69
1:1A:359:C:H4'	20:1Y:73:ARG:HD3	1.74	0.69
23:11:52:ARG:NH2	23:11:55:GLY:O	2.25	0.69
32:2a:1030(A):G:H21	32:2a:1030(C):G:H3'	1.57	0.69
32:2a:1348:U:H4'	40:2i:120:ARG:HD2	1.75	0.69
32:1a:945:G:OP1	61:1a:3308:HOH:O	2.11	0.69
23:21:75:GLU:HA	23:21:78:LYS:HE2	1.73	0.69
32:2a:937:A:OP2	61:2a:3208:HOH:O	2.11	0.69
32:2a:1182:G:H4'	32:2a:1183:A:H3'	1.75	0.69
1:1A:168:G:N7	61:1A:4208:HOH:O	2.27	0.68
5:2F:21:ALA:HB3	5:2F:22:ALA:HA	1.74	0.68
21:2Z:31:ARG:NH1	61:2Z:302:HOH:O	2.26	0.68
32:2a:461:A:O2'	32:2a:471:G:N7	2.25	0.68
40:2i:46:ALA:HB2	40:2i:74:ILE:HG23	1.73	0.68
32:1a:1047:G:H5''	45:1n:4:LYS:HD3	1.74	0.68
1:2A:1087:G:H1	1:2A:1102:C:H42	1.41	0.68
2:2B:14:U:OP2	2:2B:70:C:O2'	2.11	0.68
43:1l:117:ARG:HG2	43:1l:122:THR:HB	1.73	0.68
1:2A:1793:C:OP1	61:2A:3820:HOH:O	2.11	0.68
4:2E:11:MET:HG2	4:2E:24:THR:HG22	1.75	0.68
32:2a:407:G:H5''	35:2d:115:ARG:HG2	1.74	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:2i:21:PRO:HA	40:2i:59:PHE:HA	1.75	0.68
1:2A:2815:C:H5'	27:25:29:THR:HG21	1.75	0.68
1:1A:136:G:OP2	61:1A:4131:HOH:O	2.12	0.68
1:1A:1694:G:OP1	61:1A:4130:HOH:O	2.11	0.68
1:1A:2776:G:OP2	61:1A:4132:HOH:O	2.12	0.68
32:1a:1414:U:H3	32:1a:1486:G:H1	1.42	0.68
1:2A:1664:A:OP1	61:2A:3819:HOH:O	2.11	0.68
32:2a:1346:A:H5''	40:2i:120:ARG:HH12	1.57	0.68
32:1a:8:A:N7	35:1d:208:SER:OG	2.27	0.68
32:1a:77:G:H1	32:1a:92:C:H42	1.42	0.68
1:2A:2602:A:H1'	1:2A:2603:G:C5'	2.23	0.68
1:2A:2499:C:OP2	61:2A:3823:HOH:O	2.12	0.68
8:2I:4:ILE:HG12	8:2I:18:VAL:HG22	1.75	0.68
26:24:18:CYS:SG	26:24:39:CYS:HB3	2.34	0.68
1:1A:1679:A:N7	61:1A:4214:HOH:O	2.27	0.67
1:2A:2107:C:N3	1:2A:2182:G:N2	2.35	0.67
32:2a:1274:G:N2	32:2a:1275:A:N7	2.42	0.67
32:2a:1508:G:OP1	61:2a:3203:HOH:O	2.11	0.67
38:2g:76:ARG:HH21	38:2g:89:MET:HG3	1.58	0.67
2:1B:82:G:OP2	61:1B:3102:HOH:O	2.12	0.67
1:2A:111:A:N3	61:2A:3903:HOH:O	2.26	0.67
1:2A:2431:U:OP1	61:2A:3821:HOH:O	2.11	0.67
1:1A:1747:A:OP2	61:1A:4136:HOH:O	2.12	0.67
15:1T:39:ARG:HH12	15:1T:41:ARG:HD3	1.57	0.67
32:1a:1435:G:H2'	32:1a:1436:U:C6	2.29	0.67
7:2H:113:VAL:HG11	7:2H:151:ILE:HD13	1.74	0.67
34:2c:6:HIS:CD2	45:2n:49:HIS:HB3	2.29	0.67
34:2c:22:TRP:HA	41:2j:93:GLY:HA2	1.76	0.67
39:2h:121:ASP:N	39:2h:121:ASP:OD1	2.28	0.67
23:11:21:ARG:HD3	23:11:35:THR:HG21	1.74	0.67
6:2G:3:LEU:O	6:2G:8:LYS:NZ	2.27	0.67
25:23:13:ILE:O	61:23:201:HOH:O	2.12	0.67
1:2A:1264:G:OP1	27:25:19:ARG:NH2	2.17	0.67
8:2I:55:ALA:HA	8:2I:58:LEU:HB3	1.77	0.67
53:2y:52:ALA:HB2	53:2y:77:LEU:HD21	1.76	0.67
1:1A:1039:G:OP1	16:1U:50:ARG:NH2	2.27	0.67
1:1A:1748:A:OP2	61:1A:4135:HOH:O	2.12	0.67
1:1A:2459:G:OP2	61:1A:4133:HOH:O	2.12	0.67
20:1Y:102:CYS:SG	20:1Y:103:GLY:N	2.67	0.67
32:1a:137:C:N4	32:1a:226:G:O6	2.18	0.67
32:1a:1305:G:N7	61:1a:3326:HOH:O	2.27	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:84:A:N1	1:2A:98:G:O2'	2.27	0.67
1:2A:2285:C:OP2	28:26:6:ARG:NH1	2.27	0.67
33:2b:16:HIS:HB3	33:2b:210:SER:HB3	1.76	0.67
45:1n:3:ARG:NH2	61:1n:601:HOH:O	2.23	0.67
1:1A:2460:A:OP1	61:1A:4137:HOH:O	2.13	0.67
4:2E:28:ALA:HB3	4:2E:93:VAL:HG12	1.77	0.67
32:2a:31:G:O2'	32:2a:48:C:N4	2.28	0.67
7:1H:97:ARG:NE	7:1H:104:GLU:OE1	2.28	0.67
1:2A:1281:G:N7	61:2A:3920:HOH:O	2.28	0.67
32:2a:474:G:H2'	32:2a:475:G:H8	1.59	0.67
39:2h:103:VAL:HG21	39:2h:110:ALA:HB2	1.75	0.67
1:2A:526:A:OP1	61:2A:3826:HOH:O	2.13	0.66
1:2A:2267:A:OP2	61:2A:3825:HOH:O	2.12	0.66
1:2A:2504:U:OP2	61:2A:3824:HOH:O	2.12	0.66
1:1A:455:A:OP1	61:1A:4134:HOH:O	2.12	0.66
32:1a:877:C:OP1	39:1h:88:LYS:NZ	2.28	0.66
1:2A:530:G:O6	61:2A:3822:HOH:O	2.12	0.66
32:2a:1002:G:H2'	32:2a:1003:G:C8	2.29	0.66
33:2b:187:LEU:HA	33:2b:201:ILE:HB	1.76	0.66
1:1A:1361:C:OP2	61:1A:4118:HOH:O	2.14	0.66
6:1G:139:LEU:HD21	6:1G:149:VAL:HG11	1.77	0.66
23:11:50:ARG:HG2	23:11:59:THR:HG22	1.76	0.66
32:1a:1182:G:H4'	32:1a:1183:A:H5'	1.75	0.66
1:2A:1064:C:H3'	1:2A:1065:U:H5'	1.76	0.66
7:2H:3:ARG:HE	7:2H:54:ARG:HH12	1.43	0.66
19:2X:53:LYS:HB3	19:2X:82:GLN:HB3	1.78	0.66
33:2b:217:ARG:HA	33:2b:220:ASP:HB2	1.78	0.66
1:1A:1871:G:N7	61:1A:4222:HOH:O	2.28	0.66
1:2A:1771:C:OP1	61:2A:3829:HOH:O	2.13	0.66
32:2a:1119:C:H2'	32:2a:1120:G:H8	1.61	0.66
41:2j:51:ARG:O	45:2n:45:ARG:NH1	2.28	0.66
32:2a:954:G:H21	32:2a:1227:A:H62	1.43	0.66
33:1b:134:GLU:HG3	33:1b:137:ARG:HH21	1.59	0.66
1:2A:365:C:OP2	61:2A:3827:HOH:O	2.13	0.66
4:2E:199:ARG:NH1	61:2E:401:HOH:O	2.20	0.66
14:2S:50:SER:O	14:2S:76:LYS:NZ	2.29	0.66
1:1A:272:U:OP1	8:1I:50:ARG:NH1	2.29	0.66
1:1A:1847:G:O6	3:1D:35:LYS:NZ	2.24	0.66
2:1B:6:C:H2'	2:1B:7:G:H5''	1.77	0.66
32:1a:1077:G:N2	32:1a:1080:A:OP2	2.28	0.66
50:1s:63:THR:OG1	50:1s:65:ASN:OD1	2.14	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:881:G:H1	1:2A:895:U:H3	1.41	0.66
1:2A:1064:C:H3'	1:2A:1065:U:C5'	2.25	0.66
1:2A:2759:G:N2	7:2H:139:GLN:OE1	2.28	0.66
26:24:59:PHE:HA	26:24:60:GLN:C	2.19	0.66
32:2a:574:A:OP2	61:2a:3204:HOH:O	2.13	0.66
32:2a:976:G:H5'	32:2a:1358:U:O2'	1.96	0.66
32:2a:1456:G:N1	51:2t:51:GLU:OE2	2.27	0.66
22:10:11:ARG:O	22:10:14:ARG:NH2	2.26	0.66
32:1a:812:C:N3	61:1a:3327:HOH:O	2.28	0.66
1:2A:999:U:OP2	61:2A:3828:HOH:O	2.13	0.66
23:11:51:VAL:HG11	23:11:74:VAL:HG21	1.76	0.66
32:1a:278:G:OP2	48:1q:92:ARG:NH2	2.29	0.66
1:2A:1110:G:H1'	1:2A:1111:A:C8	2.31	0.66
1:2A:1780:A:OP1	61:2A:3815:HOH:O	2.14	0.66
1:2A:2237:G:OP1	61:2A:3832:HOH:O	2.14	0.66
27:25:16:ARG:NH1	27:25:17:ASP:OD1	2.29	0.66
1:1A:1941:A:O2'	32:1a:1517:G:N3	2.28	0.65
1:1A:2320:G:O2'	1:1A:2322:A:N7	2.24	0.65
1:2A:1322:A:OP1	61:2A:3834:HOH:O	2.14	0.65
1:1A:273:G:H21	8:1I:50:ARG:HD3	1.61	0.65
11:1P:42:SER:O	61:1P:301:HOH:O	2.14	0.65
32:1a:255:G:H1'	48:1q:16:GLN:HE21	1.61	0.65
1:2A:131:G:OP1	61:2A:3831:HOH:O	2.14	0.65
6:2G:72:ARG:HG2	6:2G:87:PRO:HA	1.79	0.65
1:1A:1428:G:N7	61:1A:4232:HOH:O	2.29	0.65
1:1A:1529:G:H1	1:1A:1552:C:H42	1.43	0.65
3:1D:69:ARG:NH2	3:1D:128:GLY:O	2.29	0.65
5:1F:185:ASP:HA	5:1F:188:ARG:HD3	1.77	0.65
17:1V:74:LYS:HB2	17:1V:83:ARG:HB2	1.77	0.65
35:1d:83:SER:O	61:1d:401:HOH:O	2.14	0.65
1:2A:1371:G:N7	61:2A:3919:HOH:O	2.28	0.65
17:1V:40:LEU:HB2	17:1V:46:VAL:HG13	1.79	0.65
32:1a:100:C:H2'	32:1a:101:A:C8	2.30	0.65
35:1d:81:GLU:OE2	35:1d:139:ARG:NH1	2.27	0.65
1:2A:990:A:OP2	61:2A:3836:HOH:O	2.14	0.65
1:2A:994:C:OP2	16:2U:54:LYS:NZ	2.26	0.65
1:2A:1445:A:OP1	61:2A:3833:HOH:O	2.14	0.65
1:2A:2111:C:H42	1:2A:2147:G:H22	1.44	0.65
32:2a:21:G:OP1	61:2a:3209:HOH:O	2.13	0.65
1:1A:1059:C:OP2	61:1A:4139:HOH:O	2.14	0.65
1:1A:2060:G:O6	61:1A:4125:HOH:O	2.08	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:1S:93:LYS:O	61:1S:8101:HOH:O	2.13	0.65
1:2A:2429:G:OP1	61:2A:3809:HOH:O	2.13	0.65
6:2G:47:LYS:HG3	6:2G:48:GLU:H	1.61	0.65
23:21:37:ILE:O	61:21:8101:HOH:O	2.15	0.65
32:2a:949:A:H61	32:2a:1232:U:H3	1.43	0.65
31:29:2:LYS:NZ	31:29:31:LYS:O	2.30	0.65
32:2a:1013:G:N2	32:2a:1016:A:OP2	2.25	0.65
1:1A:1199:C:OP2	61:1A:4120:HOH:O	2.15	0.65
3:1D:108:PRO:HD2	3:1D:111:LEU:HG	1.79	0.65
36:1e:100:VAL:O	36:1e:107:ARG:NH2	2.25	0.65
21:2Z:52:SER:O	61:2Z:301:HOH:O	2.13	0.65
32:2a:1262:C:H42	32:2a:1273:G:H1	1.44	0.65
1:1A:555:G:N1	1:1A:2045:G:OP1	2.27	0.65
1:1A:1717:C:OP2	61:1A:4107:HOH:O	2.15	0.65
33:1b:82:ARG:NH1	33:1b:92:TYR:OH	2.29	0.65
35:2d:163:GLU:O	35:2d:166:LYS:HG2	1.96	0.65
53:2y:5:ILE:HG23	53:2y:39:ILE:HB	1.77	0.65
4:1E:29:GLY:HA3	61:1E:3105:HOH:O	1.96	0.65
21:1Z:144:LEU:HD21	21:1Z:150:LEU:HD13	1.79	0.65
1:2A:395:U:O2'	61:2A:3835:HOH:O	2.14	0.65
6:2G:113:ARG:NH1	6:2G:139:LEU:O	2.30	0.65
12:2Q:11:LYS:NZ	12:2Q:88:GLY:O	2.22	0.65
23:21:20:ARG:NH1	61:21:8103:HOH:O	2.29	0.65
32:2a:1295:G:O2'	44:2m:14:ARG:NH1	2.29	0.65
32:2a:1352:C:H42	32:2a:1370:G:H1	1.43	0.65
38:2g:27:ILE:HD12	38:2g:40:ALA:HA	1.79	0.65
53:2y:40:ILE:HB	53:2y:51:ASP:HB2	1.79	0.65
39:1h:10:LEU:HD22	39:1h:83:ILE:HD11	1.78	0.64
2:2B:115:G:N7	61:2B:3109:HOH:O	2.29	0.64
3:2D:235:GLY:O	61:2D:401:HOH:O	2.14	0.64
32:2a:41:G:H2'	32:2a:42:G:C8	2.32	0.64
5:1F:12:LEU:HD13	5:1F:124:LEU:HD11	1.79	0.64
1:2A:2379:G:O2'	14:2S:17:ARG:NH1	2.31	0.64
1:1A:655:G:OP2	30:18:15:LYS:NZ	2.28	0.64
1:1A:1070:G:OP2	61:1A:4113:HOH:O	2.14	0.64
1:1A:2324:U:H5'	6:1G:88:ILE:HD11	1.78	0.64
58:1F:314:ARG:N	61:1F:403:HOH:O	2.31	0.64
32:1a:1007:C:N3	32:1a:1022:G:O6	2.31	0.64
32:1a:1291:G:OP1	38:1g:41:ARG:NH2	2.30	0.64
1:2A:1189:A:OP2	61:2A:3840:HOH:O	2.15	0.64
1:1A:206:G:OP2	61:1A:4142:HOH:O	2.15	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2163:G:O6	1:1A:2172:U:O2	2.15	0.64
1:2A:2589:A:OP1	61:2A:3837:HOH:O	2.15	0.64
1:1A:1556:A:H2'	1:1A:1557:A:O4'	1.98	0.64
33:1b:88:ALA:HB2	33:1b:219:VAL:HG13	1.80	0.64
34:1c:35:GLU:OE1	34:1c:59:ARG:NH2	2.31	0.64
1:2A:2805:G:H2'	1:2A:2807:G:H8	1.63	0.64
6:2G:57:ALA:HB2	6:2G:90:LEU:HD13	1.80	0.64
28:26:14:THR:OG1	28:26:48:VAL:O	2.16	0.64
36:2e:69:VAL:HG21	36:2e:113:ALA:HB1	1.78	0.64
41:2j:61:GLU:OE2	45:2n:58:LYS:NZ	2.28	0.64
50:2s:50:ALA:HB1	50:2s:57:HIS:HB3	1.80	0.64
1:1A:407:U:OP1	61:1A:4143:HOH:O	2.15	0.64
5:1F:122:LYS:HB3	5:1F:191:ARG:HG3	1.79	0.64
32:1a:1069:C:OP2	61:1a:3309:HOH:O	2.14	0.64
40:1i:9:ARG:HG2	40:1i:14:VAL:HG13	1.80	0.64
32:2a:1500:A:OP2	61:2a:3210:HOH:O	2.15	0.64
1:1A:1705:C:OP1	61:1A:4141:HOH:O	2.15	0.64
8:1I:130:TYR:HB3	8:1I:138:ILE:HB	1.79	0.64
1:2A:326:G:N7	61:2A:3933:HOH:O	2.30	0.64
1:2A:1667:G:O2'	1:2A:1991:U:O4	2.13	0.64
1:2A:2376:A:N3	14:2S:106:ARG:NH2	2.46	0.64
32:2a:1278:U:H5''	32:2a:1279:A:H5'	1.78	0.64
32:1a:1068:G:H8	32:1a:1068:G:OP2	1.81	0.63
1:2A:127:A:H5''	1:2A:128:C:C6	2.33	0.63
7:2H:98:LEU:HD22	7:2H:125:VAL:HG23	1.80	0.63
32:1a:656:C:O2'	46:1o:28:GLN:NE2	2.31	0.63
32:1a:309:G:O2'	32:1a:607:A:N1	2.31	0.63
39:1h:116:LYS:HD3	39:1h:127:LEU:HD23	1.79	0.63
32:2a:390:C:O3'	47:2p:28:ARG:NH2	2.31	0.63
41:2j:62:HIS:HB3	45:2n:59:ALA:HB3	1.79	0.63
36:1e:37:ARG:HH12	36:1e:111:GLU:HG2	1.63	0.63
1:2A:2328:A:H2'	1:2A:2329:G:C8	2.33	0.63
32:2a:450:G:H4'	47:2p:41:PRO:HB2	1.80	0.63
34:2c:6:HIS:HD2	45:2n:49:HIS:HB3	1.63	0.63
5:1F:93:LYS:O	61:1F:401:HOH:O	2.15	0.63
5:1F:116:ASP:OD1	5:1F:119:ARG:NH2	2.32	0.63
1:2A:688:U:OP1	61:2A:3839:HOH:O	2.15	0.63
7:2H:143:GLN:NE2	7:2H:147:ASN:OD1	2.29	0.63
32:2a:944:G:N1	32:2a:1338:G:OP2	2.28	0.63
1:1A:1220:U:O2'	1:1A:1221:G:O5'	2.15	0.63
1:2A:1796:U:H2'	1:2A:1797:C:C6	2.34	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2070:G:OP2	61:2A:3838:HOH:O	2.15	0.63
44:2m:49:THR:HG22	44:2m:51:ALA:H	1.64	0.63
1:1A:1016:C:OP2	61:1A:4149:HOH:O	2.16	0.63
46:1o:16:ALA:HB1	46:1o:21:ASP:HB3	1.80	0.63
46:1o:39:LEU:HD13	46:1o:56:LEU:HB2	1.80	0.63
1:2A:2364:C:OP1	22:20:55:ARG:NH1	2.32	0.63
15:2T:30:VAL:HG22	15:2T:86:ILE:HG12	1.78	0.63
23:21:50:ARG:HG2	23:21:59:THR:HG22	1.79	0.63
32:1a:1189:C:OP1	41:1j:51:ARG:NH2	2.26	0.63
5:2F:122:LYS:NZ	5:2F:152:GLU:OE2	2.28	0.63
32:2a:1227:A:OP1	50:2s:80:TYR:OH	2.10	0.63
1:1A:354:A:H2	1:1A:1255:A:HO2'	1.47	0.63
1:1A:776:G:C6	3:1D:208:LYS:HB2	2.34	0.63
1:2A:857:C:OP2	22:20:77:ARG:NH2	2.32	0.63
15:2T:41:ARG:NH2	32:2a:346:G:OP1	2.30	0.63
4:1E:36:ARG:NH1	4:1E:85:ASN:OD1	2.32	0.62
32:1a:1027:C:O2	32:1a:1034:G:C2	2.52	0.62
32:1a:1028:C:N3	32:1a:1033:G:O6	2.32	0.62
1:2A:630:G:N2	1:2A:633:A:OP2	2.27	0.62
1:2A:796:C:H2'	1:2A:797:C:C6	2.34	0.62
8:2I:126:TYR:O	8:2I:142:VAL:N	2.31	0.62
3:1D:148:GLU:HB2	3:1D:151:LYS:HD2	1.80	0.62
12:1Q:111:GLU:OE2	12:1Q:133:ARG:NH2	2.32	0.62
5:2F:129:PHE:CD2	5:2F:163:VAL:HG21	2.34	0.62
32:1a:965:A:OP2	53:1y:8:LYS:NZ	2.32	0.62
1:2A:2753:A:N3	31:29:15:LYS:NZ	2.47	0.62
26:24:24:THR:OG1	26:24:25:TYR:N	2.31	0.62
32:2a:1028:C:H2'	32:2a:1033:G:N2	2.15	0.62
33:2b:98:LEU:H	33:2b:101:MET:HE3	1.64	0.62
34:2c:181:ASN:N	34:2c:205:GLY:O	2.31	0.62
1:1A:272:U:H4'	8:1I:50:ARG:HH22	1.64	0.62
1:1A:1115:A:O2'	1:1A:1119:A:N6	2.30	0.62
33:1b:161:ALA:HB1	33:1b:185:ILE:HD11	1.80	0.62
41:1j:35:SER:N	41:1j:73:ASP:O	2.32	0.62
53:1y:71:TYR:HA	53:1y:74:ILE:HD12	1.81	0.62
32:2a:1047:G:H5''	45:2n:4:LYS:HD3	1.80	0.62
53:2y:12:ILE:HG23	53:2y:16:ILE:HG23	1.81	0.62
1:1A:1057:G:OP1	16:1U:77:SER:OG	2.16	0.62
1:1A:2331:G:H22	14:1S:3:ARG:CD	2.06	0.62
26:14:61:ARG:HG3	26:14:62:ARG:H	1.64	0.62
32:1a:1499:A:OP2	61:1a:3311:HOH:O	2.16	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1285:A:H4'	32:2a:1286:A:H5'	1.80	0.62
40:2i:26:VAL:HG22	40:2i:61:ALA:HB3	1.81	0.62
1:1A:546:G:O6	61:1A:4140:HOH:O	2.15	0.62
1:1A:1202:A:OP1	16:1U:55:ARG:NH1	2.32	0.62
1:1A:1273:G:OP2	16:1U:16:LYS:NZ	2.32	0.62
1:1A:2331:G:N2	14:1S:3:ARG:HD3	2.06	0.62
19:1X:54:VAL:HG22	19:1X:81:VAL:HG12	1.80	0.62
1:2A:631:A:OP1	11:2P:65:ARG:NH1	2.33	0.62
12:2Q:43:THR:N	12:2Q:46:GLN:OE1	2.28	0.62
32:2a:222:U:H2'	32:2a:223:U:C6	2.34	0.62
1:1A:130:G:O6	61:1A:4144:HOH:O	2.15	0.62
8:1I:109:ILE:HG13	8:1I:130:TYR:CZ	2.34	0.62
16:1U:33:ARG:NH2	61:1U:303:HOH:O	2.31	0.62
41:1j:11:PHE:HE1	41:1j:67:THR:HG22	1.64	0.62
2:2B:13:A:N1	2:2B:69:G:O2'	2.32	0.62
32:2a:1366:C:O2'	41:2j:60:ARG:NH2	2.27	0.62
1:2A:2312:U:H5'	6:2G:88:ILE:HD11	1.80	0.62
11:2P:126:VAL:HG12	11:2P:148:LEU:HD23	1.82	0.62
32:2a:1318:A:H1'	50:2s:37:ARG:HH11	1.64	0.62
1:2A:1104:C:H2'	1:2A:1105:U:H6	1.65	0.62
36:2e:78:HIS:HE1	36:2e:143:ARG:H	1.47	0.62
7:1H:101:ARG:HG2	7:1H:117:PRO:HG2	1.81	0.62
46:1o:55:GLY:HA2	46:1o:58:MET:HE3	1.81	0.62
1:2A:568:U:O2'	61:2A:3830:HOH:O	2.13	0.62
1:1A:1410:G:N7	23:11:3:LYS:HE2	2.15	0.61
1:1A:2849:G:H5'	13:1R:46:GLY:HA2	1.81	0.61
1:2A:726:G:O6	61:2A:3841:HOH:O	2.16	0.61
1:1A:640:A:OP2	61:1A:4152:HOH:O	2.16	0.61
1:1A:2412:G:OP2	61:1A:4150:HOH:O	2.16	0.61
1:1A:2859:U:OP2	15:1T:95:ARG:NH1	2.32	0.61
53:2y:7:SER:OG	53:2y:10:MET:O	2.18	0.61
32:1a:377:G:OP1	47:1p:3:LYS:NZ	2.28	0.61
32:1a:976:G:H5'	32:1a:1358:U:O2'	2.00	0.61
1:1A:2010:C:OP2	61:1A:4148:HOH:O	2.16	0.61
22:10:27:GLU:HG3	22:10:68:GLU:HA	1.83	0.61
1:2A:302:C:H42	1:2A:315:G:H1	1.48	0.61
1:2A:2134:A:O2'	1:2A:2159:G:N3	2.33	0.61
32:2a:1286:A:H8	32:2a:1287:A:H4'	1.62	0.61
1:2A:2136:C:N3	1:2A:2155:G:N2	2.48	0.61
1:2A:2318:G:N2	14:2S:3:ARG:HE	1.98	0.61
6:2G:106:LEU:HA	6:2G:110:ALA:HB3	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:2H:24:VAL:HG13	7:2H:37:VAL:HG21	1.83	0.61
32:2a:974:A:OP2	45:2n:29:ARG:NH2	2.32	0.61
34:2c:77:ILE:HG12	34:2c:103:VAL:HG21	1.82	0.61
36:2e:143:ARG:NE	39:2h:77:GLU:OE2	2.33	0.61
44:2m:80:ARG:HH22	50:2s:69:HIS:HE1	1.48	0.61
1:1A:2124:U:O2	1:1A:2209:G:O6	2.19	0.61
18:2W:2:GLU:OE2	18:2W:72:LYS:NZ	2.31	0.61
24:22:19:VAL:HG12	24:22:23:LYS:HE3	1.81	0.61
32:2a:573:A:N3	32:2a:883:C:O2'	2.32	0.61
5:1F:195:ASP:HB2	5:1F:198:ALA:H	1.66	0.61
12:1Q:119:ARG:NH1	61:1Q:303:HOH:O	2.31	0.61
3:2D:133:LEU:HB3	3:2D:173:VAL:HG11	1.82	0.61
32:2a:1128:C:H1'	32:2a:1147:C:H42	1.65	0.61
44:2m:87:TYR:HA	44:2m:90:LEU:HD12	1.83	0.61
50:2s:41:VAL:HG12	50:2s:44:MET:HG3	1.83	0.61
1:1A:310:C:H2'	1:1A:311:C:C6	2.36	0.61
1:1A:676:G:OP1	30:18:19:SER:OG	2.17	0.61
1:1A:1532:A:H2'	1:1A:1533:G:H8	1.65	0.61
33:1b:219:VAL:HA	33:1b:222:ILE:HD12	1.81	0.61
21:2Z:23:LYS:HD3	21:2Z:40:ASP:HA	1.81	0.61
32:2a:406:G:H4'	35:2d:5:ILE:HD11	1.81	0.61
32:2a:1376:U:O4	38:2g:10:ARG:NH1	2.33	0.61
44:1m:36:LYS:HG3	44:1m:59:TYR:CZ	2.35	0.61
1:2A:1186:G:OP2	61:2A:3836:HOH:O	2.15	0.61
1:2A:2079:U:O3'	23:21:35:THR:OG1	2.19	0.61
1:2A:2099:U:O2	1:2A:2190:G:N2	2.32	0.61
1:2A:2659:G:H4'	7:2H:175:LYS:HD3	1.81	0.61
6:2G:105:LYS:NZ	6:2G:143:GLU:OE2	2.27	0.61
25:23:7:LYS:HE3	25:23:32:GLN:HE21	1.66	0.61
32:2a:769:G:H4'	32:2a:1513:A:H4'	1.83	0.61
34:2c:155:GLY:HA3	34:2c:196:LEU:HD22	1.83	0.61
44:2m:34:LEU:HD13	44:2m:41:PRO:HA	1.83	0.61
1:1A:762:G:C2	46:1o:56:LEU:HD21	2.36	0.61
1:1A:1111:U:O2	1:1A:1112:U:N3	2.34	0.61
1:1A:2137:G:H2'	1:1A:2139:A:N6	2.16	0.61
1:1A:2164:C:O2	1:1A:2171:G:N1	2.33	0.61
32:2a:134:A:N6	47:2p:25:ARG:HH22	1.99	0.61
44:2m:81:LEU:HD22	44:2m:88:ARG:HD3	1.81	0.61
1:1A:1218:G:O2'	1:1A:1219:A:O5'	2.19	0.60
21:1Z:158:PRO:HG2	21:1Z:161:VAL:HG11	1.82	0.60
28:16:2:ALA:N	61:16:601:HOH:O	2.33	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:673:G:H2'	32:1a:674:G:C8	2.35	0.60
32:1a:1015:A:H2'	32:1a:1016:A:C8	2.36	0.60
32:1a:1124:G:N2	32:1a:1125:U:O4	2.30	0.60
32:1a:1505:G:OP1	61:1a:3306:HOH:O	2.16	0.60
33:1b:15:VAL:HG22	33:1b:209:ARG:HB3	1.83	0.60
39:1h:51:VAL:HG12	39:1h:52:ASP:H	1.66	0.60
14:2S:93:LYS:NZ	61:2S:202:HOH:O	2.33	0.60
1:1A:2189:U:H2'	1:1A:2190:G:C8	2.36	0.60
19:1X:31:HIS:HD2	19:1X:33:LYS:H	1.49	0.60
32:1a:955:U:O2'	50:1s:83:HIS:HD2	1.83	0.60
44:1m:3:ARG:HG2	44:1m:8:GLU:HG3	1.82	0.60
48:1q:57:VAL:HG12	48:1q:76:LEU:HA	1.83	0.60
1:2A:404:C:OP2	61:2A:3846:HOH:O	2.16	0.60
1:2A:1783:A:OP2	61:2A:3847:HOH:O	2.17	0.60
8:2I:4:ILE:HD11	8:2I:44:LEU:HD12	1.82	0.60
32:2a:17:U:H2'	32:2a:18:C:C6	2.36	0.60
32:2a:1164:G:H1	32:2a:1172:C:N4	1.98	0.60
1:1A:1223:C:H2'	1:1A:1224:C:C6	2.36	0.60
16:1U:55:ARG:NH2	61:1U:302:HOH:O	2.29	0.60
35:1d:15:GLU:OE2	35:1d:66:ARG:NH1	2.34	0.60
15:2T:51:ARG:HB2	15:2T:98:LYS:HD3	1.83	0.60
16:2U:10:ARG:NH1	61:2U:302:HOH:O	2.34	0.60
1:1A:2859:U:H4'	1:1A:2878:A:C2	2.36	0.60
32:1a:1318:A:H5''	50:1s:3:ARG:HH12	1.66	0.60
35:1d:76:ARG:NH1	35:1d:80:GLU:OE1	2.34	0.60
39:1h:51:VAL:HG11	39:1h:60:ARG:HH12	1.65	0.60
1:2A:362:U:O2'	1:2A:363:G:H5'	2.00	0.60
1:2A:2870:C:H2'	1:2A:2871:C:O4'	2.00	0.60
14:2S:27:SER:HA	14:2S:88:ASP:HB3	1.82	0.60
32:2a:59:A:H5''	32:2a:60:A:H5''	1.83	0.60
41:2j:49:VAL:HG23	45:2n:41:ARG:HB2	1.84	0.60
1:1A:2465:A:OP1	61:1A:4147:HOH:O	2.15	0.60
2:1B:66:A:H61	2:1B:108:U:H2'	1.66	0.60
14:1S:27:SER:HA	14:1S:88:ASP:HB3	1.83	0.60
20:1Y:92:ASN:N	20:1Y:93:GLY:HA2	2.16	0.60
32:1a:1316:G:H4'	45:1n:18:VAL:HG11	1.84	0.60
35:1d:18:LYS:NZ	35:1d:31:CYS:SG	2.72	0.60
1:2A:309:G:N3	1:2A:329:G:O2'	2.35	0.60
1:2A:1062:G:N7	1:2A:1070:A:H1'	2.16	0.60
12:2Q:68:ILE:HG22	12:2Q:101:ARG:HE	1.64	0.60
35:2d:79:PHE:HE1	35:2d:204:ILE:HD13	1.65	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1532:A:H2'	1:1A:1533:G:C8	2.36	0.60
1:1A:2649:U:OP2	61:1A:4146:HOH:O	2.15	0.60
44:1m:87:TYR:HA	44:1m:90:LEU:HD12	1.82	0.60
1:2A:2001:A:H2'	1:2A:2002:G:C8	2.37	0.60
22:20:17:GLN:NE2	61:20:5003:HOH:O	2.34	0.60
32:2a:353:A:H5'	32:2a:353:A:H8	1.66	0.60
32:2a:457:C:H2'	32:2a:458:C:H6	1.65	0.60
32:2a:533:A:O2'	32:2a:535:A:OP2	2.20	0.60
32:2a:632:A:H3'	32:2a:633:G:H8	1.65	0.60
32:2a:1256:A:N6	32:2a:1278:U:H1'	2.12	0.60
37:2f:61:LEU:HB3	37:2f:63:TYR:HE2	1.65	0.60
38:2g:115:ARG:HB3	38:2g:118:VAL:HG23	1.82	0.60
53:2y:3:MET:HG3	53:2y:37:PRO:HG2	1.83	0.60
7:1H:11:VAL:HG13	7:1H:15:VAL:HG22	1.84	0.60
7:2H:98:LEU:HD13	7:2H:103:LEU:HD13	1.84	0.60
33:2b:178:ARG:HH22	39:2h:74:PRO:HB3	1.66	0.60
15:1T:96:ARG:NH2	61:1T:303:HOH:O	2.33	0.60
21:1Z:69:THR:HG22	21:1Z:90:VAL:HA	1.82	0.60
26:14:16:CYS:SG	26:14:17:GLY:N	2.74	0.60
32:1a:642:A:N3	39:1h:113:SER:OG	2.29	0.60
32:1a:757:U:O2'	32:1a:879:C:O2	2.20	0.60
1:2A:586:A:N1	1:2A:809:G:O2'	2.29	0.60
1:2A:2417:C:OP1	11:2P:65:ARG:NH2	2.35	0.60
7:2H:113:VAL:HG21	7:2H:151:ILE:HG21	1.84	0.60
32:2a:443:C:H2'	32:2a:444:C:C6	2.37	0.60
1:2A:1101:U:H2'	1:2A:1102:C:H6	1.67	0.60
34:2c:63:ASN:HB2	34:2c:98:ASN:HB2	1.82	0.60
35:2d:108:LEU:HD21	35:2d:183:GLY:HA3	1.83	0.60
1:1A:1827:U:H2'	1:1A:1828:C:C6	2.36	0.60
1:1A:2348:A:H61	22:10:43:THR:HG22	1.67	0.60
12:1Q:109:VAL:HG13	12:1Q:113:GLN:HB2	1.84	0.60
32:1a:352:C:O2'	32:1a:354:G:OP1	2.20	0.60
32:1a:794:A:OP2	61:1a:3310:HOH:O	2.16	0.60
5:2F:178:PRO:HB2	5:2F:201:VAL:HG21	1.83	0.60
1:1A:2164:C:N3	1:1A:2171:G:O6	2.35	0.59
39:1h:14:ARG:O	39:1h:18:ARG:HG2	2.02	0.59
1:2A:1007:C:OP1	9:2N:35:ARG:NH1	2.35	0.59
1:2A:1507:A:O2'	1:2A:1508:A:O5'	2.20	0.59
1:1A:492:A:OP1	29:17:34:ARG:NH1	2.35	0.59
1:1A:2416:C:O3'	11:1P:77:ARG:NH2	2.35	0.59
32:1a:171:A:H2'	32:1a:172:A:C8	2.37	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:1q:62:SER:HB3	48:1q:72:ARG:HH11	1.66	0.59
1:2A:1009:A:OP2	61:2A:3844:HOH:O	2.16	0.59
26:24:48:ARG:HD2	26:24:52:THR:HA	1.82	0.59
32:2a:164:U:H2'	32:2a:165:C:C6	2.37	0.59
33:2b:83:MET:SD	33:2b:234:PRO:HB2	2.42	0.59
1:1A:1140:U:H1'	1:1A:1143:U:H5	1.66	0.59
5:1F:53:THR:CG2	5:1F:55:GLY:H	2.14	0.59
28:16:14:THR:O	28:16:17:LYS:NZ	2.34	0.59
21:2Z:33:LEU:HD11	21:2Z:90:VAL:HG21	1.84	0.59
33:2b:178:ARG:HB3	39:2h:72:PRO:HA	1.84	0.59
35:2d:122:ARG:NH1	35:2d:134:ASP:O	2.36	0.59
1:1A:1313:U:OP1	61:1A:4151:HOH:O	2.16	0.59
32:1a:1062:U:H2'	32:1a:1063:C:C6	2.37	0.59
32:1a:1191:A:H5''	34:1c:4:LYS:HE3	1.85	0.59
32:1a:1356:G:H2'	32:1a:1357:A:C8	2.38	0.59
32:1a:1510:U:H2'	32:1a:1511:G:C8	2.37	0.59
1:2A:271(L):U:H5'	8:2I:50:ARG:HH12	1.66	0.59
1:2A:2119:A:H61	1:2A:2168:G:H21	1.48	0.59
1:2A:2128:C:H1'	1:2A:2173:A:H2	1.67	0.59
7:2H:3:ARG:NH1	7:2H:5:GLY:H	2.00	0.59
33:2b:63:MET:HG2	33:2b:225:ALA:HB1	1.83	0.59
1:1A:1124:U:H4'	1:1A:1125:C:H5'	1.85	0.59
1:1A:1889:G:O6	61:1A:4145:HOH:O	2.15	0.59
17:2V:52:VAL:HG23	17:2V:55:ALA:HB3	1.83	0.59
32:2a:931:C:H42	32:2a:1386:G:H1	1.50	0.59
1:1A:2045:G:H5'	1:1A:2629:C:H4'	1.83	0.59
32:1a:116:A:H61	32:1a:313:A:H1'	1.68	0.59
34:1c:6:HIS:HD2	34:1c:8:ILE:H	1.51	0.59
1:2A:2526:G:O6	61:2A:3842:HOH:O	2.16	0.59
17:2V:40:LEU:HB2	17:2V:46:VAL:HG13	1.84	0.59
26:24:16:CYS:SG	26:24:17:GLY:N	2.75	0.59
33:2b:84:GLU:HB3	33:2b:219:VAL:HG21	1.84	0.59
51:1t:33:ILE:O	51:1t:37:SER:OG	2.15	0.59
1:2A:2155:G:C2	1:2A:2156:G:H1'	2.37	0.59
33:2b:91:PRO:HG3	33:2b:155:LEU:HD13	1.83	0.59
34:2c:6:HIS:NE2	34:2c:8:ILE:HB	2.17	0.59
44:2m:90:LEU:HD23	44:2m:93:ARG:HH21	1.67	0.59
1:1A:1218:G:O2'	1:1A:1219:A:O4'	2.21	0.59
1:1A:1398:U:OP1	61:1A:4154:HOH:O	2.17	0.59
1:1A:1475:G:H2'	1:1A:1476:C:C6	2.38	0.59
5:1F:41:LEU:HA	5:1F:44:ARG:HD3	1.85	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:1u:17:THR:O	52:1u:22:ARG:NH1	2.35	0.59
1:2A:2128:C:N4	1:2A:2160:G:H1	2.00	0.59
6:2G:5:VAL:HG23	6:2G:8:LYS:HB3	1.84	0.59
32:2a:474:G:H2'	32:2a:475:G:C8	2.37	0.59
32:2a:1513:A:H2'	32:2a:1514:C:C6	2.37	0.59
1:1A:2136:A:H3'	1:1A:2137:G:C8	2.37	0.59
32:1a:300:A:O2'	32:1a:564:C:N3	2.32	0.59
36:1e:78:HIS:ND1	39:1h:104:ARG:HD2	2.18	0.59
1:2A:2327:A:H2'	1:2A:2328:A:C8	2.37	0.59
1:2A:2355:C:H1'	22:20:39:ARG:HH21	1.67	0.59
14:2S:74:ALA:HB2	14:2S:105:ALA:HA	1.85	0.59
15:2T:65:LYS:HE3	15:2T:67:SER:HB2	1.85	0.59
32:2a:1003:G:H3'	32:2a:1003:G:N3	2.18	0.59
6:1G:66:GLN:NE2	6:1G:93:THR:O	2.36	0.59
8:1I:77:LEU:HD12	8:1I:104:GLN:HE21	1.66	0.59
32:1a:79:G:N1	32:1a:90:U:N3	2.51	0.59
32:2a:1006:C:H2'	32:2a:1007:C:C6	2.37	0.59
32:2a:1129:C:H2'	32:2a:1139:G:N7	2.18	0.59
1:1A:1001:G:O6	61:1A:4138:HOH:O	2.13	0.58
48:1q:66:SER:O	48:1q:70:ARG:NH1	2.36	0.58
1:2A:2104:G:N2	1:2A:2105:C:N3	2.51	0.58
27:25:16:ARG:HG2	27:25:16:ARG:HH11	1.68	0.58
28:26:35:GLU:OE2	28:26:50:ARG:NH1	2.36	0.58
32:2a:501:C:H2'	32:2a:502:G:C8	2.38	0.58
1:1A:1317:G:OP2	61:1A:4130:HOH:O	2.16	0.58
1:1A:2339:A:H2'	1:1A:2340:A:C8	2.38	0.58
44:1m:11:ARG:O	44:1m:13:LYS:N	2.36	0.58
48:1q:9:VAL:HG22	48:1q:56:VAL:HG22	1.83	0.58
1:2A:2144:U:H5''	1:2A:2145:C:C5	2.38	0.58
8:2I:5:LEU:HD21	8:2I:12:LEU:HD22	1.85	0.58
24:22:1:MET:SD	24:22:56:GLN:NE2	2.74	0.58
44:2m:23:TYR:HB3	44:2m:67:GLU:HA	1.84	0.58
1:1A:645:G:H5'	1:1A:645:G:N3	2.18	0.58
1:1A:2442:A:H2'	1:1A:2442:A:N3	2.17	0.58
34:1c:180:ALA:HB1	34:1c:203:PHE:HE1	1.68	0.58
36:1e:81:GLU:HG2	36:1e:90:VAL:HG13	1.84	0.58
32:2a:131:C:H2'	32:2a:132:C:H6	1.68	0.58
32:2a:1512:U:H2'	32:2a:1513:A:C8	2.38	0.58
32:1a:533:A:O2'	32:1a:535:A:OP2	2.17	0.58
32:1a:538:G:H5''	43:1I:114:LYS:HB2	1.86	0.58
1:2A:1065:U:H3	1:2A:1073:A:H61	1.51	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:2F:132:VAL:HG21	5:2F:163:VAL:HG22	1.86	0.58
32:2a:1251:A:O2'	32:2a:1369:C:O2'	2.21	0.58
40:2i:4:TYR:HB2	40:2i:19:LEU:HB2	1.86	0.58
1:1A:1053:C:OP1	9:1N:35:ARG:NH1	2.37	0.58
28:16:13:CYS:SG	28:16:47:THR:HG21	2.44	0.58
36:1e:78:HIS:HD1	39:1h:104:ARG:HD2	1.67	0.58
41:1j:39:PRO:HA	41:1j:70:ARG:HD3	1.85	0.58
1:2A:1818:U:O2'	3:2D:154:LYS:O	2.20	0.58
32:2a:1143:G:H2'	32:2a:1144:G:H8	1.68	0.58
40:2i:5:TYR:HE1	40:2i:16:ARG:HB3	1.68	0.58
40:2i:51:ARG:HG2	40:2i:56:LEU:HD21	1.85	0.58
1:1A:1232:G:H5''	17:1V:81:TYR:CE1	2.37	0.58
1:1A:2703:C:OP2	61:1A:4159:HOH:O	2.17	0.58
1:2A:1669:A:OP2	61:2A:3849:HOH:O	2.17	0.58
1:2A:2206:G:H5''	1:2A:2207:G:C8	2.38	0.58
10:2O:36:GLY:HA3	10:2O:109:LYS:HD2	1.85	0.58
32:2a:1004:A:H62	32:2a:1037:C:H3'	1.67	0.58
32:2a:1068:G:H8	32:2a:1068:G:OP2	1.85	0.58
49:2r:25:THR:HG23	49:2r:26:LEU:HD13	1.84	0.58
9:1N:70:LYS:HD3	9:1N:87:LEU:HD12	1.84	0.58
32:1a:17:U:H2'	32:1a:18:C:C6	2.39	0.58
32:2a:1435:G:H2'	32:2a:1436:U:C6	2.38	0.58
33:2b:155:LEU:HD21	33:2b:159:PRO:HG3	1.85	0.58
35:2d:60:GLU:HG3	35:2d:202:LEU:HD12	1.85	0.58
1:1A:2104:A:N1	61:1A:4269:HOH:O	2.32	0.58
1:1A:2534:U:O2'	1:1A:2659:U:OP1	2.20	0.58
32:1a:176:C:H2'	32:1a:177:C:H6	1.68	0.58
32:1a:262:A:H2'	32:1a:263:A:C8	2.39	0.58
32:1a:992:U:H4'	32:1a:993:G:H5'	1.85	0.58
39:1h:41:ARG:NH2	39:1h:123:GLU:OE2	2.36	0.58
1:2A:800:A:H8	1:2A:800:A:OP1	1.87	0.58
1:2A:1828:G:OP1	61:2A:3850:HOH:O	2.17	0.58
1:2A:2315:G:H2'	1:2A:2316:C:C6	2.39	0.58
1:2A:2596:U:OP2	61:2A:3843:HOH:O	2.16	0.58
13:2R:29:LEU:HB3	13:2R:75:LEU:HD21	1.84	0.58
24:22:65:ASN:OD1	24:22:69:ARG:NH1	2.36	0.58
32:2a:663:A:H5''	49:2r:61:LYS:HZ1	1.69	0.58
32:2a:992:U:H4'	32:2a:993:G:O5'	2.03	0.58
32:2a:1301:U:O2'	32:2a:1302:U:H5'	2.04	0.58
36:2e:101:ILE:O	36:2e:120:THR:OG1	2.22	0.58
53:2y:23:ARG:HG3	53:2y:78:ILE:HG13	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:437:G:OP1	61:1A:4157:HOH:O	2.17	0.58
32:1a:828:A:H2'	32:1a:829:G:O4'	2.03	0.58
32:1a:840:C:H4'	32:1a:841:U:OP2	2.02	0.58
44:1m:37:THR:O	44:1m:55:ARG:NH1	2.36	0.58
7:2H:127:GLU:C	7:2H:129:THR:H	2.11	0.58
4:1E:121:ASN:ND2	61:1E:3103:HOH:O	2.36	0.58
1:2A:1405:U:H2'	1:2A:1406:U:C6	2.37	0.58
3:2D:108:PRO:HB3	3:2D:143:HIS:CE1	2.39	0.58
32:2a:316:G:OP2	32:2a:351:G:O2'	2.21	0.58
1:1A:2156:A:O2'	1:1A:2181:G:N3	2.37	0.57
1:1A:2705:A:H2'	1:1A:2706:G:H8	1.69	0.57
16:1U:78:THR:HG22	16:1U:117:GLN:HE22	1.68	0.57
32:1a:745:C:H2'	32:1a:746:A:C8	2.39	0.57
32:1a:1240:U:OP2	38:1g:116:ALA:N	2.35	0.57
32:1a:1492:A:H4'	32:1a:1493:A:C2	2.39	0.57
36:1e:122:GLU:O	36:1e:126:ARG:NH1	2.36	0.57
40:1i:50:LEU:HG	40:1i:81:ILE:HD12	1.85	0.57
2:2B:58:A:OP2	61:2B:3102:HOH:O	2.16	0.57
2:2B:75:G:O3'	21:2Z:10:ARG:NH2	2.37	0.57
4:2E:111:ARG:HD3	4:2E:160:TYR:CE2	2.39	0.57
6:2G:137:GLU:HG2	6:2G:152:LEU:HD22	1.85	0.57
40:2i:7:THR:HG1	40:2i:83:ARG:NH1	2.02	0.57
32:1a:138:G:H1	32:1a:225:C:H42	1.52	0.57
32:1a:1003:G:C2'	32:1a:1004:A:H4'	2.34	0.57
33:1b:231:GLU:HB3	33:1b:232:PRO:HD2	1.85	0.57
44:2m:79:LYS:HA	44:2m:82:MET:HE2	1.86	0.57
58:1B:228:ARG:N	61:1B:3108:HOH:O	2.37	0.57
11:1P:75:ILE:O	61:1P:302:HOH:O	2.18	0.57
47:1p:20:VAL:HG21	47:1p:32:TYR:CD2	2.39	0.57
1:2A:1803:A:O2'	3:2D:259:THR:HG21	2.04	0.57
32:2a:991:U:H2'	32:2a:1212:U:C4	2.39	0.57
32:2a:1244:C:N4	32:2a:1293:G:H1	2.01	0.57
1:1A:664:U:H2'	1:1A:665:C:C6	2.39	0.57
1:1A:1114:G:O2'	1:1A:1142:A:O2'	1.99	0.57
1:2A:78:A:H2'	1:2A:79:G:C8	2.39	0.57
3:2D:69:ARG:NH2	3:2D:105:ILE:HD13	2.20	0.57
6:2G:7:LEU:HD23	6:2G:100:TRP:HE3	1.69	0.57
32:2a:67:C:H2'	32:2a:68:G:C8	2.39	0.57
12:1Q:122:GLY:O	61:1Q:301:HOH:O	2.17	0.57
1:2A:873:G:H1	1:2A:904:C:H42	1.51	0.57
1:2A:1073:A:H2'	1:2A:1074:G:C8	2.39	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2356:C:O3'	22:20:20:ARG:HD3	2.05	0.57
8:2I:94:ALA:HB2	8:2I:116:LEU:HD22	1.84	0.57
32:2a:1491:G:O2'	32:2a:1492:A:OP1	2.20	0.57
47:2p:18:ARG:HD3	47:2p:35:LYS:HD2	1.87	0.57
48:2q:6:LEU:HD23	48:2q:23:VAL:HG11	1.87	0.57
3:1D:253:GLN:HB3	61:1D:403:HOH:O	2.03	0.57
32:1a:189(A):C:H42	32:1a:189(J):G:H1	1.53	0.57
40:1i:121:ARG:NH1	40:1i:122:ALA:O	2.38	0.57
21:2Z:157:LEU:HD11	21:2Z:163:LEU:HB2	1.86	0.57
32:2a:663:A:H5''	49:2r:61:LYS:NZ	2.18	0.57
32:2a:1030(A):G:H2'	32:2a:1030(B):C:H5''	1.86	0.57
50:2s:38:SER:HB2	50:2s:71:LEU:HD13	1.86	0.57
51:2t:65:LYS:HA	51:2t:68:LYS:HD3	1.87	0.57
8:1I:116:LEU:HD11	8:1I:120:ILE:HG13	1.87	0.57
32:1a:1496:C:OP2	61:1a:3312:HOH:O	2.17	0.57
32:1a:1518:MA6:N6	32:1a:1519:MA6:H103	2.18	0.57
51:1t:57:ARG:HH12	51:1t:100:ILE:HD12	1.70	0.57
1:2A:1364:G:OP2	23:21:3:LYS:HG3	2.04	0.57
7:2H:86:GLU:OE2	7:2H:132:ARG:NH2	2.38	0.57
32:2a:1011:G:N2	32:2a:1018:C:N3	2.51	0.57
1:1A:1834:A:O2'	3:1D:259:THR:HG21	2.04	0.57
10:1O:20:MET:HE3	10:1O:44:LYS:HE3	1.87	0.57
21:1Z:136:PHE:HE1	21:1Z:138:GLU:HG3	1.69	0.57
35:1d:108:LEU:HD23	35:1d:110:PHE:CZ	2.40	0.57
1:2A:1266:G:O5'	18:2W:15:ARG:NH2	2.38	0.57
26:24:61:ARG:NH2	50:2s:9:VAL:HG11	2.19	0.57
32:2a:1030(C):G:N7	32:2a:1031:G:N2	2.52	0.57
1:1A:347:G:C8	5:1F:171:PRO:HG3	2.40	0.57
8:1I:77:LEU:HB3	8:1I:142:VAL:HG22	1.85	0.57
11:1P:63:PRO:HD3	30:18:27:THR:HG22	1.87	0.57
1:2A:652(T):C:H2'	1:2A:652(U):G:C8	2.40	0.57
1:2A:1014:U:H2'	1:2A:1015:G:H8	1.68	0.57
5:2F:190:GLU:O	61:2F:3101:HOH:O	2.17	0.57
32:2a:503:C:OP2	43:2l:116:SER:HB3	2.05	0.57
32:2a:601:C:H2'	32:2a:602:A:H8	1.68	0.57
32:2a:1070:U:H2'	32:2a:1071:C:C6	2.37	0.57
34:2c:181:ASN:HB3	34:2c:205:GLY:H	1.70	0.57
38:2g:65:ALA:HB1	38:2g:127:ALA:HB3	1.86	0.57
1:1A:1485:A:OP1	61:1A:4162:HOH:O	2.18	0.57
1:1A:2155:G:H3'	1:1A:2179:G:H21	1.69	0.57
47:1p:20:VAL:HG23	47:1p:35:LYS:HA	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:991:C:OP2	61:2A:3836:HOH:O	2.17	0.57
1:2A:1062:G:H1	1:2A:1088:A:H8	1.52	0.57
5:2F:185:ASP:HA	5:2F:188:ARG:HD3	1.87	0.57
32:2a:1412:C:H2'	32:2a:1413:A:C8	2.39	0.57
1:1A:240:A:C5	1:1A:241:G:H1'	2.40	0.56
32:1a:428:G:OP2	35:1d:10:ARG:NH1	2.37	0.56
1:2A:588:U:H2'	1:2A:589:C:C6	2.39	0.56
1:2A:2099:U:O4	1:2A:2190:G:O6	2.23	0.56
1:2A:2584:U:H2'	1:2A:2585:U:H2'	1.86	0.56
6:2G:54:GLU:O	6:2G:58:GLN:N	2.34	0.56
7:2H:11:VAL:HG21	7:2H:50:VAL:HG23	1.87	0.56
32:2a:201:C:H42	32:2a:216:G:H1	1.52	0.56
32:2a:1347:G:N2	32:2a:1373:G:H2'	2.20	0.56
34:2c:58:GLU:HB3	41:2j:92:THR:HG21	1.85	0.56
52:2u:6:ARG:NH2	52:2u:15:ARG:HH22	2.03	0.56
1:1A:1398:U:OP2	61:1A:4155:HOH:O	2.17	0.56
7:1H:40:GLU:CD	7:1H:60:ARG:HH12	2.12	0.56
18:1W:37:ARG:NH1	27:15:48:GLU:OE2	2.38	0.56
32:1a:181:G:H4'	32:1a:182:U:H5'	1.88	0.56
1:2A:1031:G:H21	31:29:36:GLN:HE22	1.53	0.56
1:2A:2161:C:O2'	1:2A:2173:A:O2'	2.22	0.56
15:2T:53:ARG:HB3	15:2T:53:ARG:NH1	2.21	0.56
16:2U:8:VAL:HG13	16:2U:11:ARG:HH21	1.69	0.56
17:2V:72:VAL:HG13	17:2V:85:LYS:HB3	1.87	0.56
22:20:23:VAL:HG22	22:20:38:VAL:HG22	1.88	0.56
31:29:14:CYS:HA	31:29:27:CYS:HB2	1.86	0.56
39:2h:95:VAL:HB	39:2h:99:GLU:HG2	1.86	0.56
1:1A:483:A:OP2	61:1A:4161:HOH:O	2.17	0.56
1:1A:1809:U:H2'	1:1A:1815:A:N6	2.20	0.56
3:1D:206:LEU:HD22	3:1D:211:ARG:HG2	1.87	0.56
32:1a:162:A:H3'	32:1a:163:C:H4'	1.86	0.56
32:1a:1227:A:OP2	44:1m:111:LYS:NZ	2.38	0.56
51:1t:57:ARG:HH22	51:1t:100:ILE:HD12	1.69	0.56
1:2A:574:C:N3	4:2E:145:LYS:NZ	2.51	0.56
1:2A:1356:G:OP1	61:2A:3848:HOH:O	2.17	0.56
1:2A:2295:C:H5	14:2S:13:ARG:HH12	1.51	0.56
1:2A:2810:A:N6	1:2A:2891:G:O2'	2.37	0.56
32:2a:471:G:H2'	32:2a:472:A:H8	1.70	0.56
32:2a:1352:C:N4	32:2a:1370:G:H1	2.04	0.56
33:2b:162:ILE:HD11	33:2b:184:VAL:HG22	1.87	0.56
34:2c:6:HIS:CD2	34:2c:9:GLY:H	2.22	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:2i:26:VAL:HB	40:2i:33:PHE:HB2	1.87	0.56
52:2u:17:THR:O	52:2u:22:ARG:NH1	2.39	0.56
1:1A:2037:A:N3	27:15:4:HIS:HE1	2.03	0.56
1:2A:483:A:H5''	20:2Y:50:ARG:HD3	1.86	0.56
1:2A:2136:C:N4	1:2A:2155:G:N1	2.51	0.56
32:2a:660:G:OP2	46:2o:5:LYS:NZ	2.39	0.56
38:2g:50:ILE:HD11	38:2g:58:PRO:HA	1.87	0.56
38:2g:89:MET:SD	38:2g:155:ARG:HB2	2.46	0.56
44:2m:80:ARG:HH22	50:2s:69:HIS:CE1	2.24	0.56
52:2u:9:ARG:HG2	52:2u:13:ILE:HD11	1.88	0.56
11:1P:82:GLY:HA2	11:1P:113:LYS:O	2.04	0.56
32:1a:600:C:H2'	32:1a:601:C:H6	1.70	0.56
32:1a:1070:U:H2'	32:1a:1071:C:C6	2.41	0.56
33:1b:166:ASP:HB3	33:1b:169:LYS:HB3	1.88	0.56
37:1f:69:GLU:O	37:1f:72:VAL:HG12	2.05	0.56
1:2A:572:A:OP2	17:2V:78:LYS:NZ	2.39	0.56
11:2P:63:PRO:HD3	30:28:27:THR:HG22	1.86	0.56
15:1T:93:ARG:NH2	61:1T:305:HOH:O	2.38	0.56
22:10:24:LYS:O	22:10:25:ARG:NH1	2.37	0.56
32:1a:406:G:H5'	35:1d:5:ILE:HD11	1.88	0.56
33:1b:167:PRO:HG3	33:1b:186:ALA:HB1	1.87	0.56
36:1e:148:VAL:HG21	39:1h:107:LEU:HB3	1.87	0.56
1:2A:1324:G:N7	61:2A:3963:HOH:O	2.33	0.56
1:2A:1889:A:H2'	1:2A:1890:A:C8	2.40	0.56
1:2A:2134:A:N7	1:2A:2157:G:H5'	2.20	0.56
32:2a:73:G:H1	32:2a:96:U:H3	1.54	0.56
32:2a:117:G:OP2	61:2a:3211:HOH:O	2.18	0.56
32:2a:926:G:C6	53:2y:87:LYS:HG3	2.40	0.56
33:2b:174:VAL:O	33:2b:178:ARG:HG2	2.06	0.56
36:2e:87:SER:HB3	36:2e:131:ILE:HD13	1.88	0.56
48:2q:22:LEU:HD13	48:2q:41:LYS:HG2	1.88	0.56
6:1G:59:GLU:OE2	6:1G:153:ARG:NH2	2.38	0.56
1:2A:855:G:H2'	1:2A:856:C:C6	2.41	0.56
1:2A:2206:G:H8	1:2A:2207:G:N7	2.04	0.56
1:2A:2602:A:H4'	1:2A:2603:G:OP1	2.05	0.56
4:2E:143:ASN:HD22	4:2E:147:PRO:HD3	1.70	0.56
32:2a:501:C:OP1	43:2l:117:ARG:NH2	2.36	0.56
32:2a:673:G:H2'	32:2a:674:G:C8	2.41	0.56
32:1a:60:A:H4'	32:1a:61:G:H5'	1.87	0.56
32:1a:1070:U:H2'	32:1a:1071:C:H6	1.71	0.56
1:2A:382:G:OP2	61:2A:3851:HOH:O	2.18	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2590:A:O3'	3:2D:239:ARG:NH2	2.39	0.56
1:2A:2689:U:OP2	1:2A:2719:G:N2	2.36	0.56
4:2E:52:LEU:HB3	4:2E:53:PRO:HD2	1.87	0.56
32:2a:224:C:H2'	32:2a:225:C:C6	2.41	0.56
32:2a:1014:A:H2	32:2a:1219:U:H1'	1.71	0.56
36:2e:93:PRO:HG2	39:2h:105:ARG:HE	1.70	0.56
1:1A:1476:C:H2'	1:1A:1477:U:C6	2.41	0.56
38:1g:48:LYS:O	38:1g:52:GLU:HG2	2.05	0.56
1:2A:1796:U:H2'	1:2A:1797:C:H6	1.69	0.56
1:2A:1864:U:OP1	1:2A:2410:G:O2'	2.20	0.56
23:21:3:LYS:HB2	23:21:61:ARG:HH22	1.70	0.56
32:2a:328:C:H4'	32:2a:329:A:H5'	1.88	0.56
32:2a:1030(C):G:H2'	32:2a:1030(D):A:H8	1.71	0.56
1:1A:2511:C:OP1	61:1A:4137:HOH:O	2.18	0.56
5:1F:143:ALA:HB1	5:1F:148:LEU:HB2	1.88	0.56
1:2A:2131:G:OP1	1:2A:2132:U:H5'	2.06	0.56
2:2B:116:G:N7	61:2B:3112:HOH:O	2.33	0.56
5:2F:143:ALA:HB1	5:2F:148:LEU:HB2	1.88	0.56
32:2a:110:C:O2'	47:2p:25:ARG:O	2.24	0.56
36:2e:93:PRO:HB2	39:2h:105:ARG:HH21	1.71	0.56
1:1A:1129:U:H1'	1:1A:1132:A:N6	2.21	0.55
32:1a:184:G:H2'	32:1a:185:A:H8	1.71	0.55
43:1l:53:ARG:HB3	43:1l:69:TYR:HE1	1.71	0.55
48:1q:58:GLU:OE2	48:1q:75:ARG:NH2	2.39	0.55
1:2A:1011:G:OP2	16:2U:66:ASN:ND2	2.37	0.55
1:2A:1187:G:H5'	17:2V:81:TYR:CE1	2.41	0.55
32:2a:1012:U:H2'	32:2a:1013:G:C8	2.41	0.55
32:2a:1014:A:C2	32:2a:1219:U:H1'	2.41	0.55
1:1A:831:A:H5'	1:1A:832:G:OP1	2.06	0.55
19:1X:31:HIS:CD2	19:1X:33:LYS:H	2.24	0.55
19:1X:41:ASN:O	19:1X:45:THR:HG23	2.05	0.55
32:1a:222:U:H2'	32:1a:223:U:C6	2.41	0.55
1:2A:328:U:H4'	20:2Y:68:HIS:CD2	2.41	0.55
1:2A:1278:A:OP1	13:2R:36:THR:HG23	2.06	0.55
1:2A:1514:U:H2'	1:2A:1515:G:H8	1.70	0.55
1:2A:2150:U:H2'	1:2A:2151:G:C8	2.41	0.55
3:2D:224:ALA:O	61:2D:402:HOH:O	2.18	0.55
6:2G:46:ALA:HB2	6:2G:53:LEU:HD12	1.88	0.55
19:2X:46:ALA:HB1	24:22:33:MET:HE1	1.88	0.55
1:1A:1613:A:OP1	3:1D:211:ARG:NH1	2.36	0.55
8:1I:57:ARG:O	8:1I:61:ARG:HG2	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:868:C:H2'	32:1a:869:G:O4'	2.06	0.55
32:1a:1074:G:O2'	32:1a:1101:A:N1	2.40	0.55
1:2A:2316:C:H2'	1:2A:2317:C:H6	1.72	0.55
1:2A:2537:U:H2'	1:2A:2538:C:C6	2.42	0.55
30:28:13:ARG:O	61:28:8101:HOH:O	2.18	0.55
32:2a:1402:4OC:HM22	32:2a:1403:C:H5'	1.88	0.55
32:1a:1027:C:O2	32:1a:1034:G:N1	2.40	0.55
1:2A:615:G:OP1	5:2F:40:GLN:HG3	2.06	0.55
1:2A:1153:C:OP2	61:2A:3828:HOH:O	2.18	0.55
7:2H:87:LEU:HD23	7:2H:164:TYR:HA	1.88	0.55
1:1A:312:C:H2'	1:1A:313:A:H8	1.71	0.55
1:1A:1425:A:H4'	1:1A:1426:G:OP2	2.06	0.55
10:1O:48:PRO:HB3	32:1a:1422:G:H5''	1.87	0.55
32:1a:1027:C:N3	32:1a:1034:G:O6	2.39	0.55
35:1d:173:TRP:CD2	35:1d:189:PRO:HG3	2.41	0.55
1:2A:212:G:H2'	1:2A:213:A:O4'	2.07	0.55
1:2A:2122:U:H3	1:2A:2176:A:N6	2.04	0.55
32:2a:438:G:H4'	35:2d:123:HIS:HD2	1.71	0.55
32:2a:664:G:H22	32:2a:741:G:H1	1.54	0.55
32:2a:1255:G:N1	32:2a:1279:A:N7	2.55	0.55
34:2c:180:ALA:HB1	34:2c:203:PHE:HE1	1.71	0.55
38:2g:113:GLU:HG2	38:2g:119:ARG:HG2	1.88	0.55
46:2o:39:LEU:HD13	46:2o:56:LEU:HB2	1.89	0.55
1:1A:173:C:H2'	1:1A:174:U:C6	2.42	0.55
1:1A:611:U:H2'	1:1A:612:C:C6	2.42	0.55
24:12:65:ASN:O	24:12:69:ARG:HG3	2.07	0.55
1:2A:984:A:H5''	1:2A:985:C:H5	1.71	0.55
1:2A:1041:C:N4	1:2A:1114:G:H1	1.97	0.55
19:2X:43:VAL:HG21	19:2X:81:VAL:HG11	1.89	0.55
32:1a:434:U:H2'	32:1a:435:C:C6	2.42	0.55
2:2B:28:C:OP1	14:2S:36:TYR:OH	2.23	0.55
5:2F:184:TYR:CE2	5:2F:188:ARG:HD2	2.42	0.55
32:2a:224:C:H2'	32:2a:225:C:H6	1.70	0.55
33:2b:229:VAL:HG12	33:2b:230:VAL:H	1.72	0.55
35:2d:22:LYS:O	35:2d:113:SER:HB3	2.06	0.55
39:2h:20:TYR:HA	39:2h:65:TYR:CZ	2.42	0.55
40:2i:15:ALA:HB2	40:2i:65:VAL:HG23	1.88	0.55
1:1A:1754:G:O6	61:1A:4158:HOH:O	2.17	0.55
1:1A:2705:A:H2'	1:1A:2706:G:C8	2.42	0.55
26:24:59:PHE:HA	26:24:61:ARG:N	2.21	0.55
32:2a:1503:A:H5'	32:2a:1531:A:H1'	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2121:U:H3	1:1A:2212:G:H1	1.55	0.55
1:1A:2899:C:H2'	1:1A:2900:G:O4'	2.07	0.55
32:1a:626:U:H2'	32:1a:627:G:C8	2.41	0.55
32:1a:1218:C:H2'	32:1a:1219:U:C6	2.41	0.55
35:1d:173:TRP:CD1	35:1d:173:TRP:H	2.24	0.55
40:1i:49:PRO:HD2	40:1i:81:ILE:HD11	1.89	0.55
46:1o:64:ARG:HH12	46:1o:68:ARG:NH2	2.05	0.55
1:2A:1068:G:H3'	1:2A:1096:A:OP2	2.07	0.55
1:2A:2584:U:H5''	1:2A:2602:A:C2	2.42	0.55
1:2A:2849:U:O4	15:2T:23:ARG:NH2	2.39	0.55
32:2a:977:A:O3'	32:2a:980:C:N4	2.39	0.55
32:2a:1015:A:H2'	32:2a:1016:A:C8	2.42	0.55
35:2d:88:VAL:HG22	36:2e:96:PRO:HB2	1.89	0.55
44:2m:13:LYS:HA	44:2m:44:ARG:HH11	1.71	0.55
1:1A:625:G:O2'	1:1A:702:A:N6	2.40	0.55
6:1G:16:ARG:NE	6:1G:31:VAL:HG21	2.20	0.55
32:1a:631:G:H2'	32:1a:632:A:C8	2.41	0.55
36:1e:8:GLU:OE2	36:1e:63:ARG:NH2	2.39	0.55
1:2A:23:G:OP1	1:2A:504:U:N3	2.40	0.55
1:2A:2074:U:H2'	1:2A:2075:U:C6	2.41	0.55
25:23:9:VAL:HG12	25:23:32:GLN:HE22	1.72	0.55
31:29:25:VAL:HB	31:29:34:GLN:HB2	1.89	0.55
32:2a:600:C:H2'	32:2a:601:C:C6	2.42	0.55
6:1G:9:ARG:NH1	6:1G:13:GLU:OE2	2.40	0.54
6:1G:67:LYS:HD3	26:14:5:ILE:HB	1.89	0.54
32:1a:56:U:H2'	32:1a:57:G:C8	2.41	0.54
32:1a:1118:C:H1'	32:1a:1179:A:C4	2.42	0.54
32:1a:1132:C:H2'	32:1a:1133:G:H8	1.72	0.54
1:2A:271(M):G:O2'	1:2A:271(N):U:O5'	2.22	0.54
1:2A:635:C:O2'	1:2A:639:U:OP1	2.23	0.54
1:2A:1166:C:H2'	1:2A:1167:U:C6	2.42	0.54
1:2A:1937:A:H1'	1:2A:1939:5MU:H72	1.89	0.54
4:2E:181:LEU:HD11	15:2T:6:LEU:HD23	1.89	0.54
8:2I:117:GLU:HG3	8:2I:118:LYS:H	1.71	0.54
47:2p:53:VAL:HG13	47:2p:79:VAL:HG22	1.89	0.54
3:1D:4:LYS:HB3	3:1D:18:VAL:HG23	1.89	0.54
30:18:28:GLY:O	30:18:36:LYS:NZ	2.37	0.54
32:1a:649:G:H2'	32:1a:650:G:H8	1.72	0.54
1:2A:277:C:HO2'	1:2A:278:A:P	2.27	0.54
1:2A:1639:U:H2'	1:2A:1640:C:H5''	1.90	0.54
32:2a:1305:G:N2	32:2a:1331:G:H1'	2.22	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:2i:28:VAL:HG13	40:2i:63:ILE:HG22	1.90	0.54
9:1N:46:VAL:HG23	9:1N:48:MET:HG2	1.89	0.54
20:1Y:23:ARG:NH1	61:1Y:601:HOH:O	2.30	0.54
32:1a:263:A:OP1	51:1t:79:ARG:NH1	2.40	0.54
6:2G:80:PHE:O	6:2G:82:LEU:N	2.40	0.54
17:2V:95:LEU:HD22	17:2V:97:LYS:HD3	1.89	0.54
32:2a:986:A:N3	50:2s:52:TYR:OH	2.33	0.54
34:2c:5:ILE:HD11	45:2n:49:HIS:HE1	1.72	0.54
1:1A:924:U:H2'	1:1A:925:A:H5''	1.89	0.54
9:1N:13:TRP:CE2	9:1N:133:GLN:HG2	2.43	0.54
32:1a:411:A:OP1	35:1d:30:LYS:NZ	2.36	0.54
33:1b:36:ARG:O	33:1b:38:GLY:N	2.40	0.54
1:2A:2375:G:N1	61:2A:3961:HOH:O	2.33	0.54
22:20:49:LYS:HG2	22:20:50:ASN:ND2	2.22	0.54
32:2a:1516:G:H2'	32:2a:1518:MA6:OP2	2.07	0.54
33:2b:24:TRP:CD1	33:2b:24:TRP:H	2.24	0.54
1:1A:354:A:H2	1:1A:1255:A:O2'	1.90	0.54
1:1A:2151:C:N3	1:1A:2181:G:O6	2.40	0.54
8:1I:72:LEU:C	8:1I:74:ASN:H	2.15	0.54
32:1a:619:U:C2	35:1d:135:LEU:HD22	2.43	0.54
37:1f:1:MET:HE3	37:1f:66:GLU:HG2	1.90	0.54
1:2A:2171:A:H4'	1:2A:2172:U:OP1	2.07	0.54
32:2a:1510:U:H2'	32:2a:1511:G:C8	2.42	0.54
33:2b:119:GLU:HG3	33:2b:153:ARG:HH12	1.72	0.54
42:2k:62:GLN:HG3	42:2k:97:ALA:HB2	1.90	0.54
1:1A:1099:C:N3	1:1A:1152:G:O6	2.41	0.54
1:1A:2348:A:H61	22:10:43:THR:CG2	2.20	0.54
16:1U:69:CYS:HB3	16:1U:74:LEU:HD12	1.90	0.54
32:1a:107:G:N7	51:1t:15:ARG:NH2	2.56	0.54
32:1a:677:U:H3	32:1a:713:G:H22	1.56	0.54
32:1a:993:G:O2'	32:1a:995:C:N4	2.29	0.54
1:2A:11:G:C2'	1:2A:12:U:H5'	2.36	0.54
11:2P:97:PRO:HD3	11:2P:126:VAL:O	2.07	0.54
14:2S:43:GLU:OE2	22:20:49:LYS:NZ	2.37	0.54
32:2a:118:U:H3'	32:2a:288:A:H61	1.73	0.54
32:2a:415:A:H2'	32:2a:416:G:O4'	2.07	0.54
32:2a:718:G:H5'	42:2k:117:ASN:OD1	2.07	0.54
32:2a:1028:C:H2'	32:2a:1033:G:H22	1.71	0.54
32:2a:1129:C:N3	32:2a:1143:G:N2	2.53	0.54
1:1A:238:C:O2	30:18:12:LYS:NZ	2.37	0.54
5:1F:164:ARG:HE	58:1F:314:ARG:HH12	1.55	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:1T:24:PRO:HA	15:1T:49:VAL:HG22	1.89	0.54
33:1b:160:ASP:N	33:1b:160:ASP:OD1	2.40	0.54
1:2A:2123:G:O6	1:2A:2175:C:N3	2.41	0.54
32:2a:41:G:H2'	32:2a:42:G:H8	1.72	0.54
32:2a:102:G:O2'	32:2a:151:A:N3	2.36	0.54
32:2a:1079:G:O3'	36:2e:14:ARG:NH2	2.40	0.54
32:2a:1452:C:H4'	32:2a:1457:G:C8	2.42	0.54
1:1A:1346:U:H4'	1:1A:1347:A:H5''	1.89	0.54
1:1A:2892:A:OP1	13:1R:96:ARG:NH1	2.38	0.54
3:1D:69:ARG:HG2	3:1D:69:ARG:HH11	1.73	0.54
24:12:22:GLU:OE2	24:12:68:ARG:NH2	2.41	0.54
32:1a:503:C:OP1	43:1l:119:LYS:NZ	2.29	0.54
33:1b:231:GLU:HB3	33:1b:232:PRO:CD	2.37	0.54
36:1e:12:LEU:HB3	36:1e:31:LEU:HB2	1.90	0.54
36:1e:107:ARG:NH1	61:1e:3101:HOH:O	2.41	0.54
1:2A:876:C:H2'	1:2A:877:U:O4'	2.08	0.54
1:2A:1063:G:N2	1:2A:1075:C:N3	2.56	0.54
8:2I:40:THR:HG23	8:2I:43:ASN:HB2	1.90	0.54
19:2X:31:HIS:CD2	19:2X:33:LYS:H	2.26	0.54
32:2a:624:C:H2'	32:2a:625:G:H8	1.72	0.54
47:2p:43:LYS:HG2	47:2p:48:TRP:CD2	2.42	0.54
1:1A:215:G:H21	1:1A:217:A:H62	1.55	0.54
1:1A:957:A:H2'	12:1Q:9:TYR:OH	2.08	0.54
1:1A:1110:C:N4	1:1A:1111:U:O2	2.41	0.54
1:1A:2144:U:H3	1:1A:2198:A:H61	1.56	0.54
1:1A:2389:A:H2'	1:1A:2390:A:C8	2.43	0.54
37:1f:68:PRO:HG2	37:1f:71:ARG:HD2	1.89	0.54
40:1i:3:GLN:NE2	40:1i:20:ARG:HH21	2.05	0.54
1:2A:78:A:H2'	1:2A:79:G:H8	1.73	0.54
1:2A:2314:C:H2'	1:2A:2315:G:C8	2.43	0.54
3:2D:69:ARG:HH21	3:2D:105:ILE:HD13	1.73	0.54
6:2G:101:ILE:HG22	6:2G:105:LYS:HE2	1.89	0.54
14:2S:89:ARG:NH1	61:2S:203:HOH:O	2.39	0.54
25:23:6:VAL:HG22	25:23:56:VAL:HG22	1.90	0.54
1:1A:482:C:H4'	61:1A:4543:HOH:O	2.07	0.54
8:1I:27:ARG:HD2	23:1I:71:TYR:CE2	2.43	0.54
10:1O:64:ARG:HD3	10:1O:79:PHE:CD1	2.43	0.54
1:2A:271(L):U:H5'	8:2I:50:ARG:HH22	1.73	0.54
1:2A:614(C):A:C4	5:2F:180:GLY:HA2	2.42	0.54
5:2F:40:GLN:HE22	5:2F:182:ASN:HB2	1.73	0.54
23:21:31:GLY:O	61:21:8102:HOH:O	2.19	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:2f:61:LEU:HB3	37:2f:63:TYR:CE2	2.43	0.54
1:1A:936:C:O2'	1:1A:937:A:O5'	2.26	0.53
6:1G:16:ARG:HB2	6:1G:17:PRO:HD3	1.89	0.53
9:1N:12:ARG:NH1	9:1N:50:ASP:OD2	2.40	0.53
13:1R:33:ARG:NH2	27:15:57:VAL:O	2.27	0.53
1:2A:729:G:C6	3:2D:208:LYS:HB2	2.42	0.53
1:2A:1316:U:H2'	1:2A:1317:A:H8	1.73	0.53
1:2A:2130:U:H2'	1:2A:2158:A:H61	1.73	0.53
10:2O:115:VAL:HG13	10:2O:121:VAL:HG21	1.89	0.53
17:2V:28:GLU:O	17:2V:61:VAL:HG21	2.08	0.53
32:2a:1029:C:N4	32:2a:1030:C:H41	2.05	0.53
32:2a:1224:G:H4'	44:2m:102:ARG:NH1	2.14	0.53
32:2a:1362:C:H2'	32:2a:1363:C:H5''	1.89	0.53
39:2h:7:ALA:HB2	39:2h:85:ARG:HG3	1.90	0.53
4:1E:143:ASN:HD22	4:1E:147:PRO:HD3	1.73	0.53
32:1a:316:G:OP2	32:1a:351:G:O2'	2.23	0.53
32:1a:426:G:OP1	35:1d:38:TYR:OH	2.21	0.53
35:1d:156:GLU:O	35:1d:160:GLN:HG2	2.07	0.53
44:1m:11:ARG:C	44:1m:13:LYS:H	2.16	0.53
47:1p:42:ARG:HB2	47:1p:44:THR:HG23	1.90	0.53
49:1r:32:ARG:HA	49:1r:69:THR:HG21	1.90	0.53
1:2A:641:C:O2'	1:2A:2350:C:OP1	2.17	0.53
1:2A:1057:A:N7	1:2A:1086:A:H2'	2.23	0.53
6:2G:15:VAL:HG22	6:2G:175:LEU:HB3	1.89	0.53
32:2a:662:G:H2'	32:2a:663:A:C8	2.43	0.53
32:2a:949:A:H1'	32:2a:1364:U:H3	1.71	0.53
51:2t:43:LEU:O	51:2t:47:GLY:N	2.41	0.53
1:1A:2291:G:O6	22:10:14:ARG:HG3	2.08	0.53
61:1A:6219:HOH:O	18:1W:92:ARG:HD2	2.08	0.53
3:1D:71:ASP:HB3	3:1D:103:ARG:NH2	2.23	0.53
3:1D:85:ASP:OD2	3:1D:88:ARG:HD2	2.08	0.53
23:11:3:LYS:O	23:11:12:PRO:HD3	2.09	0.53
32:1a:1318:A:H5''	50:1s:3:ARG:NH1	2.22	0.53
44:1m:78:ILE:HG22	44:1m:82:MET:HE2	1.90	0.53
1:2A:1001:A:OP2	61:2A:3852:HOH:O	2.19	0.53
1:2A:1188:U:H4'	17:2V:79:VAL:HG22	1.89	0.53
13:2R:56:LYS:NZ	13:2R:90:ARG:O	2.41	0.53
32:2a:279:A:N6	48:2q:98:LEU:O	2.41	0.53
1:1A:2340:A:H2'	1:1A:2341:G:C8	2.43	0.53
21:1Z:144:LEU:HD11	21:1Z:150:LEU:HD22	1.90	0.53
32:1a:747:C:H3'	32:1a:748:C:C6	2.43	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:322:A:OP2	5:2F:169:ASN:HB2	2.08	0.53
1:2A:1246:A:OP1	5:2F:38:ARG:NH1	2.41	0.53
1:2A:1538:G:H2'	1:2A:1539:G:H8	1.73	0.53
1:2A:2125:G:H22	1:2A:2172:U:H3'	1.72	0.53
1:2A:2140:C:H2'	1:2A:2141:G:H8	1.73	0.53
1:2A:2540:C:H2'	1:2A:2541:A:O4'	2.08	0.53
5:2F:116:ASP:OD2	11:2P:1:MET:N	2.38	0.53
18:2W:12:ILE:HD13	18:2W:17:VAL:HG13	1.90	0.53
22:20:9:SER:OG	22:20:10:THR:N	2.40	0.53
32:2a:501:C:H2'	32:2a:502:G:H8	1.74	0.53
32:2a:580:U:H5''	46:2o:58:MET:HG2	1.91	0.53
33:2b:88:ALA:HB2	33:2b:219:VAL:HG13	1.90	0.53
33:2b:134:GLU:HA	33:2b:137:ARG:HH21	1.74	0.53
47:2p:43:LYS:HG2	47:2p:48:TRP:CG	2.44	0.53
1:1A:1071:G:C4	1:1A:1180:C:H1'	2.44	0.53
1:1A:1360:C:OP1	61:1A:4118:HOH:O	2.19	0.53
32:1a:651:C:H2'	32:1a:652:U:C6	2.43	0.53
1:2A:667:U:O2	30:28:2:PRO:HD2	2.09	0.53
8:2I:72:LEU:HD21	8:2I:107:VAL:HG11	1.90	0.53
12:2Q:34:LEU:HB2	12:2Q:118:LEU:HD22	1.89	0.53
19:2X:12:VAL:HG22	19:2X:29:TRP:CE2	2.44	0.53
32:2a:189:G:H2'	32:2a:189(A):C:C6	2.44	0.53
40:2i:28:VAL:HA	40:2i:63:ILE:O	2.08	0.53
53:2y:13:THR:OG1	53:2y:16:ILE:HG22	2.09	0.53
1:1A:630:U:OP1	5:1F:102:PRO:HA	2.08	0.53
1:1A:1845:G:H4'	3:1D:51:VAL:HG21	1.91	0.53
1:1A:2814:C:H2'	1:1A:2815:C:C6	2.44	0.53
4:1E:101:ARG:CZ	4:1E:171:GLU:HB2	2.39	0.53
1:2A:995:C:O2	9:2N:3:THR:OG1	2.21	0.53
1:2A:1028:A:N6	1:2A:1125:G:H2'	2.24	0.53
2:2B:4:C:H2'	2:2B:5:C:C6	2.43	0.53
32:2a:425:G:O3'	35:2d:45:GLN:NE2	2.41	0.53
32:2a:517:G:N1	32:2a:533:A:OP2	2.39	0.53
32:2a:601:C:H2'	32:2a:602:A:C8	2.44	0.53
46:2o:5:LYS:O	46:2o:9:GLN:HG2	2.09	0.53
1:1A:323:A:N1	1:1A:346:A:O2'	2.38	0.53
1:1A:669:A:H4'	1:1A:670:C:H5	1.74	0.53
1:1A:1310:G:OP1	27:15:19:ARG:NH2	2.27	0.53
1:1A:1899:A:H5'	1:1A:1900:G:OP2	2.09	0.53
11:1P:50:ARG:HD3	30:18:7:HIS:CD2	2.44	0.53
14:1S:11:LYS:HG3	14:1S:91:PRO:HD3	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1131:G:H1	32:1a:1143:G:H21	1.55	0.53
35:1d:173:TRP:CE3	35:1d:174:LEU:HG	2.44	0.53
40:1i:3:GLN:HG3	40:1i:20:ARG:HG2	1.90	0.53
1:2A:1525:G:H2'	1:2A:1526:G:C8	2.43	0.53
1:2A:2136:C:C4	1:2A:2155:G:N1	2.70	0.53
7:2H:154:PRO:HB3	7:2H:163:TYR:CZ	2.44	0.53
32:2a:1030:C:N3	32:2a:1031:G:C2	2.76	0.53
50:1s:41:VAL:HG12	50:1s:44:MET:HG3	1.90	0.53
1:2A:11:G:N7	61:2A:3971:HOH:O	2.34	0.53
1:2A:125:G:O6	29:27:10:ARG:NH1	2.42	0.53
1:2A:300:A:H1'	1:2A:319:C:H1'	1.90	0.53
1:2A:479:A:N3	1:2A:481:G:H5''	2.24	0.53
1:2A:1910:G:H2'	1:2A:1911:PSU:H6	1.73	0.53
1:2A:2673:G:O2'	61:2A:3853:HOH:O	2.19	0.53
32:2a:1051:C:N4	32:2a:1207:2MG:HN1	2.06	0.53
1:1A:636:G:O2'	1:1A:640:A:N1	2.38	0.53
1:1A:1941:A:N1	32:1a:1495:U:O2'	2.31	0.53
11:1P:56:SER:N	61:1P:304:HOH:O	2.29	0.53
12:1Q:21:THR:HG21	12:1Q:101:ARG:N	2.23	0.53
32:1a:437:U:H5'	35:1d:155:LEU:HD21	1.91	0.53
47:1p:23:ASP:OD1	47:1p:25:ARG:HG2	2.09	0.53
48:1q:9:VAL:HG21	48:1q:84:LEU:HD12	1.89	0.53
1:2A:323:G:O2'	1:2A:1205:U:N3	2.33	0.53
12:2Q:31:ASP:OD1	12:2Q:134:ARG:NH1	2.30	0.53
32:2a:434:U:H2'	32:2a:435:C:C6	2.43	0.53
32:2a:615:C:H2'	32:2a:616:G:O4'	2.09	0.53
32:2a:826:C:O2	39:2h:15:ASN:ND2	2.42	0.53
32:2a:1122:U:C4	32:2a:1123:A:N7	2.77	0.53
43:2l:70:ILE:HG12	43:2l:100:ILE:HD12	1.91	0.53
34:1c:47:LEU:HD13	34:1c:68:VAL:HG11	1.91	0.53
1:2A:1688:U:O2	1:2A:1700:A:H5'	2.10	0.53
9:2N:4:TYR:O	16:2U:64:ARG:NH2	2.35	0.53
34:2c:17:ASP:OD1	34:2c:18:TRP:N	2.42	0.53
1:1A:1285:G:H2'	1:1A:1286:U:O4'	2.09	0.52
10:1O:2:ILE:HD12	10:1O:6:THR:HG21	1.90	0.52
32:1a:221:C:H2'	32:1a:222:U:H6	1.74	0.52
1:2A:607:U:OP1	5:2F:102:PRO:HA	2.08	0.52
6:2G:12:TYR:HA	6:2G:16:ARG:CG	2.39	0.52
32:2a:460:G:H2'	32:2a:461:A:H2'	1.91	0.52
39:2h:86:ILE:HG21	39:2h:133:LEU:HD22	1.90	0.52
48:2q:12:SER:HB3	48:2q:20:THR:HB	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1529:G:H1	1:1A:1552:C:N4	2.07	0.52
32:1a:1402:4OC:HM22	32:1a:1403:C:H5'	1.91	0.52
33:2b:223:ILE:HA	33:2b:226:ARG:HB2	1.91	0.52
34:2c:5:ILE:HD11	45:2n:49:HIS:CE1	2.44	0.52
40:2i:26:VAL:HA	40:2i:61:ALA:O	2.09	0.52
1:1A:821:A:HO2'	1:1A:822:G:H8	1.57	0.52
1:1A:1495:G:O2'	1:1A:1575:A:N1	2.40	0.52
2:1B:77:U:OP1	21:1Z:19:ARG:NH2	2.42	0.52
4:1E:111:ARG:HD2	4:1E:160:TYR:CD2	2.45	0.52
7:1H:7:LEU:HD12	7:1H:8:PRO:HD2	1.91	0.52
10:1O:64:ARG:HG2	10:1O:83:ALA:HB3	1.92	0.52
24:12:64:LEU:HD21	24:12:68:ARG:HE	1.74	0.52
32:1a:270:A:H2'	32:1a:271:C:C6	2.45	0.52
32:1a:664:G:N2	32:1a:741:G:H1	2.05	0.52
32:1a:1019:C:H2'	32:1a:1020:U:O4'	2.10	0.52
47:1p:43:LYS:HG2	47:1p:48:TRP:CE2	2.44	0.52
1:2A:315:G:H2'	1:2A:316:C:C6	2.45	0.52
1:2A:2319:G:N1	14:2S:3:ARG:HA	2.24	0.52
1:2A:2546:U:OP1	61:2A:3854:HOH:O	2.19	0.52
12:2Q:58:PHE:O	12:2Q:60:ARG:N	2.42	0.52
32:2a:141:A:H1'	32:2a:182:U:O2	2.10	0.52
32:2a:1007:C:N3	32:2a:1022:G:O6	2.42	0.52
33:2b:24:TRP:HZ3	33:2b:29:ALA:HB2	1.75	0.52
49:2r:23:LYS:NZ	61:2r:8101:HOH:O	2.38	0.52
53:2y:61:LEU:HD13	53:2y:81:LEU:HD22	1.91	0.52
1:1A:2227:G:H2'	1:1A:2228:G:C2	2.44	0.52
6:1G:43:LEU:HD11	6:1G:153:ARG:HD3	1.91	0.52
6:1G:101:ILE:HD13	26:14:25:TYR:HB2	1.91	0.52
7:1H:159:GLU:HG2	7:1H:169:VAL:HG11	1.91	0.52
32:1a:6:G:H4'	32:1a:298:A:H4'	1.90	0.52
32:1a:1117:G:H4'	40:1i:104:ARG:NH1	2.24	0.52
41:1j:35:SER:HB3	41:1j:73:ASP:HB2	1.92	0.52
1:2A:885:C:H2'	1:2A:886:C:H4'	1.92	0.52
5:2F:192:LEU:HD13	5:2F:194:MET:HE2	1.92	0.52
8:2I:130:TYR:HB3	8:2I:138:ILE:HB	1.90	0.52
20:2Y:44:ILE:HD13	20:2Y:64:GLU:HG3	1.91	0.52
20:2Y:77:PRO:HD2	20:2Y:106:LEU:HD23	1.91	0.52
32:2a:881:G:P	43:2l:12:ARG:HH22	2.32	0.52
32:2a:1118:C:N3	32:2a:1156:G:N2	2.57	0.52
32:2a:1245:A:H2'	32:2a:1246:C:O4'	2.09	0.52
32:2a:1504:G:OP1	32:2a:1507:A:H4'	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:2i:42:ARG:HH22	40:2i:74:ILE:HB	1.74	0.52
1:1A:1452:U:H2'	1:1A:1453:C:C6	2.44	0.52
6:1G:179:PRO:HG3	26:14:43:TYR:OH	2.10	0.52
32:1a:1136:U:H5''	32:1a:1137:C:C2	2.44	0.52
2:2B:2:C:H2'	2:2B:3:C:C6	2.45	0.52
4:2E:52:LEU:O	4:2E:76:ARG:N	2.41	0.52
6:2G:15:VAL:HG21	6:2G:176:LEU:HD23	1.91	0.52
10:2O:76:ALA:O	15:2T:74:ARG:HG3	2.09	0.52
35:2d:173:TRP:CD1	35:2d:174:LEU:HG	2.45	0.52
36:2e:137:GLU:OE1	36:2e:141:GLN:NE2	2.39	0.52
1:1A:276:C:H2'	1:1A:277:G:O4'	2.09	0.52
1:1A:1140:U:H1'	1:1A:1143:U:C5	2.44	0.52
4:1E:40:GLU:OE1	4:1E:40:GLU:N	2.30	0.52
6:1G:41:GLN:HB3	6:1G:43:LEU:HD13	1.91	0.52
15:1T:96:ARG:HB3	15:1T:96:ARG:HH11	1.73	0.52
16:1U:33:ARG:NH1	61:1U:306:HOH:O	2.42	0.52
32:1a:166:G:H2'	32:1a:167:G:C8	2.44	0.52
32:1a:1297:C:O2'	38:1g:114:ARG:NH1	2.42	0.52
32:1a:1338:G:H2'	32:1a:1339:A:C8	2.44	0.52
32:1a:1513:A:H2'	32:1a:1514:C:C6	2.45	0.52
46:1o:83:GLU:C	46:1o:85:LEU:H	2.17	0.52
50:1s:12:ASP:O	50:1s:14:HIS:N	2.43	0.52
1:2A:1778:U:H2'	1:2A:1784:A:N6	2.25	0.52
1:2A:1783:A:OP1	61:2A:3857:HOH:O	2.19	0.52
4:2E:50:GLY:O	4:2E:51:PHE:HB2	2.08	0.52
4:2E:111:ARG:HD3	4:2E:160:TYR:CD2	2.44	0.52
15:2T:28:VAL:HG13	15:2T:86:ILE:HG23	1.92	0.52
23:21:40:ARG:NH2	23:21:42:GLN:HG2	2.25	0.52
26:24:48:ARG:HG3	26:24:52:THR:HG23	1.91	0.52
32:2a:1212:U:H4'	32:2a:1213:A:C8	2.45	0.52
32:2a:1319:A:OP2	50:2s:3:ARG:HD2	2.08	0.52
32:2a:1410:G:N1	32:2a:1490:C:N3	2.48	0.52
40:2i:17:VAL:HG11	40:2i:80:GLY:C	2.35	0.52
1:1A:847:A:H8	1:1A:847:A:OP1	1.92	0.52
1:1A:2658:C:H2'	1:1A:2659:U:O4'	2.10	0.52
4:1E:119:ARG:HD2	4:1E:120:TRP:CE2	2.45	0.52
32:1a:79:G:N1	32:1a:90:U:C2	2.77	0.52
32:1a:1277:C:H1'	32:1a:1282:C:O2	2.09	0.52
32:1a:1400:5MC:N3	53:1y:63:ALA:HA	2.24	0.52
36:1e:110:LEU:HD13	36:1e:118:ILE:HG21	1.92	0.52
44:1m:40:ASN:HB3	44:1m:43:THR:HG23	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1503:U:H2'	1:2A:1504:C:C6	2.45	0.52
2:2B:24:G:H4'	2:2B:25:A:C8	2.45	0.52
32:2a:56:U:H2'	32:2a:57:G:C8	2.45	0.52
32:2a:141:A:H1'	32:2a:182:U:H1'	1.92	0.52
32:2a:438:G:H4'	35:2d:123:HIS:CD2	2.45	0.52
32:2a:977:A:O2'	32:2a:979:C:OP2	2.25	0.52
32:2a:1376:U:H2'	32:2a:1377:A:C8	2.39	0.52
32:2a:1401:G:C2	32:2a:1402:4OC:H1'	2.44	0.52
41:2j:38:ILE:HD11	41:2j:71:LEU:HD22	1.92	0.52
42:2k:20:TYR:CZ	42:2k:83:ILE:HD12	2.44	0.52
1:1A:153:C:OP2	23:11:92:LYS:NZ	2.33	0.52
1:1A:196:A:H2'	1:1A:197:C:O4'	2.10	0.52
1:1A:742:G:OP1	1:1A:1426:G:O2'	2.28	0.52
11:1P:140:ALA:O	25:23:38:GLU:HG2	2.10	0.52
29:17:34:ARG:NE	29:17:39:ARG:HG3	2.22	0.52
46:1o:25:THR:HG21	46:1o:70:LEU:HB2	1.90	0.52
1:2A:2526:G:H5'	1:2A:2742:C:O2'	2.09	0.52
2:2B:33:G:H1'	2:2B:50:G:H22	1.75	0.52
2:2B:42:C:O2'	61:2B:3103:HOH:O	2.18	0.52
5:2F:11:VAL:HG22	5:2F:125:LEU:HB2	1.92	0.52
32:2a:707:C:H2'	32:2a:708:C:C6	2.45	0.52
32:2a:1086:U:H3	32:2a:1099:G:H22	1.57	0.52
48:2q:24:GLU:HG3	48:2q:39:SER:HB3	1.92	0.52
1:1A:174:U:H4'	1:1A:207:A:H4'	1.92	0.52
1:1A:2132:G:OP1	1:1A:2140:U:N3	2.42	0.52
6:1G:18:GLU:OE2	6:1G:21:ARG:NH1	2.43	0.52
32:1a:255:G:H1'	48:1q:16:GLN:NE2	2.23	0.52
32:1a:1277:C:O2'	32:1a:1279:A:H1'	2.10	0.52
1:2A:774:A:H2'	1:2A:774:A:N3	2.25	0.52
1:2A:1420:U:O2'	1:2A:1421:G:OP1	2.26	0.52
1:2A:1952:A:OP1	10:2O:42:SER:OG	2.21	0.52
1:2A:2102:U:O2	1:2A:2187:G:O6	2.27	0.52
1:2A:2104:G:N2	1:2A:2105:C:C2	2.78	0.52
1:2A:2313:C:H2'	1:2A:2314:C:C6	2.45	0.52
1:2A:2462:U:H2'	1:2A:2463:C:C6	2.45	0.52
21:2Z:10:ARG:NH1	21:2Z:26:GLY:O	2.43	0.52
32:2a:600:C:H2'	32:2a:601:C:H6	1.74	0.52
32:2a:976:G:P	45:2n:32:SER:H	2.33	0.52
32:2a:1203:C:H2'	32:2a:1204:A:O4'	2.09	0.52
1:1A:1073:A:C2	1:1A:2500:A:H5'	2.45	0.52
1:1A:2205:C:H2'	1:1A:2206:G:H8	1.75	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:1E:47:VAL:HG12	4:1E:49:LEU:HD13	1.91	0.52
17:1V:21:ARG:HD3	17:1V:91:TYR:CD1	2.44	0.52
19:1X:2:LYS:NZ	19:1X:38:GLU:OE2	2.38	0.52
35:1d:162:LEU:HD13	35:1d:181:MET:HG2	1.92	0.52
1:2A:271(R):G:OP1	23:21:76:ARG:NH1	2.43	0.52
1:2A:2445:G:OP1	5:2F:74:ARG:NH2	2.43	0.52
32:2a:1030(A):G:H1'	32:2a:1030(C):G:N7	2.24	0.52
32:2a:1410:G:H2'	32:2a:1411:C:C6	2.45	0.52
1:1A:1554:A:H4'	1:1A:1556:A:C5	2.45	0.51
32:1a:1371:G:OP1	40:1i:11:LYS:HB3	2.10	0.51
1:2A:659:C:H2'	1:2A:660:G:H8	1.74	0.51
1:2A:2023:G:H5'	1:2A:2617:C:H4'	1.92	0.51
1:2A:2286:A:H4'	1:2A:2287:A:O4'	2.10	0.51
5:2F:24:LEU:HD23	5:2F:115:ALA:HA	1.92	0.51
5:2F:40:GLN:NE2	5:2F:182:ASN:HB2	2.24	0.51
32:2a:714:G:N2	32:2a:777:A:N3	2.53	0.51
32:2a:1442:G:O2'	32:2a:1442(A):G:O5'	2.27	0.51
37:2f:67:MET:HE1	37:2f:75:LEU:HD22	1.91	0.51
1:1A:207:A:N6	61:1A:4387:HOH:O	2.43	0.51
1:1A:933:C:H3'	1:1A:934:A:H5''	1.92	0.51
1:1A:2576:A:C2	1:1A:2659:U:H4'	2.45	0.51
32:1a:8:A:N6	35:1d:205:GLU:O	2.43	0.51
33:1b:102:LEU:HB3	33:1b:180:LEU:HD12	1.92	0.51
36:1e:33:VAL:HG13	36:1e:112:LEU:HD12	1.92	0.51
50:1s:51:VAL:O	50:1s:58:VAL:N	2.40	0.51
1:2A:1748:G:H2'	1:2A:1749:A:O4'	2.10	0.51
1:2A:1794:U:H2'	1:2A:1795:C:C6	2.45	0.51
1:2A:2299:G:N1	1:2A:2318:G:N7	2.58	0.51
1:2A:2687:U:H2'	1:2A:2688:U:O4'	2.10	0.51
3:2D:124:PRO:HB2	3:2D:126:GLN:HG2	1.93	0.51
10:2O:15:GLY:O	10:2O:47:ILE:HG13	2.10	0.51
32:2a:737:A:H2'	32:2a:738:C:C6	2.46	0.51
39:2h:10:LEU:HD22	39:2h:83:ILE:HD11	1.91	0.51
47:2p:20:VAL:HG21	47:2p:32:TYR:CG	2.45	0.51
1:1A:1087:C:H5'	1:1A:1088:G:OP2	2.10	0.51
1:1A:2137:G:H2'	1:1A:2139:A:H61	1.75	0.51
3:1D:77:ALA:HB2	3:1D:97:TYR:CD1	2.46	0.51
3:1D:242:ARG:HD2	3:1D:246:PRO:HG3	1.93	0.51
7:1H:3:ARG:NH2	7:1H:65:HIS:HB3	2.25	0.51
7:1H:86:GLU:OE2	7:1H:132:ARG:NH2	2.44	0.51
24:12:59:ARG:NH2	61:12:103:HOH:O	2.42	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:649:G:H2'	32:1a:650:G:C8	2.46	0.51
32:1a:1124:G:N7	32:1a:1145:C:O2'	2.40	0.51
32:1a:1458:G:OP1	51:1t:35:THR:OG1	2.25	0.51
33:1b:73:THR:OG1	33:1b:170:GLU:OE2	2.24	0.51
1:2A:2400:G:H4'	28:26:18:ARG:HG2	1.92	0.51
9:2N:58:ASP:N	9:2N:58:ASP:OD1	2.43	0.51
17:2V:5:VAL:HG11	17:2V:57:VAL:HG21	1.92	0.51
32:2a:444:C:H42	32:2a:490:G:H1	1.56	0.51
32:2a:979:C:H42	45:2n:18:VAL:HB	1.76	0.51
46:2o:25:THR:HG21	46:2o:70:LEU:HB2	1.92	0.51
1:1A:1370:G:N7	61:1A:4278:HOH:O	2.34	0.51
31:19:15:LYS:HE2	31:19:17:ILE:HD13	1.92	0.51
32:1a:687:A:N3	32:1a:688:G:H1'	2.25	0.51
32:1a:1251:A:H2'	32:1a:1252:A:C8	2.45	0.51
1:2A:300:A:H2'	1:2A:334:C:H1'	1.91	0.51
1:2A:1445(A):C:H2'	1:2A:1446:C:H6	1.75	0.51
1:2A:2318:G:H21	14:2S:3:ARG:HE	1.57	0.51
1:2A:2467:C:H4'	12:2Q:123:HIS:CD2	2.46	0.51
2:2B:75:G:H22	21:2Z:73:GLN:NE2	2.08	0.51
3:2D:148:GLU:HB2	3:2D:151:LYS:HD2	1.92	0.51
6:2G:101:ILE:HD13	26:24:25:TYR:HB2	1.91	0.51
12:2Q:141:GLN:HE22	21:2Z:74:VAL:HG13	1.76	0.51
16:2U:34:LYS:NZ	16:2U:37:GLU:OE1	2.41	0.51
25:23:8:LEU:HG	25:23:31:LEU:HD22	1.91	0.51
32:2a:936:C:H2'	32:2a:937:A:O4'	2.11	0.51
32:2a:1108:G:H5'	34:2c:176:HIS:HD2	1.75	0.51
53:2y:74:ILE:O	53:2y:78:ILE:HG12	2.09	0.51
1:1A:2164:C:H2'	1:1A:2165:C:C6	2.45	0.51
3:1D:137:PRO:O	3:1D:140:THR:HG23	2.10	0.51
32:1a:396:G:O2'	32:1a:398:C:OP1	2.24	0.51
1:2A:740:U:OP2	61:2A:3857:HOH:O	2.19	0.51
1:2A:1096:A:C5	1:2A:1097:U:H5	2.29	0.51
1:2A:1104:C:H2'	1:2A:1105:U:C6	2.45	0.51
1:2A:2127:G:H2'	1:2A:2128:C:O4'	2.10	0.51
1:2A:2267:A:H5''	1:2A:2268:A:H5'	1.91	0.51
32:2a:1004:A:H5''	32:2a:1025:U:C5	2.45	0.51
32:2a:1218:C:H2'	32:2a:1219:U:C6	2.45	0.51
32:2a:1240:U:C2	38:2g:32:ARG:HG3	2.46	0.51
35:2d:114:ARG:HA	35:2d:117:ALA:HB3	1.92	0.51
38:2g:46:ALA:HA	38:2g:49:ILE:HD12	1.93	0.51
53:2y:53:THR:HG22	53:2y:62:VAL:HG12	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1117:G:O2'	1:1A:1135:G:H2'	2.09	0.51
1:1A:1219:A:H1'	1:1A:1220:U:H5'	1.92	0.51
1:2A:2680:C:H5'	4:2E:189:PRO:HA	1.93	0.51
26:24:34:GLU:HG2	26:24:35:VAL:HG12	1.92	0.51
26:24:40:HIS:HB3	26:24:43:TYR:CD2	2.46	0.51
32:2a:1275:A:H2'	32:2a:1276:G:O4'	2.10	0.51
41:2j:16:LEU:HD23	41:2j:70:ARG:HG2	1.93	0.51
41:2j:37:PRO:HA	41:2j:72:VAL:HG12	1.92	0.51
1:1A:959:U:OP1	61:1A:4165:HOH:O	2.19	0.51
21:1Z:1:MET:N	21:1Z:135:GLU:OE2	2.43	0.51
32:1a:558:G:OP1	61:1a:3313:HOH:O	2.19	0.51
33:1b:24:TRP:CZ3	33:1b:26:PRO:HA	2.46	0.51
1:2A:120:U:OP2	61:2A:3856:HOH:O	2.19	0.51
1:2A:207:A:OP2	61:2A:3855:HOH:O	2.19	0.51
1:2A:888:C:H2'	1:2A:889:C:N3	2.26	0.51
1:2A:1066:U:O2'	1:2A:1068:G:OP2	2.27	0.51
1:2A:1073:A:H2'	1:2A:1074:G:H8	1.76	0.51
2:2B:102:A:OP2	61:2B:3104:HOH:O	2.19	0.51
32:2a:443:C:H2'	32:2a:444:C:H6	1.75	0.51
32:2a:719:C:O2'	49:2r:49:LYS:HB3	2.11	0.51
32:1a:452:A:H4'	47:1p:72:ARG:NH1	2.26	0.51
32:1a:1129:C:H5''	40:1i:16:ARG:HH12	1.75	0.51
32:1a:1305:G:N2	32:1a:1331:G:H1'	2.26	0.51
35:1d:168:ARG:N	35:1d:168:ARG:HH11	2.09	0.51
37:1f:78:GLU:O	37:1f:81:ILE:HG22	2.11	0.51
44:1m:11:ARG:HA	44:1m:45:VAL:HB	1.93	0.51
1:2A:2115:G:H2'	1:2A:2115:G:N3	2.26	0.51
8:2I:62:LYS:O	8:2I:66:GLU:HG2	2.11	0.51
23:21:53:VAL:HG22	23:21:74:VAL:HG13	1.93	0.51
32:2a:181:G:N2	32:2a:182:U:O4	2.23	0.51
32:2a:1108:G:H5'	34:2c:176:HIS:CD2	2.46	0.51
32:2a:1352:C:H2'	32:2a:1353:G:C8	2.45	0.51
44:2m:40:ASN:HB3	44:2m:43:THR:HG23	1.93	0.51
50:2s:22:LEU:O	50:2s:26:GLY:N	2.36	0.51
1:1A:1264:G:OP2	16:1U:19:LYS:NZ	2.37	0.51
1:1A:2316:G:H22	1:1A:2324:U:H3	1.57	0.51
8:1I:130:TYR:HD2	8:1I:138:ILE:HD12	1.76	0.51
32:1a:77:G:H1	32:1a:92:C:N4	2.07	0.51
32:1a:448:A:OP2	32:1a:485:G:N2	2.30	0.51
32:1a:1003:G:H2'	32:1a:1004:A:H4'	1.92	0.51
32:1a:1298:C:H2'	38:1g:114:ARG:NH2	2.26	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:1d:107:ARG:NH2	35:1d:194:LEU:HD21	2.26	0.51
1:2A:452:G:OP2	61:2A:3859:HOH:O	2.19	0.51
1:2A:668:G:H5'	1:2A:669:G:OP2	2.11	0.51
1:2A:911:A:H2'	12:2Q:9:TYR:OH	2.10	0.51
1:2A:1101:U:H2'	1:2A:1102:C:C6	2.45	0.51
6:2G:145:THR:OG1	6:2G:146:TYR:N	2.40	0.51
21:2Z:102:LEU:HD23	21:2Z:137:ILE:HB	1.92	0.51
32:2a:56:U:H2'	32:2a:57:G:H8	1.75	0.51
34:2c:103:VAL:HG12	34:2c:104:GLN:H	1.76	0.51
1:1A:2377:G:N7	30:18:39:LYS:NZ	2.48	0.51
6:1G:16:ARG:O	6:1G:20:ILE:HG13	2.10	0.51
8:1I:46:ALA:O	8:1I:50:ARG:HG2	2.11	0.51
15:1T:51:ARG:HG3	15:1T:98:LYS:HE3	1.93	0.51
34:1c:69:HIS:CD2	34:1c:104:GLN:HG2	2.46	0.51
34:1c:70:VAL:O	34:1c:106:VAL:N	2.40	0.51
40:1i:5:TYR:HE1	40:1i:16:ARG:HB3	1.76	0.51
1:2A:2022:U:O2'	1:2A:2617:C:H5'	2.11	0.51
3:2D:80:ALA:HB3	3:2D:94:LEU:HD23	1.91	0.51
3:2D:102:LYS:C	3:2D:103:ARG:HG2	2.36	0.51
10:2O:86:ILE:HG22	10:2O:94:ARG:HD3	1.93	0.51
14:2S:14:VAL:O	14:2S:18:ILE:HG12	2.11	0.51
30:28:23:VAL:HG11	30:28:47:LYS:HD3	1.93	0.51
32:2a:993:G:H1	32:2a:1045:C:H42	1.58	0.51
32:2a:1062:U:H2'	32:2a:1063:C:C6	2.46	0.51
32:2a:1144:G:N2	32:2a:1146:A:H62	2.07	0.51
1:1A:1829:U:OP1	61:1A:4164:HOH:O	2.19	0.50
7:1H:124:GLU:HG3	7:1H:132:ARG:HB3	1.94	0.50
8:1I:77:LEU:HD12	8:1I:104:GLN:NE2	2.26	0.50
11:1P:88:LEU:HD11	11:1P:114:ILE:HD12	1.93	0.50
11:1P:138:LEU:HD23	11:1P:145:PRO:HB3	1.94	0.50
13:1R:59:ASP:OD1	13:1R:59:ASP:N	2.41	0.50
32:1a:7:G:H5'	32:1a:298:A:O4'	2.10	0.50
32:1a:353:A:H5'	32:1a:353:A:H8	1.76	0.50
32:1a:489:C:OP1	35:1d:132:ARG:NH2	2.44	0.50
32:1a:527:7MG:O6	43:1l:49:ASN:ND2	2.40	0.50
32:1a:747:C:H3'	32:1a:748:C:H6	1.76	0.50
32:1a:1003:G:O2'	32:1a:1004:A:H4'	2.11	0.50
32:1a:1014:A:C2	32:1a:1219:U:H1'	2.46	0.50
32:1a:1033:G:H2'	32:1a:1034:G:H8	1.75	0.50
38:1g:75:VAL:HG21	38:1g:144:MET:HG3	1.92	0.50
1:2A:962:G:OP1	61:2A:3858:HOH:O	2.19	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1412:A:H2'	1:2A:1413:G:H8	1.76	0.50
1:2A:2698:U:H2'	1:2A:2699:C:C6	2.46	0.50
15:2T:60:THR:HG22	15:2T:77:PRO:HA	1.93	0.50
35:2d:165:MET:SD	35:2d:168:ARG:NH1	2.75	0.50
36:2e:50:GLU:HB2	36:2e:53:LEU:HD13	1.92	0.50
44:2m:84:ILE:HB	50:2s:66:MET:HE2	1.93	0.50
1:1A:1682:G:N2	61:1A:4403:HOH:O	2.44	0.50
32:1a:186:C:H2'	32:1a:187:C:C6	2.46	0.50
32:1a:1239:A:H62	32:1a:1299:A:N6	2.08	0.50
32:2a:1256:A:H61	32:2a:1278:U:C1'	2.15	0.50
45:2n:4:LYS:O	45:2n:7:ILE:HG12	2.10	0.50
1:1A:2044:U:O2'	1:1A:2629:C:H5'	2.12	0.50
2:1B:15:A:OP1	2:1B:108:U:O2'	2.26	0.50
4:1E:116:VAL:HG13	4:1E:122:PHE:HB2	1.92	0.50
32:1a:769:G:H4'	32:1a:1513:A:H4'	1.93	0.50
34:1c:3:ASN:OD1	34:1c:3:ASN:N	2.44	0.50
1:2A:1707:G:H2'	1:2A:1708:C:C6	2.46	0.50
4:2E:105:THR:HG21	4:2E:164:ARG:HE	1.76	0.50
35:2d:72:GLU:OE2	35:2d:207:TYR:OH	2.28	0.50
38:2g:133:GLY:HA2	38:2g:136:LYS:HB2	1.92	0.50
40:2i:3:GLN:HE22	40:2i:20:ARG:HH21	1.59	0.50
41:2j:11:PHE:CE1	41:2j:67:THR:HG22	2.46	0.50
41:2j:35:SER:HB3	41:2j:73:ASP:HB2	1.93	0.50
42:2k:84:VAL:HG21	42:2k:95:ILE:HD11	1.93	0.50
45:2n:45:ARG:O	45:2n:49:HIS:HD2	1.93	0.50
4:1E:119:ARG:HG3	4:1E:160:TYR:HB2	1.92	0.50
6:1G:77:ILE:HB	6:1G:82:LEU:HB2	1.93	0.50
8:1I:40:THR:O	8:1I:44:LEU:HB2	2.11	0.50
32:1a:1305:G:OP1	52:1u:2:GLY:N	2.44	0.50
40:1i:17:VAL:HG11	40:1i:80:GLY:C	2.35	0.50
44:1m:15:VAL:HG11	44:1m:48:LEU:HD21	1.92	0.50
1:2A:1754:C:P	15:2T:96:ARG:HH12	2.35	0.50
1:2A:2314:C:H2'	1:2A:2315:G:H8	1.76	0.50
8:2I:14:ASP:O	8:2I:17:GLN:HB2	2.10	0.50
40:2i:18:PHE:HB2	40:2i:62:TYR:HB3	1.94	0.50
1:1A:1255:A:H5''	1:1A:1257:G:O4'	2.11	0.50
1:1A:1633:A:H2'	1:1A:1634:C:C6	2.47	0.50
1:1A:1964:5MC:OP2	1:1A:1965:U:O2'	2.24	0.50
1:1A:2204:G:H2'	1:1A:2205:C:C6	2.46	0.50
1:1A:2897:U:H2'	1:1A:2898:C:C6	2.46	0.50
3:1D:155:LEU:HD23	3:1D:177:LEU:HD22	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:355:C:O2'	32:1a:388:G:N3	2.32	0.50
32:1a:890:G:O2'	32:1a:906:G:O6	2.24	0.50
46:1o:18:PHE:HB2	46:1o:19:PRO:HD2	1.92	0.50
1:2A:84:A:H5'	20:2Y:8:LYS:HB3	1.93	0.50
1:2A:154(A):C:N3	1:2A:171:G:N2	2.60	0.50
1:2A:577:G:O2'	1:2A:1254:A:OP1	2.26	0.50
1:2A:886:C:H2'	1:2A:887:A:O4'	2.12	0.50
2:2B:2:C:H2'	2:2B:3:C:H6	1.77	0.50
7:2H:104:GLU:HA	7:2H:113:VAL:O	2.12	0.50
1:1A:2089:G:N7	61:1A:4289:HOH:O	2.35	0.50
32:1a:568:G:O2'	32:1a:574:A:N1	2.42	0.50
32:1a:1243:C:H2'	32:1a:1244:C:H6	1.76	0.50
33:1b:16:HIS:HB2	33:1b:204:ASN:HB3	1.94	0.50
36:1e:91:LEU:HD12	36:1e:120:THR:HG22	1.93	0.50
1:2A:245:G:O6	30:28:8:LYS:NZ	2.43	0.50
1:2A:2166:G:H2'	1:2A:2167:U:O4'	2.11	0.50
5:2F:183:VAL:O	5:2F:187:VAL:HG23	2.11	0.50
28:26:35:GLU:HA	28:26:49:HIS:O	2.12	0.50
32:2a:473:G:C2	32:2a:474:G:C4	2.99	0.50
33:2b:16:HIS:O	33:2b:18:GLY:N	2.45	0.50
1:1A:1836:U:O2	3:1D:50:THR:HB	2.11	0.50
32:1a:1236:A:H4'	32:1a:1304:G:H4'	1.93	0.50
35:1d:107:ARG:CZ	35:1d:194:LEU:HD21	2.41	0.50
1:2A:27:G:O2'	1:2A:28:A:OP2	2.28	0.50
1:2A:154(A):C:N4	1:2A:171:G:H1	2.08	0.50
1:2A:528:A:O2'	1:2A:529:A:H5'	2.11	0.50
1:2A:1427:A:H4'	1:2A:1428:C:O5'	2.12	0.50
1:2A:2327:A:O3'	21:2Z:200:GLY:HA2	2.11	0.50
7:2H:35:VAL:HG13	7:2H:71:LEU:HD22	1.93	0.50
17:2V:60:GLU:HB2	17:2V:97:LYS:HE2	1.94	0.50
32:2a:402:G:O2'	32:2a:620:C:N3	2.45	0.50
34:2c:71:ALA:HB1	34:2c:109:PRO:HG3	1.92	0.50
35:2d:8:VAL:HG22	35:2d:21:LEU:HD13	1.93	0.50
35:2d:173:TRP:CD1	35:2d:189:PRO:HG3	2.47	0.50
44:2m:14:ARG:HE	44:2m:42:ALA:HA	1.77	0.50
48:2q:4:LYS:H	48:2q:61:GLU:HG2	1.75	0.50
1:1A:7:G:H2'	1:1A:8:A:O4'	2.12	0.50
1:1A:105:C:H2'	1:1A:106:U:H6	1.75	0.50
1:1A:1128:U:C4	1:1A:1132:A:N1	2.78	0.50
33:1b:124:SER:N	33:1b:126:GLU:OE2	2.44	0.50
1:2A:1412:A:H2'	1:2A:1413:G:C8	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2129:C:N3	1:2A:2159:G:O6	2.45	0.50
1:2A:2189:U:H2'	1:2A:2190:G:C8	2.47	0.50
7:2H:10:PRO:HA	7:2H:49:VAL:HG22	1.92	0.50
11:2P:88:LEU:HD11	11:2P:114:ILE:HD12	1.92	0.50
32:2a:890:G:O2'	32:2a:906:G:O6	2.23	0.50
35:2d:31:CYS:SG	35:2d:33:MET:HB2	2.51	0.50
40:2i:16:ARG:HB2	40:2i:64:THR:HG22	1.94	0.50
41:2j:11:PHE:HE1	41:2j:67:THR:HG22	1.77	0.50
42:2k:65:ALA:HB3	42:2k:97:ALA:HB3	1.94	0.50
45:2n:26:ARG:HD3	45:2n:43:CYS:HB3	1.94	0.50
1:1A:383:A:H2'	1:1A:384:G:O4'	2.12	0.50
5:1F:150:GLY:HA2	5:1F:172:TRP:CE3	2.46	0.50
32:1a:1442:G:H2'	32:1a:1442:G:N3	2.27	0.50
35:1d:60:GLU:HG3	35:1d:202:LEU:HD12	1.94	0.50
1:2A:1005:C:O2'	9:2N:28:THR:HG21	2.11	0.50
1:2A:1075:C:H2'	1:2A:1076:C:H5'	1.92	0.50
15:2T:95:ARG:HG2	15:2T:95:ARG:HH11	1.76	0.50
32:2a:149:A:H2'	32:2a:150:C:C6	2.46	0.50
32:2a:325:A:H2'	32:2a:326:G:O4'	2.12	0.50
32:2a:757:U:H2'	32:2a:758:G:O4'	2.11	0.50
32:2a:975:A:N1	41:2j:48:THR:HB	2.26	0.50
32:2a:1188:A:H2'	32:2a:1189:C:O4'	2.11	0.50
1:1A:236:G:H4'	1:1A:413:G:C5	2.47	0.49
27:15:16:ARG:HG3	27:15:17:ASP:N	2.25	0.49
32:1a:608:A:OP2	61:1a:3314:HOH:O	2.20	0.49
37:1f:95:GLU:O	49:1r:32:ARG:NH1	2.39	0.49
46:1o:64:ARG:HH12	46:1o:68:ARG:HH21	1.59	0.49
1:2A:30:G:H2'	1:2A:31:C:C6	2.47	0.49
16:2U:6:THR:HG21	16:2U:10:ARG:HH21	1.77	0.49
32:2a:401:C:H1'	32:2a:622:A:H1'	1.94	0.49
32:2a:537:G:H5''	43:2l:113:ARG:NH1	2.27	0.49
1:1A:310:C:H2'	1:1A:311:C:H6	1.75	0.49
1:1A:331:G:H21	1:1A:354:A:H62	1.58	0.49
1:1A:715:G:H5'	1:1A:716:G:OP2	2.11	0.49
1:1A:911:G:N7	12:1Q:22:LYS:NZ	2.60	0.49
1:1A:2244:U:P	23:11:40:ARG:HH12	2.36	0.49
11:1P:121:LYS:HB3	11:1P:123:LEU:HG	1.94	0.49
32:1a:254:G:H21	48:1q:16:GLN:NE2	2.10	0.49
32:1a:269:C:H2'	32:1a:270:A:C8	2.47	0.49
32:1a:271:C:H2'	32:1a:272:C:H6	1.77	0.49
41:1j:55:LYS:HE3	41:1j:56:HIS:CE1	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:1k:84:VAL:HG11	42:1k:91:ARG:HD2	1.94	0.49
1:2A:900:A:H2'	1:2A:901:A:O4'	2.12	0.49
1:2A:927:G:H2'	1:2A:928:G:O4'	2.10	0.49
1:2A:1783:A:H5'	1:2A:2608:G:H4'	1.94	0.49
1:2A:2159:G:C2	1:2A:2160:G:H1'	2.47	0.49
2:2B:5:C:OP1	2:2B:61:G:O2'	2.29	0.49
4:2E:59:VAL:HG21	4:2E:74:PRO:HB3	1.94	0.49
6:2G:109:VAL:HG21	26:24:14:ILE:HG21	1.93	0.49
6:2G:131:TYR:HB3	6:2G:159:VAL:HG13	1.94	0.49
8:2I:127:VAL:HA	8:2I:141:LYS:HA	1.94	0.49
12:2Q:45:GLN:OE1	12:2Q:45:GLN:N	2.44	0.49
32:2a:258:G:H1	32:2a:268:C:H42	1.59	0.49
32:2a:1145:C:H4'	32:2a:1146:A:H8	1.77	0.49
33:2b:121:LEU:HA	33:2b:125:PRO:HG2	1.92	0.49
1:1A:1129:U:H1'	1:1A:1132:A:H61	1.76	0.49
1:1A:1312:G:O5'	18:1W:15:ARG:NH2	2.45	0.49
4:1E:11:MET:O	4:1E:12:THR:HG23	2.12	0.49
19:1X:40:LYS:HG3	19:1X:51:VAL:HB	1.94	0.49
25:13:6:VAL:CG1	25:13:54:VAL:HG11	2.42	0.49
29:17:35:ARG:NH1	61:17:201:HOH:O	2.44	0.49
32:1a:1149:C:H2'	32:1a:1150:U:C6	2.47	0.49
32:1a:1263:C:H2'	32:1a:1264:C:C6	2.48	0.49
32:1a:1412:C:H2'	32:1a:1413:A:C8	2.48	0.49
34:1c:8:ILE:HD11	34:1c:184:TYR:HB3	1.94	0.49
48:1q:62:SER:OG	48:1q:72:ARG:HG3	2.12	0.49
2:2B:3:C:H2'	2:2B:4:C:C6	2.47	0.49
8:2I:93:THR:HG22	8:2I:119:PRO:HB3	1.92	0.49
14:2S:3:ARG:NH1	14:2S:4:LEU:O	2.45	0.49
16:2U:5:LYS:HE2	61:2U:306:HOH:O	2.12	0.49
17:2V:62:LEU:HD12	17:2V:93:GLU:HG2	1.94	0.49
32:2a:137:C:H2'	32:2a:138:G:C8	2.47	0.49
32:1a:656:C:C2'	46:1o:28:GLN:HE22	2.26	0.49
32:1a:1315:U:H2'	32:1a:1316:G:O4'	2.13	0.49
35:1d:178:VAL:HG12	35:1d:179:GLU:H	1.77	0.49
1:2A:299:A:N1	1:2A:322:A:O2'	2.37	0.49
13:2R:95:THR:HG22	13:2R:116:LEU:HD23	1.95	0.49
41:2j:44:VAL:HG22	41:2j:66:ARG:HG2	1.94	0.49
45:2n:26:ARG:NH1	45:2n:46:GLU:OE1	2.37	0.49
1:1A:1070:G:O2'	1:1A:1190:G:O2'	2.30	0.49
25:13:3:ARG:HD2	25:13:60:GLU:CD	2.37	0.49
25:13:54:VAL:HG12	25:13:55:ARG:N	2.28	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:14:46:GLN:O	26:14:48:ARG:N	2.44	0.49
28:16:6:ARG:NH1	28:16:26:ASN:HB2	2.27	0.49
38:1g:50:ILE:HD11	38:1g:58:PRO:HA	1.93	0.49
42:1k:48:ILE:HD13	42:1k:63:LEU:HD12	1.94	0.49
1:2A:746:A:H2'	1:2A:2612:C:H5''	1.93	0.49
1:2A:2260:C:OP1	61:2A:3863:HOH:O	2.20	0.49
1:2A:2787:C:H1'	4:2E:62:PRO:HG3	1.92	0.49
5:2F:161:GLU:O	5:2F:165:ARG:HG3	2.13	0.49
26:24:59:PHE:CZ	50:2s:64:GLU:HG2	2.48	0.49
31:29:12:ASP:OD1	31:29:12:ASP:N	2.46	0.49
1:1A:636:G:N2	1:1A:640:A:O2'	2.45	0.49
1:1A:860:U:H2'	1:1A:861:C:C6	2.48	0.49
1:1A:967:G:O6	61:1A:4160:HOH:O	2.17	0.49
1:1A:1549:U:H2'	1:1A:1550:C:H6	1.77	0.49
1:1A:2880:C:H2'	1:1A:2881:C:O4'	2.13	0.49
3:1D:204:ILE:O	61:1D:401:HOH:O	2.18	0.49
4:1E:47:VAL:HG23	4:1E:84:PHE:O	2.13	0.49
9:1N:75:TYR:CE2	9:1N:77:GLY:HA2	2.48	0.49
25:13:49:LYS:O	61:13:201:HOH:O	2.20	0.49
32:1a:1320:C:H2'	32:1a:1321:C:O4'	2.12	0.49
41:1j:16:LEU:HD22	41:1j:68:HIS:HB2	1.95	0.49
1:2A:42:G:H2'	1:2A:43:A:O4'	2.12	0.49
1:2A:922:U:H2'	1:2A:923:C:C6	2.48	0.49
1:2A:1316:U:H2'	1:2A:1317:A:C8	2.47	0.49
1:2A:2243:U:H2'	1:2A:2244:U:C6	2.48	0.49
26:24:46:GLN:O	26:24:48:ARG:N	2.45	0.49
32:2a:189(B):C:H2'	32:2a:189(C):C:C6	2.48	0.49
32:2a:921:U:O2	36:2e:19:MET:HB2	2.13	0.49
1:1A:1219:A:H4'	1:1A:1220:U:OP1	2.12	0.49
1:1A:1222:A:H2'	1:1A:1222:A:N3	2.28	0.49
1:1A:2108:U:H2'	1:1A:2109:G:C8	2.48	0.49
4:1E:181:LEU:HD11	15:1T:6:LEU:HD23	1.95	0.49
9:1N:138:LEU:HB3	9:1N:140:VAL:HG13	1.94	0.49
24:12:36:ARG:HD3	61:12:107:HOH:O	2.12	0.49
32:1a:266:G:H2'	32:1a:266:G:N3	2.26	0.49
1:2A:1815:A:OP2	61:2A:3860:HOH:O	2.20	0.49
1:2A:1876:A:H2'	1:2A:1877:A:C8	2.47	0.49
1:2A:2062:A:H2'	1:2A:2062:A:N3	2.27	0.49
1:2A:2115:G:N2	1:2A:2119:A:H5'	2.27	0.49
1:2A:2704:C:H2'	1:2A:2705:A:O4'	2.13	0.49
26:24:18:CYS:HB2	26:24:20:ASN:H	1.76	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:632:A:H5'	32:2a:633:G:OP2	2.13	0.49
32:2a:1516:G:N2	32:2a:1519:MA6:OP2	2.44	0.49
35:2d:163:GLU:HA	35:2d:166:LYS:HD3	1.95	0.49
40:2i:3:GLN:NE2	40:2i:20:ARG:HH21	2.11	0.49
1:1A:465:G:H2'	1:1A:466:G:C8	2.47	0.49
1:1A:1110:C:C4	1:1A:1120:G:N1	2.81	0.49
26:14:15:ILE:HB	26:14:32:TYR:CD1	2.48	0.49
32:1a:996:A:H2'	32:1a:997:U:C6	2.48	0.49
40:1i:106:ALA:O	40:1i:108:VAL:HG23	2.13	0.49
41:1j:61:GLU:OE2	45:1n:58:LYS:NZ	2.41	0.49
44:1m:45:VAL:HG13	44:1m:48:LEU:HD12	1.94	0.49
36:2e:77:PRO:HD2	36:2e:142:LEU:HD22	1.94	0.49
41:2j:38:ILE:O	41:2j:38:ILE:HG13	2.13	0.49
1:1A:211:A:H3'	1:1A:448:U:H5'	1.95	0.49
1:1A:1766:G:H2'	1:1A:1769:G:O6	2.13	0.49
1:1A:2575:U:H4'	10:1O:28:SER:HA	1.95	0.49
10:1O:115:VAL:O	57:1a:1854:MPD:H13	2.13	0.49
32:1a:841:U:C5	32:1a:848:C:H1'	2.48	0.49
32:1a:920:U:H2'	32:1a:921:U:C6	2.47	0.49
44:1m:5:ALA:HB1	44:1m:61:GLU:HG2	1.94	0.49
1:2A:297:C:H2'	1:2A:298:G:O4'	2.13	0.49
1:2A:1062:G:C5	1:2A:1070:A:H1'	2.47	0.49
1:2A:1079:C:C4	1:2A:1080:C:C2	3.00	0.49
1:2A:1165:U:H2'	1:2A:1166:C:C6	2.47	0.49
1:2A:1428:C:O2'	1:2A:1569:A:OP2	2.18	0.49
1:2A:1680:U:N3	1:2A:1764:G:OP2	2.40	0.49
1:2A:2320:A:N3	1:2A:2320:A:H2'	2.27	0.49
1:2A:2689:U:H5'	1:2A:2689:U:O2	2.13	0.49
2:2B:75:G:H21	21:2Z:85:HIS:CE1	2.31	0.49
23:21:21:ARG:NH2	61:21:8105:HOH:O	2.45	0.49
32:2a:131:C:H2'	32:2a:132:C:C6	2.48	0.49
32:2a:1142:G:H2'	32:2a:1143:G:O4'	2.13	0.49
39:2h:20:TYR:HA	39:2h:65:TYR:CE1	2.47	0.49
53:2y:6:THR:HB	53:2y:40:ILE:HG12	1.95	0.49
1:1A:590:A:OP2	11:1P:29:LYS:NZ	2.44	0.49
1:1A:2084:A:N3	1:1A:2084:A:H2'	2.26	0.49
29:17:30:VAL:O	29:17:34:ARG:HG2	2.13	0.49
32:1a:547:A:OP1	61:1a:3315:HOH:O	2.20	0.49
32:1a:1030(C):G:N7	32:1a:1031:G:N2	2.61	0.49
33:1b:55:PHE:HD1	33:1b:58:ILE:HD12	1.78	0.49
40:1i:15:ALA:HB2	40:1i:65:VAL:HG23	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1y:23:ARG:HH11	53:1y:26:LYS:HD2	1.77	0.49
1:2A:1287:A:H8	13:2R:104:ARG:HD3	1.78	0.49
26:24:61:ARG:HH22	50:2s:9:VAL:HG11	1.77	0.49
32:2a:1224:G:N1	32:2a:1322:C:O4'	2.45	0.49
33:2b:16:HIS:CB	33:2b:210:SER:HB3	2.42	0.49
34:2c:71:ALA:HA	34:2c:106:VAL:HB	1.94	0.49
38:2g:108:ALA:O	38:2g:119:ARG:HD2	2.12	0.49
1:1A:1091:A:H4'	1:1A:1091:A:OP1	2.13	0.48
1:1A:2094:G:N2	61:1A:4429:HOH:O	2.45	0.48
1:1A:2326:C:H2'	1:1A:2327:G:C8	2.47	0.48
5:1F:38:ARG:NH2	61:1F:408:HOH:O	2.46	0.48
6:1G:43:LEU:C	6:1G:45:GLU:H	2.21	0.48
7:1H:40:GLU:OE2	7:1H:60:ARG:NH1	2.46	0.48
8:1I:115:ALA:HB2	8:1I:131:LYS:HE2	1.95	0.48
21:1Z:141:VAL:HB	21:1Z:144:LEU:HD12	1.95	0.48
28:16:23:THR:OG1	28:16:24:GLU:N	2.46	0.48
32:1a:233:C:H2'	32:1a:234:C:H6	1.78	0.48
32:1a:1010:G:N2	32:1a:1020:U:H1'	2.27	0.48
34:1c:18:TRP:O	34:1c:21:ARG:NH1	2.45	0.48
38:1g:75:VAL:HG13	38:1g:145:ALA:HA	1.94	0.48
39:1h:51:VAL:HG11	39:1h:60:ARG:NH1	2.28	0.48
51:1t:58:LYS:HA	51:1t:58:LYS:HD2	1.60	0.48
1:2A:455:C:N3	1:2A:472:A:H2'	2.28	0.48
61:2A:4393:HOH:O	5:2F:74:ARG:HG3	2.12	0.48
2:2B:84:C:OP1	25:23:15:TYR:OH	2.24	0.48
32:2a:110:C:H2'	32:2a:111:G:O4'	2.13	0.48
32:2a:949:A:N6	32:2a:1232:U:H3	2.10	0.48
32:2a:1004:A:H5''	32:2a:1025:U:O4	2.13	0.48
1:1A:1817:A:H1'	1:1A:1960:A:N6	2.28	0.48
1:1A:1874:C:H5'	3:1D:253:GLN:OE1	2.13	0.48
1:1A:2157:A:H62	1:1A:2178:G:N2	2.11	0.48
12:1Q:108:GLY:HA3	21:1Z:116:VAL:HG13	1.95	0.48
12:1Q:110:THR:HG23	12:1Q:113:GLN:OE1	2.13	0.48
25:13:3:ARG:NH1	25:13:60:GLU:OE2	2.45	0.48
32:1a:191:G:H2'	32:1a:192:U:O4'	2.13	0.48
32:1a:337:C:H2'	32:1a:338:A:C8	2.48	0.48
32:1a:946:A:H2'	32:1a:947:G:C8	2.48	0.48
32:1a:1391:U:H2'	32:1a:1392:G:C8	2.48	0.48
38:1g:50:ILE:HG22	38:1g:125:MET:HG3	1.94	0.48
1:2A:2161:C:HO2'	1:2A:2173:A:HO2'	1.53	0.48
3:2D:101:GLU:OE2	3:2D:103:ARG:HD3	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:29:27:CYS:SG	31:29:28:GLU:N	2.86	0.48
38:2g:26:PHE:O	38:2g:30:ILE:HG13	2.13	0.48
40:2i:127:LYS:NZ	53:2y:60:VAL:HG11	2.28	0.48
44:2m:3:ARG:HB2	44:2m:9:ILE:H	1.77	0.48
1:1A:952:G:O6	61:1A:4166:HOH:O	2.20	0.48
4:1E:59:VAL:HG21	4:1E:74:PRO:HB3	1.94	0.48
32:1a:57:G:H2'	32:1a:58:C:C6	2.48	0.48
32:1a:598:U:H2'	32:1a:599:C:H6	1.77	0.48
32:1a:1134:G:N3	32:1a:1134:G:H2'	2.27	0.48
32:1a:1329:A:P	44:1m:28:ALA:HB3	2.53	0.48
33:1b:54:THR:HG21	33:1b:201:ILE:HD11	1.95	0.48
36:1e:71:LEU:HD21	36:1e:115:VAL:HG22	1.95	0.48
1:2A:272(I):U:H3	1:2A:363(A):A:H61	1.61	0.48
1:2A:1292:U:H2'	1:2A:1293:C:C6	2.48	0.48
4:2E:54:GLN:OE1	4:2E:55:ASN:N	2.44	0.48
12:2Q:135:ASP:OD1	12:2Q:136:ALA:N	2.45	0.48
18:2W:45:TYR:OH	18:2W:49:LYS:NZ	2.33	0.48
32:2a:551:U:H2'	32:2a:552:U:C6	2.47	0.48
32:2a:685:G:O2'	32:2a:686:U:H5'	2.14	0.48
35:2d:146:ILE:HD12	35:2d:146:ILE:H	1.79	0.48
1:1A:71:U:OP1	61:1A:4163:HOH:O	2.19	0.48
1:1A:230:A:H5''	61:1A:6566:HOH:O	2.13	0.48
1:1A:572:A:N6	17:1V:19:LYS:H	2.11	0.48
1:1A:2710:U:H2'	1:1A:2711:C:C6	2.49	0.48
15:1T:16:ARG:HG2	15:1T:18:ASP:OD1	2.14	0.48
15:1T:68:TYR:CE2	57:1T:204:MPD:H51	2.48	0.48
32:1a:743:U:H2'	32:1a:744:C:C6	2.48	0.48
32:1a:1183:A:H3'	32:1a:1184:G:C5'	2.42	0.48
34:1c:6:HIS:CD2	34:1c:8:ILE:H	2.31	0.48
34:1c:180:ALA:HB1	34:1c:203:PHE:CE1	2.48	0.48
37:1f:96:PRO:HB3	49:1r:30:ASP:CG	2.39	0.48
53:1y:23:ARG:HG3	53:1y:78:ILE:HG13	1.96	0.48
1:2A:1063:G:H2'	1:2A:1065:U:C6	2.48	0.48
1:2A:1292:U:H2'	1:2A:1293:C:H6	1.78	0.48
1:2A:1786:A:H1'	1:2A:1938:A:N6	2.27	0.48
1:2A:2441:C:OP2	1:2A:2586:C:O2'	2.31	0.48
8:2I:77:LEU:HD21	8:2I:100:ALA:HB3	1.93	0.48
32:2a:137:C:H2'	32:2a:138:G:H8	1.77	0.48
32:2a:1338:G:H2'	32:2a:1339:A:C8	2.48	0.48
50:2s:49:ILE:O	50:2s:60:VAL:N	2.45	0.48
1:1A:70:A:N7	19:1X:31:HIS:HE1	2.11	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:91:G:H2'	1:1A:92:C:H6	1.79	0.48
1:1A:572:A:H61	17:1V:19:LYS:H	1.59	0.48
1:1A:794:U:O2	1:1A:2036:A:H1'	2.13	0.48
1:1A:1033:G:O2'	1:1A:1046:A:N3	2.43	0.48
1:1A:2018:C:H4'	1:1A:2019:G:OP1	2.12	0.48
1:1A:2164:C:C2	1:1A:2171:G:N1	2.81	0.48
1:1A:2326:C:H2'	1:1A:2327:G:H8	1.79	0.48
2:1B:106:G:H5'	21:1Z:31:ARG:HG2	1.96	0.48
7:1H:13:LYS:HA	7:1H:14:GLY:HA2	1.60	0.48
31:19:17:ILE:HD12	31:19:17:ILE:HA	1.72	0.48
32:1a:461:A:O2'	32:1a:470:C:H5'	2.14	0.48
32:1a:692:U:H1'	32:1a:695:A:N7	2.28	0.48
38:1g:74:GLU:OE2	38:1g:95:ARG:NE	2.46	0.48
42:1k:99:GLN:HG3	42:1k:105:VAL:HG11	1.95	0.48
43:1l:7:ILE:O	43:1l:11:VAL:HG23	2.14	0.48
44:1m:95:GLY:O	44:1m:110:ARG:HB3	2.13	0.48
1:2A:372:G:H8	23:21:65:SER:O	1.96	0.48
1:2A:373:U:H2'	1:2A:374:A:H8	1.78	0.48
1:2A:1666:G:H1'	10:2O:3:GLN:HE21	1.78	0.48
1:2A:1807:G:OP1	61:2A:3861:HOH:O	2.20	0.48
1:2A:2157:G:H5''	1:2A:2158:A:H5'	1.94	0.48
1:2A:2639:A:H2'	1:2A:2640:G:O4'	2.14	0.48
6:2G:77:ILE:HG21	6:2G:80:PHE:CD2	2.48	0.48
15:1T:51:ARG:NH1	61:1T:306:HOH:O	2.38	0.48
16:1U:36:ARG:NH2	61:1U:307:HOH:O	2.47	0.48
32:1a:184:G:H2'	32:1a:185:A:C8	2.47	0.48
32:1a:1024:G:H2'	32:1a:1024:G:N3	2.28	0.48
35:1d:85:LYS:HD3	35:1d:92:VAL:HG11	1.95	0.48
1:2A:495:G:N3	18:2W:61:ASN:ND2	2.58	0.48
1:2A:2544:G:H1'	1:2A:2646:C:H4'	1.95	0.48
1:2A:2646:C:H2'	1:2A:2647:U:O4'	2.13	0.48
31:29:29:ASN:HB3	31:29:32:HIS:ND1	2.28	0.48
34:2c:184:TYR:HA	34:2c:200:ALA:O	2.14	0.48
49:2r:54:ARG:HB3	49:2r:54:ARG:HH11	1.78	0.48
1:1A:1103:A:N1	1:1A:1127:U:O4	2.47	0.48
17:1V:21:ARG:HD3	17:1V:91:TYR:CE1	2.48	0.48
20:1Y:6:HIS:H	20:1Y:6:HIS:CD2	2.30	0.48
32:1a:1036:G:H2'	32:1a:1036:G:N3	2.28	0.48
32:1a:1183:A:H3'	32:1a:1184:G:H5''	1.94	0.48
33:1b:115:LEU:O	33:1b:119:GLU:HG2	2.12	0.48
34:1c:17:ASP:OD2	34:1c:21:ARG:HD3	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:1c:56:ASP:HB2	34:1c:67:THR:HB	1.96	0.48
1:2A:208:C:H2'	1:2A:209:C:C6	2.48	0.48
1:2A:1287:A:C8	13:2R:104:ARG:HD3	2.48	0.48
7:2H:89:ILE:HB	7:2H:129:THR:HA	1.96	0.48
11:2P:95:VAL:CG2	11:2P:125:VAL:HG12	2.44	0.48
12:2Q:138:ASP:OD2	21:2Z:81:ARG:NH1	2.47	0.48
32:2a:1366:C:H2'	32:2a:1367:C:C6	2.48	0.48
40:2i:86:VAL:HG13	40:2i:90:PRO:HA	1.95	0.48
1:1A:1674:G:H2'	1:1A:1675:U:C6	2.49	0.48
1:1A:1814:A:H5'	1:1A:2620:G:H4'	1.96	0.48
7:1H:23:ARG:HD2	7:1H:34:GLU:OE1	2.14	0.48
32:1a:176:C:H2'	32:1a:177:C:C6	2.47	0.48
32:1a:1133:G:H1	32:1a:1141:C:H42	1.62	0.48
34:1c:13:GLY:HA3	45:1n:57:ARG:HH21	1.79	0.48
38:1g:16:LEU:HD21	40:1i:45:ALA:HB2	1.95	0.48
53:1y:76:GLU:O	53:1y:80:LYS:HG3	2.14	0.48
1:2A:251:A:C5	1:2A:252:G:H1'	2.48	0.48
1:2A:265:A:N1	1:2A:427:U:O2'	2.45	0.48
1:2A:1581:G:H2'	1:2A:1582:C:O4'	2.14	0.48
8:2I:31:LEU:HD21	8:2I:38:LEU:HG	1.94	0.48
12:2Q:111:GLU:OE2	12:2Q:133:ARG:NH2	2.46	0.48
14:2S:23:ARG:HH11	14:2S:84:GLN:HB3	1.79	0.48
20:2Y:7:VAL:HG21	20:2Y:72:VAL:HG12	1.96	0.48
26:24:48:ARG:HB3	26:24:52:THR:OG1	2.13	0.48
32:2a:1004:A:OP1	32:2a:1024:G:N2	2.46	0.48
32:2a:1512:U:H2'	32:2a:1513:A:H8	1.77	0.48
6:1G:27:ASN:HB3	6:1G:30:GLU:HG3	1.96	0.48
6:1G:114:ILE:HG12	6:1G:140:ILE:HG12	1.94	0.48
32:1a:67:C:H2'	32:1a:68:G:C8	2.49	0.48
32:1a:576:G:O6	32:1a:880:C:O2'	2.31	0.48
32:1a:718:G:H5'	42:1k:117:ASN:HB2	1.96	0.48
33:1b:48:MET:HE2	33:1b:48:MET:HA	1.95	0.48
34:1c:32:LEU:HD13	34:1c:59:ARG:HH11	1.79	0.48
35:1d:114:ARG:HA	35:1d:117:ALA:HB3	1.96	0.48
1:2A:1607:C:H4'	1:2A:1608:A:O5'	2.13	0.48
1:2A:2316:C:H2'	1:2A:2317:C:C6	2.48	0.48
1:2A:2391:G:O6	1:2A:2425:A:H8	1.97	0.48
1:2A:2639:A:OP2	61:2A:3864:HOH:O	2.20	0.48
6:2G:115:ARG:HD3	6:2G:136:ARG:HH22	1.78	0.48
32:2a:577:G:C8	32:2a:816:A:C6	3.02	0.48
32:2a:625:G:H4'	47:2p:16:HIS:CD2	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:2c:148:GLY:HA3	34:2c:172:ARG:O	2.14	0.48
39:2h:86:ILE:HG12	39:2h:135:CYS:HA	1.94	0.48
1:1A:167:G:OP2	61:1A:4169:HOH:O	2.20	0.48
1:1A:303:C:H42	1:1A:385:G:H1	1.62	0.48
1:1A:1719:C:OP1	61:1A:4171:HOH:O	2.20	0.48
1:1A:2353:G:H2'	1:1A:2354:C:C6	2.49	0.48
32:1a:10:A:OP2	36:1e:126:ARG:HD2	2.14	0.48
32:1a:1060:C:C5	34:1c:2:GLY:HA3	2.49	0.48
32:1a:1202:G:O4'	45:1n:29:ARG:NH1	2.47	0.48
34:1c:19:GLU:HG2	34:1c:54:ARG:NH1	2.28	0.48
1:2A:539:G:H2'	1:2A:540:C:C6	2.49	0.48
4:2E:36:ARG:NH1	4:2E:85:ASN:OD1	2.47	0.48
20:2Y:97:ARG:HB3	20:2Y:106:LEU:HD12	1.94	0.48
26:24:13:ARG:HH12	26:24:23:GLU:HG2	1.78	0.48
32:2a:376:G:H4'	47:2p:5:ARG:NH1	2.29	0.48
34:2c:32:LEU:O	34:2c:36:ASP:HB2	2.13	0.48
44:2m:108:ARG:HA	44:2m:108:ARG:HD3	1.64	0.48
46:2o:4:THR:HG23	46:2o:7:GLU:H	1.78	0.48
47:2p:3:LYS:O	47:2p:21:VAL:HA	2.13	0.48
1:1A:840:A:OP2	1:1A:2093:A:O2'	2.29	0.47
1:1A:1793:A:H2'	61:1A:6306:HOH:O	2.14	0.47
1:1A:1834:A:H4'	3:1D:259:THR:HG23	1.96	0.47
1:1A:2175:G:H2'	1:1A:2176:G:C8	2.49	0.47
9:1N:62:VAL:HG11	9:1N:66:LYS:HB2	1.95	0.47
32:1a:1183:A:O2'	32:1a:1184:G:OP1	2.32	0.47
33:1b:208:ILE:HA	33:1b:211:ILE:HD12	1.96	0.47
36:1e:40:ARG:NH2	36:1e:68:GLU:OE2	2.47	0.47
41:1j:8:LEU:HB2	41:1j:70:ARG:HB2	1.95	0.47
1:2A:1079:C:N4	1:2A:1080:C:N3	2.62	0.47
1:2A:1237:A:OP1	61:2A:3867:HOH:O	2.20	0.47
1:2A:1776:G:OP1	61:2A:3866:HOH:O	2.20	0.47
1:2A:2732:G:H3'	1:2A:2733:A:O4'	2.13	0.47
5:2F:28:ILE:HG23	5:2F:112:MET:HE3	1.94	0.47
5:2F:172:TRP:H	5:2F:172:TRP:CD1	2.31	0.47
5:2F:179:GLU:CD	5:2F:179:GLU:H	2.22	0.47
19:2X:65:ARG:HB3	19:2X:70:LEU:HD23	1.96	0.47
32:2a:857:C:H2'	32:2a:858:G:O4'	2.14	0.47
32:2a:1015:A:H4'	45:2n:15:LYS:NZ	2.29	0.47
32:2a:1097:C:H1'	32:2a:1170:A:H1'	1.96	0.47
32:2a:1172:C:H2'	32:2a:1173:G:H8	1.79	0.47
37:2f:91:VAL:HG11	49:2r:72:ARG:NH1	2.28	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:802:C:O2'	1:1A:803:C:H5'	2.14	0.47
1:1A:2255:U:H2'	1:1A:2256:U:C6	2.49	0.47
5:1F:9:ILE:HG21	5:1F:125:LEU:HD22	1.95	0.47
32:1a:1328:C:OP1	52:1u:21:TYR:OH	2.22	0.47
39:1h:6:ILE:O	39:1h:10:LEU:HG	2.14	0.47
1:2A:1579:A:H2'	1:2A:1580:A:C8	2.48	0.47
1:2A:2657:A:O2'	7:2H:160:LYS:NZ	2.46	0.47
13:2R:44:LEU:HD22	13:2R:48:VAL:HG23	1.96	0.47
32:2a:237:C:O3'	48:2q:25:ARG:NH2	2.47	0.47
32:2a:767:A:H2'	32:2a:768:A:O4'	2.15	0.47
32:2a:922:G:H4'	36:2e:20:GLN:HA	1.95	0.47
32:2a:1119:C:H2'	32:2a:1120:G:C8	2.45	0.47
45:2n:29:ARG:HD3	45:2n:40:CYS:SG	2.54	0.47
47:2p:19:ILE:N	47:2p:37:GLY:O	2.46	0.47
4:1E:12:THR:HG21	15:1T:11:GLU:OE2	2.14	0.47
5:1F:51:THR:HB	5:1F:88:VAL:HG11	1.96	0.47
8:1I:9:LEU:HD12	8:1I:9:LEU:HA	1.72	0.47
12:1Q:7:MET:HE1	21:1Z:194:PRO:HB2	1.97	0.47
20:1Y:15:VAL:O	20:1Y:22:GLY:N	2.42	0.47
32:1a:688:G:O2'	32:1a:704:A:N1	2.33	0.47
33:1b:74:LYS:HE3	33:1b:166:ASP:HB2	1.96	0.47
33:1b:84:GLU:HB3	33:1b:219:VAL:HG21	1.96	0.47
40:1i:29:ASN:ND2	40:1i:65:VAL:O	2.41	0.47
42:1k:40:ILE:HG22	42:1k:75:TYR:HD2	1.79	0.47
1:2A:1180:C:H2'	1:2A:1181:C:C6	2.50	0.47
1:2A:2125:G:N2	1:2A:2172:U:H3'	2.29	0.47
1:2A:2564:A:C2	1:2A:2647:U:H4'	2.48	0.47
5:2F:36:VAL:O	5:2F:40:GLN:HB2	2.14	0.47
6:2G:55:LYS:O	6:2G:59:GLU:N	2.40	0.47
7:2H:45:VAL:HA	7:2H:50:VAL:HG22	1.95	0.47
23:21:59:THR:HG23	61:21:8114:HOH:O	2.13	0.47
32:2a:1241:G:H2'	32:2a:1242:C:C6	2.50	0.47
33:2b:137:ARG:O	33:2b:141:GLU:N	2.42	0.47
1:1A:1053:C:OP1	9:1N:37:LYS:NZ	2.47	0.47
1:1A:1211:U:H2'	1:1A:1212:C:C6	2.50	0.47
1:1A:1217:G:H5'	61:1A:4221:HOH:O	2.14	0.47
1:1A:1766:G:H5'	1:1A:1767:A:OP2	2.15	0.47
1:1A:2804:C:H5'	1:1A:2902:G:N2	2.30	0.47
3:1D:12:SER:HB3	3:1D:208:LYS:HB3	1.97	0.47
21:1Z:103:ARG:HD3	21:1Z:136:PHE:CD1	2.49	0.47
32:1a:738:C:H2'	32:1a:739:C:H6	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1028:C:O2	32:1a:1033:G:N1	2.38	0.47
32:1a:1278:U:H5'	32:1a:1279:A:O4'	2.14	0.47
34:1c:63:ASN:HB3	34:1c:98:ASN:HB2	1.97	0.47
1:2A:994:C:O2'	1:2A:996:A:OP1	2.31	0.47
1:2A:1647:G:H3'	1:2A:1647:G:OP2	2.14	0.47
10:2O:35:VAL:HG22	10:2O:65:THR:HG23	1.96	0.47
32:2a:611:A:H61	32:2a:629:G:H1	1.63	0.47
32:2a:651:C:N4	32:2a:753:A:OP2	2.46	0.47
32:2a:662:G:O2'	32:2a:836:G:OP1	2.32	0.47
32:2a:1255:G:HO2'	32:2a:1258:G:HO2'	1.62	0.47
51:2t:57:ARG:NH2	51:2t:100:ILE:HD12	2.22	0.47
1:1A:2584:A:N7	4:1E:144:ARG:HD2	2.30	0.47
7:1H:124:GLU:OE2	7:1H:132:ARG:HD2	2.15	0.47
10:1O:39:ILE:HD12	10:1O:41:ALA:HB2	1.97	0.47
14:1S:14:VAL:O	14:1S:18:ILE:HG12	2.14	0.47
32:1a:631:G:H2'	32:1a:632:A:H8	1.79	0.47
32:1a:715:A:H2'	32:1a:716:A:C8	2.50	0.47
32:1a:1273:G:H3'	32:1a:1274:G:H8	1.78	0.47
37:1f:11:ASN:HB3	37:1f:14:LEU:HG	1.96	0.47
50:1s:36:ARG:NH1	50:1s:52:TYR:O	2.45	0.47
1:2A:422:A:N7	61:2A:3990:HOH:O	2.35	0.47
1:2A:691:C:OP1	61:2A:3862:HOH:O	2.20	0.47
1:2A:720:C:H2'	1:2A:721:C:H6	1.79	0.47
1:2A:2103:C:N4	1:2A:2104:G:O6	2.47	0.47
11:2P:98:GLU:H	11:2P:98:GLU:CD	2.23	0.47
21:2Z:150:LEU:HB3	21:2Z:171:ILE:HD11	1.96	0.47
26:24:45:GLY:C	26:24:47:GLN:H	2.23	0.47
32:2a:1240:U:N3	38:2g:30:ILE:O	2.33	0.47
32:2a:1314:C:OP2	50:2s:4:SER:OG	2.25	0.47
32:2a:1400:5MC:N4	53:2y:62:VAL:HG23	2.30	0.47
50:2s:52:TYR:HB2	50:2s:57:HIS:CE1	2.50	0.47
3:1D:146:GLU:HG2	3:1D:152:GLY:C	2.39	0.47
6:1G:150:ASP:OD1	6:1G:151:ALA:N	2.47	0.47
32:1a:674:G:H2'	32:1a:675:A:C8	2.49	0.47
32:1a:1001:A:H2'	32:1a:1001(A):G:H8	1.80	0.47
32:1a:1004:A:O2'	32:1a:1038:C:O2	2.23	0.47
1:2A:271(E):U:H2'	1:2A:271(F):C:C6	2.50	0.47
1:2A:1155:A:H5''	16:2U:55:ARG:HD3	1.96	0.47
1:2A:1379:A:H4'	1:2A:1380:G:OP2	2.15	0.47
1:2A:1538:G:H2'	1:2A:1539:G:C8	2.50	0.47
6:2G:11:TYR:CZ	6:2G:16:ARG:HD3	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:2G:82:LEU:HA	6:2G:86:MET:SD	2.55	0.47
15:2T:24:PRO:HA	15:2T:49:VAL:HG23	1.96	0.47
21:2Z:35:ARG:HD2	21:2Z:35:ARG:HA	1.54	0.47
32:2a:7:G:H5'	32:2a:298:A:O4'	2.14	0.47
32:2a:1304:G:C6	32:2a:1305:G:N1	2.82	0.47
38:2g:113:GLU:CG	38:2g:119:ARG:HG2	2.45	0.47
1:1A:91:G:H2'	1:1A:92:C:C6	2.49	0.47
1:1A:268:G:H5'	23:11:81:LYS:HE2	1.96	0.47
1:1A:2045:G:H4'	1:1A:2629:C:O3'	2.15	0.47
1:1A:2213:G:H5'	1:1A:2214:G:OP2	2.14	0.47
1:1A:2298:A:H4'	1:1A:2299:A:O4'	2.15	0.47
3:1D:69:ARG:HG2	3:1D:69:ARG:NH1	2.30	0.47
6:1G:77:ILE:HG22	6:1G:80:PHE:H	1.80	0.47
11:1P:76:LYS:NZ	61:1P:309:HOH:O	2.47	0.47
11:1P:112:LEU:HD23	11:1P:113:LYS:N	2.29	0.47
18:1W:68:ARG:HH11	18:1W:111:HIS:HA	1.80	0.47
24:12:22:GLU:HG3	24:12:64:LEU:HD11	1.96	0.47
28:16:18:ARG:HD2	28:16:42:TRP:CD1	2.50	0.47
32:1a:160:A:H2'	32:1a:161:A:O4'	2.15	0.47
32:1a:1492:A:H4'	32:1a:1493:A:C6	2.50	0.47
45:1n:4:LYS:O	45:1n:7:ILE:HG12	2.15	0.47
1:2A:82:G:N1	1:2A:103:A:OP2	2.42	0.47
1:2A:271(L):U:O5'	1:2A:271(L):U:H6	1.98	0.47
1:2A:458:G:O2'	1:2A:469:G:O6	2.30	0.47
1:2A:578:A:H3'	61:2A:4047:HOH:O	2.15	0.47
9:2N:39:ARG:HE	9:2N:48:MET:HE3	1.79	0.47
18:2W:64:MET:HE3	18:2W:109:GLU:HG3	1.96	0.47
20:2Y:13:VAL:HB	20:2Y:72:VAL:HG13	1.97	0.47
23:21:76:ARG:HH22	23:21:97:LEU:HB3	1.79	0.47
26:24:53:GLU:H	26:24:53:GLU:CD	2.22	0.47
26:24:64:GLY:C	26:24:66:SER:H	2.23	0.47
32:2a:409:G:H2'	32:2a:410:G:O4'	2.13	0.47
32:2a:420:U:H2'	32:2a:422:C:C5	2.50	0.47
34:2c:8:ILE:HG12	34:2c:184:TYR:HB3	1.95	0.47
51:2t:14:LYS:O	51:2t:18:GLN:HG3	2.15	0.47
1:1A:297:C:H42	1:1A:387:G:H1	1.63	0.47
1:1A:638:U:H5''	58:1F:314:ARG:N	2.30	0.47
1:1A:1093:G:O2'	1:1A:1094:A:H8	1.97	0.47
1:1A:2177:G:H3'	1:1A:2178:G:C8	2.50	0.47
6:1G:115:ARG:H	6:1G:136:ARG:NH2	2.12	0.47
8:1I:117:GLU:HG3	8:1I:118:LYS:H	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:575:G:O2'	32:1a:821:G:H5'	2.15	0.47
32:1a:1004:A:O4'	32:1a:1025:U:N3	2.48	0.47
33:1b:189:ASP:OD1	33:1b:189:ASP:N	2.48	0.47
37:1f:22:GLU:OE2	37:1f:82:ARG:NH2	2.41	0.47
52:1u:5:ASP:O	52:1u:11:GLY:HA3	2.14	0.47
1:2A:2134:A:H5''	1:2A:2156:G:H22	1.79	0.47
1:2A:2298:A:N6	1:2A:2318:G:C8	2.82	0.47
32:2a:60:A:H4'	32:2a:61:G:O5'	2.15	0.47
32:2a:250:A:H4'	32:2a:251:G:O5'	2.15	0.47
32:2a:280:C:N3	48:2q:39:SER:OG	2.41	0.47
32:2a:1256:A:OP2	34:2c:26:LYS:NZ	2.30	0.47
41:2j:8:LEU:HB2	41:2j:70:ARG:HB2	1.95	0.47
1:1A:2053:A:C6	1:1A:2510:C:H1'	2.50	0.47
58:1B:228:ARG:HE	58:1B:228:ARG:HB3	1.64	0.47
6:1G:43:LEU:HB3	6:1G:44:GLY:H	1.58	0.47
15:1T:53:ARG:HB3	15:1T:53:ARG:CZ	2.45	0.47
19:1X:12:VAL:HG21	19:1X:27:THR:HG22	1.96	0.47
36:1e:18:ARG:HE	36:1e:20:GLN:NE2	2.13	0.47
39:1h:64:LYS:HG2	39:1h:79:VAL:HG21	1.97	0.47
1:2A:171:G:H2'	1:2A:172:C:C6	2.50	0.47
1:2A:674:G:O2'	5:2F:74:ARG:HD3	2.15	0.47
1:2A:981:A:N1	1:2A:2027:G:O2'	2.48	0.47
1:2A:1410:G:H2'	1:2A:1411:C:H6	1.80	0.47
1:2A:2308:G:H5''	1:2A:2310:A:OP2	2.15	0.47
12:2Q:51:ARG:O	12:2Q:55:VAL:HG12	2.15	0.47
32:2a:1262:C:N4	32:2a:1273:G:H1	2.11	0.47
33:2b:55:PHE:CD1	33:2b:221:LEU:HD13	2.49	0.47
44:2m:102:ARG:HH21	44:2m:104:ARG:HD3	1.78	0.47
1:1A:858:U:H2'	11:1P:21:ARG:HA	1.96	0.47
1:1A:2228:G:O2'	1:1A:2229:A:OP1	2.31	0.47
1:1A:2250:G:N3	1:1A:2250:G:H2'	2.29	0.47
3:1D:91:ARG:N	61:1D:408:HOH:O	2.40	0.47
11:1P:94:GLU:HA	11:1P:124:LYS:O	2.15	0.47
1:2A:271(P):C:O3'	8:2I:42:SER:OG	2.31	0.47
1:2A:840:C:H2'	1:2A:841:A:C8	2.50	0.47
1:2A:1010:A:OP2	61:2A:3844:HOH:O	2.20	0.47
1:2A:1489:U:HO2'	1:2A:1490:A:H8	1.58	0.47
1:2A:2273:A:H2'	1:2A:2274:A:C8	2.50	0.47
1:2A:2390:U:P	30:28:35:GLN:HE22	2.37	0.47
4:2E:11:MET:HE2	4:2E:11:MET:HB3	1.86	0.47
11:2P:91:PHE:CE1	11:2P:99:LEU:HD21	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:2Q:73:PRO:HB3	12:2Q:93:TYR:CE1	2.49	0.47
13:2R:87:TYR:OH	13:2R:117:VAL:O	2.14	0.47
39:2h:6:ILE:HG22	39:2h:10:LEU:HD11	1.97	0.47
49:2r:53:ARG:NH1	49:2r:60:ALA:HB2	2.29	0.47
1:1A:1091:A:O2'	1:1A:1093:G:C4	2.67	0.46
2:1B:66:A:N6	2:1B:108:U:H2'	2.29	0.46
6:1G:135:LEU:O	6:1G:154:GLY:HA3	2.15	0.46
32:1a:131:C:H2'	32:1a:132:C:C6	2.50	0.46
32:1a:237:C:OP2	48:1q:40:LYS:NZ	2.47	0.46
32:1a:1028:C:N3	32:1a:1033:G:C6	2.83	0.46
32:1a:1248:A:N3	40:1i:70:LYS:HE3	2.30	0.46
1:2A:51:G:H4'	1:2A:52:A:H5'	1.97	0.46
1:2A:856:C:H2'	1:2A:857:C:C6	2.50	0.46
1:2A:1503:U:H2'	1:2A:1504:C:H6	1.79	0.46
1:2A:2109:U:O2	1:2A:2181:G:N2	2.48	0.46
14:2S:26:LEU:HD22	14:2S:87:PHE:HD1	1.80	0.46
27:25:15:ARG:NH1	61:25:601:HOH:O	2.33	0.46
32:2a:442:C:H42	32:2a:492:G:H1	1.63	0.46
32:2a:952:U:H4'	32:2a:964:A:N1	2.30	0.46
32:2a:1030:C:N4	32:2a:1031:G:C6	2.78	0.46
32:2a:1324:A:O4'	32:2a:1362:C:H4'	2.15	0.46
48:2q:18:THR:HG1	48:2q:69:LYS:HZ2	1.61	0.46
52:2u:9:ARG:O	52:2u:13:ILE:HG13	2.15	0.46
1:1A:265:U:H2'	1:1A:266:C:C6	2.50	0.46
1:1A:560:C:O3'	16:1U:53:ARG:NH1	2.48	0.46
1:1A:2164:C:N3	1:1A:2171:G:C6	2.84	0.46
1:1A:2169:G:H2'	1:1A:2170:G:O4'	2.15	0.46
1:1A:2441:G:OP1	61:1A:4109:HOH:O	2.21	0.46
1:1A:2694:U:O2'	15:1T:58:ASN:ND2	2.48	0.46
22:10:43:THR:OG1	22:10:46:LYS:HG2	2.13	0.46
32:1a:1129:C:O2'	32:1a:1139:G:N7	2.32	0.46
32:1a:1186:G:H21	45:1n:61:TRP:C	2.24	0.46
32:1a:1243:C:H2'	32:1a:1244:C:C6	2.49	0.46
37:1f:69:GLU:H	37:1f:69:GLU:CD	2.24	0.46
41:1j:31:GLY:HA2	41:1j:32:ALA:HA	1.45	0.46
48:1q:86:GLU:O	48:1q:90:ILE:N	2.43	0.46
1:2A:1817:G:OP1	3:2D:88:ARG:NH2	2.41	0.46
32:2a:560:U:H4'	32:2a:561:U:O5'	2.14	0.46
32:2a:598:U:H2'	32:2a:599:C:C6	2.50	0.46
41:2j:35:SER:N	41:2j:73:ASP:O	2.46	0.46
50:2s:50:ALA:HA	50:2s:58:VAL:O	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:209:G:O2'	1:1A:222:A:N3	2.39	0.46
1:1A:1118:C:N4	1:1A:1144:A:OP2	2.49	0.46
1:1A:2186:C:H3'	1:1A:2187:G:C8	2.51	0.46
1:1A:2376:C:H2'	1:1A:2377:G:O4'	2.14	0.46
1:1A:2602:A:O3'	3:1D:239:ARG:NH2	2.48	0.46
32:1a:441:A:H3'	32:1a:442:C:C6	2.50	0.46
32:1a:1148:U:H2'	32:1a:1149:C:O4'	2.16	0.46
36:1e:96:PRO:O	36:1e:98:THR:N	2.46	0.46
51:1t:92:LEU:O	51:1t:96:GLY:N	2.48	0.46
1:2A:79:G:O2'	1:2A:346:A:N3	2.44	0.46
1:2A:747:U:O2	1:2A:2014:A:H1'	2.15	0.46
1:2A:1506:C:H2'	1:2A:1507:A:H5'	1.96	0.46
1:2A:2533:A:OP1	1:2A:2665:A:O2'	2.31	0.46
1:2A:2684:U:OP2	61:2A:3865:HOH:O	2.20	0.46
1:2A:2749:A:OP1	7:2H:3:ARG:NH1	2.48	0.46
4:2E:79:ARG:HA	4:2E:79:ARG:HD3	1.76	0.46
11:2P:50:ARG:HD3	30:28:7:HIS:CD2	2.50	0.46
32:2a:786:G:C2	32:2a:797:C:C2	3.04	0.46
33:2b:54:THR:HG21	33:2b:201:ILE:HD11	1.97	0.46
48:2q:66:SER:O	48:2q:70:ARG:NH1	2.47	0.46
1:1A:1104:G:O6	1:1A:1126:C:N3	2.49	0.46
1:1A:1210:G:H2'	1:1A:1211:U:C6	2.51	0.46
1:1A:1343:C:H5''	61:1A:4124:HOH:O	2.15	0.46
1:1A:1604:C:H5''	1:1A:1605:A:OP2	2.16	0.46
14:1S:15:ARG:HE	14:1S:88:ASP:CG	2.23	0.46
20:1Y:90:LEU:HB3	20:1Y:92:ASN:HD22	1.80	0.46
26:14:62:ARG:HD3	26:14:62:ARG:HA	1.57	0.46
32:1a:79:G:N2	32:1a:90:U:O2	2.48	0.46
32:1a:560:U:O2'	32:1a:561:U:OP2	2.28	0.46
33:1b:183:PRO:HA	33:1b:198:ASP:OD2	2.15	0.46
38:1g:22:LEU:HG	38:1g:62:PHE:HE2	1.80	0.46
1:2A:271(D):G:H2'	1:2A:271(E):U:C6	2.50	0.46
1:2A:644:A:H4'	1:2A:645:C:H5	1.80	0.46
1:2A:2119:A:O2'	1:2A:2120:G:H5'	2.16	0.46
1:2A:2364:C:H2'	1:2A:2365:G:O4'	2.15	0.46
1:2A:2377:A:H2'	1:2A:2378:A:C8	2.50	0.46
8:2I:64:GLU:O	8:2I:68:LEU:HB2	2.15	0.46
26:24:40:HIS:HB3	26:24:43:TYR:CE2	2.50	0.46
32:2a:1073:U:H2'	32:2a:1074:G:H8	1.81	0.46
32:2a:1312:G:H5'	50:2s:5:LEU:HD21	1.97	0.46
32:2a:1360:A:H2'	32:2a:1361:G:O4'	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:2c:47:LEU:HD13	34:2c:68:VAL:HG11	1.97	0.46
1:1A:272:U:H4'	8:1I:50:ARG:NH2	2.28	0.46
1:1A:1008:U:H2'	1:1A:1009:C:C6	2.50	0.46
1:1A:1102:G:N2	1:1A:1150:C:N3	2.64	0.46
1:1A:2762:A:OP1	7:1H:3:ARG:NH1	2.48	0.46
26:14:56:VAL:HG22	26:14:60:GLN:OE1	2.15	0.46
32:1a:346:G:H3'	57:1a:1854:MPD:O4	2.15	0.46
32:1a:626:U:H2'	32:1a:627:G:H8	1.79	0.46
32:1a:1187:G:H4'	40:1i:111:ARG:HH11	1.79	0.46
32:1a:1236:A:H2'	32:1a:1237:C:C6	2.51	0.46
33:1b:16:HIS:HB3	33:1b:210:SER:HB2	1.98	0.46
44:1m:4:ILE:HA	44:1m:5:ALA:HA	1.62	0.46
1:2A:2630:G:H2'	1:2A:2631:G:O4'	2.16	0.46
3:2D:145:VAL:HG12	3:2D:146:GLU:O	2.16	0.46
11:2P:82:GLY:HA2	11:2P:113:LYS:O	2.15	0.46
16:2U:106:PHE:O	16:2U:110:VAL:HG23	2.15	0.46
32:2a:23:C:OP2	32:2a:561:U:N3	2.37	0.46
32:2a:397:A:N7	32:2a:547:A:O2'	2.45	0.46
32:2a:399:G:H2'	32:2a:400:C:C6	2.49	0.46
32:2a:748:C:H4'	32:2a:749:C:O5'	2.16	0.46
41:2j:25:GLU:O	41:2j:29:ARG:HG3	2.16	0.46
1:1A:1144:A:H2'	1:1A:1145:G:O4'	2.15	0.46
1:1A:1355:G:OP1	29:17:9:ARG:HG3	2.15	0.46
1:1A:1733:C:H2'	1:1A:1734:G:O4'	2.16	0.46
1:1A:1753:U:OP1	61:1A:4168:HOH:O	2.20	0.46
1:1A:2331:G:N1	14:1S:3:ARG:HA	2.30	0.46
1:1A:2623:U:C4	27:15:3:LYS:HG2	2.51	0.46
5:1F:184:TYR:CE2	5:1F:188:ARG:HD2	2.50	0.46
19:1X:53:LYS:HB3	19:1X:82:GLN:HB3	1.96	0.46
20:1Y:99:CYS:HB2	20:1Y:106:LEU:HD21	1.98	0.46
25:13:44:ARG:O	25:13:48:GLU:HG3	2.15	0.46
32:1a:344:A:H4'	32:1a:345:C:OP2	2.16	0.46
32:1a:452:A:H1'	32:1a:453:A:C8	2.50	0.46
32:1a:542:G:H2'	32:1a:543:C:H6	1.81	0.46
32:1a:572:A:OP1	61:1a:3316:HOH:O	2.21	0.46
32:1a:593:G:H2'	32:1a:594:G:O4'	2.16	0.46
32:1a:765:G:C6	32:1a:812:C:C2	3.04	0.46
32:1a:986:A:H2'	32:1a:987:G:O4'	2.16	0.46
41:1j:26:ALA:HA	41:1j:29:ARG:NH2	2.31	0.46
51:1t:18:GLN:O	51:1t:22:ARG:HG3	2.15	0.46
53:1y:55:ASN:OD1	53:1y:60:VAL:HG12	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1002:G:H2'	1:2A:1003:G:O4'	2.16	0.46
1:2A:2092:U:H4'	1:2A:2093:G:O5'	2.16	0.46
1:2A:2484:G:C2	1:2A:2485:G:C8	3.03	0.46
5:2F:207:GLY:O	61:2F:3102:HOH:O	2.20	0.46
13:2R:67:LEU:HD13	13:2R:76:VAL:HG21	1.98	0.46
14:2S:10:ARG:HH21	14:2S:91:PRO:HB2	1.81	0.46
15:2T:29:ARG:NH2	15:2T:46:GLU:OE1	2.48	0.46
16:2U:11:ARG:O	16:2U:15:LYS:HG3	2.15	0.46
17:2V:43:GLU:OE1	17:2V:43:GLU:N	2.48	0.46
21:2Z:5:LEU:HB3	21:2Z:59:LEU:HD23	1.98	0.46
32:2a:849:C:H2'	32:2a:850:U:O4'	2.16	0.46
32:2a:938:A:C6	32:2a:939:G:C5	3.03	0.46
32:2a:1005:A:H3'	32:2a:1006:C:O4'	2.15	0.46
32:2a:1054:C:H41	53:2y:46:GLN:HG3	1.79	0.46
32:2a:1079:G:H4'	36:2e:14:ARG:HH22	1.80	0.46
32:2a:1263:C:H2'	32:2a:1264:C:H6	1.79	0.46
32:2a:1496:C:H2'	32:2a:1497:G:O4'	2.16	0.46
37:2f:22:GLU:OE2	37:2f:84:ASN:ND2	2.40	0.46
1:1A:1220:U:H1'	1:1A:1221:G:OP1	2.16	0.46
1:1A:1221:G:H21	1:1A:1223:C:P	2.38	0.46
1:1A:1617:A:H2'	1:1A:1618:A:C8	2.50	0.46
1:1A:2299:A:O2'	1:1A:2300:A:H3'	2.15	0.46
17:1V:14:VAL:HB	17:1V:96:ILE:HG13	1.98	0.46
18:1W:68:ARG:HH12	18:1W:112:GLY:H	1.64	0.46
21:1Z:19:ARG:NH1	21:1Z:84:GLU:O	2.49	0.46
32:1a:731:G:H5'	32:1a:766:A:H4'	1.97	0.46
32:1a:1216:G:H5''	45:1n:5:ALA:HB2	1.97	0.46
33:1b:19:HIS:O	33:1b:20:GLU:HB2	2.15	0.46
33:1b:20:GLU:HG2	33:1b:23:ARG:HD3	1.98	0.46
38:1g:71:PRO:HA	38:1g:138:LYS:HG3	1.98	0.46
38:1g:94:ARG:O	38:1g:97:GLN:HB3	2.16	0.46
1:2A:514:A:N3	1:2A:581:C:O2'	2.46	0.46
1:2A:1065:U:H4'	1:2A:1066:U:O5'	2.16	0.46
1:2A:2383:G:OP2	30:28:37:SER:HB2	2.16	0.46
3:2D:133:LEU:HD23	3:2D:136:ILE:HD12	1.97	0.46
6:2G:32:PRO:HB3	6:2G:163:ALA:HB2	1.98	0.46
32:2a:163:C:H2'	32:2a:164:U:O4'	2.15	0.46
32:2a:965:A:N7	53:2y:8:LYS:NZ	2.51	0.46
32:2a:1129:C:N4	32:2a:1143:G:N1	2.61	0.46
32:2a:1248:A:H2'	32:2a:1249:C:H6	1.81	0.46
33:2b:16:HIS:HB2	33:2b:204:ASN:CB	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:2d:173:TRP:NE1	35:2d:189:PRO:HG3	2.29	0.46
40:2i:127:LYS:HZ1	53:2y:60:VAL:HG11	1.80	0.46
44:2m:3:ARG:N	44:2m:8:GLU:HA	2.31	0.46
50:2s:30:LEU:HD11	50:2s:50:ALA:HB2	1.98	0.46
1:1A:172:C:N4	1:1A:202:A:H61	2.14	0.46
1:1A:1003:U:H5''	12:1Q:14:ARG:HD3	1.97	0.46
1:1A:1715:A:H4'	1:1A:1716:A:O5'	2.16	0.46
4:1E:143:ASN:HD22	4:1E:147:PRO:CD	2.28	0.46
32:1a:926:G:O6	53:1y:87:LYS:HE2	2.15	0.46
44:1m:89:GLY:O	44:1m:93:ARG:HG3	2.15	0.46
47:1p:14:ASN:OD1	47:1p:42:ARG:NH1	2.49	0.46
52:1u:18:TYR:CD1	52:1u:24:ARG:HB3	2.50	0.46
1:2A:952:G:OP1	12:2Q:16:ARG:NH2	2.47	0.46
1:2A:1365:A:O2'	23:21:11:ARG:NH1	2.49	0.46
1:2A:2723:C:OP1	13:2R:3:HIS:ND1	2.30	0.46
2:2B:61:G:H2'	2:2B:62:C:C6	2.51	0.46
6:2G:39:ILE:O	6:2G:91:ARG:HB2	2.16	0.46
7:2H:117:PRO:HG3	7:2H:123:PHE:CE2	2.51	0.46
25:23:57:GLU:HG2	25:23:59:VAL:HG13	1.97	0.46
26:24:1:MET:HE2	26:24:6:HIS:CE1	2.50	0.46
32:2a:192:U:H2'	32:2a:193:C:H6	1.80	0.46
32:2a:1004:A:H5''	32:2a:1025:U:C4	2.51	0.46
32:2a:1305:G:H22	32:2a:1331:G:H1'	1.77	0.46
38:2g:92:SER:O	38:2g:96:GLN:HG3	2.16	0.46
39:2h:112:LEU:HA	39:2h:134:ILE:HG12	1.98	0.46
1:1A:181:C:O2'	1:1A:849:A:N3	2.46	0.46
1:1A:1335:C:H2'	1:1A:1336:C:C6	2.51	0.46
1:1A:2125:C:N3	1:1A:2208:G:N2	2.49	0.46
1:1A:2138:G:P	1:1A:2188:G:H21	2.38	0.46
61:1A:4275:HOH:O	16:1U:13:LYS:NZ	2.42	0.46
17:1V:2:PHE:CE2	17:1V:41:GLY:HA3	2.51	0.46
21:1Z:146:ILE:HA	21:1Z:147:GLY:HA2	1.68	0.46
33:1b:16:HIS:CG	33:1b:17:PHE:N	2.84	0.46
33:1b:178:ARG:HH21	33:1b:196:LEU:HA	1.80	0.46
34:1c:15:THR:HG21	34:1c:181:ASN:HA	1.97	0.46
1:2A:384:U:H2'	1:2A:385:C:H6	1.79	0.46
1:2A:996:A:H4'	16:2U:91:ASP:OD2	2.16	0.46
1:2A:1014:U:H2'	1:2A:1015:G:C8	2.48	0.46
1:2A:2319:G:H1	14:2S:3:ARG:HA	1.80	0.46
1:2A:2321:G:O2'	1:2A:2322:A:OP1	2.27	0.46
1:2A:2782:G:OP2	61:2A:3868:HOH:O	2.21	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:2H:98:LEU:HD12	7:2H:102:ALA:O	2.15	0.46
8:2I:77:LEU:HD13	8:2I:101:LEU:HD23	1.97	0.46
13:2R:72:ASP:OD1	61:2R:301:HOH:O	2.21	0.46
32:2a:192:U:O2'	51:2t:60:GLU:OE1	2.28	0.46
32:2a:685:G:C2	32:2a:686:U:C4	3.04	0.46
32:2a:707:C:H2'	32:2a:708:C:H6	1.79	0.46
32:2a:1053:G:N7	32:2a:1200:C:H5''	2.31	0.46
32:2a:1191:A:OP1	34:2c:3:ASN:HB3	2.16	0.46
34:2c:114:PRO:HA	34:2c:185:GLY:HA3	1.98	0.46
35:2d:63:LYS:HD2	35:2d:198:VAL:HG22	1.98	0.46
1:1A:329:U:H2'	1:1A:330:U:C6	2.51	0.46
1:1A:928:G:H2'	1:1A:929:G:O4'	2.16	0.46
1:1A:1405:A:H61	1:1A:1418:U:H3	1.63	0.46
1:1A:2136:A:H3'	1:1A:2137:G:H8	1.79	0.46
6:1G:11:TYR:HA	6:1G:15:VAL:HB	1.98	0.46
30:18:23:VAL:HG13	30:18:47:LYS:HB3	1.98	0.46
32:1a:580:U:H2'	32:1a:581:G:O4'	2.16	0.46
32:1a:1302:U:C5	44:1m:17:VAL:HG21	2.51	0.46
35:1d:59:ARG:HA	35:1d:59:ARG:HD3	1.49	0.46
1:2A:69:C:O2	1:2A:73:A:O2'	2.30	0.46
1:2A:1913:A:H2	32:2a:1491:G:N2	2.14	0.46
1:2A:2310:A:H61	6:2G:79:ASN:HD22	1.64	0.46
1:2A:2723:C:OP2	4:2E:109:LYS:NZ	2.49	0.46
1:2A:2849:U:H4'	1:2A:2868:A:C2	2.51	0.46
16:2U:91:ASP:N	17:2V:11:GLN:OE1	2.38	0.46
32:2a:1010:G:H2'	32:2a:1011:G:C8	2.51	0.46
32:2a:1387:G:H2'	32:2a:1388:C:C6	2.51	0.46
33:2b:167:PRO:HD3	33:2b:187:LEU:O	2.16	0.46
38:2g:94:ARG:O	38:2g:97:GLN:HB3	2.16	0.46
50:2s:41:VAL:HG13	50:2s:43:GLU:H	1.81	0.46
1:1A:2205:C:H2'	1:1A:2206:G:C8	2.51	0.45
6:1G:131:TYR:HB3	6:1G:159:VAL:HG13	1.97	0.45
14:1S:10:ARG:O	14:1S:14:VAL:HG13	2.15	0.45
32:1a:457:C:H2'	32:1a:458:C:C6	2.51	0.45
32:1a:1479:C:H2'	32:1a:1480:G:C8	2.51	0.45
34:1c:137:ALA:HA	34:1c:140:ARG:HE	1.81	0.45
36:1e:143:ARG:NH1	39:1h:77:GLU:OE2	2.49	0.45
1:2A:1025:G:C4	1:2A:1135:C:H1'	2.51	0.45
1:2A:2315:G:H2'	1:2A:2316:C:H6	1.80	0.45
1:2A:2648:C:H2'	1:2A:2649:U:C6	2.51	0.45
1:2A:2712:U:H2'	1:2A:2714:G:H5''	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:2N:104:LYS:HE2	9:2N:117:PHE:CZ	2.50	0.45
13:2R:36:THR:HG22	13:2R:37:THR:H	1.81	0.45
21:2Z:110:GLY:HA3	21:2Z:174:VAL:HG11	1.97	0.45
32:2a:64:G:H4'	32:2a:65:U:H3'	1.97	0.45
34:2c:143:GLU:C	34:2c:145:GLY:H	2.24	0.45
39:2h:6:ILE:O	39:2h:10:LEU:HG	2.16	0.45
43:2l:56:ALA:HB3	43:2l:100:ILE:HD11	1.98	0.45
1:1A:268:G:O2'	1:1A:269:G:OP2	2.30	0.45
1:1A:733:G:OP2	61:1A:4170:HOH:O	2.20	0.45
1:1A:795:G:C8	18:1W:89:ALA:HB1	2.51	0.45
1:1A:2050:U:H2'	1:1A:2051:G:O4'	2.15	0.45
1:1A:2245:U:H2'	1:1A:2246:G:C8	2.52	0.45
1:1A:2662:U:H2'	1:1A:2663:C:C6	2.50	0.45
1:1A:2701:U:H4'	1:1A:2702:C:H5'	1.97	0.45
6:1G:77:ILE:HG21	6:1G:80:PHE:CD2	2.52	0.45
7:1H:3:ARG:NH1	7:1H:5:GLY:H	2.13	0.45
7:1H:17:VAL:HG22	7:1H:26:VAL:HG22	1.97	0.45
12:1Q:2:LEU:HG	12:1Q:69:PHE:CE1	2.51	0.45
20:1Y:15:VAL:HG21	20:1Y:42:VAL:HG11	1.98	0.45
25:13:7:LYS:HE3	25:13:32:GLN:NE2	2.30	0.45
32:1a:673:G:H5''	37:1f:87:ARG:CZ	2.46	0.45
35:1d:119:GLN:HG2	35:1d:123:HIS:CD2	2.51	0.45
38:1g:27:ILE:HD12	38:1g:40:ALA:HA	1.97	0.45
1:2A:1092:C:H2'	1:2A:1092:C:O2	2.17	0.45
1:2A:1366:A:H2'	1:2A:1367:A:O4'	2.16	0.45
1:2A:2261:C:H1'	1:2A:2388:A:N3	2.30	0.45
6:2G:27:ASN:OD1	6:2G:28:VAL:N	2.48	0.45
21:2Z:152:ALA:O	21:2Z:155:LEU:HB2	2.16	0.45
32:2a:114:U:H1'	32:2a:353:A:H1'	1.98	0.45
32:2a:193:C:H2'	32:2a:194:C:C6	2.51	0.45
32:2a:1004:A:N6	32:2a:1037:C:C6	2.84	0.45
33:2b:97:TRP:HH2	33:2b:176:GLU:CD	2.24	0.45
1:1A:965:G:N2	1:1A:2281:A:OP2	2.49	0.45
1:1A:1841:A:H2'	1:1A:1842:G:O4'	2.16	0.45
7:1H:24:VAL:HG22	7:1H:35:VAL:HB	1.98	0.45
17:1V:22:VAL:HG23	17:1V:23:GLU:O	2.15	0.45
32:1a:1347:G:N2	32:1a:1373:G:H2'	2.32	0.45
34:1c:8:ILE:HG23	34:1c:16:ARG:HD3	1.98	0.45
34:1c:179:ARG:NH1	34:1c:206:GLU:OE1	2.49	0.45
36:1e:90:VAL:O	36:1e:120:THR:HA	2.16	0.45
36:1e:102:ALA:HB1	36:1e:106:PRO:HG2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:1h:6:ILE:HD11	39:1h:31:PHE:HD2	1.81	0.45
50:1s:80:TYR:CZ	50:1s:82:GLY:HA2	2.51	0.45
1:2A:328:U:H4'	20:2Y:68:HIS:CG	2.51	0.45
1:2A:862:G:H2'	1:2A:863:A:O4'	2.16	0.45
6:2G:16:ARG:HH22	6:2G:28:VAL:HB	1.82	0.45
26:24:57:GLU:HA	26:24:58:ARG:HA	1.44	0.45
30:28:62:LEU:HB3	30:28:65:GLU:HG2	1.99	0.45
32:2a:259:G:H2'	32:2a:260:G:O4'	2.17	0.45
32:2a:390:C:H2'	32:2a:391:G:C8	2.51	0.45
32:2a:977:A:H2'	32:2a:978:A:H5'	1.98	0.45
46:2o:55:GLY:HA2	46:2o:58:MET:HE3	1.98	0.45
51:2t:89:ARG:HE	51:2t:89:ARG:HB3	1.49	0.45
1:1A:582:G:H22	16:1U:49:HIS:CE1	2.35	0.45
1:1A:1541:A:C6	1:1A:1542:A:C6	3.04	0.45
1:1A:1700:G:H3'	13:1R:2:ARG:HD3	1.98	0.45
1:1A:2830:A:P	13:1R:2:ARG:HH22	2.39	0.45
3:1D:3:VAL:HG13	3:1D:17:THR:HB	1.98	0.45
3:1D:71:ASP:HB3	3:1D:103:ARG:HH22	1.80	0.45
6:1G:7:LEU:HD23	6:1G:7:LEU:HA	1.75	0.45
10:1O:64:ARG:NH2	10:1O:99:PHE:O	2.49	0.45
16:1U:81:HIS:CE1	16:1U:85:LYS:HD2	2.51	0.45
24:12:53:LEU:HD23	24:12:53:LEU:HA	1.72	0.45
30:18:23:VAL:CG1	30:18:47:LYS:HD3	2.47	0.45
32:1a:540:G:H2'	32:1a:541:G:O4'	2.16	0.45
35:1d:139:ARG:HE	35:1d:139:ARG:HB2	1.54	0.45
41:1j:78:ASN:O	41:1j:81:THR:HG23	2.15	0.45
1:2A:517:C:OP1	27:25:16:ARG:NH2	2.49	0.45
1:2A:740:U:H2'	1:2A:741:G:C8	2.52	0.45
1:2A:1204:A:H61	1:2A:1240:U:H2'	1.81	0.45
1:2A:2032:G:OP2	1:2A:2454:G:O2'	2.34	0.45
16:2U:9:VAL:O	16:2U:13:LYS:HG3	2.17	0.45
32:2a:359:U:H2'	32:2a:360:A:C8	2.51	0.45
32:2a:957:U:H4'	50:2s:79:THR:HB	1.99	0.45
33:2b:77:ALA:HB2	33:2b:211:ILE:HD13	1.98	0.45
33:2b:111:ARG:HD3	33:2b:111:ARG:HA	1.77	0.45
46:2o:8:LYS:O	46:2o:12:ILE:HG13	2.16	0.45
17:1V:6:LYS:HG2	61:1V:3118:HOH:O	2.16	0.45
32:1a:458:C:H2'	32:1a:460:G:O4'	2.17	0.45
32:1a:627:G:H2'	32:1a:628:G:H8	1.81	0.45
32:1a:1261:A:H3'	32:1a:1262:C:C6	2.51	0.45
1:2A:375:C:H2'	1:2A:376:C:C6	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1598:C:H2'	1:2A:1599:C:H6	1.82	0.45
1:2A:2168:G:H2'	1:2A:2170:A:OP2	2.17	0.45
1:2A:2473:U:O2	1:2A:2473:U:H2'	2.17	0.45
1:2A:2872:G:C2	1:2A:2873:A:N6	2.85	0.45
57:2A:3710:MPD:HM2	61:2A:4463:HOH:O	2.15	0.45
3:2D:158:ALA:O	3:2D:161:THR:OG1	2.34	0.45
4:2E:52:LEU:H	4:2E:76:ARG:HB2	1.80	0.45
15:2T:64:ARG:HB2	15:2T:73:GLU:HG2	1.99	0.45
32:2a:657:G:C2	32:2a:750:G:C5	3.05	0.45
32:2a:775:G:N2	32:2a:804:U:O4	2.49	0.45
32:2a:1346:A:N1	32:2a:1374:A:H5''	2.32	0.45
32:2a:1468:A:H2'	32:2a:1469:G:O4'	2.16	0.45
1:1A:402:C:H2'	1:1A:403:C:C6	2.52	0.45
1:1A:1119:A:N3	1:1A:1119:A:H2'	2.32	0.45
1:1A:1740:U:H1'	3:1D:14:ARG:NH1	2.32	0.45
1:1A:2119:C:H2'	1:1A:2120:U:O4'	2.17	0.45
1:1A:2639:G:O2'	1:1A:2794:A:N1	2.43	0.45
5:1F:64:ILE:HD11	5:1F:75:HIS:HB2	1.97	0.45
19:1X:76:ARG:HG3	61:1X:201:HOH:O	2.17	0.45
21:1Z:31:ARG:H	21:1Z:31:ARG:HG3	1.46	0.45
32:1a:1237:C:H3'	32:1a:1336:C:H41	1.82	0.45
33:1b:80:ILE:HD11	33:1b:212:GLN:HA	1.98	0.45
35:1d:129:ASN:HD21	35:1d:144:ASP:HB3	1.81	0.45
53:1y:3:MET:HB3	53:1y:3:MET:HE2	1.69	0.45
1:2A:445:C:OP1	16:2U:2:PRO:HA	2.16	0.45
1:2A:1110:G:H1'	1:2A:1111:A:H8	1.77	0.45
1:2A:2262:U:H4'	1:2A:2328:A:C2	2.52	0.45
20:2Y:39:VAL:HB	20:2Y:42:VAL:HB	1.99	0.45
32:2a:546:G:OP1	35:2d:73:ARG:HG2	2.17	0.45
32:2a:671:G:H2'	32:2a:672:U:O4'	2.15	0.45
32:2a:1255:G:O2'	32:2a:1258:G:O2'	2.32	0.45
33:2b:24:TRP:CZ3	33:2b:26:PRO:HA	2.52	0.45
40:2i:18:PHE:HD2	40:2i:62:TYR:CD2	2.35	0.45
44:2m:22:ILE:HD12	44:2m:25:ILE:HD12	1.98	0.45
1:1A:2155:G:H3'	1:1A:2179:G:N2	2.31	0.45
32:1a:1232:U:OP1	40:1i:124:GLN:NE2	2.29	0.45
33:1b:214:ILE:HD13	33:1b:214:ILE:HA	1.82	0.45
38:1g:106:GLN:O	38:1g:110:GLN:HG2	2.16	0.45
46:1o:23:GLY:N	61:1o:3101:HOH:O	2.27	0.45
1:2A:994:C:H3'	16:2U:54:LYS:HE3	1.98	0.45
1:2A:1533:G:N2	1:2A:1536:C:N3	2.64	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2497:A:H5''	61:2A:4548:HOH:O	2.16	0.45
11:2P:99:LEU:HD23	11:2P:100:LEU:HD23	1.98	0.45
32:2a:457:C:H2'	32:2a:458:C:C6	2.50	0.45
32:2a:1269:A:H2	32:2a:1312:G:N3	2.15	0.45
41:2j:16:LEU:HD12	41:2j:94:VAL:HG22	1.98	0.45
47:2p:74:LEU:HD23	47:2p:79:VAL:HG11	1.99	0.45
1:1A:1124:U:C4	1:1A:1134:A:H5''	2.52	0.45
1:1A:1221:G:N2	1:1A:1223:C:OP1	2.40	0.45
1:1A:1405:A:N6	1:1A:1418:U:H3	2.14	0.45
1:1A:1594:C:H2'	1:1A:1595:C:H6	1.82	0.45
1:1A:1895:U:OP1	1:1A:2422:G:O2'	2.25	0.45
1:1A:1942:4OC:HM22	1:1A:1943:G:H5'	1.99	0.45
1:1A:2347:A:OP2	14:1S:13:ARG:HG3	2.16	0.45
1:1A:2455:C:OP1	5:1F:68:LYS:HD3	2.17	0.45
1:1A:2699:U:H2'	1:1A:2700:U:O4'	2.16	0.45
11:1P:94:GLU:HG3	11:1P:124:LYS:HD3	1.99	0.45
20:1Y:56:PRO:C	20:1Y:58:GLY:H	2.24	0.45
32:1a:328:C:H4'	32:1a:329:A:H5'	1.97	0.45
32:1a:1016:A:H2'	32:1a:1017:G:O4'	2.17	0.45
32:1a:1304:G:C6	32:1a:1305:G:N1	2.85	0.45
33:1b:79:ASP:O	33:1b:83:MET:HG2	2.16	0.45
1:2A:623:G:H2'	1:2A:624:C:C6	2.52	0.45
1:2A:1224:C:O2'	17:2V:85:LYS:HA	2.17	0.45
1:2A:2298:A:H2'	1:2A:2299:G:O4'	2.16	0.45
32:2a:107:G:N7	51:2t:15:ARG:NH2	2.64	0.45
32:2a:1251:A:HO2'	32:2a:1369:C:HO2'	1.55	0.45
32:2a:1466:C:H2'	32:2a:1467:G:O4'	2.17	0.45
34:2c:5:ILE:HD12	34:2c:5:ILE:HA	1.80	0.45
43:2l:58:VAL:O	43:2l:65:GLU:HA	2.16	0.45
46:2o:35:ARG:NH2	46:2o:59:MET:HE2	2.31	0.45
47:2p:21:VAL:HG22	47:2p:33:ILE:HD12	1.99	0.45
1:1A:2190:G:C2	1:1A:2193:A:C8	3.05	0.45
4:1E:7:VAL:HG13	4:1E:27:LEU:HB3	1.99	0.45
32:1a:79:G:C6	32:1a:90:U:N3	2.85	0.45
32:1a:834:C:C2	32:1a:853:G:C2	3.04	0.45
32:1a:1236:A:OP1	52:1u:3:LYS:HG3	2.17	0.45
32:1a:1366:C:H2'	32:1a:1367:C:H6	1.81	0.45
39:1h:21:LYS:O	39:1h:65:TYR:OH	2.27	0.45
1:2A:1098:A:H3'	1:2A:1099:G:H8	1.82	0.45
1:2A:1818:U:O4	3:2D:154:LYS:HD2	2.17	0.45
4:2E:101:ARG:NH1	4:2E:171:GLU:HB2	2.32	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:2G:11:TYR:HA	6:2G:15:VAL:HB	1.98	0.45
9:2N:60:ILE:HG13	9:2N:61:ARG:H	1.80	0.45
14:2S:85:VAL:HG11	14:2S:110:LEU:HG	1.99	0.45
20:2Y:38:ILE:HD13	20:2Y:66:PRO:HA	1.97	0.45
32:2a:582:U:C2	32:2a:760:G:C6	3.05	0.45
32:2a:1281:U:O5'	32:2a:1282:C:H5	2.00	0.45
52:2u:2:GLY:O	52:2u:4:GLY:N	2.50	0.45
1:1A:215:G:N2	1:1A:217:A:H62	2.15	0.45
1:1A:1417:G:H2'	1:1A:1418:U:H5	1.82	0.45
12:1Q:21:THR:HG23	12:1Q:99:PRO:O	2.17	0.45
21:1Z:75:ASN:O	21:1Z:84:GLU:HG2	2.17	0.45
32:1a:141:A:H1'	32:1a:182:U:O2	2.16	0.45
32:1a:629:G:H2'	32:1a:630:G:O4'	2.17	0.45
32:1a:1410:G:H2'	32:1a:1411:C:C6	2.52	0.45
35:1d:61:LYS:HD2	35:1d:207:TYR:OH	2.16	0.45
1:2A:471:A:H8	1:2A:471:A:O5'	2.00	0.45
1:2A:874:G:O2'	21:2Z:120:ILE:HD11	2.17	0.45
1:2A:1035:U:H2'	1:2A:1036:G:C8	2.52	0.45
1:2A:1831:G:H2'	1:2A:1832:C:C6	2.52	0.45
2:2B:17:C:H2'	2:2B:18:G:O4'	2.16	0.45
7:2H:140:LYS:HB2	7:2H:140:LYS:HE3	1.82	0.45
12:2Q:111:GLU:O	12:2Q:115:MET:HG2	2.17	0.45
15:2T:95:ARG:HG2	15:2T:95:ARG:NH1	2.32	0.45
22:20:10:THR:O	61:20:5001:HOH:O	2.21	0.45
32:2a:458:C:H2'	32:2a:460:G:O4'	2.17	0.45
32:2a:1084:G:H5'	32:2a:1102:A:OP2	2.17	0.45
32:2a:1423:G:H2'	32:2a:1424:C:C6	2.51	0.45
33:2b:33:TYR:N	33:2b:41:ILE:O	2.32	0.45
1:1A:416:G:O6	11:1P:70:GLN:HB3	2.17	0.44
1:1A:1926:G:O2'	1:1A:1950:A:N1	2.49	0.44
2:1B:93:G:OP1	21:1Z:80:ARG:NH2	2.48	0.44
10:1O:64:ARG:HB2	10:1O:79:PHE:CG	2.52	0.44
23:11:69:LYS:HA	23:11:69:LYS:HD2	1.81	0.44
32:1a:279:A:N6	48:1q:98:LEU:O	2.49	0.44
32:1a:418:C:H1'	32:1a:540:G:O2'	2.17	0.44
32:1a:1479:C:H2'	32:1a:1480:G:H8	1.82	0.44
50:1s:61:TYR:HE2	50:1s:63:THR:HG22	1.82	0.44
53:1y:40:ILE:HB	53:1y:51:ASP:HB2	1.99	0.44
1:2A:184:C:H2'	1:2A:185:U:C6	2.52	0.44
1:2A:422:A:H2'	1:2A:423:A:C8	2.53	0.44
1:2A:1589:C:H2'	1:2A:1590:U:H6	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1916:A:H2'	1:2A:1917:PSU:O4'	2.17	0.44
1:2A:2788:C:N3	1:2A:2789:C:N4	2.64	0.44
4:2E:9:VAL:HG22	4:2E:25:VAL:HB	1.98	0.44
6:2G:15:VAL:HA	6:2G:175:LEU:HD23	1.99	0.44
10:2O:105:GLU:OE1	10:2O:105:GLU:N	2.48	0.44
26:24:53:GLU:HG2	26:24:55:ARG:H	1.81	0.44
32:2a:189(F):U:C4	48:2q:72:ARG:NH1	2.85	0.44
32:2a:1221:G:OP1	32:2a:1320:C:N4	2.50	0.44
32:2a:1493:A:H2'	32:2a:1494:G:H5'	1.99	0.44
33:2b:236:TYR:CG	33:2b:237:ALA:N	2.86	0.44
34:2c:6:HIS:CE1	34:2c:184:TYR:HD2	2.35	0.44
35:2d:155:LEU:HB3	35:2d:158:ILE:HG22	1.99	0.44
1:1A:924:U:C2'	1:1A:925:A:H5''	2.48	0.44
1:1A:1296:G:N7	11:1P:18:ARG:NH1	2.61	0.44
1:1A:1829:U:H5'	3:1D:259:THR:CG2	2.39	0.44
1:1A:2495:C:N3	12:1Q:124:LYS:NZ	2.55	0.44
1:1A:2724:U:OP1	1:1A:2727:G:H4'	2.17	0.44
4:1E:125:GLY:O	61:1E:3101:HOH:O	2.21	0.44
5:1F:102:PRO:O	5:1F:106:ARG:HG3	2.17	0.44
6:1G:7:LEU:HD22	6:1G:176:LEU:HD22	1.98	0.44
6:1G:32:PRO:HB3	6:1G:163:ALA:HB2	1.98	0.44
9:1N:67:LEU:O	9:1N:88:GLU:HG3	2.17	0.44
20:1Y:47:LYS:HD2	20:1Y:63:LYS:HE3	1.98	0.44
32:1a:164:U:H2'	32:1a:165:C:C6	2.52	0.44
32:1a:491:G:H2'	32:1a:492:G:O4'	2.16	0.44
32:1a:714:G:H2'	32:1a:715:A:C8	2.52	0.44
35:1d:178:VAL:C	35:1d:180:GLY:H	2.25	0.44
1:2A:335:C:H4'	20:2Y:73:ARG:HD2	1.99	0.44
1:2A:1514:U:H2'	1:2A:1515:G:C8	2.50	0.44
1:2A:1583:A:OP1	1:2A:1584:C:H5	2.00	0.44
1:2A:2693:A:H2'	1:2A:2694:G:H8	1.82	0.44
3:2D:16:MET:HG3	3:2D:206:LEU:O	2.16	0.44
5:2F:32:LEU:O	5:2F:36:VAL:HG23	2.17	0.44
32:2a:256:U:H2'	32:2a:257:G:C8	2.53	0.44
32:2a:620:C:C2	35:2d:135:LEU:HG	2.53	0.44
32:2a:839:U:H5''	32:2a:840:C:H5	1.82	0.44
32:2a:1328:C:H2'	32:2a:1329:A:O4'	2.17	0.44
34:2c:152:ILE:HG12	34:2c:167:TRP:HB2	1.99	0.44
37:2f:46:ARG:HB3	37:2f:60:PHE:CE2	2.52	0.44
38:2g:22:LEU:HG	38:2g:62:PHE:HE2	1.83	0.44
39:2h:10:LEU:HG	39:2h:10:LEU:H	1.62	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:2t:67:ALA:HB2	51:2t:77:ALA:HB2	1.99	0.44
52:2u:2:GLY:C	52:2u:4:GLY:H	2.26	0.44
1:1A:208:G:OP2	61:1A:4172:HOH:O	2.21	0.44
1:1A:272:U:H5'	8:1I:50:ARG:HH12	1.83	0.44
1:1A:312:C:H2'	1:1A:313:A:C8	2.52	0.44
1:1A:843:C:H2'	1:1A:844:C:C6	2.53	0.44
1:1A:1549:U:H2'	1:1A:1550:C:C6	2.51	0.44
3:1D:260:ARG:NH2	3:1D:266:SER:OG	2.48	0.44
6:1G:106:LEU:HA	6:1G:110:ALA:HB3	1.99	0.44
9:1N:62:VAL:CG1	9:1N:66:LYS:HB2	2.46	0.44
32:1a:1003:G:C2	32:1a:1004:A:N3	2.85	0.44
32:1a:1196:U:H3	34:1c:162:GLN:HE22	1.66	0.44
32:1a:1504:G:OP1	32:1a:1507:A:H4'	2.18	0.44
43:1l:54:LYS:HD2	43:1l:54:LYS:N	2.32	0.44
49:1r:47:THR:HG23	49:1r:49:LYS:HG3	1.99	0.44
1:2A:1085:A:H2'	1:2A:1085:A:N3	2.33	0.44
1:2A:2114:A:C2	1:2A:2115:G:H1'	2.52	0.44
1:2A:2184:G:H2'	1:2A:2185:C:O4'	2.17	0.44
6:2G:139:LEU:HA	6:2G:144:ILE:HB	1.99	0.44
16:2U:88:ILE:HG22	16:2U:90:VAL:HG23	1.99	0.44
32:2a:244:U:H4'	32:2a:245:C:H5''	1.99	0.44
35:2d:111:ALA:HB1	35:2d:116:GLN:HE21	1.81	0.44
42:2k:16:SER:O	42:2k:35:PRO:HG3	2.17	0.44
47:2p:23:ASP:OD1	47:2p:25:ARG:HG2	2.17	0.44
49:2r:33:ASP:OD2	49:2r:36:ASN:HB2	2.16	0.44
1:1A:1338:U:H2'	1:1A:1339:C:C6	2.52	0.44
1:1A:1374:G:O2'	1:1A:1375:U:H2'	2.18	0.44
1:1A:2211:U:H2'	1:1A:2212:G:H8	1.82	0.44
1:1A:2579:G:H2'	1:1A:2580:C:C6	2.52	0.44
4:1E:9:VAL:HG22	4:1E:25:VAL:HB	1.98	0.44
26:14:15:ILE:HB	26:14:32:TYR:HD1	1.81	0.44
27:15:34:PRO:HG2	27:15:35:GLU:OE1	2.17	0.44
32:1a:736:C:H2'	32:1a:737:A:C8	2.52	0.44
32:1a:967:5MC:H2'	32:1a:968:A:C8	2.52	0.44
33:1b:134:GLU:CG	33:1b:137:ARG:HH21	2.30	0.44
1:2A:760:G:H2'	1:2A:761:A:O4'	2.17	0.44
1:2A:782:A:H5'	1:2A:783:A:N7	2.33	0.44
1:2A:2811:G:OP1	4:2E:60:ASN:HB2	2.17	0.44
4:2E:5:LEU:HD11	4:2E:79:ARG:HB2	2.00	0.44
20:2Y:102:CYS:SG	20:2Y:103:GLY:N	2.91	0.44
32:2a:309:G:H2'	32:2a:310:G:H8	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:848:C:H2'	32:2a:849:C:H6	1.81	0.44
32:2a:1038:C:O5'	32:2a:1038:C:H6	2.01	0.44
32:2a:1206:G:H4'	34:2c:192:THR:O	2.16	0.44
34:2c:177:THR:HG22	34:2c:179:ARG:HG2	1.99	0.44
35:2d:119:GLN:O	35:2d:123:HIS:ND1	2.50	0.44
40:2i:85:LEU:O	40:2i:89:ASN:N	2.43	0.44
44:2m:14:ARG:HH21	44:2m:42:ALA:HB2	1.81	0.44
1:1A:1109:G:H5''	1:1A:1111:U:H5	1.83	0.44
1:1A:2717:A:H2'	1:1A:2718:G:O4'	2.18	0.44
31:19:25:VAL:O	31:19:33:LYS:HA	2.17	0.44
32:1a:102:G:O2'	32:1a:151:A:N3	2.47	0.44
32:1a:110:C:H2'	32:1a:111:G:O4'	2.16	0.44
35:1d:187:ARG:NH2	35:1d:193:ASP:OD2	2.49	0.44
39:1h:86:ILE:HG13	39:1h:133:LEU:HD22	2.00	0.44
1:2A:1448:G:H1'	1:2A:1528:A:N1	2.32	0.44
5:2F:33:LEU:HD12	5:2F:33:LEU:HA	1.78	0.44
8:2I:26:ALA:O	8:2I:31:LEU:HB2	2.17	0.44
32:2a:557:G:C6	32:2a:558:G:C6	3.06	0.44
32:2a:1151:A:O2'	32:2a:1152:A:H8	2.01	0.44
46:2o:39:LEU:HB3	46:2o:56:LEU:HD13	1.97	0.44
47:2p:43:LYS:HA	47:2p:48:TRP:HB3	2.00	0.44
1:1A:231:G:C8	30:18:5:LYS:HG2	2.52	0.44
1:1A:2357:G:N3	1:1A:2393:C:H2'	2.33	0.44
61:1A:5741:HOH:O	3:1D:229:VAL:HG22	2.17	0.44
4:1E:170:LEU:HB3	4:1E:184:VAL:CG2	2.48	0.44
5:1F:140:LEU:HD11	5:1F:170:LEU:HD11	2.00	0.44
5:1F:183:VAL:HG13	61:1F:437:HOH:O	2.16	0.44
6:1G:5:VAL:CG2	6:1G:8:LYS:H	2.30	0.44
9:1N:99:LEU:HD23	9:1N:99:LEU:HA	1.76	0.44
14:1S:110:LEU:HD12	14:1S:110:LEU:HA	1.73	0.44
15:1T:37:GLY:HA2	15:1T:38:ASN:HA	1.62	0.44
32:1a:186:C:H2'	32:1a:187:C:H6	1.82	0.44
32:1a:789:U:O2'	32:1a:791:G:N7	2.37	0.44
32:1a:1162:C:H2'	32:1a:1163:C:C6	2.53	0.44
32:1a:1226:C:H4'	32:1a:1227:A:OP1	2.18	0.44
32:1a:1254:C:H42	32:1a:1283:G:H1	1.64	0.44
32:1a:1400:5MC:C2	53:1y:63:ALA:HA	2.53	0.44
36:1e:110:LEU:HD13	36:1e:118:ILE:HD13	1.98	0.44
51:1t:43:LEU:O	51:1t:47:GLY:N	2.51	0.44
1:2A:443:A:N7	5:2F:45:ARG:HG2	2.33	0.44
1:2A:720:C:H2'	1:2A:721:C:C6	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1131:G:O6	1:2A:2040:C:H1'	2.17	0.44
1:2A:1991:U:H2'	1:2A:1992:G:H5''	1.98	0.44
1:2A:2142:C:H2'	1:2A:2143:C:C6	2.53	0.44
10:2O:15:GLY:HA2	10:2O:47:ILE:HD11	1.99	0.44
15:2T:53:ARG:HB3	15:2T:53:ARG:CZ	2.46	0.44
32:2a:765:G:H5''	32:2a:766:A:OP1	2.18	0.44
32:2a:947:G:O3'	44:2m:109:THR:OG1	2.36	0.44
34:2c:112:SER:O	34:2c:116:VAL:HG23	2.17	0.44
34:2c:131:ARG:HD3	34:2c:166:GLU:OE2	2.17	0.44
42:2k:18:ARG:NH2	42:2k:35:PRO:O	2.49	0.44
43:2l:110:VAL:HB	43:2l:113:ARG:HG2	2.00	0.44
44:2m:91:ARG:NE	44:2m:97:PRO:O	2.49	0.44
1:1A:116:A:C8	1:1A:117:A:C8	3.05	0.44
1:1A:1110:C:OP2	1:1A:1111:U:H6	2.01	0.44
1:1A:1140:U:C2	1:1A:1142:A:H5''	2.53	0.44
1:1A:2334:A:H2'	1:1A:2335:G:O4'	2.17	0.44
5:1F:34:TRP:NE1	11:1P:8:PRO:HD3	2.32	0.44
6:1G:58:GLN:O	6:1G:62:LEU:HG	2.17	0.44
32:1a:7:G:H21	36:1e:121:LYS:HG2	1.80	0.44
32:1a:1151:A:O2'	32:1a:1152:A:H8	2.01	0.44
32:1a:1343:G:O2'	40:1i:121:ARG:HD2	2.18	0.44
32:1a:1456:G:N1	51:1t:51:GLU:OE2	2.49	0.44
35:1d:107:ARG:NH2	35:1d:114:ARG:HH22	2.14	0.44
41:1j:30:SER:OG	41:1j:81:THR:HG22	2.17	0.44
50:1s:48:THR:HG22	50:1s:61:TYR:HD1	1.83	0.44
1:2A:875:G:H2'	1:2A:876:C:O4'	2.17	0.44
1:2A:1032:A:H2	1:2A:1122:G:H22	1.65	0.44
1:2A:1495:A:H2'	1:2A:1496:A:C8	2.53	0.44
1:2A:2143:C:H2'	1:2A:2144:U:H5'	2.00	0.44
1:2A:2693:A:H2'	1:2A:2694:G:C8	2.53	0.44
4:2E:28:ALA:HB3	4:2E:93:VAL:CG1	2.46	0.44
6:2G:142:PRO:O	26:24:31:ILE:HD13	2.17	0.44
8:2I:62:LYS:HG2	8:2I:133:HIS:CE1	2.53	0.44
17:2V:31:ALA:O	17:2V:61:VAL:HG22	2.17	0.44
31:29:3:VAL:HA	31:29:35:ARG:O	2.17	0.44
32:2a:222:U:H2'	32:2a:223:U:H6	1.79	0.44
32:2a:373:A:O2'	32:2a:451:A:N7	2.50	0.44
32:2a:1135:U:H2'	32:2a:1137:C:N3	2.32	0.44
32:2a:1190:G:H5'	34:2c:176:HIS:HE1	1.83	0.44
33:2b:46:LYS:O	33:2b:50:GLU:HG2	2.18	0.44
35:2d:22:LYS:HD2	60:2d:501:SF4:S3	2.58	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:2n:23:ARG:NH1	45:2n:30:ALA:HB2	2.32	0.44
1:1A:2135:U:O4	1:1A:2190:G:H4'	2.17	0.44
1:1A:2137:G:N3	1:1A:2139:A:N6	2.66	0.44
5:1F:129:PHE:O	5:1F:132:VAL:HG13	2.18	0.44
15:1T:108:ARG:HA	15:1T:111:ARG:NH1	2.33	0.44
32:1a:96:U:H2'	32:1a:97:G:C8	2.53	0.44
32:1a:235:C:H5'	48:1q:70:ARG:HG3	2.00	0.44
32:1a:401:C:OP2	35:1d:73:ARG:NH2	2.51	0.44
32:1a:998:G:H2'	32:1a:999:C:C6	2.53	0.44
44:1m:49:THR:HG22	44:1m:51:ALA:H	1.83	0.44
1:2A:108:U:H2'	1:2A:109:G:C8	2.53	0.44
1:2A:1097:U:H2'	1:2A:1098:A:O4'	2.17	0.44
1:2A:1518:U:H2'	1:2A:1519:G:O4'	2.18	0.44
1:2A:1550:C:OP1	1:2A:1720:U:O2'	2.28	0.44
9:2N:60:ILE:HG13	9:2N:61:ARG:N	2.33	0.44
11:2P:38:GLN:HB3	11:2P:45:LEU:HD23	2.00	0.44
16:2U:8:VAL:HG13	16:2U:11:ARG:NH2	2.32	0.44
19:2X:2:LYS:NZ	19:2X:38:GLU:OE2	2.41	0.44
20:2Y:43:ASN:HD22	20:2Y:67:LEU:HD21	1.83	0.44
32:2a:545:C:H5'	35:2d:72:GLU:HB2	2.00	0.44
32:2a:944:G:C2	32:2a:1340:A:C6	3.06	0.44
32:2a:1229:A:H1'	53:2y:4:ASN:HD21	1.83	0.44
32:2a:1346:A:H61	32:2a:1374:A:H3'	1.83	0.44
33:2b:48:MET:HA	33:2b:51:LEU:HD12	2.00	0.44
34:2c:8:ILE:HG23	34:2c:16:ARG:CD	2.47	0.44
34:2c:111:LEU:HD21	34:2c:146:ALA:HB2	1.99	0.44
40:2i:102:LEU:HD12	40:2i:103:THR:HB	2.00	0.44
44:2m:51:ALA:HA	44:2m:54:VAL:HG22	1.99	0.44
1:1A:1099:C:O2	1:1A:1152:G:N1	2.49	0.44
1:1A:2411:G:H3'	61:1A:4150:HOH:O	2.17	0.44
12:1Q:35:VAL:CG1	12:1Q:130:LYS:HB3	2.48	0.44
13:1R:79:LEU:HA	13:1R:83:ILE:HB	2.00	0.44
21:1Z:125:LEU:HB3	21:1Z:165:VAL:HG13	2.00	0.44
32:1a:473:G:H2'	32:1a:474:G:C8	2.52	0.44
32:1a:684:A:O2'	42:1k:39:PRO:O	2.33	0.44
38:1g:54:THR:O	38:1g:56:GLN:N	2.50	0.44
45:1n:48:ALA:HB2	45:1n:53:LEU:HD12	1.99	0.44
1:2A:102:G:OP1	24:22:7:ARG:NH2	2.50	0.44
1:2A:833:U:O2	11:2P:55:ARG:NH1	2.49	0.44
1:2A:1939:5MU:OP1	1:2A:2604:U:O2'	2.36	0.44
6:2G:12:TYR:HA	6:2G:16:ARG:HG3	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:2N:34:LEU:HD12	9:2N:34:LEU:HA	1.88	0.44
19:2X:94:GLY:HA3	19:2X:95:LEU:C	2.43	0.44
21:2Z:29:TYR:HB3	21:2Z:34:ASN:HD22	1.83	0.44
21:2Z:151:HIS:HA	21:2Z:170:THR:HA	1.99	0.44
26:24:68:ARG:O	26:24:69:LYS:HB3	2.18	0.44
32:2a:500:G:H2'	32:2a:501:C:C6	2.53	0.44
32:2a:870:U:H6	32:2a:870:U:H5'	1.83	0.44
32:2a:953:G:C6	32:2a:954:G:C4	3.06	0.44
36:2e:19:MET:SD	36:2e:24:ARG:HB3	2.58	0.44
1:1A:387:G:H2'	1:1A:388:A:H8	1.83	0.43
1:1A:1314:A:H2'	1:1A:1315:A:O4'	2.18	0.43
1:1A:1630:A:H5'	1:1A:1631:C:OP1	2.18	0.43
1:1A:2162:C:N3	1:1A:2173:G:O6	2.51	0.43
1:1A:2371:C:H2'	1:1A:2372:A:O4'	2.18	0.43
1:1A:2874:G:OP1	15:1T:119:LYS:HD2	2.18	0.43
5:1F:178:PRO:HB2	5:1F:201:VAL:CG2	2.48	0.43
5:1F:192:LEU:HD13	5:1F:194:MET:HE2	2.00	0.43
12:1Q:58:PHE:O	12:1Q:60:ARG:N	2.50	0.43
32:1a:189(K):U:H2'	32:1a:189(L):G:C8	2.53	0.43
36:1e:80:ILE:HG22	36:1e:91:LEU:HB2	1.99	0.43
38:1g:152:ALA:O	38:1g:155:ARG:NH1	2.51	0.43
46:1o:21:ASP:OD1	46:1o:24:SER:HB3	2.18	0.43
1:2A:1016:G:C4	1:2A:1017:G:C8	3.06	0.43
1:2A:1772:G:O6	57:2A:3710:MPD:H32	2.18	0.43
1:2A:2051:A:H5'	1:2A:2578:G:O4'	2.17	0.43
1:2A:2141:G:C6	1:2A:2151:G:C6	3.06	0.43
1:2A:2287:A:O2'	1:2A:2289:G:N7	2.36	0.43
1:2A:2323:G:H1	1:2A:2332:U:H3	1.66	0.43
1:2A:2611:U:H6	1:2A:2611:U:H5'	1.83	0.43
1:2A:2836:U:H2'	1:2A:2837:G:C8	2.53	0.43
7:2H:13:LYS:HA	7:2H:14:GLY:HA2	1.59	0.43
20:2Y:73:ARG:HG2	20:2Y:73:ARG:HH11	1.82	0.43
21:2Z:182:LYS:HD2	61:2Z:306:HOH:O	2.18	0.43
32:2a:613:C:H4'	61:2d:602:HOH:O	2.17	0.43
34:2c:109:PRO:HB3	34:2c:115:LEU:HD23	1.99	0.43
39:2h:49:GLU:HG2	39:2h:62:TYR:HE2	1.83	0.43
41:2j:5:ARG:N	61:2j:8101:HOH:O	2.50	0.43
48:2q:6:LEU:O	48:2q:58:GLU:HA	2.17	0.43
1:1A:1686:U:H4'	1:1A:2711:C:H4'	2.00	0.43
1:1A:2346:G:H5'	14:1S:9:ARG:HG2	1.99	0.43
7:1H:84:SER:HA	7:1H:133:VAL:O	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:1V:58:VAL:HG12	17:1V:97:LYS:HB2	1.99	0.43
20:1Y:92:ASN:HB2	20:1Y:94:LYS:N	2.19	0.43
24:12:32:LEU:HD22	24:12:36:ARG:NH1	2.34	0.43
25:13:55:ARG:NH1	61:13:202:HOH:O	2.51	0.43
32:1a:376:G:OP1	47:1p:5:ARG:HB2	2.18	0.43
32:1a:392:G:H2'	32:1a:393:A:H8	1.84	0.43
32:1a:936:C:H2'	32:1a:937:A:O4'	2.18	0.43
32:1a:1508:G:H2'	32:1a:1509:C:O4'	2.18	0.43
37:1f:99:ALA:HB2	49:1r:31:LEU:HD11	2.00	0.43
41:1j:64:GLU:OE2	41:1j:66:ARG:HD2	2.17	0.43
44:1m:19:LEU:HD11	44:1m:56:LEU:HD21	1.99	0.43
51:1t:47:GLY:HA2	51:1t:48:LYS:HB2	1.99	0.43
1:2A:244:A:C2	1:2A:255:A:C4	3.06	0.43
1:2A:1504:C:H2'	1:2A:1505:C:C6	2.54	0.43
2:2B:42:C:N4	6:2G:91:ARG:HH22	2.16	0.43
3:2D:84:TYR:HE2	3:2D:86:PRO:HB3	1.83	0.43
9:2N:30:ILE:HG23	9:2N:52:VAL:HG11	2.00	0.43
13:2R:63:ARG:O	13:2R:67:LEU:HB2	2.18	0.43
15:2T:118:ARG:HG2	32:2a:1442(A):G:C8	2.53	0.43
16:2U:34:LYS:HA	16:2U:34:LYS:HD2	1.70	0.43
32:2a:38:G:H22	32:2a:397:A:H5''	1.83	0.43
32:2a:254:G:OP1	48:2q:66:SER:OG	2.24	0.43
32:2a:262:A:H4'	51:2t:75:ASN:HB2	2.00	0.43
32:2a:404:U:H2'	32:2a:405:U:C6	2.53	0.43
32:2a:1289:A:N1	32:2a:1371:G:O2'	2.36	0.43
33:2b:118:LEU:O	33:2b:122:PHE:HB3	2.18	0.43
53:2y:52:ALA:HB1	53:2y:81:LEU:HD11	2.00	0.43
1:1A:123:G:O2'	29:17:48:LYS:HE3	2.17	0.43
1:1A:637:U:H5'	1:1A:640:A:N6	2.33	0.43
1:1A:929:G:H1	1:1A:940:C:H42	1.66	0.43
1:1A:1634:C:H2'	1:1A:1635:C:C6	2.52	0.43
1:1A:1815:A:H4'	1:1A:1816:A:O5'	2.18	0.43
1:1A:2071:G:H5''	61:1A:4313:HOH:O	2.17	0.43
1:1A:2533:C:C4	1:1A:2534:U:C4	3.06	0.43
1:1A:2858:G:H3'	15:1T:95:ARG:O	2.18	0.43
1:1A:2889:C:OP2	61:1A:4173:HOH:O	2.21	0.43
26:14:49:PHE:HB3	26:14:50:VAL:H	1.47	0.43
31:19:25:VAL:HB	31:19:34:GLN:HB2	1.99	0.43
32:1a:1162:C:H2'	32:1a:1163:C:H6	1.82	0.43
32:1a:1360:A:H2'	32:1a:1361:G:O4'	2.18	0.43
32:1a:1519:MA6:H8	32:1a:1519:MA6:O5'	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1e:95:ALA:HB1	36:1e:96:PRO:HD2	2.00	0.43
1:2A:459:U:H4'	29:27:40:TRP:CZ3	2.52	0.43
1:2A:724:U:H2'	1:2A:725:G:O4'	2.18	0.43
5:2F:132:VAL:O	5:2F:133:ASN:ND2	2.51	0.43
6:2G:161:THR:CG2	6:2G:163:ALA:H	2.31	0.43
26:24:8:LYS:O	26:24:27:THR:HG22	2.18	0.43
32:2a:1029:C:O2	32:2a:1032:G:N1	2.51	0.43
32:2a:1029:C:N3	32:2a:1032:G:O6	2.51	0.43
32:2a:1030(A):G:H1'	32:2a:1030(C):G:C5	2.52	0.43
32:2a:1086:U:H2'	32:2a:1087:G:H8	1.83	0.43
33:2b:128:GLU:CD	33:2b:135:GLN:HE21	2.26	0.43
45:2n:27:CYS:SG	45:2n:29:ARG:HB2	2.59	0.43
1:1A:465:G:H2'	1:1A:466:G:H8	1.83	0.43
1:1A:599:U:H2'	1:1A:600:G:C8	2.54	0.43
1:1A:956:A:N1	1:1A:2289:G:H1'	2.34	0.43
1:1A:2402:U:P	30:18:35:GLN:HE22	2.42	0.43
2:1B:13:A:N1	2:1B:69:G:O2'	2.45	0.43
3:1D:108:PRO:HG3	3:1D:143:HIS:CE1	2.53	0.43
11:1P:141:ALA:HA	25:23:38:GLU:HG2	2.01	0.43
32:1a:45:U:H2'	32:1a:46:G:C8	2.53	0.43
32:1a:114:U:H1'	32:1a:353:A:H1'	2.00	0.43
32:1a:1034:G:C2	32:1a:1035:A:H1'	2.53	0.43
32:1a:1505:G:OP2	61:1a:3311:HOH:O	2.21	0.43
35:1d:188:LEU:HA	35:1d:189:PRO:HD3	1.88	0.43
1:2A:1450:G:H2'	1:2A:1450(A):C:C6	2.53	0.43
1:2A:2130:U:H3'	1:2A:2130:U:H6	1.84	0.43
1:2A:2553:G:O4'	1:2A:2582:G:O2'	2.34	0.43
2:2B:52:A:C6	14:2S:33:LYS:HE3	2.52	0.43
5:2F:24:LEU:HD21	5:2F:114:VAL:HG12	1.99	0.43
5:2F:101:LEU:HD12	5:2F:102:PRO:HD2	2.00	0.43
7:2H:11:VAL:HG23	7:2H:49:VAL:HA	2.00	0.43
9:2N:73:THR:HA	9:2N:83:LYS:O	2.19	0.43
20:2Y:5:MET:HE2	20:2Y:32:PRO:HA	2.01	0.43
32:2a:59:A:H3'	32:2a:331:G:H22	1.82	0.43
32:2a:129(A):G:C6	32:2a:189(E):U:H4'	2.53	0.43
32:2a:192:U:H2'	32:2a:193:C:C6	2.52	0.43
32:2a:1318:A:O2'	50:2s:37:ARG:HB3	2.18	0.43
32:2a:1323:G:H2'	32:2a:1324:A:C8	2.53	0.43
36:2e:5:ASP:N	36:2e:5:ASP:OD1	2.51	0.43
37:2f:2:ARG:CZ	37:2f:69:GLU:HG2	2.48	0.43
1:1A:297:C:N4	1:1A:298:G:O6	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:886:U:H2'	1:1A:887:C:C6	2.53	0.43
1:1A:1810:U:H2'	61:1A:4556:HOH:O	2.17	0.43
4:1E:16:ARG:NH1	4:1E:171:GLU:OE2	2.42	0.43
5:1F:117:ARG:NH2	61:1F:411:HOH:O	2.51	0.43
9:1N:12:ARG:HG2	9:1N:14:VAL:HG23	2.01	0.43
28:16:12:GLU:OE1	28:16:19:ARG:NH1	2.51	0.43
32:1a:19:C:O2'	32:1a:572:A:N1	2.48	0.43
32:1a:814:A:N7	32:1a:816:A:C4	2.87	0.43
35:1d:196:LEU:O	35:1d:198:VAL:N	2.46	0.43
36:1e:131:ILE:HD13	36:1e:131:ILE:HA	1.85	0.43
40:1i:4:TYR:HA	40:1i:87:GLN:NE2	2.32	0.43
47:1p:8:ARG:C	47:1p:9:PHE:HD1	2.25	0.43
1:2A:93:G:H2'	1:2A:94:C:C6	2.53	0.43
1:2A:1045:A:H5'	1:2A:1047:G:O5'	2.17	0.43
1:2A:1359:A:H61	1:2A:1372:U:H3	1.65	0.43
1:2A:1409:C:H2'	1:2A:1410:G:C8	2.53	0.43
1:2A:1507:A:O2'	1:2A:1508:A:O4'	2.32	0.43
1:2A:1668:A:O2'	1:2A:1674:G:N7	2.46	0.43
1:2A:1847:A:H3'	1:2A:1848:A:H5'	2.00	0.43
1:2A:1952:A:C6	1:2A:1953:A:N1	2.86	0.43
1:2A:1996:C:H4'	1:2A:1997:G:OP1	2.18	0.43
1:2A:2179:C:C4	1:2A:2180:U:C4	3.07	0.43
6:2G:33:ARG:HH21	6:2G:162:THR:HG21	1.83	0.43
9:2N:39:ARG:NH2	9:2N:41:ASP:OD2	2.50	0.43
15:2T:9:LEU:O	15:2T:12:SER:OG	2.35	0.43
25:23:6:VAL:HG13	25:23:54:VAL:HG13	1.99	0.43
32:2a:555:C:H2'	32:2a:556:C:C6	2.53	0.43
32:2a:1034:G:H3'	32:2a:1035:A:H8	1.84	0.43
33:2b:24:TRP:H	33:2b:24:TRP:HD1	1.66	0.43
35:2d:142:PRO:HA	35:2d:185:PHE:HD2	1.83	0.43
51:2t:54:LYS:HB3	51:2t:54:LYS:HE2	1.82	0.43
1:1A:704:U:H2'	1:1A:705:C:C6	2.54	0.43
1:1A:1140:U:O2'	1:1A:1142:A:N7	2.46	0.43
1:1A:2283:G:OP1	22:10:18:ALA:HB1	2.19	0.43
1:1A:2549:U:H2'	1:1A:2550:C:C6	2.54	0.43
8:1I:75:LEU:HD13	8:1I:105:HIS:ND1	2.34	0.43
9:1N:12:ARG:HB3	9:1N:50:ASP:OD1	2.19	0.43
21:1Z:136:PHE:CE1	21:1Z:138:GLU:HG3	2.51	0.43
26:14:69:LYS:HA	50:1s:20:LEU:HD13	2.00	0.43
28:16:44:ARG:HG2	28:16:44:ARG:HH11	1.82	0.43
32:1a:1003:G:N2	32:1a:1004:A:H1'	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1264:C:H2'	32:1a:1265:G:H8	1.84	0.43
32:1a:1299:A:N3	32:1a:1299:A:H5''	2.34	0.43
38:1g:104:LEU:HD13	38:1g:104:LEU:HA	1.92	0.43
40:1i:4:TYR:HB2	40:1i:19:LEU:HB2	2.00	0.43
1:2A:887:A:O2'	1:2A:888:C:H3'	2.18	0.43
1:2A:888:C:OP1	44:2m:93:ARG:NH1	2.52	0.43
1:2A:993:G:N2	17:2V:23:GLU:OE2	2.52	0.43
1:2A:1015:G:O2'	1:2A:1016:G:H5'	2.19	0.43
1:2A:1223:G:N2	1:2A:1226:A:OP2	2.38	0.43
1:2A:1430:C:H2'	1:2A:1431:U:C6	2.53	0.43
1:2A:1504:C:H2'	1:2A:1505:C:H6	1.83	0.43
1:2A:2567:G:H2'	1:2A:2568:C:C6	2.53	0.43
5:2F:74:ARG:HD2	61:2F:3107:HOH:O	2.19	0.43
6:2G:15:VAL:HG13	6:2G:175:LEU:HD23	2.00	0.43
18:2W:29:LEU:HD21	18:2W:33:ARG:NH2	2.33	0.43
21:2Z:99:TYR:HA	21:2Z:124:ILE:O	2.18	0.43
32:2a:448:A:P	32:2a:485:G:H22	2.42	0.43
32:2a:931:C:N4	32:2a:1386:G:H1	2.15	0.43
32:2a:939:G:H2'	32:2a:940:C:H6	1.84	0.43
32:2a:1054:C:H41	53:2y:46:GLN:CG	2.31	0.43
32:2a:1292:U:H5'	40:2i:38:GLN:HE21	1.84	0.43
32:2a:1349:A:C4	32:2a:1350:A:C8	3.07	0.43
1:1A:217:A:H2'	1:1A:219:U:O4'	2.19	0.43
1:1A:233:A:C2	1:1A:244:A:C4	3.07	0.43
6:1G:72:ARG:HG2	6:1G:87:PRO:HA	2.00	0.43
6:1G:110:ALA:HA	6:1G:140:ILE:O	2.19	0.43
7:1H:20:ALA:HB1	7:1H:21:PRO:HD2	2.00	0.43
32:1a:359:U:H2'	32:1a:360:A:C8	2.53	0.43
32:1a:376:G:H4'	47:1p:5:ARG:NH1	2.34	0.43
32:1a:1374:A:OP1	38:1g:36:LYS:NZ	2.52	0.43
34:1c:22:TRP:HB3	34:1c:59:ARG:HB2	2.01	0.43
37:1f:61:LEU:HD23	37:1f:63:TYR:OH	2.18	0.43
39:1h:14:ARG:NH1	39:1h:83:ILE:O	2.50	0.43
39:1h:19:VAL:HG23	39:1h:21:LYS:HG2	2.00	0.43
40:1i:16:ARG:HB2	40:1i:64:THR:HG22	2.01	0.43
44:1m:15:VAL:HG13	44:1m:43:THR:O	2.18	0.43
47:1p:6:LEU:HB3	47:1p:17:TYR:CD1	2.54	0.43
1:2A:361:G:O2'	1:2A:362:U:H5'	2.18	0.43
1:2A:2461:C:H2'	1:2A:2462:U:C6	2.54	0.43
4:2E:11:MET:CG	4:2E:24:THR:HG22	2.46	0.43
4:2E:36:ARG:HG2	4:2E:47:VAL:HG12	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:78:G:C2	32:2a:79:G:H1'	2.54	0.43
32:2a:187:C:H2'	32:2a:188:C:H6	1.83	0.43
32:2a:273:A:H1'	48:2q:16:GLN:NE2	2.34	0.43
32:2a:542:G:OP1	35:2d:10:ARG:NH1	2.42	0.43
32:2a:848:C:O5'	32:2a:848:C:H6	2.02	0.43
33:2b:40:HIS:HB2	33:2b:190:THR:HG21	2.00	0.43
34:2c:139:GLN:HE21	34:2c:143:GLU:HG3	1.83	0.43
35:2d:111:ALA:HB1	35:2d:116:GLN:HG2	2.01	0.43
36:2e:90:VAL:O	36:2e:120:THR:HA	2.18	0.43
41:2j:6:ILE:HB	41:2j:72:VAL:HG22	2.01	0.43
1:1A:1335:C:H2'	1:1A:1336:C:H6	1.83	0.43
1:1A:1935:A:C2	32:1a:1493:A:H8	2.36	0.43
1:1A:2603:C:H2'	1:1A:2604:G:C8	2.54	0.43
2:1B:96:U:H2'	2:1B:97:G:C8	2.54	0.43
26:14:40:HIS:HB3	26:14:43:TYR:HD2	1.84	0.43
38:1g:22:LEU:HD13	38:1g:97:GLN:OE1	2.19	0.43
42:1k:32:ILE:HG22	42:1k:77:MET:HE3	2.00	0.43
47:1p:20:VAL:HG21	47:1p:32:TYR:CG	2.54	0.43
1:2A:207:A:H2'	1:2A:208:C:O4'	2.19	0.43
1:2A:478:A:N1	1:2A:500:G:H4'	2.33	0.43
1:2A:570:G:H5''	61:2A:5018:HOH:O	2.18	0.43
1:2A:1315:C:OP2	61:2A:3810:HOH:O	2.20	0.43
1:2A:1525:G:H2'	1:2A:1526:G:H8	1.83	0.43
1:2A:2037:G:H2'	1:2A:2038:G:C8	2.54	0.43
1:2A:2602:A:H1'	1:2A:2603:G:O5'	2.17	0.43
2:2B:43:C:C4	2:2B:45:A:C6	3.07	0.43
7:2H:40:GLU:OE1	7:2H:60:ARG:NH1	2.49	0.43
24:22:10:LEU:HD21	24:22:59:ARG:HD2	2.01	0.43
24:22:53:LEU:HD23	24:22:53:LEU:HA	1.88	0.43
25:23:6:VAL:HG12	25:23:28:LEU:HD11	2.00	0.43
32:2a:539:A:H2'	32:2a:540:G:C8	2.54	0.43
32:2a:598:U:H4'	39:2h:94:TYR:CD2	2.53	0.43
32:2a:1281:U:H6	32:2a:1281:U:H2'	1.65	0.43
46:2o:16:ALA:HB1	46:2o:21:ASP:HB3	2.01	0.43
50:2s:41:VAL:HG22	50:2s:42:PRO:HD2	1.99	0.43
1:1A:592:U:C4	1:1A:593:G:C6	3.07	0.43
1:1A:1557:A:H2'	1:1A:1558:G:O4'	2.19	0.43
1:1A:1566:U:H2'	1:1A:1567:G:O4'	2.19	0.43
1:1A:1825:U:H2'	1:1A:1826:C:H6	1.84	0.43
1:1A:2388:A:H2'	1:1A:2389:A:O4'	2.19	0.43
1:1A:2846:U:H2'	1:1A:2847:G:C8	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:1F:108:LYS:HD2	5:1F:112:MET:HE3	2.01	0.43
6:1G:46:ALA:HB1	6:1G:51:ARG:HA	2.01	0.43
13:1R:118:GLU:H	13:1R:118:GLU:CD	2.27	0.43
16:1U:58:ARG:HA	16:1U:61:TRP:CE3	2.54	0.43
21:1Z:182:LYS:O	21:1Z:185:GLU:HG2	2.19	0.43
27:15:40:LYS:NZ	27:15:44:THR:O	2.52	0.43
29:17:34:ARG:NH2	61:17:202:HOH:O	2.51	0.43
32:1a:79:G:C2	32:1a:90:U:O2	2.71	0.43
32:1a:1060:C:H2'	32:1a:1061:G:H8	1.83	0.43
35:1d:108:LEU:HD12	35:1d:174:LEU:HD13	2.00	0.43
37:1f:45:LEU:HD12	37:1f:59:TYR:HD1	1.83	0.43
40:1i:37:PHE:HA	40:1i:40:LEU:HD12	2.00	0.43
47:1p:3:LYS:HB3	47:1p:3:LYS:HE2	1.82	0.43
1:2A:140:G:N2	1:2A:1596:A:H4'	2.34	0.43
1:2A:479:A:H4'	1:2A:480:A:OP1	2.18	0.43
1:2A:848:G:H2'	1:2A:849:A:C8	2.54	0.43
1:2A:1291:C:H2'	1:2A:1292:U:C6	2.54	0.43
5:2F:150:GLY:HA2	5:2F:172:TRP:CD2	2.54	0.43
12:2Q:39:PRO:HD3	12:2Q:99:PRO:HG3	2.00	0.43
32:2a:108:G:C6	51:2t:15:ARG:HG2	2.54	0.43
32:2a:447:G:O6	32:2a:485:G:O2'	2.33	0.43
32:2a:969:A:H2'	32:2a:970:C:O4'	2.19	0.43
32:2a:1103:C:H5''	33:2b:98:LEU:HD22	2.01	0.43
35:2d:92:VAL:HG12	35:2d:96:LEU:HD13	2.00	0.43
37:2f:2:ARG:O	37:2f:66:GLU:HA	2.19	0.43
44:2m:33:ALA:HB2	44:2m:64:TRP:CH2	2.54	0.43
51:2t:14:LYS:HA	51:2t:17:ARG:CZ	2.49	0.43
51:2t:86:ARG:O	51:2t:90:GLN:HB2	2.19	0.43
1:1A:171:A:H2	1:1A:460:C:O2	2.01	0.43
1:1A:187:C:H5'	1:1A:2256:U:OP1	2.19	0.43
1:1A:904:C:N4	1:1A:905:U:O4	2.52	0.43
1:1A:1109:G:H1	1:1A:1121:C:N4	2.17	0.43
1:1A:1825:U:H2'	1:1A:1826:C:C6	2.53	0.43
2:1B:78:A:C2	2:1B:100:A:C4	3.07	0.43
3:1D:242:ARG:HG3	3:1D:242:ARG:NH1	2.24	0.43
12:1Q:37:LEU:HD21	12:1Q:130:LYS:HE2	1.99	0.43
14:1S:11:LYS:HD3	14:1S:15:ARG:HH12	1.84	0.43
20:1Y:28:LYS:HG3	20:1Y:40:GLU:HG3	2.01	0.43
32:1a:130:A:C8	48:1q:63:ARG:HD3	2.54	0.43
32:1a:565:U:OP2	32:1a:566:G:O2'	2.33	0.43
32:1a:673:G:O3'	37:1f:87:ARG:NH2	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:1k:20:TYR:HB2	42:1k:31:THR:HG23	2.00	0.43
48:1q:87:LYS:HA	48:1q:87:LYS:HD2	1.91	0.43
1:2A:242:G:C8	30:28:5:LYS:HG2	2.54	0.43
1:2A:634:C:H2'	1:2A:635:C:C6	2.53	0.43
1:2A:781:A:H2	1:2A:1776:G:N3	2.17	0.43
5:2F:120:GLU:HB3	5:2F:122:LYS:HG2	2.01	0.43
7:2H:12:PRO:O	7:2H:15:VAL:HG22	2.19	0.43
28:26:14:THR:O	28:26:17:LYS:NZ	2.48	0.43
32:2a:109:A:C6	32:2a:326:G:C6	3.07	0.43
32:2a:411:A:O2'	32:2a:413:G:H5'	2.19	0.43
32:2a:1125:U:C2	41:2j:38:ILE:HD13	2.54	0.43
32:2a:1133:G:H2'	32:2a:1134:G:C8	2.54	0.43
1:1A:441:C:H2'	1:1A:442:A:C8	2.54	0.42
1:1A:537:G:N1	61:1A:4190:HOH:O	2.24	0.42
1:1A:1224:C:H2'	1:1A:1225:C:H6	1.84	0.42
1:1A:1730:C:H2'	1:1A:1731:C:C6	2.54	0.42
1:1A:2585:C:H3'	61:1A:4593:HOH:O	2.19	0.42
3:1D:113:VAL:HG12	61:1D:475:HOH:O	2.19	0.42
6:1G:133:LEU:HD11	6:1G:157:ILE:HD12	2.01	0.42
20:1Y:92:ASN:HD22	20:1Y:92:ASN:H	1.67	0.42
32:1a:227:G:H2'	32:1a:228:A:O4'	2.18	0.42
32:1a:542:G:H5'	35:1d:41:GLY:HA3	2.00	0.42
32:1a:1366:C:H2'	32:1a:1367:C:C6	2.54	0.42
32:1a:1431:C:H2'	32:1a:1432:G:O4'	2.19	0.42
32:1a:1492:A:H4'	32:1a:1493:A:N1	2.33	0.42
33:1b:215:LEU:O	33:1b:219:VAL:HG23	2.19	0.42
35:1d:61:LYS:HD3	35:1d:206:PHE:CD2	2.53	0.42
40:1i:26:VAL:HG22	40:1i:61:ALA:HB3	2.01	0.42
47:1p:21:VAL:HG12	47:1p:34:GLU:O	2.19	0.42
48:1q:13:ASP:N	48:1q:13:ASP:OD1	2.52	0.42
1:2A:9:U:O4	1:2A:2629:A:H2	2.02	0.42
1:2A:196:A:N3	1:2A:196:A:H2'	2.34	0.42
1:2A:783:A:H2'	1:2A:783:A:N3	2.33	0.42
1:2A:897:C:H2'	1:2A:898:C:C6	2.54	0.42
1:2A:1540:U:H2'	1:2A:1541:G:O4'	2.19	0.42
1:2A:2153:G:H2'	1:2A:2154:G:C8	2.54	0.42
1:2A:2218:U:O4'	23:21:52:ARG:NH2	2.52	0.42
4:2E:181:LEU:HD12	4:2E:181:LEU:HA	1.71	0.42
10:2O:4:PRO:O	10:2O:5:GLN:HB2	2.19	0.42
10:2O:107:ARG:HE	10:2O:107:ARG:HB3	1.53	0.42
14:2S:15:ARG:HB3	14:2S:19:LYS:HE3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:2T:29:ARG:HB3	15:2T:87:ASP:HB2	2.00	0.42
15:2T:73:GLU:OE2	15:2T:103:ARG:NE	2.41	0.42
17:2V:76:LYS:HB2	17:2V:81:TYR:HB3	2.01	0.42
32:2a:396:G:O2'	32:2a:398:C:OP1	2.26	0.42
32:2a:614:A:H2'	32:2a:615:C:C6	2.54	0.42
32:2a:745:C:H4'	32:2a:836:G:H21	1.83	0.42
32:2a:1146:A:H2'	32:2a:1147:C:O4'	2.19	0.42
40:2i:102:LEU:HD12	40:2i:103:THR:N	2.34	0.42
53:2y:85:LEU:O	53:2y:89:GLN:HG2	2.19	0.42
1:1A:1653:C:H4'	1:1A:1654:A:O5'	2.19	0.42
1:1A:2303:U:H2'	1:1A:2304:C:C6	2.53	0.42
1:1A:2761:A:H5'	7:1H:4:ILE:HD12	2.01	0.42
1:1A:2804:C:OP2	1:1A:2804:C:H6	2.02	0.42
3:1D:71:ASP:OD2	3:1D:103:ARG:NH2	2.45	0.42
12:1Q:3:MET:HE2	61:1Q:322:HOH:O	2.17	0.42
13:1R:28:LEU:O	13:1R:32:GLY:N	2.49	0.42
26:14:57:GLU:HB2	26:14:58:ARG:HA	2.01	0.42
31:19:7:VAL:HG12	31:19:34:GLN:HB3	2.00	0.42
32:1a:616:G:C2'	32:1a:617:G:H5'	2.49	0.42
32:1a:911:U:OP2	43:1l:97:ARG:NH2	2.33	0.42
35:1d:15:GLU:OE2	35:1d:59:ARG:NH1	2.52	0.42
35:1d:153:ARG:HA	35:1d:158:ILE:HD11	2.00	0.42
36:1e:87:SER:OG	36:1e:125:SER:O	2.36	0.42
40:1i:8:GLY:HA2	40:1i:79:LEU:HD23	2.00	0.42
53:1y:85:LEU:O	53:1y:89:GLN:HG2	2.18	0.42
1:2A:493:G:H2'	1:2A:494:G:O4'	2.18	0.42
1:2A:566:U:H2'	1:2A:567:A:O4'	2.19	0.42
1:2A:1016:G:H2'	1:2A:1017:G:O4'	2.18	0.42
1:2A:1539:G:H2'	1:2A:1540:U:H6	1.84	0.42
1:2A:1739:U:O2'	1:2A:1740:G:H8	2.02	0.42
1:2A:2128:C:H1'	1:2A:2173:A:C2	2.51	0.42
1:2A:2715:C:H2'	1:2A:2716:U:H6	1.84	0.42
61:2A:3820:HOH:O	32:2a:773:G:OP1	2.21	0.42
2:2B:66:A:H61	2:2B:109:C:H5''	1.84	0.42
2:2B:95:C:H2'	2:2B:96:U:C6	2.54	0.42
32:2a:755:G:OP2	46:2o:65:ARG:HD2	2.19	0.42
32:2a:978:A:O2'	32:2a:1322:C:N3	2.46	0.42
32:2a:1179:A:H2'	32:2a:1180:A:O4'	2.19	0.42
37:2f:69:GLU:O	37:2f:72:VAL:HG13	2.19	0.42
39:2h:49:GLU:OE2	39:2h:62:TYR:OH	2.34	0.42
48:2q:13:ASP:OD1	48:2q:13:ASP:N	2.48	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:211:A:H5''	1:1A:448:U:OP1	2.19	0.42
1:1A:721:G:H1'	5:1F:74:ARG:HD3	2.02	0.42
1:1A:1347:A:C8	1:1A:1349:G:C8	3.07	0.42
1:1A:2177:G:H3'	1:1A:2178:G:H8	1.84	0.42
2:1B:96:U:H2'	2:1B:97:G:H8	1.84	0.42
15:1T:99:LEU:O	15:1T:102:ILE:HG12	2.19	0.42
18:1W:1:MET:HE2	18:1W:62:HIS:HB3	2.01	0.42
20:1Y:53:PRO:O	20:1Y:56:PRO:HD3	2.19	0.42
32:1a:262:A:C6	32:1a:263:A:C6	3.08	0.42
32:1a:838:G:H5'	32:1a:839:U:OP2	2.19	0.42
32:1a:1250:A:H4'	40:1i:68:GLY:N	2.34	0.42
39:1h:86:ILE:HG12	39:1h:135:CYS:HA	2.00	0.42
53:1y:23:ARG:HA	53:1y:23:ARG:HD3	1.48	0.42
1:2A:140:G:N3	1:2A:142:A:N6	2.58	0.42
1:2A:1069:A:H2'	1:2A:1073:A:N7	2.35	0.42
1:2A:1631(A):A:OP1	61:2A:3870:HOH:O	2.21	0.42
1:2A:2430:A:H5'	1:2A:2431:U:OP2	2.19	0.42
1:2A:2647:U:H2'	1:2A:2648:C:C6	2.54	0.42
1:2A:2776:A:H4'	1:2A:2777:G:H5''	2.00	0.42
1:2A:2818:G:OP2	13:2R:42:LYS:NZ	2.52	0.42
4:2E:78:LEU:HD12	4:2E:78:LEU:HA	1.87	0.42
7:2H:124:GLU:HB2	7:2H:132:ARG:HB3	2.01	0.42
32:2a:606:G:H5''	32:2a:607:A:H5'	2.00	0.42
32:2a:942:G:C2	32:2a:1342:C:C2	3.07	0.42
32:2a:1263:C:H2'	32:2a:1264:C:C6	2.53	0.42
32:2a:1370:G:N7	40:2i:109:VAL:HG11	2.35	0.42
35:2d:36:ARG:HD2	35:2d:38:TYR:OH	2.19	0.42
43:2l:92:0TD:H4	43:2l:92:0TD:H8	1.87	0.42
1:1A:502:G:H4'	1:1A:527:A:N1	2.35	0.42
1:1A:574:G:O2'	1:1A:1265:A:N3	2.47	0.42
1:1A:1115:A:H4'	1:1A:1116:A:H5''	2.01	0.42
1:1A:1144:A:H3'	1:1A:1145:G:H8	1.84	0.42
1:1A:1432:C:H2'	1:1A:1433:C:C6	2.54	0.42
1:1A:1749:G:H2'	1:1A:1750:G:O4'	2.19	0.42
1:1A:2155:G:C2	1:1A:2179:G:H2'	2.54	0.42
1:1A:2159:C:N4	1:1A:2176:G:N1	2.34	0.42
1:1A:2383:G:H21	28:16:46:HIS:CE1	2.37	0.42
8:1I:133:HIS:ND1	8:1I:134:PRO:O	2.48	0.42
22:10:43:THR:O	22:10:43:THR:HG23	2.20	0.42
32:1a:486:U:H2'	32:1a:487:A:H8	1.85	0.42
32:1a:546:G:OP1	35:1d:73:ARG:HG2	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:594:G:H1	32:1a:645:C:H42	1.66	0.42
32:1a:911:U:H2'	32:1a:912:C:C6	2.55	0.42
32:1a:1226:C:H4'	50:1s:80:TYR:OH	2.19	0.42
33:1b:12:GLU:OE2	33:1b:48:MET:HE3	2.19	0.42
35:1d:172:PRO:HB2	35:1d:187:ARG:NH2	2.25	0.42
39:1h:112:LEU:HD23	39:1h:133:LEU:HA	2.01	0.42
39:1h:121:ASP:OD1	39:1h:121:ASP:N	2.52	0.42
42:1k:18:ARG:HB2	42:1k:33:THR:OG1	2.19	0.42
43:1l:7:ILE:HD13	43:1l:7:ILE:HA	1.89	0.42
53:1y:38:HIS:O	53:1y:52:ALA:HA	2.19	0.42
1:2A:566:U:H5''	11:2P:29:LYS:HE3	2.00	0.42
1:2A:1000:A:H62	1:2A:1154:G:H2'	1.84	0.42
1:2A:2750:A:H8	1:2A:2750:A:OP1	2.02	0.42
6:2G:114:ILE:HB	6:2G:117:PHE:HD1	1.83	0.42
25:23:5:LYS:NZ	25:23:57:GLU:OE1	2.38	0.42
32:2a:1239:A:O2'	38:2g:114:ARG:O	2.34	0.42
33:2b:189:ASP:OD1	33:2b:189:ASP:N	2.37	0.42
36:2e:78:HIS:HE1	36:2e:143:ARG:N	2.16	0.42
1:1A:441:C:H4'	1:1A:1901:C:O2	2.19	0.42
1:1A:553:A:O2'	1:1A:554:A:H5'	2.20	0.42
1:1A:842:C:H2'	1:1A:843:C:C6	2.54	0.42
1:1A:933:C:C3'	1:1A:934:A:H5''	2.49	0.42
1:1A:1333:A:H8	13:1R:104:ARG:HD3	1.84	0.42
1:1A:1815:A:OP1	61:1A:4176:HOH:O	2.22	0.42
1:1A:2279:A:H5''	1:1A:2280:A:H5'	2.00	0.42
1:1A:2639:G:N2	1:1A:2790:G:OP2	2.52	0.42
11:1P:97:PRO:HD3	11:1P:126:VAL:O	2.19	0.42
12:1Q:48:GLU:O	12:1Q:52:VAL:HG23	2.20	0.42
32:1a:299:G:O5'	32:1a:299:G:H8	2.03	0.42
32:1a:1090:U:H2'	32:1a:1091:U:C6	2.54	0.42
36:1e:74:GLY:HA3	36:1e:116:THR:HG22	2.00	0.42
48:1q:86:GLU:O	48:1q:90:ILE:HG12	2.19	0.42
1:2A:172:C:H2'	1:2A:173:G:H8	1.85	0.42
1:2A:414:C:H2'	1:2A:415:A:C8	2.55	0.42
1:2A:1045:A:N3	1:2A:1045:A:H2'	2.34	0.42
1:2A:1902:C:H5'	3:2D:246:PRO:HD3	2.02	0.42
7:2H:13:LYS:HE3	7:2H:13:LYS:HB2	1.70	0.42
7:2H:154:PRO:HB3	7:2H:163:TYR:CE1	2.54	0.42
14:2S:76:LYS:HE2	14:2S:76:LYS:HB3	1.70	0.42
21:2Z:72:ARG:HD3	21:2Z:72:ARG:HA	1.86	0.42
32:2a:939:G:H2'	32:2a:940:C:C6	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:2b:32:ILE:HD13	33:2b:40:HIS:CD2	2.55	0.42
35:2d:191:ARG:HA	35:2d:191:ARG:HD2	1.83	0.42
40:2i:22:GLY:HA3	40:2i:60:ASP:OD2	2.20	0.42
1:1A:217:A:OP1	11:1P:76:LYS:HE3	2.19	0.42
1:1A:767:C:H2'	1:1A:768:C:C6	2.54	0.42
1:1A:776:G:C5	3:1D:208:LYS:HB2	2.54	0.42
1:1A:1113:A:H2'	1:1A:1113:A:N3	2.34	0.42
1:1A:1634:C:H2'	1:1A:1635:C:H6	1.84	0.42
1:1A:1652:G:H5''	1:1A:1653:C:OP1	2.19	0.42
1:1A:2071:G:N7	61:1A:4315:HOH:O	2.37	0.42
12:1Q:35:VAL:HG13	12:1Q:130:LYS:HB3	2.00	0.42
27:15:33:CYS:HB2	27:15:40:LYS:HD3	2.01	0.42
30:18:23:VAL:HG11	30:18:47:LYS:HD3	2.00	0.42
31:19:33:LYS:HG3	61:19:604:HOH:O	2.19	0.42
32:1a:119:A:H4'	32:1a:120:A:C8	2.54	0.42
32:1a:674:G:H2'	32:1a:675:A:H8	1.83	0.42
32:1a:864:A:H2'	32:1a:865:A:C8	2.55	0.42
32:1a:1004:A:C5	32:1a:1037:C:C2	3.08	0.42
32:1a:1201:A:H4'	32:1a:1202:G:O5'	2.19	0.42
35:1d:121:VAL:O	35:1d:134:ASP:HA	2.20	0.42
40:1i:26:VAL:HG13	40:1i:61:ALA:HB3	2.01	0.42
40:1i:79:LEU:HD22	40:1i:104:ARG:HB2	2.02	0.42
40:1i:100:GLY:O	40:1i:103:THR:HG22	2.19	0.42
41:1j:19:SER:O	41:1j:23:ILE:HG12	2.20	0.42
1:2A:643:A:C8	28:26:44:ARG:NH1	2.88	0.42
1:2A:897:C:H2'	1:2A:898:C:H6	1.85	0.42
1:2A:1341:U:OP2	1:2A:1394:U:O2'	2.28	0.42
1:2A:1720:U:H2'	1:2A:1721:G:O4'	2.19	0.42
1:2A:1826:G:H4'	3:2D:242:ARG:CZ	2.50	0.42
1:2A:2112:G:H2'	1:2A:2113:U:C6	2.54	0.42
1:2A:2296:U:OP2	14:2S:6:ALA:HB2	2.20	0.42
5:2F:31:HIS:HB2	11:2P:9:ASN:OD1	2.20	0.42
5:2F:157:VAL:HB	5:2F:194:MET:HG2	2.01	0.42
21:2Z:102:LEU:HD11	21:2Z:124:ILE:HB	2.01	0.42
32:2a:910:C:H2'	32:2a:911:U:O4'	2.20	0.42
32:2a:1002:G:C4	32:2a:1003:G:C8	3.08	0.42
32:2a:1002:G:N3	32:2a:1003:G:H8	2.18	0.42
32:2a:1346:A:H5''	40:2i:120:ARG:NH1	2.32	0.42
33:2b:74:LYS:NZ	33:2b:166:ASP:HB2	2.34	0.42
39:2h:9:MET:HG3	39:2h:26:VAL:HG11	2.01	0.42
50:2s:17:GLU:O	50:2s:21:GLU:N	2.42	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:2t:38:LYS:HB2	51:2t:38:LYS:HE3	1.70	0.42
1:1A:1219:A:C1'	1:1A:1220:U:H5'	2.49	0.42
1:1A:2686:G:H5''	10:1O:26:LYS:HE3	2.02	0.42
8:1I:9:LEU:HD23	8:1I:12:LEU:HD13	2.02	0.42
21:1Z:4:ARG:NE	21:1Z:60:GLU:OE2	2.43	0.42
26:14:8:LYS:HE3	26:14:10:VAL:HG12	2.02	0.42
32:1a:427:U:H5'	35:1d:41:GLY:HA2	2.02	0.42
32:1a:584:G:H5'	48:1q:91:ARG:HH21	1.85	0.42
32:1a:1005:A:C2	32:1a:1025:U:H1'	2.55	0.42
38:1g:50:ILE:HD12	38:1g:61:VAL:HB	2.02	0.42
38:1g:79:ARG:HA	38:1g:84:ASN:HA	2.00	0.42
51:1t:14:LYS:HG2	51:1t:18:GLN:HE21	1.85	0.42
1:2A:58:G:O2'	1:2A:73:A:N1	2.49	0.42
1:2A:390:A:H4'	1:2A:391:G:H5'	2.02	0.42
1:2A:981:A:H8	1:2A:982:C:C5	2.38	0.42
1:2A:1410:G:H2'	1:2A:1411:C:C6	2.55	0.42
1:2A:1721:G:H8	1:2A:1741:A:H62	1.66	0.42
6:2G:171:ALA:O	6:2G:175:LEU:HB2	2.19	0.42
8:2I:12:LEU:HD23	8:2I:19:VAL:HG21	2.01	0.42
32:2a:563:A:H2'	32:2a:567:G:C8	2.55	0.42
32:2a:818:G:O2'	32:2a:819:A:H5'	2.19	0.42
32:2a:1255:G:OP1	41:2j:45:ARG:NH2	2.53	0.42
35:2d:122:ARG:HA	35:2d:122:ARG:HD2	1.88	0.42
36:2e:91:LEU:HD12	36:2e:120:THR:HG22	2.01	0.42
38:2g:104:LEU:HD12	38:2g:104:LEU:HA	1.90	0.42
41:2j:32:ALA:HB1	41:2j:33:GLN:HA	2.01	0.42
42:2k:20:TYR:CE1	42:2k:83:ILE:HD12	2.54	0.42
51:2t:89:ARG:O	51:2t:93:GLU:HG2	2.20	0.42
1:1A:517:A:H2'	1:1A:518:G:O4'	2.19	0.42
1:1A:1014:U:H2'	1:1A:1015:C:C6	2.54	0.42
1:1A:1315:A:H2'	1:1A:1316:C:C6	2.54	0.42
1:1A:2251:G:H5'	3:1D:251:GLY:HA3	2.01	0.42
3:1D:13:ARG:HA	3:1D:13:ARG:HD2	1.75	0.42
14:1S:58:LEU:HD23	14:1S:58:LEU:HA	1.76	0.42
32:1a:256:U:H2'	32:1a:257:G:O4'	2.20	0.42
32:1a:954:G:H2'	32:1a:955:U:O4'	2.20	0.42
34:1c:35:GLU:HB3	34:1c:59:ARG:HH22	1.83	0.42
39:1h:81:HIS:N	39:1h:138:TRP:O	2.53	0.42
39:1h:104:ARG:HD3	39:1h:104:ARG:HA	1.63	0.42
43:1l:109:GLY:HA3	43:1l:121:GLY:O	2.20	0.42
45:1n:39:LEU:HD11	45:1n:47:LEU:HD12	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:511:U:H4'	1:2A:1235:G:H4'	2.01	0.42
1:2A:531:C:H4'	1:2A:532:A:H5''	2.01	0.42
1:2A:639:U:H2'	1:2A:640:C:C6	2.55	0.42
1:2A:1053:C:H4'	1:2A:1054:A:OP1	2.19	0.42
1:2A:1069:A:H5'	1:2A:1096:A:H5'	2.00	0.42
1:2A:1260:G:C6	1:2A:1261:C:C4	3.08	0.42
1:2A:1371:G:O2'	1:2A:1372:U:H5	2.03	0.42
1:2A:2627:G:N2	1:2A:2777:G:OP2	2.45	0.42
1:2A:2689:U:H4'	1:2A:2690:C:H5'	2.02	0.42
6:2G:41:GLN:HG3	6:2G:60:LEU:HD22	2.02	0.42
12:2Q:29:PHE:HB2	12:2Q:105:GLU:OE1	2.19	0.42
17:2V:4:ILE:HD12	17:2V:39:LEU:HD22	2.01	0.42
32:2a:176:C:H2'	32:2a:177:C:H6	1.85	0.42
32:2a:1277:C:O2'	32:2a:1279:A:C8	2.73	0.42
32:2a:1387:G:H2'	32:2a:1388:C:H6	1.85	0.42
33:2b:7:VAL:O	33:2b:217:ARG:NH1	2.52	0.42
37:2f:95:GLU:O	49:2r:32:ARG:NH1	2.52	0.42
38:2g:18:TYR:HB3	38:2g:59:LEU:HD22	2.02	0.42
39:2h:103:VAL:CG2	39:2h:110:ALA:HB2	2.46	0.42
1:1A:518:G:H2'	1:1A:519:G:O4'	2.20	0.42
1:1A:589:U:H2'	1:1A:590:A:O4'	2.20	0.42
1:1A:831:A:C8	1:1A:839:G:C5	3.08	0.42
1:1A:1497:G:H2'	1:1A:1498:C:C6	2.55	0.42
1:1A:1695:C:OP1	61:1A:4130:HOH:O	2.21	0.42
1:1A:2864:G:H2'	1:1A:2865:C:C6	2.54	0.42
7:1H:87:LEU:HD23	7:1H:164:TYR:HA	2.02	0.42
12:1Q:110:THR:OG1	12:1Q:113:GLN:HG3	2.20	0.42
22:10:10:THR:HG22	22:10:12:ASN:H	1.84	0.42
32:1a:220:G:C6	32:1a:221:C:C4	3.08	0.42
32:1a:1261:A:H3'	32:1a:1262:C:H6	1.85	0.42
33:1b:24:TRP:CD1	33:1b:24:TRP:H	2.37	0.42
33:1b:108:ILE:O	33:1b:111:ARG:HB3	2.20	0.42
1:2A:118:A:N3	1:2A:178:G:H1'	2.35	0.42
1:2A:271(Q):G:H2'	1:2A:271(R):G:C8	2.55	0.42
1:2A:407:G:H5''	61:2A:3964:HOH:O	2.18	0.42
1:2A:483:A:O4'	20:2Y:48:ALA:HB1	2.19	0.42
1:2A:1059:G:C5	1:2A:1060:U:N3	2.88	0.42
1:2A:1138:G:N3	9:2N:106:MET:HE2	2.34	0.42
1:2A:1324:G:C4	1:2A:1328:G:O6	2.72	0.42
1:2A:2165:G:H2'	1:2A:2166:G:O4'	2.19	0.42
7:2H:26:VAL:HG12	7:2H:79:VAL:HG21	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:2O:1:MET:HE2	10:2O:1:MET:HB3	1.76	0.42
14:2S:30:ARG:HG3	14:2S:97:ARG:CZ	2.50	0.42
17:2V:52:VAL:CG2	17:2V:55:ALA:HB3	2.48	0.42
18:2W:88:ARG:NH1	18:2W:94:ASP:OD2	2.52	0.42
21:2Z:146:ILE:HA	21:2Z:174:VAL:HG12	2.01	0.42
25:23:52:HIS:CD2	25:23:53:LEU:HG	2.54	0.42
29:27:1:MET:HE3	29:27:1:MET:HB2	1.89	0.42
32:2a:19:C:H5'	36:2e:86:ALA:HB3	2.00	0.42
32:2a:59:A:H1'	32:2a:354:G:N2	2.34	0.42
32:2a:184:G:H2'	32:2a:185:A:C8	2.55	0.42
32:2a:430:A:H2'	32:2a:431:A:O4'	2.20	0.42
32:2a:490:G:OP2	35:2d:132:ARG:NH2	2.52	0.42
32:2a:1249:C:O4'	40:2i:70:LYS:HE3	2.19	0.42
32:2a:1291:G:H4'	40:2i:39:GLY:HA3	2.01	0.42
32:2a:1327:C:H2'	32:2a:1328:C:C6	2.54	0.42
36:2e:89:ILE:HD12	36:2e:89:ILE:HA	1.93	0.42
40:2i:20:ARG:O	40:2i:60:ASP:HB2	2.19	0.42
1:1A:510:C:H2'	1:1A:511:C:C6	2.55	0.42
1:1A:787:U:H2'	1:1A:788:G:C8	2.54	0.42
1:1A:895:G:H2'	1:1A:896:A:C8	2.55	0.42
1:1A:1141:A:H2'	1:1A:1142:A:C8	2.55	0.42
1:1A:2846:U:C4	1:1A:2893:A:N6	2.87	0.42
1:1A:2875:U:OP2	15:1T:119:LYS:NZ	2.50	0.42
8:1I:14:ASP:OD1	8:1I:15:VAL:N	2.53	0.42
9:1N:14:VAL:HG13	9:1N:138:LEU:HG	2.02	0.42
28:16:7:ILE:HD11	28:16:25:LYS:HE2	2.01	0.42
32:1a:737:A:H2'	32:1a:738:C:C6	2.55	0.42
32:1a:974:A:OP1	45:1n:29:ARG:NH2	2.53	0.42
32:1a:1187:G:H4'	40:1i:111:ARG:NH1	2.35	0.42
33:1b:174:VAL:O	33:1b:178:ARG:HB2	2.20	0.42
40:1i:10:ARG:HG2	40:1i:75:ASP:HB2	2.02	0.42
47:1p:23:ASP:OD2	47:1p:25:ARG:NH1	2.53	0.42
1:2A:384:U:H2'	1:2A:385:C:C6	2.53	0.42
1:2A:1171:G:N2	1:2A:1179:C:C2	2.87	0.42
1:2A:2103:C:O2	1:2A:2187:G:N1	2.53	0.42
1:2A:2137:C:H2'	1:2A:2138:C:O4'	2.20	0.42
1:2A:2397:G:N2	1:2A:2420:C:H1'	2.35	0.42
1:2A:2712(A):A:OP2	61:2A:3872:HOH:O	2.22	0.42
17:2V:71:LEU:HD23	17:2V:71:LEU:HA	1.86	0.42
32:2a:1025:U:H4'	32:2a:1026:G:C8	2.54	0.42
38:2g:106:GLN:O	38:2g:110:GLN:HG2	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:105:C:H2'	1:1A:106:U:C6	2.54	0.41
1:1A:548:C:H2'	1:1A:549:U:O4'	2.19	0.41
1:1A:561:A:H2'	1:1A:562:C:C6	2.55	0.41
1:1A:1055:A:OP2	9:1N:37:LYS:NZ	2.48	0.41
1:1A:1096:A:C2	1:1A:2764:G:C4	3.08	0.41
1:1A:1387:U:O4'	19:1X:57:LEU:HD23	2.19	0.41
1:1A:1594:C:H2'	1:1A:1595:C:C6	2.55	0.41
1:1A:2317:A:H5''	6:1G:134:GLY:HA3	2.00	0.41
1:1A:2596:U:H2'	1:1A:2597:U:H2'	2.02	0.41
3:1D:70:TRP:HB3	3:1D:190:TYR:CE2	2.55	0.41
8:1I:109:ILE:HD12	8:1I:109:ILE:HA	1.77	0.41
9:1N:62:VAL:HG13	9:1N:66:LYS:HD2	2.02	0.41
11:1P:63:PRO:HG2	30:18:25:MET:HB2	2.01	0.41
18:1W:68:ARG:NH1	18:1W:112:GLY:H	2.18	0.41
25:13:31:LEU:HD23	25:13:31:LEU:HA	1.80	0.41
30:18:15:LYS:HB3	57:18:102:MPD:H52	2.01	0.41
32:1a:656:C:H2'	46:1o:28:GLN:HE22	1.84	0.41
32:1a:667:G:H4'	46:1o:51:HIS:ND1	2.35	0.41
40:1i:89:ASN:O	40:1i:92:TYR:HB2	2.20	0.41
1:2A:118:A:H1'	1:2A:178:G:O4'	2.20	0.41
1:2A:271(Q):G:H2'	1:2A:271(R):G:H8	1.85	0.41
1:2A:515:A:H1'	1:2A:581:C:H1'	2.01	0.41
1:2A:1274:A:N3	1:2A:1297:C:H1'	2.35	0.41
1:2A:2745:C:C4	1:2A:2746:U:C4	3.08	0.41
4:2E:13:ARG:O	15:2T:57:PHE:HE2	2.02	0.41
10:2O:2:ILE:HD12	10:2O:6:THR:HG21	2.01	0.41
19:2X:11:PRO:HB3	19:2X:92:LEU:HD11	2.02	0.41
32:2a:392:G:OP1	47:2p:8:ARG:NH2	2.53	0.41
33:2b:15:VAL:O	33:2b:209:ARG:HB2	2.20	0.41
33:2b:133:LYS:O	33:2b:136:VAL:HG12	2.20	0.41
35:2d:121:VAL:HG22	35:2d:126:ILE:HG13	2.02	0.41
1:1A:269:G:H2'	1:1A:270:C:C6	2.55	0.41
1:1A:542:C:OP2	27:15:13:LYS:HE3	2.19	0.41
1:1A:2156:A:N6	1:1A:2179:G:H4'	2.35	0.41
1:1A:2573:A:H2	10:1O:23:ARG:NH2	2.18	0.41
6:1G:66:GLN:OE1	6:1G:98:ARG:NE	2.50	0.41
6:1G:133:LEU:HG	6:1G:157:ILE:HB	2.00	0.41
32:1a:22:G:H4'	32:1a:885:G:C8	2.55	0.41
32:1a:67:C:O2'	32:1a:171:A:H1'	2.20	0.41
32:1a:510:A:H5''	32:1a:511:C:P	2.60	0.41
32:1a:604:G:H2'	32:1a:605:U:O4'	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:1c:17:ASP:OD1	34:1c:18:TRP:N	2.53	0.41
35:1d:166:LYS:HA	35:1d:166:LYS:HD2	1.68	0.41
36:1e:7:GLU:O	36:1e:34:VAL:HA	2.19	0.41
38:1g:28:ASN:HD21	38:1g:36:LYS:NZ	2.17	0.41
1:2A:108:U:OP1	1:2A:293:U:O2'	2.38	0.41
1:2A:1527:G:H5''	1:2A:1528:A:OP1	2.20	0.41
1:2A:1899:G:H2'	1:2A:1899:G:N3	2.34	0.41
1:2A:2252:G:H2'	1:2A:2253:G:H8	1.85	0.41
3:2D:17:THR:O	3:2D:211:ARG:NH2	2.53	0.41
5:2F:152:GLU:OE1	5:2F:191:ARG:HD2	2.20	0.41
7:2H:127:GLU:C	7:2H:129:THR:N	2.78	0.41
8:2I:87:LYS:HD2	8:2I:87:LYS:HA	1.86	0.41
8:2I:87:LYS:HE2	8:2I:121:LYS:HG3	2.02	0.41
14:2S:41:ASP:OD2	14:2S:44:LYS:HB2	2.20	0.41
14:2S:93:LYS:HG2	14:2S:95:HIS:HB3	2.01	0.41
21:2Z:5:LEU:O	21:2Z:59:LEU:HA	2.21	0.41
25:23:4:LEU:O	25:23:36:VAL:HA	2.20	0.41
25:23:8:LEU:HB2	25:23:28:LEU:HD13	2.02	0.41
32:2a:444:C:N4	32:2a:490:G:H1	2.16	0.41
32:2a:560:U:H5'	32:2a:566:G:N2	2.35	0.41
33:2b:51:LEU:HD22	33:2b:55:PHE:HE2	1.85	0.41
1:1A:142:G:H1'	19:1X:37:THR:HG21	2.01	0.41
1:1A:360:C:HO2'	20:1Y:35:TYR:HH	1.64	0.41
1:1A:894:U:OP2	61:1A:4175:HOH:O	2.22	0.41
1:1A:909:G:H2'	1:1A:910:A:O4'	2.20	0.41
1:1A:1473:A:H4'	1:1A:1474:C:O4'	2.20	0.41
8:1I:72:LEU:C	8:1I:74:ASN:N	2.78	0.41
11:1P:141:ALA:HA	25:23:38:GLU:CG	2.50	0.41
26:14:47:GLN:C	26:14:49:PHE:H	2.28	0.41
32:1a:299:G:C6	32:1a:300:A:C6	3.08	0.41
32:1a:657:G:O2'	46:1o:23:GLY:HA2	2.20	0.41
32:1a:1212:U:H4'	32:1a:1213:A:C8	2.56	0.41
33:1b:98:LEU:O	33:1b:101:MET:HB2	2.20	0.41
35:1d:105:VAL:HG13	35:1d:110:PHE:HB2	2.01	0.41
35:1d:122:ARG:HA	35:1d:122:ARG:HD2	1.71	0.41
38:1g:27:ILE:CD1	38:1g:40:ALA:HA	2.50	0.41
40:1i:17:VAL:HA	40:1i:63:ILE:HG12	2.01	0.41
42:1k:59:TYR:CZ	42:1k:63:LEU:HD21	2.55	0.41
1:2A:17:G:C6	1:2A:18:C:N4	2.89	0.41
1:2A:57:C:H2'	1:2A:58:G:O4'	2.20	0.41
1:2A:108:U:H2'	1:2A:109:G:H8	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:825:C:O2	11:2P:55:ARG:NH1	2.45	0.41
1:2A:2251:OMG:HM23	1:2A:2251:OMG:H1'	1.76	0.41
1:2A:2406:U:OP2	1:2A:2406:U:H2'	2.20	0.41
1:2A:2498:C:OP2	61:2A:3823:HOH:O	2.21	0.41
2:2B:50:G:OP2	14:2S:62:LYS:HB2	2.21	0.41
2:2B:73:A:C4	2:2B:105:A:C2	3.08	0.41
5:2F:23:ASP:O	5:2F:24:LEU:HD12	2.20	0.41
20:2Y:1:MET:HE2	20:2Y:1:MET:HB3	1.81	0.41
32:2a:967:5MC:H2'	32:2a:968:A:C8	2.54	0.41
32:2a:1343:G:C2	32:2a:1344:C:C2	3.08	0.41
33:2b:66:GLY:HA3	33:2b:160:ASP:OD2	2.20	0.41
34:2c:40:ARG:NH1	34:2c:55:VAL:O	2.53	0.41
36:2e:12:LEU:HD23	36:2e:13:ILE:N	2.34	0.41
46:2o:87:ILE:O	46:2o:88:ARG:HB3	2.20	0.41
53:2y:87:LYS:O	53:2y:91:LYS:HB2	2.20	0.41
1:1A:564:G:H2'	1:1A:565:C:C6	2.56	0.41
1:1A:1086:C:H2'	1:1A:1087:C:O4'	2.20	0.41
1:1A:2137:G:N2	1:1A:2141:A:N7	2.68	0.41
2:1B:90:A:N7	2:1B:91:C:H1'	2.35	0.41
18:1W:65:LEU:HA	18:1W:65:LEU:HD23	1.76	0.41
23:11:50:ARG:HG2	23:11:59:THR:CG2	2.49	0.41
32:1a:131:C:H2'	32:1a:132:C:H6	1.85	0.41
32:1a:555:C:H2'	32:1a:556:C:C6	2.55	0.41
32:1a:600:C:H2'	32:1a:601:C:C6	2.51	0.41
32:1a:975:A:N6	32:1a:1367:C:O4'	2.53	0.41
33:1b:80:ILE:HD13	33:1b:211:ILE:HG22	2.02	0.41
36:1e:135:THR:O	36:1e:139:LEU:HG	2.21	0.41
41:1j:81:THR:C	41:1j:83:GLU:H	2.28	0.41
47:1p:40:ASP:HB3	47:1p:48:TRP:HB2	2.03	0.41
53:1y:74:ILE:O	53:1y:78:ILE:HG12	2.21	0.41
1:2A:116:C:H2'	1:2A:117:G:O4'	2.21	0.41
1:2A:118:A:C8	1:2A:119:A:C8	3.08	0.41
1:2A:997:G:H5''	16:2U:92:ARG:NH1	2.35	0.41
1:2A:1076:C:H4'	1:2A:1077:A:OP1	2.20	0.41
1:2A:1429:G:H2'	1:2A:1430:C:C6	2.55	0.41
1:2A:1827:C:C2'	1:2A:1828:G:H5'	2.51	0.41
1:2A:2271:G:C5	1:2A:2272:U:C4	3.08	0.41
1:2A:2344:U:H3'	28:26:37:ARG:O	2.20	0.41
1:2A:2785:C:O2'	4:2E:66:HIS:ND1	2.42	0.41
2:2B:17:C:N4	2:2B:109:C:N3	2.68	0.41
2:2B:31:C:N4	14:2S:32:LEU:HD22	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:2D:38:LYS:HA	3:2D:38:LYS:HD2	1.88	0.41
6:2G:3:LEU:HD22	26:24:25:TYR:OH	2.19	0.41
8:2I:29:TYR:HD2	8:2I:30:LEU:HD23	1.86	0.41
20:2Y:6:HIS:CD2	20:2Y:7:VAL:HG23	2.55	0.41
20:2Y:19:LYS:HE2	20:2Y:19:LYS:HB3	1.79	0.41
21:2Z:76:LEU:H	21:2Z:76:LEU:HD12	1.85	0.41
26:24:14:ILE:O	26:24:21:VAL:HA	2.21	0.41
26:24:14:ILE:HB	26:24:22:ILE:HD13	2.02	0.41
32:2a:1015:A:H4'	45:2n:15:LYS:HZ1	1.86	0.41
32:2a:1262:C:H2'	32:2a:1263:C:H6	1.84	0.41
34:2c:6:HIS:CE1	34:2c:8:ILE:HB	2.55	0.41
38:2g:18:TYR:CD1	38:2g:59:LEU:HB2	2.55	0.41
38:2g:79:ARG:HA	38:2g:84:ASN:HA	2.02	0.41
1:1A:227:C:C2	1:1A:249:G:C2	3.08	0.41
1:1A:605:G:H2'	1:1A:606:G:C8	2.56	0.41
1:1A:1588:G:H3'	1:1A:1589:A:H2'	2.03	0.41
1:1A:1730:C:H2'	1:1A:1731:C:H6	1.85	0.41
1:1A:2073:A:H4'	4:1E:141:ILE:HG12	2.03	0.41
1:1A:2123:G:H2'	1:1A:2124:U:O4'	2.20	0.41
2:1B:11:C:OP2	2:1B:12:C:N4	2.45	0.41
4:1E:3:GLY:HA3	4:1E:81:ILE:HD12	2.02	0.41
5:1F:133:ASN:C	5:1F:162:LEU:HD23	2.46	0.41
31:19:4:ARG:O	31:19:36:GLN:HA	2.20	0.41
31:19:8:LYS:H	31:19:34:GLN:HE22	1.68	0.41
32:1a:375:U:C2	32:1a:376:G:C8	3.09	0.41
32:1a:583:A:H2'	32:1a:584:G:O4'	2.20	0.41
32:1a:1220:G:N2	50:1s:54:GLY:O	2.49	0.41
32:1a:1379:G:OP2	38:1g:6:ARG:HG2	2.20	0.41
1:2A:1221(A):C:C2	1:2A:1229:G:C2	3.09	0.41
1:2A:1288:U:C2	1:2A:1327:C:O2	2.74	0.41
1:2A:1493:C:N4	1:2A:2206:G:O2'	2.53	0.41
1:2A:1686:C:H2'	1:2A:1687:G:O4'	2.20	0.41
1:2A:2031:A:C6	1:2A:2498:C:H1'	2.55	0.41
1:2A:2119:A:H61	1:2A:2168:G:N2	2.18	0.41
1:2A:2187:G:N7	1:2A:2188:C:C4	2.89	0.41
1:2A:2366:A:OP1	61:2A:3875:HOH:O	2.22	0.41
4:2E:14:ILE:HG13	4:2E:21:VAL:HG13	2.01	0.41
4:2E:167:VAL:CG1	4:2E:189:PRO:HD3	2.50	0.41
8:2I:14:ASP:OD1	8:2I:15:VAL:N	2.53	0.41
21:2Z:128:VAL:HG23	21:2Z:160:GLY:O	2.19	0.41
23:21:81:LYS:HB3	23:21:81:LYS:HE3	1.87	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:26:13:CYS:SG	28:26:47:THR:HG21	2.59	0.41
32:2a:130:A:H1'	32:2a:263:A:O2'	2.20	0.41
32:2a:189(D):C:H2'	32:2a:189(E):U:O4'	2.21	0.41
32:2a:336:C:H2'	32:2a:337:C:C6	2.55	0.41
32:2a:539:A:C6	32:2a:540:G:C6	3.08	0.41
32:2a:539:A:OP2	43:2l:115:LYS:NZ	2.54	0.41
32:2a:540:G:C6	32:2a:541:G:C5	3.09	0.41
32:2a:1030:C:N4	32:2a:1032:G:O6	2.53	0.41
32:2a:1402:4OC:CM2	32:2a:1403:C:H5'	2.51	0.41
34:2c:6:HIS:HE1	34:2c:184:TYR:HD2	1.67	0.41
35:2d:174:LEU:HD23	35:2d:185:PHE:HA	2.02	0.41
53:2y:70:MET:O	53:2y:74:ILE:HG13	2.20	0.41
1:1A:18:C:O2'	1:1A:577:U:OP1	2.35	0.41
1:1A:27:G:C2	1:1A:537:G:N3	2.89	0.41
1:1A:551:A:H2'	61:1A:4675:HOH:O	2.21	0.41
1:1A:1314:A:C2	1:1A:2035:A:C4	3.09	0.41
1:1A:2157:A:H61	1:1A:2177:G:N2	2.18	0.41
5:1F:148:LEU:HD22	5:1F:154:VAL:HG21	2.03	0.41
15:1T:33:LYS:HG3	15:1T:34:VAL:N	2.35	0.41
32:1a:264:U:H4'	48:1q:63:ARG:HD2	2.03	0.41
32:1a:1086:U:H3	32:1a:1099:G:N2	2.11	0.41
32:1a:1346:A:C2'	38:1g:10:ARG:HH22	2.34	0.41
36:1e:96:PRO:C	36:1e:98:THR:H	2.29	0.41
40:1i:53:VAL:HG21	40:1i:85:LEU:HD13	2.03	0.41
47:1p:45:THR:OG1	47:1p:46:PRO:HD2	2.21	0.41
1:2A:480:A:OP2	20:2Y:47:LYS:HD3	2.20	0.41
1:2A:1539:G:H2'	1:2A:1540:U:C6	2.56	0.41
1:2A:1557:C:H5''	1:2A:1558:A:OP2	2.20	0.41
3:2D:97:TYR:C	3:2D:99:ASP:N	2.76	0.41
4:2E:12:THR:HG21	15:2T:11:GLU:OE2	2.20	0.41
6:2G:34:LEU:HD11	6:2G:176:LEU:HD13	2.01	0.41
6:2G:55:LYS:HA	6:2G:58:GLN:HB3	2.02	0.41
10:2O:49:ARG:NH1	32:2a:1422:G:O3'	2.54	0.41
14:2S:14:VAL:HG21	14:2S:90:GLY:O	2.20	0.41
32:2a:67:C:H2'	32:2a:68:G:H8	1.86	0.41
32:2a:509:A:N3	32:2a:543:C:O2'	2.47	0.41
32:2a:662:G:H2'	32:2a:663:A:H8	1.86	0.41
32:2a:691:G:H2'	32:2a:692:U:C6	2.56	0.41
32:2a:983:A:H2	32:2a:984:C:C6	2.38	0.41
32:2a:1005:A:N3	32:2a:1005:A:H2'	2.35	0.41
33:2b:16:HIS:HB2	33:2b:204:ASN:HB3	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:2l:27:LEU:O	43:2l:33:ARG:NE	2.46	0.41
43:2l:117:ARG:NH2	43:2l:124:LYS:HB2	2.35	0.41
47:2p:9:PHE:HE2	47:2p:18:ARG:HD2	1.85	0.41
49:2r:53:ARG:HD2	49:2r:60:ALA:HA	2.03	0.41
52:2u:6:ARG:HE	52:2u:15:ARG:HH12	1.68	0.41
1:1A:302:A:H2'	1:1A:303:C:C6	2.55	0.41
1:1A:556:C:H4'	1:1A:557:A:H5''	2.02	0.41
1:1A:1291:G:OP1	11:1P:13:ASN:ND2	2.36	0.41
1:1A:1516:A:H2'	1:1A:1517:G:O4'	2.21	0.41
1:1A:2703:C:O3'	1:1A:2881:C:H4'	2.19	0.41
3:1D:255:LYS:O	61:1D:403:HOH:O	2.22	0.41
7:1H:149:ARG:NH1	7:1H:167:GLU:OE2	2.49	0.41
8:1I:8:PRO:HD3	8:1I:15:VAL:HB	2.01	0.41
14:1S:11:LYS:HD3	14:1S:15:ARG:NH1	2.36	0.41
18:1W:20:VAL:O	18:1W:23:LEU:HB2	2.19	0.41
32:1a:9:G:H5''	36:1e:126:ARG:HD3	2.03	0.41
32:1a:58:C:O2'	32:1a:388:G:N7	2.35	0.41
32:1a:691:G:H2'	32:1a:692:U:C6	2.56	0.41
33:1b:12:GLU:O	33:1b:15:VAL:HG12	2.21	0.41
33:1b:69:LEU:HD13	33:1b:155:LEU:HD22	2.03	0.41
36:1e:84:PHE:CE2	36:1e:133:TYR:HD2	2.38	0.41
37:1f:38:GLU:OE1	37:1f:64:GLN:NE2	2.54	0.41
39:1h:17:THR:HG22	39:1h:63:LEU:HG	2.02	0.41
46:1o:33:THR:HG21	46:1o:85:LEU:HD22	2.02	0.41
51:1t:15:ARG:HA	51:1t:15:ARG:HD3	1.86	0.41
1:2A:9:U:H3	1:2A:2629:A:H2	1.67	0.41
1:2A:489:G:N7	18:2W:49:LYS:NZ	2.69	0.41
1:2A:884:C:H42	1:2A:892:G:H1	1.68	0.41
1:2A:1203:G:C6	1:2A:1204:A:N6	2.89	0.41
1:2A:1486:A:H2'	1:2A:1487:G:H8	1.85	0.41
1:2A:2252:G:H2'	1:2A:2253:G:C8	2.55	0.41
1:2A:2601:C:H5''	1:2A:2602:A:OP2	2.21	0.41
1:2A:2682:U:O2'	15:2T:58:ASN:ND2	2.53	0.41
3:2D:206:LEU:HD23	3:2D:206:LEU:HA	1.76	0.41
10:2O:7:TYR:CE1	10:2O:20:MET:HB2	2.55	0.41
12:2Q:57:HIS:NE2	12:2Q:116:GLU:HB3	2.36	0.41
18:2W:67:ASP:OD1	18:2W:67:ASP:N	2.53	0.41
21:2Z:69:THR:HG22	21:2Z:90:VAL:HA	2.03	0.41
32:2a:352:C:O2'	32:2a:354:G:OP1	2.33	0.41
32:2a:889:A:H4'	32:2a:890:G:OP1	2.21	0.41
32:2a:1002:G:N3	32:2a:1003:G:C8	2.89	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1073:U:H2'	32:2a:1074:G:C8	2.56	0.41
32:2a:1320:C:H2'	32:2a:1321:C:O4'	2.21	0.41
34:2c:56:ASP:HB2	34:2c:69:HIS:HE1	1.85	0.41
41:2j:85:LEU:HD23	41:2j:85:LEU:HA	1.89	0.41
42:2k:59:TYR:O	42:2k:63:LEU:HG	2.20	0.41
44:2m:80:ARG:NH2	50:2s:69:HIS:HE1	2.13	0.41
1:1A:1821:C:H2'	1:1A:1822:A:C5	2.55	0.41
1:1A:2321:A:H2'	1:1A:2322:A:O4'	2.20	0.41
8:1I:105:HIS:CD2	8:1I:105:HIS:N	2.86	0.41
21:1Z:145:GLU:O	21:1Z:148:ASP:N	2.33	0.41
30:18:26:LYS:HD2	30:18:48:PHE:CD2	2.55	0.41
32:1a:166:G:H2'	32:1a:167:G:H8	1.83	0.41
32:1a:414:A:H2'	32:1a:415:A:H8	1.86	0.41
32:1a:1288:A:H2'	32:1a:1289:A:O4'	2.21	0.41
35:1d:12:CYS:SG	35:1d:19:LEU:HB2	2.60	0.41
40:1i:16:ARG:HB2	40:1i:64:THR:CG2	2.51	0.41
40:1i:97:LYS:HB3	40:1i:98:PRO:HD3	2.02	0.41
1:2A:754:C:H2'	1:2A:755:C:C6	2.55	0.41
1:2A:910:A:C6	1:2A:911:A:C6	3.09	0.41
1:2A:1053:C:H2'	1:2A:1054:A:H8	1.84	0.41
1:2A:1056:G:H5''	1:2A:1057:A:H5'	2.03	0.41
1:2A:1065:U:H3	1:2A:1073:A:N6	2.17	0.41
1:2A:1590:U:H2'	1:2A:1591:G:C8	2.55	0.41
1:2A:1598:C:H2'	1:2A:1599:C:C6	2.56	0.41
1:2A:1915:5MU:H2'	1:2A:1916:A:O4'	2.21	0.41
1:2A:1952:A:N3	10:2O:22:ILE:HD12	2.36	0.41
7:2H:3:ARG:HH21	7:2H:54:ARG:NH1	2.19	0.41
7:2H:144:VAL:O	7:2H:148:ILE:HG12	2.20	0.41
9:2N:1:MET:HE1	16:2U:94:ASN:ND2	2.35	0.41
20:2Y:56:PRO:C	20:2Y:58:GLY:H	2.29	0.41
22:20:51:VAL:HG22	22:20:81:VAL:HG23	2.02	0.41
32:2a:297:G:N2	32:2a:300:A:OP2	2.53	0.41
32:2a:580:U:H2'	32:2a:581:G:O4'	2.21	0.41
32:2a:677:U:H1'	42:2k:119:CYS:SG	2.61	0.41
32:2a:932:C:H2'	32:2a:933:G:C8	2.55	0.41
32:2a:1207:2MG:H2'	32:2a:1208:C:H6	1.85	0.41
32:2a:1276:G:H2'	32:2a:1277:C:C6	2.55	0.41
32:2a:1338:G:C6	32:2a:1339:A:C6	3.09	0.41
33:2b:204:ASN:OD1	33:2b:205:ASP:N	2.54	0.41
49:2r:45:SER:OG	49:2r:47:THR:HG22	2.20	0.41
1:1A:831:A:C6	3:1D:229:VAL:HG11	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1049:G:O2'	1:1A:1056:A:N1	2.47	0.41
1:1A:1066:A:N1	1:1A:1186:U:O2'	2.40	0.41
1:1A:1074:A:H61	1:1A:1171:G:H2'	1.85	0.41
1:1A:1501:U:O2'	1:1A:1502:G:N7	2.50	0.41
1:1A:1699:A:O2'	1:1A:1700:G:H5'	2.21	0.41
1:1A:1716:A:C8	10:1O:5:GLN:HG3	2.56	0.41
1:1A:1857:G:OP1	3:1D:224:ALA:N	2.52	0.41
1:1A:2360:U:O4	1:1A:2394:G:N1	2.54	0.41
1:1A:2843:G:O2'	1:1A:2844:G:H5'	2.20	0.41
1:1A:2860:A:H2	13:1R:61:HIS:CG	2.38	0.41
4:1E:144:ARG:HB3	4:1E:145:LYS:H	1.53	0.41
7:1H:22:GLY:HA2	7:1H:37:VAL:O	2.21	0.41
12:1Q:137:TYR:O	12:1Q:141:GLN:HG2	2.21	0.41
16:1U:62:ILE:O	16:1U:66:ASN:HB2	2.21	0.41
19:1X:72:LYS:HB3	19:1X:72:LYS:HE3	1.91	0.41
23:11:67:ILE:N	23:11:68:PRO:HD2	2.36	0.41
32:1a:92:C:H2'	32:1a:93:G:C8	2.55	0.41
32:1a:161:A:N1	32:1a:347:G:O2'	2.52	0.41
32:1a:537:G:H5''	43:1l:113:ARG:NH1	2.36	0.41
32:1a:620:C:H2'	32:1a:621:A:O4'	2.20	0.41
32:1a:655:A:H2'	32:1a:656:C:O4'	2.21	0.41
32:1a:1030(C):G:H2'	32:1a:1030(D):A:H8	1.86	0.41
32:1a:1144:G:N2	32:1a:1146:A:H62	2.19	0.41
32:1a:1446:U:O2'	32:1a:1447:A:C8	2.69	0.41
33:1b:27:LYS:O	33:1b:30:ARG:NH1	2.54	0.41
34:1c:56:ASP:OD2	34:1c:69:HIS:HE1	2.04	0.41
35:1d:150:GLU:HG3	35:1d:151:LYS:N	2.35	0.41
39:1h:120:THR:HG23	39:1h:123:GLU:OE1	2.20	0.41
40:1i:127:LYS:HB3	40:1i:127:LYS:HE2	1.68	0.41
41:1j:11:PHE:CE1	41:1j:67:THR:HG22	2.50	0.41
43:1l:34:ARG:HD3	43:1l:105:TYR:CE2	2.56	0.41
43:1l:92:0TD:H4	43:1l:92:0TD:H8	1.85	0.41
51:1t:38:LYS:HA	51:1t:41:ILE:HB	2.03	0.41
51:1t:72:LEU:HD23	51:1t:72:LEU:HA	1.87	0.41
1:2A:64:A:O3'	19:2X:71:GLY:HA3	2.21	0.41
1:2A:111:A:H4'	24:22:69:ARG:NH1	2.35	0.41
1:2A:556:G:H2'	1:2A:557:U:C6	2.56	0.41
1:2A:747:U:C5	27:25:4:HIS:CE1	3.09	0.41
1:2A:811:U:H2'	11:2P:21:ARG:HA	2.03	0.41
1:2A:820:A:H1'	1:2A:943:U:H1'	2.03	0.41
1:2A:1027:A:C6	1:2A:1126:A:C4	3.09	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1065:U:H4'	1:2A:1066:U:C5'	2.51	0.41
1:2A:1091:G:H2'	1:2A:1091:G:N3	2.36	0.41
1:2A:1341:U:O4	19:2X:16:LYS:HE2	2.20	0.41
1:2A:1449:A:N3	1:2A:1529:G:H1'	2.35	0.41
1:2A:1587:A:H2'	1:2A:1588:C:C6	2.56	0.41
1:2A:1709:U:H2'	1:2A:1710:C:C6	2.56	0.41
1:2A:1881:C:H2'	1:2A:1882:C:C6	2.56	0.41
1:2A:2104:G:N7	1:2A:2186:G:N2	2.69	0.41
1:2A:2302:G:C2	1:2A:2303:G:C8	3.09	0.41
1:2A:2461:C:H2'	1:2A:2462:U:H6	1.85	0.41
2:2B:70:C:H2'	2:2B:71:C:H6	1.86	0.41
3:2D:69:ARG:HD2	3:2D:130:ALA:CB	2.51	0.41
4:2E:96:PHE:O	4:2E:175:VAL:HG11	2.20	0.41
18:2W:60:ASN:N	18:2W:60:ASN:HD22	2.19	0.41
21:2Z:45:ASP:O	21:2Z:49:ARG:HG3	2.20	0.41
21:2Z:144:LEU:HD11	21:2Z:150:LEU:HD22	2.03	0.41
32:2a:20:U:H2'	32:2a:21:G:O4'	2.20	0.41
32:2a:173:U:OP2	32:2a:174:C:H5	2.04	0.41
32:2a:625:G:H4'	47:2p:16:HIS:CG	2.56	0.41
32:2a:709:G:H2'	32:2a:710:G:H8	1.85	0.41
32:2a:1077:G:N1	32:2a:1081:G:C6	2.89	0.41
32:2a:1111:A:N1	34:2c:177:THR:OG1	2.45	0.41
32:2a:1129:C:H5''	32:2a:1129:C:H6	1.85	0.41
32:2a:1323:G:H4'	32:2a:1363:C:C4	2.56	0.41
33:2b:73:THR:HA	33:2b:94:ASN:O	2.20	0.41
35:2d:68:TYR:OH	35:2d:98:GLU:OE2	2.27	0.41
35:2d:189:PRO:HB2	35:2d:194:LEU:HD11	2.02	0.41
38:2g:22:LEU:HG	38:2g:62:PHE:CE2	2.56	0.41
40:2i:100:GLY:O	40:2i:103:THR:HG22	2.21	0.41
40:2i:102:LEU:H	40:2i:102:LEU:HG	1.70	0.41
40:2i:106:ALA:O	40:2i:108:VAL:HG23	2.21	0.41
41:2j:9:ARG:HG2	41:2j:69:ASN:ND2	2.36	0.41
41:2j:50:ILE:HG22	41:2j:52:GLY:H	1.85	0.41
44:2m:51:ALA:O	44:2m:55:ARG:N	2.46	0.41
45:2n:24:CYS:HB3	45:2n:29:ARG:H	1.86	0.41
45:2n:52:GLN:O	45:2n:53:LEU:HD23	2.21	0.41
51:2t:76:ALA:O	51:2t:80:ARG:HG2	2.21	0.41
1:1A:624:C:O2	1:1A:628:C:H4'	2.21	0.41
1:1A:1140:U:H2'	1:1A:1142:A:OP2	2.21	0.41
1:1A:2141:A:N6	1:1A:2193:A:N7	2.69	0.41
1:1A:2271:G:C8	1:1A:2439:C:C4	3.09	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:1E:14:ILE:HB	15:1T:14:TYR:CZ	2.56	0.41
4:1E:119:ARG:HD3	61:1E:3133:HOH:O	2.22	0.41
4:1E:146:THR:HA	4:1E:147:PRO:HA	1.86	0.41
7:1H:154:PRO:HB3	7:1H:163:TYR:CE1	2.56	0.41
8:1I:10:GLU:O	8:1I:11:ASN:C	2.64	0.41
18:1W:79:GLY:HA3	18:1W:100:THR:HG22	2.03	0.41
23:11:23:LYS:HB3	23:11:29:GLY:HA3	2.03	0.41
32:1a:44:G:H2'	32:1a:45:U:O4'	2.21	0.41
32:1a:300:A:H2'	32:1a:301:G:O4'	2.21	0.41
32:1a:441:A:H8	32:1a:441:A:OP2	2.03	0.41
32:1a:453:A:C5	32:1a:454:C:C4	3.09	0.41
32:1a:1027:C:H2'	32:1a:1028:C:C4	2.56	0.41
32:1a:1328:C:H2'	32:1a:1329:A:O4'	2.20	0.41
43:1l:113:ARG:HD2	43:1l:113:ARG:HA	1.79	0.41
1:2A:26:G:C6	1:2A:27:G:N1	2.89	0.41
1:2A:281:G:H1'	1:2A:359:A:H61	1.85	0.41
1:2A:662:G:H5''	11:2P:16:ARG:HG2	2.03	0.41
1:2A:699:A:H2'	1:2A:700:G:O4'	2.20	0.41
1:2A:1055:G:H3'	1:2A:1056:G:H8	1.86	0.41
1:2A:1319:G:C6	1:2A:1320:C:N4	2.89	0.41
1:2A:1498:C:O4'	1:2A:1577:C:H4'	2.21	0.41
1:2A:1509(B):A:H2'	1:2A:1510:G:C8	2.56	0.41
1:2A:2086:U:H2'	1:2A:2087:G:C8	2.56	0.41
61:2A:4295:HOH:O	27:25:15:ARG:HG2	2.20	0.41
4:2E:9:VAL:HG13	4:2E:25:VAL:O	2.21	0.41
23:21:62:VAL:HG22	23:21:63:ALA:O	2.21	0.41
32:2a:11:G:H1	32:2a:23:C:H42	1.68	0.41
32:2a:304:U:H2'	32:2a:305:G:C8	2.56	0.41
32:2a:955:U:O2'	50:2s:83:HIS:HD2	2.04	0.41
32:2a:1208:C:H2'	32:2a:1209:C:O4'	2.21	0.41
34:2c:34:LEU:O	34:2c:38:ARG:HG3	2.20	0.41
50:2s:3:ARG:HE	50:2s:7:LYS:HB2	1.86	0.41
1:1A:223:C:H2'	1:1A:224:U:H6	1.86	0.40
1:1A:707:G:O3'	5:1F:38:ARG:NH2	2.54	0.40
1:1A:1223:C:H2'	1:1A:1224:C:H6	1.82	0.40
1:1A:2507:G:O2'	12:1Q:83:MET:HE3	2.21	0.40
1:1A:2745:G:OP1	4:1E:203:LYS:NZ	2.41	0.40
61:1A:4412:HOH:O	11:1P:39:LYS:HD3	2.20	0.40
6:1G:56:ALA:O	6:1G:59:GLU:HB2	2.21	0.40
8:1I:76:THR:O	8:1I:105:HIS:HE1	2.04	0.40
12:1Q:7:MET:HE3	12:1Q:7:MET:HB2	1.52	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:187:C:H4'	51:1t:86:ARG:HG3	2.02	0.40
32:1a:688:G:H2'	32:1a:689:C:C6	2.56	0.40
32:1a:708:C:H2'	32:1a:709:G:H8	1.86	0.40
32:1a:779:C:H2'	32:1a:780:A:O4'	2.21	0.40
32:1a:1179:A:H2'	32:1a:1180:A:O4'	2.20	0.40
33:1b:112:VAL:HG12	33:1b:149:LEU:HD13	2.04	0.40
34:1c:110:ASN:O	34:1c:111:LEU:HD23	2.22	0.40
35:1d:11:LEU:HD23	35:1d:66:ARG:HB3	2.01	0.40
35:1d:87:GLY:N	61:1d:402:HOH:O	2.49	0.40
35:1d:88:VAL:HA	36:1e:97:GLY:HA3	2.02	0.40
35:1d:194:LEU:O	35:1d:196:LEU:HD12	2.22	0.40
43:1l:47:LYS:HA	43:1l:48:PRO:HA	1.75	0.40
48:1q:66:SER:OG	48:1q:67:LYS:O	2.38	0.40
1:2A:1031:G:N2	31:29:36:GLN:HE22	2.17	0.40
1:2A:1204:A:OP1	1:2A:1204:A:H8	2.04	0.40
1:2A:1359:A:N6	1:2A:1372:U:H3	2.18	0.40
1:2A:1657:C:H2'	1:2A:1658:C:C6	2.56	0.40
12:2Q:35:VAL:HG23	12:2Q:101:ARG:C	2.46	0.40
15:2T:18:ASP:OD1	15:2T:18:ASP:N	2.53	0.40
32:2a:93:G:H2'	32:2a:96:U:O4'	2.21	0.40
32:2a:1165:C:H2'	32:2a:1166:G:O4'	2.21	0.40
32:2a:1201:A:H4'	32:2a:1202:G:H5''	2.03	0.40
35:2d:25:ARG:HA	35:2d:28:SER:HB3	2.03	0.40
42:2k:116:HIS:N	42:2k:117:ASN:HA	2.37	0.40
43:2l:57:LYS:HD3	43:2l:65:GLU:OE2	2.21	0.40
53:2y:30:TRP:CD1	53:2y:89:GLN:HG3	2.56	0.40
1:1A:1122:C:O2'	1:1A:1123:A:OP2	2.33	0.40
1:1A:2515:2MA:O2'	1:1A:2517:G:OP2	2.28	0.40
5:1F:20:LEU:HG	5:1F:21:ALA:N	2.36	0.40
7:1H:137:ASP:HB3	7:1H:140:LYS:HB3	2.03	0.40
8:1I:14:ASP:O	8:1I:17:GLN:HB3	2.21	0.40
10:1O:17:ARG:NH1	10:1O:47:ILE:HD13	2.36	0.40
24:12:3:LEU:HD23	24:12:3:LEU:HA	1.89	0.40
26:14:53:GLU:HB2	26:14:55:ARG:H	1.84	0.40
32:1a:115:G:H4'	32:1a:116:A:O5'	2.21	0.40
32:1a:688:G:H2'	32:1a:689:C:H6	1.85	0.40
32:1a:1182:G:C4'	32:1a:1183:A:H5'	2.47	0.40
32:1a:1287:A:N3	32:1a:1353:G:O2'	2.48	0.40
34:1c:52:LEU:HD12	34:1c:53:ALA:H	1.86	0.40
43:1l:24:VAL:HB	43:1l:27:LEU:HD22	2.02	0.40
48:1q:22:LEU:HD13	48:1q:41:LYS:HG2	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:1r:26:LEU:HD22	49:1r:39:VAL:HG13	2.03	0.40
1:2A:27:G:N2	1:2A:512:G:H1'	2.36	0.40
1:2A:324:A:N6	1:2A:338:G:O2'	2.53	0.40
1:2A:363(D):G:H2'	1:2A:363(E):U:O4'	2.22	0.40
1:2A:411:G:C5	11:2P:72:PRO:HB3	2.56	0.40
1:2A:477:A:H2'	1:2A:478:A:C8	2.56	0.40
1:2A:478:A:C6	1:2A:480:A:C6	3.09	0.40
1:2A:659:C:H2'	1:2A:660:G:C8	2.55	0.40
1:2A:685:A:H5''	61:2A:3845:HOH:O	2.21	0.40
1:2A:907:U:C2'	1:2A:908:C:H5'	2.51	0.40
1:2A:2307:G:H8	1:2A:2307:G:OP1	2.04	0.40
1:2A:2751:G:H3'	1:2A:2752:C:C6	2.56	0.40
1:2A:2821:A:H2'	1:2A:2822:G:C8	2.57	0.40
7:2H:88:LEU:N	7:2H:163:TYR:O	2.52	0.40
12:2Q:75:THR:HA	12:2Q:89:ASN:O	2.20	0.40
21:2Z:44:PHE:CZ	21:2Z:86:VAL:HG11	2.57	0.40
32:2a:410:G:H21	32:2a:432:A:H62	1.68	0.40
32:2a:438:G:C4'	35:2d:123:HIS:HD2	2.33	0.40
32:2a:445:G:H2'	32:2a:446:G:O4'	2.20	0.40
32:2a:472:A:H5''	47:2p:80:PHE:HB3	2.03	0.40
32:2a:1005:A:H1'	32:2a:1025:U:C2	2.57	0.40
37:2f:100:ASN:ND2	49:2r:23:LYS:HE2	2.35	0.40
40:2i:9:ARG:H	40:2i:79:LEU:HD23	1.86	0.40
1:1A:27:G:N2	1:1A:537:G:H1'	2.36	0.40
1:1A:261:A:N1	1:1A:291:G:O2'	2.48	0.40
1:1A:603:C:H2'	1:1A:604:C:C6	2.56	0.40
1:1A:1217:G:H3'	1:1A:1218:G:H5'	2.03	0.40
12:1Q:75:THR:HG22	61:1Q:329:HOH:O	2.21	0.40
20:1Y:19:LYS:HB3	20:1Y:19:LYS:HE2	1.90	0.40
21:1Z:54:HIS:HD2	21:1Z:99:TYR:O	2.05	0.40
32:1a:736:C:H2'	32:1a:737:A:H8	1.85	0.40
32:1a:1014:A:H4'	50:1s:14:HIS:CE1	2.56	0.40
32:1a:1264:C:H2'	32:1a:1265:G:C8	2.57	0.40
32:1a:1456:G:N2	51:1t:43:LEU:HD11	2.37	0.40
33:1b:55:PHE:O	33:1b:59:GLU:HG2	2.21	0.40
34:1c:116:VAL:HG21	34:1c:202:ILE:HD11	2.02	0.40
35:1d:30:LYS:HA	35:1d:35:ARG:HE	1.87	0.40
41:1j:29:ARG:O	41:1j:31:GLY:N	2.54	0.40
1:2A:468:G:N7	29:27:39:ARG:NH2	2.63	0.40
1:2A:483:A:O2'	20:2Y:49:VAL:O	2.31	0.40
1:2A:2516:G:C2'	1:2A:2517:C:H5'	2.52	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:2G:17:PRO:HA	6:2G:20:ILE:HB	2.03	0.40
18:2W:38:TYR:CE1	27:25:41:PRO:HD3	2.56	0.40
20:2Y:7:VAL:HG11	20:2Y:13:VAL:HG11	2.03	0.40
21:2Z:145:GLU:HB2	21:2Z:148:ASP:OD2	2.21	0.40
23:21:8:SER:HB3	23:21:66:HIS:CD2	2.56	0.40
28:26:37:ARG:NH1	61:26:603:HOH:O	2.53	0.40
32:2a:69:G:H2'	32:2a:70:G:H8	1.87	0.40
32:2a:954:G:H5'	53:2y:17:ARG:NH2	2.37	0.40
32:2a:1400:5MC:C2	53:2y:63:ALA:HA	2.56	0.40
32:2a:1442:G:N3	32:2a:1442:G:H2'	2.36	0.40
36:2e:98:THR:HB	36:2e:117:ASP:HB3	2.03	0.40
40:2i:3:GLN:NE2	40:2i:20:ARG:HE	2.19	0.40
40:2i:127:LYS:HE3	53:2y:60:VAL:HG21	2.04	0.40
44:2m:33:ALA:HB2	44:2m:64:TRP:HH2	1.87	0.40
1:1A:214:A:O2'	1:1A:246:A:H4'	2.22	0.40
1:1A:669:A:H4'	1:1A:670:C:C5	2.55	0.40
1:1A:1463:C:H2'	1:1A:1464:G:O4'	2.20	0.40
1:1A:1688:A:H2'	1:1A:1689:G:O4'	2.22	0.40
1:1A:1756:U:H2'	1:1A:1757:C:C6	2.57	0.40
1:1A:2159:C:C2	1:1A:2176:G:N2	2.84	0.40
1:1A:2564:2MU:H2'	1:1A:2566:U:OP2	2.20	0.40
1:1A:2828:G:O2'	1:1A:2829:G:H5'	2.22	0.40
2:1B:24:G:N7	2:1B:56:G:H2'	2.36	0.40
8:1I:14:ASP:OD1	8:1I:15:VAL:HG12	2.21	0.40
8:1I:42:SER:HB2	61:1I:5007:HOH:O	2.21	0.40
8:1I:134:PRO:C	8:1I:136:VAL:H	2.30	0.40
32:1a:62:U:H1'	32:1a:379:C:H1'	2.04	0.40
32:1a:130:A:C8	48:1q:63:ARG:HB2	2.56	0.40
32:1a:581:G:OP1	46:1o:61:GLY:HA3	2.21	0.40
32:1a:1057:G:C4	32:1a:1204:A:C2	3.09	0.40
41:1j:44:VAL:HG22	41:1j:66:ARG:HG2	2.04	0.40
43:1l:33:ARG:HA	43:1l:33:ARG:HD3	1.71	0.40
50:1s:52:TYR:HB2	50:1s:57:HIS:CE1	2.57	0.40
51:1t:34:LYS:O	51:1t:38:LYS:HG2	2.22	0.40
1:2A:74:A:H4'	1:2A:75:G:O5'	2.21	0.40
1:2A:182:A:H2	1:2A:433:C:O2	2.03	0.40
1:2A:373:U:H2'	1:2A:374:A:C8	2.55	0.40
1:2A:571:A:C8	1:2A:2030:A:N6	2.89	0.40
1:2A:1614:A:C2	18:2W:93:ALA:HB2	2.56	0.40
1:2A:1669:A:H5''	1:2A:2550:G:OP1	2.20	0.40
1:2A:1946:U:H2'	1:2A:1947:C:C6	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2116:G:H3'	1:2A:2117:A:C8	2.57	0.40
1:2A:2238:G:N3	1:2A:2238:G:H2'	2.36	0.40
3:2D:142:VAL:HG23	3:2D:193:VAL:HA	2.03	0.40
6:2G:97:ASP:HA	6:2G:100:TRP:CD1	2.46	0.40
8:2I:72:LEU:HD12	8:2I:138:ILE:HG21	2.02	0.40
12:2Q:36:ALA:HB2	12:2Q:103:MET:SD	2.61	0.40
12:2Q:110:THR:OG1	12:2Q:112:GLU:HG3	2.22	0.40
14:2S:34:HIS:O	14:2S:97:ARG:NH2	2.54	0.40
14:2S:38:GLN:HB2	14:2S:47:THR:HG23	2.04	0.40
15:2T:119:LYS:O	15:2T:123:GLN:HB2	2.21	0.40
26:24:47:GLN:O	26:24:48:ARG:HB2	2.21	0.40
32:2a:66:G:H8	32:2a:66:G:OP1	2.05	0.40
32:2a:472:A:H4'	47:2p:80:PHE:O	2.22	0.40
32:2a:1034:G:H3'	32:2a:1035:A:C8	2.56	0.40
32:2a:1481:U:H2'	32:2a:1482:G:C8	2.57	0.40
38:2g:133:GLY:O	38:2g:137:LYS:N	2.47	0.40
41:2j:35:SER:HB3	41:2j:73:ASP:H	1.87	0.40
53:2y:39:ILE:HA	53:2y:51:ASP:O	2.21	0.40
1:1A:322:G:H5''	1:1A:323:A:OP1	2.22	0.40
1:1A:426:G:OP2	61:1A:4177:HOH:O	2.22	0.40
1:1A:1882:U:H2'	1:1A:1883:C:O4'	2.21	0.40
1:1A:2473:C:H2'	1:1A:2474:U:C6	2.57	0.40
6:1G:129:GLY:O	6:1G:161:THR:HB	2.20	0.40
15:1T:111:ARG:NH2	32:1a:1464:G:OP2	2.53	0.40
19:1X:5:TYR:CZ	24:12:30:ARG:HB2	2.56	0.40
19:1X:94:GLY:HA3	19:1X:95:LEU:C	2.45	0.40
32:1a:437:U:O2'	35:1d:123:HIS:HD2	2.04	0.40
32:1a:437:U:O3'	35:1d:125:HIS:HE1	2.04	0.40
32:1a:909:A:H2'	32:1a:910:C:O4'	2.20	0.40
33:1b:71:VAL:HB	33:1b:164:VAL:HG22	2.03	0.40
34:1c:6:HIS:HD2	34:1c:8:ILE:N	2.18	0.40
40:1i:18:PHE:HD2	40:1i:62:TYR:HD2	1.68	0.40
44:1m:59:TYR:CE1	44:1m:63:THR:HG21	2.57	0.40
46:1o:18:PHE:O	46:1o:19:PRO:C	2.64	0.40
46:1o:83:GLU:C	46:1o:85:LEU:N	2.79	0.40
1:2A:90:U:H1'	1:2A:92:A:C8	2.57	0.40
1:2A:247:G:H4'	1:2A:386:G:C5	2.57	0.40
1:2A:2563:U:O2	1:2A:2565:A:H8	2.04	0.40
1:2A:2820:A:OP1	13:2R:2:ARG:NH2	2.55	0.40
2:2B:27:C:H5''	14:2S:54:LEU:HD11	2.04	0.40
2:2B:32:C:C4	2:2B:33:G:N7	2.90	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:2F:110:LEU:HD11	5:2F:181:LEU:HG	2.03	0.40
5:2F:197:ASP:OD1	5:2F:198:ALA:N	2.55	0.40
7:2H:148:ILE:HG22	7:2H:162:ILE:HD13	2.03	0.40
9:2N:15:LEU:HD23	9:2N:16:ILE:N	2.37	0.40
13:2R:72:ASP:OD2	13:2R:75:LEU:HB2	2.21	0.40
15:2T:91:ARG:HD2	15:2T:120:ARG:NH1	2.37	0.40
32:2a:17:U:O2'	32:2a:1079:G:H1'	2.21	0.40
32:2a:255:G:OP1	48:2q:69:LYS:NZ	2.33	0.40
32:2a:277:C:H5''	48:2q:68:ARG:NH2	2.37	0.40
32:2a:406:G:H21	35:2d:119:GLN:NE2	2.19	0.40
32:2a:1250:A:H4'	40:2i:68:GLY:N	2.37	0.40
33:2b:33:TYR:HB2	33:2b:43:ASP:HA	2.02	0.40
35:2d:61:LYS:NZ	35:2d:62:GLN:OE1	2.45	0.40
40:2i:9:ARG:O	40:2i:104:ARG:NE	2.54	0.40
43:2l:28:LYS:N	43:2l:29:GLY:HA2	2.37	0.40
43:2l:79:GLU:HG2	43:2l:80:HIS:CD2	2.56	0.40
50:2s:22:LEU:HD13	50:2s:28:LYS:N	2.29	0.40
50:2s:22:LEU:HB3	50:2s:27:GLU:HA	2.02	0.40
50:2s:33:THR:HG22	50:2s:50:ALA:O	2.22	0.40
51:2t:50:GLU:O	51:2t:100:ILE:HD11	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	1D	273/276 (99%)	258 (94%)	15 (6%)	0	100	100
3	2D	273/276 (99%)	258 (94%)	15 (6%)	0	100	100
4	1E	202/206 (98%)	192 (95%)	9 (4%)	1 (0%)	24	48
4	2E	202/206 (98%)	192 (95%)	9 (4%)	1 (0%)	24	48

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	1F	201/210 (96%)	191 (95%)	9 (4%)	1 (0%)	24	48
5	2F	201/210 (96%)	191 (95%)	7 (4%)	3 (2%)	8	22
6	1G	179/182 (98%)	163 (91%)	15 (8%)	1 (1%)	21	44
6	2G	179/182 (98%)	166 (93%)	10 (6%)	3 (2%)	7	19
7	1H	172/180 (96%)	162 (94%)	9 (5%)	1 (1%)	21	44
7	2H	171/180 (95%)	152 (89%)	19 (11%)	0	100	100
8	1I	145/148 (98%)	129 (89%)	15 (10%)	1 (1%)	18	41
8	2I	144/148 (97%)	130 (90%)	12 (8%)	2 (1%)	9	23
9	1N	138/140 (99%)	135 (98%)	3 (2%)	0	100	100
9	2N	138/140 (99%)	130 (94%)	7 (5%)	1 (1%)	18	41
10	1O	120/122 (98%)	111 (92%)	8 (7%)	1 (1%)	16	37
10	2O	120/122 (98%)	111 (92%)	8 (7%)	1 (1%)	16	37
11	1P	147/150 (98%)	138 (94%)	9 (6%)	0	100	100
11	2P	147/150 (98%)	137 (93%)	9 (6%)	1 (1%)	18	41
12	1Q	139/141 (99%)	134 (96%)	4 (3%)	1 (1%)	18	41
12	2Q	139/141 (99%)	131 (94%)	7 (5%)	1 (1%)	18	41
13	1R	116/118 (98%)	113 (97%)	3 (3%)	0	100	100
13	2R	116/118 (98%)	109 (94%)	7 (6%)	0	100	100
14	1S	108/112 (96%)	99 (92%)	8 (7%)	1 (1%)	14	35
14	2S	108/112 (96%)	96 (89%)	12 (11%)	0	100	100
15	1T	129/146 (88%)	121 (94%)	7 (5%)	1 (1%)	16	37
15	2T	129/146 (88%)	121 (94%)	8 (6%)	0	100	100
16	1U	114/118 (97%)	113 (99%)	1 (1%)	0	100	100
16	2U	114/118 (97%)	109 (96%)	5 (4%)	0	100	100
17	1V	99/101 (98%)	97 (98%)	1 (1%)	1 (1%)	12	32
17	2V	99/101 (98%)	93 (94%)	5 (5%)	1 (1%)	12	32
18	1W	110/113 (97%)	107 (97%)	3 (3%)	0	100	100
18	2W	110/113 (97%)	107 (97%)	3 (3%)	0	100	100
19	1X	93/96 (97%)	91 (98%)	1 (1%)	1 (1%)	11	29
19	2X	93/96 (97%)	89 (96%)	3 (3%)	1 (1%)	11	29
20	1Y	105/110 (96%)	95 (90%)	10 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
20	2Y	105/110 (96%)	98 (93%)	7 (7%)	0	100	100
21	1Z	201/206 (98%)	189 (94%)	12 (6%)	0	100	100
21	2Z	199/206 (97%)	183 (92%)	16 (8%)	0	100	100
22	10	75/85 (88%)	73 (97%)	2 (3%)	0	100	100
22	20	75/85 (88%)	72 (96%)	3 (4%)	0	100	100
23	11	95/98 (97%)	93 (98%)	1 (1%)	1 (1%)	11	29
23	21	95/98 (97%)	93 (98%)	1 (1%)	1 (1%)	11	29
24	12	68/72 (94%)	67 (98%)	1 (2%)	0	100	100
24	22	68/72 (94%)	66 (97%)	2 (3%)	0	100	100
25	13	57/60 (95%)	56 (98%)	1 (2%)	0	100	100
25	23	57/60 (95%)	55 (96%)	1 (2%)	1 (2%)	6	18
26	14	67/71 (94%)	52 (78%)	12 (18%)	3 (4%)	2	4
26	24	67/71 (94%)	53 (79%)	9 (13%)	5 (8%)	1	1
27	15	57/60 (95%)	57 (100%)	0	0	100	100
27	25	57/60 (95%)	55 (96%)	1 (2%)	1 (2%)	6	18
28	16	51/54 (94%)	48 (94%)	3 (6%)	0	100	100
28	26	51/54 (94%)	47 (92%)	4 (8%)	0	100	100
29	17	46/49 (94%)	46 (100%)	0	0	100	100
29	27	46/49 (94%)	45 (98%)	1 (2%)	0	100	100
30	18	62/65 (95%)	62 (100%)	0	0	100	100
30	28	62/65 (95%)	62 (100%)	0	0	100	100
31	19	35/37 (95%)	35 (100%)	0	0	100	100
31	29	35/37 (95%)	34 (97%)	1 (3%)	0	100	100
33	1b	229/256 (90%)	200 (87%)	20 (9%)	9 (4%)	2	5
33	2b	229/256 (90%)	200 (87%)	22 (10%)	7 (3%)	3	8
34	1c	204/239 (85%)	191 (94%)	12 (6%)	1 (0%)	24	48
34	2c	204/239 (85%)	172 (84%)	29 (14%)	3 (2%)	8	22
35	1d	206/209 (99%)	192 (93%)	13 (6%)	1 (0%)	24	48
35	2d	206/209 (99%)	189 (92%)	16 (8%)	1 (0%)	24	48
36	1e	146/162 (90%)	141 (97%)	3 (2%)	2 (1%)	9	23
36	2e	146/162 (90%)	134 (92%)	12 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
37	1f	98/101 (97%)	93 (95%)	5 (5%)	0	100	100
37	2f	98/101 (97%)	91 (93%)	7 (7%)	0	100	100
38	1g	153/156 (98%)	145 (95%)	7 (5%)	1 (1%)	18	41
38	2g	153/156 (98%)	144 (94%)	7 (5%)	2 (1%)	9	25
39	1h	135/138 (98%)	128 (95%)	7 (5%)	0	100	100
39	2h	135/138 (98%)	127 (94%)	7 (5%)	1 (1%)	18	41
40	1i	125/128 (98%)	112 (90%)	12 (10%)	1 (1%)	16	37
40	2i	124/128 (97%)	111 (90%)	10 (8%)	3 (2%)	4	12
41	1j	95/105 (90%)	77 (81%)	15 (16%)	3 (3%)	3	7
41	2j	94/105 (90%)	80 (85%)	12 (13%)	2 (2%)	5	15
42	1k	112/129 (87%)	102 (91%)	9 (8%)	1 (1%)	14	35
42	2k	112/129 (87%)	100 (89%)	11 (10%)	1 (1%)	14	35
43	1l	119/132 (90%)	115 (97%)	4 (3%)	0	100	100
43	2l	119/132 (90%)	108 (91%)	11 (9%)	0	100	100
44	1m	114/126 (90%)	104 (91%)	8 (7%)	2 (2%)	6	18
44	2m	112/126 (89%)	98 (88%)	12 (11%)	2 (2%)	6	18
45	1n	58/61 (95%)	56 (97%)	2 (3%)	0	100	100
45	2n	58/61 (95%)	53 (91%)	5 (9%)	0	100	100
46	1o	86/89 (97%)	82 (95%)	1 (1%)	3 (4%)	3	6
46	2o	86/89 (97%)	83 (96%)	2 (2%)	1 (1%)	10	27
47	1p	80/88 (91%)	72 (90%)	7 (9%)	1 (1%)	9	25
47	2p	80/88 (91%)	68 (85%)	11 (14%)	1 (1%)	9	25
48	1q	97/105 (92%)	92 (95%)	5 (5%)	0	100	100
48	2q	97/105 (92%)	92 (95%)	5 (5%)	0	100	100
49	1r	66/88 (75%)	65 (98%)	1 (2%)	0	100	100
49	2r	66/88 (75%)	63 (96%)	3 (4%)	0	100	100
50	1s	81/93 (87%)	71 (88%)	8 (10%)	2 (2%)	4	11
50	2s	81/93 (87%)	73 (90%)	8 (10%)	0	100	100
51	1t	94/106 (89%)	87 (93%)	5 (5%)	2 (2%)	5	15
51	2t	96/106 (91%)	89 (93%)	3 (3%)	4 (4%)	2	4
52	1u	21/27 (78%)	21 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
52	2u	21/27 (78%)	16 (76%)	4 (19%)	1 (5%)	2	3
53	1y	95/113 (84%)	90 (95%)	5 (5%)	0	100	100
53	2y	94/113 (83%)	88 (94%)	6 (6%)	0	100	100
All	All	11629/12354 (94%)	10827 (93%)	706 (6%)	96 (1%)	16	37

All (96) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
26	14	47	GLN
26	14	55	ARG
33	1b	21	ARG
4	2E	51	PHE
6	2G	78	SER
6	2G	81	LYS
8	2I	10	GLU
12	2Q	59	ARG
33	2b	17	PHE
40	2i	54	ASP
6	1G	52	ILE
12	1Q	59	ARG
14	1S	59	LYS
15	1T	127	ALA
17	1V	79	VAL
33	1b	17	PHE
33	1b	20	GLU
33	1b	126	GLU
34	1c	107	GLN
38	1g	55	GLY
41	1j	77	PRO
44	1m	3	ARG
5	2F	130	ALA
10	2O	5	GLN
17	2V	79	VAL
23	21	3	LYS
26	24	62	ARG
33	2b	95	GLN
40	2i	44	VAL
41	2j	78	ASN
51	2t	47	GLY
51	2t	95	ALA
4	1E	52	LEU

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Mol	Chain	Res	Type
19	1X	94	GLY
23	11	3	LYS
26	14	39	CYS
36	1e	96	PRO
41	1j	55	LYS
46	1o	19	PRO
6	2G	43	LEU
26	24	44	THR
26	24	47	GLN
33	2b	16	HIS
52	2u	3	LYS
5	1F	130	ALA
7	1H	159	GLU
8	1I	85	GLU
10	1O	5	GLN
33	1b	37	ASN
33	1b	95	GLN
41	1j	30	SER
44	1m	12	ASN
47	1p	28	ARG
50	1s	12	ASP
50	1s	27	GLU
5	2F	21	ALA
19	2X	94	GLY
33	2b	128	GLU
38	2g	7	ALA
40	2i	96	LEU
42	2k	89	ALA
47	2p	44	THR
51	2t	100	ILE
51	2t	102	GLY
35	1d	124	GLY
36	1e	97	GLY
8	2I	132	PRO
26	24	49	PHE
27	25	35	GLU
33	2b	9	GLU
34	2c	108	ASN
34	2c	156	ARG
38	2g	97	GLN
44	2m	95	GLY
46	2o	88	ARG

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Mol	Chain	Res	Type
33	1b	127	ILE
33	1b	232	PRO
46	1o	84	LYS
26	24	55	ARG
33	2b	21	ARG
34	2c	99	VAL
39	2h	51	VAL
9	2N	129	PRO
5	2F	171	PRO
11	2P	122	PRO
41	2j	37	PRO
44	2m	7	VAL
25	23	59	VAL
35	2d	171	GLY
40	1i	44	VAL
42	1k	105	VAL
51	1t	47	GLY
51	1t	100	ILE
33	2b	125	PRO
46	1o	86	GLY
33	1b	125	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	1D	214/218 (98%)	192 (90%)	22 (10%)	7	18
3	2D	215/218 (99%)	195 (91%)	20 (9%)	8	21
4	1E	164/166 (99%)	150 (92%)	14 (8%)	10	25
4	2E	164/166 (99%)	150 (92%)	14 (8%)	10	25
5	1F	160/166 (96%)	145 (91%)	15 (9%)	8	21
5	2F	159/166 (96%)	144 (91%)	15 (9%)	8	21
6	1G	144/156 (92%)	128 (89%)	16 (11%)	6	15
6	2G	142/156 (91%)	127 (89%)	15 (11%)	6	17

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	1H	144/148 (97%)	137 (95%)	7 (5%)	22	49
7	2H	143/148 (97%)	133 (93%)	10 (7%)	14	34
8	1I	111/124 (90%)	101 (91%)	10 (9%)	9	23
8	2I	108/124 (87%)	101 (94%)	7 (6%)	15	37
9	1N	119/119 (100%)	112 (94%)	7 (6%)	18	42
9	2N	118/119 (99%)	110 (93%)	8 (7%)	14	35
10	1O	100/100 (100%)	95 (95%)	5 (5%)	22	48
10	2O	100/100 (100%)	97 (97%)	3 (3%)	36	66
11	1P	115/116 (99%)	109 (95%)	6 (5%)	21	47
11	2P	115/116 (99%)	108 (94%)	7 (6%)	17	40
12	1Q	111/111 (100%)	105 (95%)	6 (5%)	20	45
12	2Q	111/111 (100%)	107 (96%)	4 (4%)	31	60
13	1R	101/101 (100%)	91 (90%)	10 (10%)	7	19
13	2R	101/101 (100%)	89 (88%)	12 (12%)	5	13
14	1S	87/88 (99%)	80 (92%)	7 (8%)	11	28
14	2S	85/88 (97%)	78 (92%)	7 (8%)	10	27
15	1T	115/127 (91%)	107 (93%)	8 (7%)	14	34
15	2T	113/127 (89%)	105 (93%)	8 (7%)	13	33
16	1U	93/94 (99%)	87 (94%)	6 (6%)	15	37
16	2U	93/94 (99%)	89 (96%)	4 (4%)	26	54
17	1V	81/82 (99%)	73 (90%)	8 (10%)	7	19
17	2V	80/82 (98%)	75 (94%)	5 (6%)	16	39
18	1W	90/92 (98%)	80 (89%)	10 (11%)	6	15
18	2W	90/92 (98%)	81 (90%)	9 (10%)	7	19
19	1X	77/78 (99%)	72 (94%)	5 (6%)	15	37
19	2X	77/78 (99%)	72 (94%)	5 (6%)	15	37
20	1Y	86/91 (94%)	78 (91%)	8 (9%)	8	21
20	2Y	86/91 (94%)	82 (95%)	4 (5%)	23	51
21	1Z	169/179 (94%)	153 (90%)	16 (10%)	8	20
21	2Z	165/179 (92%)	158 (96%)	7 (4%)	26	55
22	10	61/67 (91%)	58 (95%)	3 (5%)	22	49

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
22	20	61/67 (91%)	60 (98%)	1 (2%)	55	80
23	11	79/83 (95%)	75 (95%)	4 (5%)	21	48
23	21	81/83 (98%)	77 (95%)	4 (5%)	22	49
24	12	65/67 (97%)	64 (98%)	1 (2%)	57	81
24	22	66/67 (98%)	63 (96%)	3 (4%)	24	52
25	13	51/52 (98%)	47 (92%)	4 (8%)	11	29
25	23	50/52 (96%)	47 (94%)	3 (6%)	17	41
26	14	58/63 (92%)	55 (95%)	3 (5%)	21	47
26	24	54/63 (86%)	53 (98%)	1 (2%)	50	77
27	15	51/52 (98%)	44 (86%)	7 (14%)	3	9
27	25	50/52 (96%)	47 (94%)	3 (6%)	17	41
28	16	51/52 (98%)	47 (92%)	4 (8%)	11	29
28	26	50/52 (96%)	46 (92%)	4 (8%)	11	28
29	17	41/42 (98%)	36 (88%)	5 (12%)	5	12
29	27	41/42 (98%)	40 (98%)	1 (2%)	43	72
30	18	54/55 (98%)	50 (93%)	4 (7%)	13	32
30	28	54/55 (98%)	49 (91%)	5 (9%)	8	21
31	19	34/34 (100%)	32 (94%)	2 (6%)	18	42
31	29	34/34 (100%)	32 (94%)	2 (6%)	18	42
33	1b	191/220 (87%)	177 (93%)	14 (7%)	13	32
33	2b	187/220 (85%)	178 (95%)	9 (5%)	23	50
34	1c	144/188 (77%)	138 (96%)	6 (4%)	26	55
34	2c	140/188 (74%)	132 (94%)	8 (6%)	18	43
35	1d	171/181 (94%)	161 (94%)	10 (6%)	18	42
35	2d	172/181 (95%)	166 (96%)	6 (4%)	32	61
36	1e	114/123 (93%)	109 (96%)	5 (4%)	25	53
36	2e	114/123 (93%)	107 (94%)	7 (6%)	17	40
37	1f	85/90 (94%)	79 (93%)	6 (7%)	13	33
37	2f	85/90 (94%)	82 (96%)	3 (4%)	32	61
38	1g	120/127 (94%)	114 (95%)	6 (5%)	22	48
38	2g	119/127 (94%)	112 (94%)	7 (6%)	18	42

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
39	1h	116/119 (98%)	109 (94%)	7 (6%)	17	41
39	2h	114/119 (96%)	104 (91%)	10 (9%)	9	23
40	1i	91/99 (92%)	89 (98%)	2 (2%)	45	74
40	2i	88/99 (89%)	82 (93%)	6 (7%)	14	35
41	1j	68/92 (74%)	66 (97%)	2 (3%)	37	67
41	2j	68/92 (74%)	65 (96%)	3 (4%)	25	53
42	1k	83/99 (84%)	78 (94%)	5 (6%)	17	41
42	2k	83/99 (84%)	75 (90%)	8 (10%)	8	20
43	1l	96/108 (89%)	91 (95%)	5 (5%)	21	47
43	2l	96/108 (89%)	93 (97%)	3 (3%)	35	65
44	1m	90/101 (89%)	84 (93%)	6 (7%)	15	36
44	2m	87/101 (86%)	82 (94%)	5 (6%)	18	43
45	1n	49/50 (98%)	47 (96%)	2 (4%)	27	56
45	2n	49/50 (98%)	48 (98%)	1 (2%)	48	76
46	1o	78/80 (98%)	74 (95%)	4 (5%)	21	48
46	2o	78/80 (98%)	77 (99%)	1 (1%)	61	83
47	1p	69/74 (93%)	66 (96%)	3 (4%)	26	54
47	2p	68/74 (92%)	62 (91%)	6 (9%)	9	23
48	1q	94/97 (97%)	90 (96%)	4 (4%)	26	54
48	2q	94/97 (97%)	90 (96%)	4 (4%)	26	54
49	1r	59/77 (77%)	57 (97%)	2 (3%)	32	62
49	2r	59/77 (77%)	53 (90%)	6 (10%)	7	18
50	1s	68/80 (85%)	67 (98%)	1 (2%)	57	81
50	2s	67/80 (84%)	61 (91%)	6 (9%)	9	23
51	1t	71/82 (87%)	67 (94%)	4 (6%)	19	44
51	2t	70/82 (85%)	63 (90%)	7 (10%)	7	19
52	1u	18/22 (82%)	17 (94%)	1 (6%)	19	44
52	2u	18/22 (82%)	17 (94%)	1 (6%)	19	44
53	1y	82/98 (84%)	75 (92%)	7 (8%)	10	25
53	2y	79/98 (81%)	74 (94%)	5 (6%)	16	39
All	All	9524/10260 (93%)	8896 (93%)	628 (7%)	15	36

All (628) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	1D	3	VAL
3	1D	13	ARG
3	1D	39	LYS
3	1D	61	LEU
3	1D	63	ARG
3	1D	69	ARG
3	1D	88	ARG
3	1D	103	ARG
3	1D	106	ILE
3	1D	111	LEU
3	1D	113	VAL
3	1D	138	VAL
3	1D	140	THR
3	1D	141	VAL
3	1D	173	VAL
3	1D	183	ARG
3	1D	193	VAL
3	1D	211	ARG
3	1D	221	VAL
3	1D	229	VAL
3	1D	242	ARG
3	1D	259	THR
4	1E	1	MET
4	1E	7	VAL
4	1E	9	VAL
4	1E	33	VAL
4	1E	34	VAL
4	1E	49	LEU
4	1E	75	VAL
4	1E	78	LEU
4	1E	116	VAL
4	1E	119	ARG
4	1E	144	ARG
4	1E	175	VAL
4	1E	181	LEU
4	1E	195	LEU
5	1F	53	THR
5	1F	57	VAL
5	1F	74	ARG
5	1F	88	VAL
5	1F	110	LEU
5	1F	125	LEU

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Mol	Chain	Res	Type
5	1F	132	VAL
5	1F	157	VAL
5	1F	158	THR
5	1F	170	LEU
5	1F	183	VAL
5	1F	191	ARG
5	1F	192	LEU
5	1F	197	ASP
5	1F	201	VAL
6	1G	5	VAL
6	1G	7	LEU
6	1G	28	VAL
6	1G	43	LEU
6	1G	47	LYS
6	1G	49	ASP
6	1G	52	ILE
6	1G	53	LEU
6	1G	58	GLN
6	1G	105	LYS
6	1G	135	LEU
6	1G	140	ILE
6	1G	153	ARG
6	1G	159	VAL
6	1G	175	LEU
6	1G	181	ARG
7	1H	15	VAL
7	1H	71	LEU
7	1H	85	LYS
7	1H	122	THR
7	1H	134	SER
7	1H	141	VAL
7	1H	149	ARG
8	1I	5	LEU
8	1I	12	LEU
8	1I	38	LEU
8	1I	41	GLU
8	1I	44	LEU
8	1I	92	VAL
8	1I	101	LEU
8	1I	109	ILE
8	1I	116	LEU
8	1I	127	VAL

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Mol	Chain	Res	Type
9	1N	5	VAL
9	1N	15	LEU
9	1N	34	LEU
9	1N	48	MET
9	1N	62	VAL
9	1N	67	LEU
9	1N	99	LEU
10	1O	10	VAL
10	1O	24	VAL
10	1O	94	ARG
10	1O	98	VAL
10	1O	108	GLU
11	1P	59	LEU
11	1P	75	ILE
11	1P	83	VAL
11	1P	95	VAL
11	1P	101	VAL
11	1P	125	VAL
12	1Q	2	LEU
12	1Q	6	ARG
12	1Q	7	MET
12	1Q	55	VAL
12	1Q	81	VAL
12	1Q	109	VAL
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	100	LEU
13	1R	111	LEU
14	1S	14	VAL
14	1S	25	ARG
14	1S	50	SER
14	1S	52	SER
14	1S	59	LYS
14	1S	85	VAL
14	1S	110	LEU
15	1T	28	VAL

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Mol	Chain	Res	Type
15	1T	33	LYS
15	1T	34	VAL
15	1T	49	VAL
15	1T	65	LYS
15	1T	89	VAL
15	1T	96	ARG
15	1T	118	ARG
16	1U	8	VAL
16	1U	30	LYS
16	1U	74	LEU
16	1U	77	SER
16	1U	83	LEU
16	1U	95	LEU
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	15	ARG
18	1W	17	VAL
18	1W	19	LEU
18	1W	23	LEU
18	1W	49	LYS
18	1W	95	ILE
18	1W	96	ILE
18	1W	100	THR
18	1W	107	LEU
19	1X	35	THR
19	1X	38	GLU
19	1X	45	THR
19	1X	52	VAL
19	1X	66	LEU
20	1Y	7	VAL
20	1Y	43	ASN
20	1Y	63	LYS
20	1Y	64	GLU
20	1Y	72	VAL
20	1Y	85	VAL

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Mol	Chain	Res	Type
20	1Y	90	LEU
20	1Y	99	CYS
21	1Z	18	LEU
21	1Z	31	ARG
21	1Z	46	LYS
21	1Z	58	VAL
21	1Z	61	LEU
21	1Z	74	VAL
21	1Z	76	LEU
21	1Z	86	VAL
21	1Z	91	LEU
21	1Z	120	ILE
21	1Z	126	VAL
21	1Z	150	LEU
21	1Z	155	LEU
21	1Z	161	VAL
21	1Z	162	GLU
21	1Z	170	THR
22	10	39	ARG
22	10	55	ARG
22	10	59	LEU
23	11	21	ARG
23	11	30	VAL
23	11	59	THR
23	11	95	LEU
24	12	53	LEU
25	13	6	VAL
25	13	8	LEU
25	13	23	LEU
25	13	55	ARG
26	14	49	PHE
26	14	53	GLU
26	14	56	VAL
27	15	6	VAL
27	15	16	ARG
27	15	26	THR
27	15	29	THR
27	15	40	LYS
27	15	58	LEU
27	15	60	VAL
28	16	14	THR
28	16	19	ARG

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Mol	Chain	Res	Type
28	16	48	VAL
28	16	52	VAL
29	17	1	MET
29	17	24	THR
29	17	43	THR
29	17	46	VAL
29	17	47	ARG
30	18	14	VAL
30	18	23	VAL
30	18	32	LEU
30	18	58	ILE
31	19	17	ILE
31	19	35	ARG
33	1b	7	VAL
33	1b	15	VAL
33	1b	20	GLU
33	1b	32	ILE
33	1b	44	LEU
33	1b	71	VAL
33	1b	107	THR
33	1b	112	VAL
33	1b	130	ARG
33	1b	160	ASP
33	1b	184	VAL
33	1b	185	ILE
33	1b	196	LEU
33	1b	200	ILE
34	1c	3	ASN
34	1c	32	LEU
34	1c	105	GLU
34	1c	112	SER
34	1c	154	SER
34	1c	206	GLU
35	1d	17	VAL
35	1d	19	LEU
35	1d	28	SER
35	1d	59	ARG
35	1d	112	VAL
35	1d	127	THR
35	1d	135	LEU
35	1d	157	LEU
35	1d	188	LEU

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Mol	Chain	Res	Type
35	1d	194	LEU
36	1e	31	LEU
36	1e	41	VAL
36	1e	69	VAL
36	1e	91	LEU
36	1e	131	ILE
37	1f	40	VAL
37	1f	45	LEU
37	1f	48	LEU
37	1f	63	TYR
37	1f	69	GLU
37	1f	72	VAL
38	1g	12	LEU
38	1g	27	ILE
38	1g	75	VAL
38	1g	91	VAL
38	1g	104	LEU
38	1g	115	ARG
39	1h	25	ASP
39	1h	26	VAL
39	1h	39	LEU
39	1h	51	VAL
39	1h	63	LEU
39	1h	99	GLU
39	1h	104	ARG
40	1i	27	THR
40	1i	47	LEU
41	1j	34	VAL
41	1j	72	VAL
42	1k	16	SER
42	1k	83	ILE
42	1k	84	VAL
42	1k	112	THR
42	1k	114	VAL
43	1l	27	LEU
43	1l	60	LEU
43	1l	83	VAL
43	1l	113	ARG
43	1l	117	ARG
44	1m	9	ILE
44	1m	19	LEU
44	1m	70	LEU

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Mol	Chain	Res	Type
44	1m	98	VAL
44	1m	102	ARG
44	1m	117	VAL
45	1n	18	VAL
45	1n	42	ILE
46	1o	3	ILE
46	1o	24	SER
46	1o	66	LEU
46	1o	87	ILE
47	1p	2	VAL
47	1p	29	ASP
47	1p	62	VAL
48	1q	26	GLN
48	1q	57	VAL
48	1q	63	ARG
48	1q	97	SER
49	1r	37	VAL
49	1r	42	ARG
50	1s	41	VAL
51	1t	10	LEU
51	1t	11	SER
51	1t	24	LEU
51	1t	84	LEU
52	1u	24	ARG
53	1y	3	MET
53	1y	16	ILE
53	1y	23	ARG
53	1y	24	LEU
53	1y	42	SER
53	1y	60	VAL
53	1y	88	LEU
3	2D	3	VAL
3	2D	32	SER
3	2D	69	ARG
3	2D	71	ASP
3	2D	82	ILE
3	2D	94	LEU
3	2D	103	ARG
3	2D	111	LEU
3	2D	138	VAL
3	2D	142	VAL
3	2D	173	VAL

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Mol	Chain	Res	Type
3	2D	193	VAL
3	2D	211	ARG
3	2D	217	ARG
3	2D	221	VAL
3	2D	229	VAL
3	2D	237	GLU
3	2D	242	ARG
3	2D	259	THR
3	2D	274	ARG
4	2E	7	VAL
4	2E	9	VAL
4	2E	21	VAL
4	2E	38	THR
4	2E	72	VAL
4	2E	75	VAL
4	2E	78	LEU
4	2E	93	VAL
4	2E	116	VAL
4	2E	167	VAL
4	2E	175	VAL
4	2E	181	LEU
4	2E	182	LEU
4	2E	184	VAL
5	2F	20	LEU
5	2F	33	LEU
5	2F	38	ARG
5	2F	57	VAL
5	2F	60	SER
5	2F	74	ARG
5	2F	88	VAL
5	2F	132	VAL
5	2F	153	SER
5	2F	157	VAL
5	2F	158	THR
5	2F	168	ARG
5	2F	174	VAL
5	2F	183	VAL
5	2F	192	LEU
6	2G	5	VAL
6	2G	7	LEU
6	2G	28	VAL
6	2G	60	LEU

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Mol	Chain	Res	Type
6	2G	62	LEU
6	2G	71	THR
6	2G	79	ASN
6	2G	88	ILE
6	2G	92	VAL
6	2G	109	VAL
6	2G	133	LEU
6	2G	140	ILE
6	2G	159	VAL
6	2G	161	THR
6	2G	181	ARG
7	2H	24	VAL
7	2H	47	GLU
7	2H	56	SER
7	2H	71	LEU
7	2H	89	ILE
7	2H	98	LEU
7	2H	127	GLU
7	2H	134	SER
7	2H	136	ILE
7	2H	139	GLN
8	2I	40	THR
8	2I	44	LEU
8	2I	64	GLU
8	2I	68	LEU
8	2I	116	LEU
8	2I	127	VAL
8	2I	140	LEU
9	2N	28	THR
9	2N	34	LEU
9	2N	46	VAL
9	2N	60	ILE
9	2N	62	VAL
9	2N	71	ILE
9	2N	99	LEU
9	2N	140	VAL
10	2O	24	VAL
10	2O	35	VAL
10	2O	108	GLU
11	2P	4	SER
11	2P	59	LEU
11	2P	65	ARG

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Mol	Chain	Res	Type
11	2P	83	VAL
11	2P	112	LEU
11	2P	117	GLU
11	2P	126	VAL
12	2Q	55	VAL
12	2Q	109	VAL
12	2Q	110	THR
12	2Q	112	GLU
13	2R	6	SER
13	2R	17	ARG
13	2R	24	GLN
13	2R	29	LEU
13	2R	36	THR
13	2R	44	LEU
13	2R	65	LEU
13	2R	67	LEU
13	2R	75	LEU
13	2R	96	ARG
13	2R	100	LEU
13	2R	111	LEU
14	2S	8	GLU
14	2S	28	VAL
14	2S	30	ARG
14	2S	50	SER
14	2S	52	SER
14	2S	64	GLU
14	2S	69	VAL
15	2T	28	VAL
15	2T	31	SER
15	2T	49	VAL
15	2T	51	ARG
15	2T	53	ARG
15	2T	89	VAL
15	2T	95	ARG
15	2T	96	ARG
16	2U	31	SER
16	2U	34	LYS
16	2U	59	ARG
16	2U	95	LEU
17	2V	18	LEU
17	2V	39	LEU
17	2V	46	VAL

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Mol	Chain	Res	Type
17	2V	72	VAL
17	2V	79	VAL
18	2W	15	ARG
18	2W	17	VAL
18	2W	19	LEU
18	2W	23	LEU
18	2W	49	LYS
18	2W	67	ASP
18	2W	86	LEU
18	2W	100	THR
18	2W	107	LEU
19	2X	2	LYS
19	2X	35	THR
19	2X	49	VAL
19	2X	57	LEU
19	2X	81	VAL
20	2Y	3	VAL
20	2Y	28	LYS
20	2Y	44	ILE
20	2Y	72	VAL
21	2Z	33	LEU
21	2Z	74	VAL
21	2Z	86	VAL
21	2Z	107	THR
21	2Z	150	LEU
21	2Z	170	THR
21	2Z	175	VAL
22	20	9	SER
23	21	11	ARG
23	21	35	THR
23	21	51	VAL
23	21	85	LEU
24	22	1	MET
24	22	25	VAL
24	22	53	LEU
25	23	23	LEU
25	23	31	LEU
25	23	54	VAL
26	24	52	THR
27	25	6	VAL
27	25	29	THR
27	25	58	LEU

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Mol	Chain	Res	Type
28	26	7	ILE
28	26	14	THR
28	26	40	CYS
28	26	48	VAL
29	27	46	VAL
30	28	14	VAL
30	28	23	VAL
30	28	30	ARG
30	28	32	LEU
30	28	37	SER
31	29	7	VAL
31	29	17	ILE
33	2b	15	VAL
33	2b	23	ARG
33	2b	44	LEU
33	2b	83	MET
33	2b	112	VAL
33	2b	127	ILE
33	2b	189	ASP
33	2b	190	THR
33	2b	209	ARG
34	2c	15	THR
34	2c	33	LEU
34	2c	68	VAL
34	2c	103	VAL
34	2c	166	GLU
34	2c	195	VAL
34	2c	196	LEU
34	2c	207	VAL
35	2d	8	VAL
35	2d	83	SER
35	2d	108	LEU
35	2d	122	ARG
35	2d	135	LEU
35	2d	175	SER
36	2e	18	ARG
36	2e	31	LEU
36	2e	34	VAL
36	2e	41	VAL
36	2e	72	GLN
36	2e	75	THR
36	2e	152	ARG

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Mol	Chain	Res	Type
37	2f	61	LEU
37	2f	63	TYR
37	2f	72	VAL
38	2g	42	ILE
38	2g	50	ILE
38	2g	75	VAL
38	2g	77	SER
38	2g	104	LEU
38	2g	113	GLU
38	2g	155	ARG
39	2h	10	LEU
39	2h	26	VAL
39	2h	29	SER
39	2h	38	ILE
39	2h	45	ILE
39	2h	85	ARG
39	2h	91	ARG
39	2h	104	ARG
39	2h	121	ASP
39	2h	137	VAL
40	2i	9	ARG
40	2i	17	VAL
40	2i	27	THR
40	2i	51	ARG
40	2i	102	LEU
40	2i	108	VAL
41	2j	30	SER
41	2j	94	VAL
41	2j	100	THR
42	2k	32	ILE
42	2k	47	VAL
42	2k	48	ILE
42	2k	66	LEU
42	2k	79	SER
42	2k	83	ILE
42	2k	109	VAL
42	2k	114	VAL
43	2l	36	VAL
43	2l	83	VAL
43	2l	112	ASP
44	2m	4	ILE
44	2m	60	VAL

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Mol	Chain	Res	Type
44	2m	79	LYS
44	2m	99	ARG
44	2m	102	ARG
45	2n	6	LEU
46	2o	39	LEU
47	2p	1	MET
47	2p	2	VAL
47	2p	21	VAL
47	2p	62	VAL
47	2p	69	THR
47	2p	74	LEU
48	2q	9	VAL
48	2q	56	VAL
48	2q	60	ILE
48	2q	70	ARG
49	2r	26	LEU
49	2r	37	VAL
49	2r	54	ARG
49	2r	55	ARG
49	2r	76	LEU
49	2r	85	LEU
50	2s	37	ARG
50	2s	41	VAL
50	2s	48	THR
50	2s	49	ILE
50	2s	64	GLU
50	2s	71	LEU
51	2t	15	ARG
51	2t	31	SER
51	2t	56	MET
51	2t	62	LEU
51	2t	71	THR
51	2t	86	ARG
51	2t	100	ILE
52	2u	24	ARG
53	2y	5	ILE
53	2y	6	THR
53	2y	32	THR
53	2y	61	LEU
53	2y	93	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (139) such sidechains are listed below:

Mol	Chain	Res	Type
3	1D	87	ASN
3	1D	166	GLN
4	1E	55	ASN
4	1E	143	ASN
5	1F	67	GLN
5	1F	69	HIS
5	1F	203	GLN
6	1G	26	GLN
6	1G	79	ASN
8	1I	11	ASN
8	1I	74	ASN
8	1I	104	GLN
8	1I	105	HIS
9	1N	94	HIS
10	1O	89	ASN
13	1R	31	HIS
13	1R	50	HIS
13	1R	71	GLN
14	1S	95	HIS
15	1T	58	ASN
16	1U	72	HIS
16	1U	81	HIS
16	1U	94	ASN
16	1U	117	GLN
18	1W	111	HIS
19	1X	31	HIS
20	1Y	6	HIS
20	1Y	43	ASN
20	1Y	92	ASN
21	1Z	55	HIS
21	1Z	65	GLN
21	1Z	73	GLN
21	1Z	132	ASN
21	1Z	151	HIS
23	11	19	GLN
24	12	70	GLN
25	13	32	GLN
25	13	46	ASN
26	14	47	GLN
27	15	4	HIS
31	19	34	GLN
33	1b	224	GLN
34	1c	6	HIS

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Mol	Chain	Res	Type
34	1c	69	HIS
34	1c	98	ASN
34	1c	102	ASN
34	1c	118	GLN
34	1c	162	GLN
35	1d	45	GLN
35	1d	77	ASN
35	1d	116	GLN
35	1d	123	HIS
35	1d	129	ASN
35	1d	160	GLN
36	1e	20	GLN
36	1e	141	GLN
37	1f	64	GLN
37	1f	100	ASN
38	1g	28	ASN
39	1h	82	HIS
40	1i	3	GLN
40	1i	73	GLN
41	1j	21	GLN
41	1j	56	HIS
41	1j	69	ASN
41	1j	84	GLN
42	1k	93	GLN
42	1k	116	HIS
43	1l	99	HIS
46	1o	28	GLN
47	1p	16	HIS
48	1q	16	GLN
50	1s	83	HIS
51	1t	18	GLN
53	1y	31	GLN
53	1y	38	HIS
3	2D	87	ASN
3	2D	126	GLN
3	2D	253	GLN
4	2E	48	GLN
5	2F	40	GLN
5	2F	69	HIS
5	2F	133	ASN
6	2G	26	GLN
6	2G	79	ASN

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Mol	Chain	Res	Type
8	2I	43	ASN
9	2N	94	HIS
10	2O	3	GLN
11	2P	27	HIS
12	2Q	89	ASN
12	2Q	113	GLN
12	2Q	123	HIS
12	2Q	141	GLN
13	2R	31	HIS
16	2U	94	ASN
18	2W	34	ASN
18	2W	60	ASN
19	2X	31	HIS
19	2X	82	GLN
20	2Y	92	ASN
21	2Z	73	GLN
21	2Z	75	ASN
25	23	32	GLN
28	26	20	ASN
30	28	35	GLN
31	29	36	GLN
33	2b	40	HIS
34	2c	3	ASN
34	2c	6	HIS
34	2c	139	GLN
34	2c	176	HIS
35	2d	77	ASN
35	2d	116	GLN
35	2d	161	ASN
36	2e	78	HIS
37	2f	100	ASN
38	2g	11	GLN
38	2g	13	GLN
38	2g	28	ASN
38	2g	56	GLN
38	2g	64	GLN
38	2g	109	ASN
39	2h	82	HIS
40	2i	3	GLN
40	2i	73	GLN
41	2j	56	HIS
41	2j	68	HIS

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Mol	Chain	Res	Type
42	2k	22	HIS
43	2l	99	HIS
44	2m	92	HIS
45	2n	49	HIS
46	2o	28	GLN
47	2p	16	HIS
50	2s	69	HIS
50	2s	83	HIS
53	2y	4	ASN
53	2y	38	HIS
53	2y	84	GLN
53	2y	89	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1A	2865/2915 (98%)	421 (14%)	29 (1%)
1	2A	2858/2915 (98%)	493 (17%)	36 (1%)
2	1B	119/121 (98%)	11 (9%)	0
2	2B	119/121 (98%)	18 (15%)	0
32	1a	1497/1521 (98%)	234 (15%)	0
32	2a	1501/1521 (98%)	262 (17%)	0
All	All	8959/9114 (98%)	1439 (16%)	65 (0%)

All (1439) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1A	12	U
1	1A	14	A
1	1A	15	G
1	1A	34	C
1	1A	45	C
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	164	G
1	1A	166	G
1	1A	170	A

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Mol	Chain	Res	Type
1	1A	171	A
1	1A	177	G
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	253	C
1	1A	254	A
1	1A	265	U
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	297	C
1	1A	298	G
1	1A	299	G
1	1A	303	C
1	1A	304	C
1	1A	307	A
1	1A	335	A
1	1A	354	A
1	1A	376	G
1	1A	381	A
1	1A	384	G
1	1A	387	G
1	1A	413	G
1	1A	423	G
1	1A	432	U
1	1A	438	G
1	1A	448	U
1	1A	449	A

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Mol	Chain	Res	Type
1	1A	455	A
1	1A	474	U
1	1A	482	C
1	1A	483	A
1	1A	507	G
1	1A	530	A
1	1A	534	C
1	1A	553	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	597	C
1	1A	598	A
1	1A	626	A
1	1A	627	G
1	1A	630	U
1	1A	639	G
1	1A	641	G
1	1A	652	A
1	1A	662	A
1	1A	670	C
1	1A	693	G
1	1A	697	C
1	1A	698	G
1	1A	701	A
1	1A	716	G
1	1A	733	G
1	1A	764	G
1	1A	777	C
1	1A	785	G
1	1A	804	U
1	1A	821	A
1	1A	822	G
1	1A	823	G
1	1A	829	A
1	1A	831	A
1	1A	832	G

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Mol	Chain	Res	Type
1	1A	837	C
1	1A	839	G
1	1A	852	G
1	1A	859	C
1	1A	874	U
1	1A	875	U
1	1A	906	G
1	1A	913	A
1	1A	925	A
1	1A	926	G
1	1A	929	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	943	C
1	1A	945	A
1	1A	953	U
1	1A	956	A
1	1A	977	G
1	1A	983	G
1	1A	990	A
1	1A	991	G
1	1A	1003	U
1	1A	1004	A
1	1A	1006	C
1	1A	1008	U
1	1A	1019	G
1	1A	1020	C
1	1A	1029	A
1	1A	1042	A
1	1A	1045	U
1	1A	1058	U
1	1A	1059	C
1	1A	1068	G
1	1A	1072	U
1	1A	1079	U
1	1A	1084	C

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Mol	Chain	Res	Type
1	1A	1085	G
1	1A	1088	G
1	1A	1089	C
1	1A	1091	A
1	1A	1092	A
1	1A	1093	G
1	1A	1094	A
1	1A	1099	C
1	1A	1100	A
1	1A	1106	U
1	1A	1107	U
1	1A	1108	G
1	1A	1109	G
1	1A	1111	U
1	1A	1114	G
1	1A	1116	A
1	1A	1117	G
1	1A	1119	A
1	1A	1121	C
1	1A	1123	A
1	1A	1124	U
1	1A	1125	C
1	1A	1129	U
1	1A	1133	G
1	1A	1134	A
1	1A	1136	U
1	1A	1137	G
1	1A	1142	A
1	1A	1143	U
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	1196	C
1	1A	1216	G
1	1A	1217	G

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Mol	Chain	Res	Type
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	1255	A
1	1A	1256	U
1	1A	1263	C
1	1A	1275	G
1	1A	1299	A
1	1A	1302	G
1	1A	1317	G
1	1A	1318	A
1	1A	1327	G
1	1A	1346	U
1	1A	1347	A
1	1A	1351	C
1	1A	1367	A
1	1A	1398	U
1	1A	1405	A
1	1A	1406	A
1	1A	1411	A
1	1A	1416	C
1	1A	1426	G
1	1A	1430	A
1	1A	1431	G
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	1491	A
1	1A	1497	G
1	1A	1500	A
1	1A	1502	G
1	1A	1506	G
1	1A	1508	G
1	1A	1514	C
1	1A	1518	A
1	1A	1529	G

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Mol	Chain	Res	Type
1	1A	1539	C
1	1A	1552	C
1	1A	1554	A
1	1A	1555	C
1	1A	1556	A
1	1A	1589	A
1	1A	1590	C
1	1A	1605	A
1	1A	1613	A
1	1A	1616	A
1	1A	1625	U
1	1A	1628	G
1	1A	1629	C
1	1A	1631	C
1	1A	1632	A
1	1A	1654	A
1	1A	1655	A
1	1A	1656	A
1	1A	1695	C
1	1A	1701	A
1	1A	1711	A
1	1A	1721	G
1	1A	1747	A
1	1A	1748	A
1	1A	1766	G
1	1A	1767	A
1	1A	1768	U
1	1A	1777	G
1	1A	1787	G
1	1A	1794	G
1	1A	1795	G
1	1A	1804	A
1	1A	1811	A
1	1A	1813	C
1	1A	1822	A
1	1A	1831	C
1	1A	1832	G
1	1A	1843	A
1	1A	1847	G
1	1A	1860	A
1	1A	1870	G
1	1A	1878	A

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Mol	Chain	Res	Type
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	1951	G
1	1A	1952	G
1	1A	1959	A
1	1A	1960	A
1	1A	1974	A
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	2015	U
1	1A	2019	G
1	1A	2042	A
1	1A	2045	G
1	1A	2053	A
1	1A	2054	G
1	1A	2055	A
1	1A	2065	C
1	1A	2077	C
1	1A	2078	G
1	1A	2082	A
1	1A	2083	G
1	1A	2085	C
1	1A	2091	G
1	1A	2121	U
1	1A	2125	C
1	1A	2129	C
1	1A	2130	C
1	1A	2138	G
1	1A	2139	A
1	1A	2141	A
1	1A	2145	G
1	1A	2148	A
1	1A	2149	G

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Mol	Chain	Res	Type
1	1A	2153	G
1	1A	2154	U
1	1A	2155	G
1	1A	2156	A
1	1A	2157	A
1	1A	2158	C
1	1A	2161	C
1	1A	2164	C
1	1A	2167	C
1	1A	2168	C
1	1A	2170	G
1	1A	2180	A
1	1A	2181	G
1	1A	2188	G
1	1A	2195	A
1	1A	2198	A
1	1A	2207	C
1	1A	2209	G
1	1A	2213	G
1	1A	2214	G
1	1A	2215	G
1	1A	2220	A
1	1A	2227	G
1	1A	2228	G
1	1A	2229	A
1	1A	2237	A
1	1A	2244	U
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	2317	A
1	1A	2320	G
1	1A	2332	A
1	1A	2337	G
1	1A	2338	C
1	1A	2346	G
1	1A	2359	C

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Mol	Chain	Res	Type
1	1A	2362	C
1	1A	2395	G
1	1A	2397	C
1	1A	2417	G
1	1A	2418	U
1	1A	2421	G
1	1A	2426	G
1	1A	2434	A
1	1A	2435	U
1	1A	2437	A
1	1A	2440	G
1	1A	2441	G
1	1A	2442	A
1	1A	2443	U
1	1A	2444	A
1	1A	2447	A
1	1A	2451	A
1	1A	2453	C
1	1A	2460	A
1	1A	2480	G
1	1A	2481	A
1	1A	2488	A
1	1A	2510	C
1	1A	2514	G
1	1A	2517	G
1	1A	2530	A
1	1A	2541	G
1	1A	2547	G
1	1A	2566	U
1	1A	2567	U
1	1A	2578	A
1	1A	2579	G
1	1A	2585	C
1	1A	2597	U
1	1A	2614	A
1	1A	2615	G
1	1A	2621	U
1	1A	2623	U
1	1A	2624	C
1	1A	2641	A
1	1A	2642	G
1	1A	2666	A

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Mol	Chain	Res	Type
1	1A	2674	A
1	1A	2701	U
1	1A	2702	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	2782	C
1	1A	2791	A
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	2846	U
1	1A	2882	G
1	1A	2883	A
1	1A	2890	C
1	1A	2901	A
1	1A	2903	G
2	1B	7	G
2	1B	15	A
2	1B	32	C
2	1B	45	A
2	1B	53	A
2	1B	56	G
2	1B	73	A
2	1B	84	C
2	1B	106	G
2	1B	110	G
2	1B	116	G
32	1a	5	U
32	1a	9	G

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Mol	Chain	Res	Type
32	1a	32	A
32	1a	39	G
32	1a	48	C
32	1a	51	A
32	1a	61	G
32	1a	79	G
32	1a	101	A
32	1a	115	G
32	1a	116	A
32	1a	121	C
32	1a	131	C
32	1a	156	G
32	1a	159	G
32	1a	163	C
32	1a	169	C
32	1a	173	U
32	1a	174	C
32	1a	182	U
32	1a	189(F)	U
32	1a	195	A
32	1a	197	A
32	1a	199	G
32	1a	202	U
32	1a	203	U
32	1a	204	U
32	1a	216	G
32	1a	220	G
32	1a	231	G
32	1a	247	G
32	1a	251	G
32	1a	254	G
32	1a	258	G
32	1a	266	G
32	1a	267	C
32	1a	289	G
32	1a	301	G
32	1a	306	G
32	1a	321	A
32	1a	328	C
32	1a	332	G
32	1a	348	G
32	1a	352	C

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Mol	Chain	Res	Type
32	1a	353	A
32	1a	354	G
32	1a	356	A
32	1a	367	U
32	1a	372	C
32	1a	373	A
32	1a	384	G
32	1a	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	443	C
32	1a	444	C
32	1a	452	A
32	1a	456	C
32	1a	461	A
32	1a	470	C
32	1a	475	G
32	1a	477	A
32	1a	485	G
32	1a	496	A
32	1a	498	U
32	1a	505	G
32	1a	506	G
32	1a	509	A
32	1a	510	A
32	1a	511	C
32	1a	518	C
32	1a	521	G
32	1a	532	A
32	1a	547	A
32	1a	550	G
32	1a	559	A
32	1a	561	U
32	1a	572	A
32	1a	573	A

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Mol	Chain	Res	Type
32	1a	576	G
32	1a	577	G
32	1a	607	A
32	1a	617	G
32	1a	619	U
32	1a	630	G
32	1a	631	G
32	1a	632	A
32	1a	633	G
32	1a	642	A
32	1a	650	G
32	1a	653	A
32	1a	661	G
32	1a	665	A
32	1a	671	G
32	1a	687	A
32	1a	688	G
32	1a	693	G
32	1a	723	U
32	1a	728	A
32	1a	731	G
32	1a	750	G
32	1a	755	G
32	1a	777	A
32	1a	793	U
32	1a	794	A
32	1a	817	C
32	1a	821	G
32	1a	828	A
32	1a	829	G
32	1a	836	G
32	1a	839	U
32	1a	840	C
32	1a	841	U
32	1a	848	C
32	1a	858	G
32	1a	902	G
32	1a	914	A
32	1a	926	G
32	1a	927	G
32	1a	934	C
32	1a	935	A

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Mol	Chain	Res	Type
32	1a	960	U
32	1a	961	U
32	1a	968	A
32	1a	969	A
32	1a	971	G
32	1a	975	A
32	1a	976	G
32	1a	977	A
32	1a	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	1003	G
32	1a	1004	A
32	1a	1009	G
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(A)	G
32	1a	1032	G
32	1a	1037	C
32	1a	1044	A
32	1a	1053	G
32	1a	1065	U
32	1a	1066	C
32	1a	1068	G
32	1a	1070	U
32	1a	1081	G
32	1a	1094	G
32	1a	1095	U
32	1a	1100	C
32	1a	1101	A
32	1a	1124	G
32	1a	1126	U
32	1a	1130	A

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Mol	Chain	Res	Type
32	1a	1134	G
32	1a	1136	U
32	1a	1137	C
32	1a	1139	G
32	1a	1140	C
32	1a	1146	A
32	1a	1152	A
32	1a	1159	U
32	1a	1183	A
32	1a	1184	G
32	1a	1196	U
32	1a	1197	G
32	1a	1202	G
32	1a	1208	C
32	1a	1213	A
32	1a	1214	C
32	1a	1224	G
32	1a	1227	A
32	1a	1238	A
32	1a	1240	U
32	1a	1256	A
32	1a	1257	U
32	1a	1258	G
32	1a	1263	C
32	1a	1269	A
32	1a	1270	C
32	1a	1278	U
32	1a	1280	A
32	1a	1286	A
32	1a	1287	A
32	1a	1299	A
32	1a	1300	G
32	1a	1302	U
32	1a	1320	C
32	1a	1322	C
32	1a	1338	G
32	1a	1340	A
32	1a	1346	A
32	1a	1347	G
32	1a	1353	G
32	1a	1360	A
32	1a	1363	C

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Mol	Chain	Res	Type
32	1a	1370	G
32	1a	1397	C
32	1a	1406	U
32	1a	1419	G
32	1a	1422	G
32	1a	1442	G
32	1a	1442(A)	G
32	1a	1447	A
32	1a	1452	C
32	1a	1456	G
32	1a	1492	A
32	1a	1493	A
32	1a	1503	A
32	1a	1504	G
32	1a	1505	G
32	1a	1506	U
32	1a	1507	A
32	1a	1517	G
32	1a	1520	G
32	1a	1529	G
32	1a	1530	G
32	1a	1531	A
1	2A	9	U
1	2A	10	G
1	2A	12	U
1	2A	34	C
1	2A	36	G
1	2A	45	C
1	2A	61	G
1	2A	63	U
1	2A	71	A
1	2A	74	A
1	2A	75	G
1	2A	84	A
1	2A	90	U
1	2A	94	C
1	2A	118	A
1	2A	119	A
1	2A	120	U
1	2A	131	G
1	2A	141	A
1	2A	157	U

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Mol	Chain	Res	Type
1	2A	181	A
1	2A	182	A
1	2A	196	A
1	2A	199	A
1	2A	205	G
1	2A	215	G
1	2A	216	A
1	2A	221	A
1	2A	222	A
1	2A	225	A
1	2A	228	A
1	2A	229	A
1	2A	230	U
1	2A	233	A
1	2A	248	G
1	2A	265	A
1	2A	271(K)	U
1	2A	271(L)	U
1	2A	271(M)	G
1	2A	271(N)	U
1	2A	271(O)	C
1	2A	272(A)	U
1	2A	272(B)	G
1	2A	272(J)	C
1	2A	277	C
1	2A	278	A
1	2A	303	U
1	2A	311	A
1	2A	312	G
1	2A	317	G
1	2A	324	A
1	2A	327	G
1	2A	329	G
1	2A	330	A
1	2A	333	G
1	2A	352	G
1	2A	363	G
1	2A	370	G
1	2A	386	G
1	2A	396	G
1	2A	405	U
1	2A	411	G

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Mol	Chain	Res	Type
1	2A	412	A
1	2A	444	C
1	2A	455	C
1	2A	456	C
1	2A	457	A
1	2A	470	A
1	2A	481	G
1	2A	504	U
1	2A	505	A
1	2A	509	C
1	2A	530	G
1	2A	531	C
1	2A	532	A
1	2A	533	G
1	2A	545	G
1	2A	563	G
1	2A	573	G
1	2A	574	C
1	2A	575	A
1	2A	586	A
1	2A	595	C
1	2A	603	A
1	2A	604	G
1	2A	607	U
1	2A	609	A
1	2A	614(B)	G
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(U)	G
1	2A	669	G
1	2A	677	A
1	2A	686	G
1	2A	717	G
1	2A	726	G
1	2A	730	C
1	2A	740	U

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Mol	Chain	Res	Type
1	2A	751	A
1	2A	752	A
1	2A	753	C
1	2A	775	G
1	2A	776	G
1	2A	782	A
1	2A	784	A
1	2A	785	G
1	2A	792	G
1	2A	805	G
1	2A	812	C
1	2A	815	C
1	2A	827	U
1	2A	828	U
1	2A	847	U
1	2A	853	G
1	2A	857	C
1	2A	859	G
1	2A	877	U
1	2A	880	G
1	2A	886	C
1	2A	887	A
1	2A	888	C
1	2A	889	C
1	2A	890	A
1	2A	893	C
1	2A	896	A
1	2A	897	C
1	2A	901	A
1	2A	908	C
1	2A	910	A
1	2A	911	A
1	2A	917	A
1	2A	932	G
1	2A	938	G
1	2A	941	A
1	2A	945	A
1	2A	946	G
1	2A	959	A
1	2A	961	C
1	2A	974	G
1	2A	975	C

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Mol	Chain	Res	Type
1	2A	983	A
1	2A	996	A
1	2A	1005	C
1	2A	1012	U
1	2A	1013	C
1	2A	1033	U
1	2A	1038	C
1	2A	1041	C
1	2A	1044	G
1	2A	1045	A
1	2A	1046	A
1	2A	1047	G
1	2A	1052	C
1	2A	1054	A
1	2A	1055	G
1	2A	1058	G
1	2A	1060	U
1	2A	1064	C
1	2A	1065	U
1	2A	1066	U
1	2A	1067	A
1	2A	1068	G
1	2A	1069	A
1	2A	1070	A
1	2A	1071	G
1	2A	1073	A
1	2A	1074	G
1	2A	1076	C
1	2A	1077	A
1	2A	1078	U
1	2A	1079	C
1	2A	1080	C
1	2A	1082	U
1	2A	1083	U
1	2A	1084	A
1	2A	1085	A
1	2A	1086	A
1	2A	1088	A
1	2A	1090	U
1	2A	1091	G
1	2A	1092	C
1	2A	1093	G

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Mol	Chain	Res	Type
1	2A	1094	U
1	2A	1095	A
1	2A	1096	A
1	2A	1105	U
1	2A	1109	C
1	2A	1110	G
1	2A	1111	A
1	2A	1112	G
1	2A	1116	C
1	2A	1117	G
1	2A	1129	A
1	2A	1130	U
1	2A	1135	C
1	2A	1136	G
1	2A	1141	U
1	2A	1142(A)	A
1	2A	1169	G
1	2A	1171	G
1	2A	1195	G
1	2A	1211	U
1	2A	1212	G
1	2A	1219	G
1	2A	1220	A
1	2A	1241	A
1	2A	1253	A
1	2A	1256	G
1	2A	1271	G
1	2A	1272	A
1	2A	1273	U
1	2A	1287	A
1	2A	1300	U
1	2A	1301	A
1	2A	1303	G
1	2A	1308	A
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	1384	A

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Mol	Chain	Res	Type
1	2A	1385	G
1	2A	1386	C
1	2A	1392	A
1	2A	1416	G
1	2A	1417	C
1	2A	1420	U
1	2A	1421	G
1	2A	1427	A
1	2A	1428	C
1	2A	1445	A
1	2A	1450	G
1	2A	1455	G
1	2A	1459	G
1	2A	1467	C
1	2A	1471	A
1	2A	1482	G
1	2A	1490	A
1	2A	1493	C
1	2A	1497	U
1	2A	1508	A
1	2A	1509	C
1	2A	1509(A)	A
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	1583	A
1	2A	1584	C
1	2A	1586	A
1	2A	1595	G
1	2A	1608	A
1	2A	1610	A
1	2A	1629	U
1	2A	1640	C
1	2A	1648	C
1	2A	1654	A
1	2A	1674	G

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Mol	Chain	Res	Type
1	2A	1675	C
1	2A	1696	G
1	2A	1700	A
1	2A	1701	A
1	2A	1703	G
1	2A	1721	G
1	2A	1722	A
1	2A	1746	G
1	2A	1750	G
1	2A	1756	G
1	2A	1762	A
1	2A	1763	G
1	2A	1764	G
1	2A	1773	A
1	2A	1780	A
1	2A	1782	C
1	2A	1791	A
1	2A	1800	C
1	2A	1801	G
1	2A	1816	G
1	2A	1828	G
1	2A	1829	A
1	2A	1835	G
1	2A	1839	G
1	2A	1847	A
1	2A	1848	A
1	2A	1858	G
1	2A	1877	A
1	2A	1878	G
1	2A	1882	C
1	2A	1900	A
1	2A	1906	G
1	2A	1913	A
1	2A	1914	C
1	2A	1921	G
1	2A	1929	G
1	2A	1930	G
1	2A	1937	A
1	2A	1938	A
1	2A	1955	U
1	2A	1963	U
1	2A	1967	C

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Mol	Chain	Res	Type
1	2A	1970	A
1	2A	1971	A
1	2A	1972	A
1	2A	1993	U
1	2A	1997	G
1	2A	2020	A
1	2A	2023	G
1	2A	2031	A
1	2A	2033	A
1	2A	2043	C
1	2A	2055	C
1	2A	2056	G
1	2A	2060	A
1	2A	2061	G
1	2A	2062	A
1	2A	2069	G
1	2A	2095	C
1	2A	2096	U
1	2A	2099	U
1	2A	2100	G
1	2A	2103	C
1	2A	2104	G
1	2A	2105	C
1	2A	2106	G
1	2A	2107	C
1	2A	2108	C
1	2A	2109	U
1	2A	2110	G
1	2A	2111	C
1	2A	2112	G
1	2A	2115	G
1	2A	2116	G
1	2A	2117	A
1	2A	2118	U
1	2A	2119	A
1	2A	2120	G
1	2A	2123	G
1	2A	2126	A
1	2A	2127	G
1	2A	2129	C
1	2A	2131	G
1	2A	2132	U

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Mol	Chain	Res	Type
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	2145	C
1	2A	2146	C
1	2A	2147	G
1	2A	2148	G
1	2A	2149	G
1	2A	2150	U
1	2A	2151	G
1	2A	2158	A
1	2A	2159	G
1	2A	2161	C
1	2A	2162	G
1	2A	2163	C
1	2A	2164	C
1	2A	2165	G
1	2A	2166	G
1	2A	2172	U
1	2A	2173	A
1	2A	2176	A
1	2A	2178	C
1	2A	2181	G
1	2A	2184	G
1	2A	2186	G
1	2A	2187	G
1	2A	2189	U
1	2A	2192	G
1	2A	2198	A
1	2A	2206	G
1	2A	2207	G
1	2A	2208	A
1	2A	2218	U
1	2A	2219	G
1	2A	2225	A
1	2A	2239	G
1	2A	2243	U
1	2A	2268	A
1	2A	2269	A

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Mol	Chain	Res	Type
1	2A	2275	C
1	2A	2280	G
1	2A	2283	C
1	2A	2287	A
1	2A	2289	G
1	2A	2292	C
1	2A	2302	G
1	2A	2305	A
1	2A	2308	G
1	2A	2311	A
1	2A	2312	U
1	2A	2318	G
1	2A	2319	G
1	2A	2320	A
1	2A	2321	G
1	2A	2322	A
1	2A	2325	G
1	2A	2334	G
1	2A	2335	A
1	2A	2336	A
1	2A	2343	C
1	2A	2347	C
1	2A	2350	C
1	2A	2354	G
1	2A	2358	G
1	2A	2366	A
1	2A	2379	G
1	2A	2383	G
1	2A	2385	C
1	2A	2402	C
1	2A	2406	U
1	2A	2407	G
1	2A	2410	G
1	2A	2414	G
1	2A	2419	U
1	2A	2422	A
1	2A	2423	U
1	2A	2425	A
1	2A	2429	G
1	2A	2430	A
1	2A	2435	A
1	2A	2439	A

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Mol	Chain	Res	Type
1	2A	2441	C
1	2A	2448	A
1	2A	2459	A
1	2A	2470	G
1	2A	2474	C
1	2A	2476	A
1	2A	2478	A
1	2A	2487	G
1	2A	2502	G
1	2A	2505	G
1	2A	2517	C
1	2A	2518	A
1	2A	2520	C
1	2A	2529	G
1	2A	2554	U
1	2A	2555	U
1	2A	2566	A
1	2A	2567	G
1	2A	2573	C
1	2A	2585	U
1	2A	2602	A
1	2A	2603	G
1	2A	2611	U
1	2A	2612	C
1	2A	2629	A
1	2A	2630	G
1	2A	2654	A
1	2A	2663	G
1	2A	2682	U
1	2A	2689	U
1	2A	2690	C
1	2A	2703	C
1	2A	2712(A)	A
1	2A	2713	A
1	2A	2714	G
1	2A	2721	A
1	2A	2726	U
1	2A	2733	A
1	2A	2757	A
1	2A	2758	A
1	2A	2765	A
1	2A	2778	A

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Mol	Chain	Res	Type
1	2A	2802	G
1	2A	2803	C
1	2A	2818	G
1	2A	2820	A
1	2A	2821	A
1	2A	2833	G
1	2A	2835	A
1	2A	2872	G
1	2A	2880	C
1	2A	2891	G
1	2A	2894	G
2	2B	2	C
2	2B	8	U
2	2B	13	A
2	2B	30	C
2	2B	31	C
2	2B	32	C
2	2B	42	C
2	2B	51	G
2	2B	56	G
2	2B	64	C
2	2B	67	G
2	2B	73	A
2	2B	79	C
2	2B	84	C
2	2B	108	U
2	2B	110	G
2	2B	118	G
2	2B	120	A
32	2a	5	U
32	2a	6	G
32	2a	7	G
32	2a	9	G
32	2a	22	G
32	2a	32	A
32	2a	39	G
32	2a	47	C
32	2a	48	C
32	2a	50	A
32	2a	51	A
32	2a	59	A
32	2a	61	G

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Mol	Chain	Res	Type
32	2a	65	U
32	2a	66	G
32	2a	79	G
32	2a	88	A
32	2a	89	C
32	2a	101	A
32	2a	116	A
32	2a	121	C
32	2a	131	C
32	2a	148	G
32	2a	156	G
32	2a	163	C
32	2a	173	U
32	2a	174	C
32	2a	182	U
32	2a	189(C)	C
32	2a	189(E)	U
32	2a	189(F)	U
32	2a	195	A
32	2a	197	A
32	2a	202	U
32	2a	203	U
32	2a	204	U
32	2a	216	G
32	2a	227	G
32	2a	247	G
32	2a	251	G
32	2a	258	G
32	2a	262	A
32	2a	266	G
32	2a	267	C
32	2a	269	C
32	2a	281	G
32	2a	289	G
32	2a	298	A
32	2a	306	G
32	2a	321	A
32	2a	328	C
32	2a	332	G
32	2a	345	C
32	2a	351	G
32	2a	352	C

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Mol	Chain	Res	Type
32	2a	353	A
32	2a	354	G
32	2a	360	A
32	2a	367	U
32	2a	372	C
32	2a	384	G
32	2a	397	A
32	2a	398	C
32	2a	406	G
32	2a	412	A
32	2a	413	G
32	2a	421	U
32	2a	424	G
32	2a	429	U
32	2a	430	A
32	2a	439	A
32	2a	441	A
32	2a	442	C
32	2a	446	G
32	2a	451	A
32	2a	452	A
32	2a	458	C
32	2a	461	A
32	2a	470	C
32	2a	471	G
32	2a	476	G
32	2a	477	A
32	2a	482	A
32	2a	484	G
32	2a	485	G
32	2a	496	A
32	2a	498	U
32	2a	505	G
32	2a	506	G
32	2a	509	A
32	2a	510	A
32	2a	511	C
32	2a	518	C
32	2a	532	A
32	2a	533	A
32	2a	547	A
32	2a	559	A

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Mol	Chain	Res	Type
32	2a	561	U
32	2a	562	C
32	2a	564	C
32	2a	572	A
32	2a	573	A
32	2a	576	G
32	2a	592	G
32	2a	596	C
32	2a	630	G
32	2a	631	G
32	2a	632	A
32	2a	641	U
32	2a	653	A
32	2a	665	A
32	2a	672	U
32	2a	685	G
32	2a	688	G
32	2a	695	A
32	2a	723	U
32	2a	724	G
32	2a	731	G
32	2a	734	G
32	2a	735	C
32	2a	748	C
32	2a	749	C
32	2a	753	A
32	2a	755	G
32	2a	777	A
32	2a	793	U
32	2a	794	A
32	2a	817	C
32	2a	821	G
32	2a	828	A
32	2a	829	G
32	2a	836	G
32	2a	840	C
32	2a	841	U
32	2a	851	G
32	2a	859	A
32	2a	870	U
32	2a	902	G
32	2a	914	A

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Mol	Chain	Res	Type
32	2a	916	G
32	2a	926	G
32	2a	927	G
32	2a	931	C
32	2a	934	C
32	2a	958	A
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	989	C
32	2a	992	U
32	2a	993	G
32	2a	994	A
32	2a	995	C
32	2a	996	A
32	2a	1004	A
32	2a	1005	A
32	2a	1006	C
32	2a	1009	G
32	2a	1017	G
32	2a	1020	U
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	1034	G
32	2a	1041	A
32	2a	1043	C
32	2a	1047	G
32	2a	1053	G
32	2a	1054	C
32	2a	1065	U

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Mol	Chain	Res	Type
32	2a	1066	C
32	2a	1068	G
32	2a	1081	G
32	2a	1094	G
32	2a	1095	U
32	2a	1097	C
32	2a	1101	A
32	2a	1117	G
32	2a	1122	U
32	2a	1125	U
32	2a	1129	C
32	2a	1136	U
32	2a	1137	C
32	2a	1138	G
32	2a	1139	G
32	2a	1140	C
32	2a	1146	A
32	2a	1147	C
32	2a	1152	A
32	2a	1157	A
32	2a	1159	U
32	2a	1168	A
32	2a	1176	A
32	2a	1183	A
32	2a	1184	G
32	2a	1196	U
32	2a	1197	G
32	2a	1211	U
32	2a	1212	U
32	2a	1224	G
32	2a	1227	A
32	2a	1228	C
32	2a	1238	A
32	2a	1256	A
32	2a	1257	U
32	2a	1258	G
32	2a	1269	A
32	2a	1270	C
32	2a	1278	U
32	2a	1279	A
32	2a	1281	U
32	2a	1282	C

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Mol	Chain	Res	Type
32	2a	1283	G
32	2a	1285	A
32	2a	1286	A
32	2a	1287	A
32	2a	1290	G
32	2a	1300	G
32	2a	1302	U
32	2a	1303	C
32	2a	1305	G
32	2a	1316	G
32	2a	1317	C
32	2a	1319	A
32	2a	1320	C
32	2a	1340	A
32	2a	1346	A
32	2a	1347	G
32	2a	1353	G
32	2a	1363	C
32	2a	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	1458	G
32	2a	1492	A
32	2a	1497	G
32	2a	1499	A
32	2a	1503	A
32	2a	1504	G
32	2a	1505	G
32	2a	1506	U
32	2a	1507	A
32	2a	1517	G
32	2a	1520	G
32	2a	1529	G
32	2a	1530	G
32	2a	1531	A

All (65) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1A	115	G
1	1A	302	A
1	1A	509	A
1	1A	732	A
1	1A	793	A
1	1A	811	A
1	1A	821	A
1	1A	874	U
1	1A	913	A
1	1A	935	C
1	1A	941	U
1	1A	1003	U
1	1A	1019	G
1	1A	1067	A
1	1A	1093	G
1	1A	1188	A
1	1A	1201	A
1	1A	1219	A
1	1A	1220	U
1	1A	1221	G
1	1A	1255	A
1	1A	1654	A
1	1A	1700	G
1	1A	2250	G
1	1A	2418	U
1	1A	2434	A
1	1A	2442	A
1	1A	2614	A
1	1A	2701	U
1	2A	9	U
1	2A	195	A
1	2A	249	C
1	2A	266	G
1	2A	271(M)	G
1	2A	277	C
1	2A	685	A
1	2A	752	A
1	2A	764	A
1	2A	827	U
1	2A	840	C
1	2A	856	C
1	2A	900	A
1	2A	1053	C

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Mol	Chain	Res	Type
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	1240	U
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	2288	A
1	2A	2317	C
1	2A	2321	G
1	2A	2406	U
1	2A	2601	C
1	2A	2602	A
1	2A	2689	U
1	2A	2756	U

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

48 non-standard protein/DNA/RNA residues are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
32	5MC	1a	1400	32	19,22,23	1.80	3 (15%)	26,32,35	1.18	3 (11%)
32	5MC	1a	1407	32	19,22,23	1.71	2 (10%)	26,32,35	1.21	3 (11%)
32	4OC	1a	1402	32	20,23,24	0.72	0	25,32,35	0.99	2 (8%)
32	5MC	2a	1407	32	19,22,23	1.63	3 (15%)	26,32,35	1.18	3 (11%)
1	5MU	1A	1937	1	19,22,23	1.44	5 (26%)	27,32,35	2.22	8 (29%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	2MU	1A	2564	54,1	19,22,24	1.34	4 (21%)	25,31,36	1.87	6 (24%)
32	7MG	1a	527	54,32	23,26,27	1.40	3 (13%)	27,39,42	2.43	6 (22%)
32	PSU	1a	516	54,32	18,21,22	1.40	2 (11%)	21,30,33	1.93	4 (19%)
32	PSU	2a	516	54,32	18,21,22	1.33	2 (11%)	21,30,33	2.07	5 (23%)
1	PSU	1A	2617	54,1	18,21,22	1.39	3 (16%)	21,30,33	1.94	5 (23%)
32	5MC	2a	1404	32	19,22,23	1.76	3 (15%)	26,32,35	1.24	4 (15%)
1	5MU	2A	1939	1	19,22,23	1.45	5 (26%)	27,32,35	2.30	6 (22%)
32	UR3	1a	1498	32	19,22,23	0.96	1 (5%)	26,32,35	1.85	4 (15%)
32	2MG	1a	1207	32	23,26,27	1.24	2 (8%)	33,38,41	2.46	10 (30%)
43	0TD	2l	92	43	8,9,10	4.44	1 (12%)	6,11,13	4.29	3 (50%)
1	4OC	1A	1942	1	19,22,24	0.80	0	25,31,35	0.90	1 (4%)
1	PSU	1A	1933	1	18,21,22	1.39	2 (11%)	21,30,33	2.18	5 (23%)
32	MA6	1a	1518	32	23,26,27	1.56	5 (21%)	33,38,41	2.21	12 (36%)
1	PSU	2A	2605	1	18,21,22	1.41	3 (16%)	21,30,33	1.96	5 (23%)
1	5MU	1A	1961	54,1	19,22,23	1.44	5 (26%)	27,32,35	2.21	6 (22%)
1	5MC	1A	1984	54,1	19,22,23	1.65	3 (15%)	26,32,35	1.22	4 (15%)
32	5MC	1a	1404	32	19,22,23	1.68	3 (15%)	26,32,35	1.14	3 (11%)
32	2MG	2a	1207	32	23,26,27	1.23	3 (13%)	33,38,41	2.07	8 (24%)
1	OMG	1A	2263	54,1	23,26,27	1.27	3 (13%)	32,38,41	2.07	6 (18%)
32	MA6	2a	1519	32	23,26,27	1.56	5 (21%)	33,38,41	2.40	13 (39%)
32	M2G	1a	966	32	24,27,28	1.28	3 (12%)	33,40,43	1.83	6 (18%)
43	0TD	1l	92	43	8,9,10	4.56	1 (12%)	6,11,13	3.20	3 (50%)
32	4OC	2a	1402	32	20,23,24	0.77	0	25,32,35	1.11	1 (4%)
1	5MC	2A	1942	1	19,22,23	1.70	3 (15%)	26,32,35	1.20	2 (7%)
32	MA6	1a	1519	32	23,26,27	1.56	5 (21%)	33,38,41	2.20	11 (33%)
1	5MU	2A	1915	1	19,22,23	1.43	4 (21%)	27,32,35	2.21	8 (29%)
1	4OC	2A	1920	1	19,22,24	0.80	0	25,31,35	0.95	1 (4%)
32	5MC	2a	967	32	19,22,23	2.03	3 (15%)	26,32,35	1.19	3 (11%)
1	2MA	1A	2515	54,1	22,25,26	1.45	5 (22%)	32,37,40	2.36	7 (21%)
32	UR3	2a	1498	54,32	19,22,23	0.95	1 (5%)	26,32,35	1.79	3 (11%)
1	5MC	1A	1964	54,1	19,22,23	1.47	3 (15%)	26,32,35	1.11	2 (7%)
1	5MC	2A	1962	54,1	19,22,23	1.53	3 (15%)	26,32,35	1.09	2 (7%)
1	OMG	2A	2251	54,1	23,26,27	1.17	3 (13%)	32,38,41	2.01	7 (21%)
32	MA6	2a	1518	32	23,26,27	1.64	4 (17%)	33,38,41	2.23	12 (36%)
32	M2G	2a	966	32	24,27,28	1.38	4 (16%)	33,40,43	1.83	5 (15%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	PSU	1A	1939	1	18,21,22	1.35	2 (11%)	21,30,33	1.87	4 (19%)
32	5MC	1a	967	32	19,22,23	1.59	3 (15%)	26,32,35	1.14	2 (7%)
32	7MG	2a	527	54,32	23,26,27	1.34	4 (17%)	27,39,42	2.58	5 (18%)
32	5MC	2a	1400	32	19,22,23	1.67	3 (15%)	26,32,35	1.21	2 (7%)
1	2MU	2A	2552	54,1	19,22,24	1.23	3 (15%)	25,31,36	2.02	6 (24%)
1	PSU	2A	1917	1	18,21,22	1.34	2 (11%)	21,30,33	2.09	3 (14%)
1	2MA	2A	2503	54,1	22,25,26	1.41	5 (22%)	32,37,40	2.35	9 (28%)
1	PSU	2A	1911	1	18,21,22	1.40	2 (11%)	21,30,33	2.06	3 (14%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
32	5MC	1a	1400	32	-	1/7/25/26	0/2/2/2
32	5MC	1a	1407	32	-	0/7/25/26	0/2/2/2
32	4OC	1a	1402	32	-	2/9/29/30	0/2/2/2
32	5MC	2a	1407	32	-	0/7/25/26	0/2/2/2
1	5MU	1A	1937	1	-	2/7/25/26	0/2/2/2
1	2MU	1A	2564	54,1	-	0/9/27/28	0/2/2/2
32	7MG	1a	527	54,32	-	1/7/37/38	0/3/3/3
32	PSU	1a	516	54,32	-	0/7/25/26	0/2/2/2
32	PSU	2a	516	54,32	-	0/7/25/26	0/2/2/2
1	PSU	1A	2617	54,1	-	0/7/25/26	0/2/2/2
32	5MC	2a	1404	32	-	0/7/25/26	0/2/2/2
1	5MU	2A	1939	1	-	0/7/25/26	0/2/2/2
32	UR3	1a	1498	32	-	0/7/25/26	0/2/2/2
32	2MG	1a	1207	32	-	2/9/27/28	0/3/3/3
43	0TD	2l	92	43	-	1/7/12/14	-
1	4OC	1A	1942	1	-	1/9/27/30	0/2/2/2
1	PSU	1A	1933	1	-	0/7/25/26	0/2/2/2
32	MA6	1a	1518	32	-	3/11/29/30	0/3/3/3
1	PSU	2A	2605	1	-	0/7/25/26	0/2/2/2
1	5MU	1A	1961	54,1	-	0/7/25/26	0/2/2/2
1	5MC	1A	1984	54,1	-	2/7/25/26	0/2/2/2
32	5MC	1a	1404	32	-	0/7/25/26	0/2/2/2
32	2MG	2a	1207	32	-	0/9/27/28	0/3/3/3
1	OMG	1A	2263	54,1	-	1/9/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
32	MA6	2a	1519	32	-	4/11/29/30	0/3/3/3
32	M2G	1a	966	32	-	0/11/29/30	0/3/3/3
43	0TD	1l	92	43	-	3/7/12/14	-
32	4OC	2a	1402	32	-	2/9/29/30	0/2/2/2
1	5MC	2A	1942	1	-	0/7/25/26	0/2/2/2
32	MA6	1a	1519	32	-	3/11/29/30	0/3/3/3
1	5MU	2A	1915	1	-	2/7/25/26	0/2/2/2
1	4OC	2A	1920	1	-	0/9/27/30	0/2/2/2
32	5MC	2a	967	32	-	0/7/25/26	0/2/2/2
1	2MA	1A	2515	54,1	-	2/7/25/26	0/3/3/3
32	UR3	2a	1498	54,32	-	0/7/25/26	0/2/2/2
1	5MC	1A	1964	54,1	-	0/7/25/26	0/2/2/2
1	5MC	2A	1962	54,1	-	0/7/25/26	0/2/2/2
1	OMG	2A	2251	54,1	-	0/9/27/28	0/3/3/3
32	MA6	2a	1518	32	-	2/11/29/30	0/3/3/3
32	M2G	2a	966	32	-	0/11/29/30	0/3/3/3
1	PSU	1A	1939	1	-	0/7/25/26	0/2/2/2
32	5MC	1a	967	32	-	0/7/25/26	0/2/2/2
32	7MG	2a	527	54,32	-	0/7/37/38	0/3/3/3
32	5MC	2a	1400	32	-	0/7/25/26	0/2/2/2
1	2MU	2A	2552	54,1	-	0/9/27/28	0/2/2/2
1	PSU	2A	1917	1	-	0/7/25/26	0/2/2/2
1	2MA	2A	2503	54,1	-	1/7/25/26	0/3/3/3
1	PSU	2A	1911	1	-	0/7/25/26	0/2/2/2

All (137) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
43	1l	92	0TD	CB-SB	-12.47	1.69	1.82
43	2l	92	0TD	CB-SB	-12.21	1.70	1.82
32	2a	967	5MC	C5-C4	7.77	1.50	1.44
32	1a	1400	5MC	C5-C4	6.69	1.49	1.44
32	2a	1404	5MC	C5-C4	6.56	1.49	1.44
32	1a	1407	5MC	C5-C4	6.29	1.48	1.44
32	1a	1404	5MC	C5-C4	6.22	1.48	1.44
1	2A	1942	5MC	C5-C4	6.22	1.48	1.44
32	2a	1400	5MC	C5-C4	6.11	1.48	1.44
32	2a	1407	5MC	C5-C4	5.83	1.48	1.44
1	1A	1984	5MC	C5-C4	5.83	1.48	1.44
32	1a	967	5MC	C5-C4	5.50	1.48	1.44
1	2A	1962	5MC	C5-C4	5.38	1.48	1.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
32	2a	1518	MA6	C5-C4	5.31	1.48	1.39
1	1A	1964	5MC	C5-C4	4.97	1.47	1.44
32	1a	1519	MA6	C5-C4	4.80	1.47	1.39
32	1a	1518	MA6	C5-C4	4.71	1.47	1.39
32	2a	1519	MA6	C5-C4	4.65	1.47	1.39
1	2A	2503	2MA	C5-C4	3.95	1.46	1.39
1	1A	2515	2MA	C5-C4	3.93	1.46	1.39
32	1a	527	7MG	C4-N9	-3.84	1.33	1.37
1	2A	1911	PSU	C6-C5	3.61	1.39	1.35
1	1A	1933	PSU	C6-C5	3.60	1.39	1.35
32	1a	516	PSU	C6-C5	3.54	1.39	1.35
1	1A	1939	PSU	C6-C5	3.52	1.39	1.35
32	2a	966	M2G	C5-C4	3.49	1.48	1.38
1	2A	1917	PSU	C6-C5	3.37	1.39	1.35
32	2a	1519	MA6	C5-C6	3.30	1.49	1.41
32	1a	527	7MG	C5-C4	3.29	1.47	1.37
32	2a	1207	2MG	C5-C4	3.27	1.47	1.38
32	2a	1518	MA6	C5-C6	3.19	1.49	1.41
32	2a	527	7MG	C5-C4	3.17	1.47	1.37
1	1A	2617	PSU	C6-C5	3.11	1.38	1.35
32	2a	966	M2G	C2-N2	3.11	1.40	1.35
1	2A	2605	PSU	C6-C5	3.08	1.38	1.35
32	2a	516	PSU	C6-C5	3.05	1.38	1.35
1	1A	2263	OMG	C5-C4	3.05	1.47	1.38
1	1A	1961	5MU	C4-N3	-3.03	1.33	1.38
1	2A	1915	5MU	C2-N1	3.03	1.43	1.38
1	1A	1937	5MU	C2-N1	3.03	1.43	1.38
1	1A	2617	PSU	C4-N3	-3.02	1.33	1.38
32	1a	966	M2G	C5-C4	3.01	1.47	1.38
1	2A	2251	OMG	C5-C4	2.98	1.46	1.38
32	1a	1207	2MG	C5-C4	2.98	1.46	1.38
1	1A	2263	OMG	C6-N1	-2.95	1.33	1.38
1	1A	2564	2MU	C4-N3	-2.93	1.33	1.38
1	2A	1939	5MU	C4-C5	2.91	1.49	1.44
32	2a	527	7MG	C4-N9	-2.91	1.34	1.37
32	1a	1518	MA6	C5-C6	2.88	1.48	1.41
1	2A	1915	5MU	C6-C5	2.88	1.39	1.34
1	2A	1939	5MU	C6-C5	2.87	1.39	1.34
32	2a	967	5MC	C6-C5	2.82	1.39	1.34
32	1a	1407	5MC	C6-C5	2.81	1.39	1.34
32	1a	966	M2G	C2-N2	2.80	1.40	1.35
1	2A	1962	5MC	C6-C5	2.79	1.39	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	2A	2605	PSU	C4-N3	-2.78	1.33	1.38
32	2a	1407	5MC	C6-C5	2.75	1.39	1.34
1	1A	1937	5MU	C6-C5	2.75	1.39	1.34
1	1A	2515	2MA	C5-N7	-2.72	1.34	1.39
32	1a	1519	MA6	C5-C6	2.72	1.48	1.41
1	1A	1961	5MU	C6-C5	2.69	1.39	1.34
1	1A	1984	5MC	C6-C5	2.68	1.39	1.34
32	2a	1404	5MC	C6-C5	2.65	1.38	1.34
32	1a	967	5MC	C6-C5	2.64	1.38	1.34
32	1a	1404	5MC	C6-C5	2.63	1.38	1.34
1	1A	1984	5MC	C6-N1	-2.63	1.33	1.38
1	1A	1964	5MC	C6-C5	2.62	1.38	1.34
32	2a	1400	5MC	C6-C5	2.62	1.38	1.34
32	1a	1519	MA6	C5-N7	-2.61	1.34	1.39
1	2A	2552	2MU	C4-N3	-2.61	1.34	1.38
32	1a	1400	5MC	C6-N1	-2.61	1.33	1.38
32	2a	966	M2G	C6-N1	-2.60	1.34	1.38
32	2a	527	7MG	C6-N1	-2.58	1.34	1.38
1	2A	1911	PSU	C4-N3	-2.57	1.34	1.38
32	1a	1400	5MC	C6-C5	2.54	1.38	1.34
1	2A	1942	5MC	C6-C5	2.53	1.38	1.34
1	2A	1939	5MU	C4-N3	-2.53	1.34	1.38
32	1a	966	M2G	C6-N1	-2.52	1.34	1.38
32	1a	516	PSU	C4-N3	-2.51	1.34	1.38
1	1A	1939	PSU	C4-N3	-2.50	1.34	1.38
32	1a	1207	2MG	C6-N1	-2.50	1.34	1.38
1	2A	1917	PSU	C4-N3	-2.49	1.34	1.38
1	2A	1915	5MU	C4-N3	-2.49	1.34	1.38
1	1A	1964	5MC	C6-N1	-2.49	1.33	1.38
1	1A	1937	5MU	C4-N3	-2.47	1.34	1.38
1	1A	2564	2MU	C5-C4	2.47	1.49	1.43
32	1a	1518	MA6	C5-N7	-2.46	1.34	1.39
1	2A	2503	2MA	C5-N7	-2.45	1.34	1.39
32	2a	1518	MA6	C8-N7	2.45	1.36	1.31
1	2A	2605	PSU	C2-N3	-2.45	1.33	1.37
1	1A	1933	PSU	C4-N3	-2.44	1.34	1.38
32	2a	1519	MA6	C8-N7	2.43	1.36	1.31
1	2A	2503	2MA	C5-C6	2.41	1.47	1.41
32	1a	1518	MA6	C4-N9	-2.41	1.32	1.37
1	2A	1942	5MC	C6-N1	-2.41	1.33	1.38
1	1A	2515	2MA	C4-N9	-2.41	1.32	1.37
1	1A	1961	5MU	C2-N3	-2.40	1.33	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
32	2a	516	PSU	C4-N3	-2.40	1.34	1.38
32	1a	527	7MG	C6-N1	-2.39	1.34	1.38
1	2A	2251	OMG	C6-N1	-2.39	1.34	1.38
1	1A	1961	5MU	C4-C5	2.36	1.48	1.44
1	1A	2515	2MA	C8-N7	2.34	1.36	1.31
32	1a	1518	MA6	C8-N7	2.34	1.36	1.31
1	2A	1915	5MU	C4-C5	2.33	1.48	1.44
32	2a	1400	5MC	C6-N1	-2.32	1.34	1.38
1	2A	1962	5MC	C6-N1	-2.30	1.34	1.38
1	2A	2503	2MA	C4-N9	-2.30	1.32	1.37
1	1A	1937	5MU	C4-C5	2.29	1.48	1.44
32	2a	1404	5MC	C6-N1	-2.25	1.34	1.38
1	2A	1939	5MU	C6-N1	-2.25	1.34	1.38
1	1A	2617	PSU	C2-N3	-2.24	1.33	1.37
32	1a	967	5MC	C6-N1	-2.23	1.34	1.38
32	1a	1519	MA6	C8-N7	2.22	1.35	1.31
32	2a	966	M2G	C5-N7	-2.22	1.34	1.39
1	1A	2515	2MA	C5-C6	2.21	1.47	1.41
32	2a	967	5MC	C6-N1	-2.19	1.34	1.38
1	2A	1939	5MU	C2-N1	2.19	1.41	1.38
1	2A	2552	2MU	C2-N3	-2.18	1.34	1.38
1	2A	2251	OMG	C5-N7	-2.18	1.34	1.39
1	1A	2564	2MU	C2-N3	-2.17	1.34	1.38
1	2A	2552	2MU	C5-C4	2.15	1.48	1.43
1	1A	1961	5MU	C6-N1	-2.14	1.34	1.38
32	2a	1518	MA6	C5-N7	-2.13	1.35	1.39
32	2a	1498	UR3	C6-C5	2.13	1.40	1.35
32	2a	1207	2MG	C5-N7	-2.12	1.34	1.39
32	1a	1404	5MC	C6-N1	-2.11	1.34	1.38
32	2a	1407	5MC	C6-N1	-2.11	1.34	1.38
1	1A	2564	2MU	C6-C5	2.10	1.40	1.35
32	1a	1519	MA6	C4-N9	-2.10	1.33	1.37
32	2a	1519	MA6	C4-N9	-2.10	1.33	1.37
1	1A	2263	OMG	C5-N7	-2.09	1.34	1.39
1	2A	2503	2MA	C8-N7	2.08	1.35	1.31
32	2a	1519	MA6	C5-N7	-2.07	1.35	1.39
32	2a	527	7MG	C8-N9	2.05	1.47	1.45
32	2a	1207	2MG	C6-N1	-2.05	1.35	1.38
1	1A	1937	5MU	C2-N3	-2.02	1.34	1.38
32	1a	1498	UR3	C6-C5	2.01	1.39	1.35

All (242) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
43	2l	92	0TD	CSB-SB-CB	-9.81	84.73	102.36
1	1A	2515	2MA	C5-C4-N3	-8.66	118.06	127.18
32	2a	527	7MG	N9-C4-N3	8.50	137.92	125.46
32	1a	527	7MG	N9-C4-N3	8.21	137.50	125.46
1	2A	2503	2MA	C5-C4-N3	-7.68	119.09	127.18
32	1a	1498	UR3	C4-N3-C2	-7.51	118.53	124.58
32	2a	1498	UR3	C4-N3-C2	-7.33	118.68	124.58
32	1a	1207	2MG	C2-N3-C4	7.28	121.10	112.00
1	1A	1933	PSU	N1-C2-N3	6.81	122.35	115.17
1	2A	1911	PSU	N1-C2-N3	6.48	122.00	115.17
1	1A	2515	2MA	N3-C4-N9	6.43	135.15	126.99
1	1A	2263	OMG	C5-C4-N3	-6.41	118.19	128.39
32	2a	966	M2G	C5-C4-N3	-6.39	118.22	128.39
32	2a	1207	2MG	C2-N3-C4	6.38	119.98	112.00
1	2A	1917	PSU	N1-C2-N3	6.31	121.82	115.17
32	2a	516	PSU	N1-C2-N3	6.27	121.79	115.17
1	2A	2503	2MA	N3-C4-N9	6.25	134.93	126.99
1	1A	2617	PSU	N1-C2-N3	6.17	121.67	115.17
43	1l	92	0TD	CSB-SB-CB	-6.17	91.28	102.36
1	2A	2251	OMG	C5-C4-N3	-6.00	118.85	128.39
1	2A	2605	PSU	N1-C2-N3	5.98	121.47	115.17
32	1a	516	PSU	N1-C2-N3	5.92	121.41	115.17
1	2A	1939	5MU	C4-N3-C2	-5.80	119.73	127.34
1	2A	1939	5MU	N3-C2-N1	5.79	122.43	114.89
32	2a	527	7MG	N9-C8-N7	-5.75	95.23	103.37
32	1a	1519	MA6	C5-C4-N3	-5.69	118.89	126.72
32	1a	1207	2MG	C5-C4-N3	-5.67	119.36	128.39
32	2a	1519	MA6	C5-C4-N3	-5.59	119.02	126.72
32	1a	966	M2G	C5-C4-N3	-5.59	119.50	128.39
1	1A	1939	PSU	N1-C2-N3	5.53	121.00	115.17
1	2A	2552	2MU	N3-C2-N1	5.47	122.00	114.89
32	2a	1207	2MG	C5-C4-N3	-5.45	119.71	128.39
1	1A	2564	2MU	N3-C2-N1	5.36	121.87	114.89
1	1A	1961	5MU	C4-N3-C2	-5.33	120.35	127.34
32	2a	1518	MA6	C5-C4-N3	-5.30	119.42	126.72
32	2a	527	7MG	C5-C4-N3	-5.30	118.18	128.13
1	1A	2263	OMG	C2-N3-C4	5.19	121.24	112.30
1	2A	2251	OMG	C2-N3-C4	5.16	121.18	112.30
32	1a	527	7MG	N9-C8-N7	-5.10	96.15	103.37
1	1A	1961	5MU	C5-C4-N3	5.04	119.70	115.32
32	1a	527	7MG	C5-C4-N3	-4.98	118.79	128.13
32	1a	1518	MA6	C5-C4-N3	-4.94	119.92	126.72
1	1A	1961	5MU	N3-C2-N1	4.89	121.26	114.89

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	2A	2552	2MU	C4-N3-C2	-4.87	120.57	126.61
1	2A	1915	5MU	N3-C2-N1	4.85	121.20	114.89
1	1A	1937	5MU	N3-C2-N1	4.82	121.17	114.89
32	1a	1518	MA6	C9-N6-C6	-4.82	108.27	120.52
32	2a	966	M2G	N9-C4-N3	4.79	135.53	125.95
32	2a	1519	MA6	C4-C5-N7	-4.71	105.19	110.58
32	2a	1519	MA6	C10-N6-C6	-4.68	108.61	120.52
1	2A	2251	OMG	N9-C4-N3	4.66	135.27	125.95
32	2a	1518	MA6	C2-N1-C6	4.60	123.07	111.83
1	2A	1915	5MU	C4-N3-C2	-4.60	121.31	127.34
1	1A	1937	5MU	C4-N3-C2	-4.58	121.34	127.34
1	2A	1917	PSU	O2-C2-N1	-4.57	118.07	122.79
1	1A	2263	OMG	N9-C4-N3	4.54	135.02	125.95
1	2A	1939	5MU	C5-C6-N1	-4.48	118.45	123.31
1	1A	1961	5MU	C5-C6-N1	-4.45	118.47	123.31
32	2a	527	7MG	C2-N3-C4	4.44	119.94	112.30
32	2a	966	M2G	C2-N3-C4	4.43	120.71	112.51
32	1a	1518	MA6	C2-N1-C6	4.41	122.61	111.83
1	1A	1933	PSU	O2-C2-N1	-4.36	118.30	122.79
1	1A	1937	5MU	C5-C4-N3	4.33	119.09	115.32
32	2a	1518	MA6	C9-N6-C6	-4.33	109.50	120.52
32	1a	1207	2MG	C6-C5-N7	4.31	138.14	130.29
32	1a	966	M2G	C2-N3-C4	4.27	120.41	112.51
1	1A	1933	PSU	C4-N3-C2	-4.26	120.50	126.37
32	1a	1519	MA6	N3-C4-N9	4.24	134.37	127.17
32	1a	1518	MA6	C4-C5-N7	-4.23	105.74	110.58
32	1a	1519	MA6	C2-N1-C6	4.19	122.07	111.83
32	2a	1519	MA6	C2-N1-C6	4.16	122.00	111.83
1	2A	1915	5MU	C1'-N1-C2	4.13	125.01	117.59
1	1A	1937	5MU	C1'-N1-C2	4.12	125.00	117.59
32	2a	516	PSU	C4-N3-C2	-4.12	120.69	126.37
1	2A	1911	PSU	C4-N3-C2	-4.12	120.69	126.37
1	2A	1915	5MU	C5-C4-N3	4.12	118.90	115.32
32	2a	1518	MA6	C4-C5-N7	-4.09	105.90	110.58
1	2A	1939	5MU	C5-C4-N3	4.09	118.88	115.32
1	2A	1915	5MU	O4-C4-C5	-4.09	120.24	124.92
1	1A	1937	5MU	O4-C4-C5	-4.09	120.24	124.92
1	2A	2605	PSU	C4-N3-C2	-4.08	120.75	126.37
32	1a	1519	MA6	C9-N6-C6	-4.08	110.15	120.52
1	2A	1917	PSU	C4-N3-C2	-4.08	120.76	126.37
32	1a	527	7MG	C2-N3-C4	4.04	119.26	112.30
1	1A	2564	2MU	C4-N3-C2	-4.01	121.63	126.61

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	2a	1400	5MC	C5-C6-N1	-4.00	118.96	123.31
32	1a	966	M2G	N9-C4-N3	3.97	133.90	125.95
32	2a	1207	2MG	N9-C4-N3	3.88	133.71	125.95
1	1A	2617	PSU	C4-N3-C2	-3.85	121.07	126.37
32	2a	1404	5MC	C5-C6-N1	-3.81	119.17	123.31
32	2a	516	PSU	O2-C2-N1	-3.81	118.86	122.79
32	2a	1518	MA6	N3-C4-N9	3.80	133.64	127.17
1	1A	1961	5MU	O4-C4-C5	-3.78	120.59	124.92
43	1l	92	0TD	OD2-CG-CB	3.76	121.27	113.15
32	1a	1207	2MG	N1-C2-N2	3.76	120.39	116.56
32	1a	516	PSU	C4-N3-C2	-3.75	121.20	126.37
1	2A	2552	2MU	O2-C2-N1	-3.75	117.92	122.80
1	2A	1939	5MU	O4-C4-C5	-3.74	120.64	124.92
1	1A	1939	PSU	C4-N3-C2	-3.73	121.23	126.37
32	2a	1519	MA6	N3-C4-N9	3.73	133.51	127.17
32	1a	1400	5MC	C5-C6-N1	-3.71	119.28	123.31
32	1a	1519	MA6	C4-C5-N7	-3.70	106.35	110.58
32	2a	1519	MA6	C2-N3-C4	3.69	120.84	111.83
1	2A	2503	2MA	C4-N9-C8	3.68	109.60	105.74
32	1a	966	M2G	C6-C5-N7	3.63	136.89	130.29
1	1A	2564	2MU	C2'-C1'-N1	-3.57	107.46	114.24
1	1A	2263	OMG	C6-C5-N7	3.54	136.72	130.29
32	2a	1519	MA6	C9-N6-C6	-3.54	111.53	120.52
1	2A	2503	2MA	C4-C5-N7	-3.51	106.57	110.58
32	1a	1519	MA6	C2-N3-C4	3.50	120.39	111.83
1	2A	1962	5MC	C5-C6-N1	-3.50	119.52	123.31
1	2A	1911	PSU	O2-C2-N1	-3.50	119.18	122.79
1	1A	1964	5MC	C5-C6-N1	-3.47	119.55	123.31
32	2a	967	5MC	C5-C6-N1	-3.46	119.56	123.31
1	1A	1937	5MU	C1'-N1-C6	-3.45	115.47	121.15
1	2A	1915	5MU	C1'-N1-C6	-3.43	115.50	121.15
32	2a	1518	MA6	C2-N3-C4	3.43	120.21	111.83
1	2A	2503	2MA	N6-C6-N1	3.41	121.62	117.03
32	1a	1207	2MG	N9-C4-N3	3.39	132.74	125.95
1	2A	1942	5MC	C5-C6-N1	-3.39	119.64	123.31
1	1A	2515	2MA	N6-C6-N1	3.37	121.57	117.03
32	1a	1404	5MC	C5-C6-N1	-3.36	119.66	123.31
32	1a	1518	MA6	C2-N3-C4	3.35	120.00	111.83
1	1A	2515	2MA	C4-C5-N7	-3.34	106.76	110.58
32	1a	1518	MA6	N3-C4-N9	3.33	132.82	127.17
32	1a	1498	UR3	C5-C4-N3	3.33	119.42	115.04
32	1a	516	PSU	O2-C2-N1	-3.32	119.36	122.79

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	2a	1498	UR3	C5-C4-N3	3.32	119.41	115.04
32	2a	1407	5MC	C5-C6-N1	-3.27	119.76	123.31
32	2a	1207	2MG	C6-C5-N7	3.27	136.24	130.29
32	2a	1518	MA6	N1-C2-N3	-3.22	123.71	128.58
32	1a	1207	2MG	C4-C5-N7	-3.22	105.57	110.67
1	1A	1939	PSU	O2-C2-N1	-3.20	119.49	122.79
1	2A	1939	5MU	O2-C2-N1	-3.18	118.66	122.80
1	2A	2251	OMG	C6-C5-N7	3.17	136.06	130.29
1	1A	1961	5MU	O2-C2-N1	-3.14	118.71	122.80
32	2a	1519	MA6	N1-C2-N3	-3.13	123.84	128.58
32	1a	1518	MA6	N1-C2-N3	-3.13	123.85	128.58
32	2a	1519	MA6	C5-N7-C8	3.10	108.33	103.45
32	1a	967	5MC	C5-C6-N1	-3.07	119.97	123.31
32	1a	1519	MA6	N1-C2-N3	-3.03	124.00	128.58
32	2a	1519	MA6	C10-N6-C9	-3.01	106.51	116.18
1	1A	2263	OMG	C4-C5-N7	-2.99	105.93	110.67
32	1a	1407	5MC	C5-C6-N1	-2.97	120.08	123.31
32	2a	967	5MC	C5-C4-N3	-2.93	118.75	121.75
1	2A	2503	2MA	C5-N7-C8	2.92	108.05	103.45
1	2A	2552	2MU	O4-C4-C5	-2.92	120.13	125.16
32	1a	1207	2MG	N2-C2-N3	-2.92	116.79	120.51
1	2A	2503	2MA	N9-C8-N7	-2.91	109.80	113.94
32	1a	1407	5MC	C5-C4-N3	-2.88	118.80	121.75
1	2A	2552	2MU	C2'-C1'-N1	-2.88	108.77	114.24
32	1a	1518	MA6	C10-N6-C6	-2.88	113.19	120.52
43	2l	92	0TD	OD2-CG-CB	2.82	119.25	113.15
32	2a	1207	2MG	N1-C2-N2	2.79	119.41	116.56
1	1A	1984	5MC	C5-C6-N1	-2.79	120.29	123.31
32	2a	1519	MA6	C6-C5-N7	2.78	137.87	133.43
32	2a	527	7MG	C5-C6-N1	2.77	115.81	110.94
32	1a	1400	5MC	C5-C4-N3	-2.76	118.93	121.75
32	1a	1518	MA6	C5-N7-C8	2.74	107.76	103.45
32	2a	1518	MA6	C10-N6-C9	-2.74	107.39	116.18
32	1a	966	M2G	C4-C5-N7	-2.73	106.35	110.67
1	2A	2552	2MU	C5-C4-N3	2.73	118.62	114.80
32	2a	1404	5MC	C5-C4-N3	-2.71	118.97	121.75
1	1A	1984	5MC	C5-C4-N3	-2.71	118.98	121.75
32	2a	966	M2G	C6-C5-N7	2.70	135.20	130.29
32	1a	1519	MA6	N1-C6-N6	2.69	120.13	116.86
32	2a	1407	5MC	C5-C4-N3	-2.67	119.01	121.75
1	2A	1942	5MC	C5-C4-N3	-2.64	119.05	121.75
32	2a	1518	MA6	C5-N7-C8	2.64	107.59	103.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	1a	1518	MA6	C6-C5-N7	2.63	137.63	133.43
1	1A	1964	5MC	C5-C4-N3	-2.62	119.06	121.75
32	1a	1407	5MC	O2-C2-N3	-2.61	118.21	122.33
1	1A	2564	2MU	O2-C2-N1	-2.57	119.45	122.80
32	2a	1207	2MG	C4-C5-N7	-2.56	106.61	110.67
1	1A	1939	PSU	C6-C5-C4	-2.56	116.45	118.17
32	2a	1402	4OC	C6-C5-C4	2.56	120.08	117.00
32	2a	1518	MA6	C10-N6-C6	-2.56	114.02	120.52
1	1A	1937	5MU	O2-C2-N3	-2.55	116.79	121.49
32	2a	1207	2MG	N2-C2-N3	-2.54	117.27	120.51
43	1l	92	0TD	OD1-CG-CB	-2.51	117.19	122.44
32	1a	1404	5MC	C5-C4-N3	-2.50	119.19	121.75
1	1A	2617	PSU	O2-C2-N1	-2.50	120.21	122.79
1	1A	1984	5MC	CM5-C5-C6	-2.50	119.47	122.85
32	1a	1498	UR3	C3U-N3-C2	2.50	121.68	117.33
1	2A	2251	OMG	O6-C6-C5	-2.49	119.95	126.53
32	1a	967	5MC	C5-C4-N3	-2.47	119.22	121.75
32	1a	1519	MA6	C5-N7-C8	2.47	107.33	103.45
32	2a	1519	MA6	C4-N9-C8	2.44	108.30	105.74
1	1A	2515	2MA	C4-N9-C8	2.44	108.30	105.74
1	2A	2605	PSU	O2-C2-N1	-2.41	120.30	122.79
1	1A	1942	4OC	O2-C2-N3	-2.40	118.55	122.33
32	2a	1407	5MC	O2-C2-N3	-2.39	118.56	122.33
32	1a	1402	4OC	C6-C5-C4	2.39	119.88	117.00
32	2a	516	PSU	O4'-C1'-C2'	2.38	108.45	105.15
32	2a	967	5MC	CM5-C5-C6	-2.36	119.65	122.85
32	1a	527	7MG	C5-C6-N1	2.36	115.08	110.94
1	2A	1920	4OC	O2-C2-N3	-2.35	118.62	122.33
1	1A	2515	2MA	C5-N7-C8	2.34	107.13	103.45
1	1A	2564	2MU	C5-C4-N3	2.33	118.06	114.80
1	2A	1915	5MU	C5-C6-N1	-2.32	120.80	123.31
32	1a	1207	2MG	O3'-C3'-C2'	2.32	119.24	111.82
1	2A	2251	OMG	C4-C5-N7	-2.31	107.01	110.67
1	2A	2605	PSU	C5-C6-N1	-2.30	118.94	122.14
32	1a	1402	4OC	CM4-N4-C4	-2.30	117.96	122.45
1	1A	2617	PSU	C5-C6-N1	-2.30	118.95	122.14
1	2A	2503	2MA	C6-C5-N7	2.29	136.51	132.09
32	2a	1519	MA6	N9-C8-N7	-2.28	110.70	113.94
1	2A	1962	5MC	C5-C4-N3	-2.28	119.42	121.75
1	1A	1937	5MU	C5-C6-N1	-2.28	120.84	123.31
32	2a	1400	5MC	C5-C4-N3	-2.28	119.42	121.75
32	2a	516	PSU	C5-C6-N1	-2.28	118.98	122.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	1a	1518	MA6	C4-N9-C8	2.27	108.12	105.74
32	2a	966	M2G	C4-C5-N7	-2.26	107.08	110.67
32	1a	1518	MA6	C10-N6-C9	-2.25	108.94	116.18
1	2A	1915	5MU	O2-C2-N3	-2.24	117.36	121.49
1	1A	1984	5MC	C1'-N1-C6	-2.24	117.47	121.15
1	2A	2503	2MA	C2-N1-C6	2.24	121.54	118.10
32	2a	1404	5MC	O2-C2-N3	-2.23	118.81	122.33
32	1a	516	PSU	O4'-C1'-C2'	2.19	108.18	105.15
1	1A	1933	PSU	C5-C6-N1	-2.16	119.14	122.14
32	2a	1518	MA6	C6-C5-N7	2.16	136.88	133.43
32	1a	1519	MA6	C10-N6-C6	-2.16	115.03	120.52
32	2a	1207	2MG	O6-C6-C5	-2.12	120.94	126.53
1	1A	2617	PSU	O2-C2-N3	-2.11	118.11	121.86
1	1A	2564	2MU	C6'-O2'-C2'	-2.10	109.07	114.47
32	2a	1498	UR3	C3U-N3-C4	2.09	120.76	117.87
32	1a	1400	5MC	CM5-C5-C6	-2.08	120.03	122.85
32	1a	1519	MA6	C4-N9-C8	2.08	107.92	105.74
32	2a	1518	MA6	C4-N9-C8	2.07	107.91	105.74
32	1a	1207	2MG	O3'-C3'-C4'	2.06	117.01	111.08
32	1a	1404	5MC	CM5-C5-C6	-2.06	120.07	122.85
1	1A	2515	2MA	N9-C8-N7	-2.05	111.03	113.94
32	1a	527	7MG	C5-C4-N9	-2.05	103.71	106.33
1	2A	2251	OMG	C5-C6-N1	2.05	118.47	113.25
1	2A	2605	PSU	O2-C2-N3	-2.05	118.22	121.86
1	1A	1933	PSU	O4'-C1'-C2'	2.05	107.98	105.15
32	1a	966	M2G	O6-C6-C5	-2.04	121.16	126.53
32	1a	1207	2MG	CM2-N2-C2	-2.03	119.28	123.65
32	1a	1498	UR3	C6-N1-C2	-2.02	120.14	121.80
1	1A	2263	OMG	C8-N7-C5	2.01	107.84	104.26
43	2l	92	0TD	OD1-CG-CB	-2.01	118.24	122.44
32	2a	1404	5MC	CM5-C5-C6	-2.01	120.14	122.85

There are no chirality outliers.

All (35) 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
32	1a	1207	2MG	N1-C2-N2-CM2
32	1a	1207	2MG	N3-C2-N2-CM2
32	1a	1518	MA6	C5-C6-N6-C9
32	1a	1519	MA6	O4'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
43	1l	92	0TD	O-C-CA-CB
1	2A	1915	5MU	O4'-C1'-N1-C2
1	2A	1915	5MU	O4'-C1'-N1-C6
32	2a	1402	4OC	O4'-C4'-C5'-O5'
32	2a	1519	MA6	O4'-C4'-C5'-O5'
32	1a	1518	MA6	N1-C6-N6-C9
32	1a	1519	MA6	C3'-C4'-C5'-O5'
32	2a	1402	4OC	C3'-C4'-C5'-O5'
32	1a	1519	MA6	C5-C6-N6-C10
32	2a	1518	MA6	C5-C6-N6-C10
32	2a	1519	MA6	C5-C6-N6-C9
32	2a	1519	MA6	C5-C6-N6-C10
32	2a	1519	MA6	C3'-C4'-C5'-O5'
43	1l	92	0TD	CG-CB-SB-CSB
43	2l	92	0TD	CG-CB-SB-CSB
32	1a	1402	4OC	O4'-C4'-C5'-O5'
32	1a	1518	MA6	C5-C6-N6-C10
32	2a	1518	MA6	C5-C6-N6-C9
1	1A	2515	2MA	C4'-C5'-O5'-P
1	2A	2503	2MA	O4'-C4'-C5'-O5'
43	1l	92	0TD	SB-CB-CG-OD2
32	1a	1400	5MC	O4'-C4'-C5'-O5'
32	1a	1402	4OC	C3'-C2'-O2'-CM2
1	1A	2515	2MA	O4'-C4'-C5'-O5'
1	1A	1984	5MC	C2'-C1'-N1-C6
1	1A	2263	OMG	C4'-C5'-O5'-P
1	1A	1942	4OC	C2'-C1'-N1-C2
1	1A	1984	5MC	O4'-C1'-N1-C6
32	1a	527	7MG	C3'-C4'-C5'-O5'

There are no ring outliers.

23 monomers are involved in 30 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
32	1a	1400	5MC	2	0
32	1a	1402	4OC	1	0
1	1A	2564	2MU	1	0
32	1a	527	7MG	1	0
1	2A	1939	5MU	2	0
43	2l	92	0TD	1	0
1	1A	1942	4OC	1	0
32	1a	1518	MA6	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
32	2a	1207	2MG	3	0
32	2a	1519	MA6	1	0
43	1l	92	0TD	1	0
32	2a	1402	4OC	3	0
32	1a	1519	MA6	2	0
1	2A	1915	5MU	1	0
32	2a	967	5MC	1	0
1	1A	2515	2MA	1	0
1	1A	1964	5MC	1	0
1	2A	2251	OMG	1	0
32	2a	1518	MA6	1	0
32	1a	967	5MC	1	0
32	2a	1400	5MC	2	0
1	2A	1917	PSU	1	0
1	2A	1911	PSU	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2389 ligands modelled in this entry, 2376 are monoatomic - leaving 13 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
57	MPD	18	102	-	7,7,7	0.31	0	9,10,10	0.38	0
57	MPD	2B	3020	-	7,7,7	0.31	0	9,10,10	0.31	0
58	ARG	1B	228	54	10,11,11	0.76	1 (10%)	9,13,13	1.07	1 (11%)
57	MPD	1T	204	-	7,7,7	0.35	0	9,10,10	0.37	0
56	EZP	1A	3987	-	26,26,26	2.59	3 (11%)	32,35,35	1.55	4 (12%)
57	MPD	2A	3711	-	7,7,7	0.32	0	9,10,10	0.27	0
58	ARG	1F	314	-	10,11,11	0.72	0	9,13,13	0.86	1 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
57	MPD	2A	3710	-	7,7,7	0.41	0	9,10,10	0.33	0
60	SF4	2d	501	35	0,12,12	-	-	-		
57	MPD	1A	3988	-	7,7,7	0.31	0	9,10,10	0.28	0
60	SF4	1d	302	35	0,12,12	-	-	-		
56	EZP	2A	3709	-	26,26,26	3.25	3 (11%)	32,35,35	0.85	1 (3%)
57	MPD	1a	1854	-	7,7,7	0.41	0	9,10,10	0.41	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
57	MPD	18	102	-	-	3/5/5/5	-
57	MPD	2B	3020	-	-	5/5/5/5	-
58	ARG	1B	228	54	-	4/11/11/11	-
57	MPD	1T	204	-	-	1/5/5/5	-
56	EZP	1A	3987	-	-	8/24/26/26	0/2/2/2
57	MPD	2A	3711	-	-	3/5/5/5	-
58	ARG	1F	314	-	-	3/11/11/11	-
57	MPD	2A	3710	-	-	0/5/5/5	-
60	SF4	2d	501	35	-	-	0/6/5/5
57	MPD	1A	3988	-	-	3/5/5/5	-
60	SF4	1d	302	35	-	-	0/6/5/5
56	EZP	2A	3709	-	-	8/24/26/26	0/2/2/2
57	MPD	1a	1854	-	-	3/5/5/5	-

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
56	2A	3709	EZP	OAC-NAY	13.29	1.45	1.22
56	1A	3987	EZP	OAC-NAY	9.03	1.38	1.22
56	2A	3709	EZP	CAT-CAW	-8.15	1.39	1.51
56	1A	3987	EZP	CAT-CAW	-7.51	1.40	1.51
56	1A	3987	EZP	CAU-NAY	-4.66	1.34	1.45
56	2A	3709	EZP	CAU-NAY	-4.32	1.34	1.45
58	1B	228	ARG	OXT-C	-2.18	1.23	1.30

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
56	1A	3987	EZP	CAT-CAW-CAX	4.85	120.42	111.72
56	1A	3987	EZP	CAW-CAX-NAP	4.58	118.30	110.03
58	1B	228	ARG	OXT-C-O	-2.67	118.01	124.08
58	1F	314	ARG	OXT-C-O	-2.43	118.57	124.08
56	2A	3709	EZP	CAW-CAX-NAP	2.39	114.35	110.03
56	1A	3987	EZP	CA-C-NAP	-2.36	113.01	116.21
56	1A	3987	EZP	CAI-CAU-NAY	2.15	121.22	119.34

There are no chirality outliers.

All (41) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
56	1A	3987	EZP	NAP-C-CA-CB
56	1A	3987	EZP	O-C-CA-CB
56	1A	3987	EZP	C-CA-CB-CG
56	2A	3709	EZP	NAP-C-CA-N
56	2A	3709	EZP	NAP-C-CA-CB
56	2A	3709	EZP	O-C-CA-N
56	2A	3709	EZP	O-C-CA-CB
56	2A	3709	EZP	C-CA-CB-CG
56	2A	3709	EZP	N-CA-CB-CG
57	18	102	MPD	C2-C3-C4-C5
57	2B	3020	MPD	C2-C3-C4-C5
56	1A	3987	EZP	CA-CB-CG-CD2
56	1A	3987	EZP	CA-CB-CG-ND1
58	1B	228	ARG	NE-CD-CG-CB
56	1A	3987	EZP	CAM-CAX-NAP-C
56	2A	3709	EZP	CA-CB-CG-CD2
56	2A	3709	EZP	CA-CB-CG-ND1
58	1B	228	ARG	CA-CB-CG-CD
56	1A	3987	EZP	N-CA-CB-CG
57	1a	1854	MPD	CM-C2-C3-C4
57	2A	3711	MPD	C1-C2-C3-C4
57	1T	204	MPD	C2-C3-C4-C5
57	1a	1854	MPD	C2-C3-C4-C5
56	1A	3987	EZP	OAE-CAW-CAX-CAM
58	1F	314	ARG	CG-CD-NE-CZ
57	1A	3988	MPD	O2-C2-C3-C4
57	2B	3020	MPD	O2-C2-C3-C4
57	2A	3711	MPD	C2-C3-C4-O4
57	2B	3020	MPD	C2-C3-C4-O4
57	1A	3988	MPD	C1-C2-C3-C4
57	1A	3988	MPD	CM-C2-C3-C4

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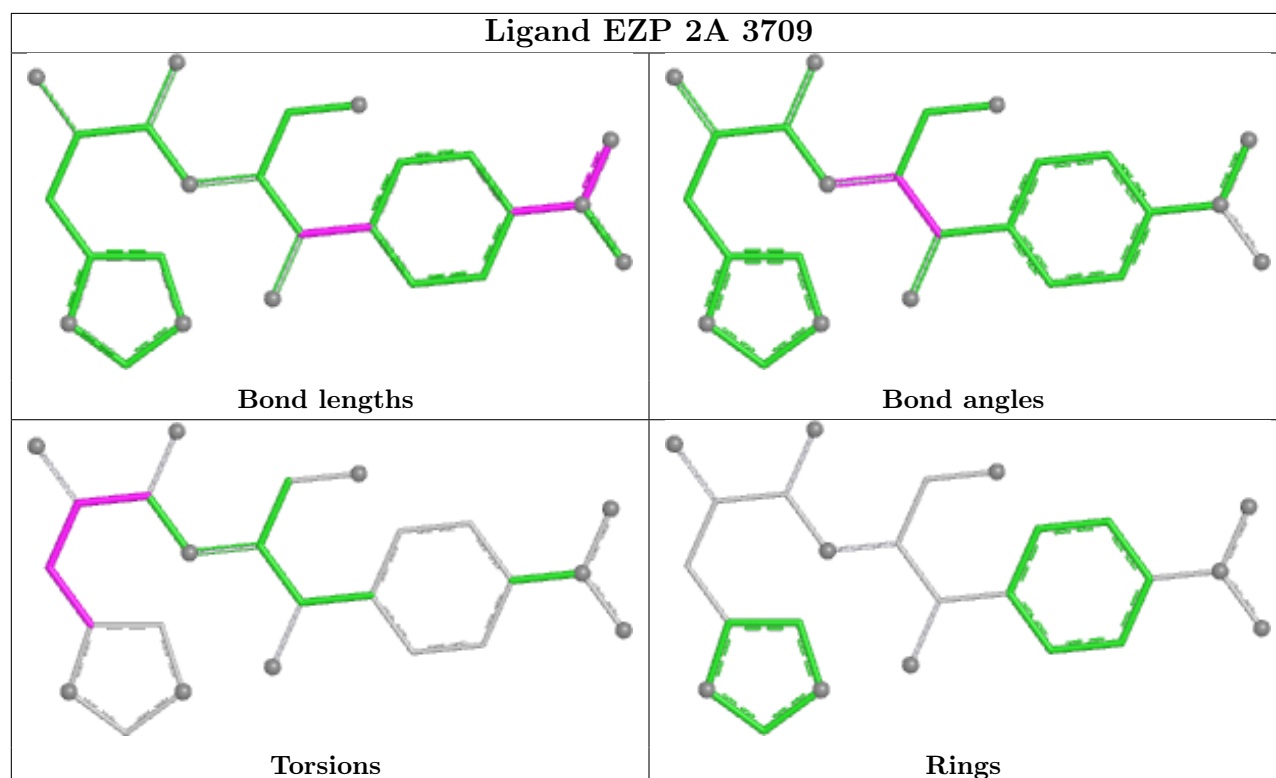
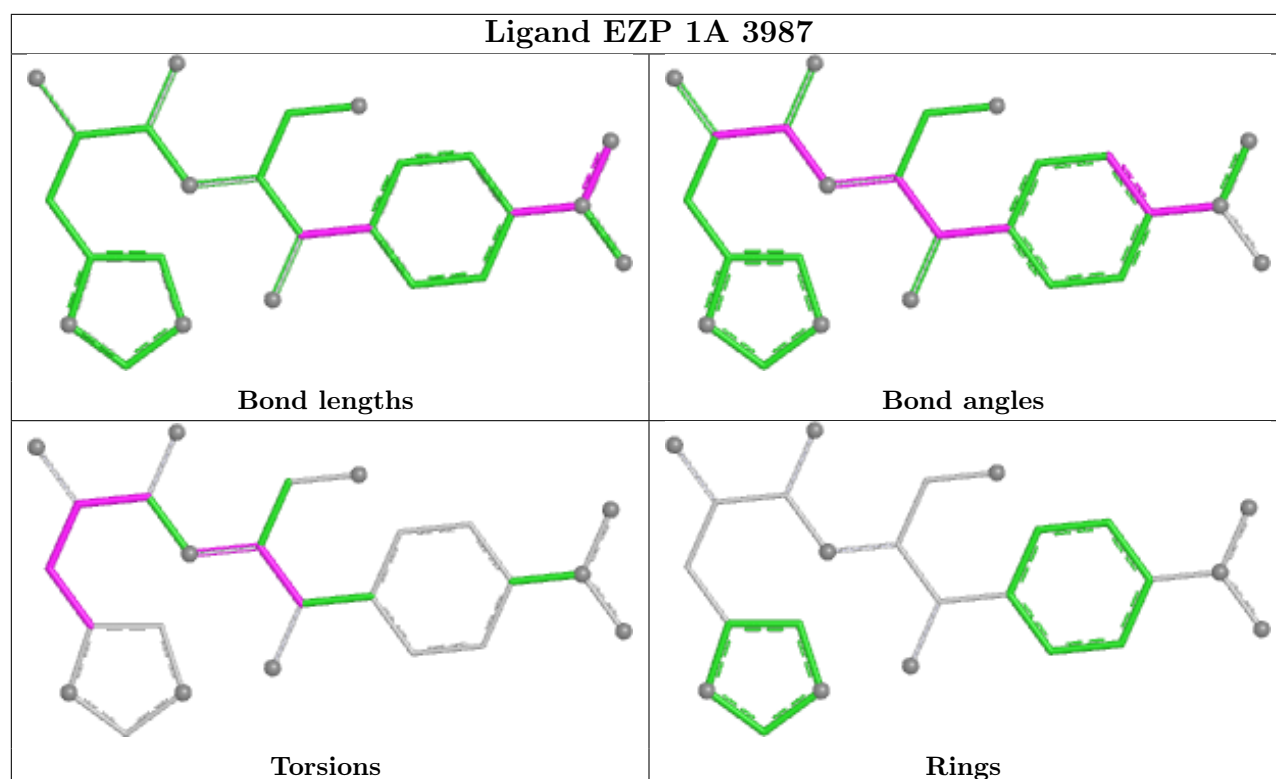
Mol	Chain	Res	Type	Atoms
57	18	102	MPD	C1-C2-C3-C4
57	18	102	MPD	CM-C2-C3-C4
57	1a	1854	MPD	C1-C2-C3-C4
57	2A	3711	MPD	CM-C2-C3-C4
57	2B	3020	MPD	C1-C2-C3-C4
57	2B	3020	MPD	CM-C2-C3-C4
58	1B	228	ARG	OXT-C-CA-N
58	1F	314	ARG	OXT-C-CA-N
58	1B	228	ARG	N-CA-CB-CG
58	1F	314	ARG	O-C-CA-N

There are no ring outliers.

7 monomers are involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
57	18	102	MPD	1	0
58	1B	228	ARG	3	0
57	1T	204	MPD	1	0
58	1F	314	ARG	3	0
57	2A	3710	MPD	2	0
60	2d	501	SF4	1	0
57	1a	1854	MPD	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	1A	2861/2915 (98%)	-0.65	114 (3%) 42 38	15, 31, 89, 105	0
1	2A	2856/2915 (97%)	-0.19	134 (4%) 36 33	27, 50, 92, 103	0
2	1B	120/121 (99%)	-0.53	1 (0%) 82 81	24, 44, 58, 80	0
2	2B	120/121 (99%)	0.72	8 (6%) 24 21	52, 74, 83, 90	0
3	1D	275/276 (99%)	-0.35	1 (0%) 88 87	17, 32, 46, 65	0
3	2D	275/276 (99%)	-0.01	2 (0%) 84 83	26, 44, 56, 76	0
4	1E	204/206 (99%)	-0.28	1 (0%) 87 86	16, 34, 55, 70	0
4	2E	204/206 (99%)	0.14	3 (1%) 72 70	29, 50, 66, 79	0
5	1F	203/210 (96%)	-0.22	1 (0%) 87 86	16, 35, 60, 83	0
5	2F	203/210 (96%)	0.25	0 100 100	29, 60, 72, 85	0
6	1G	181/182 (99%)	0.33	4 (2%) 62 59	39, 56, 72, 80	0
6	2G	181/182 (99%)	1.21	25 (13%) 6 5	68, 77, 85, 89	0
7	1H	174/180 (96%)	0.01	2 (1%) 78 76	32, 46, 59, 64	0
7	2H	173/180 (96%)	0.97	11 (6%) 25 22	62, 75, 82, 86	0
8	1I	147/148 (99%)	0.57	5 (3%) 48 44	34, 66, 76, 83	0
8	2I	146/148 (98%)	0.85	10 (6%) 23 20	51, 69, 81, 84	0
9	1N	140/140 (100%)	-0.34	0 100 100	22, 32, 53, 67	0
9	2N	140/140 (100%)	0.23	0 100 100	43, 57, 71, 76	0
10	1O	122/122 (100%)	-0.33	0 100 100	23, 34, 50, 58	0
10	2O	122/122 (100%)	0.15	1 (0%) 82 81	38, 51, 61, 69	0
11	1P	149/150 (99%)	-0.20	0 100 100	15, 38, 58, 71	0
11	2P	149/150 (99%)	0.28	3 (2%) 65 62	32, 59, 77, 80	0
12	1Q	141/141 (100%)	-0.30	0 100 100	21, 35, 46, 62	0
12	2Q	141/141 (100%)	0.46	3 (2%) 63 61	40, 57, 67, 76	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
13	1R	118/118 (100%)	-0.42	0 100 100	21, 29, 44, 50	0
13	2R	118/118 (100%)	-0.07	0 100 100	31, 44, 55, 65	0
14	1S	110/112 (98%)	0.03	1 (0%) 81 80	34, 45, 56, 65	0
14	2S	110/112 (98%)	1.17	16 (14%) 6 5	59, 69, 76, 81	0
15	1T	131/146 (89%)	-0.13	4 (3%) 51 48	28, 38, 62, 75	0
15	2T	131/146 (89%)	0.13	1 (0%) 82 81	41, 52, 70, 76	0
16	1U	116/118 (98%)	-0.52	0 100 100	18, 25, 39, 57	0
16	2U	116/118 (98%)	0.25	1 (0%) 81 80	33, 52, 67, 74	0
17	1V	101/101 (100%)	-0.47	0 100 100	15, 35, 54, 67	0
17	2V	101/101 (100%)	0.38	0 100 100	31, 62, 72, 77	0
18	1W	112/113 (99%)	-0.47	0 100 100	19, 27, 46, 75	0
18	2W	112/113 (99%)	0.01	1 (0%) 81 80	29, 43, 59, 84	0
19	1X	95/96 (98%)	-0.25	1 (1%) 78 76	23, 32, 58, 68	0
19	2X	95/96 (98%)	0.43	1 (1%) 78 76	43, 54, 69, 74	0
20	1Y	107/110 (97%)	0.02	1 (0%) 81 80	29, 42, 62, 67	0
20	2Y	107/110 (97%)	0.91	5 (4%) 36 33	49, 63, 73, 82	0
21	1Z	203/206 (98%)	0.10	2 (0%) 79 78	35, 51, 66, 76	0
21	2Z	201/206 (97%)	0.89	8 (3%) 42 38	57, 71, 79, 88	0
22	10	77/85 (90%)	-0.25	0 100 100	24, 31, 48, 54	0
22	20	77/85 (90%)	0.60	2 (2%) 57 54	43, 57, 67, 72	0
23	11	97/98 (98%)	0.02	1 (1%) 79 78	22, 39, 61, 69	0
23	21	97/98 (98%)	0.32	2 (2%) 63 61	35, 49, 71, 73	0
24	12	70/72 (97%)	-0.12	1 (1%) 73 72	29, 44, 57, 78	0
24	22	70/72 (97%)	0.49	0 100 100	53, 64, 71, 73	0
25	13	59/60 (98%)	-0.41	0 100 100	20, 30, 55, 63	0
25	23	59/60 (98%)	0.36	1 (1%) 69 67	45, 55, 69, 77	0
26	14	69/71 (97%)	0.89	14 (20%) 3 2	50, 69, 86, 90	0
26	24	69/71 (97%)	1.37	13 (18%) 3 3	70, 83, 88, 91	0
27	15	59/60 (98%)	-0.50	0 100 100	17, 27, 44, 54	0
27	25	59/60 (98%)	-0.17	0 100 100	29, 44, 59, 68	0
28	16	53/54 (98%)	-0.45	0 100 100	28, 36, 48, 55	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
28	26	53/54 (98%)	0.20	1 (1%) 66 63	46, 54, 63, 68	0
29	17	48/49 (97%)	-0.32	1 (2%) 63 61	17, 24, 49, 58	0
29	27	48/49 (97%)	-0.07	2 (4%) 40 37	28, 36, 58, 65	0
30	18	64/65 (98%)	-0.47	0 100 100	23, 28, 34, 47	0
30	28	64/65 (98%)	0.21	1 (1%) 70 68	38, 49, 56, 63	0
31	19	37/37 (100%)	-0.29	0 100 100	22, 32, 49, 53	0
31	29	37/37 (100%)	0.76	1 (2%) 56 53	50, 60, 68, 69	0
32	1a	1488/1521 (97%)	0.10	38 (2%) 57 54	32, 62, 89, 104	0
32	2a	1492/1521 (98%)	0.42	61 (4%) 41 37	42, 71, 91, 103	0
33	1b	231/256 (90%)	0.94	28 (12%) 8 7	61, 74, 83, 88	0
33	2b	231/256 (90%)	1.30	45 (19%) 3 2	66, 80, 86, 90	0
34	1c	206/239 (86%)	0.74	15 (7%) 21 18	53, 67, 77, 81	0
34	2c	206/239 (86%)	1.34	37 (17%) 3 3	70, 79, 84, 91	0
35	1d	208/209 (99%)	0.75	12 (5%) 29 25	51, 66, 75, 81	0
35	2d	208/209 (99%)	0.93	10 (4%) 35 32	55, 68, 77, 79	0
36	1e	148/162 (91%)	0.28	0 100 100	46, 59, 69, 80	0
36	2e	148/162 (91%)	0.75	4 (2%) 56 53	57, 68, 76, 83	0
37	1f	100/101 (99%)	0.41	1 (1%) 79 78	43, 60, 70, 74	0
37	2f	100/101 (99%)	0.31	0 100 100	52, 62, 70, 76	0
38	1g	155/156 (99%)	0.49	3 (1%) 66 63	56, 65, 76, 85	0
38	2g	155/156 (99%)	0.87	10 (6%) 25 22	68, 74, 81, 87	0
39	1h	137/138 (99%)	0.41	2 (1%) 72 70	51, 62, 71, 74	0
39	2h	137/138 (99%)	0.67	2 (1%) 72 70	58, 69, 74, 82	0
40	1i	127/128 (99%)	1.05	14 (11%) 10 9	52, 73, 79, 82	0
40	2i	126/128 (98%)	1.74	42 (33%) 1 1	67, 80, 85, 87	0
41	1j	97/105 (92%)	1.03	10 (10%) 12 10	52, 72, 83, 86	0
41	2j	96/105 (91%)	2.17	53 (55%) 0 0	71, 80, 85, 87	0
42	1k	114/129 (88%)	0.27	1 (0%) 81 80	39, 58, 69, 73	0
42	2k	114/129 (88%)	0.72	8 (7%) 22 19	50, 66, 75, 81	0
43	1l	121/132 (91%)	0.20	3 (2%) 58 55	42, 54, 65, 70	0
43	2l	121/132 (91%)	0.63	3 (2%) 58 55	54, 62, 69, 77	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
44	1m	116/126 (92%)	0.82	8 (6%) 23 20	52, 68, 75, 79	0
44	2m	114/126 (90%)	1.42	21 (18%) 3 3	73, 80, 85, 87	0
45	1n	60/61 (98%)	0.84	3 (5%) 34 30	57, 64, 72, 79	0
45	2n	60/61 (98%)	1.90	22 (36%) 1 0	71, 79, 85, 88	0
46	1o	88/89 (98%)	0.58	3 (3%) 48 44	43, 60, 71, 77	0
46	2o	88/89 (98%)	0.69	2 (2%) 61 58	54, 67, 75, 78	0
47	1p	82/88 (93%)	1.36	13 (15%) 5 4	55, 67, 77, 80	0
47	2p	82/88 (93%)	1.03	6 (7%) 21 18	55, 65, 75, 82	0
48	1q	99/105 (94%)	0.65	2 (2%) 65 62	48, 63, 72, 73	0
48	2q	99/105 (94%)	0.58	2 (2%) 65 62	53, 63, 73, 79	0
49	1r	68/88 (77%)	0.24	0 100 100	51, 60, 73, 76	0
49	2r	68/88 (77%)	0.45	1 (1%) 72 70	59, 67, 74, 76	0
50	1s	83/93 (89%)	0.74	2 (2%) 59 56	59, 70, 76, 79	0
50	2s	83/93 (89%)	1.55	22 (26%) 1 1	70, 82, 86, 88	0
51	1t	96/106 (90%)	1.00	9 (9%) 14 12	53, 66, 76, 82	0
51	2t	98/106 (92%)	0.66	9 (9%) 14 12	53, 64, 75, 77	0
52	1u	23/27 (85%)	0.94	0 100 100	61, 66, 69, 72	0
52	2u	23/27 (85%)	2.45	14 (60%) 0 0	73, 76, 80, 82	0
53	1y	97/113 (85%)	0.47	4 (4%) 41 37	45, 56, 67, 71	0
53	2y	96/113 (84%)	1.38	20 (20%) 2 2	60, 72, 79, 83	0
All	All	20766/21468 (96%)	0.18	976 (4%) 36 33	15, 57, 84, 105	0

All (976) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	1A	1133	G	9.1
45	2n	2	ALA	8.8
1	1A	1110	C	7.0
1	2A	2602	A	6.9
51	1t	103	GLY	6.8
1	1A	1135	G	6.4
1	1A	1122	C	6.3
1	1A	1124	U	6.1
1	1A	1123	A	6.1
1	1A	1134	A	6.0

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Mol	Chain	Res	Type	RSRZ
1	1A	1111	U	6.0
1	1A	1118	C	5.8
1	1A	1126	C	5.6
41	2j	37	PRO	5.6
32	2a	1030(A)	G	5.5
32	2a	1030(B)	C	5.5
53	2y	98	ALA	5.4
1	1A	1136	U	5.3
52	2u	14	TRP	5.3
40	2i	125	TYR	5.3
1	1A	1137	G	5.2
32	1a	1036	G	5.2
44	2m	102	ARG	5.1
1	2A	2174	C	5.0
51	2t	6	PRO	5.0
1	1A	1132	A	4.9
1	1A	2139	A	4.9
32	2a	1001(A)	G	4.9
53	1y	98	ALA	4.9
1	1A	1112	U	4.8
52	2u	2	GLY	4.8
1	2A	2145	C	4.8
1	1A	1127	U	4.7
14	2S	32	LEU	4.6
26	14	56	VAL	4.6
40	2i	102	LEU	4.6
1	1A	1120	G	4.6
1	2A	2106	G	4.6
15	1T	131	ALA	4.5
39	2h	2	LEU	4.5
33	1b	7	VAL	4.5
1	1A	1138	C	4.5
1	1A	2614	A	4.5
1	1A	1125	C	4.4
52	2u	6	ARG	4.4
23	1l	2	SER	4.4
1	1A	1131	A	4.4
41	1j	4	ILE	4.4
1	1A	1150	C	4.4
7	1H	2	SER	4.3
2	2B	1	U	4.3
45	1n	2	ALA	4.3

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Mol	Chain	Res	Type	RSRZ
1	2A	1085	A	4.3
8	2I	146	ALA	4.3
41	2j	36	GLY	4.3
1	1A	1149	A	4.3
41	2j	75	ILE	4.3
26	14	50	VAL	4.3
1	2A	1076	C	4.3
45	2n	60	SER	4.2
35	1d	179	GLU	4.2
45	2n	18	VAL	4.2
1	2A	2162	G	4.2
45	2n	55	GLY	4.2
1	1A	1121	C	4.2
1	2A	1075	C	4.2
41	2j	40	LEU	4.2
20	2Y	1	MET	4.1
34	1c	90	GLU	4.1
1	2A	2130	U	4.1
40	2i	109	VAL	4.1
14	2S	33	LYS	4.1
1	2A	34	C	4.1
1	2A	2802	G	4.0
53	2y	8	LYS	4.0
45	2n	59	ALA	4.0
1	2A	2147	G	4.0
8	2I	3	VAL	4.0
40	2i	127	LYS	4.0
1	2A	1046	A	4.0
1	2A	2153	G	3.9
1	2A	2142	C	3.9
6	2G	147	ASP	3.9
32	1a	1030	C	3.9
1	1A	1109	G	3.9
1	1A	1117	G	3.9
1	2A	2159	G	3.9
1	1A	1103	A	3.9
50	2s	9	VAL	3.9
41	2j	69	ASN	3.9
1	2A	2107	C	3.9
40	2i	126	SER	3.9
32	2a	1002	G	3.9
1	1A	1128	U	3.9

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Mol	Chain	Res	Type	RSRZ
1	2A	2132	U	3.9
53	1y	94	ALA	3.8
41	2j	71	LEU	3.8
15	1T	130	ALA	3.8
40	1i	106	ALA	3.8
40	2i	106	ALA	3.8
44	1m	2	ALA	3.8
41	2j	34	VAL	3.8
26	24	56	VAL	3.8
45	1n	3	ARG	3.8
1	2A	2169	A	3.8
41	2j	55	LYS	3.8
6	2G	53	LEU	3.8
23	21	2	SER	3.8
26	24	49	PHE	3.8
51	1t	9	ASN	3.7
40	2i	56	LEU	3.7
1	1A	1148	C	3.7
14	2S	17	ARG	3.7
32	1a	1034	G	3.7
1	1A	935	C	3.7
33	2b	237	ALA	3.7
34	2c	8	ILE	3.7
6	2G	146	TYR	3.7
50	2s	2	PRO	3.7
1	2A	652(B)	A	3.6
1	2A	1086	A	3.6
41	2j	38	ILE	3.6
32	2a	1031	G	3.6
1	2A	2135	A	3.6
32	2a	1003	G	3.6
41	2j	63	PHE	3.6
40	2i	5	TYR	3.6
1	2A	2160	G	3.6
32	1a	1026	G	3.6
1	2A	2134	A	3.6
48	2q	98	LEU	3.6
40	2i	7	THR	3.5
1	2A	2138	C	3.5
50	1s	13	ASP	3.5
1	2A	2118	U	3.5
41	2j	65	LEU	3.5

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Mol	Chain	Res	Type	RSRZ
32	2a	1202	G	3.5
53	2y	38	HIS	3.5
34	2c	124	ILE	3.5
1	2A	1084	A	3.5
1	2A	2143	C	3.5
32	1a	1037	C	3.5
32	2a	1030	C	3.5
41	2j	46	ARG	3.5
53	2y	54	ILE	3.5
1	2A	2133	G	3.5
1	1A	1151	U	3.5
32	1a	1001	A	3.5
33	1b	214	ILE	3.4
47	1p	19	ILE	3.4
1	2A	2136	C	3.4
1	2A	2168	G	3.4
34	2c	33	LEU	3.4
1	1A	1113	A	3.4
1	1A	2141	A	3.4
1	2A	1070	A	3.4
6	2G	159	VAL	3.4
1	2A	1064	C	3.4
45	2n	25	VAL	3.4
1	1A	2169	G	3.4
1	2A	1089	G	3.4
52	2u	16	GLY	3.4
12	2Q	59	ARG	3.4
41	2j	76	ASN	3.4
33	1b	229	VAL	3.4
1	1A	1129	U	3.4
1	1A	1139	G	3.3
1	2A	2152	G	3.3
1	2A	2897	U	3.3
1	2A	2124	G	3.3
50	2s	77	THR	3.3
1	2A	2146	C	3.3
33	1b	17	PHE	3.3
1	2A	2127	G	3.3
1	2A	2154	G	3.3
32	1a	1030(A)	G	3.3
32	2a	1030(C)	G	3.3
32	2a	1036	G	3.3

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Mol	Chain	Res	Type	RSRZ
40	2i	18	PHE	3.3
43	2l	18	VAL	3.3
50	1s	9	VAL	3.3
52	2u	13	ILE	3.3
1	1A	2164	C	3.2
1	2A	2803	C	3.2
44	1m	102	ARG	3.2
45	2n	3	ARG	3.2
41	2j	68	HIS	3.2
1	2A	1091	G	3.2
1	2A	2125	G	3.2
1	2A	2144	U	3.2
53	1y	95	ARG	3.2
1	2A	1509	C	3.2
1	2A	2111	C	3.2
1	2A	2175	C	3.2
33	2b	236	TYR	3.2
44	1m	4	ILE	3.2
1	2A	2150	U	3.2
1	2A	2172	U	3.2
41	2j	8	LEU	3.2
33	1b	131	PRO	3.2
1	1A	2138	G	3.2
1	2A	2113	U	3.2
1	2A	2155	G	3.2
47	1p	59	TRP	3.2
34	2c	92	ALA	3.2
47	2p	19	ILE	3.2
1	1A	2815	C	3.1
40	2i	10	ARG	3.1
41	2j	45	ARG	3.1
38	1g	16	LEU	3.1
40	1i	56	LEU	3.1
6	2G	2	PRO	3.1
41	2j	39	PRO	3.1
1	2A	1082	U	3.1
1	2A	1083	U	3.1
6	2G	20	ILE	3.1
26	14	49	PHE	3.1
41	2j	54	PHE	3.1
1	2A	2157	G	3.1
32	1a	1030(C)	G	3.1

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Mol	Chain	Res	Type	RSRZ
41	2j	7	LYS	3.1
1	1A	2161	C	3.1
34	2c	52	LEU	3.1
1	2A	2119	A	3.1
44	2m	45	VAL	3.1
30	28	46	ARG	3.1
33	2b	10	LEU	3.1
1	2A	1087	G	3.1
41	2j	93	GLY	3.1
15	2T	131	ALA	3.1
14	2S	29	PHE	3.1
52	2u	23	PRO	3.1
1	1A	2806	G	3.1
1	2A	2116	G	3.1
32	2a	1190	G	3.1
51	2t	103	GLY	3.1
52	2u	11	GLY	3.1
29	27	48	LYS	3.1
40	1i	46	ALA	3.1
41	1j	44	VAL	3.1
32	1a	1286	A	3.0
34	1c	193	TYR	3.0
26	14	54	GLY	3.0
1	2A	2805	G	3.0
40	1i	126	SER	3.0
34	2c	91	LEU	3.0
1	1A	1130	A	3.0
1	2A	2173	A	3.0
29	17	48	LYS	3.0
41	2j	42	THR	3.0
21	2Z	191	VAL	3.0
35	1d	194	LEU	3.0
26	24	63	TYR	3.0
1	2A	2793	G	3.0
32	2a	1032	G	3.0
53	2y	9	GLN	3.0
44	2m	46	LYS	3.0
45	2n	58	LYS	3.0
1	2A	2896	C	3.0
32	1a	1035	A	3.0
35	1d	3	ARG	3.0
33	2b	38	GLY	3.0

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Mol	Chain	Res	Type	RSRZ
33	1b	237	ALA	3.0
33	2b	57	PHE	3.0
50	2s	10	PHE	3.0
33	2b	44	LEU	3.0
44	2m	6	GLY	3.0
1	1A	1108	G	3.0
1	1A	1555	C	3.0
32	1a	63	C	3.0
2	2B	26	A	3.0
47	1p	6	LEU	2.9
3	1D	275	LYS	2.9
53	2y	45	PRO	2.9
53	2y	40	ILE	2.9
26	24	45	GLY	2.9
33	1b	18	GLY	2.9
34	2c	195	VAL	2.9
41	2j	72	VAL	2.9
1	1A	2816	G	2.9
1	2A	1079	C	2.9
1	2A	2129	C	2.9
32	1a	1033	G	2.9
32	2a	972	C	2.9
32	2a	1037	C	2.9
32	2a	1001	A	2.9
14	1S	3	ARG	2.9
52	2u	9	ARG	2.9
6	2G	157	ILE	2.9
35	2d	158	ILE	2.9
40	2i	6	GLY	2.9
42	2k	31	THR	2.9
1	1A	2167	C	2.9
32	2a	1038	C	2.9
41	2j	43	ARG	2.9
1	2A	2109	U	2.9
32	2a	1257	U	2.9
44	2m	106	ASN	2.9
6	2G	88	ILE	2.9
15	1T	37	GLY	2.9
14	2S	3	ARG	2.9
14	2S	35	ILE	2.9
1	1A	1072	U	2.9
1	1A	2195	A	2.9

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Mol	Chain	Res	Type	RSRZ
1	2A	2108	C	2.9
50	2s	82	GLY	2.9
34	2c	191	THR	2.9
1	1A	2137	G	2.9
6	2G	160	VAL	2.9
34	2c	207	VAL	2.9
50	2s	35	SER	2.8
26	14	51	ASP	2.8
40	2i	114	TYR	2.8
44	2m	98	VAL	2.8
1	1A	1144	A	2.8
1	2A	1096	A	2.8
1	1A	2168	C	2.8
1	2A	2137	C	2.8
23	2l	83	GLU	2.8
1	1A	1104	G	2.8
33	2b	21	ARG	2.8
8	1I	147	GLN	2.8
47	2p	82	GLN	2.8
41	2j	59	SER	2.8
35	2d	20	TYR	2.8
41	2j	67	THR	2.8
45	2n	20	ALA	2.8
12	2Q	104	PHE	2.8
33	2b	7	VAL	2.8
35	1d	178	VAL	2.8
40	2i	101	PHE	2.8
41	1j	64	GLU	2.8
32	2a	968	A	2.8
51	1t	18	GLN	2.8
1	1A	1099	C	2.8
1	1A	2165	C	2.8
32	1a	1030(B)	C	2.8
26	24	66	SER	2.8
1	1A	1221	G	2.8
1	2A	2151	G	2.8
32	2a	1124	G	2.8
33	2b	72	GLY	2.8
51	1t	13	LEU	2.8
33	2b	67	THR	2.8
14	2S	36	TYR	2.8
33	1b	230	VAL	2.8

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Mol	Chain	Res	Type	RSRZ
35	1d	149	ALA	2.8
41	2j	44	VAL	2.8
29	27	1	MET	2.8
41	2j	41	PRO	2.8
1	1A	2189	U	2.8
1	2A	1097	U	2.8
33	2b	133	LYS	2.8
1	1A	218	A	2.8
1	1A	2180	A	2.8
1	2A	229	A	2.8
1	2A	1057	A	2.8
1	2A	2176	A	2.8
32	2a	1280	A	2.8
33	1b	11	LEU	2.8
38	2g	80	VAL	2.8
40	2i	14	VAL	2.8
41	2j	70	ARG	2.8
50	2s	3	ARG	2.8
45	2n	14	PRO	2.7
20	2Y	88	LYS	2.7
6	2G	133	LEU	2.7
1	1A	1119	A	2.7
1	2A	1088	A	2.7
26	14	45	GLY	2.7
34	2c	3	ASN	2.7
41	2j	78	ASN	2.7
44	2m	100	GLY	2.7
47	1p	1	MET	2.7
1	1A	2129	C	2.7
1	2A	2140	C	2.7
26	14	59	PHE	2.7
32	1a	1027	C	2.7
32	2a	1039	C	2.7
38	2g	2	ALA	2.7
43	2l	89	ARG	2.7
52	2u	24	ARG	2.7
32	1a	630	G	2.7
32	2a	1034	G	2.7
32	2a	1271	G	2.7
32	2a	1000	U	2.7
6	2G	145	THR	2.7
21	2Z	192	ALA	2.7

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Mol	Chain	Res	Type	RSRZ
41	2j	47	PHE	2.7
33	1b	232	PRO	2.7
51	1t	74	LYS	2.7
20	2Y	5	MET	2.7
1	1A	2175	G	2.7
1	2A	1074	G	2.7
1	2A	2893	G	2.7
38	2g	32	ARG	2.7
40	1i	66	ARG	2.7
21	1Z	192	ALA	2.7
21	2Z	86	VAL	2.7
33	2b	136	VAL	2.7
32	1a	841	U	2.7
32	2a	1150	U	2.7
40	1i	125	TYR	2.7
32	1a	1492	A	2.7
41	2j	6	ILE	2.7
1	2A	2179	C	2.7
32	1a	1029	C	2.7
11	2P	15	ARG	2.7
40	2i	115	GLY	2.7
33	2b	163	PHE	2.7
43	1l	17	LYS	2.7
1	1A	2181	G	2.6
1	2A	2141	G	2.6
32	1a	1031	G	2.6
32	2a	1033	G	2.6
1	1A	2140	U	2.6
1	2A	271(K)	U	2.6
32	2a	1040	U	2.6
41	2j	96	ILE	2.6
53	2y	35	ILE	2.6
50	2s	71	LEU	2.6
41	2j	64	GLU	2.6
1	1A	2807	C	2.6
20	2Y	34	LYS	2.6
45	2n	50	LYS	2.6
51	2t	9	ASN	2.6
51	2t	74	LYS	2.6
6	1G	76	SER	2.6
7	2H	45	VAL	2.6
51	2t	11	SER	2.6

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Mol	Chain	Res	Type	RSRZ
40	2i	105	ASP	2.6
32	1a	1257	U	2.6
19	1X	95	LEU	2.6
44	2m	90	LEU	2.6
1	2A	6	A	2.6
8	1I	107	VAL	2.6
6	2G	71	THR	2.6
52	2u	17	THR	2.6
1	2A	2128	C	2.6
1	2A	2804	C	2.6
6	1G	146	TYR	2.6
41	2j	16	LEU	2.6
2	1B	1	U	2.6
3	2D	28	GLU	2.6
40	2i	2	GLU	2.6
7	2H	166	GLY	2.6
1	1A	2134	G	2.6
1	1A	2188	G	2.6
1	2A	2131	G	2.6
1	2A	2148	G	2.6
41	2j	18	ALA	2.6
6	2G	161	THR	2.6
14	2S	53	SER	2.6
33	2b	97	TRP	2.6
53	2y	64	SER	2.6
1	1A	1141	A	2.6
6	2G	52	ILE	2.6
1	2A	2139	C	2.6
1	2A	2161	C	2.6
32	2a	1149	C	2.6
40	2i	79	LEU	2.6
44	2m	59	TYR	2.6
47	1p	17	TYR	2.6
40	1i	127	LYS	2.6
45	2n	4	LYS	2.6
34	2c	2	GLY	2.6
35	1d	2	GLY	2.6
14	2S	46	VAL	2.6
1	1A	299	G	2.5
1	2A	1047	G	2.5
1	2A	2110	G	2.5
1	2A	2120	G	2.5

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Mol	Chain	Res	Type	RSRZ
32	1a	1001(A)	G	2.5
33	1b	200	ILE	2.5
33	2b	214	ILE	2.5
35	2d	5	ILE	2.5
41	2j	74	ILE	2.5
8	2I	140	LEU	2.5
40	2i	66	ARG	2.5
53	2y	66	LYS	2.5
14	2S	7	TYR	2.5
40	2i	88	TYR	2.5
53	2y	93	GLU	2.5
1	1A	2160	C	2.5
1	2A	1072	C	2.5
32	1a	1028	C	2.5
40	1i	8	GLY	2.5
33	2b	165	VAL	2.5
40	2i	21	PRO	2.5
33	2b	152	PHE	2.5
34	2c	189	ALA	2.5
35	2d	161	ASN	2.5
50	2s	79	THR	2.5
7	2H	136	ILE	2.5
44	2m	19	LEU	2.5
1	2A	1062	G	2.5
1	2A	2894	G	2.5
1	2A	2892	A	2.5
32	1a	1447	A	2.5
32	2a	1030(D)	A	2.5
47	2p	38	TYR	2.5
47	1p	46	PRO	2.5
37	1f	90	VAL	2.5
47	1p	62	VAL	2.5
1	1A	2183	C	2.5
1	1A	2196	C	2.5
1	2A	1536	C	2.5
2	2B	88	C	2.5
45	1n	13	THR	2.5
34	2c	77	ILE	2.5
32	2a	1126	U	2.5
38	2g	5	ARG	2.5
41	2j	90	LEU	2.5
52	2u	5	ASP	2.5

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Mol	Chain	Res	Type	RSRZ
1	2A	2167	U	2.5
44	2m	69	GLU	2.5
38	2g	154	TYR	2.5
46	1o	89	GLY	2.5
32	2a	1035	A	2.5
45	2n	33	VAL	2.5
33	2b	225	ALA	2.5
42	2k	15	ALA	2.5
33	2b	132	LYS	2.5
42	2k	117	ASN	2.5
53	2y	4	ASN	2.5
35	2d	146	ILE	2.5
50	2s	4	SER	2.5
1	1A	2814	C	2.5
32	2a	1128	C	2.5
1	1A	2166	U	2.5
32	2a	1281	U	2.5
8	1I	84	GLY	2.5
40	2i	49	PRO	2.5
40	2i	92	TYR	2.5
26	24	50	VAL	2.5
40	2i	86	VAL	2.5
38	2g	7	ALA	2.5
3	2D	276	LYS	2.4
1	2A	2062	A	2.4
41	1j	43	ARG	2.4
1	2A	2149	G	2.4
14	2S	34	HIS	2.4
33	1b	19	HIS	2.4
42	2k	36	ASP	2.4
1	2A	1080	C	2.4
1	2A	2105	C	2.4
1	2A	2183	C	2.4
21	2Z	1	MET	2.4
32	2a	1125	U	2.4
33	2b	131	PRO	2.4
33	1b	236	TYR	2.4
6	2G	149	VAL	2.4
40	2i	11	LYS	2.4
42	2k	13	GLN	2.4
47	1p	76	GLN	2.4
33	1b	13	ALA	2.4

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Mol	Chain	Res	Type	RSRZ
51	1t	8	ARG	2.4
34	2c	94	LEU	2.4
36	2e	109	ILE	2.4
1	1A	1092	A	2.4
1	2A	1077	A	2.4
1	2A	1095	A	2.4
50	2s	34	TRP	2.4
38	1g	8	GLU	2.4
1	1A	2155	G	2.4
1	1A	2163	G	2.4
1	2A	2121	G	2.4
1	1A	2133	C	2.4
1	2A	645	C	2.4
33	1b	165	VAL	2.4
1	1A	1140	U	2.4
1	1A	2131	U	2.4
1	2A	614(A)	U	2.4
40	2i	4	TYR	2.4
8	2I	55	ALA	2.4
44	2m	110	ARG	2.4
45	2n	5	ALA	2.4
7	2H	71	LEU	2.4
7	2H	87	LEU	2.4
14	2S	47	THR	2.4
33	2b	11	LEU	2.4
8	2I	10	GLU	2.4
34	2c	18	TRP	2.4
32	1a	196	A	2.4
32	2a	1183	A	2.4
47	2p	10	GLY	2.4
26	14	60	GLN	2.4
34	1c	99	VAL	2.4
1	1A	2171	G	2.4
1	2A	1071	G	2.4
1	2A	2318	G	2.4
32	1a	1021	G	2.4
40	2i	36	TYR	2.4
42	2k	75	TYR	2.4
41	2j	88	LEU	2.4
44	2m	66	LEU	2.4
1	1A	34	C	2.4
32	2a	1025	U	2.4

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Mol	Chain	Res	Type	RSRZ
34	2c	15	THR	2.4
45	2n	13	THR	2.4
32	2a	1028	C	2.4
32	2a	1066	C	2.4
34	2c	7	PRO	2.4
43	1l	63	GLY	2.4
26	14	47	GLN	2.4
1	1A	2191	A	2.4
1	2A	2126	A	2.4
1	2A	2171	A	2.4
33	1b	34	ALA	2.4
33	2b	17	PHE	2.4
35	1d	188	LEU	2.3
53	2y	53	THR	2.3
1	1A	2170	G	2.3
1	1A	2172	U	2.3
1	2A	652(C)	G	2.3
1	2A	1081	U	2.3
32	1a	1024	G	2.3
34	1c	62	ASP	2.3
44	2m	113	PRO	2.3
5	1F	208	GLY	2.3
6	2G	127	GLY	2.3
34	1c	2	GLY	2.3
41	2j	10	GLY	2.3
40	1i	42	ARG	2.3
40	2i	83	ARG	2.3
47	1p	81	ARG	2.3
40	2i	108	VAL	2.3
8	2l	38	LEU	2.3
34	1c	52	LEU	2.3
34	2c	163	ALA	2.3
45	2n	39	LEU	2.3
26	14	63	TYR	2.3
34	2c	48	TYR	2.3
35	1d	138	TYR	2.3
1	1A	2192	A	2.3
1	2A	2158	A	2.3
39	2h	3	THR	2.3
34	2c	90	GLU	2.3
32	2a	1020	U	2.3
25	23	2	PRO	2.3

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Mol	Chain	Res	Type	RSRZ
47	2p	48	TRP	2.3
32	1a	380	G	2.3
32	1a	1003	G	2.3
26	24	54	GLY	2.3
44	2m	24	GLY	2.3
52	2u	10	ARG	2.3
34	2c	68	VAL	2.3
40	2i	17	VAL	2.3
14	2S	48	LEU	2.3
33	2b	158	LEU	2.3
40	2i	59	PHE	2.3
34	2c	65	ALA	2.3
53	2y	52	ALA	2.3
44	1m	116	THR	2.3
45	2n	21	TYR	2.3
26	14	69	LYS	2.3
26	24	28	LYS	2.3
1	1A	2193	A	2.3
32	2a	1157	A	2.3
40	2i	107	ARG	2.3
33	1b	14	GLY	2.3
7	2H	52	VAL	2.3
21	2Z	90	VAL	2.3
43	1l	18	VAL	2.3
33	2b	69	LEU	2.3
45	2n	36	PHE	2.3
51	2t	13	LEU	2.3
34	2c	152	ILE	2.3
35	2d	164	ALA	2.3
44	2m	72	ALA	2.3
1	1A	2177	G	2.3
1	2A	1056	G	2.3
1	2A	2123	G	2.3
32	2a	973	G	2.3
4	2E	1	MET	2.3
41	2j	48	THR	2.3
53	1y	2	THR	2.3
41	1j	76	ASN	2.3
41	2j	30	SER	2.3
42	2k	126	ARG	2.3
46	2o	88	ARG	2.3
48	1q	68	ARG	2.3

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Mol	Chain	Res	Type	RSRZ
1	1A	934	A	2.3
1	2A	1445	A	2.3
1	2A	2117	A	2.3
32	2a	965	A	2.3
34	2c	159	GLY	2.3
42	2k	118	GLY	2.3
50	2s	26	GLY	2.3
8	2I	92	VAL	2.3
33	2b	15	VAL	2.3
34	1c	47	LEU	2.3
1	1A	271	U	2.2
1	1A	2152	U	2.2
38	2g	128	ALA	2.2
41	2j	82	ILE	2.2
1	2A	1092	C	2.2
2	2B	4	C	2.2
1	1A	1218	G	2.2
1	1A	2147	G	2.2
1	1A	2182	G	2.2
1	1A	2902	G	2.2
1	2A	2165	G	2.2
1	2A	2319	G	2.2
32	1a	1032	G	2.2
33	1b	37	ASN	2.2
7	2H	128	PRO	2.2
22	20	9	SER	2.2
24	12	70	GLN	2.2
51	2t	102	GLY	2.2
6	2G	29	TRP	2.2
41	2j	49	VAL	2.2
51	1t	10	LEU	2.2
1	2A	1067	A	2.2
1	2A	2114	A	2.2
32	1a	1004	A	2.2
33	1b	39	ILE	2.2
7	2H	41	MET	2.2
1	1A	2135	U	2.2
33	2b	190	THR	2.2
41	1j	100	THR	2.2
12	2Q	60	ARG	2.2
15	1T	129	ARG	2.2
1	1A	155	C	2.2

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Mol	Chain	Res	Type	RSRZ
26	24	46	GLN	2.2
32	2a	1029	C	2.2
32	2a	1114	C	2.2
41	1j	31	GLY	2.2
41	2j	58	ASP	2.2
52	2u	4	GLY	2.2
53	2y	92	GLY	2.2
34	1c	87	LEU	2.2
40	1i	78	LYS	2.2
41	1j	80	LYS	2.2
45	2n	17	LYS	2.2
8	2I	79	ILE	2.2
33	2b	162	ILE	2.2
46	1o	3	ILE	2.2
34	2c	129	ALA	2.2
6	1G	48	GLU	2.2
1	2A	1073	A	2.2
2	2B	25	A	2.2
44	2m	43	THR	2.2
1	2A	1026	U	2.2
6	2G	136	ARG	2.2
26	14	48	ARG	2.2
33	2b	144	ARG	2.2
39	1h	84	ARG	2.2
53	2y	83	ARG	2.2
41	2j	53	PRO	2.2
6	1G	182	LYS	2.2
14	2S	31	SER	2.2
21	2Z	166	SER	2.2
33	1b	187	LEU	2.2
34	1c	45	LYS	2.2
45	2n	6	LEU	2.2
51	2t	7	LYS	2.2
7	2H	115	VAL	2.2
33	2b	229	VAL	2.2
50	2s	60	VAL	2.2
53	2y	3	MET	2.2
1	2A	1049	C	2.2
32	2a	1325	C	2.2
34	2c	10	PHE	2.2
34	2c	57	ILE	2.2
35	2d	70	ILE	2.2

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Mol	Chain	Res	Type	RSRZ
33	2b	123	ALA	2.2
34	2c	187	ALA	2.2
41	2j	32	ALA	2.2
1	1A	1102	G	2.2
1	1A	2179	G	2.2
1	2A	1044	G	2.2
8	1I	117	GLU	2.2
31	29	28	GLU	2.2
40	1i	7	THR	2.2
47	1p	44	THR	2.2
45	2n	29	ARG	2.2
1	1A	2084	A	2.2
7	2H	21	PRO	2.2
1	1A	1143	U	2.2
1	1A	2194	U	2.2
20	2Y	4	LYS	2.2
32	1a	1025	U	2.2
32	1a	1532	U	2.2
48	2q	93	GLN	2.2
35	1d	169	LYS	2.2
44	2m	65	LYS	2.2
34	1c	94	LEU	2.2
48	1q	98	LEU	2.2
20	1Y	1	MET	2.2
40	1i	75	ASP	2.2
4	2E	72	VAL	2.2
33	2b	233	SER	2.2
33	2b	172	ILE	2.2
34	1c	64	VAL	2.2
42	1k	14	VAL	2.2
4	2E	204	ALA	2.1
28	26	42	TRP	2.1
33	1b	97	TRP	2.1
34	2c	53	ALA	2.1
16	2U	89	GLU	2.1
1	1A	2130	C	2.1
1	2A	1109	C	2.1
2	2B	12	C	2.1
7	1H	6	ARG	2.1
19	2X	68	ARG	2.1
32	2a	1027	C	2.1
32	2a	1116	C	2.1

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Mol	Chain	Res	Type	RSRZ
34	2c	95	THR	2.1
35	1d	76	ARG	2.1
50	2s	29	ARG	2.1
52	2u	15	ARG	2.1
1	2A	1171	G	2.1
2	2B	118	G	2.1
40	2i	123	PRO	2.1
34	1c	28	GLN	2.1
41	1j	78	ASN	2.1
40	1i	5	TYR	2.1
40	2i	62	TYR	2.1
1	2A	2170	A	2.1
32	2a	1447	A	2.1
40	2i	30	GLY	2.1
44	1m	112	GLY	2.1
32	2a	992	U	2.1
33	1b	15	VAL	2.1
33	2b	200	ILE	2.1
34	2c	66	VAL	2.1
41	2j	62	HIS	2.1
33	1b	122	PHE	2.1
8	1I	108	THR	2.1
33	1b	125	PRO	2.1
44	1m	113	PRO	2.1
47	1p	43	LYS	2.1
50	2s	76	PRO	2.1
8	2I	54	GLN	2.1
32	2a	1119	C	2.1
26	14	67	TYR	2.1
26	24	67	TYR	2.1
44	2m	48	LEU	2.1
50	2s	80	TYR	2.1
1	1A	1114	G	2.1
1	1A	1145	G	2.1
1	1A	2227	G	2.1
1	2A	2184	G	2.1
6	2G	77	ILE	2.1
32	1a	181	G	2.1
32	1a	1023	G	2.1
32	2a	993	G	2.1
32	2a	1026	G	2.1
33	2b	93	VAL	2.1

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Mol	Chain	Res	Type	RSRZ
33	2b	208	ILE	2.1
38	2g	9	VAL	2.1
39	1h	134	ILE	2.1
40	2i	53	VAL	2.1
45	2n	7	ILE	2.1
35	1d	110	PHE	2.1
1	1A	572	A	2.1
1	1A	2641	A	2.1
4	1E	163	GLU	2.1
32	1a	90	U	2.1
34	2c	60	ALA	2.1
41	1j	32	ALA	2.1
7	2H	95	ARG	2.1
33	1b	24	TRP	2.1
33	2b	226	ARG	2.1
44	2m	3	ARG	2.1
53	2y	37	PRO	2.1
34	2c	170	GLN	2.1
40	1i	19	LEU	2.1
41	2j	85	LEU	2.1
11	2P	116	GLY	2.1
14	2S	90	GLY	2.1
33	1b	228	GLY	2.1
6	2G	39	ILE	2.1
21	2Z	197	ILE	2.1
32	1a	163	C	2.1
32	1a	1038	C	2.1
32	2a	1063	C	2.1
32	2a	1277	C	2.1
34	1c	86	VAL	2.1
35	1d	170	VAL	2.1
36	2e	115	VAL	2.1
33	2b	122	PHE	2.1
21	2Z	187	ALA	2.1
38	2g	8	GLU	2.1
40	2i	94	ALA	2.1
47	1p	25	ARG	2.1
51	2t	97	ALA	2.1
1	1A	1101	G	2.1
1	1A	2190	G	2.1
1	2A	2166	G	2.1
32	2a	1127	G	2.1

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Mol	Chain	Res	Type	RSRZ
33	2b	22	LYS	2.1
21	1Z	1	MET	2.1
38	2g	16	LEU	2.1
10	2O	74	GLY	2.1
50	2s	68	GLY	2.1
51	1t	69	GLY	2.1
44	1m	59	TYR	2.1
47	2p	39	TYR	2.1
53	2y	39	ILE	2.1
34	1c	68	VAL	2.1
34	2c	173	VAL	2.1
41	2j	24	VAL	2.1
33	2b	70	PHE	2.1
35	2d	110	PHE	2.1
6	2G	33	ARG	2.0
33	1b	130	ARG	2.0
40	2i	12	GLU	2.0
40	2i	93	ARG	2.0
53	2y	95	ARG	2.0
36	2e	104	ALA	2.0
1	1A	2151	C	2.0
1	2A	1104	C	2.0
43	2l	47	LYS	2.0
50	2s	28	LYS	2.0
22	20	43	THR	2.0
26	24	27	THR	2.0
41	2j	92	THR	2.0
50	2s	48	THR	2.0
6	2G	17	PRO	2.0
33	2b	101	MET	2.0
47	1p	41	PRO	2.0
50	2s	59	PRO	2.0
1	1A	288	U	2.0
1	1A	1107	U	2.0
34	2c	87	LEU	2.0
35	2d	160	GLN	2.0
35	2d	162	LEU	2.0
1	1A	2142	G	2.0
1	2A	2156	G	2.0
2	2B	110	G	2.0
32	2a	963	G	2.0
32	2a	1178	G	2.0

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Mol	Chain	Res	Type	RSRZ
32	2a	1184	G	2.0
32	2a	1224	G	2.0
32	2a	1286	A	2.0
11	2P	109	GLY	2.0
26	14	64	GLY	2.0
26	24	15	ILE	2.0
33	2b	39	ILE	2.0
33	2b	99	GLY	2.0
33	2b	201	ILE	2.0
33	2b	223	ILE	2.0
36	2e	114	GLY	2.0
44	1m	100	GLY	2.0
46	1o	87	ILE	2.0
6	2G	12	TYR	2.0
8	2I	107	VAL	2.0
41	2j	94	VAL	2.0
41	2j	9	ARG	2.0
33	1b	12	GLU	2.0
33	2b	207	ALA	2.0
34	2c	160	ALA	2.0
38	1g	156	TRP	2.0
41	2j	15	THR	2.0
1	1A	936	C	2.0
1	2A	2163	C	2.0
14	2S	58	LEU	2.0
32	2a	1019	C	2.0
34	2c	175	LEU	2.0
40	2i	117	HIS	2.0
1	2A	1090	U	2.0
32	1a	1446	U	2.0
40	2i	29	ASN	2.0
44	2m	9	ILE	2.0
46	2o	86	GLY	2.0
49	2r	57	GLY	2.0
51	1t	101	GLY	2.0
6	2G	109	VAL	2.0
6	2G	181	ARG	2.0
18	2W	92	ARG	2.0
26	24	35	VAL	2.0
50	2s	11	VAL	2.0
50	2s	36	ARG	2.0
34	1c	201	TYR	2.0

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

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
32	2MG	2a	1207	24/25	0.82	0.12	76,86,91,102	0
1	5MU	1A	1937	21/22	0.83	0.12	67,74,83,94	0
1	5MU	2A	1915	21/22	0.85	0.11	76,82,88,101	0
1	PSU	2A	1917	20/21	0.86	0.10	71,78,90,90	0
32	PSU	2a	516	20/21	0.87	0.11	71,76,80,84	0
43	0TD	1l	92	10/11	0.88	0.13	50,54,59,76	0
1	PSU	2A	1911	20/21	0.89	0.09	56,70,76,78	0
43	0TD	2l	92	10/11	0.89	0.14	60,65,71,95	0
1	PSU	1A	1939	20/21	0.90	0.09	62,68,77,77	0
32	M2G	2a	966	25/26	0.90	0.16	57,67,81,92	0
32	5MC	2a	967	21/22	0.91	0.16	63,68,77,88	0
32	2MG	1a	1207	24/25	0.92	0.10	56,66,69,71	0
1	4OC	2A	1920	21/23	0.93	0.10	61,65,72,73	0
32	7MG	2a	527	24/25	0.93	0.11	61,67,73,74	0
32	5MC	2a	1400	21/22	0.94	0.13	65,70,73,74	0
32	4OC	2a	1402	22/23	0.94	0.11	53,63,68,71	0
1	PSU	1A	1933	20/21	0.94	0.08	55,62,65,66	0
32	5MC	1a	967	21/22	0.95	0.11	53,58,65,71	0
32	PSU	1a	516	20/21	0.95	0.08	56,60,64,65	0
32	5MC	2a	1404	21/22	0.95	0.09	51,60,63,66	0
32	5MC	2a	1407	21/22	0.95	0.10	50,60,64,68	0
32	MA6	2a	1518	24/25	0.95	0.11	51,61,66,67	0
32	7MG	1a	527	24/25	0.95	0.09	42,51,54,59	0
32	UR3	1a	1498	21/22	0.96	0.08	43,46,52,60	0
32	MA6	1a	1519	24/25	0.96	0.09	37,43,46,49	0
32	4OC	1a	1402	22/23	0.96	0.09	42,47,55,56	0
32	UR3	2a	1498	21/22	0.96	0.08	52,58,63,66	0
1	5MC	2A	1942	21/22	0.96	0.08	36,48,53,54	0
32	MA6	2a	1519	24/25	0.96	0.10	51,60,64,67	0
32	5MC	1a	1407	21/22	0.96	0.08	36,45,49,56	0
1	5MC	1A	1964	21/22	0.97	0.06	26,32,38,47	0
32	MA6	1a	1518	24/25	0.97	0.09	34,41,46,51	0
1	5MU	2A	1939	21/22	0.97	0.08	29,36,41,43	0
32	5MC	1a	1400	21/22	0.97	0.08	40,45,49,51	0
1	5MC	2A	1962	21/22	0.97	0.08	33,43,48,58	0
1	2MA	2A	2503	23/24	0.97	0.08	24,30,35,37	0
1	2MU	2A	2552	21/23	0.97	0.08	30,36,39,41	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	0.97	0.08	51,53,58,61	0
32	5MC	1a	1404	21/22	0.97	0.08	35,44,46,49	0
1	4OC	1A	1942	21/23	0.97	0.09	39,54,59,60	0
1	OMG	1A	2263	24/25	0.98	0.06	15,21,23,26	0
1	2MA	1A	2515	23/24	0.98	0.07	16,20,24,31	0
1	PSU	2A	2605	20/21	0.98	0.07	29,35,39,44	0
1	2MU	1A	2564	21/23	0.98	0.06	20,26,28,29	0
1	PSU	1A	2617	20/21	0.98	0.07	18,22,28,28	0
1	5MU	1A	1961	21/22	0.98	0.07	18,24,27,32	0
1	5MC	1A	1984	21/22	0.98	0.07	25,33,37,45	0
1	OMG	2A	2251	24/25	0.98	0.07	32,36,38,39	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1a	1851	1/1	0.36	0.40	94,94,94,94	0
54	MG	1a	1752	1/1	0.47	0.31	71,71,71,71	0
54	MG	2A	3318	1/1	0.54	0.21	78,78,78,78	0
54	MG	1a	1846	1/1	0.59	0.23	74,74,74,74	0
54	MG	2A	3466	1/1	0.59	0.22	68,68,68,68	0
54	MG	1A	3957	1/1	0.62	0.21	79,79,79,79	0
54	MG	2A	3219	1/1	0.63	0.17	74,74,74,74	0
54	MG	2A	3685	1/1	0.64	0.19	75,75,75,75	0
54	MG	1A	3082	1/1	0.65	0.14	55,55,55,55	0
54	MG	2A	3197	1/1	0.65	0.16	73,73,73,73	0
54	MG	2B	3015	1/1	0.65	0.13	74,74,74,74	0
54	MG	2A	3586	1/1	0.66	0.29	84,84,84,84	0
54	MG	2A	3676	1/1	0.67	0.26	66,66,66,66	0
54	MG	2A	3171	1/1	0.68	0.15	58,58,58,58	0
54	MG	1A	3434	1/1	0.68	0.16	44,44,44,44	0
54	MG	1A	3721	1/1	0.68	0.12	25,25,25,25	0
54	MG	2A	3648	1/1	0.69	0.26	73,73,73,73	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	2A	3215	1/1	0.69	0.55	73,73,73,73	0
54	MG	2A	3548	1/1	0.70	0.18	54,54,54,54	0
54	MG	2B	3003	1/1	0.70	0.26	74,74,74,74	0
54	MG	1A	3937	1/1	0.70	0.14	74,74,74,74	0
54	MG	2A	3167	1/1	0.71	0.22	74,74,74,74	0
54	MG	1a	1828	1/1	0.71	0.18	62,62,62,62	0
54	MG	1a	1840	1/1	0.71	0.16	45,45,45,45	0
54	MG	2A	3355	1/1	0.71	0.18	46,46,46,46	0
54	MG	1A	3941	1/1	0.72	0.15	68,68,68,68	0
54	MG	1a	1817	1/1	0.72	0.23	57,57,57,57	0
54	MG	1A	3191	1/1	0.72	0.19	51,51,51,51	0
54	MG	1a	1704	1/1	0.72	0.23	77,77,77,77	0
54	MG	2A	3370	1/1	0.72	0.23	70,70,70,70	0
54	MG	2A	3454	1/1	0.72	0.36	70,70,70,70	0
54	MG	1a	1845	1/1	0.72	0.19	78,78,78,78	0
54	MG	1a	1754	1/1	0.73	0.24	68,68,68,68	0
54	MG	2A	3251	1/1	0.73	0.25	60,60,60,60	0
54	MG	2a	1700	1/1	0.73	0.19	48,48,48,48	0
54	MG	2A	3388	1/1	0.74	0.21	51,51,51,51	0
54	MG	2A	3413	1/1	0.74	0.28	63,63,63,63	0
54	MG	1a	1751	1/1	0.74	0.17	69,69,69,69	0
54	MG	2A	3338	1/1	0.74	0.17	53,53,53,53	0
54	MG	1A	3934	1/1	0.74	0.24	50,50,50,50	0
54	MG	2I	3001	1/1	0.74	0.15	71,71,71,71	0
54	MG	1A	3942	1/1	0.74	0.23	73,73,73,73	0
54	MG	1A	3875	1/1	0.75	0.18	49,49,49,49	0
54	MG	1I	3002	1/1	0.75	0.10	72,72,72,72	0
54	MG	1A	3327	1/1	0.75	0.18	33,33,33,33	0
54	MG	1A	3602	1/1	0.75	0.17	54,54,54,54	0
54	MG	2B	3014	1/1	0.75	0.12	71,71,71,71	0
54	MG	2A	3467	1/1	0.75	0.29	79,79,79,79	0
54	MG	1A	3364	1/1	0.75	0.08	13,13,13,13	0
54	MG	1A	3837	1/1	0.75	0.20	56,56,56,56	0
54	MG	2a	1719	1/1	0.75	0.28	67,67,67,67	0
54	MG	2a	1729	1/1	0.75	0.18	64,64,64,64	0
54	MG	1a	1700	1/1	0.76	0.31	65,65,65,65	0
54	MG	2G	3003	1/1	0.76	0.15	79,79,79,79	0
54	MG	1A	3575	1/1	0.76	0.19	65,65,65,65	0
54	MG	2A	3493	1/1	0.76	0.17	55,55,55,55	0
54	MG	1a	1737	1/1	0.76	0.10	62,62,62,62	0
54	MG	2a	1725	1/1	0.76	0.20	64,64,64,64	0
54	MG	1a	1755	1/1	0.76	0.17	68,68,68,68	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	2j	8001	1/1	0.76	0.12	82,82,82,82	0
58	ARG	1F	314	12/12	0.76	0.17	47,65,78,79	0
54	MG	1A	3404	1/1	0.77	0.22	65,65,65,65	0
54	MG	2A	3398	1/1	0.77	0.15	55,55,55,55	0
54	MG	2A	3198	1/1	0.77	0.26	60,60,60,60	0
54	MG	2A	3426	1/1	0.77	0.16	58,58,58,58	0
54	MG	1A	3794	1/1	0.77	0.14	53,53,53,53	0
54	MG	1a	1766	1/1	0.77	0.29	67,67,67,67	0
54	MG	1f	3001	1/1	0.77	0.23	64,64,64,64	0
54	MG	1A	3597	1/1	0.77	0.27	62,62,62,62	0
54	MG	2A	3142	1/1	0.77	0.16	68,68,68,68	0
54	MG	2A	3567	1/1	0.77	0.15	40,40,40,40	0
54	MG	2A	3579	1/1	0.77	0.36	65,65,65,65	0
54	MG	1A	3379	1/1	0.77	0.26	73,73,73,73	0
54	MG	1A	3921	1/1	0.77	0.22	58,58,58,58	0
54	MG	14	502	1/1	0.78	0.15	72,72,72,72	0
54	MG	1a	1608	1/1	0.78	0.12	63,63,63,63	0
54	MG	2A	3385	1/1	0.78	0.15	47,47,47,47	0
54	MG	2A	3115	1/1	0.78	0.22	63,63,63,63	0
54	MG	2B	3002	1/1	0.78	0.19	71,71,71,71	0
54	MG	1a	1686	1/1	0.78	0.27	61,61,61,61	0
54	MG	1a	1783	1/1	0.78	0.23	64,64,64,64	0
54	MG	1a	1807	1/1	0.78	0.30	67,67,67,67	0
54	MG	1a	1810	1/1	0.78	0.16	63,63,63,63	0
54	MG	1A	3499	1/1	0.78	0.18	50,50,50,50	0
54	MG	1a	1701	1/1	0.78	0.12	71,71,71,71	0
54	MG	2a	1703	1/1	0.78	0.28	61,61,61,61	0
54	MG	2A	3489	1/1	0.78	0.23	69,69,69,69	0
54	MG	1A	3501	1/1	0.78	0.28	59,59,59,59	0
54	MG	1A	3730	1/1	0.78	0.13	26,26,26,26	0
54	MG	1A	3908	1/1	0.78	0.13	52,52,52,52	0
54	MG	1A	3748	1/1	0.78	0.15	68,68,68,68	0
54	MG	2A	3673	1/1	0.79	0.25	68,68,68,68	0
54	MG	2A	3675	1/1	0.79	0.12	73,73,73,73	0
54	MG	1a	1767	1/1	0.79	0.17	58,58,58,58	0
54	MG	2A	3425	1/1	0.79	0.23	68,68,68,68	0
54	MG	1a	1778	1/1	0.79	0.24	60,60,60,60	0
54	MG	2A	3450	1/1	0.79	0.13	55,55,55,55	0
54	MG	1A	3649	1/1	0.79	0.15	58,58,58,58	0
54	MG	1a	1802	1/1	0.79	0.38	62,62,62,62	0
54	MG	1a	1803	1/1	0.79	0.26	64,64,64,64	0
54	MG	1A	3817	1/1	0.79	0.16	65,65,65,65	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1A	3577	1/1	0.79	0.15	26,26,26,26	0
54	MG	2A	3506	1/1	0.79	0.13	63,63,63,63	0
54	MG	1A	3567	1/1	0.79	0.22	62,62,62,62	0
54	MG	2A	3170	1/1	0.79	0.13	60,60,60,60	0
54	MG	1A	3887	1/1	0.79	0.10	69,69,69,69	0
54	MG	2A	3393	1/1	0.79	0.19	55,55,55,55	0
54	MG	1A	3177	1/1	0.79	0.14	51,51,51,51	0
54	MG	2A	3335	1/1	0.80	0.13	56,56,56,56	0
54	MG	2A	3451	1/1	0.80	0.21	49,49,49,49	0
54	MG	1A	3969	1/1	0.80	0.20	45,45,45,45	0
54	MG	1a	1835	1/1	0.80	0.15	67,67,67,67	0
54	MG	2B	3001	1/1	0.80	0.13	68,68,68,68	0
54	MG	1D	302	1/1	0.80	0.20	42,42,42,42	0
54	MG	1a	1843	1/1	0.80	0.17	78,78,78,78	0
54	MG	2B	3007	1/1	0.80	0.13	71,71,71,71	0
54	MG	1A	3138	1/1	0.80	0.26	59,59,59,59	0
54	MG	1a	1702	1/1	0.80	0.15	52,52,52,52	0
54	MG	1a	1759	1/1	0.80	0.20	64,64,64,64	0
54	MG	2A	3551	1/1	0.80	0.18	61,61,61,61	0
54	MG	20	101	1/1	0.80	0.24	75,75,75,75	0
54	MG	25	502	1/1	0.80	0.18	59,59,59,59	0
54	MG	2a	1664	1/1	0.80	0.15	61,61,61,61	0
54	MG	1a	1808	1/1	0.80	0.21	74,74,74,74	0
54	MG	2A	3569	1/1	0.80	0.21	51,51,51,51	0
54	MG	1A	3422	1/1	0.80	0.12	41,41,41,41	0
54	MG	1a	1681	1/1	0.80	0.13	60,60,60,60	0
54	MG	2A	3602	1/1	0.80	0.20	46,46,46,46	0
54	MG	2a	1742	1/1	0.80	0.34	65,65,65,65	0
54	MG	2A	3646	1/1	0.80	0.13	60,60,60,60	0
54	MG	2A	3429	1/1	0.80	0.14	59,59,59,59	0
54	MG	2A	3386	1/1	0.81	0.15	68,68,68,68	0
54	MG	1A	3745	1/1	0.81	0.22	60,60,60,60	0
54	MG	2A	3534	1/1	0.81	0.25	65,65,65,65	0
54	MG	1A	3935	1/1	0.81	0.13	55,55,55,55	0
54	MG	1a	1662	1/1	0.81	0.22	56,56,56,56	0
54	MG	2A	3555	1/1	0.81	0.16	61,61,61,61	0
54	MG	1h	3002	1/1	0.81	0.16	64,64,64,64	0
54	MG	2A	3419	1/1	0.81	0.23	59,59,59,59	0
54	MG	2A	3242	1/1	0.81	0.13	63,63,63,63	0
54	MG	1a	1731	1/1	0.81	0.27	56,56,56,56	0
54	MG	2A	3274	1/1	0.81	0.15	53,53,53,53	0
54	MG	2a	1672	1/1	0.81	0.33	62,62,62,62	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	2a	1687	1/1	0.81	0.29	67,67,67,67	0
54	MG	1a	1773	1/1	0.81	0.20	61,61,61,61	0
54	MG	1a	1674	1/1	0.81	0.18	65,65,65,65	0
54	MG	2A	3662	1/1	0.81	0.16	56,56,56,56	0
54	MG	2A	3672	1/1	0.81	0.14	55,55,55,55	0
54	MG	2a	1726	1/1	0.81	0.33	62,62,62,62	0
54	MG	1A	3131	1/1	0.81	0.11	48,48,48,48	0
54	MG	2a	1736	1/1	0.81	0.31	61,61,61,61	0
54	MG	1A	3411	1/1	0.81	0.18	46,46,46,46	0
54	MG	1F	311	1/1	0.81	0.19	45,45,45,45	0
54	MG	2A	3193	1/1	0.81	0.13	47,47,47,47	0
54	MG	2A	3108	1/1	0.82	0.19	62,62,62,62	0
54	MG	2A	3288	1/1	0.82	0.20	49,49,49,49	0
54	MG	1a	1830	1/1	0.82	0.35	66,66,66,66	0
54	MG	1A	3618	1/1	0.82	0.21	42,42,42,42	0
54	MG	2A	3605	1/1	0.82	0.15	62,62,62,62	0
54	MG	2A	3619	1/1	0.82	0.21	66,66,66,66	0
54	MG	2A	3635	1/1	0.82	0.23	64,64,64,64	0
54	MG	2a	1669	1/1	0.82	0.39	63,63,63,63	0
54	MG	1A	3398	1/1	0.82	0.15	26,26,26,26	0
54	MG	1G	3002	1/1	0.82	0.10	66,66,66,66	0
54	MG	1A	3473	1/1	0.82	0.14	63,63,63,63	0
54	MG	1A	3796	1/1	0.82	0.15	45,45,45,45	0
54	MG	1a	1617	1/1	0.82	0.13	58,58,58,58	0
54	MG	2A	3504	1/1	0.82	0.12	60,60,60,60	0
54	MG	1A	3256	1/1	0.82	0.24	51,51,51,51	0
54	MG	2A	3202	1/1	0.82	0.20	62,62,62,62	0
54	MG	1f	3002	1/1	0.82	0.14	53,53,53,53	0
54	MG	1a	1772	1/1	0.82	0.25	57,57,57,57	0
54	MG	1A	3832	1/1	0.82	0.21	57,57,57,57	0
57	MPD	2B	3020	8/8	0.82	0.23	61,66,69,79	0
54	MG	1y	3004	1/1	0.82	0.19	76,76,76,76	0
54	MG	2A	3503	1/1	0.83	0.23	54,54,54,54	0
54	MG	1A	3764	1/1	0.83	0.13	44,44,44,44	0
54	MG	1a	1634	1/1	0.83	0.26	69,69,69,69	0
54	MG	2A	3515	1/1	0.83	0.15	54,54,54,54	0
54	MG	1a	1637	1/1	0.83	0.23	67,67,67,67	0
54	MG	2A	3177	1/1	0.83	0.17	56,56,56,56	0
54	MG	1A	3906	1/1	0.83	0.17	55,55,55,55	0
54	MG	2D	301	1/1	0.83	0.21	56,56,56,56	0
54	MG	2A	3195	1/1	0.83	0.19	54,54,54,54	0
54	MG	2A	3389	1/1	0.83	0.17	47,47,47,47	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1a	1790	1/1	0.83	0.17	60,60,60,60	0
54	MG	2l	101	1/1	0.83	0.12	67,67,67,67	0
54	MG	1a	1665	1/1	0.83	0.17	59,59,59,59	0
54	MG	2a	1603	1/1	0.83	0.19	57,57,57,57	0
54	MG	2a	1641	1/1	0.83	0.40	66,66,66,66	0
54	MG	1A	3786	1/1	0.83	0.17	40,40,40,40	0
54	MG	1a	1680	1/1	0.83	0.18	70,70,70,70	0
54	MG	1A	3124	1/1	0.83	0.11	40,40,40,40	0
54	MG	2a	1677	1/1	0.83	0.20	53,53,53,53	0
54	MG	1R	203	1/1	0.83	0.15	34,34,34,34	0
54	MG	2a	1689	1/1	0.83	0.27	62,62,62,62	0
54	MG	2a	1693	1/1	0.83	0.21	55,55,55,55	0
54	MG	2a	1699	1/1	0.83	0.24	71,71,71,71	0
54	MG	2A	3633	1/1	0.83	0.11	43,43,43,43	0
54	MG	1A	3950	1/1	0.83	0.13	80,80,80,80	0
54	MG	2A	3252	1/1	0.83	0.23	61,61,61,61	0
54	MG	2A	3647	1/1	0.83	0.23	57,57,57,57	0
54	MG	2A	3261	1/1	0.83	0.16	43,43,43,43	0
54	MG	2A	3656	1/1	0.83	0.20	48,48,48,48	0
54	MG	1a	1822	1/1	0.83	0.28	60,60,60,60	0
54	MG	1A	3457	1/1	0.83	0.12	64,64,64,64	0
54	MG	1a	1768	1/1	0.83	0.19	69,69,69,69	0
57	MPD	2A	3711	8/8	0.83	0.25	48,60,64,64	0
54	MG	2A	3332	1/1	0.83	0.10	65,65,65,65	0
54	MG	2A	3150	1/1	0.83	0.20	62,62,62,62	0
54	MG	1A	3485	1/1	0.84	0.10	47,47,47,47	0
54	MG	2B	3005	1/1	0.84	0.17	61,61,61,61	0
54	MG	2A	3545	1/1	0.84	0.21	53,53,53,53	0
54	MG	2B	3008	1/1	0.84	0.16	66,66,66,66	0
54	MG	1A	3508	1/1	0.84	0.12	29,29,29,29	0
54	MG	1S	8001	1/1	0.84	0.17	62,62,62,62	0
54	MG	10	105	1/1	0.84	0.14	59,59,59,59	0
54	MG	1A	3905	1/1	0.84	0.14	53,53,53,53	0
54	MG	1d	307	1/1	0.84	0.10	89,89,89,89	0
54	MG	2A	3412	1/1	0.84	0.10	61,61,61,61	0
54	MG	2A	3216	1/1	0.84	0.20	54,54,54,54	0
54	MG	2A	3589	1/1	0.84	0.24	57,57,57,57	0
54	MG	28	8003	1/1	0.84	0.17	56,56,56,56	0
54	MG	1a	1794	1/1	0.84	0.25	67,67,67,67	0
54	MG	2a	1614	1/1	0.84	0.22	74,74,74,74	0
54	MG	2a	1630	1/1	0.84	0.12	62,62,62,62	0
54	MG	2a	1637	1/1	0.84	0.22	63,63,63,63	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	2A	3236	1/1	0.84	0.11	61,61,61,61	0
54	MG	2a	1655	1/1	0.84	0.36	63,63,63,63	0
54	MG	2A	3610	1/1	0.84	0.20	51,51,51,51	0
54	MG	1A	3947	1/1	0.84	0.11	67,67,67,67	0
54	MG	2A	3628	1/1	0.84	0.21	60,60,60,60	0
54	MG	1A	3741	1/1	0.84	0.10	48,48,48,48	0
54	MG	1a	1805	1/1	0.84	0.14	52,52,52,52	0
54	MG	2A	3640	1/1	0.84	0.15	52,52,52,52	0
54	MG	1A	3635	1/1	0.84	0.10	62,62,62,62	0
54	MG	1A	3964	1/1	0.84	0.38	36,36,36,36	0
54	MG	2A	3281	1/1	0.84	0.21	59,59,59,59	0
54	MG	1a	1649	1/1	0.84	0.25	41,41,41,41	0
54	MG	2A	3659	1/1	0.84	0.22	49,49,49,49	0
54	MG	2A	3475	1/1	0.84	0.17	30,30,30,30	0
54	MG	1A	3831	1/1	0.84	0.10	19,19,19,19	0
54	MG	1B	207	1/1	0.84	0.14	41,41,41,41	0
54	MG	1a	1824	1/1	0.84	0.24	55,55,55,55	0
54	MG	1B	211	1/1	0.84	0.26	64,64,64,64	0
54	MG	2a	1745	1/1	0.84	0.24	67,67,67,67	0
54	MG	2A	3680	1/1	0.84	0.11	50,50,50,50	0
54	MG	1A	3205	1/1	0.84	0.10	42,42,42,42	0
54	MG	1A	3679	1/1	0.84	0.14	52,52,52,52	0
54	MG	2A	3533	1/1	0.84	0.15	51,51,51,51	0
54	MG	1a	1812	1/1	0.85	0.10	59,59,59,59	0
54	MG	2A	3435	1/1	0.85	0.13	60,60,60,60	0
54	MG	1a	1715	1/1	0.85	0.20	58,58,58,58	0
54	MG	1A	3548	1/1	0.85	0.11	34,34,34,34	0
54	MG	2A	3214	1/1	0.85	0.17	56,56,56,56	0
54	MG	1A	3551	1/1	0.85	0.11	43,43,43,43	0
54	MG	2A	3707	1/1	0.85	0.20	61,61,61,61	0
54	MG	1a	1747	1/1	0.85	0.38	56,56,56,56	0
54	MG	2A	3469	1/1	0.85	0.32	61,61,61,61	0
54	MG	2A	3470	1/1	0.85	0.16	43,43,43,43	0
54	MG	2B	3004	1/1	0.85	0.16	58,58,58,58	0
54	MG	1a	1749	1/1	0.85	0.12	46,46,46,46	0
54	MG	2A	3477	1/1	0.85	0.15	59,59,59,59	0
54	MG	1A	3158	1/1	0.85	0.12	41,41,41,41	0
54	MG	1a	1837	1/1	0.85	0.10	44,44,44,44	0
54	MG	1A	3440	1/1	0.85	0.12	18,18,18,18	0
54	MG	1U	201	1/1	0.85	0.19	38,38,38,38	0
54	MG	1A	3751	1/1	0.85	0.20	55,55,55,55	0
54	MG	1A	3927	1/1	0.85	0.12	42,42,42,42	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	2A	3520	1/1	0.85	0.17	54,54,54,54	0
54	MG	1A	3452	1/1	0.85	0.14	21,21,21,21	0
54	MG	2A	3285	1/1	0.85	0.13	65,65,65,65	0
54	MG	1A	3330	1/1	0.85	0.14	15,15,15,15	0
54	MG	2A	3303	1/1	0.85	0.10	40,40,40,40	0
54	MG	2A	3314	1/1	0.85	0.12	30,30,30,30	0
54	MG	2A	3552	1/1	0.85	0.16	63,63,63,63	0
54	MG	1A	3403	1/1	0.85	0.10	50,50,50,50	0
54	MG	2A	3558	1/1	0.85	0.20	58,58,58,58	0
54	MG	2A	3563	1/1	0.85	0.13	60,60,60,60	0
54	MG	2a	1656	1/1	0.85	0.18	63,63,63,63	0
54	MG	2a	1658	1/1	0.85	0.29	60,60,60,60	0
54	MG	1A	3939	1/1	0.85	0.26	55,55,55,55	0
54	MG	1A	3940	1/1	0.85	0.42	67,67,67,67	0
54	MG	1A	3337	1/1	0.85	0.12	55,55,55,55	0
54	MG	2A	3339	1/1	0.85	0.15	71,71,71,71	0
54	MG	2a	1681	1/1	0.85	0.18	57,57,57,57	0
54	MG	1a	1779	1/1	0.85	0.18	58,58,58,58	0
54	MG	2A	3078	1/1	0.85	0.13	63,63,63,63	0
54	MG	1a	1782	1/1	0.85	0.23	61,61,61,61	0
54	MG	1A	3805	1/1	0.85	0.11	54,54,54,54	0
54	MG	1A	3486	1/1	0.85	0.09	21,21,21,21	0
54	MG	1A	3820	1/1	0.85	0.13	50,50,50,50	0
54	MG	2a	1704	1/1	0.85	0.27	63,63,63,63	0
54	MG	2a	1717	1/1	0.85	0.17	60,60,60,60	0
54	MG	2A	3629	1/1	0.85	0.13	51,51,51,51	0
54	MG	2a	1721	1/1	0.85	0.35	76,76,76,76	0
54	MG	1A	3823	1/1	0.85	0.20	29,29,29,29	0
54	MG	1A	3271	1/1	0.85	0.13	49,49,49,49	0
54	MG	2A	3406	1/1	0.85	0.13	54,54,54,54	0
54	MG	1A	3670	1/1	0.85	0.13	25,25,25,25	0
54	MG	2a	1737	1/1	0.85	0.28	60,60,60,60	0
54	MG	1A	3419	1/1	0.85	0.14	47,47,47,47	0
54	MG	2A	3179	1/1	0.85	0.30	65,65,65,65	0
54	MG	1A	3849	1/1	0.85	0.12	58,58,58,58	0
54	MG	2p	3001	1/1	0.85	0.37	61,61,61,61	0
54	MG	1A	3371	1/1	0.85	0.21	49,49,49,49	0
54	MG	2A	3428	1/1	0.85	0.26	53,53,53,53	0
54	MG	2A	3663	1/1	0.85	0.14	61,61,61,61	0
54	MG	1B	206	1/1	0.86	0.09	45,45,45,45	0
54	MG	1A	3784	1/1	0.86	0.12	42,42,42,42	0
54	MG	1a	1774	1/1	0.86	0.12	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1A	3203	1/1	0.86	0.25	55,55,55,55	0
54	MG	2A	3708	1/1	0.86	0.13	58,58,58,58	0
54	MG	2A	3476	1/1	0.86	0.14	54,54,54,54	0
54	MG	1B	224	1/1	0.86	0.09	43,43,43,43	0
54	MG	1g	3002	1/1	0.86	0.12	60,60,60,60	0
54	MG	2A	3492	1/1	0.86	0.14	66,66,66,66	0
54	MG	1B	230	1/1	0.86	0.08	68,68,68,68	0
54	MG	1A	3789	1/1	0.86	0.14	31,31,31,31	0
54	MG	1y	3001	1/1	0.86	0.12	61,61,61,61	0
54	MG	2A	3286	1/1	0.86	0.10	47,47,47,47	0
54	MG	2A	3507	1/1	0.86	0.19	54,54,54,54	0
54	MG	2B	3017	1/1	0.86	0.12	80,80,80,80	0
54	MG	1y	3002	1/1	0.86	0.11	62,62,62,62	0
54	MG	2A	3291	1/1	0.86	0.10	47,47,47,47	0
54	MG	1E	301	1/1	0.86	0.12	35,35,35,35	0
54	MG	2A	3004	1/1	0.86	0.14	44,44,44,44	0
54	MG	2A	3536	1/1	0.86	0.19	57,57,57,57	0
54	MG	2A	3049	1/1	0.86	0.23	53,53,53,53	0
54	MG	2A	3330	1/1	0.86	0.23	69,69,69,69	0
54	MG	2A	3063	1/1	0.86	0.14	58,58,58,58	0
54	MG	2A	3071	1/1	0.86	0.15	46,46,46,46	0
54	MG	2a	1627	1/1	0.86	0.26	61,61,61,61	0
54	MG	1A	3938	1/1	0.86	0.17	64,64,64,64	0
54	MG	2a	1633	1/1	0.86	0.26	68,68,68,68	0
54	MG	2A	3081	1/1	0.86	0.22	55,55,55,55	0
54	MG	2A	3097	1/1	0.86	0.33	67,67,67,67	0
54	MG	2A	3564	1/1	0.86	0.17	57,57,57,57	0
54	MG	1A	3190	1/1	0.86	0.21	45,45,45,45	0
54	MG	2A	3380	1/1	0.86	0.13	56,56,56,56	0
54	MG	2A	3382	1/1	0.86	0.14	43,43,43,43	0
54	MG	2A	3581	1/1	0.86	0.18	39,39,39,39	0
54	MG	1a	1710	1/1	0.86	0.16	63,63,63,63	0
54	MG	2a	1676	1/1	0.86	0.24	68,68,68,68	0
54	MG	2A	3124	1/1	0.86	0.10	54,54,54,54	0
54	MG	1A	3732	1/1	0.86	0.17	41,41,41,41	0
54	MG	2a	1684	1/1	0.86	0.16	60,60,60,60	0
54	MG	1a	1718	1/1	0.86	0.14	56,56,56,56	0
54	MG	2a	1688	1/1	0.86	0.20	54,54,54,54	0
54	MG	1a	1719	1/1	0.86	0.17	48,48,48,48	0
54	MG	1A	3278	1/1	0.86	0.10	38,38,38,38	0
54	MG	2A	3623	1/1	0.86	0.12	43,43,43,43	0
54	MG	2A	3627	1/1	0.86	0.17	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	2A	3404	1/1	0.86	0.19	56,56,56,56	0
54	MG	1A	3521	1/1	0.86	0.14	42,42,42,42	0
54	MG	2A	3630	1/1	0.86	0.20	52,52,52,52	0
54	MG	2A	3173	1/1	0.86	0.18	67,67,67,67	0
54	MG	2A	3175	1/1	0.86	0.21	55,55,55,55	0
54	MG	1A	3907	1/1	0.86	0.15	52,52,52,52	0
54	MG	1A	3949	1/1	0.86	0.19	68,68,68,68	0
54	MG	1a	1606	1/1	0.86	0.16	58,58,58,58	0
54	MG	1A	3589	1/1	0.86	0.13	54,54,54,54	0
54	MG	1A	3916	1/1	0.86	0.12	29,29,29,29	0
54	MG	1A	3961	1/1	0.86	0.13	38,38,38,38	0
54	MG	1A	3339	1/1	0.86	0.19	48,48,48,48	0
54	MG	1a	1640	1/1	0.86	0.23	59,59,59,59	0
54	MG	2A	3664	1/1	0.86	0.17	57,57,57,57	0
54	MG	1A	3702	1/1	0.86	0.10	27,27,27,27	0
54	MG	2A	3461	1/1	0.86	0.16	55,55,55,55	0
54	MG	1B	203	1/1	0.86	0.09	57,57,57,57	0
54	MG	2A	3691	1/1	0.87	0.10	64,64,64,64	0
54	MG	2A	3702	1/1	0.87	0.11	46,46,46,46	0
54	MG	1a	1856	1/1	0.87	0.20	67,67,67,67	0
54	MG	2A	3233	1/1	0.87	0.29	58,58,58,58	0
54	MG	1b	3001	1/1	0.87	0.23	76,76,76,76	0
54	MG	1d	306	1/1	0.87	0.15	56,56,56,56	0
54	MG	2A	3248	1/1	0.87	0.13	55,55,55,55	0
54	MG	1a	1763	1/1	0.87	0.25	64,64,64,64	0
54	MG	1A	3563	1/1	0.87	0.11	30,30,30,30	0
54	MG	1A	3882	1/1	0.87	0.11	60,60,60,60	0
54	MG	1A	3297	1/1	0.87	0.13	37,37,37,37	0
54	MG	1a	1644	1/1	0.87	0.17	60,60,60,60	0
54	MG	1A	3415	1/1	0.87	0.12	47,47,47,47	0
54	MG	1a	1654	1/1	0.87	0.15	56,56,56,56	0
54	MG	1a	1659	1/1	0.87	0.23	64,64,64,64	0
54	MG	2D	308	1/1	0.87	0.09	27,27,27,27	0
54	MG	1A	4007	1/1	0.87	0.12	23,23,23,23	0
54	MG	1A	3479	1/1	0.87	0.13	20,20,20,20	0
54	MG	2A	3308	1/1	0.87	0.21	48,48,48,48	0
54	MG	2A	3019	1/1	0.87	0.17	56,56,56,56	0
54	MG	1A	3450	1/1	0.87	0.17	27,27,27,27	0
54	MG	2A	3328	1/1	0.87	0.18	56,56,56,56	0
54	MG	1A	3801	1/1	0.87	0.06	34,34,34,34	0
54	MG	1a	1791	1/1	0.87	0.25	60,60,60,60	0
54	MG	2a	1618	1/1	0.87	0.31	66,66,66,66	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	2a	1625	1/1	0.87	0.17	67,67,67,67	0
54	MG	1a	1792	1/1	0.87	0.16	57,57,57,57	0
54	MG	1A	3913	1/1	0.87	0.17	61,61,61,61	0
54	MG	2A	3083	1/1	0.87	0.14	49,49,49,49	0
54	MG	2A	3350	1/1	0.87	0.10	31,31,31,31	0
54	MG	2a	1638	1/1	0.87	0.23	60,60,60,60	0
54	MG	2A	3096	1/1	0.87	0.16	60,60,60,60	0
54	MG	2a	1642	1/1	0.87	0.18	58,58,58,58	0
54	MG	2a	1645	1/1	0.87	0.24	62,62,62,62	0
54	MG	1a	1797	1/1	0.87	0.12	66,66,66,66	0
54	MG	2A	3106	1/1	0.87	0.11	46,46,46,46	0
54	MG	1a	1799	1/1	0.87	0.18	58,58,58,58	0
54	MG	2a	1662	1/1	0.87	0.26	67,67,67,67	0
54	MG	2A	3114	1/1	0.87	0.17	56,56,56,56	0
54	MG	1A	3522	1/1	0.87	0.09	38,38,38,38	0
54	MG	1A	3813	1/1	0.87	0.19	56,56,56,56	0
54	MG	2a	1673	1/1	0.87	0.17	56,56,56,56	0
54	MG	1A	3737	1/1	0.87	0.14	53,53,53,53	0
54	MG	2A	3612	1/1	0.87	0.10	40,40,40,40	0
54	MG	2a	1678	1/1	0.87	0.12	57,57,57,57	0
54	MG	2a	1679	1/1	0.87	0.12	53,53,53,53	0
54	MG	2a	1680	1/1	0.87	0.10	58,58,58,58	0
54	MG	2A	3146	1/1	0.87	0.22	52,52,52,52	0
54	MG	2A	3149	1/1	0.87	0.23	68,68,68,68	0
54	MG	1A	3524	1/1	0.87	0.10	46,46,46,46	0
54	MG	2A	3405	1/1	0.87	0.17	66,66,66,66	0
54	MG	2A	3164	1/1	0.87	0.17	69,69,69,69	0
54	MG	1A	3603	1/1	0.87	0.22	60,60,60,60	0
54	MG	2A	3632	1/1	0.87	0.14	49,49,49,49	0
54	MG	1A	3544	1/1	0.87	0.33	34,34,34,34	0
54	MG	1H	8001	1/1	0.87	0.23	67,67,67,67	0
54	MG	1A	3428	1/1	0.87	0.28	52,52,52,52	0
54	MG	2a	1709	1/1	0.87	0.34	48,48,48,48	0
54	MG	1A	3833	1/1	0.87	0.10	30,30,30,30	0
54	MG	1A	3835	1/1	0.87	0.08	50,50,50,50	0
54	MG	1Z	8001	1/1	0.87	0.15	60,60,60,60	0
54	MG	2A	3431	1/1	0.87	0.19	53,53,53,53	0
54	MG	1a	1738	1/1	0.87	0.11	62,62,62,62	0
54	MG	2A	3444	1/1	0.87	0.17	60,60,60,60	0
54	MG	10	104	1/1	0.87	0.11	51,51,51,51	0
54	MG	1A	3753	1/1	0.87	0.13	35,35,35,35	0
54	MG	1A	3487	1/1	0.87	0.19	51,51,51,51	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1A	3858	1/1	0.87	0.10	28,28,28,28	0
54	MG	2a	1749	1/1	0.87	0.28	64,64,64,64	0
54	MG	1A	3868	1/1	0.87	0.14	23,23,23,23	0
54	MG	1A	3870	1/1	0.87	0.09	46,46,46,46	0
57	MPD	1a	1854	8/8	0.87	0.12	46,63,67,69	0
57	MPD	2A	3710	8/8	0.87	0.23	43,49,51,57	0
54	MG	2A	3468	1/1	0.87	0.13	61,61,61,61	0
54	MG	1a	1628	1/1	0.87	0.20	49,49,49,49	0
54	MG	2A	3687	1/1	0.87	0.25	64,64,64,64	0
54	MG	2A	3205	1/1	0.88	0.26	60,60,60,60	0
54	MG	1a	1601	1/1	0.88	0.16	56,56,56,56	0
54	MG	1A	3637	1/1	0.88	0.12	47,47,47,47	0
54	MG	2A	3457	1/1	0.88	0.13	54,54,54,54	0
54	MG	1A	3189	1/1	0.88	0.21	41,41,41,41	0
54	MG	1a	1612	1/1	0.88	0.18	72,72,72,72	0
54	MG	2A	3226	1/1	0.88	0.14	53,53,53,53	0
54	MG	2A	3231	1/1	0.88	0.13	42,42,42,42	0
54	MG	1a	1756	1/1	0.88	0.25	58,58,58,58	0
54	MG	1A	3030	1/1	0.88	0.25	54,54,54,54	0
54	MG	2A	3471	1/1	0.88	0.14	61,61,61,61	0
54	MG	1A	3148	1/1	0.88	0.10	30,30,30,30	0
54	MG	1A	3966	1/1	0.88	0.17	36,36,36,36	0
54	MG	1A	3903	1/1	0.88	0.31	63,63,63,63	0
54	MG	2B	3013	1/1	0.88	0.10	80,80,80,80	0
54	MG	2A	3484	1/1	0.88	0.38	65,65,65,65	0
54	MG	1A	3437	1/1	0.88	0.16	41,41,41,41	0
54	MG	1n	502	1/1	0.88	0.13	51,51,51,51	0
54	MG	2B	3018	1/1	0.88	0.14	76,76,76,76	0
54	MG	2A	3269	1/1	0.88	0.17	32,32,32,32	0
54	MG	2D	306	1/1	0.88	0.10	56,56,56,56	0
54	MG	2D	307	1/1	0.88	0.25	43,43,43,43	0
54	MG	1A	3493	1/1	0.88	0.15	56,56,56,56	0
54	MG	1a	1648	1/1	0.88	0.12	72,72,72,72	0
54	MG	1A	3573	1/1	0.88	0.32	52,52,52,52	0
54	MG	2T	3003	1/1	0.88	0.09	61,61,61,61	0
54	MG	1a	1776	1/1	0.88	0.43	69,69,69,69	0
54	MG	2A	3509	1/1	0.88	0.24	60,60,60,60	0
54	MG	1A	3498	1/1	0.88	0.10	32,32,32,32	0
54	MG	2A	3037	1/1	0.88	0.23	56,56,56,56	0
54	MG	2A	3523	1/1	0.88	0.24	49,49,49,49	0
54	MG	2a	1605	1/1	0.88	0.09	57,57,57,57	0
54	MG	2A	3526	1/1	0.88	0.26	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	2A	3532	1/1	0.88	0.20	52,52,52,52	0
54	MG	2a	1620	1/1	0.88	0.17	56,56,56,56	0
54	MG	2a	1623	1/1	0.88	0.30	64,64,64,64	0
54	MG	2A	3041	1/1	0.88	0.13	54,54,54,54	0
54	MG	1A	3039	1/1	0.88	0.16	56,56,56,56	0
54	MG	1A	3445	1/1	0.88	0.10	21,21,21,21	0
54	MG	2A	3544	1/1	0.88	0.09	56,56,56,56	0
54	MG	1B	227	1/1	0.88	0.09	52,52,52,52	0
54	MG	1a	1669	1/1	0.88	0.11	51,51,51,51	0
54	MG	1A	3825	1/1	0.88	0.10	45,45,45,45	0
54	MG	1a	1676	1/1	0.88	0.20	46,46,46,46	0
54	MG	1A	3504	1/1	0.88	0.07	16,16,16,16	0
54	MG	1D	309	1/1	0.88	0.17	52,52,52,52	0
54	MG	2A	3103	1/1	0.88	0.23	66,66,66,66	0
54	MG	1a	1684	1/1	0.88	0.14	49,49,49,49	0
54	MG	1A	3159	1/1	0.88	0.16	38,38,38,38	0
54	MG	2A	3568	1/1	0.88	0.24	50,50,50,50	0
54	MG	2A	3111	1/1	0.88	0.14	66,66,66,66	0
54	MG	2a	1670	1/1	0.88	0.23	59,59,59,59	0
54	MG	2A	3371	1/1	0.88	0.15	26,26,26,26	0
54	MG	2A	3379	1/1	0.88	0.14	40,40,40,40	0
54	MG	1a	1691	1/1	0.88	0.17	56,56,56,56	0
54	MG	1F	302	1/1	0.88	0.09	32,32,32,32	0
54	MG	2A	3594	1/1	0.88	0.28	60,60,60,60	0
54	MG	2A	3597	1/1	0.88	0.37	61,61,61,61	0
54	MG	2A	3600	1/1	0.88	0.25	54,54,54,54	0
54	MG	2A	3384	1/1	0.88	0.23	38,38,38,38	0
54	MG	1A	3161	1/1	0.88	0.07	34,34,34,34	0
54	MG	2A	3126	1/1	0.88	0.09	42,42,42,42	0
54	MG	1A	3752	1/1	0.88	0.11	55,55,55,55	0
54	MG	1a	1809	1/1	0.88	0.22	66,66,66,66	0
54	MG	1A	3611	1/1	0.88	0.10	41,41,41,41	0
54	MG	2a	1698	1/1	0.88	0.24	50,50,50,50	0
54	MG	1a	1707	1/1	0.88	0.11	58,58,58,58	0
54	MG	2A	3399	1/1	0.88	0.13	42,42,42,42	0
54	MG	1A	3838	1/1	0.88	0.18	60,60,60,60	0
54	MG	1a	1818	1/1	0.88	0.21	62,62,62,62	0
54	MG	1a	1712	1/1	0.88	0.16	51,51,51,51	0
54	MG	2A	3408	1/1	0.88	0.13	54,54,54,54	0
54	MG	2A	3409	1/1	0.88	0.09	51,51,51,51	0
54	MG	1A	3757	1/1	0.88	0.11	48,48,48,48	0
54	MG	1A	3854	1/1	0.88	0.09	19,19,19,19	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	2A	3417	1/1	0.88	0.14	37,37,37,37	0
54	MG	1W	3001	1/1	0.88	0.21	46,46,46,46	0
54	MG	2a	1734	1/1	0.88	0.27	55,55,55,55	0
54	MG	2A	3649	1/1	0.88	0.17	38,38,38,38	0
54	MG	2A	3652	1/1	0.88	0.18	44,44,44,44	0
54	MG	2a	1741	1/1	0.88	0.27	55,55,55,55	0
54	MG	2A	3421	1/1	0.88	0.14	62,62,62,62	0
54	MG	1a	1833	1/1	0.88	0.23	60,60,60,60	0
54	MG	2a	1746	1/1	0.88	0.18	60,60,60,60	0
54	MG	2a	1747	1/1	0.88	0.27	61,61,61,61	0
54	MG	1A	3857	1/1	0.88	0.10	26,26,26,26	0
54	MG	1A	3347	1/1	0.88	0.10	36,36,36,36	0
54	MG	1A	3948	1/1	0.88	0.11	60,60,60,60	0
54	MG	1l	102	1/1	0.88	0.08	47,47,47,47	0
54	MG	1a	1748	1/1	0.88	0.19	57,57,57,57	0
54	MG	2A	3674	1/1	0.88	0.15	63,63,63,63	0
54	MG	1A	3055	1/1	0.88	0.11	45,45,45,45	0
54	MG	2A	3449	1/1	0.88	0.14	58,58,58,58	0
54	MG	2A	3677	1/1	0.89	0.11	50,50,50,50	0
54	MG	2A	3472	1/1	0.89	0.09	52,52,52,52	0
54	MG	2A	3068	1/1	0.89	0.13	59,59,59,59	0
54	MG	1T	202	1/1	0.89	0.08	48,48,48,48	0
54	MG	2A	3072	1/1	0.89	0.12	49,49,49,49	0
54	MG	2A	3482	1/1	0.89	0.14	51,51,51,51	0
54	MG	2A	3703	1/1	0.89	0.09	81,81,81,81	0
54	MG	2A	3287	1/1	0.89	0.13	42,42,42,42	0
54	MG	1a	1692	1/1	0.89	0.19	46,46,46,46	0
54	MG	1A	3777	1/1	0.89	0.08	19,19,19,19	0
54	MG	2A	3082	1/1	0.89	0.11	62,62,62,62	0
54	MG	2A	3501	1/1	0.89	0.14	43,43,43,43	0
54	MG	1A	3780	1/1	0.89	0.13	45,45,45,45	0
54	MG	2A	3094	1/1	0.89	0.12	49,49,49,49	0
54	MG	1A	3430	1/1	0.89	0.12	38,38,38,38	0
54	MG	1a	1703	1/1	0.89	0.17	60,60,60,60	0
54	MG	2B	3010	1/1	0.89	0.21	68,68,68,68	0
54	MG	2B	3011	1/1	0.89	0.10	65,65,65,65	0
54	MG	1A	3861	1/1	0.89	0.11	22,22,22,22	0
54	MG	2A	3510	1/1	0.89	0.24	64,64,64,64	0
54	MG	1A	3867	1/1	0.89	0.16	47,47,47,47	0
54	MG	1A	3785	1/1	0.89	0.17	28,28,28,28	0
54	MG	1A	3518	1/1	0.89	0.14	51,51,51,51	0
54	MG	2A	3525	1/1	0.89	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
54	MG	1A	3873	1/1	0.89	0.20	57,57,57,57	0
54	MG	2A	3528	1/1	0.89	0.14	32,32,32,32	0
54	MG	2A	3343	1/1	0.89	0.23	50,50,50,50	0
54	MG	2E	302	1/1	0.89	0.19	67,67,67,67	0
54	MG	2G	3001	1/1	0.89	0.14	71,71,71,71	0
54	MG	2G	3002	1/1	0.89	0.14	65,65,65,65	0
54	MG	1A	3719	1/1	0.89	0.18	56,56,56,56	0
54	MG	2A	3122	1/1	0.89	0.19	66,66,66,66	0
54	MG	2A	3360	1/1	0.89	0.18	48,48,48,48	0
54	MG	2W	8002	1/1	0.89	0.13	59,59,59,59	0
54	MG	2A	3542	1/1	0.89	0.15	45,45,45,45	0
54	MG	2A	3543	1/1	0.89	0.19	49,49,49,49	0
54	MG	2A	3361	1/1	0.89	0.11	33,33,33,33	0
54	MG	2A	3364	1/1	0.89	0.22	58,58,58,58	0
54	MG	1A	3214	1/1	0.89	0.16	30,30,30,30	0
54	MG	1a	1720	1/1	0.89	0.10	60,60,60,60	0
54	MG	2a	1607	1/1	0.89	0.39	64,64,64,64	0
54	MG	2a	1611	1/1	0.89	0.11	62,62,62,62	0
54	MG	2A	3137	1/1	0.89	0.21	52,52,52,52	0
54	MG	2A	3553	1/1	0.89	0.28	56,56,56,56	0
54	MG	2A	3554	1/1	0.89	0.12	49,49,49,49	0
54	MG	1a	1730	1/1	0.89	0.13	43,43,43,43	0
54	MG	1A	3983	1/1	0.89	0.11	36,36,36,36	0
54	MG	1A	3296	1/1	0.89	0.12	19,19,19,19	0
54	MG	1a	1623	1/1	0.89	0.11	47,47,47,47	0
54	MG	1a	1739	1/1	0.89	0.11	61,61,61,61	0
54	MG	2a	1634	1/1	0.89	0.21	55,55,55,55	0
54	MG	2A	3166	1/1	0.89	0.14	51,51,51,51	0
54	MG	1a	1740	1/1	0.89	0.16	59,59,59,59	0
54	MG	2A	3572	1/1	0.89	0.07	21,21,21,21	0
54	MG	1a	1743	1/1	0.89	0.19	62,62,62,62	0
54	MG	2A	3397	1/1	0.89	0.14	55,55,55,55	0
54	MG	2a	1650	1/1	0.89	0.08	58,58,58,58	0
54	MG	2a	1651	1/1	0.89	0.24	58,58,58,58	0
54	MG	2A	3582	1/1	0.89	0.17	47,47,47,47	0
54	MG	1A	3799	1/1	0.89	0.12	46,46,46,46	0
54	MG	2A	3587	1/1	0.89	0.22	44,44,44,44	0
54	MG	1a	1631	1/1	0.89	0.20	64,64,64,64	0
54	MG	2A	3403	1/1	0.89	0.15	57,57,57,57	0
54	MG	2a	1668	1/1	0.89	0.14	45,45,45,45	0
54	MG	2A	3595	1/1	0.89	0.22	53,53,53,53	0
54	MG	2A	3596	1/1	0.89	0.27	50,50,50,50	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1A	3249	1/1	0.89	0.14	34,34,34,34	0
54	MG	1a	1636	1/1	0.89	0.17	60,60,60,60	0
54	MG	2A	3178	1/1	0.89	0.20	53,53,53,53	0
54	MG	1A	3804	1/1	0.89	0.10	21,21,21,21	0
54	MG	1A	3362	1/1	0.89	0.10	36,36,36,36	0
54	MG	1B	215	1/1	0.89	0.12	61,61,61,61	0
54	MG	1d	303	1/1	0.89	0.28	68,68,68,68	0
54	MG	2A	3621	1/1	0.89	0.11	28,28,28,28	0
54	MG	2a	1682	1/1	0.89	0.14	60,60,60,60	0
54	MG	1B	219	1/1	0.89	0.09	46,46,46,46	0
54	MG	2A	3626	1/1	0.89	0.11	70,70,70,70	0
54	MG	2A	3200	1/1	0.89	0.08	45,45,45,45	0
54	MG	1A	3314	1/1	0.89	0.10	46,46,46,46	0
54	MG	1a	1760	1/1	0.89	0.25	52,52,52,52	0
54	MG	2A	3207	1/1	0.89	0.13	55,55,55,55	0
54	MG	1a	1650	1/1	0.89	0.24	62,62,62,62	0
54	MG	1A	3744	1/1	0.89	0.19	54,54,54,54	0
54	MG	1A	3182	1/1	0.89	0.09	43,43,43,43	0
54	MG	1A	3626	1/1	0.89	0.15	51,51,51,51	0
54	MG	2a	1706	1/1	0.89	0.13	63,63,63,63	0
54	MG	2a	1708	1/1	0.89	0.31	52,52,52,52	0
54	MG	1A	3749	1/1	0.89	0.09	36,36,36,36	0
54	MG	2a	1714	1/1	0.89	0.20	48,48,48,48	0
54	MG	1A	3500	1/1	0.89	0.10	44,44,44,44	0
54	MG	1A	3118	1/1	0.89	0.26	49,49,49,49	0
54	MG	2a	1720	1/1	0.89	0.22	50,50,50,50	0
54	MG	1A	3644	1/1	0.89	0.09	58,58,58,58	0
54	MG	2A	3651	1/1	0.89	0.20	58,58,58,58	0
54	MG	1a	1679	1/1	0.89	0.29	60,60,60,60	0
54	MG	2A	3654	1/1	0.89	0.18	57,57,57,57	0
54	MG	2A	3655	1/1	0.89	0.17	42,42,42,42	0
54	MG	2A	3244	1/1	0.89	0.38	44,44,44,44	0
54	MG	2A	3460	1/1	0.89	0.19	53,53,53,53	0
54	MG	2a	1738	1/1	0.89	0.32	52,52,52,52	0
54	MG	2A	3660	1/1	0.89	0.17	61,61,61,61	0
54	MG	2A	3661	1/1	0.89	0.10	47,47,47,47	0
54	MG	1A	3756	1/1	0.89	0.15	57,57,57,57	0
54	MG	2A	3465	1/1	0.89	0.15	56,56,56,56	0
54	MG	2A	3028	1/1	0.89	0.15	68,68,68,68	0
54	MG	2A	3666	1/1	0.89	0.23	51,51,51,51	0
54	MG	2e	3001	1/1	0.89	0.24	58,58,58,58	0
54	MG	2A	3669	1/1	0.89	0.18	59,59,59,59	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	2A	3671	1/1	0.89	0.14	56,56,56,56	0
54	MG	2r	8001	1/1	0.89	0.22	65,65,65,65	0
57	MPD	1T	204	8/8	0.89	0.20	57,64,66,66	0
54	MG	1A	3570	1/1	0.89	0.10	47,47,47,47	0
54	MG	1a	1683	1/1	0.89	0.16	59,59,59,59	0
54	MG	2A	3265	1/1	0.89	0.15	57,57,57,57	0
54	MG	1A	3759	1/1	0.89	0.24	43,43,43,43	0
54	MG	1A	3391	1/1	0.89	0.13	37,37,37,37	0
54	MG	1A	3678	1/1	0.90	0.12	40,40,40,40	0
54	MG	1G	3003	1/1	0.90	0.10	57,57,57,57	0
54	MG	1A	3355	1/1	0.90	0.08	33,33,33,33	0
54	MG	2A	3113	1/1	0.90	0.21	59,59,59,59	0
54	MG	1A	3688	1/1	0.90	0.13	34,34,34,34	0
54	MG	1A	3696	1/1	0.90	0.13	52,52,52,52	0
54	MG	2A	3546	1/1	0.90	0.18	41,41,41,41	0
54	MG	2D	305	1/1	0.90	0.22	53,53,53,53	0
54	MG	1A	3698	1/1	0.90	0.14	58,58,58,58	0
54	MG	1A	3187	1/1	0.90	0.13	49,49,49,49	0
54	MG	1A	3703	1/1	0.90	0.23	47,47,47,47	0
54	MG	1A	3302	1/1	0.90	0.14	27,27,27,27	0
54	MG	1A	3564	1/1	0.90	0.08	39,39,39,39	0
54	MG	1a	1819	1/1	0.90	0.27	51,51,51,51	0
54	MG	1a	1713	1/1	0.90	0.13	53,53,53,53	0
54	MG	1A	3727	1/1	0.90	0.15	22,22,22,22	0
54	MG	2A	3151	1/1	0.90	0.20	66,66,66,66	0
54	MG	2A	3162	1/1	0.90	0.16	53,53,53,53	0
54	MG	1a	1825	1/1	0.90	0.15	54,54,54,54	0
54	MG	1A	3162	1/1	0.90	0.12	41,41,41,41	0
54	MG	1A	3568	1/1	0.90	0.16	48,48,48,48	0
54	MG	19	503	1/1	0.90	0.08	50,50,50,50	0
54	MG	2a	1602	1/1	0.90	0.15	52,52,52,52	0
54	MG	2A	3401	1/1	0.90	0.08	54,54,54,54	0
54	MG	1A	3495	1/1	0.90	0.10	18,18,18,18	0
54	MG	1A	3572	1/1	0.90	0.17	46,46,46,46	0
54	MG	1a	1733	1/1	0.90	0.17	55,55,55,55	0
54	MG	2a	1612	1/1	0.90	0.09	50,50,50,50	0
54	MG	1a	1842	1/1	0.90	0.09	51,51,51,51	0
54	MG	2A	3590	1/1	0.90	0.14	58,58,58,58	0
54	MG	2A	3592	1/1	0.90	0.11	47,47,47,47	0
54	MG	1A	3316	1/1	0.90	0.10	38,38,38,38	0
54	MG	1A	3954	1/1	0.90	0.08	36,36,36,36	0
54	MG	2A	3411	1/1	0.90	0.07	55,55,55,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	2a	1629	1/1	0.90	0.18	60,60,60,60	0
54	MG	1A	3380	1/1	0.90	0.09	29,29,29,29	0
54	MG	2A	3598	1/1	0.90	0.12	53,53,53,53	0
54	MG	1a	1847	1/1	0.90	0.17	60,60,60,60	0
54	MG	2a	1636	1/1	0.90	0.19	69,69,69,69	0
54	MG	2A	3601	1/1	0.90	0.28	57,57,57,57	0
54	MG	1a	1848	1/1	0.90	0.28	53,53,53,53	0
54	MG	1a	1621	1/1	0.90	0.20	46,46,46,46	0
54	MG	1A	3383	1/1	0.90	0.09	24,24,24,24	0
54	MG	2A	3423	1/1	0.90	0.10	45,45,45,45	0
54	MG	2a	1646	1/1	0.90	0.24	63,63,63,63	0
54	MG	2A	3614	1/1	0.90	0.20	58,58,58,58	0
54	MG	1a	1624	1/1	0.90	0.10	60,60,60,60	0
54	MG	2A	3203	1/1	0.90	0.10	51,51,51,51	0
54	MG	1A	3168	1/1	0.90	0.07	46,46,46,46	0
54	MG	1A	3503	1/1	0.90	0.20	58,58,58,58	0
54	MG	1A	3392	1/1	0.90	0.13	23,23,23,23	0
54	MG	2A	3433	1/1	0.90	0.20	57,57,57,57	0
54	MG	1e	3001	1/1	0.90	0.28	56,56,56,56	0
54	MG	1A	3173	1/1	0.90	0.14	43,43,43,43	0
54	MG	1A	3160	1/1	0.90	0.16	41,41,41,41	0
54	MG	2A	3220	1/1	0.90	0.18	58,58,58,58	0
54	MG	1B	202	1/1	0.90	0.15	36,36,36,36	0
54	MG	2A	3230	1/1	0.90	0.09	55,55,55,55	0
54	MG	1A	3279	1/1	0.90	0.13	61,61,61,61	0
54	MG	2A	3458	1/1	0.90	0.18	34,34,34,34	0
54	MG	1B	204	1/1	0.90	0.19	52,52,52,52	0
54	MG	1A	3872	1/1	0.90	0.15	50,50,50,50	0
54	MG	2A	3462	1/1	0.90	0.14	53,53,53,53	0
54	MG	1A	3621	1/1	0.90	0.15	52,52,52,52	0
54	MG	1A	3408	1/1	0.90	0.16	50,50,50,50	0
54	MG	1a	1657	1/1	0.90	0.19	59,59,59,59	0
54	MG	1A	3523	1/1	0.90	0.19	48,48,48,48	0
54	MG	2A	3657	1/1	0.90	0.15	43,43,43,43	0
54	MG	2A	3017	1/1	0.90	0.22	41,41,41,41	0
54	MG	2a	1695	1/1	0.90	0.23	62,62,62,62	0
54	MG	2A	3258	1/1	0.90	0.09	36,36,36,36	0
54	MG	1A	3036	1/1	0.90	0.10	38,38,38,38	0
54	MG	1A	3894	1/1	0.90	0.13	80,80,80,80	0
54	MG	2A	3032	1/1	0.90	0.20	54,54,54,54	0
54	MG	2A	3036	1/1	0.90	0.17	57,57,57,57	0
54	MG	2A	3275	1/1	0.90	0.14	62,62,62,62	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	2A	3481	1/1	0.90	0.12	46,46,46,46	0
54	MG	1a	1668	1/1	0.90	0.40	74,74,74,74	0
54	MG	2A	3283	1/1	0.90	0.11	50,50,50,50	0
54	MG	1B	225	1/1	0.90	0.08	40,40,40,40	0
54	MG	1a	1777	1/1	0.90	0.48	61,61,61,61	0
54	MG	1A	3899	1/1	0.90	0.11	51,51,51,51	0
54	MG	1A	3639	1/1	0.90	0.13	34,34,34,34	0
54	MG	2a	1722	1/1	0.90	0.29	49,49,49,49	0
54	MG	1a	1677	1/1	0.90	0.20	64,64,64,64	0
54	MG	2A	3678	1/1	0.90	0.16	51,51,51,51	0
54	MG	1a	1678	1/1	0.90	0.22	53,53,53,53	0
54	MG	2a	1730	1/1	0.90	0.17	49,49,49,49	0
54	MG	2A	3684	1/1	0.90	0.10	65,65,65,65	0
54	MG	2A	3505	1/1	0.90	0.18	55,55,55,55	0
54	MG	1A	3527	1/1	0.90	0.09	51,51,51,51	0
54	MG	1A	3534	1/1	0.90	0.17	60,60,60,60	0
54	MG	2a	1740	1/1	0.90	0.42	59,59,59,59	0
54	MG	2A	3694	1/1	0.90	0.13	69,69,69,69	0
54	MG	2A	3696	1/1	0.90	0.09	52,52,52,52	0
54	MG	2a	1743	1/1	0.90	0.25	63,63,63,63	0
54	MG	2A	3508	1/1	0.90	0.30	57,57,57,57	0
54	MG	1D	310	1/1	0.90	0.08	62,62,62,62	0
54	MG	2A	3706	1/1	0.90	0.15	48,48,48,48	0
54	MG	2A	3320	1/1	0.90	0.19	59,59,59,59	0
54	MG	2A	3323	1/1	0.90	0.15	34,34,34,34	0
54	MG	1a	1793	1/1	0.90	0.22	63,63,63,63	0
54	MG	1A	3654	1/1	0.90	0.14	42,42,42,42	0
54	MG	2A	3524	1/1	0.90	0.13	26,26,26,26	0
57	MPD	1A	3988	8/8	0.90	0.20	48,52,54,59	0
54	MG	1a	1795	1/1	0.90	0.20	49,49,49,49	0
54	MG	1A	3668	1/1	0.90	0.19	63,63,63,63	0
54	MG	2A	3098	1/1	0.90	0.24	53,53,53,53	0
54	MG	1A	3481	1/1	0.90	0.08	48,48,48,48	0
54	MG	2B	3009	1/1	0.90	0.11	62,62,62,62	0
54	MG	2A	3342	1/1	0.90	0.21	51,51,51,51	0
54	MG	2A	3340	1/1	0.91	0.17	55,55,55,55	0
54	MG	1A	3774	1/1	0.91	0.08	12,12,12,12	0
54	MG	1A	3880	1/1	0.91	0.08	37,37,37,37	0
54	MG	2A	3346	1/1	0.91	0.16	52,52,52,52	0
54	MG	2A	3347	1/1	0.91	0.28	56,56,56,56	0
54	MG	1A	3011	1/1	0.91	0.10	47,47,47,47	0
54	MG	2A	3354	1/1	0.91	0.12	49,49,49,49	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1A	3883	1/1	0.91	0.15	47,47,47,47	0
54	MG	1A	3574	1/1	0.91	0.10	26,26,26,26	0
54	MG	1A	3889	1/1	0.91	0.10	36,36,36,36	0
54	MG	2A	3549	1/1	0.91	0.15	38,38,38,38	0
54	MG	1A	3783	1/1	0.91	0.09	48,48,48,48	0
54	MG	1A	3687	1/1	0.91	0.09	44,44,44,44	0
54	MG	1A	3332	1/1	0.91	0.14	60,60,60,60	0
54	MG	2A	3376	1/1	0.91	0.10	47,47,47,47	0
54	MG	1A	3690	1/1	0.91	0.13	46,46,46,46	0
54	MG	1A	3057	1/1	0.91	0.15	27,27,27,27	0
54	MG	2A	3562	1/1	0.91	0.14	63,63,63,63	0
54	MG	2X	101	1/1	0.91	0.09	59,59,59,59	0
54	MG	2A	3381	1/1	0.91	0.19	53,53,53,53	0
54	MG	1a	1696	1/1	0.91	0.13	70,70,70,70	0
54	MG	2A	3566	1/1	0.91	0.10	35,35,35,35	0
54	MG	1a	1811	1/1	0.91	0.17	42,42,42,42	0
54	MG	1A	3793	1/1	0.91	0.14	41,41,41,41	0
54	MG	2A	3143	1/1	0.91	0.13	41,41,41,41	0
54	MG	2A	3570	1/1	0.91	0.16	44,44,44,44	0
54	MG	1a	1813	1/1	0.91	0.16	60,60,60,60	0
54	MG	1A	3583	1/1	0.91	0.19	20,20,20,20	0
54	MG	2A	3580	1/1	0.91	0.14	36,36,36,36	0
54	MG	1P	202	1/1	0.91	0.08	66,66,66,66	0
54	MG	1A	3402	1/1	0.91	0.10	50,50,50,50	0
54	MG	1A	3058	1/1	0.91	0.07	34,34,34,34	0
54	MG	1A	3919	1/1	0.91	0.16	45,45,45,45	0
54	MG	2A	3588	1/1	0.91	0.11	48,48,48,48	0
54	MG	1A	3716	1/1	0.91	0.13	47,47,47,47	0
54	MG	1A	3718	1/1	0.91	0.10	26,26,26,26	0
54	MG	1A	3283	1/1	0.91	0.09	32,32,32,32	0
54	MG	2a	1632	1/1	0.91	0.19	59,59,59,59	0
54	MG	1A	3291	1/1	0.91	0.14	45,45,45,45	0
54	MG	1A	3815	1/1	0.91	0.07	33,33,33,33	0
54	MG	1a	1836	1/1	0.91	0.09	62,62,62,62	0
54	MG	1A	3724	1/1	0.91	0.11	27,27,27,27	0
54	MG	1A	3818	1/1	0.91	0.13	31,31,31,31	0
54	MG	2a	1639	1/1	0.91	0.24	54,54,54,54	0
54	MG	2A	3599	1/1	0.91	0.12	45,45,45,45	0
54	MG	1a	1721	1/1	0.91	0.12	42,42,42,42	0
54	MG	2A	3189	1/1	0.91	0.30	66,66,66,66	0
54	MG	1a	1726	1/1	0.91	0.25	62,62,62,62	0
54	MG	1A	3357	1/1	0.91	0.09	20,20,20,20	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1A	3612	1/1	0.91	0.07	22,22,22,22	0
54	MG	2A	3611	1/1	0.91	0.15	56,56,56,56	0
54	MG	1a	1604	1/1	0.91	0.12	62,62,62,62	0
54	MG	1A	3208	1/1	0.91	0.14	53,53,53,53	0
54	MG	1A	3829	1/1	0.91	0.13	54,54,54,54	0
54	MG	1a	1853	1/1	0.91	0.15	47,47,47,47	0
54	MG	1A	3538	1/1	0.91	0.10	55,55,55,55	0
54	MG	2A	3430	1/1	0.91	0.18	41,41,41,41	0
54	MG	1A	3739	1/1	0.91	0.13	51,51,51,51	0
54	MG	2A	3432	1/1	0.91	0.14	57,57,57,57	0
54	MG	2A	3213	1/1	0.91	0.17	67,67,67,67	0
54	MG	1a	1742	1/1	0.91	0.26	62,62,62,62	0
54	MG	1A	3416	1/1	0.91	0.13	48,48,48,48	0
54	MG	1A	3951	1/1	0.91	0.08	50,50,50,50	0
54	MG	1A	3010	1/1	0.91	0.10	38,38,38,38	0
54	MG	1A	3235	1/1	0.91	0.10	39,39,39,39	0
54	MG	2A	3453	1/1	0.91	0.16	64,64,64,64	0
54	MG	2A	3225	1/1	0.91	0.14	56,56,56,56	0
54	MG	2a	1683	1/1	0.91	0.14	57,57,57,57	0
54	MG	1A	3145	1/1	0.91	0.17	43,43,43,43	0
54	MG	1a	1633	1/1	0.91	0.09	37,37,37,37	0
54	MG	1A	3841	1/1	0.91	0.09	29,29,29,29	0
54	MG	2A	3232	1/1	0.91	0.12	44,44,44,44	0
54	MG	1A	3844	1/1	0.91	0.11	46,46,46,46	0
54	MG	2a	1694	1/1	0.91	0.21	60,60,60,60	0
54	MG	1A	3252	1/1	0.91	0.10	52,52,52,52	0
54	MG	1t	3001	1/1	0.91	0.16	52,52,52,52	0
54	MG	1a	1757	1/1	0.91	0.12	77,77,77,77	0
54	MG	1A	3850	1/1	0.91	0.13	48,48,48,48	0
54	MG	2a	1702	1/1	0.91	0.16	73,73,73,73	0
54	MG	1A	3991	1/1	0.91	0.17	43,43,43,43	0
54	MG	1A	3647	1/1	0.91	0.08	38,38,38,38	0
54	MG	1A	4023	1/1	0.91	0.21	36,36,36,36	0
54	MG	1A	3093	1/1	0.91	0.09	38,38,38,38	0
54	MG	2A	3473	1/1	0.91	0.11	60,60,60,60	0
54	MG	2a	1712	1/1	0.91	0.17	37,37,37,37	0
54	MG	1a	1652	1/1	0.91	0.32	61,61,61,61	0
54	MG	2a	1715	1/1	0.91	0.34	60,60,60,60	0
54	MG	2A	3667	1/1	0.91	0.11	49,49,49,49	0
54	MG	1a	1769	1/1	0.91	0.25	56,56,56,56	0
54	MG	1a	1771	1/1	0.91	0.17	46,46,46,46	0
54	MG	2A	3479	1/1	0.91	0.12	41,41,41,41	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	2A	3480	1/1	0.91	0.33	37,37,37,37	0
54	MG	1a	1653	1/1	0.91	0.12	60,60,60,60	0
54	MG	1A	3387	1/1	0.91	0.10	54,54,54,54	0
54	MG	2A	3483	1/1	0.91	0.08	61,61,61,61	0
54	MG	2A	3044	1/1	0.91	0.20	46,46,46,46	0
54	MG	2A	3486	1/1	0.91	0.17	56,56,56,56	0
54	MG	2A	3488	1/1	0.91	0.09	62,62,62,62	0
54	MG	2A	3047	1/1	0.91	0.20	56,56,56,56	0
54	MG	1A	3662	1/1	0.91	0.12	62,62,62,62	0
54	MG	2A	3056	1/1	0.91	0.10	46,46,46,46	0
54	MG	1a	1658	1/1	0.91	0.17	46,46,46,46	0
54	MG	1A	3502	1/1	0.91	0.21	54,54,54,54	0
54	MG	2A	3294	1/1	0.91	0.07	41,41,41,41	0
54	MG	2A	3301	1/1	0.91	0.13	56,56,56,56	0
54	MG	1A	3389	1/1	0.91	0.10	27,27,27,27	0
54	MG	1A	3760	1/1	0.91	0.29	61,61,61,61	0
54	MG	1A	3675	1/1	0.91	0.12	54,54,54,54	0
54	MG	2A	3079	1/1	0.91	0.15	47,47,47,47	0
54	MG	2A	3723	1/1	0.91	0.16	37,37,37,37	0
54	MG	1A	3765	1/1	0.91	0.08	39,39,39,39	0
54	MG	1a	1788	1/1	0.91	0.17	54,54,54,54	0
54	MG	2A	3519	1/1	0.91	0.12	54,54,54,54	0
54	MG	1a	1671	1/1	0.91	0.21	60,60,60,60	0
54	MG	2A	3087	1/1	0.91	0.13	52,52,52,52	0
54	MG	2A	3088	1/1	0.91	0.19	56,56,56,56	0
54	MG	2A	3092	1/1	0.91	0.12	46,46,46,46	0
54	MG	1a	1673	1/1	0.91	0.09	55,55,55,55	0
54	MG	1B	221	1/1	0.91	0.12	34,34,34,34	0
54	MG	1A	3881	1/1	0.92	0.19	43,43,43,43	0
54	MG	1A	3766	1/1	0.92	0.11	47,47,47,47	0
54	MG	2A	3463	1/1	0.92	0.17	62,62,62,62	0
54	MG	1D	313	1/1	0.92	0.13	43,43,43,43	0
54	MG	2A	3204	1/1	0.92	0.09	47,47,47,47	0
54	MG	2A	3688	1/1	0.92	0.14	56,56,56,56	0
54	MG	1A	3470	1/1	0.92	0.12	36,36,36,36	0
54	MG	1F	301	1/1	0.92	0.25	41,41,41,41	0
54	MG	1a	1844	1/1	0.92	0.16	58,58,58,58	0
54	MG	2A	3697	1/1	0.92	0.10	53,53,53,53	0
54	MG	1A	3885	1/1	0.92	0.08	53,53,53,53	0
54	MG	1F	309	1/1	0.92	0.12	43,43,43,43	0
54	MG	1A	3400	1/1	0.92	0.09	35,35,35,35	0
54	MG	1a	1714	1/1	0.92	0.15	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1A	3660	1/1	0.92	0.10	51,51,51,51	0
54	MG	2A	3714	1/1	0.92	0.20	45,45,45,45	0
54	MG	1a	1717	1/1	0.92	0.18	53,53,53,53	0
54	MG	1a	1855	1/1	0.92	0.07	68,68,68,68	0
54	MG	2A	3478	1/1	0.92	0.08	36,36,36,36	0
54	MG	2A	3228	1/1	0.92	0.09	58,58,58,58	0
54	MG	1A	3781	1/1	0.92	0.07	40,40,40,40	0
54	MG	1A	3340	1/1	0.92	0.09	28,28,28,28	0
54	MG	1A	3663	1/1	0.92	0.10	43,43,43,43	0
54	MG	1A	3341	1/1	0.92	0.08	36,36,36,36	0
54	MG	1A	3482	1/1	0.92	0.12	17,17,17,17	0
54	MG	2A	3485	1/1	0.92	0.11	45,45,45,45	0
54	MG	2A	3238	1/1	0.92	0.15	44,44,44,44	0
54	MG	1a	1729	1/1	0.92	0.18	60,60,60,60	0
54	MG	1e	3002	1/1	0.92	0.08	53,53,53,53	0
54	MG	2A	3245	1/1	0.92	0.30	60,60,60,60	0
54	MG	1A	3346	1/1	0.92	0.09	48,48,48,48	0
54	MG	2A	3499	1/1	0.92	0.10	30,30,30,30	0
54	MG	1A	3791	1/1	0.92	0.12	59,59,59,59	0
54	MG	1V	201	1/1	0.92	0.12	50,50,50,50	0
54	MG	1A	3910	1/1	0.92	0.09	59,59,59,59	0
54	MG	1i	3001	1/1	0.92	0.12	53,53,53,53	0
54	MG	1A	3021	1/1	0.92	0.09	38,38,38,38	0
54	MG	10	103	1/1	0.92	0.07	43,43,43,43	0
54	MG	2F	301	1/1	0.92	0.09	39,39,39,39	0
54	MG	2A	3272	1/1	0.92	0.09	38,38,38,38	0
54	MG	1A	3156	1/1	0.92	0.16	49,49,49,49	0
54	MG	1A	3917	1/1	0.92	0.11	51,51,51,51	0
54	MG	2A	3513	1/1	0.92	0.26	50,50,50,50	0
54	MG	2N	8001	1/1	0.92	0.08	70,70,70,70	0
54	MG	1A	3414	1/1	0.92	0.09	49,49,49,49	0
54	MG	2W	8001	1/1	0.92	0.14	42,42,42,42	0
54	MG	1y	3003	1/1	0.92	0.09	74,74,74,74	0
54	MG	1A	3798	1/1	0.92	0.12	35,35,35,35	0
54	MG	17	102	1/1	0.92	0.10	40,40,40,40	0
54	MG	1A	3123	1/1	0.92	0.07	32,32,32,32	0
54	MG	1A	3928	1/1	0.92	0.11	27,27,27,27	0
54	MG	1A	3496	1/1	0.92	0.10	47,47,47,47	0
54	MG	2A	3030	1/1	0.92	0.11	53,53,53,53	0
54	MG	1A	3497	1/1	0.92	0.09	46,46,46,46	0
54	MG	2a	1604	1/1	0.92	0.10	58,58,58,58	0
54	MG	1A	3065	1/1	0.92	0.22	26,26,26,26	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1A	3807	1/1	0.92	0.13	40,40,40,40	0
54	MG	2a	1608	1/1	0.92	0.15	62,62,62,62	0
54	MG	2A	3040	1/1	0.92	0.14	58,58,58,58	0
54	MG	2A	3315	1/1	0.92	0.23	73,73,73,73	0
54	MG	2A	3317	1/1	0.92	0.07	33,33,33,33	0
54	MG	1a	1614	1/1	0.92	0.08	56,56,56,56	0
54	MG	2A	3319	1/1	0.92	0.11	39,39,39,39	0
54	MG	2A	3042	1/1	0.92	0.19	49,49,49,49	0
54	MG	2a	1624	1/1	0.92	0.19	65,65,65,65	0
54	MG	2A	3321	1/1	0.92	0.09	43,43,43,43	0
54	MG	2a	1626	1/1	0.92	0.24	53,53,53,53	0
54	MG	1a	1758	1/1	0.92	0.21	52,52,52,52	0
54	MG	2A	3324	1/1	0.92	0.10	30,30,30,30	0
54	MG	2A	3045	1/1	0.92	0.09	40,40,40,40	0
54	MG	2A	3046	1/1	0.92	0.22	59,59,59,59	0
54	MG	1A	3810	1/1	0.92	0.08	37,37,37,37	0
54	MG	2A	3334	1/1	0.92	0.18	35,35,35,35	0
54	MG	1A	3099	1/1	0.92	0.11	30,30,30,30	0
54	MG	2A	3054	1/1	0.92	0.10	63,63,63,63	0
54	MG	1a	1761	1/1	0.92	0.09	57,57,57,57	0
54	MG	2A	3057	1/1	0.92	0.06	39,39,39,39	0
54	MG	2A	3060	1/1	0.92	0.21	48,48,48,48	0
54	MG	1A	3421	1/1	0.92	0.08	30,30,30,30	0
54	MG	1A	3704	1/1	0.92	0.14	50,50,50,50	0
54	MG	1A	3943	1/1	0.92	0.09	52,52,52,52	0
54	MG	1A	3100	1/1	0.92	0.11	39,39,39,39	0
54	MG	1A	3819	1/1	0.92	0.07	39,39,39,39	0
54	MG	2A	3575	1/1	0.92	0.12	41,41,41,41	0
54	MG	1a	1770	1/1	0.92	0.19	54,54,54,54	0
54	MG	2A	3356	1/1	0.92	0.15	40,40,40,40	0
54	MG	2A	3080	1/1	0.92	0.26	57,57,57,57	0
54	MG	2a	1663	1/1	0.92	0.19	48,48,48,48	0
54	MG	1A	3584	1/1	0.92	0.10	51,51,51,51	0
54	MG	2A	3583	1/1	0.92	0.13	42,42,42,42	0
54	MG	1A	3313	1/1	0.92	0.08	46,46,46,46	0
54	MG	2A	3368	1/1	0.92	0.07	30,30,30,30	0
54	MG	2a	1671	1/1	0.92	0.25	47,47,47,47	0
54	MG	1A	3590	1/1	0.92	0.09	32,32,32,32	0
54	MG	1a	1639	1/1	0.92	0.18	49,49,49,49	0
54	MG	2A	3375	1/1	0.92	0.19	64,64,64,64	0
54	MG	1A	3953	1/1	0.92	0.09	51,51,51,51	0
54	MG	1a	1643	1/1	0.92	0.17	52,52,52,52	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1A	3591	1/1	0.92	0.10	36,36,36,36	0
54	MG	2A	3095	1/1	0.92	0.10	58,58,58,58	0
54	MG	1A	3253	1/1	0.92	0.20	59,59,59,59	0
54	MG	1A	3599	1/1	0.92	0.12	45,45,45,45	0
54	MG	1A	3381	1/1	0.92	0.09	40,40,40,40	0
54	MG	2A	3102	1/1	0.92	0.13	42,42,42,42	0
54	MG	2a	1686	1/1	0.92	0.21	52,52,52,52	0
54	MG	1A	3734	1/1	0.92	0.13	26,26,26,26	0
54	MG	1A	3836	1/1	0.92	0.15	51,51,51,51	0
54	MG	2A	3392	1/1	0.92	0.16	56,56,56,56	0
54	MG	2a	1692	1/1	0.92	0.26	48,48,48,48	0
54	MG	1A	3976	1/1	0.92	0.08	38,38,38,38	0
54	MG	1A	3981	1/1	0.92	0.12	51,51,51,51	0
54	MG	1A	3144	1/1	0.92	0.18	51,51,51,51	0
54	MG	2a	1696	1/1	0.92	0.14	59,59,59,59	0
54	MG	2a	1697	1/1	0.92	0.20	59,59,59,59	0
54	MG	2A	3613	1/1	0.92	0.21	57,57,57,57	0
54	MG	1A	3986	1/1	0.92	0.12	61,61,61,61	0
54	MG	1A	3513	1/1	0.92	0.09	53,53,53,53	0
54	MG	1A	3515	1/1	0.92	0.15	30,30,30,30	0
54	MG	1a	1667	1/1	0.92	0.13	50,50,50,50	0
54	MG	2A	3625	1/1	0.92	0.06	16,16,16,16	0
54	MG	2a	1705	1/1	0.92	0.22	55,55,55,55	0
54	MG	1A	4009	1/1	0.92	0.24	42,42,42,42	0
54	MG	2A	3136	1/1	0.92	0.20	51,51,51,51	0
54	MG	1A	4015	1/1	0.92	0.13	39,39,39,39	0
54	MG	1a	1804	1/1	0.92	0.24	59,59,59,59	0
54	MG	1A	4017	1/1	0.92	0.13	34,34,34,34	0
54	MG	1a	1806	1/1	0.92	0.11	53,53,53,53	0
54	MG	2A	3147	1/1	0.92	0.26	44,44,44,44	0
54	MG	2A	3416	1/1	0.92	0.14	54,54,54,54	0
54	MG	1A	3742	1/1	0.92	0.09	32,32,32,32	0
54	MG	2A	3644	1/1	0.92	0.11	48,48,48,48	0
54	MG	2A	3418	1/1	0.92	0.09	54,54,54,54	0
54	MG	1A	3615	1/1	0.92	0.12	50,50,50,50	0
54	MG	1A	3257	1/1	0.92	0.11	42,42,42,42	0
54	MG	2a	1727	1/1	0.92	0.17	61,61,61,61	0
54	MG	2A	3422	1/1	0.92	0.07	55,55,55,55	0
54	MG	2A	3160	1/1	0.92	0.11	63,63,63,63	0
54	MG	1A	3261	1/1	0.92	0.23	36,36,36,36	0
54	MG	1A	3197	1/1	0.92	0.10	41,41,41,41	0
54	MG	1A	3630	1/1	0.92	0.11	54,54,54,54	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1A	3631	1/1	0.92	0.13	48,48,48,48	0
54	MG	1a	1816	1/1	0.92	0.13	52,52,52,52	0
54	MG	2A	3658	1/1	0.92	0.09	34,34,34,34	0
54	MG	1A	3865	1/1	0.92	0.33	35,35,35,35	0
54	MG	1A	3632	1/1	0.92	0.16	63,63,63,63	0
54	MG	1A	3272	1/1	0.92	0.13	38,38,38,38	0
54	MG	1A	3456	1/1	0.92	0.10	27,27,27,27	0
54	MG	2A	3436	1/1	0.92	0.11	56,56,56,56	0
54	MG	2a	1748	1/1	0.92	0.26	52,52,52,52	0
54	MG	2A	3440	1/1	0.92	0.11	49,49,49,49	0
54	MG	1A	3526	1/1	0.92	0.08	40,40,40,40	0
54	MG	2A	3445	1/1	0.92	0.15	41,41,41,41	0
54	MG	1A	3642	1/1	0.92	0.08	51,51,51,51	0
54	MG	2q	201	1/1	0.92	0.15	64,64,64,64	0
54	MG	2A	3670	1/1	0.92	0.13	49,49,49,49	0
54	MG	2A	3182	1/1	0.92	0.11	53,53,53,53	0
54	MG	1a	1694	1/1	0.92	0.15	32,32,32,32	0
54	MG	2A	3191	1/1	0.92	0.18	57,57,57,57	0
54	MG	1A	3102	1/1	0.92	0.10	53,53,53,53	0
54	MG	1a	1697	1/1	0.92	0.16	51,51,51,51	0
54	MG	1a	1834	1/1	0.92	0.34	58,58,58,58	0
54	MG	1A	3528	1/1	0.92	0.13	43,43,43,43	0
54	MG	1a	1629	1/1	0.93	0.12	45,45,45,45	0
54	MG	1A	3697	1/1	0.93	0.20	50,50,50,50	0
54	MG	2A	3112	1/1	0.93	0.20	44,44,44,44	0
54	MG	1a	1784	1/1	0.93	0.13	59,59,59,59	0
54	MG	1a	1786	1/1	0.93	0.27	57,57,57,57	0
54	MG	1A	3167	1/1	0.93	0.30	28,28,28,28	0
54	MG	1a	1789	1/1	0.93	0.15	69,69,69,69	0
54	MG	2A	3665	1/1	0.93	0.19	56,56,56,56	0
54	MG	1A	3816	1/1	0.93	0.09	35,35,35,35	0
54	MG	2A	3125	1/1	0.93	0.11	38,38,38,38	0
54	MG	2A	3668	1/1	0.93	0.12	48,48,48,48	0
54	MG	1A	3335	1/1	0.93	0.10	22,22,22,22	0
54	MG	1A	3405	1/1	0.93	0.06	17,17,17,17	0
54	MG	1A	3580	1/1	0.93	0.08	22,22,22,22	0
54	MG	1A	3406	1/1	0.93	0.21	52,52,52,52	0
54	MG	1A	3821	1/1	0.93	0.09	26,26,26,26	0
54	MG	2A	3144	1/1	0.93	0.17	54,54,54,54	0
54	MG	1A	3717	1/1	0.93	0.10	52,52,52,52	0
54	MG	2A	3427	1/1	0.93	0.16	57,57,57,57	0
54	MG	1a	1647	1/1	0.93	0.24	52,52,52,52	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	2A	3148	1/1	0.93	0.09	57,57,57,57	0
54	MG	2A	3679	1/1	0.93	0.12	57,57,57,57	0
54	MG	1a	1800	1/1	0.93	0.11	43,43,43,43	0
54	MG	2A	3683	1/1	0.93	0.10	73,73,73,73	0
54	MG	1A	3198	1/1	0.93	0.17	42,42,42,42	0
54	MG	1A	3958	1/1	0.93	0.12	53,53,53,53	0
54	MG	2A	3157	1/1	0.93	0.11	42,42,42,42	0
54	MG	1A	3265	1/1	0.93	0.13	46,46,46,46	0
54	MG	2A	3161	1/1	0.93	0.08	46,46,46,46	0
54	MG	1a	1651	1/1	0.93	0.12	59,59,59,59	0
54	MG	2A	3695	1/1	0.93	0.09	36,36,36,36	0
54	MG	2A	3441	1/1	0.93	0.12	47,47,47,47	0
54	MG	1A	3413	1/1	0.93	0.25	57,57,57,57	0
54	MG	1A	3722	1/1	0.93	0.20	39,39,39,39	0
54	MG	1A	3266	1/1	0.93	0.20	40,40,40,40	0
54	MG	1A	3074	1/1	0.93	0.12	45,45,45,45	0
54	MG	1A	3979	1/1	0.93	0.06	47,47,47,47	0
54	MG	1A	3729	1/1	0.93	0.16	31,31,31,31	0
54	MG	1a	1661	1/1	0.93	0.19	49,49,49,49	0
54	MG	2A	3717	1/1	0.93	0.08	61,61,61,61	0
54	MG	2A	3455	1/1	0.93	0.10	48,48,48,48	0
54	MG	2A	3456	1/1	0.93	0.08	31,31,31,31	0
54	MG	1A	3154	1/1	0.93	0.11	41,41,41,41	0
54	MG	1A	3600	1/1	0.93	0.10	27,27,27,27	0
54	MG	1A	3839	1/1	0.93	0.12	32,32,32,32	0
54	MG	2A	3180	1/1	0.93	0.14	63,63,63,63	0
54	MG	1A	4005	1/1	0.93	0.11	32,32,32,32	0
54	MG	2A	3184	1/1	0.93	0.24	68,68,68,68	0
54	MG	1A	3013	1/1	0.93	0.18	50,50,50,50	0
54	MG	1a	1820	1/1	0.93	0.13	56,56,56,56	0
54	MG	1a	1670	1/1	0.93	0.07	50,50,50,50	0
54	MG	2B	3012	1/1	0.93	0.11	50,50,50,50	0
54	MG	2A	3194	1/1	0.93	0.14	60,60,60,60	0
54	MG	1A	3354	1/1	0.93	0.06	20,20,20,20	0
54	MG	1a	1672	1/1	0.93	0.09	51,51,51,51	0
54	MG	1A	4013	1/1	0.93	0.26	29,29,29,29	0
54	MG	1a	1829	1/1	0.93	0.18	42,42,42,42	0
54	MG	1A	3848	1/1	0.93	0.10	48,48,48,48	0
54	MG	1A	3738	1/1	0.93	0.08	24,24,24,24	0
54	MG	1A	3606	1/1	0.93	0.15	42,42,42,42	0
54	MG	1B	201	1/1	0.93	0.28	34,34,34,34	0
54	MG	1A	3851	1/1	0.93	0.07	41,41,41,41	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	2A	3211	1/1	0.93	0.14	46,46,46,46	0
54	MG	1A	3043	1/1	0.93	0.26	52,52,52,52	0
54	MG	1A	3514	1/1	0.93	0.19	47,47,47,47	0
54	MG	1a	1682	1/1	0.93	0.14	59,59,59,59	0
54	MG	1A	3743	1/1	0.93	0.08	62,62,62,62	0
54	MG	2A	3218	1/1	0.93	0.23	57,57,57,57	0
54	MG	1A	3280	1/1	0.93	0.14	44,44,44,44	0
54	MG	2O	201	1/1	0.93	0.08	48,48,48,48	0
54	MG	2P	201	1/1	0.93	0.15	52,52,52,52	0
54	MG	1A	3617	1/1	0.93	0.09	38,38,38,38	0
54	MG	2A	3487	1/1	0.93	0.15	46,46,46,46	0
54	MG	1a	1687	1/1	0.93	0.19	54,54,54,54	0
54	MG	1a	1688	1/1	0.93	0.21	53,53,53,53	0
54	MG	1A	3866	1/1	0.93	0.07	35,35,35,35	0
54	MG	2A	3229	1/1	0.93	0.27	49,49,49,49	0
54	MG	2A	3494	1/1	0.93	0.08	50,50,50,50	0
54	MG	2A	3496	1/1	0.93	0.12	40,40,40,40	0
54	MG	1A	3220	1/1	0.93	0.18	31,31,31,31	0
54	MG	1A	3619	1/1	0.93	0.22	25,25,25,25	0
54	MG	1B	222	1/1	0.93	0.15	57,57,57,57	0
54	MG	1A	3869	1/1	0.93	0.13	56,56,56,56	0
54	MG	2A	3235	1/1	0.93	0.22	54,54,54,54	0
54	MG	1A	3520	1/1	0.93	0.07	38,38,38,38	0
54	MG	1A	3284	1/1	0.93	0.14	32,32,32,32	0
54	MG	2A	3239	1/1	0.93	0.16	50,50,50,50	0
54	MG	1d	305	1/1	0.93	0.14	56,56,56,56	0
54	MG	2a	1615	1/1	0.93	0.10	60,60,60,60	0
54	MG	2a	1616	1/1	0.93	0.32	60,60,60,60	0
54	MG	2a	1617	1/1	0.93	0.09	43,43,43,43	0
54	MG	1A	3368	1/1	0.93	0.12	16,16,16,16	0
54	MG	2A	3511	1/1	0.93	0.12	43,43,43,43	0
54	MG	1A	3874	1/1	0.93	0.11	43,43,43,43	0
54	MG	1A	3754	1/1	0.93	0.27	37,37,37,37	0
54	MG	1a	1705	1/1	0.93	0.11	59,59,59,59	0
54	MG	1A	3877	1/1	0.93	0.10	57,57,57,57	0
54	MG	1D	311	1/1	0.93	0.08	66,66,66,66	0
54	MG	2A	3260	1/1	0.93	0.14	53,53,53,53	0
54	MG	1A	3230	1/1	0.93	0.23	46,46,46,46	0
54	MG	2a	1631	1/1	0.93	0.17	52,52,52,52	0
54	MG	2A	3262	1/1	0.93	0.21	62,62,62,62	0
54	MG	2A	3527	1/1	0.93	0.14	38,38,38,38	0
54	MG	1g	3003	1/1	0.93	0.11	45,45,45,45	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	2a	1635	1/1	0.93	0.23	71,71,71,71	0
54	MG	2A	3531	1/1	0.93	0.11	54,54,54,54	0
54	MG	1A	3233	1/1	0.93	0.17	48,48,48,48	0
54	MG	1E	305	1/1	0.93	0.08	50,50,50,50	0
54	MG	2A	3273	1/1	0.93	0.16	51,51,51,51	0
54	MG	2a	1640	1/1	0.93	0.23	53,53,53,53	0
54	MG	1E	306	1/1	0.93	0.12	31,31,31,31	0
54	MG	2A	3538	1/1	0.93	0.07	35,35,35,35	0
54	MG	2a	1644	1/1	0.93	0.24	55,55,55,55	0
54	MG	2A	3539	1/1	0.93	0.15	41,41,41,41	0
54	MG	2A	3541	1/1	0.93	0.07	47,47,47,47	0
54	MG	2a	1649	1/1	0.93	0.07	49,49,49,49	0
54	MG	1A	3448	1/1	0.93	0.09	24,24,24,24	0
54	MG	2A	3277	1/1	0.93	0.12	38,38,38,38	0
54	MG	2A	3279	1/1	0.93	0.10	63,63,63,63	0
54	MG	1o	3001	1/1	0.93	0.15	44,44,44,44	0
54	MG	1A	3140	1/1	0.93	0.19	29,29,29,29	0
54	MG	2a	1660	1/1	0.93	0.15	55,55,55,55	0
54	MG	2A	3547	1/1	0.93	0.07	38,38,38,38	0
54	MG	1F	307	1/1	0.93	0.10	31,31,31,31	0
54	MG	1A	3884	1/1	0.93	0.07	48,48,48,48	0
54	MG	2a	1666	1/1	0.93	0.32	57,57,57,57	0
54	MG	1A	3241	1/1	0.93	0.06	43,43,43,43	0
54	MG	1A	3641	1/1	0.93	0.12	29,29,29,29	0
54	MG	2A	3001	1/1	0.93	0.15	46,46,46,46	0
54	MG	1A	3303	1/1	0.93	0.13	55,55,55,55	0
54	MG	2A	3297	1/1	0.93	0.18	51,51,51,51	0
54	MG	2A	3016	1/1	0.93	0.19	37,37,37,37	0
54	MG	2a	1675	1/1	0.93	0.17	56,56,56,56	0
54	MG	1A	3385	1/1	0.93	0.07	51,51,51,51	0
54	MG	2A	3307	1/1	0.93	0.12	51,51,51,51	0
54	MG	1N	202	1/1	0.93	0.10	56,56,56,56	0
54	MG	2A	3020	1/1	0.93	0.07	57,57,57,57	0
54	MG	2A	3021	1/1	0.93	0.08	47,47,47,47	0
54	MG	1N	203	1/1	0.93	0.08	53,53,53,53	0
54	MG	1a	1736	1/1	0.93	0.16	57,57,57,57	0
54	MG	1O	8001	1/1	0.93	0.08	43,43,43,43	0
54	MG	1A	3543	1/1	0.93	0.19	44,44,44,44	0
54	MG	1A	3901	1/1	0.93	0.11	37,37,37,37	0
54	MG	2A	3576	1/1	0.93	0.10	62,62,62,62	0
54	MG	2A	3577	1/1	0.93	0.25	68,68,68,68	0
54	MG	1A	3778	1/1	0.93	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
54	MG	2a	1691	1/1	0.93	0.17	56,56,56,56	0
54	MG	1A	3461	1/1	0.93	0.10	45,45,45,45	0
54	MG	1A	3650	1/1	0.93	0.07	38,38,38,38	0
54	MG	1a	1744	1/1	0.93	0.11	62,62,62,62	0
54	MG	1A	3651	1/1	0.93	0.11	30,30,30,30	0
54	MG	2A	3585	1/1	0.93	0.13	57,57,57,57	0
54	MG	1A	3546	1/1	0.93	0.16	52,52,52,52	0
54	MG	1A	3309	1/1	0.93	0.08	34,34,34,34	0
54	MG	2A	3048	1/1	0.93	0.26	61,61,61,61	0
54	MG	1a	1750	1/1	0.93	0.12	59,59,59,59	0
54	MG	2A	3052	1/1	0.93	0.07	40,40,40,40	0
54	MG	2A	3591	1/1	0.93	0.12	51,51,51,51	0
54	MG	2A	3341	1/1	0.93	0.10	33,33,33,33	0
54	MG	2A	3053	1/1	0.93	0.12	47,47,47,47	0
54	MG	1A	3911	1/1	0.93	0.11	46,46,46,46	0
54	MG	2a	1707	1/1	0.93	0.15	47,47,47,47	0
54	MG	2A	3055	1/1	0.93	0.11	38,38,38,38	0
54	MG	1A	3242	1/1	0.93	0.16	53,53,53,53	0
54	MG	2A	3348	1/1	0.93	0.14	42,42,42,42	0
54	MG	2A	3349	1/1	0.93	0.12	56,56,56,56	0
54	MG	1A	3557	1/1	0.93	0.08	35,35,35,35	0
54	MG	2A	3058	1/1	0.93	0.10	51,51,51,51	0
54	MG	10	106	1/1	0.93	0.17	41,41,41,41	0
54	MG	2A	3061	1/1	0.93	0.15	51,51,51,51	0
54	MG	2A	3609	1/1	0.93	0.13	45,45,45,45	0
54	MG	2A	3357	1/1	0.93	0.14	41,41,41,41	0
54	MG	2a	1724	1/1	0.93	0.20	41,41,41,41	0
54	MG	1A	3559	1/1	0.93	0.12	55,55,55,55	0
54	MG	11	103	1/1	0.93	0.09	42,42,42,42	0
54	MG	2A	3363	1/1	0.93	0.19	61,61,61,61	0
54	MG	1A	3918	1/1	0.93	0.11	38,38,38,38	0
54	MG	1A	3142	1/1	0.93	0.11	50,50,50,50	0
54	MG	2A	3074	1/1	0.93	0.11	39,39,39,39	0
54	MG	1A	3120	1/1	0.93	0.11	44,44,44,44	0
54	MG	1A	3924	1/1	0.93	0.12	45,45,45,45	0
54	MG	1a	1762	1/1	0.93	0.38	56,56,56,56	0
54	MG	2A	3377	1/1	0.93	0.11	43,43,43,43	0
54	MG	1A	3395	1/1	0.93	0.09	13,13,13,13	0
54	MG	1A	3797	1/1	0.93	0.12	34,34,34,34	0
54	MG	1A	3483	1/1	0.93	0.09	49,49,49,49	0
54	MG	2a	1744	1/1	0.93	0.20	50,50,50,50	0
54	MG	2A	3631	1/1	0.93	0.14	60,60,60,60	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	2A	3084	1/1	0.93	0.08	52,52,52,52	0
54	MG	1a	1609	1/1	0.93	0.09	51,51,51,51	0
54	MG	1A	3680	1/1	0.93	0.13	25,25,25,25	0
54	MG	1A	3936	1/1	0.93	0.15	33,33,33,33	0
54	MG	1A	3569	1/1	0.93	0.18	34,34,34,34	0
54	MG	2A	3645	1/1	0.93	0.11	40,40,40,40	0
54	MG	1a	1618	1/1	0.93	0.09	51,51,51,51	0
54	MG	1A	3325	1/1	0.93	0.08	53,53,53,53	0
54	MG	1a	1622	1/1	0.93	0.21	51,51,51,51	0
54	MG	2t	3001	1/1	0.93	0.19	45,45,45,45	0
54	MG	1A	3070	1/1	0.93	0.07	42,42,42,42	0
54	MG	2A	3100	1/1	0.93	0.14	48,48,48,48	0
54	MG	2A	3101	1/1	0.93	0.15	50,50,50,50	0
54	MG	2A	3400	1/1	0.93	0.12	36,36,36,36	0
54	MG	1A	3692	1/1	0.93	0.08	34,34,34,34	0
54	MG	1a	1626	1/1	0.93	0.28	59,59,59,59	0
58	ARG	1B	228	12/12	0.93	0.09	26,40,53,54	0
54	MG	1A	3193	1/1	0.93	0.08	44,44,44,44	0
59	ZN	2n	501	1/1	0.93	0.08	101,101,101,101	0
54	MG	1A	3480	1/1	0.94	0.10	36,36,36,36	0
54	MG	1A	4027	1/1	0.94	0.20	37,37,37,37	0
54	MG	1A	3731	1/1	0.94	0.14	40,40,40,40	0
54	MG	1a	1831	1/1	0.94	0.14	54,54,54,54	0
54	MG	1a	1832	1/1	0.94	0.07	42,42,42,42	0
54	MG	2A	3682	1/1	0.94	0.12	51,51,51,51	0
54	MG	2A	3188	1/1	0.94	0.16	51,51,51,51	0
54	MG	1A	3853	1/1	0.94	0.08	15,15,15,15	0
54	MG	2A	3452	1/1	0.94	0.16	38,38,38,38	0
54	MG	2A	3686	1/1	0.94	0.08	42,42,42,42	0
54	MG	1A	3324	1/1	0.94	0.13	39,39,39,39	0
54	MG	1A	3587	1/1	0.94	0.08	26,26,26,26	0
54	MG	2A	3689	1/1	0.94	0.11	59,59,59,59	0
54	MG	1A	3153	1/1	0.94	0.14	42,42,42,42	0
54	MG	2A	3693	1/1	0.94	0.09	50,50,50,50	0
54	MG	1A	3860	1/1	0.94	0.10	43,43,43,43	0
54	MG	2A	3196	1/1	0.94	0.14	50,50,50,50	0
54	MG	1a	1839	1/1	0.94	0.14	59,59,59,59	0
54	MG	1B	208	1/1	0.94	0.24	51,51,51,51	0
54	MG	2A	3698	1/1	0.94	0.08	40,40,40,40	0
54	MG	1a	1841	1/1	0.94	0.17	57,57,57,57	0
54	MG	1A	3184	1/1	0.94	0.16	50,50,50,50	0
54	MG	2A	3704	1/1	0.94	0.10	33,33,33,33	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1A	3484	1/1	0.94	0.07	35,35,35,35	0
54	MG	1A	3328	1/1	0.94	0.06	13,13,13,13	0
54	MG	1A	3393	1/1	0.94	0.06	18,18,18,18	0
54	MG	1A	3394	1/1	0.94	0.10	18,18,18,18	0
54	MG	2A	3716	1/1	0.94	0.18	51,51,51,51	0
54	MG	2A	3208	1/1	0.94	0.17	43,43,43,43	0
54	MG	2A	3719	1/1	0.94	0.08	48,48,48,48	0
54	MG	2A	3721	1/1	0.94	0.06	42,42,42,42	0
54	MG	1A	3490	1/1	0.94	0.08	50,50,50,50	0
54	MG	2A	3725	1/1	0.94	0.10	37,37,37,37	0
54	MG	1A	3276	1/1	0.94	0.09	26,26,26,26	0
54	MG	1A	3871	1/1	0.94	0.20	50,50,50,50	0
54	MG	1a	1852	1/1	0.94	0.18	54,54,54,54	0
54	MG	1A	3397	1/1	0.94	0.13	49,49,49,49	0
54	MG	1A	3087	1/1	0.94	0.30	26,26,26,26	0
54	MG	1A	3059	1/1	0.94	0.14	42,42,42,42	0
54	MG	1A	3236	1/1	0.94	0.26	38,38,38,38	0
54	MG	2A	3222	1/1	0.94	0.05	46,46,46,46	0
54	MG	1d	301	1/1	0.94	0.07	68,68,68,68	0
54	MG	1A	3125	1/1	0.94	0.21	30,30,30,30	0
54	MG	1d	304	1/1	0.94	0.07	56,56,56,56	0
54	MG	1A	3097	1/1	0.94	0.27	23,23,23,23	0
54	MG	1A	3285	1/1	0.94	0.20	36,36,36,36	0
54	MG	1A	3620	1/1	0.94	0.10	44,44,44,44	0
54	MG	1A	3342	1/1	0.94	0.11	48,48,48,48	0
54	MG	1A	3343	1/1	0.94	0.14	56,56,56,56	0
54	MG	1A	3628	1/1	0.94	0.09	47,47,47,47	0
54	MG	1a	1709	1/1	0.94	0.10	54,54,54,54	0
54	MG	1g	3001	1/1	0.94	0.29	52,52,52,52	0
54	MG	1F	305	1/1	0.94	0.18	34,34,34,34	0
54	MG	1A	3098	1/1	0.94	0.16	35,35,35,35	0
54	MG	1A	3293	1/1	0.94	0.10	18,18,18,18	0
54	MG	2E	303	1/1	0.94	0.14	44,44,44,44	0
54	MG	2A	3495	1/1	0.94	0.16	45,45,45,45	0
54	MG	2F	303	1/1	0.94	0.15	43,43,43,43	0
54	MG	1F	310	1/1	0.94	0.11	42,42,42,42	0
54	MG	2A	3498	1/1	0.94	0.14	30,30,30,30	0
54	MG	1A	3768	1/1	0.94	0.07	54,54,54,54	0
54	MG	1a	1716	1/1	0.94	0.14	39,39,39,39	0
54	MG	2A	3502	1/1	0.94	0.40	64,64,64,64	0
54	MG	1F	312	1/1	0.94	0.08	51,51,51,51	0
54	MG	2A	3253	1/1	0.94	0.14	25,25,25,25	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	2T	3001	1/1	0.94	0.15	50,50,50,50	0
54	MG	1G	3001	1/1	0.94	0.08	52,52,52,52	0
54	MG	1A	3895	1/1	0.94	0.07	16,16,16,16	0
54	MG	1A	3898	1/1	0.94	0.08	21,21,21,21	0
54	MG	1A	3770	1/1	0.94	0.12	27,27,27,27	0
54	MG	2A	3264	1/1	0.94	0.18	48,48,48,48	0
54	MG	1A	3900	1/1	0.94	0.08	40,40,40,40	0
54	MG	1a	1728	1/1	0.94	0.12	51,51,51,51	0
54	MG	2A	3002	1/1	0.94	0.07	53,53,53,53	0
54	MG	2a	1601	1/1	0.94	0.12	48,48,48,48	0
54	MG	1A	3773	1/1	0.94	0.10	64,64,64,64	0
54	MG	2A	3517	1/1	0.94	0.23	46,46,46,46	0
54	MG	2A	3010	1/1	0.94	0.08	54,54,54,54	0
54	MG	1A	3350	1/1	0.94	0.09	29,29,29,29	0
54	MG	2A	3521	1/1	0.94	0.27	51,51,51,51	0
54	MG	1A	3352	1/1	0.94	0.09	20,20,20,20	0
54	MG	1R	202	1/1	0.94	0.13	46,46,46,46	0
54	MG	1A	3353	1/1	0.94	0.09	18,18,18,18	0
54	MG	2a	1613	1/1	0.94	0.17	51,51,51,51	0
54	MG	1A	3779	1/1	0.94	0.10	48,48,48,48	0
54	MG	2A	3025	1/1	0.94	0.10	44,44,44,44	0
54	MG	1A	3295	1/1	0.94	0.09	19,19,19,19	0
54	MG	1T	203	1/1	0.94	0.10	52,52,52,52	0
54	MG	1A	3909	1/1	0.94	0.07	35,35,35,35	0
54	MG	1A	3063	1/1	0.94	0.10	32,32,32,32	0
54	MG	2a	1621	1/1	0.94	0.19	68,68,68,68	0
54	MG	2A	3292	1/1	0.94	0.20	47,47,47,47	0
54	MG	1A	3053	1/1	0.94	0.18	47,47,47,47	0
54	MG	2A	3296	1/1	0.94	0.07	36,36,36,36	0
54	MG	2A	3039	1/1	0.94	0.11	56,56,56,56	0
54	MG	1A	3643	1/1	0.94	0.10	56,56,56,56	0
54	MG	2A	3302	1/1	0.94	0.07	25,25,25,25	0
54	MG	1a	1746	1/1	0.94	0.17	60,60,60,60	0
54	MG	2A	3304	1/1	0.94	0.07	44,44,44,44	0
54	MG	10	102	1/1	0.94	0.06	36,36,36,36	0
54	MG	1A	3914	1/1	0.94	0.08	38,38,38,38	0
54	MG	1A	3423	1/1	0.94	0.12	51,51,51,51	0
54	MG	1A	3427	1/1	0.94	0.11	37,37,37,37	0
54	MG	1A	3361	1/1	0.94	0.13	27,27,27,27	0
54	MG	1A	3299	1/1	0.94	0.09	19,19,19,19	0
54	MG	1a	1753	1/1	0.94	0.18	66,66,66,66	0
54	MG	1A	3432	1/1	0.94	0.11	35,35,35,35	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1A	3363	1/1	0.94	0.10	28,28,28,28	0
54	MG	15	102	1/1	0.94	0.09	42,42,42,42	0
54	MG	1A	3659	1/1	0.94	0.15	52,52,52,52	0
54	MG	2a	1643	1/1	0.94	0.11	55,55,55,55	0
54	MG	2A	3325	1/1	0.94	0.11	40,40,40,40	0
54	MG	2A	3326	1/1	0.94	0.11	61,61,61,61	0
54	MG	1A	3531	1/1	0.94	0.20	40,40,40,40	0
54	MG	2a	1647	1/1	0.94	0.22	52,52,52,52	0
54	MG	2a	1648	1/1	0.94	0.25	60,60,60,60	0
54	MG	2A	3329	1/1	0.94	0.11	29,29,29,29	0
54	MG	1A	3929	1/1	0.94	0.13	38,38,38,38	0
54	MG	1a	1602	1/1	0.94	0.10	71,71,71,71	0
54	MG	2A	3059	1/1	0.94	0.09	42,42,42,42	0
54	MG	1A	3930	1/1	0.94	0.08	60,60,60,60	0
54	MG	2A	3337	1/1	0.94	0.07	38,38,38,38	0
54	MG	2A	3573	1/1	0.94	0.09	19,19,19,19	0
54	MG	1a	1605	1/1	0.94	0.20	56,56,56,56	0
54	MG	1A	3031	1/1	0.94	0.09	39,39,39,39	0
54	MG	1A	3535	1/1	0.94	0.09	38,38,38,38	0
54	MG	1A	3537	1/1	0.94	0.18	46,46,46,46	0
54	MG	1a	1610	1/1	0.94	0.06	44,44,44,44	0
54	MG	2A	3073	1/1	0.94	0.14	45,45,45,45	0
54	MG	1A	3802	1/1	0.94	0.07	47,47,47,47	0
54	MG	1A	3438	1/1	0.94	0.10	43,43,43,43	0
54	MG	1a	1616	1/1	0.94	0.12	60,60,60,60	0
54	MG	1A	3539	1/1	0.94	0.09	22,22,22,22	0
54	MG	1A	3366	1/1	0.94	0.13	16,16,16,16	0
54	MG	1a	1620	1/1	0.94	0.06	43,43,43,43	0
54	MG	1a	1775	1/1	0.94	0.20	59,59,59,59	0
54	MG	1A	3809	1/1	0.94	0.14	39,39,39,39	0
54	MG	1A	3441	1/1	0.94	0.13	34,34,34,34	0
54	MG	2A	3358	1/1	0.94	0.15	38,38,38,38	0
54	MG	2A	3593	1/1	0.94	0.08	53,53,53,53	0
54	MG	2A	3359	1/1	0.94	0.14	52,52,52,52	0
54	MG	1A	3812	1/1	0.94	0.14	35,35,35,35	0
54	MG	1A	3442	1/1	0.94	0.07	15,15,15,15	0
54	MG	1a	1780	1/1	0.94	0.15	60,60,60,60	0
54	MG	1a	1781	1/1	0.94	0.13	58,58,58,58	0
54	MG	2A	3367	1/1	0.94	0.15	47,47,47,47	0
54	MG	1A	3814	1/1	0.94	0.10	25,25,25,25	0
54	MG	1a	1627	1/1	0.94	0.22	54,54,54,54	0
54	MG	1A	3367	1/1	0.94	0.17	18,18,18,18	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	2A	3373	1/1	0.94	0.17	55,55,55,55	0
54	MG	2A	3606	1/1	0.94	0.10	50,50,50,50	0
54	MG	2A	3607	1/1	0.94	0.22	62,62,62,62	0
54	MG	2A	3099	1/1	0.94	0.14	43,43,43,43	0
54	MG	1a	1785	1/1	0.94	0.07	47,47,47,47	0
54	MG	1A	3037	1/1	0.94	0.17	39,39,39,39	0
54	MG	1A	3555	1/1	0.94	0.08	39,39,39,39	0
54	MG	1A	3260	1/1	0.94	0.07	38,38,38,38	0
54	MG	2a	1701	1/1	0.94	0.21	42,42,42,42	0
54	MG	2A	3105	1/1	0.94	0.15	46,46,46,46	0
54	MG	2A	3615	1/1	0.94	0.12	35,35,35,35	0
54	MG	2A	3617	1/1	0.94	0.14	46,46,46,46	0
54	MG	2A	3618	1/1	0.94	0.09	50,50,50,50	0
54	MG	1A	3695	1/1	0.94	0.09	49,49,49,49	0
54	MG	2A	3620	1/1	0.94	0.08	48,48,48,48	0
54	MG	1a	1635	1/1	0.94	0.10	34,34,34,34	0
54	MG	1A	3955	1/1	0.94	0.10	39,39,39,39	0
54	MG	1A	3372	1/1	0.94	0.13	47,47,47,47	0
54	MG	2a	1713	1/1	0.94	0.38	55,55,55,55	0
54	MG	1A	3375	1/1	0.94	0.07	16,16,16,16	0
54	MG	1A	3312	1/1	0.94	0.07	17,17,17,17	0
54	MG	2A	3391	1/1	0.94	0.12	49,49,49,49	0
54	MG	1a	1796	1/1	0.94	0.19	50,50,50,50	0
54	MG	2A	3118	1/1	0.94	0.18	54,54,54,54	0
54	MG	2A	3120	1/1	0.94	0.12	41,41,41,41	0
54	MG	2A	3121	1/1	0.94	0.08	53,53,53,53	0
54	MG	1A	3566	1/1	0.94	0.10	35,35,35,35	0
54	MG	2A	3634	1/1	0.94	0.14	42,42,42,42	0
54	MG	1a	1798	1/1	0.94	0.16	61,61,61,61	0
54	MG	2A	3636	1/1	0.94	0.18	47,47,47,47	0
54	MG	1A	3826	1/1	0.94	0.12	26,26,26,26	0
54	MG	2A	3402	1/1	0.94	0.08	43,43,43,43	0
54	MG	2a	1731	1/1	0.94	0.18	61,61,61,61	0
54	MG	1a	1646	1/1	0.94	0.21	48,48,48,48	0
54	MG	2A	3131	1/1	0.94	0.31	44,44,44,44	0
54	MG	2A	3133	1/1	0.94	0.16	47,47,47,47	0
54	MG	1a	1801	1/1	0.94	0.12	43,43,43,43	0
54	MG	2a	1739	1/1	0.94	0.13	51,51,51,51	0
54	MG	1A	3460	1/1	0.94	0.20	30,30,30,30	0
54	MG	1A	3050	1/1	0.94	0.10	27,27,27,27	0
54	MG	1A	3977	1/1	0.94	0.12	38,38,38,38	0
54	MG	1A	3710	1/1	0.94	0.14	38,38,38,38	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1A	3712	1/1	0.94	0.14	52,52,52,52	0
54	MG	2A	3414	1/1	0.94	0.12	46,46,46,46	0
54	MG	1A	3466	1/1	0.94	0.10	40,40,40,40	0
54	MG	1A	3468	1/1	0.94	0.09	45,45,45,45	0
54	MG	1A	3209	1/1	0.94	0.11	52,52,52,52	0
54	MG	1a	1656	1/1	0.94	0.08	63,63,63,63	0
54	MG	1A	3998	1/1	0.94	0.21	32,32,32,32	0
54	MG	2f	3001	1/1	0.94	0.08	44,44,44,44	0
54	MG	1A	3472	1/1	0.94	0.07	20,20,20,20	0
54	MG	1A	3151	1/1	0.94	0.19	40,40,40,40	0
54	MG	1A	3474	1/1	0.94	0.17	44,44,44,44	0
54	MG	1A	3478	1/1	0.94	0.09	16,16,16,16	0
54	MG	1A	3578	1/1	0.94	0.12	23,23,23,23	0
56	EZP	2A	3709	25/25	0.94	0.11	38,42,50,58	0
54	MG	1a	1666	1/1	0.94	0.12	50,50,50,50	0
54	MG	1A	4016	1/1	0.94	0.12	41,41,41,41	0
54	MG	1A	3321	1/1	0.94	0.07	16,16,16,16	0
54	MG	1a	1823	1/1	0.94	0.13	48,48,48,48	0
54	MG	1A	4020	1/1	0.94	0.27	27,27,27,27	0
54	MG	1A	4021	1/1	0.94	0.21	35,35,35,35	0
54	MG	2A	3176	1/1	0.94	0.17	42,42,42,42	0
54	MG	1a	1826	1/1	0.94	0.12	58,58,58,58	0
54	MG	2A	3438	1/1	0.94	0.11	50,50,50,50	0
54	MG	1a	1849	1/1	0.95	0.12	47,47,47,47	0
54	MG	1a	1689	1/1	0.95	0.18	55,55,55,55	0
54	MG	1B	217	1/1	0.95	0.14	61,61,61,61	0
54	MG	1B	218	1/1	0.95	0.06	50,50,50,50	0
54	MG	2A	3199	1/1	0.95	0.08	47,47,47,47	0
54	MG	1A	3852	1/1	0.95	0.17	30,30,30,30	0
54	MG	1A	3451	1/1	0.95	0.08	15,15,15,15	0
54	MG	1A	3560	1/1	0.95	0.08	40,40,40,40	0
54	MG	1a	1698	1/1	0.95	0.11	36,36,36,36	0
54	MG	1A	3714	1/1	0.95	0.11	37,37,37,37	0
54	MG	2A	3700	1/1	0.95	0.14	21,21,21,21	0
54	MG	2A	3206	1/1	0.95	0.08	45,45,45,45	0
54	MG	1A	3369	1/1	0.95	0.07	16,16,16,16	0
54	MG	1B	226	1/1	0.95	0.06	60,60,60,60	0
54	MG	2A	3705	1/1	0.95	0.44	45,45,45,45	0
54	MG	1A	3454	1/1	0.95	0.09	22,22,22,22	0
54	MG	1A	3370	1/1	0.95	0.06	21,21,21,21	0
54	MG	1A	3864	1/1	0.95	0.05	36,36,36,36	0
54	MG	1D	304	1/1	0.95	0.05	33,33,33,33	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	2A	3715	1/1	0.95	0.28	37,37,37,37	0
54	MG	1A	3232	1/1	0.95	0.17	31,31,31,31	0
54	MG	2A	3217	1/1	0.95	0.07	43,43,43,43	0
54	MG	2A	3718	1/1	0.95	0.13	44,44,44,44	0
54	MG	1A	3458	1/1	0.95	0.11	21,21,21,21	0
54	MG	1a	1711	1/1	0.95	0.22	58,58,58,58	0
54	MG	1A	3459	1/1	0.95	0.10	23,23,23,23	0
54	MG	1A	3174	1/1	0.95	0.14	34,34,34,34	0
54	MG	1A	3374	1/1	0.95	0.12	50,50,50,50	0
54	MG	1A	3464	1/1	0.95	0.10	56,56,56,56	0
54	MG	1l	3001	1/1	0.95	0.09	47,47,47,47	0
54	MG	1A	3465	1/1	0.95	0.10	33,33,33,33	0
54	MG	1A	3234	1/1	0.95	0.23	24,24,24,24	0
54	MG	2B	3006	1/1	0.95	0.18	57,57,57,57	0
54	MG	1A	3576	1/1	0.95	0.08	43,43,43,43	0
54	MG	1A	3733	1/1	0.95	0.09	42,42,42,42	0
54	MG	1A	3377	1/1	0.95	0.17	44,44,44,44	0
54	MG	1A	3735	1/1	0.95	0.08	32,32,32,32	0
54	MG	1a	1723	1/1	0.95	0.07	50,50,50,50	0
54	MG	1A	3469	1/1	0.95	0.08	29,29,29,29	0
54	MG	1A	3305	1/1	0.95	0.07	39,39,39,39	0
54	MG	2A	3491	1/1	0.95	0.13	46,46,46,46	0
54	MG	1A	3581	1/1	0.95	0.07	53,53,53,53	0
54	MG	1A	3471	1/1	0.95	0.05	31,31,31,31	0
54	MG	1A	3308	1/1	0.95	0.15	34,34,34,34	0
54	MG	2A	3247	1/1	0.95	0.06	50,50,50,50	0
54	MG	1a	1732	1/1	0.95	0.10	59,59,59,59	0
54	MG	1A	3014	1/1	0.95	0.10	44,44,44,44	0
54	MG	1A	3886	1/1	0.95	0.11	52,52,52,52	0
54	MG	1N	201	1/1	0.95	0.16	35,35,35,35	0
54	MG	1A	3310	1/1	0.95	0.11	38,38,38,38	0
54	MG	2A	3023	1/1	0.95	0.09	55,55,55,55	0
54	MG	2E	305	1/1	0.95	0.20	52,52,52,52	0
54	MG	1A	3384	1/1	0.95	0.12	14,14,14,14	0
54	MG	2F	302	1/1	0.95	0.11	49,49,49,49	0
54	MG	1A	3746	1/1	0.95	0.11	59,59,59,59	0
54	MG	2A	3263	1/1	0.95	0.13	32,32,32,32	0
54	MG	1a	1741	1/1	0.95	0.12	51,51,51,51	0
54	MG	1A	3311	1/1	0.95	0.07	35,35,35,35	0
54	MG	2A	3267	1/1	0.95	0.10	52,52,52,52	0
54	MG	2A	3033	1/1	0.95	0.20	46,46,46,46	0
54	MG	2A	3034	1/1	0.95	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
54	MG	2A	3035	1/1	0.95	0.05	29,29,29,29	0
54	MG	2Q	3001	1/1	0.95	0.13	61,61,61,61	0
54	MG	1A	3594	1/1	0.95	0.21	54,54,54,54	0
54	MG	1A	3595	1/1	0.95	0.13	16,16,16,16	0
54	MG	2A	3518	1/1	0.95	0.12	41,41,41,41	0
54	MG	1a	1745	1/1	0.95	0.13	47,47,47,47	0
54	MG	1A	3178	1/1	0.95	0.12	29,29,29,29	0
54	MG	2A	3280	1/1	0.95	0.06	58,58,58,58	0
54	MG	1A	3106	1/1	0.95	0.17	40,40,40,40	0
54	MG	2A	3282	1/1	0.95	0.12	33,33,33,33	0
54	MG	1A	3902	1/1	0.95	0.12	52,52,52,52	0
54	MG	2A	3043	1/1	0.95	0.39	68,68,68,68	0
54	MG	1A	3110	1/1	0.95	0.07	37,37,37,37	0
54	MG	1U	202	1/1	0.95	0.09	48,48,48,48	0
54	MG	1A	3755	1/1	0.95	0.07	47,47,47,47	0
54	MG	1A	3112	1/1	0.95	0.23	34,34,34,34	0
54	MG	2a	1606	1/1	0.95	0.11	45,45,45,45	0
54	MG	1A	3317	1/1	0.95	0.13	56,56,56,56	0
54	MG	2A	3293	1/1	0.95	0.07	35,35,35,35	0
54	MG	1A	3758	1/1	0.95	0.06	42,42,42,42	0
54	MG	1A	3605	1/1	0.95	0.12	44,44,44,44	0
54	MG	1A	3320	1/1	0.95	0.05	24,24,24,24	0
54	MG	1A	3763	1/1	0.95	0.11	46,46,46,46	0
54	MG	1A	3608	1/1	0.95	0.12	50,50,50,50	0
54	MG	1A	3251	1/1	0.95	0.13	23,23,23,23	0
54	MG	1A	3188	1/1	0.95	0.16	53,53,53,53	0
54	MG	2A	3305	1/1	0.95	0.10	26,26,26,26	0
54	MG	1A	3767	1/1	0.95	0.07	45,45,45,45	0
54	MG	1A	3117	1/1	0.95	0.19	39,39,39,39	0
54	MG	2a	1622	1/1	0.95	0.18	56,56,56,56	0
54	MG	1A	3086	1/1	0.95	0.17	26,26,26,26	0
54	MG	1a	1764	1/1	0.95	0.12	61,61,61,61	0
54	MG	2A	3550	1/1	0.95	0.11	31,31,31,31	0
54	MG	1A	3401	1/1	0.95	0.08	45,45,45,45	0
54	MG	2A	3065	1/1	0.95	0.08	49,49,49,49	0
54	MG	2A	3067	1/1	0.95	0.13	45,45,45,45	0
54	MG	1A	3061	1/1	0.95	0.12	43,43,43,43	0
54	MG	2A	3069	1/1	0.95	0.06	40,40,40,40	0
54	MG	2A	3322	1/1	0.95	0.15	49,49,49,49	0
54	MG	2A	3560	1/1	0.95	0.11	43,43,43,43	0
54	MG	2A	3070	1/1	0.95	0.17	42,42,42,42	0
54	MG	1A	3925	1/1	0.95	0.21	49,49,49,49	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1A	3259	1/1	0.95	0.29	62,62,62,62	0
54	MG	1A	3001	1/1	0.95	0.08	27,27,27,27	0
54	MG	2A	3327	1/1	0.95	0.11	48,48,48,48	0
54	MG	1A	3333	1/1	0.95	0.06	25,25,25,25	0
54	MG	2A	3075	1/1	0.95	0.35	42,42,42,42	0
54	MG	2A	3076	1/1	0.95	0.14	44,44,44,44	0
54	MG	2A	3077	1/1	0.95	0.07	32,32,32,32	0
54	MG	1a	1607	1/1	0.95	0.22	51,51,51,51	0
54	MG	1A	3334	1/1	0.95	0.11	25,25,25,25	0
54	MG	1A	3931	1/1	0.95	0.06	34,34,34,34	0
54	MG	1A	3932	1/1	0.95	0.08	58,58,58,58	0
54	MG	2A	3578	1/1	0.95	0.07	47,47,47,47	0
54	MG	1a	1611	1/1	0.95	0.19	37,37,37,37	0
54	MG	1A	3933	1/1	0.95	0.09	41,41,41,41	0
54	MG	1a	1613	1/1	0.95	0.09	60,60,60,60	0
54	MG	1A	3194	1/1	0.95	0.26	54,54,54,54	0
54	MG	2a	1652	1/1	0.95	0.26	48,48,48,48	0
54	MG	2a	1653	1/1	0.95	0.20	53,53,53,53	0
54	MG	1A	3264	1/1	0.95	0.25	42,42,42,42	0
54	MG	2A	3344	1/1	0.95	0.13	37,37,37,37	0
54	MG	1A	3412	1/1	0.95	0.09	45,45,45,45	0
54	MG	1A	3633	1/1	0.95	0.19	51,51,51,51	0
54	MG	2a	1661	1/1	0.95	0.32	54,54,54,54	0
54	MG	1A	3095	1/1	0.95	0.07	49,49,49,49	0
54	MG	1A	3787	1/1	0.95	0.18	40,40,40,40	0
54	MG	1A	3028	1/1	0.95	0.05	30,30,30,30	0
54	MG	2A	3351	1/1	0.95	0.12	25,25,25,25	0
54	MG	2a	1667	1/1	0.95	0.31	56,56,56,56	0
54	MG	1A	3512	1/1	0.95	0.20	40,40,40,40	0
54	MG	1A	3268	1/1	0.95	0.09	46,46,46,46	0
54	MG	1a	1625	1/1	0.95	0.07	51,51,51,51	0
54	MG	1A	3127	1/1	0.95	0.08	49,49,49,49	0
54	MG	1A	3944	1/1	0.95	0.08	47,47,47,47	0
54	MG	1A	3946	1/1	0.95	0.08	44,44,44,44	0
54	MG	1A	3204	1/1	0.95	0.22	27,27,27,27	0
54	MG	1A	3516	1/1	0.95	0.08	31,31,31,31	0
54	MG	1A	3517	1/1	0.95	0.09	48,48,48,48	0
54	MG	2A	3109	1/1	0.95	0.27	39,39,39,39	0
54	MG	2A	3365	1/1	0.95	0.20	32,32,32,32	0
54	MG	2A	3603	1/1	0.95	0.17	32,32,32,32	0
54	MG	2A	3366	1/1	0.95	0.08	31,31,31,31	0
54	MG	1A	3274	1/1	0.95	0.05	40,40,40,40	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1A	3519	1/1	0.95	0.06	38,38,38,38	0
54	MG	2A	3608	1/1	0.95	0.06	40,40,40,40	0
54	MG	2A	3369	1/1	0.95	0.24	51,51,51,51	0
54	MG	1A	3046	1/1	0.95	0.15	39,39,39,39	0
54	MG	1A	3348	1/1	0.95	0.13	41,41,41,41	0
54	MG	1A	3424	1/1	0.95	0.10	41,41,41,41	0
54	MG	2A	3116	1/1	0.95	0.26	53,53,53,53	0
54	MG	2A	3117	1/1	0.95	0.06	36,36,36,36	0
54	MG	1A	3425	1/1	0.95	0.12	35,35,35,35	0
54	MG	1a	1641	1/1	0.95	0.22	54,54,54,54	0
54	MG	1A	3808	1/1	0.95	0.18	41,41,41,41	0
54	MG	1A	3960	1/1	0.95	0.08	32,32,32,32	0
54	MG	2A	3123	1/1	0.95	0.19	49,49,49,49	0
54	MG	1A	3661	1/1	0.95	0.10	32,32,32,32	0
54	MG	2A	3622	1/1	0.95	0.12	18,18,18,18	0
54	MG	1A	3963	1/1	0.95	0.17	38,38,38,38	0
54	MG	1A	3426	1/1	0.95	0.08	14,14,14,14	0
54	MG	2A	3387	1/1	0.95	0.08	45,45,45,45	0
54	MG	2A	3128	1/1	0.95	0.26	45,45,45,45	0
54	MG	1A	3206	1/1	0.95	0.15	18,18,18,18	0
54	MG	2A	3132	1/1	0.95	0.14	43,43,43,43	0
54	MG	1A	3665	1/1	0.95	0.06	32,32,32,32	0
54	MG	1A	3974	1/1	0.95	0.19	45,45,45,45	0
54	MG	2A	3395	1/1	0.95	0.22	56,56,56,56	0
54	MG	1A	3667	1/1	0.95	0.07	40,40,40,40	0
54	MG	2a	1710	1/1	0.95	0.22	56,56,56,56	0
54	MG	2A	3139	1/1	0.95	0.09	58,58,58,58	0
54	MG	1A	3207	1/1	0.95	0.15	39,39,39,39	0
54	MG	1A	3132	1/1	0.95	0.10	40,40,40,40	0
54	MG	2A	3639	1/1	0.95	0.07	56,56,56,56	0
54	MG	2a	1716	1/1	0.95	0.37	57,57,57,57	0
54	MG	1A	3671	1/1	0.95	0.05	15,15,15,15	0
54	MG	2a	1718	1/1	0.95	0.08	63,63,63,63	0
54	MG	2A	3641	1/1	0.95	0.16	46,46,46,46	0
54	MG	2A	3642	1/1	0.95	0.18	57,57,57,57	0
54	MG	2A	3145	1/1	0.95	0.25	44,44,44,44	0
54	MG	1A	3673	1/1	0.95	0.08	28,28,28,28	0
54	MG	2a	1723	1/1	0.95	0.18	45,45,45,45	0
54	MG	1A	3529	1/1	0.95	0.09	47,47,47,47	0
54	MG	1A	3676	1/1	0.95	0.08	28,28,28,28	0
54	MG	1A	3677	1/1	0.95	0.10	43,43,43,43	0
54	MG	1A	3822	1/1	0.95	0.05	40,40,40,40	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1a	1664	1/1	0.95	0.17	51,51,51,51	0
54	MG	1A	3163	1/1	0.95	0.10	47,47,47,47	0
54	MG	2A	3653	1/1	0.95	0.11	48,48,48,48	0
54	MG	2a	1732	1/1	0.95	0.44	60,60,60,60	0
54	MG	2A	3159	1/1	0.95	0.12	50,50,50,50	0
54	MG	1A	3211	1/1	0.95	0.09	37,37,37,37	0
54	MG	1A	4010	1/1	0.95	0.35	31,31,31,31	0
54	MG	1A	3435	1/1	0.95	0.11	37,37,37,37	0
54	MG	1A	3048	1/1	0.95	0.10	33,33,33,33	0
54	MG	1A	3830	1/1	0.95	0.09	41,41,41,41	0
54	MG	1A	3286	1/1	0.95	0.09	56,56,56,56	0
54	MG	2A	3168	1/1	0.95	0.09	54,54,54,54	0
54	MG	1A	3689	1/1	0.95	0.07	22,22,22,22	0
54	MG	1A	3217	1/1	0.95	0.31	30,30,30,30	0
54	MG	2A	3172	1/1	0.95	0.10	56,56,56,56	0
54	MG	1A	3292	1/1	0.95	0.14	56,56,56,56	0
54	MG	2A	3174	1/1	0.95	0.32	45,45,45,45	0
54	MG	1A	4025	1/1	0.95	0.12	30,30,30,30	0
54	MG	1A	3081	1/1	0.95	0.31	34,34,34,34	0
54	MG	1A	3444	1/1	0.95	0.09	24,24,24,24	0
54	MG	1A	3222	1/1	0.95	0.20	32,32,32,32	0
54	MG	1A	3446	1/1	0.95	0.10	20,20,20,20	0
54	MG	1A	3700	1/1	0.95	0.08	34,34,34,34	0
54	MG	1A	3552	1/1	0.95	0.11	45,45,45,45	0
54	MG	2A	3183	1/1	0.95	0.10	53,53,53,53	0
54	MG	2A	3437	1/1	0.95	0.06	58,58,58,58	0
56	EZP	1A	3987	25/25	0.95	0.10	16,28,47,60	0
54	MG	1A	3226	1/1	0.95	0.12	32,32,32,32	0
54	MG	2A	3439	1/1	0.95	0.26	64,64,64,64	0
54	MG	2A	3186	1/1	0.95	0.17	34,34,34,34	0
57	MPD	18	102	8/8	0.95	0.13	22,28,35,36	0
54	MG	1A	3141	1/1	0.95	0.08	38,38,38,38	0
54	MG	1a	1685	1/1	0.95	0.22	40,40,40,40	0
54	MG	1B	210	1/1	0.95	0.07	50,50,50,50	0
54	MG	2A	3446	1/1	0.95	0.08	30,30,30,30	0
54	MG	2A	3192	1/1	0.95	0.08	52,52,52,52	0
54	MG	1A	3705	1/1	0.95	0.13	48,48,48,48	0
54	MG	1A	3707	1/1	0.95	0.06	40,40,40,40	0
54	MG	1A	3613	1/1	0.96	0.06	50,50,50,50	0
54	MG	1A	3965	1/1	0.96	0.18	10,10,10,10	0
54	MG	1A	3845	1/1	0.96	0.12	37,37,37,37	0
54	MG	1A	3614	1/1	0.96	0.08	17,17,17,17	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1A	3970	1/1	0.96	0.40	40,40,40,40	0
54	MG	2A	3249	1/1	0.96	0.11	45,45,45,45	0
54	MG	2A	3712	1/1	0.96	0.11	41,41,41,41	0
54	MG	2A	3250	1/1	0.96	0.12	46,46,46,46	0
54	MG	2A	3050	1/1	0.96	0.23	58,58,58,58	0
54	MG	2A	3051	1/1	0.96	0.11	38,38,38,38	0
54	MG	1a	1615	1/1	0.96	0.18	59,59,59,59	0
54	MG	2A	3257	1/1	0.96	0.12	43,43,43,43	0
54	MG	1A	3247	1/1	0.96	0.09	40,40,40,40	0
54	MG	2A	3720	1/1	0.96	0.06	44,44,44,44	0
54	MG	1A	3376	1/1	0.96	0.06	29,29,29,29	0
54	MG	2A	3722	1/1	0.96	0.10	48,48,48,48	0
54	MG	1A	3004	1/1	0.96	0.10	43,43,43,43	0
54	MG	1A	3449	1/1	0.96	0.10	17,17,17,17	0
54	MG	1A	3980	1/1	0.96	0.10	48,48,48,48	0
54	MG	1A	3250	1/1	0.96	0.21	27,27,27,27	0
54	MG	1A	3982	1/1	0.96	0.06	49,49,49,49	0
54	MG	2A	3490	1/1	0.96	0.19	44,44,44,44	0
54	MG	2A	3266	1/1	0.96	0.11	40,40,40,40	0
54	MG	1A	3002	1/1	0.96	0.07	47,47,47,47	0
54	MG	2A	3268	1/1	0.96	0.07	29,29,29,29	0
54	MG	1A	3856	1/1	0.96	0.15	42,42,42,42	0
54	MG	1A	3622	1/1	0.96	0.07	51,51,51,51	0
54	MG	2A	3064	1/1	0.96	0.11	21,21,21,21	0
54	MG	2A	3497	1/1	0.96	0.13	43,43,43,43	0
54	MG	1A	3995	1/1	0.96	0.05	26,26,26,26	0
54	MG	2A	3066	1/1	0.96	0.19	51,51,51,51	0
54	MG	2A	3276	1/1	0.96	0.08	44,44,44,44	0
54	MG	1A	3624	1/1	0.96	0.14	45,45,45,45	0
54	MG	2A	3278	1/1	0.96	0.07	25,25,25,25	0
54	MG	1A	3999	1/1	0.96	0.22	32,32,32,32	0
54	MG	1A	4001	1/1	0.96	0.12	37,37,37,37	0
54	MG	2D	303	1/1	0.96	0.11	40,40,40,40	0
54	MG	1A	3054	1/1	0.96	0.11	21,21,21,21	0
54	MG	1A	3627	1/1	0.96	0.16	30,30,30,30	0
54	MG	1A	4008	1/1	0.96	0.13	28,28,28,28	0
54	MG	2A	3284	1/1	0.96	0.05	55,55,55,55	0
54	MG	1A	3862	1/1	0.96	0.12	33,33,33,33	0
54	MG	1A	3101	1/1	0.96	0.13	30,30,30,30	0
54	MG	1A	4012	1/1	0.96	0.31	25,25,25,25	0
54	MG	2E	306	1/1	0.96	0.18	44,44,44,44	0
54	MG	1A	3629	1/1	0.96	0.07	41,41,41,41	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	2A	3289	1/1	0.96	0.08	47,47,47,47	0
54	MG	2A	3290	1/1	0.96	0.13	30,30,30,30	0
54	MG	1A	3530	1/1	0.96	0.08	44,44,44,44	0
54	MG	1A	3255	1/1	0.96	0.20	31,31,31,31	0
54	MG	1A	3071	1/1	0.96	0.25	29,29,29,29	0
54	MG	2A	3522	1/1	0.96	0.17	47,47,47,47	0
54	MG	1A	4018	1/1	0.96	0.08	36,36,36,36	0
54	MG	2A	3295	1/1	0.96	0.09	55,55,55,55	0
54	MG	1A	3040	1/1	0.96	0.09	26,26,26,26	0
54	MG	2P	202	1/1	0.96	0.09	59,59,59,59	0
54	MG	1A	3634	1/1	0.96	0.08	59,59,59,59	0
54	MG	2Q	3002	1/1	0.96	0.06	55,55,55,55	0
54	MG	2R	201	1/1	0.96	0.09	35,35,35,35	0
54	MG	1A	4022	1/1	0.96	0.06	30,30,30,30	0
54	MG	2T	3002	1/1	0.96	0.16	61,61,61,61	0
54	MG	1A	3536	1/1	0.96	0.06	26,26,26,26	0
54	MG	2T	3004	1/1	0.96	0.05	44,44,44,44	0
54	MG	1A	3388	1/1	0.96	0.11	22,22,22,22	0
54	MG	1A	3322	1/1	0.96	0.09	21,21,21,21	0
54	MG	2A	3089	1/1	0.96	0.10	41,41,41,41	0
54	MG	1A	3640	1/1	0.96	0.06	45,45,45,45	0
54	MG	2A	3535	1/1	0.96	0.05	42,42,42,42	0
54	MG	2A	3093	1/1	0.96	0.08	58,58,58,58	0
54	MG	28	8001	1/1	0.96	0.08	46,46,46,46	0
54	MG	2A	3309	1/1	0.96	0.08	25,25,25,25	0
54	MG	2A	3310	1/1	0.96	0.09	29,29,29,29	0
54	MG	1A	3390	1/1	0.96	0.13	40,40,40,40	0
54	MG	1a	1655	1/1	0.96	0.04	57,57,57,57	0
54	MG	2A	3316	1/1	0.96	0.15	41,41,41,41	0
54	MG	1A	3258	1/1	0.96	0.12	32,32,32,32	0
54	MG	1A	3878	1/1	0.96	0.13	57,57,57,57	0
54	MG	1A	3761	1/1	0.96	0.06	32,32,32,32	0
54	MG	1A	3762	1/1	0.96	0.08	19,19,19,19	0
54	MG	1a	1660	1/1	0.96	0.18	46,46,46,46	0
54	MG	1A	3108	1/1	0.96	0.20	42,42,42,42	0
54	MG	1A	3326	1/1	0.96	0.07	38,38,38,38	0
54	MG	1A	3078	1/1	0.96	0.12	47,47,47,47	0
54	MG	2A	3104	1/1	0.96	0.09	42,42,42,42	0
54	MG	1B	212	1/1	0.96	0.05	53,53,53,53	0
54	MG	1A	3550	1/1	0.96	0.12	53,53,53,53	0
54	MG	2A	3107	1/1	0.96	0.13	43,43,43,43	0
54	MG	2A	3557	1/1	0.96	0.08	22,22,22,22	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1B	216	1/1	0.96	0.07	33,33,33,33	0
54	MG	2A	3559	1/1	0.96	0.10	32,32,32,32	0
54	MG	1A	3080	1/1	0.96	0.20	37,37,37,37	0
54	MG	2A	3561	1/1	0.96	0.09	38,38,38,38	0
54	MG	1A	3329	1/1	0.96	0.06	33,33,33,33	0
54	MG	1A	3201	1/1	0.96	0.13	39,39,39,39	0
54	MG	1A	3892	1/1	0.96	0.06	39,39,39,39	0
54	MG	2a	1628	1/1	0.96	0.10	31,31,31,31	0
54	MG	1A	3655	1/1	0.96	0.13	30,30,30,30	0
54	MG	1a	1821	1/1	0.96	0.11	44,44,44,44	0
54	MG	1B	223	1/1	0.96	0.06	46,46,46,46	0
54	MG	1A	3556	1/1	0.96	0.14	39,39,39,39	0
54	MG	1A	3775	1/1	0.96	0.09	34,34,34,34	0
54	MG	2A	3119	1/1	0.96	0.20	64,64,64,64	0
54	MG	1A	3331	1/1	0.96	0.06	12,12,12,12	0
54	MG	2A	3574	1/1	0.96	0.13	52,52,52,52	0
54	MG	1A	3202	1/1	0.96	0.33	32,32,32,32	0
54	MG	2A	3345	1/1	0.96	0.21	45,45,45,45	0
54	MG	1B	229	1/1	0.96	0.06	41,41,41,41	0
54	MG	1A	3115	1/1	0.96	0.10	22,22,22,22	0
54	MG	1A	3562	1/1	0.96	0.07	32,32,32,32	0
54	MG	1A	3664	1/1	0.96	0.09	30,30,30,30	0
54	MG	1D	305	1/1	0.96	0.16	39,39,39,39	0
54	MG	2A	3127	1/1	0.96	0.07	36,36,36,36	0
54	MG	1A	3904	1/1	0.96	0.06	60,60,60,60	0
54	MG	2A	3584	1/1	0.96	0.09	46,46,46,46	0
54	MG	2A	3130	1/1	0.96	0.17	64,64,64,64	0
54	MG	1A	3782	1/1	0.96	0.06	41,41,41,41	0
54	MG	1A	3475	1/1	0.96	0.06	42,42,42,42	0
54	MG	1A	3116	1/1	0.96	0.09	28,28,28,28	0
54	MG	1A	3056	1/1	0.96	0.07	52,52,52,52	0
54	MG	1A	3023	1/1	0.96	0.09	19,19,19,19	0
54	MG	1a	1690	1/1	0.96	0.14	45,45,45,45	0
54	MG	2a	1654	1/1	0.96	0.08	58,58,58,58	0
54	MG	2A	3362	1/1	0.96	0.09	34,34,34,34	0
54	MG	1A	3273	1/1	0.96	0.11	30,30,30,30	0
54	MG	1A	3672	1/1	0.96	0.09	40,40,40,40	0
54	MG	2a	1659	1/1	0.96	0.40	48,48,48,48	0
54	MG	1a	1693	1/1	0.96	0.08	42,42,42,42	0
54	MG	1A	3407	1/1	0.96	0.08	38,38,38,38	0
54	MG	1A	3084	1/1	0.96	0.08	33,33,33,33	0
54	MG	1F	306	1/1	0.96	0.07	31,31,31,31	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1A	3571	1/1	0.96	0.22	27,27,27,27	0
54	MG	2a	1665	1/1	0.96	0.36	55,55,55,55	0
54	MG	1a	1699	1/1	0.96	0.09	57,57,57,57	0
54	MG	1F	308	1/1	0.96	0.15	29,29,29,29	0
54	MG	2A	3372	1/1	0.96	0.05	51,51,51,51	0
54	MG	1A	3122	1/1	0.96	0.08	32,32,32,32	0
54	MG	2A	3374	1/1	0.96	0.07	26,26,26,26	0
54	MG	2A	3152	1/1	0.96	0.08	58,58,58,58	0
54	MG	2A	3153	1/1	0.96	0.17	42,42,42,42	0
54	MG	2A	3154	1/1	0.96	0.19	41,41,41,41	0
54	MG	2A	3378	1/1	0.96	0.09	28,28,28,28	0
54	MG	2A	3156	1/1	0.96	0.06	41,41,41,41	0
54	MG	1A	3032	1/1	0.96	0.06	45,45,45,45	0
54	MG	2A	3158	1/1	0.96	0.06	48,48,48,48	0
54	MG	1A	3047	1/1	0.96	0.16	38,38,38,38	0
54	MG	2A	3383	1/1	0.96	0.14	64,64,64,64	0
54	MG	1A	3091	1/1	0.96	0.05	41,41,41,41	0
54	MG	2A	3616	1/1	0.96	0.09	45,45,45,45	0
54	MG	1F	313	1/1	0.96	0.04	31,31,31,31	0
54	MG	1A	3684	1/1	0.96	0.09	46,46,46,46	0
54	MG	1a	1708	1/1	0.96	0.18	32,32,32,32	0
54	MG	1A	3489	1/1	0.96	0.09	21,21,21,21	0
54	MG	1A	3926	1/1	0.96	0.06	45,45,45,45	0
54	MG	1A	3281	1/1	0.96	0.10	36,36,36,36	0
54	MG	2a	1690	1/1	0.96	0.15	68,68,68,68	0
54	MG	1H	8002	1/1	0.96	0.06	37,37,37,37	0
54	MG	1A	3169	1/1	0.96	0.25	33,33,33,33	0
54	MG	1A	3092	1/1	0.96	0.06	32,32,32,32	0
54	MG	1A	3129	1/1	0.96	0.24	26,26,26,26	0
54	MG	1A	3582	1/1	0.96	0.16	41,41,41,41	0
54	MG	1O	8002	1/1	0.96	0.08	46,46,46,46	0
54	MG	1A	3223	1/1	0.96	0.21	28,28,28,28	0
54	MG	1Q	201	1/1	0.96	0.09	38,38,38,38	0
54	MG	1Q	203	1/1	0.96	0.07	36,36,36,36	0
54	MG	1h	3001	1/1	0.96	0.07	35,35,35,35	0
54	MG	1A	3811	1/1	0.96	0.12	31,31,31,31	0
54	MG	1a	1722	1/1	0.96	0.20	56,56,56,56	0
54	MG	1A	3224	1/1	0.96	0.23	36,36,36,36	0
54	MG	2A	3637	1/1	0.96	0.08	30,30,30,30	0
54	MG	2A	3638	1/1	0.96	0.06	32,32,32,32	0
54	MG	2A	3407	1/1	0.96	0.09	50,50,50,50	0
54	MG	1a	1724	1/1	0.96	0.17	41,41,41,41	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1A	3175	1/1	0.96	0.23	35,35,35,35	0
54	MG	2A	3410	1/1	0.96	0.15	47,47,47,47	0
54	MG	2A	3187	1/1	0.96	0.09	44,44,44,44	0
54	MG	1A	3588	1/1	0.96	0.10	23,23,23,23	0
54	MG	1A	3176	1/1	0.96	0.07	49,49,49,49	0
54	MG	2A	3190	1/1	0.96	0.13	47,47,47,47	0
54	MG	1A	3294	1/1	0.96	0.07	46,46,46,46	0
54	MG	1A	3130	1/1	0.96	0.24	25,25,25,25	0
54	MG	1A	3592	1/1	0.96	0.15	44,44,44,44	0
54	MG	1A	3060	1/1	0.96	0.07	28,28,28,28	0
54	MG	1W	3002	1/1	0.96	0.12	39,39,39,39	0
54	MG	1A	3025	1/1	0.96	0.20	29,29,29,29	0
54	MG	1A	3596	1/1	0.96	0.18	38,38,38,38	0
54	MG	2A	3005	1/1	0.96	0.08	41,41,41,41	0
54	MG	2A	3007	1/1	0.96	0.12	36,36,36,36	0
54	MG	1A	3713	1/1	0.96	0.07	49,49,49,49	0
54	MG	2A	3011	1/1	0.96	0.07	21,21,21,21	0
54	MG	2A	3013	1/1	0.96	0.17	33,33,33,33	0
54	MG	2A	3014	1/1	0.96	0.18	51,51,51,51	0
54	MG	2A	3015	1/1	0.96	0.14	43,43,43,43	0
54	MG	1A	3945	1/1	0.96	0.10	36,36,36,36	0
54	MG	1A	3183	1/1	0.96	0.19	45,45,45,45	0
54	MG	2A	3434	1/1	0.96	0.10	26,26,26,26	0
54	MG	1A	3598	1/1	0.96	0.12	51,51,51,51	0
54	MG	1A	3301	1/1	0.96	0.08	27,27,27,27	0
54	MG	2A	3212	1/1	0.96	0.09	60,60,60,60	0
54	MG	1A	3062	1/1	0.96	0.12	25,25,25,25	0
54	MG	2A	3022	1/1	0.96	0.10	39,39,39,39	0
54	MG	1A	3237	1/1	0.96	0.10	28,28,28,28	0
54	MG	1A	3304	1/1	0.96	0.09	26,26,26,26	0
54	MG	15	104	1/1	0.96	0.09	62,62,62,62	0
54	MG	2A	3029	1/1	0.96	0.15	55,55,55,55	0
54	MG	17	101	1/1	0.96	0.17	54,54,54,54	0
54	MG	2A	3447	1/1	0.96	0.13	55,55,55,55	0
54	MG	2A	3031	1/1	0.96	0.16	48,48,48,48	0
54	MG	2A	3221	1/1	0.96	0.16	57,57,57,57	0
54	MG	1A	3952	1/1	0.96	0.04	46,46,46,46	0
54	MG	2A	3223	1/1	0.96	0.45	43,43,43,43	0
54	MG	2a	1751	1/1	0.96	0.08	53,53,53,53	0
54	MG	2A	3224	1/1	0.96	0.25	35,35,35,35	0
54	MG	18	101	1/1	0.96	0.06	46,46,46,46	0
54	MG	19	502	1/1	0.96	0.26	50,50,50,50	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	2A	3227	1/1	0.96	0.24	38,38,38,38	0
54	MG	1A	3604	1/1	0.96	0.05	29,29,29,29	0
54	MG	1A	3723	1/1	0.96	0.07	36,36,36,36	0
54	MG	2A	3459	1/1	0.96	0.06	38,38,38,38	0
54	MG	1A	3239	1/1	0.96	0.12	33,33,33,33	0
54	MG	2A	3038	1/1	0.96	0.09	46,46,46,46	0
54	MG	2A	3692	1/1	0.96	0.08	63,63,63,63	0
54	MG	1A	3725	1/1	0.96	0.06	36,36,36,36	0
54	MG	1A	3185	1/1	0.96	0.23	42,42,42,42	0
54	MG	1A	3959	1/1	0.96	0.21	47,47,47,47	0
54	MG	1A	3373	1/1	0.96	0.11	25,25,25,25	0
54	MG	1A	3443	1/1	0.96	0.07	25,25,25,25	0
54	MG	1A	3186	1/1	0.96	0.21	36,36,36,36	0
54	MG	2A	3699	1/1	0.96	0.10	61,61,61,61	0
54	MG	2A	3240	1/1	0.96	0.20	49,49,49,49	0
54	MG	2A	3241	1/1	0.96	0.14	47,47,47,47	0
54	MG	1A	3072	1/1	0.97	0.24	26,26,26,26	0
54	MG	1A	3646	1/1	0.97	0.08	37,37,37,37	0
54	MG	1A	3344	1/1	0.97	0.04	21,21,21,21	0
54	MG	1A	3648	1/1	0.97	0.14	32,32,32,32	0
54	MG	2A	3085	1/1	0.97	0.17	35,35,35,35	0
54	MG	1A	3790	1/1	0.97	0.07	39,39,39,39	0
54	MG	1a	1603	1/1	0.97	0.10	45,45,45,45	0
54	MG	1A	3433	1/1	0.97	0.05	32,32,32,32	0
54	MG	1A	3345	1/1	0.97	0.09	50,50,50,50	0
54	MG	1A	3532	1/1	0.97	0.07	17,17,17,17	0
54	MG	2A	3300	1/1	0.97	0.07	28,28,28,28	0
54	MG	2A	3512	1/1	0.97	0.10	51,51,51,51	0
54	MG	1A	3795	1/1	0.97	0.04	32,32,32,32	0
54	MG	2A	3514	1/1	0.97	0.19	36,36,36,36	0
54	MG	1A	3652	1/1	0.97	0.08	44,44,44,44	0
54	MG	1A	3653	1/1	0.97	0.16	41,41,41,41	0
54	MG	1a	1787	1/1	0.97	0.27	40,40,40,40	0
54	MG	1A	3533	1/1	0.97	0.06	35,35,35,35	0
54	MG	2A	3306	1/1	0.97	0.05	27,27,27,27	0
54	MG	2D	304	1/1	0.97	0.16	42,42,42,42	0
54	MG	1A	3146	1/1	0.97	0.33	34,34,34,34	0
54	MG	1A	3800	1/1	0.97	0.10	44,44,44,44	0
54	MG	1A	3656	1/1	0.97	0.10	37,37,37,37	0
54	MG	1A	3436	1/1	0.97	0.07	41,41,41,41	0
54	MG	2E	301	1/1	0.97	0.06	43,43,43,43	0
54	MG	2A	3312	1/1	0.97	0.10	39,39,39,39	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1A	3803	1/1	0.97	0.14	34,34,34,34	0
54	MG	1A	3199	1/1	0.97	0.18	38,38,38,38	0
54	MG	1A	3269	1/1	0.97	0.12	12,12,12,12	0
54	MG	2A	3530	1/1	0.97	0.06	25,25,25,25	0
54	MG	1A	3806	1/1	0.97	0.08	34,34,34,34	0
54	MG	1A	3962	1/1	0.97	0.06	55,55,55,55	0
54	MG	1A	3439	1/1	0.97	0.11	34,34,34,34	0
54	MG	1A	3200	1/1	0.97	0.14	32,32,32,32	0
54	MG	1A	3542	1/1	0.97	0.16	31,31,31,31	0
54	MG	1A	3015	1/1	0.97	0.25	29,29,29,29	0
54	MG	2A	3537	1/1	0.97	0.16	42,42,42,42	0
54	MG	1A	3967	1/1	0.97	0.12	19,19,19,19	0
54	MG	1A	3150	1/1	0.97	0.34	28,28,28,28	0
54	MG	1A	3075	1/1	0.97	0.17	32,32,32,32	0
54	MG	1A	3972	1/1	0.97	0.22	32,32,32,32	0
54	MG	1A	3669	1/1	0.97	0.10	25,25,25,25	0
54	MG	1a	1630	1/1	0.97	0.18	46,46,46,46	0
54	MG	1A	3547	1/1	0.97	0.12	29,29,29,29	0
54	MG	1a	1632	1/1	0.97	0.08	35,35,35,35	0
54	MG	1A	3275	1/1	0.97	0.08	29,29,29,29	0
54	MG	1A	3978	1/1	0.97	0.16	26,26,26,26	0
54	MG	2V	201	1/1	0.97	0.09	60,60,60,60	0
54	MG	1A	3109	1/1	0.97	0.23	31,31,31,31	0
54	MG	2A	3336	1/1	0.97	0.12	36,36,36,36	0
54	MG	1A	3358	1/1	0.97	0.06	21,21,21,21	0
54	MG	1a	1814	1/1	0.97	0.25	52,52,52,52	0
54	MG	1A	3447	1/1	0.97	0.07	34,34,34,34	0
54	MG	1a	1638	1/1	0.97	0.16	44,44,44,44	0
54	MG	1A	3553	1/1	0.97	0.07	18,18,18,18	0
54	MG	28	8002	1/1	0.97	0.08	45,45,45,45	0
54	MG	1A	3554	1/1	0.97	0.07	40,40,40,40	0
54	MG	1A	3359	1/1	0.97	0.07	15,15,15,15	0
54	MG	1A	3077	1/1	0.97	0.17	28,28,28,28	0
54	MG	1A	3111	1/1	0.97	0.18	31,31,31,31	0
54	MG	1a	1645	1/1	0.97	0.05	41,41,41,41	0
54	MG	1A	3996	1/1	0.97	0.18	27,27,27,27	0
54	MG	2A	3138	1/1	0.97	0.11	33,33,33,33	0
54	MG	1A	3682	1/1	0.97	0.06	38,38,38,38	0
54	MG	2A	3140	1/1	0.97	0.07	51,51,51,51	0
54	MG	2A	3141	1/1	0.97	0.11	39,39,39,39	0
54	MG	2A	3352	1/1	0.97	0.07	52,52,52,52	0
54	MG	2A	3353	1/1	0.97	0.06	62,62,62,62	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1A	3558	1/1	0.97	0.04	34,34,34,34	0
54	MG	2A	3571	1/1	0.97	0.17	42,42,42,42	0
54	MG	1A	4000	1/1	0.97	0.04	30,30,30,30	0
54	MG	1A	3827	1/1	0.97	0.07	21,21,21,21	0
54	MG	1A	4003	1/1	0.97	0.10	27,27,27,27	0
54	MG	2a	1619	1/1	0.97	0.18	47,47,47,47	0
54	MG	1A	3685	1/1	0.97	0.12	42,42,42,42	0
54	MG	1A	3686	1/1	0.97	0.12	32,32,32,32	0
54	MG	1A	3157	1/1	0.97	0.04	28,28,28,28	0
54	MG	1A	3038	1/1	0.97	0.12	40,40,40,40	0
54	MG	1A	3561	1/1	0.97	0.05	25,25,25,25	0
54	MG	1A	3834	1/1	0.97	0.08	31,31,31,31	0
54	MG	1A	3453	1/1	0.97	0.05	51,51,51,51	0
54	MG	1A	4014	1/1	0.97	0.16	28,28,28,28	0
54	MG	1A	3282	1/1	0.97	0.17	24,24,24,24	0
54	MG	2A	3155	1/1	0.97	0.10	48,48,48,48	0
54	MG	1A	3693	1/1	0.97	0.07	33,33,33,33	0
54	MG	1A	3694	1/1	0.97	0.06	40,40,40,40	0
54	MG	1A	3455	1/1	0.97	0.07	10,10,10,10	0
54	MG	1A	3840	1/1	0.97	0.07	33,33,33,33	0
54	MG	1A	3079	1/1	0.97	0.20	30,30,30,30	0
54	MG	1A	3210	1/1	0.97	0.15	32,32,32,32	0
54	MG	1A	3029	1/1	0.97	0.04	12,12,12,12	0
54	MG	2A	3163	1/1	0.97	0.10	53,53,53,53	0
54	MG	1A	4024	1/1	0.97	0.21	30,30,30,30	0
54	MG	1A	3699	1/1	0.97	0.07	42,42,42,42	0
54	MG	1A	4026	1/1	0.97	0.09	35,35,35,35	0
54	MG	1A	3213	1/1	0.97	0.07	33,33,33,33	0
54	MG	2A	3169	1/1	0.97	0.11	38,38,38,38	0
54	MG	1A	3701	1/1	0.97	0.09	29,29,29,29	0
54	MG	1A	3289	1/1	0.97	0.06	23,23,23,23	0
54	MG	1a	1675	1/1	0.97	0.16	42,42,42,42	0
54	MG	1A	3290	1/1	0.97	0.12	32,32,32,32	0
54	MG	1A	3463	1/1	0.97	0.10	19,19,19,19	0
54	MG	1B	205	1/1	0.97	0.05	40,40,40,40	0
54	MG	1A	3017	1/1	0.97	0.09	25,25,25,25	0
54	MG	1A	3855	1/1	0.97	0.06	25,25,25,25	0
54	MG	1A	3041	1/1	0.97	0.12	12,12,12,12	0
54	MG	1B	209	1/1	0.97	0.04	36,36,36,36	0
54	MG	1A	3708	1/1	0.97	0.04	37,37,37,37	0
54	MG	1A	3709	1/1	0.97	0.18	46,46,46,46	0
54	MG	2A	3394	1/1	0.97	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
54	MG	1A	3218	1/1	0.97	0.14	30,30,30,30	0
54	MG	2a	1657	1/1	0.97	0.11	44,44,44,44	0
54	MG	2A	3396	1/1	0.97	0.05	29,29,29,29	0
54	MG	1A	3467	1/1	0.97	0.06	49,49,49,49	0
54	MG	1A	3119	1/1	0.97	0.09	38,38,38,38	0
54	MG	1A	3221	1/1	0.97	0.23	24,24,24,24	0
54	MG	1A	3579	1/1	0.97	0.11	24,24,24,24	0
54	MG	1A	3165	1/1	0.97	0.16	28,28,28,28	0
54	MG	1A	3166	1/1	0.97	0.06	32,32,32,32	0
54	MG	1A	3042	1/1	0.97	0.13	8,8,8,8	0
54	MG	1A	3382	1/1	0.97	0.05	19,19,19,19	0
54	MG	1A	3225	1/1	0.97	0.16	32,32,32,32	0
54	MG	1A	3585	1/1	0.97	0.07	36,36,36,36	0
54	MG	2A	3624	1/1	0.97	0.06	37,37,37,37	0
54	MG	1A	3121	1/1	0.97	0.14	57,57,57,57	0
54	MG	1A	3476	1/1	0.97	0.08	14,14,14,14	0
54	MG	1A	3726	1/1	0.97	0.05	32,32,32,32	0
54	MG	1A	3227	1/1	0.97	0.18	25,25,25,25	0
54	MG	1A	3229	1/1	0.97	0.22	55,55,55,55	0
54	MG	1A	3085	1/1	0.97	0.07	36,36,36,36	0
54	MG	2A	3201	1/1	0.97	0.07	50,50,50,50	0
54	MG	1A	3879	1/1	0.97	0.07	33,33,33,33	0
54	MG	2A	3415	1/1	0.97	0.07	41,41,41,41	0
54	MG	1D	307	1/1	0.97	0.06	40,40,40,40	0
54	MG	1A	3307	1/1	0.97	0.11	31,31,31,31	0
54	MG	1A	3593	1/1	0.97	0.13	40,40,40,40	0
54	MG	1A	3231	1/1	0.97	0.17	34,34,34,34	0
54	MG	2A	3420	1/1	0.97	0.10	28,28,28,28	0
54	MG	2a	1685	1/1	0.97	0.26	52,52,52,52	0
54	MG	2A	3008	1/1	0.97	0.10	57,57,57,57	0
54	MG	1D	312	1/1	0.97	0.13	54,54,54,54	0
54	MG	2A	3210	1/1	0.97	0.07	45,45,45,45	0
54	MG	1A	3171	1/1	0.97	0.10	23,23,23,23	0
54	MG	2A	3012	1/1	0.97	0.07	43,43,43,43	0
54	MG	1A	3012	1/1	0.97	0.04	17,17,17,17	0
54	MG	1E	304	1/1	0.97	0.09	16,16,16,16	0
54	MG	1A	3006	1/1	0.97	0.07	17,17,17,17	0
54	MG	1A	3090	1/1	0.97	0.07	12,12,12,12	0
54	MG	1A	3126	1/1	0.97	0.21	33,33,33,33	0
54	MG	1A	3740	1/1	0.97	0.07	29,29,29,29	0
54	MG	1F	304	1/1	0.97	0.08	24,24,24,24	0
54	MG	1A	3488	1/1	0.97	0.09	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1A	3893	1/1	0.97	0.15	50,50,50,50	0
54	MG	1A	3033	1/1	0.97	0.07	34,34,34,34	0
54	MG	2A	3024	1/1	0.97	0.12	35,35,35,35	0
54	MG	1A	3315	1/1	0.97	0.05	25,25,25,25	0
54	MG	1A	3492	1/1	0.97	0.08	17,17,17,17	0
54	MG	1A	3238	1/1	0.97	0.20	40,40,40,40	0
54	MG	1A	3034	1/1	0.97	0.08	33,33,33,33	0
54	MG	2A	3443	1/1	0.97	0.08	47,47,47,47	0
54	MG	1A	3747	1/1	0.97	0.12	44,44,44,44	0
54	MG	1a	1727	1/1	0.97	0.17	43,43,43,43	0
54	MG	1A	3318	1/1	0.97	0.12	26,26,26,26	0
54	MG	1A	3610	1/1	0.97	0.06	27,27,27,27	0
54	MG	2a	1711	1/1	0.97	0.25	45,45,45,45	0
54	MG	2A	3448	1/1	0.97	0.05	47,47,47,47	0
54	MG	1A	3750	1/1	0.97	0.10	27,27,27,27	0
54	MG	1A	3240	1/1	0.97	0.09	37,37,37,37	0
54	MG	2A	3234	1/1	0.97	0.10	52,52,52,52	0
54	MG	1A	3179	1/1	0.97	0.16	36,36,36,36	0
54	MG	1A	3180	1/1	0.97	0.17	37,37,37,37	0
54	MG	1a	1734	1/1	0.97	0.21	47,47,47,47	0
54	MG	1a	1735	1/1	0.97	0.13	51,51,51,51	0
54	MG	1A	3323	1/1	0.97	0.08	18,18,18,18	0
54	MG	1A	3245	1/1	0.97	0.05	27,27,27,27	0
54	MG	1A	3181	1/1	0.97	0.22	57,57,57,57	0
54	MG	1A	3064	1/1	0.97	0.19	29,29,29,29	0
54	MG	1A	3094	1/1	0.97	0.24	29,29,29,29	0
54	MG	1A	3506	1/1	0.97	0.08	33,33,33,33	0
54	MG	1P	203	1/1	0.97	0.03	29,29,29,29	0
54	MG	1A	3915	1/1	0.97	0.05	25,25,25,25	0
54	MG	1A	3507	1/1	0.97	0.04	29,29,29,29	0
54	MG	1A	3035	1/1	0.97	0.09	38,38,38,38	0
54	MG	1A	3623	1/1	0.97	0.06	32,32,32,32	0
54	MG	1A	3509	1/1	0.97	0.13	41,41,41,41	0
54	MG	2a	1733	1/1	0.97	0.34	52,52,52,52	0
54	MG	2A	3256	1/1	0.97	0.12	51,51,51,51	0
54	MG	2a	1735	1/1	0.97	0.24	45,45,45,45	0
54	MG	1T	201	1/1	0.97	0.05	54,54,54,54	0
54	MG	1A	3625	1/1	0.97	0.11	35,35,35,35	0
54	MG	2A	3690	1/1	0.97	0.06	67,67,67,67	0
54	MG	1A	3922	1/1	0.97	0.12	61,61,61,61	0
54	MG	1A	3923	1/1	0.97	0.13	50,50,50,50	0
54	MG	2A	3474	1/1	0.97	0.06	50,50,50,50	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1A	3510	1/1	0.97	0.04	34,34,34,34	0
54	MG	1A	3133	1/1	0.97	0.08	27,27,27,27	0
54	MG	1V	203	1/1	0.97	0.10	55,55,55,55	0
54	MG	1A	3134	1/1	0.97	0.14	22,22,22,22	0
54	MG	1A	3137	1/1	0.97	0.06	29,29,29,29	0
54	MG	2A	3062	1/1	0.97	0.14	35,35,35,35	0
54	MG	1X	101	1/1	0.97	0.09	52,52,52,52	0
54	MG	1A	3769	1/1	0.97	0.10	19,19,19,19	0
54	MG	2A	3270	1/1	0.97	0.06	37,37,37,37	0
54	MG	10	101	1/1	0.97	0.05	47,47,47,47	0
54	MG	1A	3417	1/1	0.97	0.07	20,20,20,20	0
54	MG	1A	3066	1/1	0.97	0.16	30,30,30,30	0
54	MG	1A	3420	1/1	0.97	0.06	50,50,50,50	0
54	MG	1A	3139	1/1	0.97	0.06	29,29,29,29	0
54	MG	1A	3067	1/1	0.97	0.06	38,38,38,38	0
54	MG	2A	3713	1/1	0.97	0.37	40,40,40,40	0
54	MG	1a	1765	1/1	0.97	0.09	46,46,46,46	0
54	MG	1A	3068	1/1	0.97	0.07	23,23,23,23	0
54	MG	1A	3192	1/1	0.97	0.18	35,35,35,35	0
54	MG	13	101	1/1	0.97	0.07	53,53,53,53	0
54	MG	1A	3052	1/1	0.97	0.07	36,36,36,36	0
54	MG	1A	3262	1/1	0.97	0.07	28,28,28,28	0
54	MG	15	103	1/1	0.97	0.05	41,41,41,41	0
54	MG	1A	3263	1/1	0.97	0.13	25,25,25,25	0
54	MG	1A	3008	1/1	0.97	0.06	33,33,33,33	0
54	MG	1A	3429	1/1	0.97	0.07	41,41,41,41	0
54	MG	2A	3724	1/1	0.97	0.12	32,32,32,32	0
59	ZN	2Y	501	1/1	0.97	0.04	79,79,79,79	0
54	MG	2A	3500	1/1	0.97	0.16	51,51,51,51	0
54	MG	2A	3464	1/1	0.98	0.17	34,34,34,34	0
54	MG	1A	3681	1/1	0.98	0.09	38,38,38,38	0
54	MG	1A	3351	1/1	0.98	0.05	18,18,18,18	0
54	MG	2A	3313	1/1	0.98	0.05	33,33,33,33	0
54	MG	1A	3683	1/1	0.98	0.04	25,25,25,25	0
54	MG	2A	3026	1/1	0.98	0.07	41,41,41,41	0
54	MG	2a	1609	1/1	0.98	0.07	46,46,46,46	0
54	MG	2a	1610	1/1	0.98	0.13	45,45,45,45	0
54	MG	2A	3165	1/1	0.98	0.25	64,64,64,64	0
54	MG	2A	3027	1/1	0.98	0.07	30,30,30,30	0
54	MG	1A	3049	1/1	0.98	0.14	38,38,38,38	0
54	MG	1E	302	1/1	0.98	0.31	39,39,39,39	0
54	MG	1A	3096	1/1	0.98	0.14	25,25,25,25	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1A	3254	1/1	0.98	0.14	30,30,30,30	0
54	MG	1A	3609	1/1	0.98	0.24	41,41,41,41	0
54	MG	1E	307	1/1	0.98	0.06	53,53,53,53	0
54	MG	1A	3212	1/1	0.98	0.15	37,37,37,37	0
54	MG	1A	3540	1/1	0.98	0.06	25,25,25,25	0
54	MG	1F	303	1/1	0.98	0.12	35,35,35,35	0
54	MG	1A	3859	1/1	0.98	0.07	16,16,16,16	0
54	MG	1A	3356	1/1	0.98	0.09	37,37,37,37	0
54	MG	1A	3771	1/1	0.98	0.06	27,27,27,27	0
54	MG	1A	3772	1/1	0.98	0.21	24,24,24,24	0
54	MG	2A	3331	1/1	0.98	0.07	49,49,49,49	0
54	MG	2A	3643	1/1	0.98	0.14	34,34,34,34	0
54	MG	1A	3863	1/1	0.98	0.03	12,12,12,12	0
54	MG	2A	3181	1/1	0.98	0.09	47,47,47,47	0
54	MG	1a	1663	1/1	0.98	0.08	59,59,59,59	0
54	MG	1A	3691	1/1	0.98	0.07	17,17,17,17	0
54	MG	1A	3147	1/1	0.98	0.06	39,39,39,39	0
54	MG	2A	3185	1/1	0.98	0.07	45,45,45,45	0
54	MG	1A	3306	1/1	0.98	0.08	23,23,23,23	0
54	MG	1A	3776	1/1	0.98	0.05	26,26,26,26	0
54	MG	1A	3545	1/1	0.98	0.07	39,39,39,39	0
54	MG	1A	3020	1/1	0.98	0.14	33,33,33,33	0
54	MG	1A	3360	1/1	0.98	0.08	18,18,18,18	0
54	MG	1A	3215	1/1	0.98	0.04	35,35,35,35	0
54	MG	1G	3004	1/1	0.98	0.08	34,34,34,34	0
54	MG	1A	3549	1/1	0.98	0.05	38,38,38,38	0
54	MG	1A	3971	1/1	0.98	0.04	16,16,16,16	0
54	MG	1A	3216	1/1	0.98	0.30	29,29,29,29	0
54	MG	1A	3149	1/1	0.98	0.11	21,21,21,21	0
54	MG	1A	3975	1/1	0.98	0.06	39,39,39,39	0
54	MG	1A	3051	1/1	0.98	0.28	26,26,26,26	0
54	MG	1A	3876	1/1	0.98	0.04	27,27,27,27	0
54	MG	1P	201	1/1	0.98	0.14	27,27,27,27	0
54	MG	1A	3219	1/1	0.98	0.14	25,25,25,25	0
54	MG	1A	3009	1/1	0.98	0.10	34,34,34,34	0
54	MG	1A	3152	1/1	0.98	0.07	31,31,31,31	0
54	MG	1Q	202	1/1	0.98	0.05	29,29,29,29	0
54	MG	1A	3022	1/1	0.98	0.05	29,29,29,29	0
54	MG	1Q	204	1/1	0.98	0.09	31,31,31,31	0
54	MG	1R	201	1/1	0.98	0.13	31,31,31,31	0
54	MG	1A	3706	1/1	0.98	0.06	32,32,32,32	0
54	MG	2A	3209	1/1	0.98	0.22	43,43,43,43	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	2A	3516	1/1	0.98	0.13	19,19,19,19	0
54	MG	1A	3083	1/1	0.98	0.04	40,40,40,40	0
54	MG	1A	3984	1/1	0.98	0.03	37,37,37,37	0
54	MG	1A	3985	1/1	0.98	0.12	36,36,36,36	0
54	MG	1A	3792	1/1	0.98	0.04	12,12,12,12	0
54	MG	1A	3989	1/1	0.98	0.09	50,50,50,50	0
54	MG	2A	3681	1/1	0.98	0.07	69,69,69,69	0
54	MG	1A	3267	1/1	0.98	0.12	29,29,29,29	0
54	MG	1a	1695	1/1	0.98	0.12	37,37,37,37	0
54	MG	1A	3992	1/1	0.98	0.27	28,28,28,28	0
54	MG	1A	3993	1/1	0.98	0.09	26,26,26,26	0
54	MG	1V	202	1/1	0.98	0.04	47,47,47,47	0
54	MG	1A	3155	1/1	0.98	0.06	26,26,26,26	0
54	MG	1A	3494	1/1	0.98	0.11	38,38,38,38	0
54	MG	2A	3529	1/1	0.98	0.07	49,49,49,49	0
54	MG	1A	3997	1/1	0.98	0.12	23,23,23,23	0
54	MG	2a	1674	1/1	0.98	0.13	43,43,43,43	0
54	MG	1A	3711	1/1	0.98	0.08	30,30,30,30	0
54	MG	1A	3888	1/1	0.98	0.05	18,18,18,18	0
54	MG	1A	3319	1/1	0.98	0.06	15,15,15,15	0
54	MG	1A	3890	1/1	0.98	0.15	46,46,46,46	0
54	MG	1a	1706	1/1	0.98	0.07	28,28,28,28	0
54	MG	2A	3086	1/1	0.98	0.10	48,48,48,48	0
54	MG	1A	4002	1/1	0.98	0.24	29,29,29,29	0
54	MG	1A	3891	1/1	0.98	0.04	30,30,30,30	0
54	MG	1A	3016	1/1	0.98	0.30	17,17,17,17	0
54	MG	2A	3540	1/1	0.98	0.10	37,37,37,37	0
54	MG	2A	3701	1/1	0.98	0.05	47,47,47,47	0
54	MG	2A	3090	1/1	0.98	0.05	19,19,19,19	0
54	MG	2A	3091	1/1	0.98	0.05	61,61,61,61	0
54	MG	1A	4006	1/1	0.98	0.10	31,31,31,31	0
54	MG	1a	1838	1/1	0.98	0.08	55,55,55,55	0
54	MG	11	101	1/1	0.98	0.04	44,44,44,44	0
54	MG	2A	3390	1/1	0.98	0.04	31,31,31,31	0
54	MG	2A	3237	1/1	0.98	0.15	34,34,34,34	0
54	MG	1A	3103	1/1	0.98	0.22	25,25,25,25	0
54	MG	1A	3715	1/1	0.98	0.04	19,19,19,19	0
54	MG	1A	3128	1/1	0.98	0.05	32,32,32,32	0
54	MG	13	102	1/1	0.98	0.07	27,27,27,27	0
54	MG	1A	3896	1/1	0.98	0.06	22,22,22,22	0
54	MG	2A	3243	1/1	0.98	0.14	18,18,18,18	0
54	MG	1A	3636	1/1	0.98	0.12	17,17,17,17	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1A	3565	1/1	0.98	0.14	36,36,36,36	0
54	MG	2A	3556	1/1	0.98	0.21	35,35,35,35	0
54	MG	1A	3104	1/1	0.98	0.23	23,23,23,23	0
54	MG	1A	3720	1/1	0.98	0.04	52,52,52,52	0
54	MG	1A	3024	1/1	0.98	0.08	29,29,29,29	0
54	MG	1A	3007	1/1	0.98	0.06	26,26,26,26	0
54	MG	1A	3044	1/1	0.98	0.08	23,23,23,23	0
54	MG	1A	4019	1/1	0.98	0.06	29,29,29,29	0
54	MG	1a	1725	1/1	0.98	0.07	46,46,46,46	0
54	MG	2A	3254	1/1	0.98	0.15	51,51,51,51	0
54	MG	2A	3565	1/1	0.98	0.09	48,48,48,48	0
54	MG	2A	3255	1/1	0.98	0.04	24,24,24,24	0
54	MG	1A	3277	1/1	0.98	0.08	28,28,28,28	0
54	MG	1A	3195	1/1	0.98	0.21	33,33,33,33	0
54	MG	1A	3645	1/1	0.98	0.07	35,35,35,35	0
54	MG	1A	3505	1/1	0.98	0.03	27,27,27,27	0
54	MG	1A	3196	1/1	0.98	0.16	40,40,40,40	0
54	MG	1A	3088	1/1	0.98	0.05	32,32,32,32	0
54	MG	1A	3386	1/1	0.98	0.06	19,19,19,19	0
54	MG	1A	3912	1/1	0.98	0.06	43,43,43,43	0
54	MG	1A	3164	1/1	0.98	0.12	22,22,22,22	0
54	MG	1A	3089	1/1	0.98	0.09	26,26,26,26	0
54	MG	2B	3016	1/1	0.98	0.07	52,52,52,52	0
54	MG	1A	3511	1/1	0.98	0.04	32,32,32,32	0
54	MG	1A	3135	1/1	0.98	0.05	29,29,29,29	0
54	MG	2B	3019	1/1	0.98	0.04	65,65,65,65	0
54	MG	1A	3045	1/1	0.98	0.08	35,35,35,35	0
54	MG	2D	302	1/1	0.98	0.41	38,38,38,38	0
54	MG	2a	1728	1/1	0.98	0.10	53,53,53,53	0
54	MG	1A	3113	1/1	0.98	0.08	18,18,18,18	0
54	MG	2A	3271	1/1	0.98	0.06	23,23,23,23	0
54	MG	1A	3336	1/1	0.98	0.09	33,33,33,33	0
54	MG	1A	3658	1/1	0.98	0.03	24,24,24,24	0
54	MG	1A	3824	1/1	0.98	0.07	17,17,17,17	0
54	MG	1A	3114	1/1	0.98	0.07	22,22,22,22	0
54	MG	1a	1619	1/1	0.98	0.04	54,54,54,54	0
54	MG	2A	3129	1/1	0.98	0.06	52,52,52,52	0
54	MG	1A	3338	1/1	0.98	0.05	28,28,28,28	0
54	MG	2E	304	1/1	0.98	0.05	29,29,29,29	0
54	MG	1A	3288	1/1	0.98	0.08	16,16,16,16	0
54	MG	1B	214	1/1	0.98	0.04	35,35,35,35	0
54	MG	1A	3586	1/1	0.98	0.05	23,23,23,23	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	2A	3134	1/1	0.98	0.04	36,36,36,36	0
54	MG	1A	3396	1/1	0.98	0.07	21,21,21,21	0
54	MG	1A	3026	1/1	0.98	0.20	28,28,28,28	0
54	MG	1A	3243	1/1	0.98	0.07	35,35,35,35	0
54	MG	1A	3399	1/1	0.98	0.07	33,33,33,33	0
54	MG	1A	3244	1/1	0.98	0.15	27,27,27,27	0
54	MG	1A	3172	1/1	0.98	0.45	31,31,31,31	0
54	MG	1A	3525	1/1	0.98	0.16	37,37,37,37	0
54	MG	1A	3462	1/1	0.98	0.16	48,48,48,48	0
54	MG	2A	3006	1/1	0.98	0.20	43,43,43,43	0
54	MG	1A	3246	1/1	0.98	0.07	58,58,58,58	0
54	MG	1A	3027	1/1	0.98	0.08	34,34,34,34	0
54	MG	2A	3604	1/1	0.98	0.06	31,31,31,31	0
54	MG	2A	3009	1/1	0.98	0.05	30,30,30,30	0
54	MG	1A	3248	1/1	0.98	0.05	31,31,31,31	0
54	MG	1A	3076	1/1	0.98	0.10	27,27,27,27	0
55	K	1A	3287	1/1	0.98	0.03	27,27,27,27	0
54	MG	1A	3842	1/1	0.98	0.04	42,42,42,42	0
54	MG	2A	3298	1/1	0.98	0.09	27,27,27,27	0
54	MG	2A	3299	1/1	0.98	0.10	28,28,28,28	0
54	MG	1D	301	1/1	0.98	0.08	25,25,25,25	0
54	MG	1A	3143	1/1	0.98	0.03	26,26,26,26	0
54	MG	1D	303	1/1	0.98	0.17	44,44,44,44	0
54	MG	1A	3349	1/1	0.98	0.08	40,40,40,40	0
54	MG	1A	3846	1/1	0.98	0.07	27,27,27,27	0
54	MG	2A	3018	1/1	0.98	0.05	40,40,40,40	0
54	MG	1a	1642	1/1	0.98	0.16	39,39,39,39	0
54	MG	1A	3847	1/1	0.98	0.04	39,39,39,39	0
54	MG	1A	3019	1/1	0.98	0.20	33,33,33,33	0
59	ZN	24	501	1/1	0.98	0.08	108,108,108,108	0
54	MG	1A	3409	1/1	0.98	0.11	50,50,50,50	0
60	SF4	1d	302	8/8	0.98	0.06	48,59,66,72	0
60	SF4	2d	501	8/8	0.98	0.04	61,71,81,92	0
54	MG	1A	3300	1/1	0.99	0.03	23,23,23,23	0
54	MG	1A	3005	1/1	0.99	0.09	15,15,15,15	0
54	MG	1A	3994	1/1	0.99	0.09	26,26,26,26	0
54	MG	2A	3259	1/1	0.99	0.05	32,32,32,32	0
54	MG	2A	3311	1/1	0.99	0.06	43,43,43,43	0
54	MG	1A	3920	1/1	0.99	0.09	21,21,21,21	0
54	MG	1A	3431	1/1	0.99	0.04	34,34,34,34	0
54	MG	2A	3110	1/1	0.99	0.21	40,40,40,40	0
54	MG	1A	3073	1/1	0.99	0.13	30,30,30,30	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1A	3736	1/1	0.99	0.04	41,41,41,41	0
54	MG	1A	3607	1/1	0.99	0.04	50,50,50,50	0
54	MG	1a	1850	1/1	0.99	0.03	45,45,45,45	0
54	MG	2A	3424	1/1	0.99	0.03	52,52,52,52	0
54	MG	1A	3069	1/1	0.99	0.03	23,23,23,23	0
54	MG	1B	213	1/1	0.99	0.05	38,38,38,38	0
54	MG	1A	3828	1/1	0.99	0.06	13,13,13,13	0
54	MG	1A	3228	1/1	0.99	0.13	18,18,18,18	0
54	MG	1A	3657	1/1	0.99	0.09	31,31,31,31	0
54	MG	1A	4004	1/1	0.99	0.11	25,25,25,25	0
54	MG	1A	3105	1/1	0.99	0.13	33,33,33,33	0
54	MG	1A	3491	1/1	0.99	0.02	36,36,36,36	0
54	MG	1B	220	1/1	0.99	0.04	20,20,20,20	0
54	MG	2A	3650	1/1	0.99	0.04	36,36,36,36	0
54	MG	1A	3897	1/1	0.99	0.09	23,23,23,23	0
54	MG	1A	3418	1/1	0.99	0.06	22,22,22,22	0
54	MG	1a	1815	1/1	0.99	0.04	44,44,44,44	0
54	MG	1A	3270	1/1	0.99	0.11	11,11,11,11	0
54	MG	1A	3018	1/1	0.99	0.17	24,24,24,24	0
54	MG	1A	4011	1/1	0.99	0.13	29,29,29,29	0
54	MG	1A	3638	1/1	0.99	0.06	38,38,38,38	0
54	MG	2a	1750	1/1	0.99	0.05	59,59,59,59	0
54	MG	1A	3107	1/1	0.99	0.13	27,27,27,27	0
54	MG	2A	3442	1/1	0.99	0.08	27,27,27,27	0
54	MG	1A	3973	1/1	0.99	0.04	42,42,42,42	0
54	MG	1A	3616	1/1	0.99	0.08	16,16,16,16	0
54	MG	1A	3666	1/1	0.99	0.06	20,20,20,20	0
54	MG	2A	3135	1/1	0.99	0.14	67,67,67,67	0
54	MG	1A	3136	1/1	0.99	0.06	24,24,24,24	0
54	MG	1A	3003	1/1	0.99	0.04	31,31,31,31	0
54	MG	1A	3298	1/1	0.99	0.05	14,14,14,14	0
55	K	2A	3246	1/1	0.99	0.02	30,30,30,30	0
54	MG	1a	1827	1/1	0.99	0.06	33,33,33,33	0
54	MG	1A	3843	1/1	0.99	0.11	30,30,30,30	0
54	MG	1D	306	1/1	0.99	0.05	11,11,11,11	0
54	MG	1A	3378	1/1	0.99	0.02	20,20,20,20	0
54	MG	1D	308	1/1	0.99	0.07	31,31,31,31	0
54	MG	1A	3170	1/1	0.99	0.11	28,28,28,28	0
54	MG	1A	3410	1/1	0.99	0.07	18,18,18,18	0
54	MG	1A	3365	1/1	0.99	0.06	13,13,13,13	0
54	MG	1A	3728	1/1	0.99	0.04	38,38,38,38	0
54	MG	1A	3674	1/1	0.99	0.05	35,35,35,35	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	2A	3003	1/1	0.99	0.04	37,37,37,37	0
59	ZN	1Y	501	1/1	0.99	0.03	46,46,46,46	0
59	ZN	14	501	1/1	0.99	0.03	80,80,80,80	0
59	ZN	15	101	1/1	0.99	0.04	39,39,39,39	0
59	ZN	16	501	1/1	0.99	0.10	46,46,46,46	0
59	ZN	19	501	1/1	0.99	0.08	39,39,39,39	0
59	ZN	1n	501	1/1	0.99	0.03	60,60,60,60	0
54	MG	1A	3788	1/1	0.99	0.06	23,23,23,23	0
54	MG	1A	3601	1/1	0.99	0.06	31,31,31,31	0
59	ZN	26	501	1/1	0.99	0.04	59,59,59,59	0
59	ZN	29	501	1/1	0.99	0.03	62,62,62,62	0
54	MG	1E	303	1/1	0.99	0.05	32,32,32,32	0
54	MG	1A	3990	1/1	0.99	0.04	20,20,20,20	0
54	MG	1A	3541	1/1	0.99	0.08	19,19,19,19	0
59	ZN	25	501	1/1	1.00	0.04	44,44,44,44	0
54	MG	2A	3333	1/1	1.00	0.02	28,28,28,28	0
54	MG	1A	3956	1/1	1.00	0.04	24,24,24,24	0
54	MG	1A	3477	1/1	1.00	0.06	16,16,16,16	0
54	MG	1X	102	1/1	1.00	0.08	31,31,31,31	0
54	MG	1A	3968	1/1	1.00	0.03	11,11,11,11	0

6.5 Other polymers

There are no such residues in this entry.