



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 6, 2026 – 01:43 AM EDT

PDB ID : 5HCR / pdb_00005hcr
Title : Crystal structure of antimicrobial peptide Oncocin 10wt bound to the *Thermus thermophilus* 70S ribosome
Authors : Gagnon, M.G.; Roy, R.N.; Lomakin, I.B.; Florin, T.; Mankin, A.S.; Steitz, T.A.
Deposited on : 2016-01-04
Resolution : 2.80 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.015 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

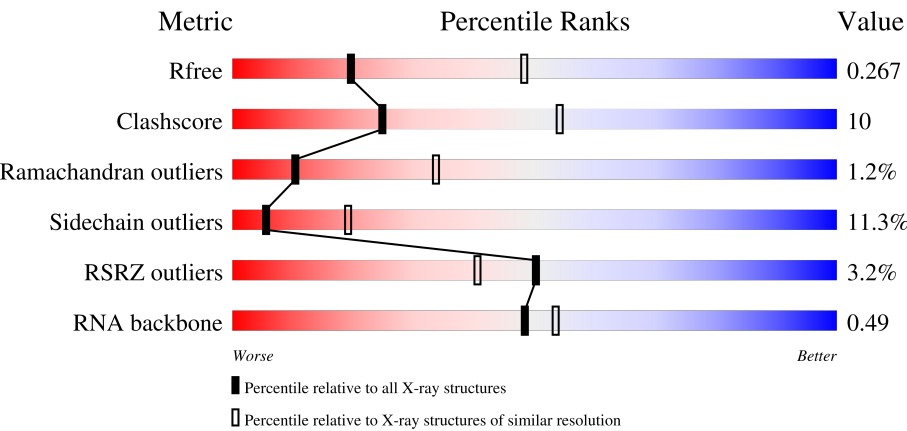
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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.



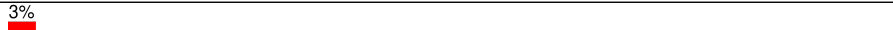
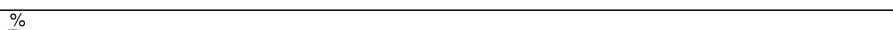
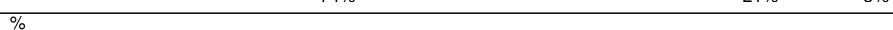
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R _{free}	180053	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)
RNA backbone	3983	1114 (3.00-2.60)

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	61%28%5%6%
1	2A	2915	53%36%7%
2	1B	121	2%73%26%
2	2B	121	3%36%52%11%

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

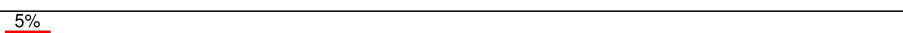
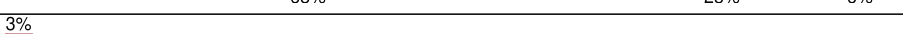
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Mol	Chain	Length	Quality of chain
15	2T	146	
16	1U	118	
16	2U	118	
17	1V	101	
17	2V	101	
18	1W	113	
18	2W	113	
19	1X	96	
19	2X	96	
20	1Y	110	
20	2Y	110	
21	1Z	206	
21	2Z	206	
22	10	85	
22	20	85	
23	11	98	
23	21	98	
24	12	72	
24	22	72	
25	13	60	
25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

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

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

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Mol	Chain	Length	Quality of chain
53	1v	24	
53	2v	24	
54	1x	77	
54	2x	77	
55	1z	19	
55	2z	19	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
56	MG	1A	3918	-	-	-	X
56	MG	1H	203	-	-	-	X

2 Entry composition

There are 59 unique types of molecules in this entry. The entry contains 288674 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	2746	Total	C	N	O	P	0	0	0
			59154	26327	11077	19005	2745			
1	2A	2790	Total	C	N	O	P	0	0	0
			60091	26746	11243	19313	2789			

- 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	1146	476	831	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
			2136	1349	423	361	3			
3	2D	275	Total	C	N	O	S	0	0	0
			2142	1352	426	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
			1425	914	256	251	4			
6	2G	181	Total	C	N	O	S	0	0	0
			1424	911	258	251	4			

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	1I	146	Total	C	N	O	S	0	0	0
			1085	693	189	202	1			
8	2I	146	Total	C	N	O	S	0	0	0
			1061	680	186	194	1			

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	1P	149	Total	C	N	O	S	0	0	0
			1139	709	231	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
			771	495	140	135	1			
17	2V	101	Total	C	N	O	S	0	0	0
			771	495	140	135	1			

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

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	1Y	107	Total	C	N	O	S	0	0	0
			806	517	152	131	6			
20	2Y	107	Total	C	N	O	S	0	0	0
			806	517	152	131	6			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
21	1Z	186	Total	C	N	O	S	0	0	0
			1470	937	262	269	2			
21	2Z	186	Total	C	N	O	S	0	0	0
			1454	929	256	267	2			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	10	75	Total	C	N	O	S	0	0	0
			598	370	127	100	1			
22	20	75	Total	C	N	O	S	0	0	0
			598	370	127	100	1			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
23	11	97	Total	C	N	O	S	0	0	0
			755	475	148	131	1			
23	21	97	Total	C	N	O	S	0	0	0
			755	475	148	131	1			

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

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	14	69	Total	C	N	O	S	0	0	0
			558	352	102	99	5			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	24	69	Total	C	N	O	S	0	0	0
			532	339	97	91	5			

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
32	1a	1477	Total	C	N	O	P	0	0	0
			31750	14131	5883	10259	1477			
32	2a	1483	Total	C	N	O	P	0	0	0
			31877	14188	5905	10301	1483			

- 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
			1786	1136	321	325	4			
33	2b	231	Total	C	N	O	S	0	0	0
			1697	1079	292	321	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
			1480	932	281	266	1			
34	2c	206	Total	C	N	O	S	0	0	0
			1412	883	269	259	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
			1618	1013	312	286	7			
35	2d	208	Total	C	N	O	S	0	0	0
			1630	1022	321	280	7			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
36	1e	148	Total	C	N	O	S	0	0	0
			1129	714	213	198	4			
36	2e	148	Total	C	N	O	S	0	0	0
			1095	695	203	193	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
			806	511	143	149	3			
37	2f	100	Total	C	N	O	S	0	0	0
			817	516	146	152	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
			1183	732	232	213	6			
38	2g	155	Total	C	N	O	S	0	0	0
			1167	728	220	213	6			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
39	1h	137	Total	C	N	O	S	0	0	0
			1088	689	206	191	2			
39	2h	137	Total	C	N	O	S	0	0	0
			1074	681	202	189	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
			976	620	189	167			
40	2i	127	Total	C	N	O	0	0	0
			932	589	177	166			

- 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
			682	424	130	128			
41	2j	96	Total	C	N	O	0	0	0
			678	424	126	128			

- 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
			826	513	156	154	3			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
42	2k	114	Total	C	N	O	S	0	0	0
			829	516	155	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
			920	579	181	159	1			
43	2l	122	Total	C	N	O	S	0	0	0
			918	576	182	159	1			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
44	1m	118	Total	C	N	O	S	0	0	0
			923	569	191	161	2			
44	2m	116	Total	C	N	O	S	0	0	0
			903	555	187	159	2			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
45	1n	60	Total	C	N	O	S	0	0	0
			482	306	100	72	4			
45	2n	60	Total	C	N	O	S	0	0	0
			459	291	93	71	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
			715	447	140	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
			671	424	133	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
			811	519	148	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	84	Total	C	N	O	S	0	0	0
			642	409	119	112	2			
50	2s	83	Total	C	N	O	S	0	0	0
			646	412	119	113	2			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
51	1t	96	Total	C	N	O	S	0	0	0
			712	435	152	123	2			
51	2t	96	Total	C	N	O	S	0	0	0
			731	449	156	124	2			

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
52	1u	23	Total	C	N	O	0	0	0
			187	116	42	29			
52	2u	23	Total	C	N	O	0	0	0
			199	122	48	29			

- Molecule 53 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
53	1v	5	Total	C	N	O	P	0	0	0
			109	49	22	33	5			
53	2v	5	Total	C	N	O	P	0	0	0
			109	49	22	33	5			

- Molecule 54 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
54	1x	76	Total	C	N	O	P	S	0	0	0
			1625	725	294	529	76	1			
54	2x	76	Total	C	N	O	P	S	0	0	0
			1625	725	294	529	76	1			

- Molecule 55 is a protein called Oncocin 10wt.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
55	1z	13	Total	C	N	O	0	0	0
			108	72	20	16			
55	2z	12	Total	C	N	O	0	0	0
			101	67	19	15			

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	1A	1096	Total	Mg	0	0
			1096	1096		
56	1B	27	Total	Mg	0	0
			27	27		
56	1D	13	Total	Mg	0	0
			13	13		
56	1E	8	Total	Mg	0	0
			8	8		
56	1F	7	Total	Mg	0	0
			7	7		
56	1G	3	Total	Mg	0	0
			3	3		
56	1H	3	Total	Mg	0	0
			3	3		
56	1N	8	Total	Mg	0	0
			8	8		
56	1O	3	Total	Mg	0	0
			3	3		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	1P	6	Total 6	Mg 6	0	0
56	1Q	7	Total 7	Mg 7	0	0
56	1R	6	Total 6	Mg 6	0	0
56	1T	6	Total 6	Mg 6	0	0
56	1U	6	Total 6	Mg 6	0	0
56	1V	1	Total 1	Mg 1	0	0
56	1W	5	Total 5	Mg 5	0	0
56	1X	1	Total 1	Mg 1	0	0
56	1Y	1	Total 1	Mg 1	0	0
56	1Z	2	Total 2	Mg 2	0	0
56	10	6	Total 6	Mg 6	0	0
56	11	4	Total 4	Mg 4	0	0
56	13	2	Total 2	Mg 2	0	0
56	15	3	Total 3	Mg 3	0	0
56	16	3	Total 3	Mg 3	0	0
56	17	6	Total 6	Mg 6	0	0
56	18	4	Total 4	Mg 4	0	0
56	19	3	Total 3	Mg 3	0	0
56	1a	307	Total 307	Mg 307	0	0
56	1b	2	Total 2	Mg 2	0	0
56	1c	1	Total 1	Mg 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	1d	2	Total 2	Mg 2	0	0
56	1e	3	Total 3	Mg 3	0	0
56	1f	1	Total 1	Mg 1	0	0
56	1h	3	Total 3	Mg 3	0	0
56	1k	1	Total 1	Mg 1	0	0
56	1l	1	Total 1	Mg 1	0	0
56	1m	2	Total 2	Mg 2	0	0
56	1n	1	Total 1	Mg 1	0	0
56	1o	2	Total 2	Mg 2	0	0
56	1q	4	Total 4	Mg 4	0	0
56	1r	3	Total 3	Mg 3	0	0
56	1t	1	Total 1	Mg 1	0	0
56	1u	1	Total 1	Mg 1	0	0
56	1x	10	Total 10	Mg 10	0	0
56	2A	559	Total 559	Mg 559	0	0
56	2B	10	Total 10	Mg 10	0	0
56	2D	6	Total 6	Mg 6	0	0
56	2E	4	Total 4	Mg 4	0	0
56	2F	3	Total 3	Mg 3	0	0
56	2G	1	Total 1	Mg 1	0	0
56	2N	1	Total 1	Mg 1	0	0

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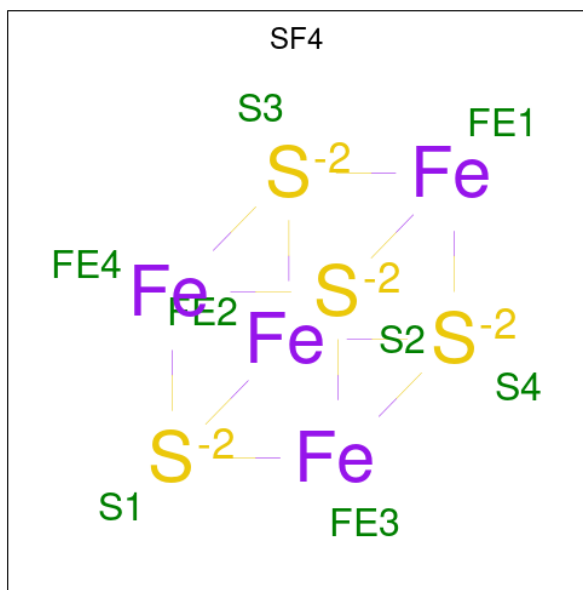
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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
56	2O	2	Total Mg 2 2	0	0
56	2Q	5	Total Mg 5 5	0	0
56	2U	2	Total Mg 2 2	0	0
56	2W	1	Total Mg 1 1	0	0
56	2Y	2	Total Mg 2 2	0	0
56	2Z	1	Total Mg 1 1	0	0
56	20	1	Total Mg 1 1	0	0
56	25	1	Total Mg 1 1	0	0
56	28	1	Total Mg 1 1	0	0
56	2a	217	Total Mg 217 217	0	0
56	2d	1	Total Mg 1 1	0	0
56	2e	3	Total Mg 3 3	0	0
56	2f	1	Total Mg 1 1	0	0
56	2k	1	Total Mg 1 1	0	0
56	2l	4	Total Mg 4 4	0	0
56	2n	1	Total Mg 1 1	0	0
56	2p	1	Total Mg 1 1	0	0
56	2q	2	Total Mg 2 2	0	0
56	2t	1	Total Mg 1 1	0	0
56	2x	5	Total Mg 5 5	0	0

- Molecule 57 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
57	1Y	1	Total Zn 1 1	0	0
57	14	1	Total Zn 1 1	0	0
57	15	1	Total Zn 1 1	0	0
57	16	1	Total Zn 1 1	0	0
57	19	1	Total Zn 1 1	0	0
57	1n	1	Total Zn 1 1	0	0
57	2Y	1	Total Zn 1 1	0	0
57	24	1	Total Zn 1 1	0	0
57	25	1	Total Zn 1 1	0	0
57	26	1	Total Zn 1 1	0	0
57	29	1	Total Zn 1 1	0	0
57	2n	1	Total Zn 1 1	0	0

- Molecule 58 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe_4S_4).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
58	1d	1	Total	Fe	S	0	0
			8	4	4		
58	2d	1	Total	Fe	S	0	0
			8	4	4		

- Molecule 59 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
59	1A	2345	Total	O	0	0
			2345	2345		
59	1B	45	Total	O	0	0
			45	45		
59	1D	20	Total	O	0	0
			20	20		
59	1E	29	Total	O	0	0
			29	29		
59	1F	18	Total	O	0	0
			18	18		
59	1G	4	Total	O	0	0
			4	4		
59	1H	4	Total	O	0	0
			4	4		
59	1I	1	Total	O	0	0
			1	1		
59	1N	12	Total	O	0	0
			12	12		
59	1O	6	Total	O	0	0
			6	6		
59	1P	16	Total	O	0	0
			16	16		
59	1Q	12	Total	O	0	0
			12	12		
59	1R	10	Total	O	0	0
			10	10		
59	1S	1	Total	O	0	0
			1	1		
59	1T	14	Total	O	0	0
			14	14		
59	1U	11	Total	O	0	0
			11	11		
59	1V	5	Total	O	0	0
			5	5		
59	1W	9	Total	O	0	0
			9	9		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
59	1X	6	Total 6	O 6	0	0
59	1Y	1	Total 1	O 1	0	0
59	1Z	6	Total 6	O 6	0	0
59	10	7	Total 7	O 7	0	0
59	11	9	Total 9	O 9	0	0
59	12	1	Total 1	O 1	0	0
59	13	5	Total 5	O 5	0	0
59	14	1	Total 1	O 1	0	0
59	15	9	Total 9	O 9	0	0
59	16	6	Total 6	O 6	0	0
59	17	3	Total 3	O 3	0	0
59	18	15	Total 15	O 15	0	0
59	19	4	Total 4	O 4	0	0
59	1a	395	Total 395	O 395	0	0
59	1b	1	Total 1	O 1	0	0
59	1d	5	Total 5	O 5	0	0
59	1e	3	Total 3	O 3	0	0
59	1f	1	Total 1	O 1	0	0
59	1h	4	Total 4	O 4	0	0
59	1i	1	Total 1	O 1	0	0
59	1j	2	Total 2	O 2	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
59	1k	2	Total 2	O 2	0	0
59	1l	3	Total 3	O 3	0	0
59	1o	3	Total 3	O 3	0	0
59	1s	1	Total 1	O 1	0	0
59	1v	2	Total 2	O 2	0	0
59	1x	11	Total 11	O 11	0	0
59	1z	1	Total 1	O 1	0	0
59	2A	810	Total 810	O 810	0	0
59	2B	10	Total 10	O 10	0	0
59	2D	15	Total 15	O 15	0	0
59	2E	9	Total 9	O 9	0	0
59	2F	4	Total 4	O 4	0	0
59	2O	2	Total 2	O 2	0	0
59	2P	6	Total 6	O 6	0	0
59	2Q	2	Total 2	O 2	0	0
59	2R	2	Total 2	O 2	0	0
59	2T	2	Total 2	O 2	0	0
59	2U	4	Total 4	O 4	0	0
59	2V	1	Total 1	O 1	0	0
59	2W	1	Total 1	O 1	0	0
59	2X	2	Total 2	O 2	0	0

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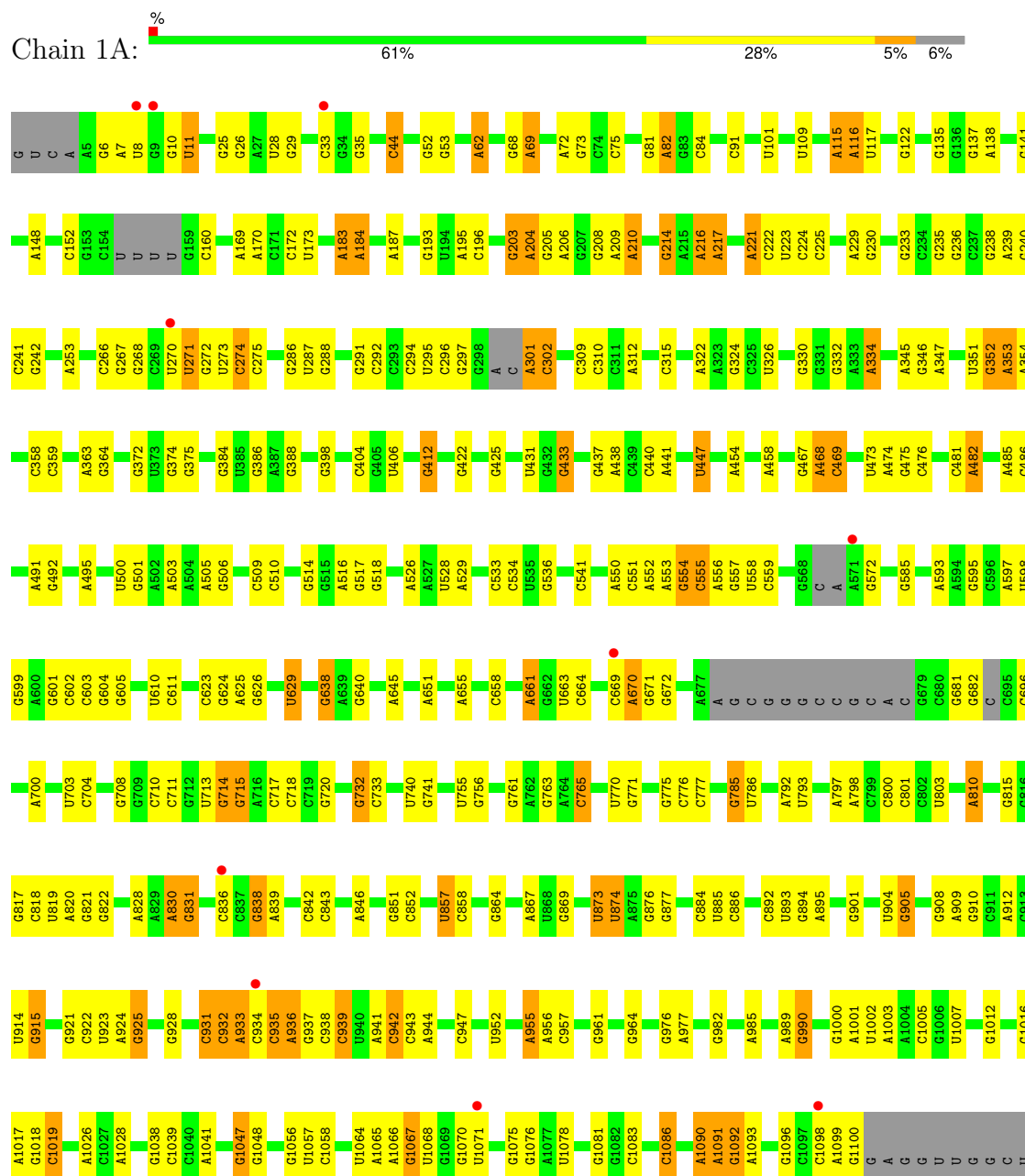
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
59	2Y	1	Total	O	0	0
			1	1		
59	2Z	4	Total	O	0	0
			4	4		
59	20	3	Total	O	0	0
			3	3		
59	21	1	Total	O	0	0
			1	1		
59	23	2	Total	O	0	0
			2	2		
59	28	4	Total	O	0	0
			4	4		
59	2a	235	Total	O	0	0
			235	235		
59	2d	2	Total	O	0	0
			2	2		
59	2e	3	Total	O	0	0
			3	3		
59	2i	1	Total	O	0	0
			1	1		
59	2m	1	Total	O	0	0
			1	1		
59	2n	1	Total	O	0	0
			1	1		
59	2p	1	Total	O	0	0
			1	1		
59	2t	4	Total	O	0	0
			4	4		
59	2x	5	Total	O	0	0
			5	5		
59	2z	1	Total	O	0	0
			1	1		

3 Residue-property plots

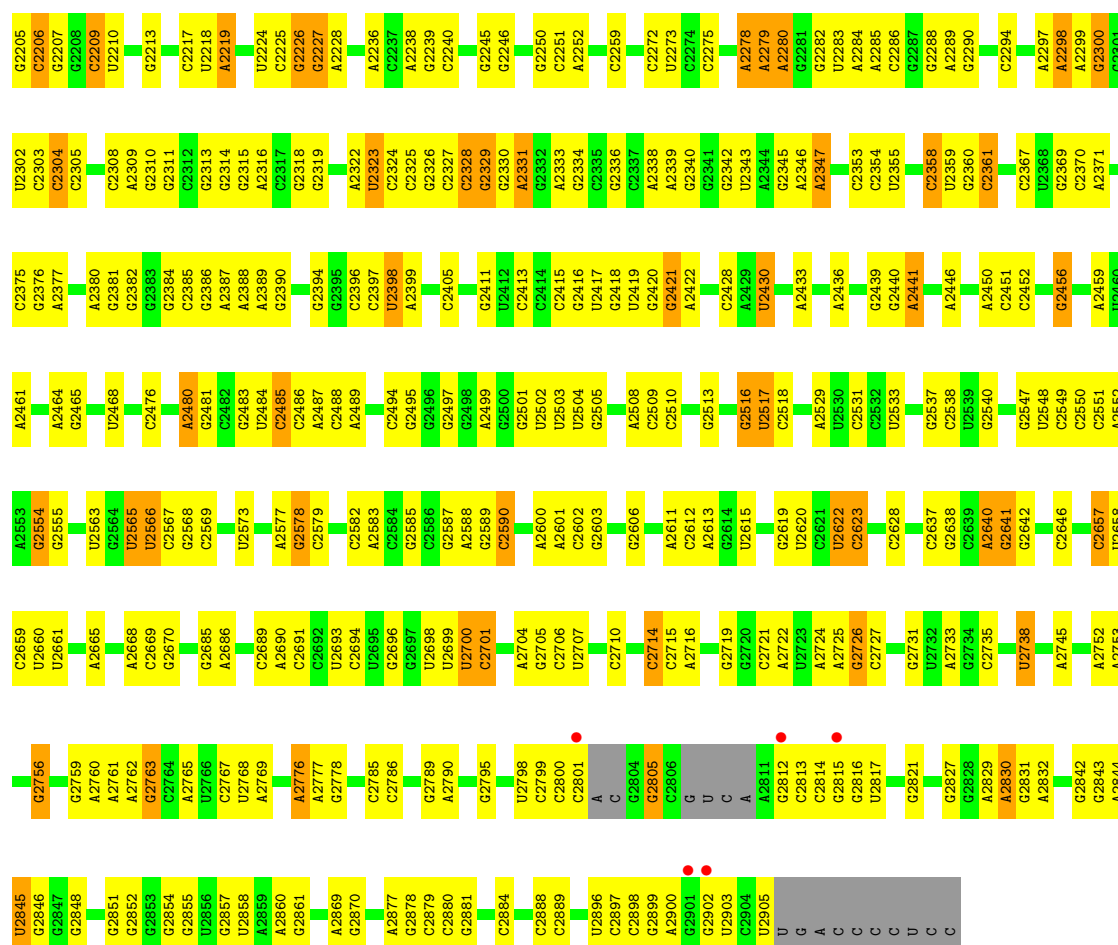
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

• Molecule 1: 23S Ribosomal RNA

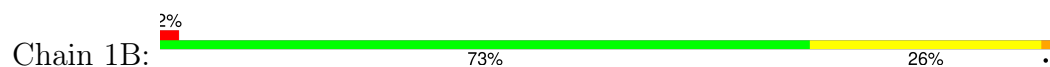


U	C	A	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C
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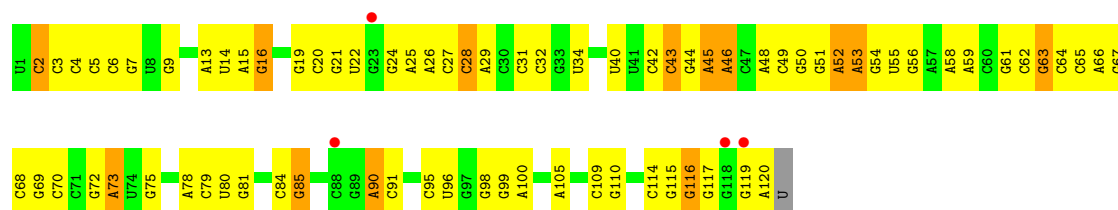
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A	C2061	G1952	U1834	C1756	G1645	C1543	G1446	U1346	G1236	G1154	U1078	U1001	A933
C	C2064	C1955	U1835	C1757	C1649	C1550	G1447	A1346	A1238	G1155	C1083	A1003	C934
C	G2067	A1958	G1845	C1758	C1652	C1551	C1448	A1347	G1239	G1156	G1084	A1004	C935
U	C2072	U1959	G1846	U1759	A1653	C1552	C1449	C1348	C1240	U1157	C1088	C1005	A956
G	A2072	U1960	G1854	G1760	A1655	C1554	U1450	G1349	G1241	U1158	C1089	C1006	G937
G	C2076	A1856	G1855	G1765	A1656	C1555	U1451	C1350	C1244	G1159	G1088	U1013	C938
A	G2077	C1857	G1856	U1767	A1663	G1557	C1452	G1354	U1248	G1160	A1090	U1014	C939
C	A2078	G1858	G1857	G1768	G1667	U1565	G1453	U1358	A1249	G1162	A1091	C1015	U940
C	A2079	A1859	G1859	G1769	G1671	G1566	U1460	C1359	U1249	C1166	A1092	G1016	C942
C	A2081	U1863	U1863	G1776	G1672	G1567	G1461	C1360	A1264	C1167	C1093	G1017	A945
C	G2082	G1869	G1869	G1777	G1673	U1570	C1462	U1361	U1265	G1170	A1094	C1018	A946
C	A2083	U1976	U1976	G1778	G1674	G1573	U1465	A1362	C1266	A1171	A1095	G1019	A947
C	G2088	U1984	C1873	C1781	G1675	A1574	G1466	A1366	G1276	U1174	A1099	U1020	C948
C	U2089	G1874	G1874	G1782	G1676	G1575	G1470	A1367	G1277	U1175	G1100	A1025	U950
C	G2090	A1877	A1877	G1783	A1677	C1576	A1472	C1372	U1279	G1176	A1101	C1027	A955
C	A2092	G1878	G1878	G1786	G1681	U1579	C1474	U1374	G1281	C1179	A1102	C1028	A956
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U	G2099	A1992	G1888	G1793	C1685	C1583	U1477	A1381	U1286	C1184	G1107	A1035	G961
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G	G2108	G2013	G1890	C1797	C1694	C1592	G1481	A1405	G1301	U1187	U1111	A1041	G964
G	G2115	C2017	U1894	A1803	A1698	C1593	G1486	A1409	C1302	A1183	G1113	G1042	G965
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C	G	G1822	G1822	C1830	G1733	C1830	G1524	A1423	U1318	C1222	U1135	A1065	U987
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C	G	A1735	A1735	A1832	U1735	A1832	G1528	G1425	A1320	C1224	U1141	G1067	A989
C	U	U1826	U1826	C1833	U1739	C1833	G1528	A1429	A1321	C1225	U1142	U1068	G990
C	A	U1827	U1827	C1834	C1740	C1834	U1534	A1430	G1322	C1225	U1143	G1069	G991
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G	G	C1829	C1829	G1836	G1741	U1836	A1536	U1439	A1331	G1231	U1150	A1072	G994
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G	G	A1948	A1948	G1831	A1744	G1831	G1537	U1440	U1333	A1233		G1075	G998
C2204													



• Molecule 2: 5S Ribosomal RNA

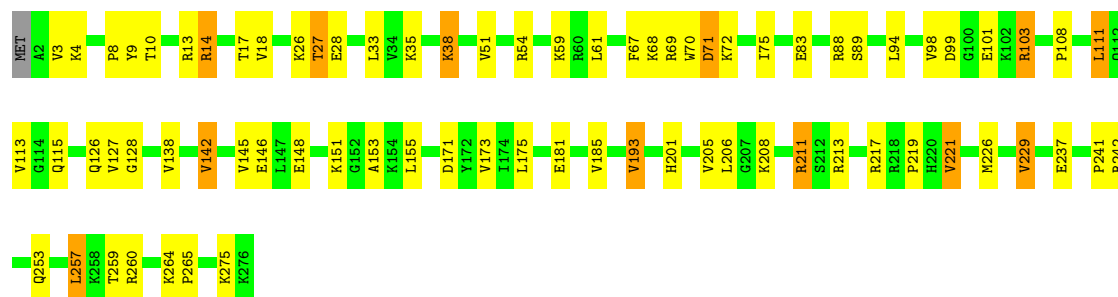


• Molecule 2: 5S Ribosomal RNA

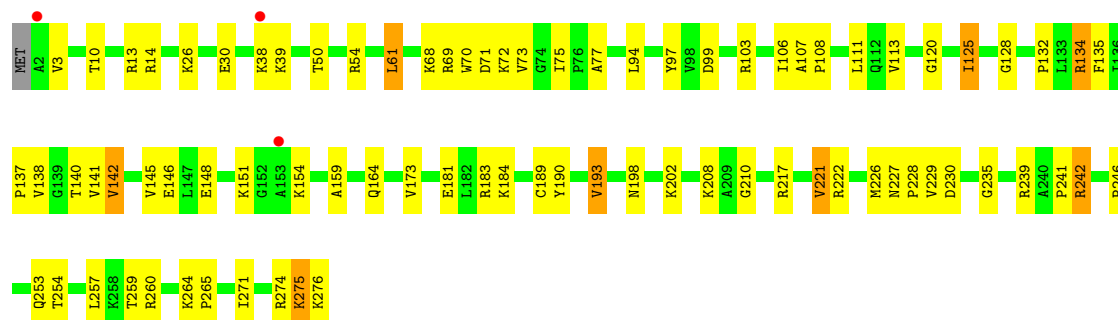


• Molecule 3: 50S ribosomal protein L2

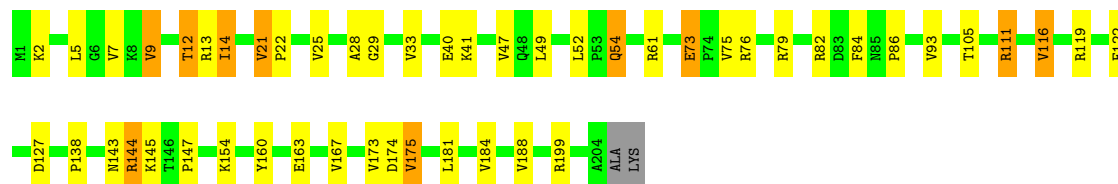
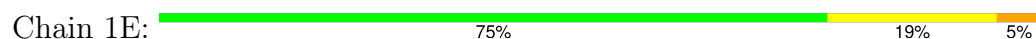




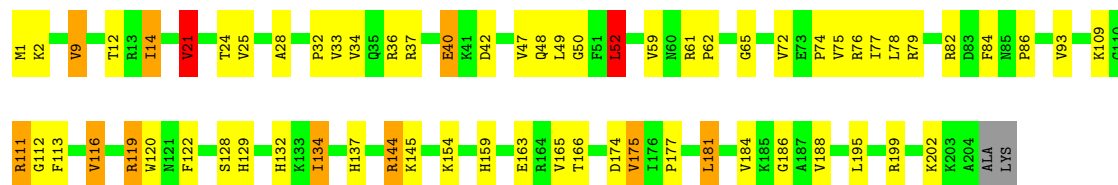
• Molecule 3: 50S ribosomal protein L2



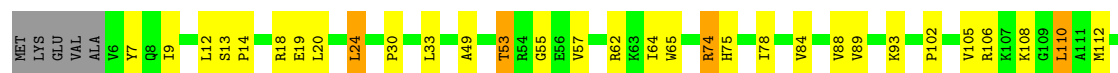
• Molecule 4: 50S ribosomal protein L3



• Molecule 4: 50S ribosomal protein L3

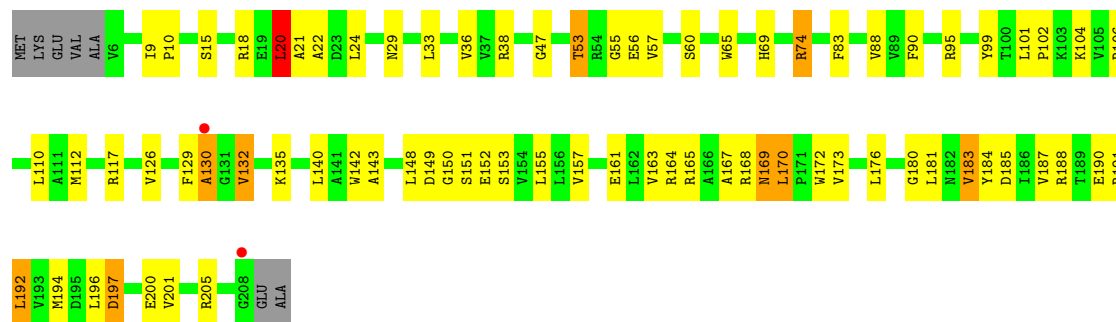


• Molecule 5: 50S ribosomal protein L4

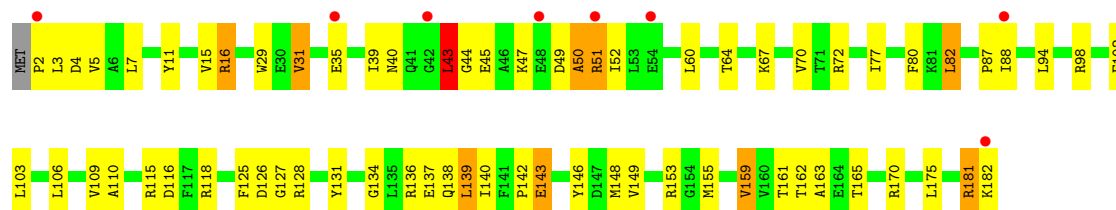




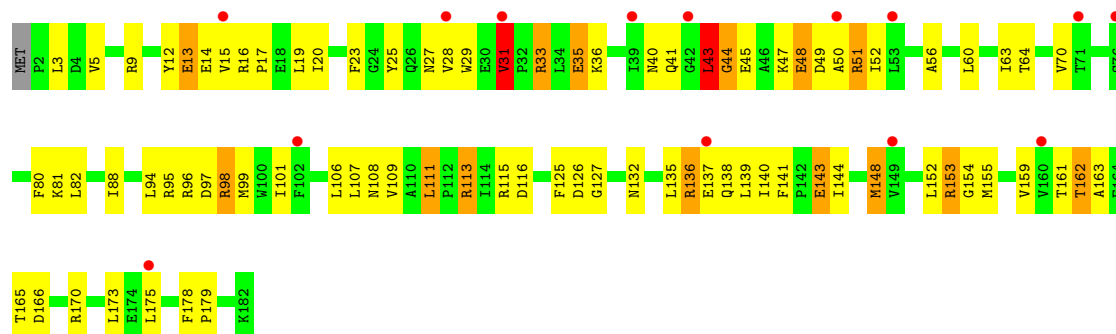
• Molecule 5: 50S ribosomal protein L4



• Molecule 6: 50S ribosomal protein L5



• Molecule 6: 50S ribosomal protein L5

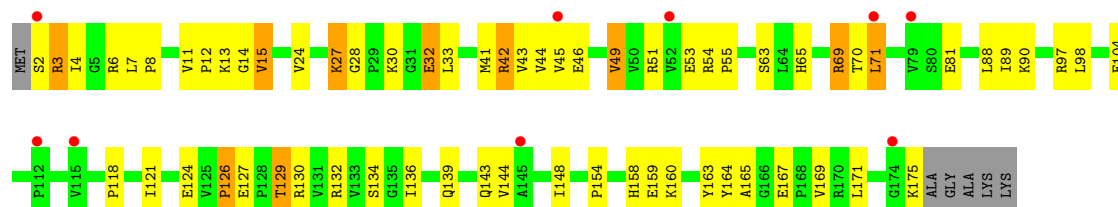


• Molecule 7: 50S ribosomal protein L6

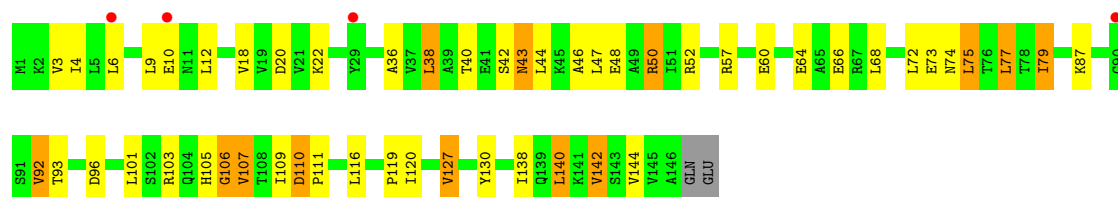




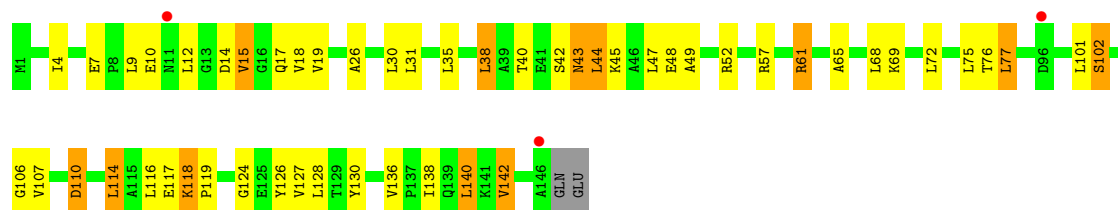
• Molecule 7: 50S ribosomal protein L6



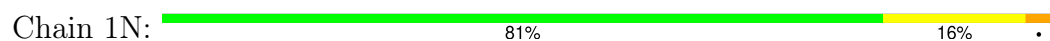
• Molecule 8: 50S ribosomal protein L9



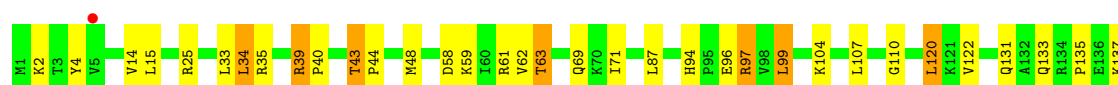
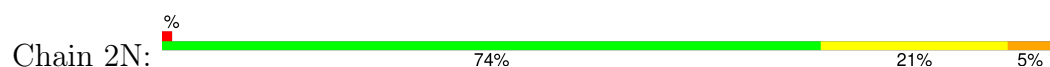
• Molecule 8: 50S ribosomal protein L9



• Molecule 9: 50S ribosomal protein L13

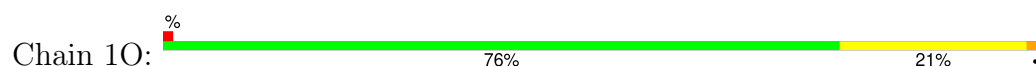


• Molecule 9: 50S ribosomal protein L13





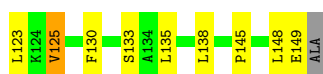
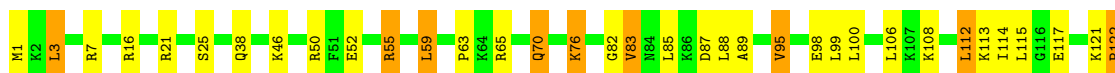
- Molecule 10: 50S ribosomal protein L14



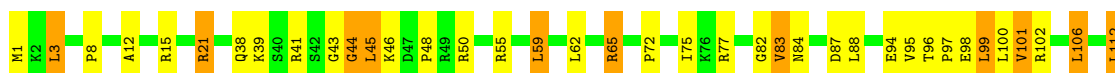
- Molecule 10: 50S ribosomal protein L14



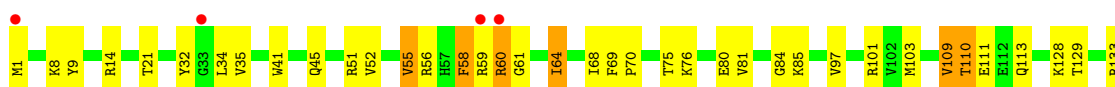
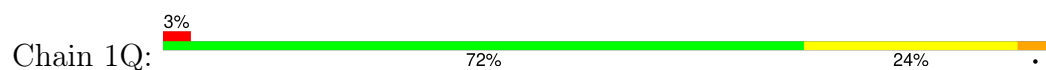
- Molecule 11: 50S ribosomal protein L15



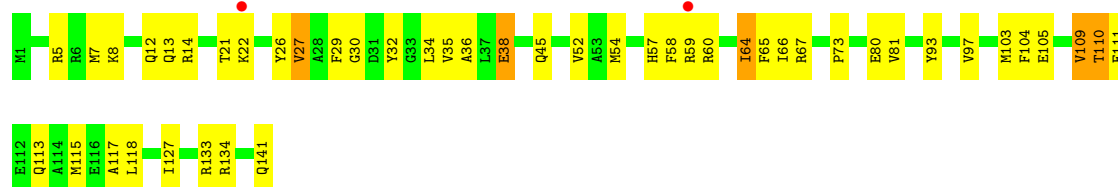
- Molecule 11: 50S ribosomal protein L15



- Molecule 12: 50S ribosomal protein L16



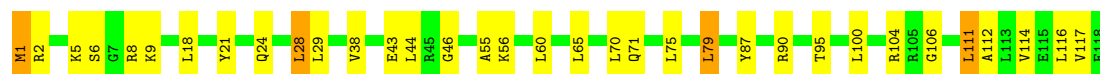
- Molecule 12: 50S ribosomal protein L16



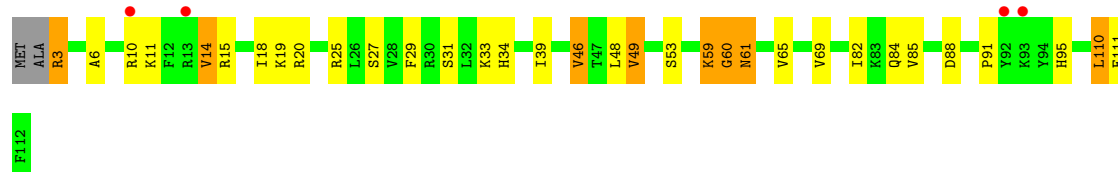
- Molecule 13: 50S ribosomal protein L17



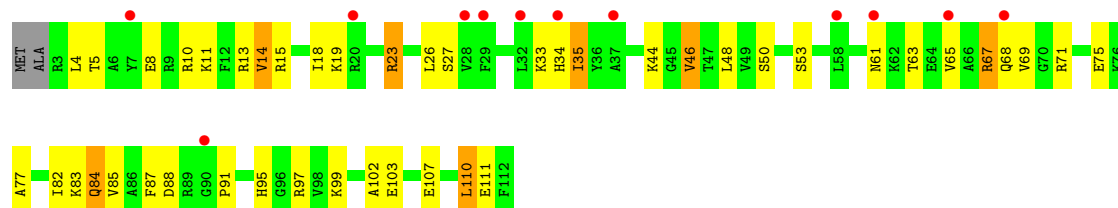
- Molecule 13: 50S ribosomal protein L17



- Molecule 14: 50S ribosomal protein L18

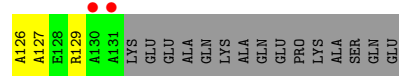


- Molecule 14: 50S ribosomal protein L18

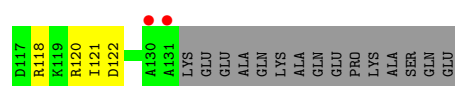
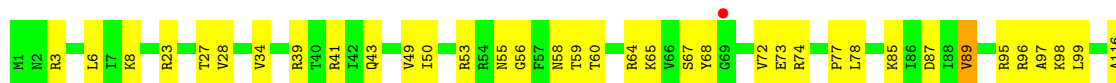


- Molecule 15: 50S ribosomal protein L19

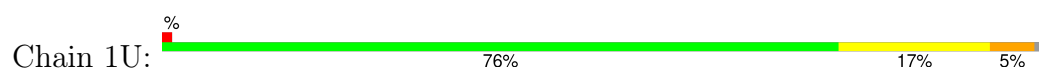




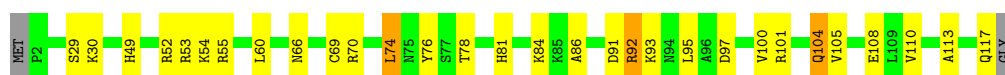
- Molecule 15: 50S ribosomal protein L19



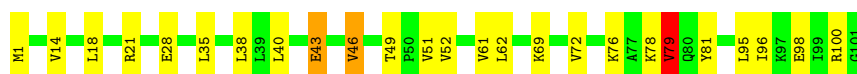
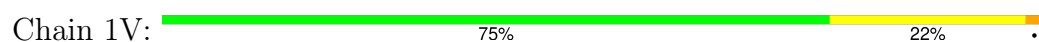
- Molecule 16: 50S ribosomal protein L20



- Molecule 16: 50S ribosomal protein L20



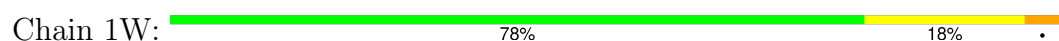
- Molecule 17: 50S ribosomal protein L21



- Molecule 17: 50S ribosomal protein L21

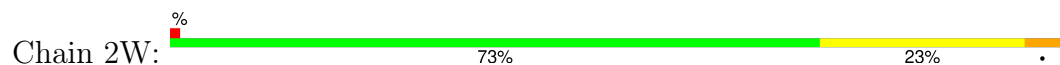


- Molecule 18: 50S ribosomal protein L22

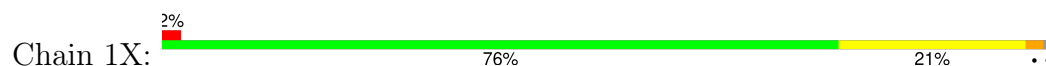




- Molecule 18: 50S ribosomal protein L22



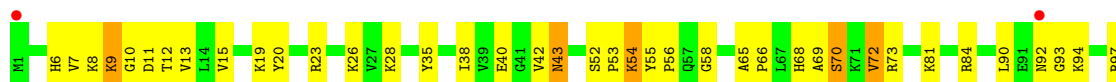
- Molecule 19: 50S ribosomal protein L23



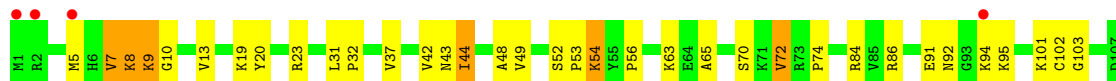
- Molecule 19: 50S ribosomal protein L23



- Molecule 20: 50S ribosomal protein L24

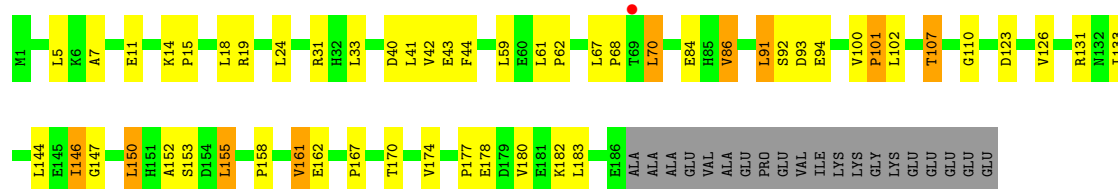


- Molecule 20: 50S ribosomal protein L24

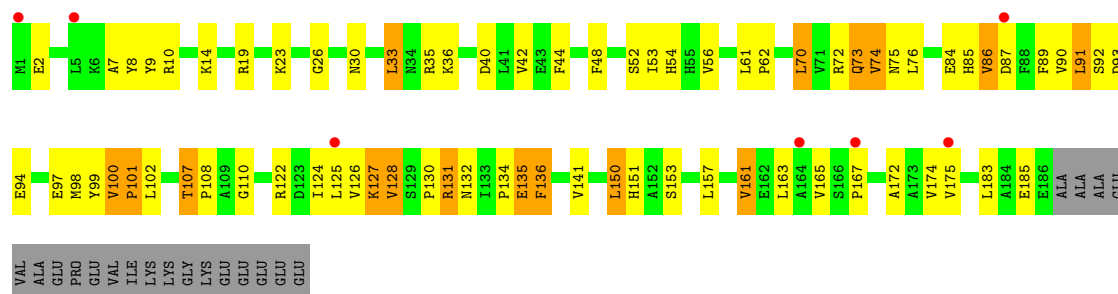


- Molecule 21: 50S ribosomal protein L25

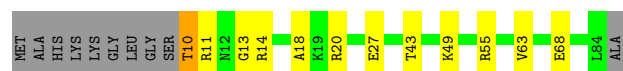




- Molecule 21: 50S ribosomal protein L25



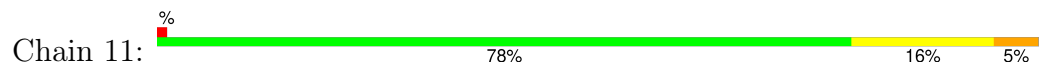
- Molecule 22: 50S ribosomal protein L27



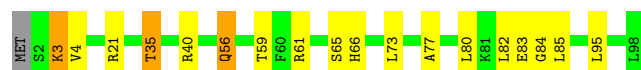
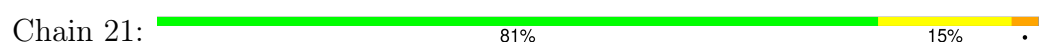
- Molecule 22: 50S ribosomal protein L27



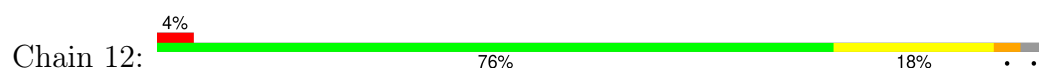
- Molecule 23: 50S ribosomal protein L28



- Molecule 23: 50S ribosomal protein L28



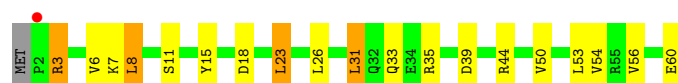
- Molecule 24: 50S ribosomal protein L29



- Molecule 24: 50S ribosomal protein L29



- Molecule 25: 50S ribosomal protein L30



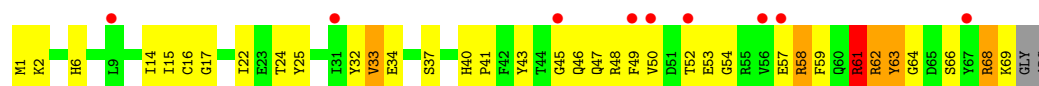
- Molecule 25: 50S ribosomal protein L30



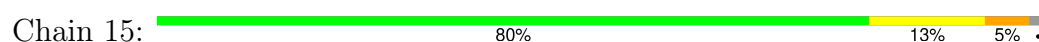
- Molecule 26: 50S ribosomal protein L31



- Molecule 26: 50S ribosomal protein L31



- Molecule 27: 50S ribosomal protein L32



- Molecule 27: 50S ribosomal protein L32

Chain 25:  78% 18% ..



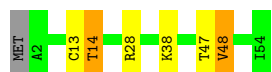
- Molecule 28: 50S ribosomal protein L33

Chain 16:  67% 28% ..



- Molecule 28: 50S ribosomal protein L33

Chain 26:  87% 7% ..



- Molecule 29: 50S ribosomal protein L34

Chain 17:  4% 59% 35% ..



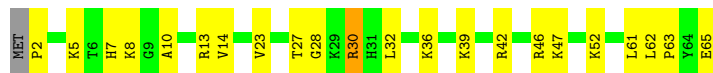
- Molecule 29: 50S ribosomal protein L34

Chain 27:  2% 73% 24% .



- Molecule 30: 50S ribosomal protein L35

Chain 18:  65% 32% ..

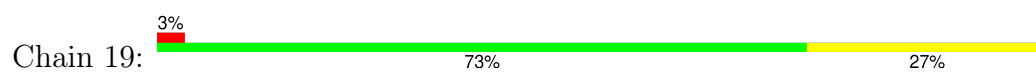


- Molecule 30: 50S ribosomal protein L35

Chain 28:  54% 42% ..



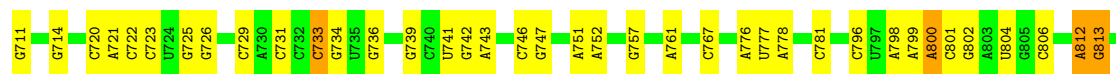
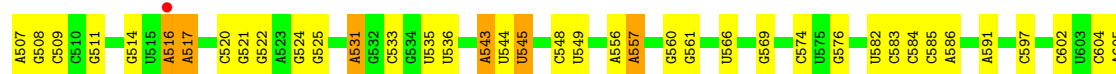
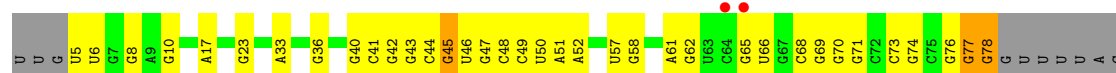
- Molecule 31: 50S ribosomal protein L36

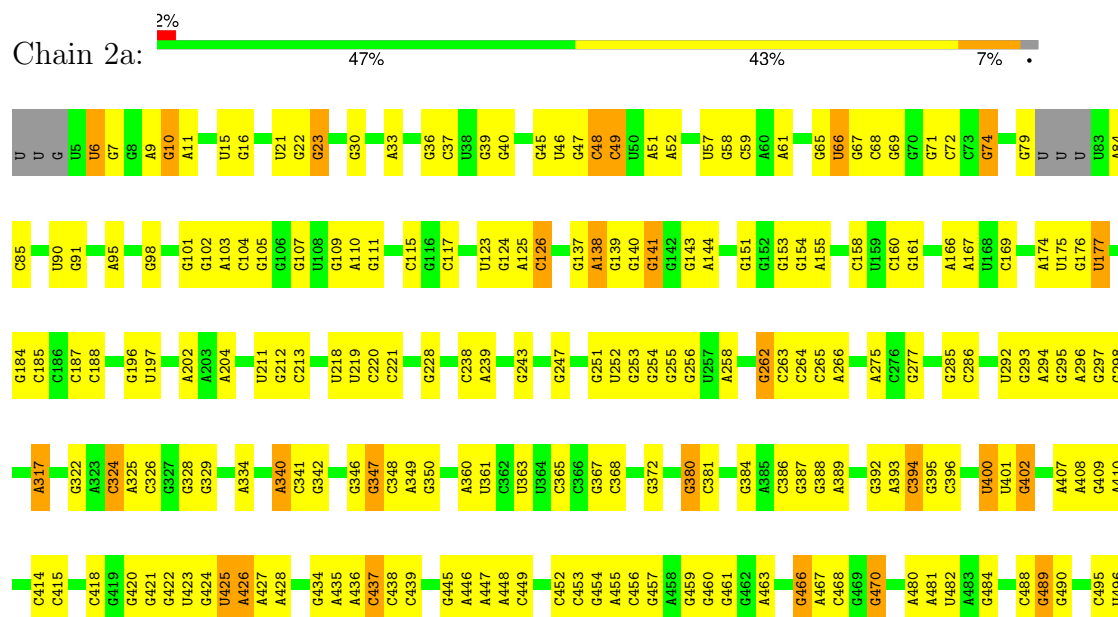
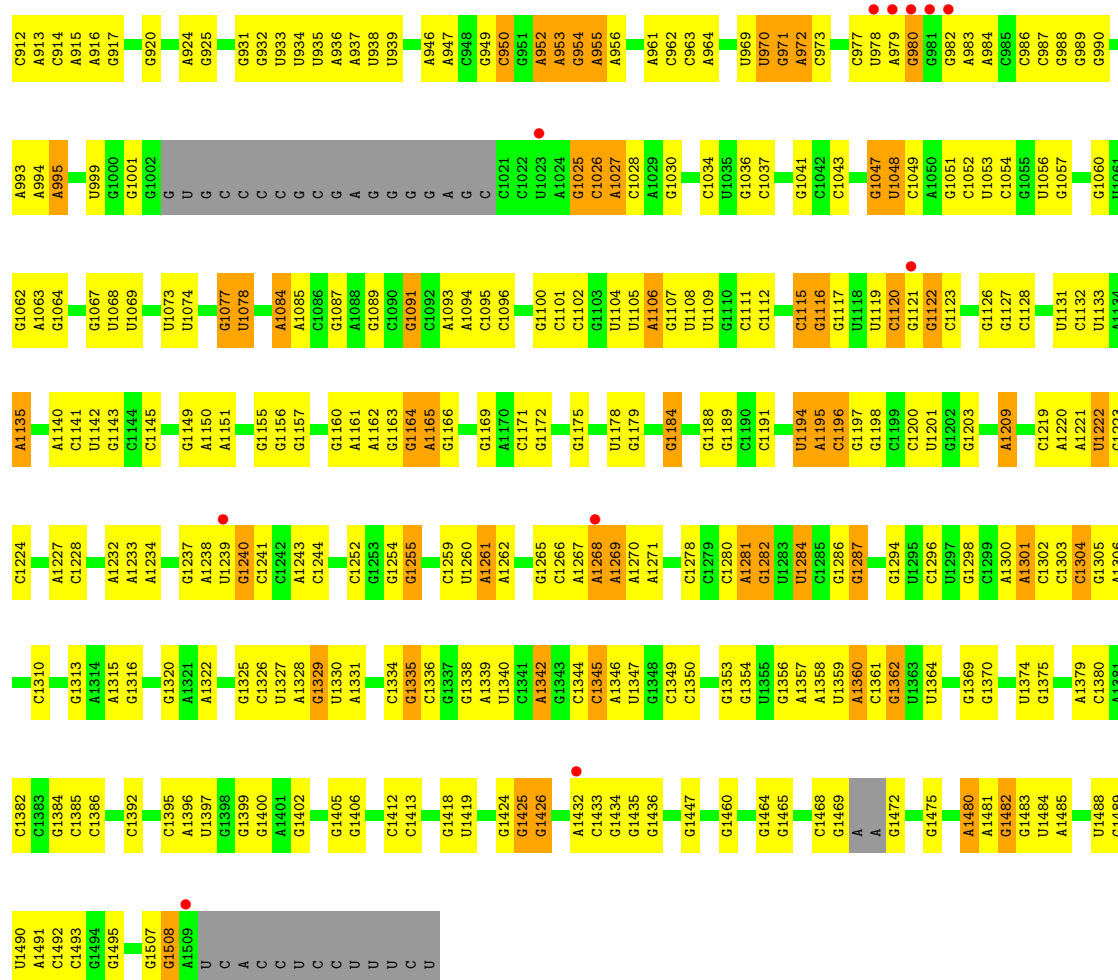


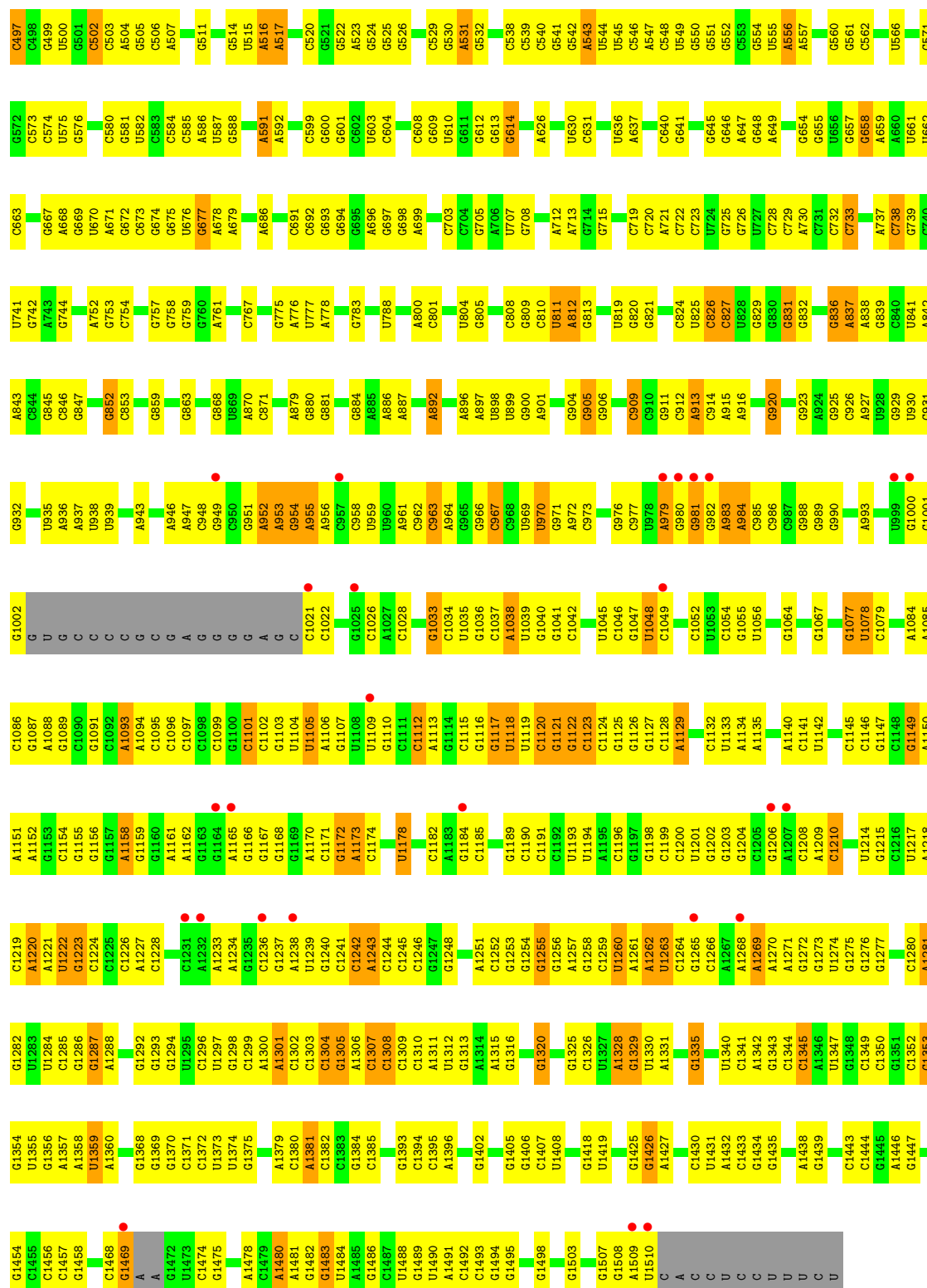
• Molecule 31: 50S ribosomal protein L36



• Molecule 32: 16S Ribosomal RNA

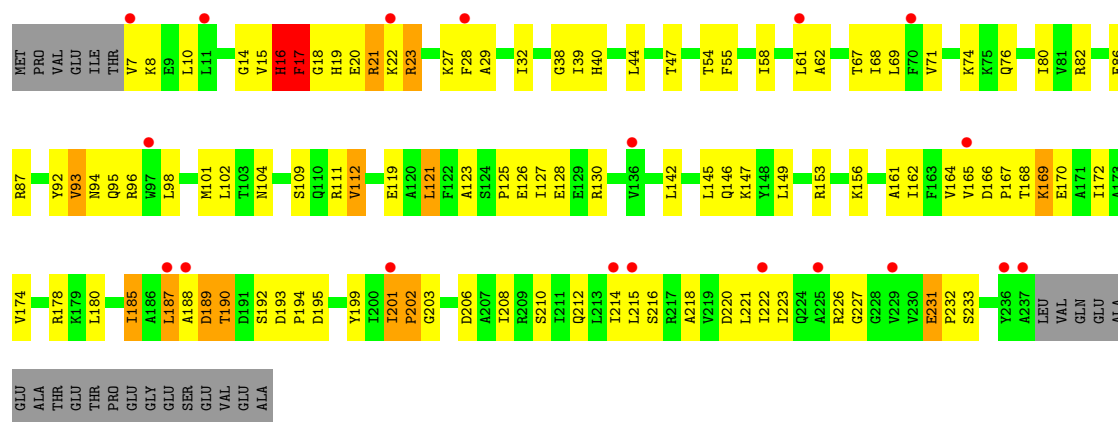




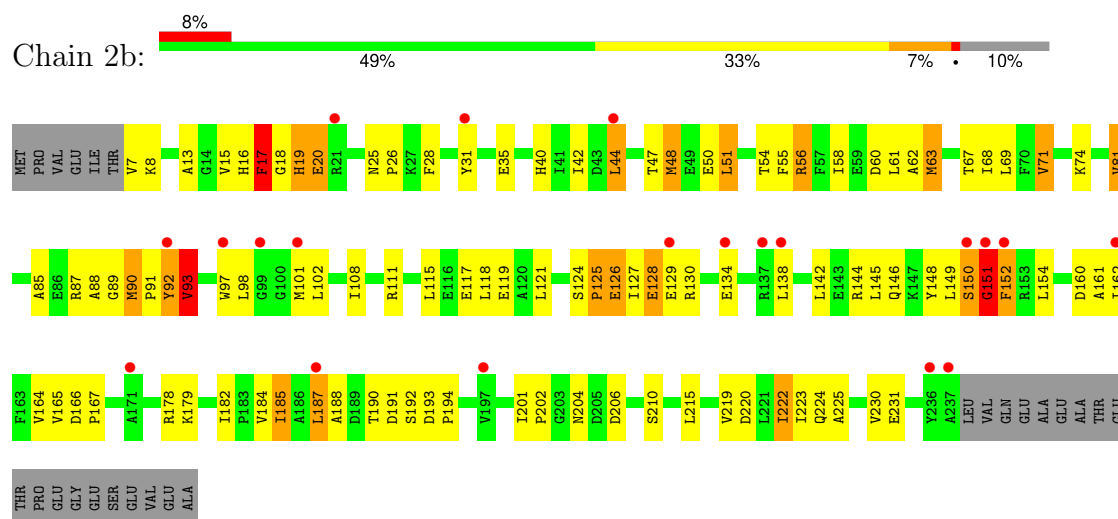


• Molecule 33: 30S ribosomal protein S2

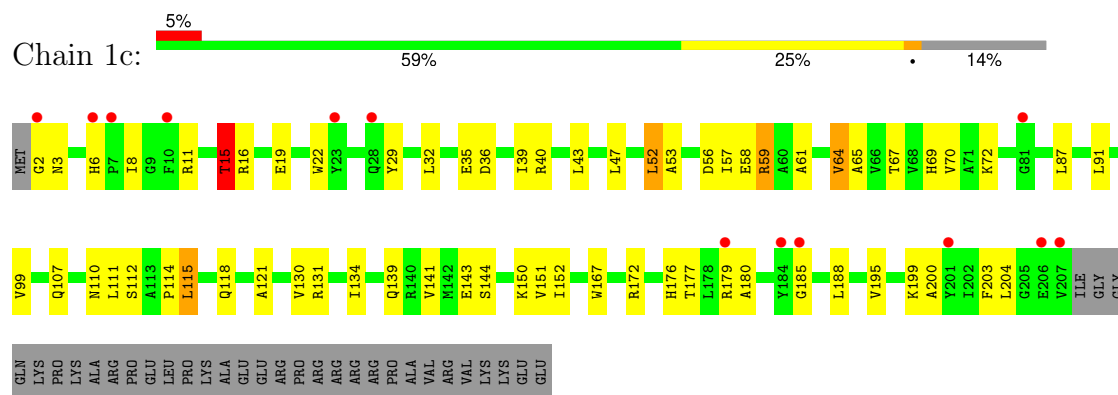




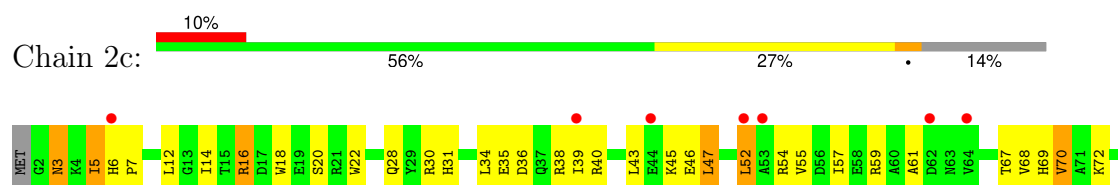
• Molecule 33: 30S ribosomal protein S2

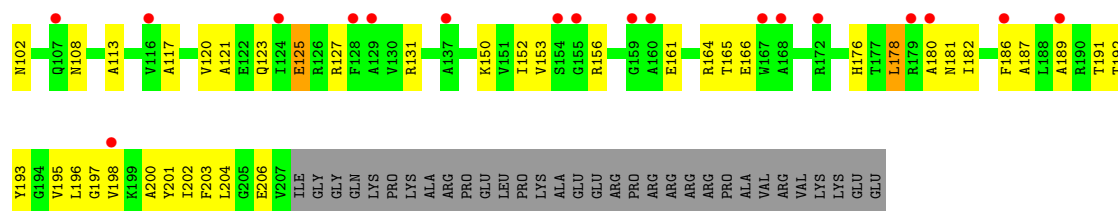


• Molecule 34: 30S ribosomal protein S3

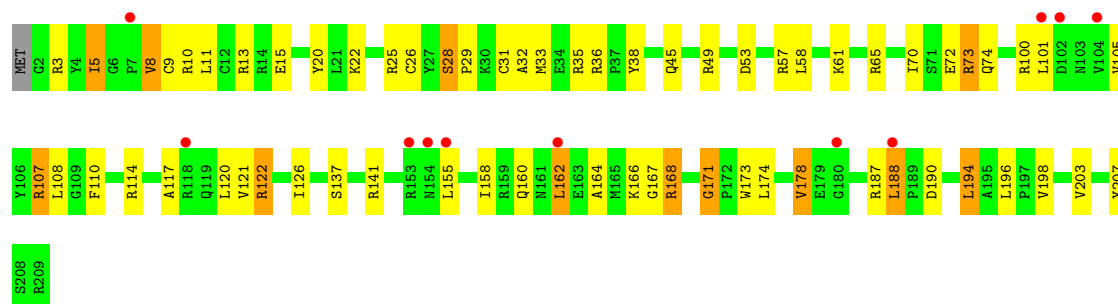


• Molecule 34: 30S ribosomal protein S3

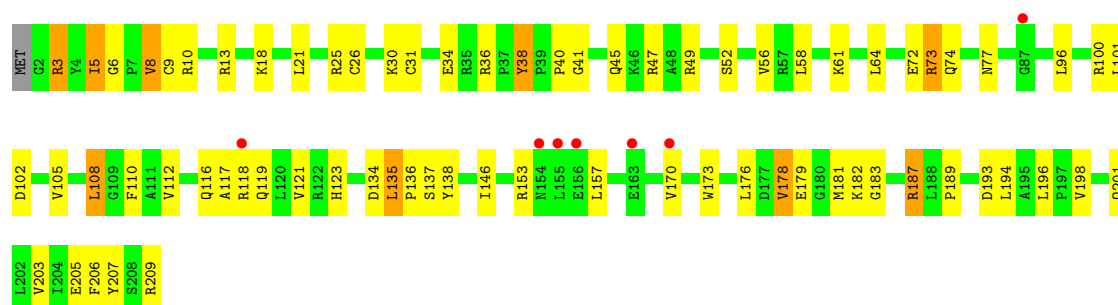




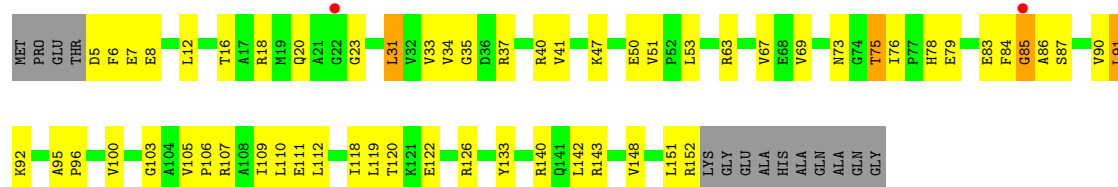
• Molecule 35: 30S ribosomal protein S4



• Molecule 35: 30S ribosomal protein S4

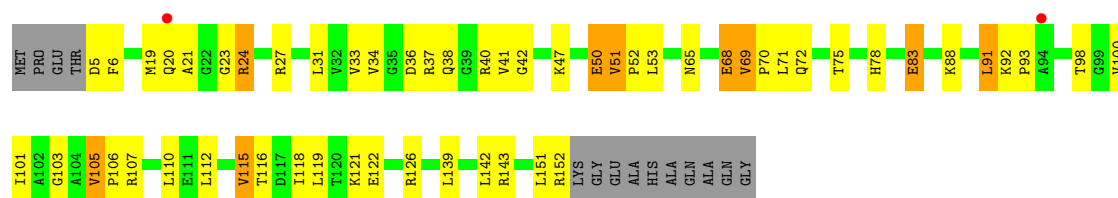


• Molecule 36: 30S ribosomal protein S5

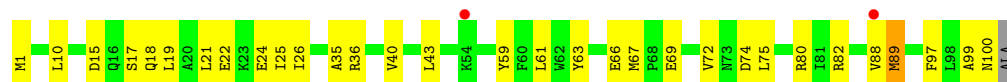


• Molecule 36: 30S ribosomal protein S5

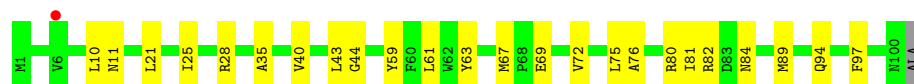
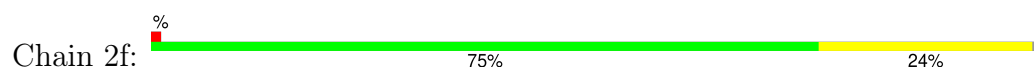




- Molecule 37: 30S ribosomal protein S6



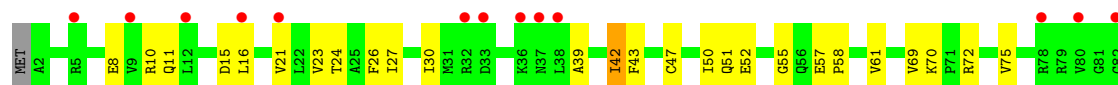
- Molecule 37: 30S ribosomal protein S6



- Molecule 38: 30S ribosomal protein S7



- Molecule 38: 30S ribosomal protein S7

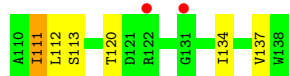


- Molecule 39: 30S ribosomal protein S8

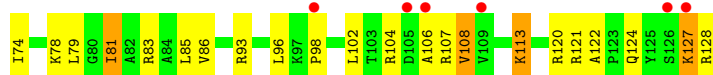
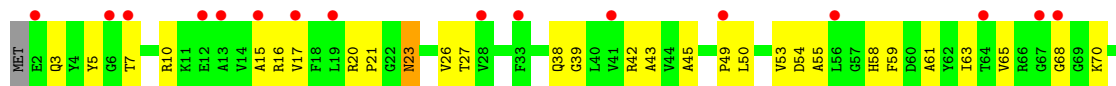




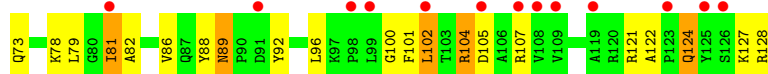
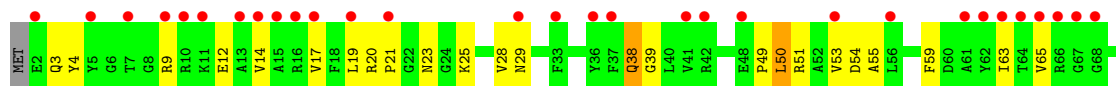
- Molecule 39: 30S ribosomal protein S8



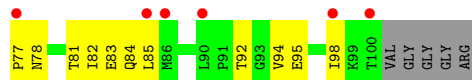
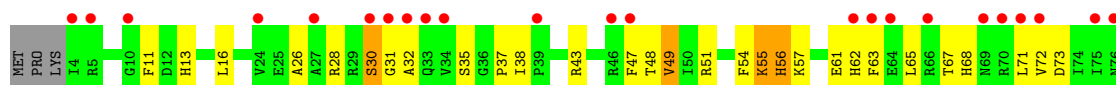
- Molecule 40: 30S ribosomal protein S9



- Molecule 40: 30S ribosomal protein S9

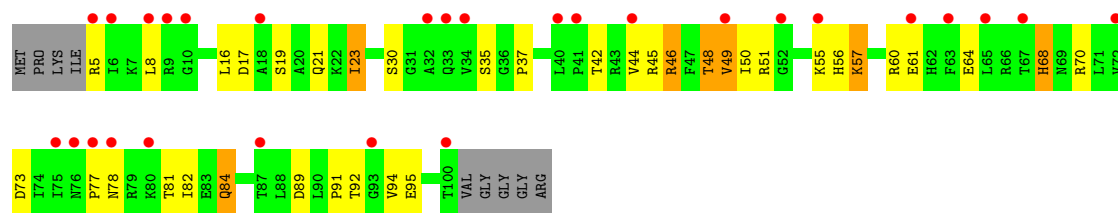


- Molecule 41: 30S ribosomal protein S10

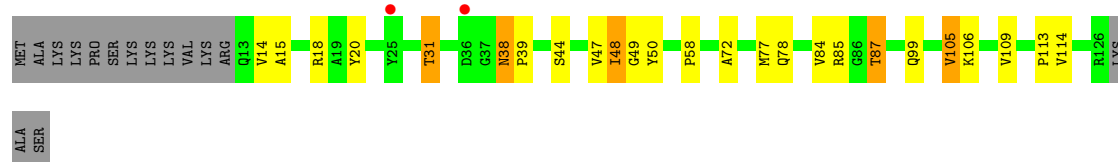


- Molecule 41: 30S ribosomal protein S10

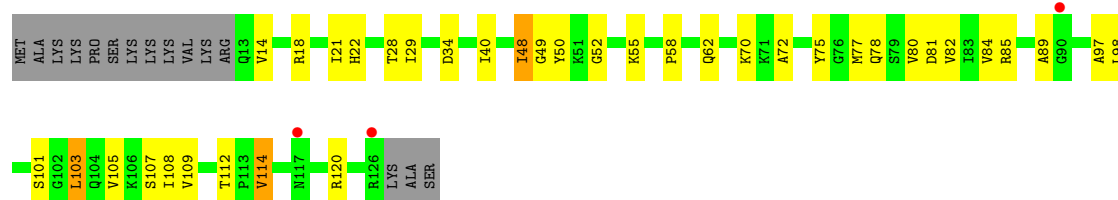




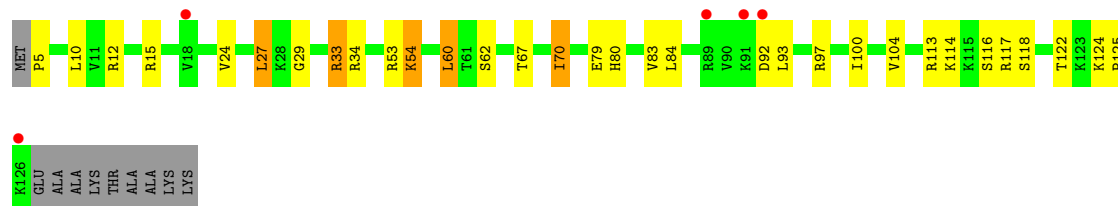
• Molecule 42: 30S ribosomal protein S11



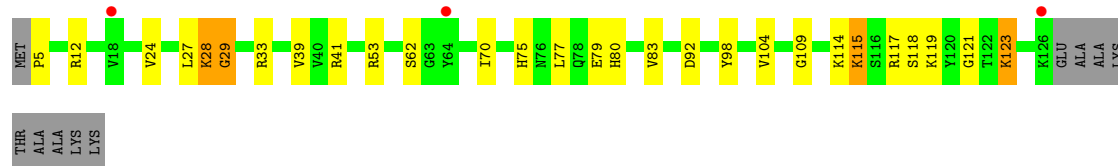
• Molecule 42: 30S ribosomal protein S11



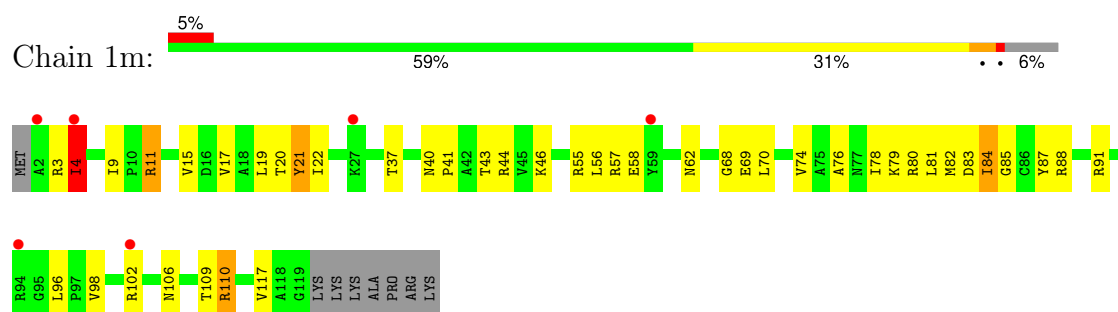
• Molecule 43: 30S ribosomal protein S12



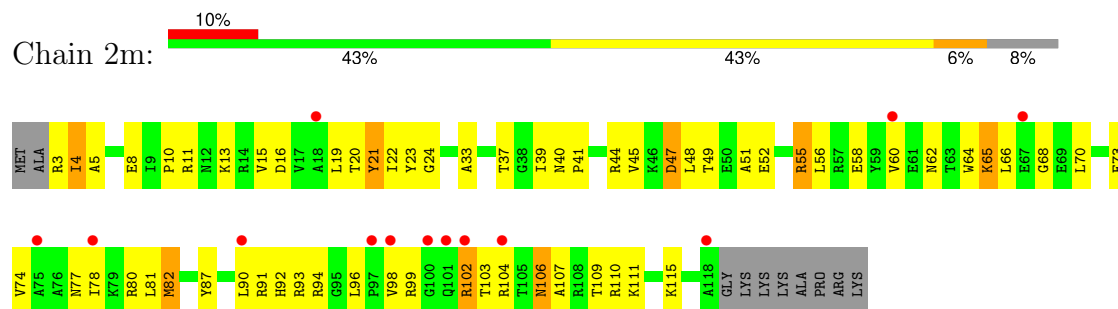
• Molecule 43: 30S ribosomal protein S12



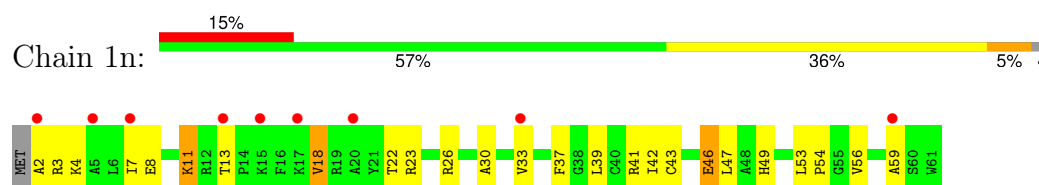
• Molecule 44: 30S ribosomal protein S13



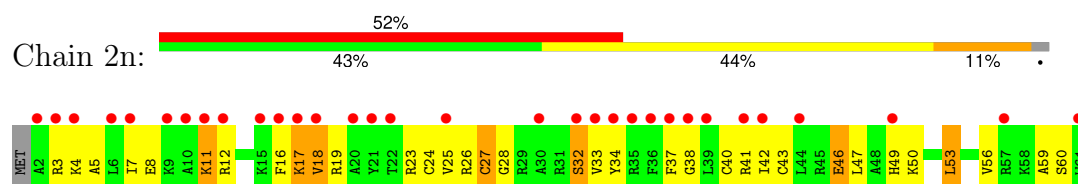
- Molecule 44: 30S ribosomal protein S13



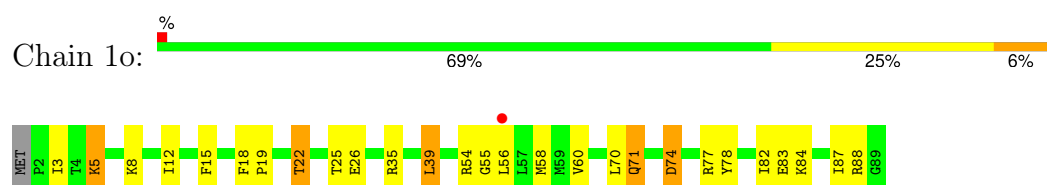
- Molecule 45: 30S ribosomal protein S14 type Z



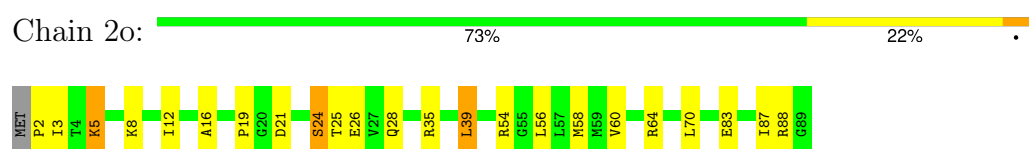
- Molecule 45: 30S ribosomal protein S14 type Z



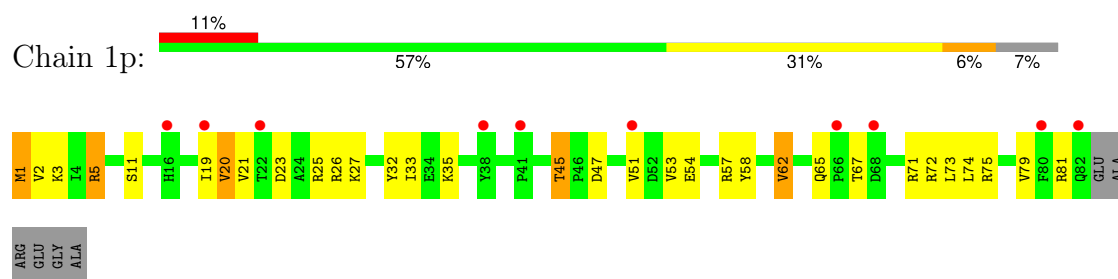
- Molecule 46: 30S ribosomal protein S15



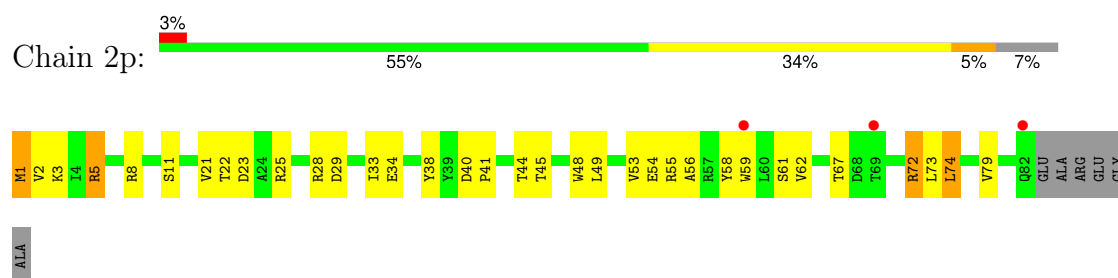
- Molecule 46: 30S ribosomal protein S15



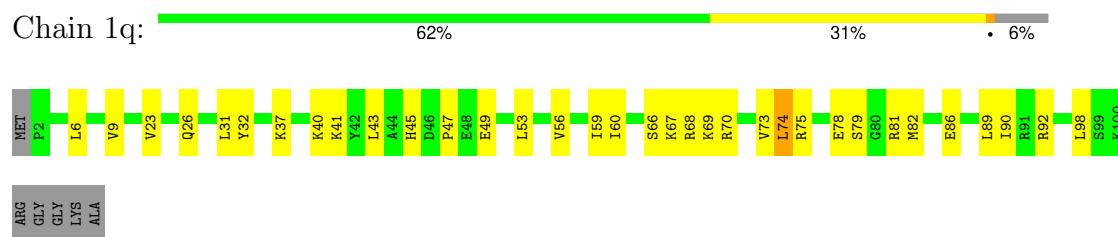
- Molecule 47: 30S ribosomal protein S16



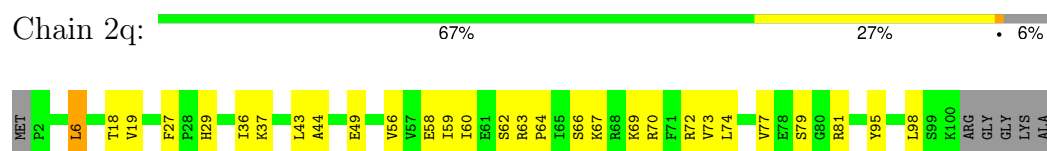
- Molecule 47: 30S ribosomal protein S16



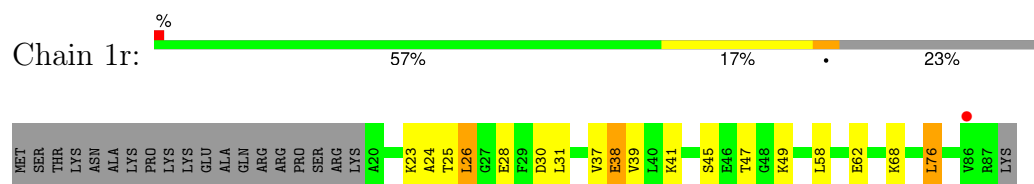
- Molecule 48: 30S ribosomal protein S17



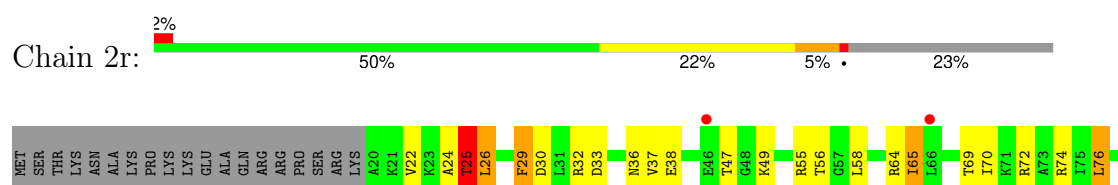
- Molecule 48: 30S ribosomal protein S17



- Molecule 49: 30S ribosomal protein S18

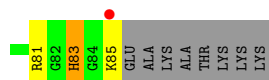


- Molecule 49: 30S ribosomal protein S18

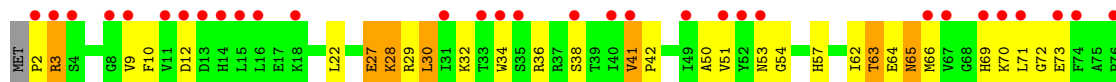




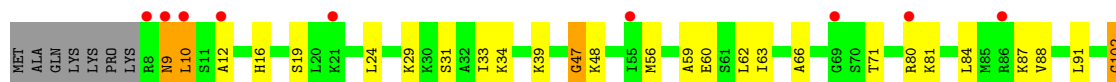
- Molecule 50: 30S ribosomal protein S19



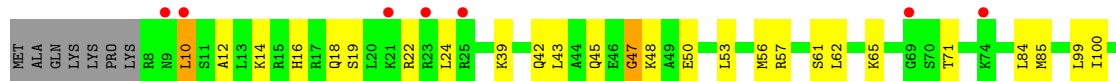
- Molecule 50: 30S ribosomal protein S19



- Molecule 51: 30S ribosomal protein S20

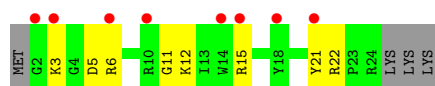


- Molecule 51: 30S ribosomal protein S20



- Molecule 52: 30S ribosomal protein Thx

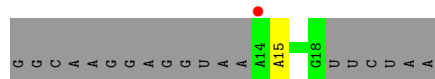




- Molecule 52: 30S ribosomal protein Thx



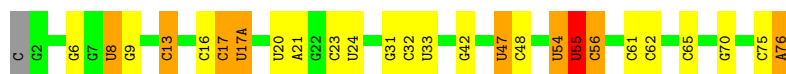
- Molecule 53: mRNA



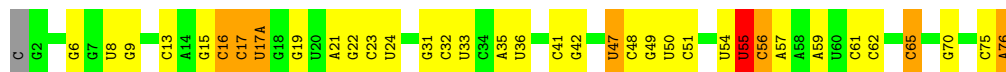
- Molecule 53: mRNA



- Molecule 54: P-site tRNA



- Molecule 54: P-site tRNA



- Molecule 55: Oncocin 10wt



- Molecule 55: Oncocin 10wt





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	209.83Å 450.81Å 622.72Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.62 – 2.80 49.62 – 2.80	Depositor EDS
% Data completeness (in resolution range)	99.1 (49.62-2.80) 99.1 (49.62-2.80)	Depositor EDS
R_{merge}	0.22	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.20 (at 2.81Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.215 , 0.268 0.215 , 0.267	Depositor DCC
R_{free} test set	71167 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å ²)	56.8	Xtriage
Anisotropy	0.225	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 55.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.42$, $\langle L^2 \rangle = 0.24$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	288674	wwPDB-VP
Average B, all atoms (Å ²)	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.67% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 5MC, PSU, MG, SF4, 4SU, 5MU, ZN

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	1A	0.32	0/66249	0.47	1/103407 (0.0%)
1	2A	0.26	0/67298	0.45	1/105044 (0.0%)
2	1B	0.25	0/2877	0.40	0/4488
2	2B	0.28	0/2878	0.45	0/4490
3	1D	0.53	0/2186	0.88	0/2944
3	2D	0.44	0/2192	0.88	3/2951 (0.1%)
4	1E	0.53	0/1592	0.87	0/2149
4	2E	0.45	0/1592	0.92	3/2149 (0.1%)
5	1F	0.53	0/1619	0.91	3/2193 (0.1%)
5	2F	0.43	0/1615	0.91	2/2188 (0.1%)
6	1G	0.43	0/1450	0.89	3/1959 (0.2%)
6	2G	0.42	0/1449	0.98	7/1958 (0.4%)
7	1H	0.46	0/1356	0.89	0/1834
7	2H	0.44	0/1356	0.96	2/1834 (0.1%)
8	1I	0.44	0/1100	0.97	5/1501 (0.3%)
8	2I	0.42	0/1076	0.98	7/1471 (0.5%)
9	1N	0.51	0/1144	0.82	0/1543
9	2N	0.41	0/1144	0.91	4/1543 (0.3%)
10	1O	0.53	0/943	0.88	5/1269 (0.4%)
10	2O	0.44	0/943	0.88	0/1269
11	1P	0.50	0/1156	0.85	0/1537
11	2P	0.44	0/1152	0.94	5/1533 (0.3%)
12	1Q	0.51	0/1143	0.85	0/1527
12	2Q	0.44	0/1143	0.88	1/1527 (0.1%)
13	1R	0.57	1/982 (0.1%)	0.85	0/1312
13	2R	0.42	0/982	0.79	0/1312
14	1S	0.46	0/887	0.85	0/1180
14	2S	0.44	0/880	0.89	0/1172
15	1T	0.46	0/1105	0.82	0/1477
15	2T	0.41	0/1097	0.83	0/1468
16	1U	0.60	0/977	0.83	0/1301
16	2U	0.46	0/977	0.86	0/1301

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
17	1V	0.50	0/782	0.82	0/1049
17	2V	0.44	0/782	0.86	0/1049
18	1W	0.59	0/897	0.85	0/1205
18	2W	0.47	0/897	0.85	0/1205
19	1X	0.52	0/764	0.83	0/1025
19	2X	0.45	0/764	0.87	0/1025
20	1Y	0.50	0/819	0.88	2/1095 (0.2%)
20	2Y	0.43	0/819	0.92	3/1095 (0.3%)
21	1Z	0.44	0/1502	0.93	5/2041 (0.2%)
21	2Z	0.44	0/1486	0.95	8/2022 (0.4%)
22	10	0.50	0/606	0.89	1/808 (0.1%)
22	20	0.38	0/606	0.91	2/808 (0.2%)
23	11	0.49	0/762	0.83	0/1014
23	21	0.44	0/762	0.82	0/1014
24	12	0.49	0/590	0.82	0/781
24	22	0.38	0/590	0.77	0/781
25	13	0.51	0/474	0.94	2/635 (0.3%)
25	23	0.38	0/469	0.88	1/630 (0.2%)
26	14	0.43	0/571	1.02	4/768 (0.5%)
26	24	0.45	0/545	1.13	3/737 (0.4%)
27	15	0.53	0/469	0.89	1/635 (0.2%)
27	25	0.45	0/469	0.89	0/635
28	16	0.45	0/460	0.78	0/613
28	26	0.41	0/456	0.78	0/608
29	17	0.58	0/426	0.83	1/561 (0.2%)
29	27	0.45	0/426	0.87	2/561 (0.4%)
30	18	0.53	0/525	0.87	0/691
30	28	0.45	0/525	0.84	0/691
31	19	0.49	0/310	0.83	0/407
31	29	0.45	0/310	0.92	0/407
32	1a	0.22	0/35537	0.40	0/55456
32	2a	0.21	0/35680	0.39	0/55681
33	1b	0.41	0/1820	0.99	8/2468 (0.3%)
33	2b	1.62	8/1728 (0.5%)	1.16	8/2352 (0.3%)
34	1c	0.39	0/1504	0.90	3/2047 (0.1%)
34	2c	0.44	0/1435	0.90	4/1960 (0.2%)
35	1d	0.41	0/1648	0.87	3/2222 (0.1%)
35	2d	0.40	0/1659	0.93	3/2230 (0.1%)
36	1e	0.40	0/1145	0.91	5/1543 (0.3%)
36	2e	0.42	0/1111	0.98	4/1504 (0.3%)
37	1f	0.39	0/819	0.79	0/1111
37	2f	0.38	0/830	0.79	0/1125
38	1g	0.39	0/1198	0.84	1/1613 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
38	2g	0.39	0/1185	0.82	0/1602
39	1h	0.38	0/1108	0.84	0/1494
39	2h	0.36	0/1094	0.90	4/1478 (0.3%)
40	1i	0.39	0/995	0.85	0/1339
40	2i	0.44	0/949	0.86	2/1284 (0.2%)
41	1j	0.44	0/695	0.96	1/950 (0.1%)
41	2j	0.44	0/690	0.98	0/943
42	1k	0.39	0/840	0.86	2/1138 (0.2%)
42	2k	0.37	0/844	0.85	1/1145 (0.1%)
43	1l	0.39	0/936	0.80	0/1263
43	2l	0.43	0/934	0.88	2/1262 (0.2%)
44	1m	0.38	0/933	0.90	1/1254 (0.1%)
44	2m	0.42	0/913	0.91	0/1230
45	1n	0.39	0/491	1.03	2/653 (0.3%)
45	2n	0.37	0/467	0.87	2/624 (0.3%)
46	1o	0.41	0/726	0.88	4/970 (0.4%)
46	2o	0.38	0/739	0.85	0/985
47	1p	0.39	0/686	0.88	2/926 (0.2%)
47	2p	0.43	0/693	0.83	2/935 (0.2%)
48	1q	0.37	0/824	0.84	0/1105
48	2q	0.36	0/836	0.86	2/1117 (0.2%)
49	1r	0.38	0/560	0.81	0/746
49	2r	0.39	0/560	0.82	1/746 (0.1%)
50	1s	0.38	0/657	0.91	0/890
50	2s	0.47	0/661	1.01	1/893 (0.1%)
51	1t	0.37	0/714	0.98	1/948 (0.1%)
51	2t	0.38	0/733	0.86	0/969
52	1u	0.36	0/191	0.75	0/252
52	2u	0.37	0/203	0.81	0/266
53	1v	0.30	0/122	0.62	0/188
53	2v	0.30	0/122	0.52	0/188
54	1x	0.30	0/1725	0.46	0/2689
54	2x	0.29	0/1725	0.46	0/2689
55	1z	0.63	0/114	1.19	0/158
55	2z	0.49	0/106	0.83	0/146
All	All	0.35	9/306288 (0.0%)	0.60	156/458204 (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
5	2F	0	1

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
33	2b	92	TYR	CD1-CE1	29.88	2.28	1.38
33	2b	92	TYR	CD2-CE2	26.93	2.19	1.38
33	2b	151	GLY	N-CA	23.93	1.80	1.45
33	2b	92	TYR	CE2-CZ	22.82	1.93	1.38
33	2b	92	TYR	CE1-CZ	22.72	1.92	1.38
33	2b	92	TYR	CG-CD1	20.81	1.83	1.39
33	2b	92	TYR	CG-CD2	19.77	1.80	1.39
33	2b	150	SER	C-N	12.55	1.51	1.33
13	1R	38	VAL	CA-CB	-5.05	1.51	1.54

All (156) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
33	2b	150	SER	CA-C-N	18.16	157.01	121.41
33	2b	150	SER	C-N-CA	18.16	157.01	121.41
33	2b	231	GLU	CA-C-N	9.91	130.53	119.83
33	2b	231	GLU	C-N-CA	9.91	130.53	119.83
33	2b	151	GLY	N-CA-C	9.32	135.27	113.18
22	20	82	ARG	CA-C-N	8.94	131.01	119.84
22	20	82	ARG	C-N-CA	8.94	131.01	119.84
45	1n	13	THR	CA-C-N	8.44	128.37	119.85
45	1n	13	THR	C-N-CA	8.44	128.37	119.85
11	2P	44	GLY	CA-C-N	7.20	134.67	121.70
11	2P	44	GLY	C-N-CA	7.20	134.67	121.70
5	1F	9	ILE	CA-C-N	7.20	127.17	119.76
5	1F	9	ILE	C-N-CA	7.20	127.17	119.76
33	1b	193	ASP	CA-C-N	7.12	126.64	119.24
33	1b	193	ASP	C-N-CA	7.12	126.64	119.24
29	27	6	GLN	CA-C-N	6.98	127.02	119.90
29	27	6	GLN	C-N-CA	6.98	127.02	119.90
36	2e	105	VAL	CA-C-N	-6.92	112.57	119.56
36	2e	105	VAL	C-N-CA	-6.92	112.57	119.56
6	2G	44	GLY	N-CA-C	-6.89	105.80	115.32
1	1A	2013	G	C2'-C3'-O3'	6.78	119.67	109.50
25	13	11	SER	CA-C-N	6.60	127.17	120.04
25	13	11	SER	C-N-CA	6.60	127.17	120.04
33	2b	152	PHE	N-CA-C	-6.58	105.29	113.38
26	14	52	THR	N-CA-C	-6.58	105.29	113.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	1m	84	ILE	N-CA-C	6.55	119.28	111.09
33	2b	130	ARG	CA-C-N	6.47	127.93	119.84
33	2b	130	ARG	C-N-CA	6.47	127.93	119.84
43	2l	28	LYS	N-CA-C	6.47	120.29	111.17
48	2q	29	HIS	CA-C-N	6.44	127.89	119.84
48	2q	29	HIS	C-N-CA	6.44	127.89	119.84
51	1t	10	LEU	N-CA-C	6.43	124.50	110.80
1	2A	2013	G	C2'-C3'-O3'	6.41	119.11	109.50
6	2G	31	VAL	CA-C-N	6.40	127.84	119.84
6	2G	31	VAL	C-N-CA	6.40	127.84	119.84
4	2E	72	VAL	N-CA-C	6.36	117.87	108.45
6	2G	141	PHE	CA-C-N	6.26	125.48	118.97
6	2G	141	PHE	C-N-CA	6.26	125.48	118.97
33	1b	14	GLY	N-CA-C	-6.26	106.90	114.66
6	1G	31	VAL	CA-C-N	6.25	127.65	119.84
6	1G	31	VAL	C-N-CA	6.25	127.65	119.84
8	1I	110	ASP	CA-C-N	6.25	126.44	119.32
8	1I	110	ASP	C-N-CA	6.25	126.44	119.32
20	2Y	91	GLU	N-CA-C	-6.16	104.47	112.23
12	2Q	27	VAL	N-CA-C	6.15	116.26	110.30
21	1Z	107	THR	CA-C-N	6.14	127.52	119.84
21	1Z	107	THR	C-N-CA	6.14	127.52	119.84
39	2h	75	ARG	CA-C-N	6.10	126.45	119.92
39	2h	75	ARG	C-N-CA	6.10	126.45	119.92
9	2N	110	GLY	CA-C-N	6.04	125.25	118.97
9	2N	110	GLY	C-N-CA	6.04	125.25	118.97
36	2e	98	THR	N-CA-C	6.02	117.54	110.97
22	10	13	GLY	N-CA-C	6.00	121.27	114.67
26	24	61	ARG	N-CA-C	-5.96	105.09	112.90
36	2e	23	GLY	N-CA-C	5.95	118.48	111.63
6	1G	43	LEU	CB-CA-C	-5.90	109.76	116.54
35	2d	178	VAL	N-CA-C	5.89	117.34	110.62
21	1Z	133	ILE	N-CA-C	5.84	113.66	107.76
26	24	53	GLU	N-CA-C	-5.82	106.15	113.72
6	2G	43	LEU	CB-CA-C	-5.81	109.86	116.54
36	1e	95	ALA	CA-C-N	5.78	127.06	119.84
36	1e	95	ALA	C-N-CA	5.78	127.06	119.84
5	2F	65	TRP	N-CA-C	5.75	113.39	108.22
29	17	47	ARG	N-CA-C	5.72	120.40	112.90
26	14	68	ARG	N-CA-C	5.70	117.68	110.33
21	2Z	107	THR	CA-C-N	5.68	126.94	119.84
21	2Z	107	THR	C-N-CA	5.68	126.94	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	1c	72	LYS	CA-C-N	5.67	125.35	119.56
34	1c	72	LYS	C-N-CA	5.67	125.35	119.56
3	2D	275	LYS	N-CA-C	-5.63	101.42	110.14
7	2H	28	GLY	CA-C-N	5.63	126.37	120.12
7	2H	28	GLY	C-N-CA	5.63	126.37	120.12
25	23	56	VAL	N-CA-C	5.61	116.66	108.53
26	24	66	SER	N-CA-C	-5.58	107.47	114.56
9	2N	39	ARG	CA-C-N	5.56	125.23	119.56
9	2N	39	ARG	C-N-CA	5.56	125.23	119.56
43	2I	29	GLY	N-CA-C	-5.56	97.18	113.30
8	1I	79	ILE	N-CA-C	5.55	113.64	108.15
8	2I	124	GLY	N-CA-C	5.55	118.70	110.60
38	1g	87	VAL	N-CA-C	5.48	113.34	108.63
5	1F	89	VAL	N-CA-C	5.47	115.72	110.74
34	2c	108	ASN	CA-C-N	5.46	124.98	119.19
34	2c	108	ASN	C-N-CA	5.46	124.98	119.19
41	1j	28	ARG	N-CA-C	-5.44	106.14	112.89
8	2I	118	LYS	CA-C-N	5.44	125.44	119.89
8	2I	118	LYS	C-N-CA	5.44	125.44	119.89
36	1e	23	GLY	N-CA-C	5.43	117.87	111.63
39	2h	73	ASP	CA-C-N	5.42	126.46	120.45
39	2h	73	ASP	C-N-CA	5.42	126.46	120.45
49	2r	81	PHE	N-CA-C	-5.41	107.23	113.88
5	2F	151	SER	N-CA-C	-5.40	106.36	113.17
35	2d	6	GLY	CA-C-N	5.40	126.59	119.84
35	2d	6	GLY	C-N-CA	5.40	126.59	119.84
21	2Z	100	VAL	CA-C-N	5.39	126.58	119.84
21	2Z	100	VAL	C-N-CA	5.39	126.58	119.84
10	1O	118	ALA	CA-C-N	5.37	124.89	119.19
10	1O	118	ALA	C-N-CA	5.37	124.89	119.19
45	2n	53	LEU	CA-C-N	5.37	126.55	119.84
45	2n	53	LEU	C-N-CA	5.37	126.55	119.84
8	2I	7	GLU	N-CA-C	5.34	113.03	108.22
4	2E	21	VAL	CA-C-N	5.33	125.50	119.90
4	2E	21	VAL	C-N-CA	5.33	125.50	119.90
34	2c	72	LYS	CA-C-N	5.31	124.98	119.56
34	2c	72	LYS	C-N-CA	5.31	124.98	119.56
3	2D	107	ALA	CA-C-N	5.30	125.21	119.85
3	2D	107	ALA	C-N-CA	5.30	125.21	119.85
10	1O	51	ALA	N-CA-C	-5.28	105.17	111.03
46	1o	18	PHE	CA-C-N	5.26	126.41	119.84
46	1o	18	PHE	C-N-CA	5.26	126.41	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	2I	110	ASP	CA-C-N	5.24	124.69	119.24
8	2I	110	ASP	C-N-CA	5.24	124.69	119.24
33	1b	130	ARG	CA-C-N	-5.24	114.25	120.11
33	1b	130	ARG	C-N-CA	-5.24	114.25	120.11
27	15	27	PRO	O-C-N	5.22	123.71	121.31
47	1p	45	THR	CA-C-N	5.22	126.36	119.84
47	1p	45	THR	C-N-CA	5.22	126.36	119.84
6	2G	48	GLU	N-CA-C	-5.21	107.05	113.41
20	2Y	31	LEU	CA-C-N	5.21	124.39	118.97
20	2Y	31	LEU	C-N-CA	5.21	124.39	118.97
34	1c	15	THR	N-CA-C	-5.20	108.69	114.62
35	1d	171	GLY	CA-C-N	5.19	126.33	119.84
35	1d	171	GLY	C-N-CA	5.19	126.33	119.84
40	2i	20	ARG	CA-C-N	5.17	125.10	119.78
40	2i	20	ARG	C-N-CA	5.17	125.10	119.78
42	2k	40	ILE	N-CA-C	-5.16	106.77	111.67
33	1b	126	GLU	CB-CA-C	-5.16	110.61	116.54
36	1e	105	VAL	CA-C-N	-5.15	114.36	119.56
36	1e	105	VAL	C-N-CA	-5.15	114.36	119.56
46	1o	74	ASP	CA-C-N	5.14	125.19	119.32
46	1o	74	ASP	C-N-CA	5.14	125.19	119.32
10	1O	47	ILE	CA-C-N	5.14	125.43	119.93
10	1O	47	ILE	C-N-CA	5.14	125.43	119.93
11	2P	43	GLY	N-CA-C	5.14	119.81	113.79
8	2I	44	LEU	N-CA-C	-5.13	105.37	111.69
33	1b	201	ILE	CA-C-N	5.11	126.23	119.84
33	1b	201	ILE	C-N-CA	5.11	126.23	119.84
21	2Z	14	LYS	CA-C-N	5.11	124.77	119.56
21	2Z	14	LYS	C-N-CA	5.11	124.77	119.56
11	2P	144	GLU	CA-C-N	5.08	125.48	119.99
11	2P	144	GLU	C-N-CA	5.08	125.48	119.99
47	2p	45	THR	CA-C-N	5.08	126.19	119.84
47	2p	45	THR	C-N-CA	5.08	126.19	119.84
8	1I	22	LYS	CA-C-N	5.08	125.11	119.32
8	1I	22	LYS	C-N-CA	5.08	125.11	119.32
35	1d	33	MET	N-CA-C	-5.06	105.95	111.82
42	1k	38	ASN	CA-C-N	5.05	124.96	119.76
42	1k	38	ASN	C-N-CA	5.05	124.96	119.76
50	2s	82	GLY	N-CA-C	5.04	117.67	110.46
21	2Z	132	ASN	CA-C-N	-5.04	119.17	122.60
21	2Z	132	ASN	C-N-CA	-5.04	119.17	122.60
20	1Y	55	TYR	CA-C-N	-5.04	115.53	120.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
20	1Y	55	TYR	C-N-CA	-5.04	115.53	120.52
26	14	40	HIS	CA-C-N	5.01	126.10	119.84
26	14	40	HIS	C-N-CA	5.01	126.10	119.84
21	1Z	100	VAL	CA-C-N	5.01	126.10	119.84
21	1Z	100	VAL	C-N-CA	5.01	126.10	119.84

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	2F	20	LEU	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1A	59154	0	29827	616	0
1	2A	60091	0	30298	789	0
2	1B	2572	0	1306	21	0
2	2B	2573	0	1306	58	0
3	1D	2136	0	2218	54	0
3	2D	2142	0	2229	51	0
4	1E	1559	0	1618	28	0
4	2E	1559	0	1618	39	0
5	1F	1584	0	1625	32	0
5	2F	1580	0	1619	49	0
6	1G	1425	0	1443	40	0
6	2G	1424	0	1434	63	0
7	1H	1330	0	1407	31	0
7	2H	1330	0	1407	42	0
8	1I	1085	0	1114	26	0
8	2I	1061	0	1080	27	0
9	1N	1117	0	1184	15	0
9	2N	1117	0	1184	19	0
10	1O	933	0	996	16	0
10	2O	933	0	996	22	0
11	1P	1139	0	1223	38	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
11	2P	1135	0	1212	47	0
12	1Q	1122	0	1178	31	0
12	2Q	1122	0	1179	29	0
13	1R	968	0	1033	16	0
13	2R	968	0	1033	19	0
14	1S	877	0	938	30	0
14	2S	870	0	923	31	0
15	1T	1091	0	1151	22	0
15	2T	1083	0	1136	24	0
16	1U	959	0	1019	16	0
16	2U	959	0	1018	22	0
17	1V	771	0	830	10	0
17	2V	771	0	830	16	0
18	1W	886	0	940	14	0
18	2W	886	0	940	16	0
19	1X	750	0	814	20	0
19	2X	750	0	814	20	0
20	1Y	806	0	881	29	0
20	2Y	806	0	881	25	0
21	1Z	1470	0	1478	23	0
21	2Z	1454	0	1452	48	0
22	10	598	0	614	7	0
22	20	598	0	614	14	0
23	11	755	0	826	12	0
23	21	755	0	826	12	0
24	12	588	0	643	12	0
24	22	588	0	643	16	0
25	13	469	0	518	9	0
25	23	464	0	514	11	0
26	14	558	0	544	28	0
26	24	532	0	503	22	0
27	15	455	0	464	11	0
27	25	455	0	465	8	0
28	16	453	0	473	11	0
28	26	449	0	469	2	0
29	17	418	0	467	17	0
29	27	418	0	467	9	0
30	18	517	0	582	22	0
30	28	517	0	582	25	0
31	19	307	0	335	7	0
31	29	307	0	335	8	0
32	1a	31750	0	16027	487	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
32	2a	31877	0	16088	546	0
33	1b	1786	0	1744	61	0
33	2b	1697	0	1574	106	0
34	1c	1480	0	1400	43	0
34	2c	1412	0	1246	53	0
35	1d	1618	0	1579	48	0
35	2d	1630	0	1633	53	0
36	1e	1129	0	1184	35	0
36	2e	1095	0	1124	39	0
37	1f	806	0	793	19	0
37	2f	817	0	808	16	0
38	1g	1183	0	1165	25	0
38	2g	1167	0	1119	28	0
39	1h	1088	0	1126	27	0
39	2h	1074	0	1100	23	0
40	1i	976	0	973	38	0
40	2i	932	0	891	34	0
41	1j	682	0	598	23	0
41	2j	678	0	612	31	0
42	1k	826	0	829	13	0
42	2k	829	0	825	17	0
43	1l	920	0	958	23	0
43	2l	918	0	947	24	0
44	1m	923	0	962	27	0
44	2m	903	0	923	49	0
45	1n	482	0	507	26	0
45	2n	459	0	467	33	0
46	1o	715	0	729	18	0
46	2o	728	0	760	14	0
47	1p	671	0	679	21	0
47	2p	677	0	686	21	0
48	1q	811	0	858	17	0
48	2q	823	0	891	18	0
49	1r	555	0	618	12	0
49	2r	555	0	618	21	0
50	1s	642	0	629	30	0
50	2s	646	0	644	30	0
51	1t	712	0	759	16	0
51	2t	731	0	807	15	0
52	1u	187	0	186	8	0
52	2u	199	0	208	7	0
53	1v	109	0	55	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
53	2v	109	0	55	0	0
54	1x	1625	0	829	15	0
54	2x	1625	0	829	21	0
55	1z	108	0	116	5	0
55	2z	101	0	109	4	0
56	10	6	0	0	0	0
56	11	4	0	0	0	0
56	13	2	0	0	0	0
56	15	3	0	0	0	0
56	16	3	0	0	0	0
56	17	6	0	0	0	0
56	18	4	0	0	0	0
56	19	3	0	0	0	0
56	1A	1096	0	0	0	0
56	1B	27	0	0	0	0
56	1D	13	0	0	0	0
56	1E	8	0	0	0	0
56	1F	7	0	0	0	0
56	1G	3	0	0	0	0
56	1H	3	0	0	0	0
56	1N	8	0	0	0	0
56	1O	3	0	0	0	0
56	1P	6	0	0	0	0
56	1Q	7	0	0	0	0
56	1R	6	0	0	0	0
56	1T	6	0	0	0	0
56	1U	6	0	0	0	0
56	1V	1	0	0	0	0
56	1W	5	0	0	0	0
56	1X	1	0	0	0	0
56	1Y	1	0	0	0	0
56	1Z	2	0	0	0	0
56	1a	307	0	0	0	0
56	1b	2	0	0	0	0
56	1c	1	0	0	0	0
56	1d	2	0	0	0	0
56	1e	3	0	0	0	0
56	1f	1	0	0	0	0
56	1h	3	0	0	0	0
56	1k	1	0	0	0	0
56	1l	1	0	0	0	0
56	1m	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
56	1n	1	0	0	0	0
56	1o	2	0	0	0	0
56	1q	4	0	0	0	0
56	1r	3	0	0	0	0
56	1t	1	0	0	0	0
56	1u	1	0	0	0	0
56	1x	10	0	0	0	0
56	20	1	0	0	0	0
56	25	1	0	0	0	0
56	28	1	0	0	0	0
56	2A	559	0	0	0	0
56	2B	10	0	0	0	0
56	2D	6	0	0	0	0
56	2E	4	0	0	0	0
56	2F	3	0	0	0	0
56	2G	1	0	0	0	0
56	2N	1	0	0	0	0
56	2O	2	0	0	0	0
56	2Q	5	0	0	0	0
56	2U	2	0	0	0	0
56	2W	1	0	0	0	0
56	2Y	2	0	0	0	0
56	2Z	1	0	0	0	0
56	2a	217	0	0	0	0
56	2d	1	0	0	0	0
56	2e	3	0	0	0	0
56	2f	1	0	0	0	0
56	2k	1	0	0	0	0
56	2l	4	0	0	0	0
56	2n	1	0	0	0	0
56	2p	1	0	0	0	0
56	2q	2	0	0	0	0
56	2t	1	0	0	0	0
56	2x	5	0	0	0	0
57	14	1	0	0	0	0
57	15	1	0	0	0	0
57	16	1	0	0	0	0
57	19	1	0	0	0	0
57	1Y	1	0	0	0	0
57	1n	1	0	0	0	0
57	24	1	0	0	0	0
57	25	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
57	26	1	0	0	0	0
57	29	1	0	0	0	0
57	2Y	1	0	0	0	0
57	2n	1	0	0	0	0
58	1d	8	0	0	0	0
58	2d	8	0	0	0	0
59	10	7	0	0	0	0
59	11	9	0	0	0	0
59	12	1	0	0	0	0
59	13	5	0	0	0	0
59	14	1	0	0	0	0
59	15	9	0	0	1	0
59	16	6	0	0	0	0
59	17	3	0	0	0	0
59	18	15	0	0	0	0
59	19	4	0	0	1	0
59	1A	2345	0	0	121	0
59	1B	45	0	0	1	0
59	1D	20	0	0	2	0
59	1E	29	0	0	3	0
59	1F	18	0	0	2	0
59	1G	4	0	0	0	0
59	1H	4	0	0	0	0
59	1I	1	0	0	0	0
59	1N	12	0	0	1	0
59	1O	6	0	0	0	0
59	1P	16	0	0	1	0
59	1Q	12	0	0	0	0
59	1R	10	0	0	1	0
59	1S	1	0	0	0	0
59	1T	14	0	0	3	0
59	1U	11	0	0	0	0
59	1V	5	0	0	1	0
59	1W	9	0	0	0	0
59	1X	6	0	0	0	0
59	1Y	1	0	0	0	0
59	1Z	6	0	0	0	0
59	1a	395	0	0	26	0
59	1b	1	0	0	0	0
59	1d	5	0	0	0	0
59	1e	3	0	0	1	0
59	1f	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
59	1h	4	0	0	0	0
59	1i	1	0	0	0	0
59	1j	2	0	0	0	0
59	1k	2	0	0	1	0
59	1l	3	0	0	1	0
59	1o	3	0	0	0	0
59	1s	1	0	0	0	0
59	1v	2	0	0	0	0
59	1x	11	0	0	1	0
59	1z	1	0	0	0	0
59	20	3	0	0	0	0
59	21	1	0	0	0	0
59	23	2	0	0	0	0
59	28	4	0	0	0	0
59	2A	810	0	0	85	0
59	2B	10	0	0	1	0
59	2D	15	0	0	0	0
59	2E	9	0	0	1	0
59	2F	4	0	0	0	0
59	2O	2	0	0	0	0
59	2P	6	0	0	0	0
59	2Q	2	0	0	0	0
59	2R	2	0	0	0	0
59	2T	2	0	0	0	0
59	2U	4	0	0	0	0
59	2V	1	0	0	1	0
59	2W	1	0	0	0	0
59	2X	2	0	0	0	0
59	2Y	1	0	0	1	0
59	2Z	4	0	0	1	0
59	2a	235	0	0	27	0
59	2d	2	0	0	0	0
59	2e	3	0	0	0	0
59	2i	1	0	0	2	0
59	2m	1	0	0	0	0
59	2n	1	0	0	1	0
59	2p	1	0	0	0	0
59	2t	4	0	0	1	0
59	2x	5	0	0	2	0
59	2z	1	0	0	0	0
All	All	288674	0	189963	4436	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 10.

All (4436) 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)
33:2b:92:TYR:CD1	33:2b:92:TYR:CG	1.83	1.67
33:2b:92:TYR:CG	33:2b:92:TYR:CD2	1.80	1.58
33:2b:92:TYR:CZ	33:2b:92:TYR:CE2	1.93	1.56
33:2b:92:TYR:CZ	33:2b:92:TYR:CE1	1.92	1.54
33:2b:151:GLY:N	33:2b:151:GLY:CA	1.80	1.45
33:2b:92:TYR:CZ	33:2b:151:GLY:N	1.88	1.40
33:2b:92:TYR:CE2	33:2b:151:GLY:N	1.91	1.35
33:2b:92:TYR:CE1	33:2b:151:GLY:N	1.95	1.33
33:2b:92:TYR:CD2	33:2b:92:TYR:CE2	2.19	1.30
33:2b:92:TYR:CD2	33:2b:151:GLY:N	2.05	1.23
33:2b:92:TYR:CD1	33:2b:92:TYR:CE1	2.28	1.22
33:2b:92:TYR:CD1	33:2b:151:GLY:N	2.10	1.19
33:2b:92:TYR:CG	33:2b:151:GLY:HA3	1.85	1.12
33:2b:92:TYR:CG	33:2b:151:GLY:N	2.20	1.09
33:2b:92:TYR:CD1	33:2b:151:GLY:CA	2.36	1.08
32:1a:77:G:H1	32:1a:87:C:N4	1.51	1.07
33:2b:92:TYR:CG	33:2b:151:GLY:CA	2.41	1.03
32:2a:1112:C:H42	32:2a:1126:G:H1	1.12	0.97
32:2a:981:G:H1	32:2a:1021:C:N4	1.62	0.96
33:2b:92:TYR:CD2	33:2b:151:GLY:CA	2.48	0.95
32:2a:981:G:H1	32:2a:1021:C:H42	1.10	0.95
22:10:11:ARG:O	22:10:14:ARG:NH2	2.02	0.93
33:2b:92:TYR:CE1	33:2b:151:GLY:CA	2.52	0.92
1:1A:353:A:H2	1:1A:1254:A:HO2'	0.99	0.91
54:2x:49:G:H1	54:2x:65:C:H42	1.07	0.91
32:2a:976:G:H1	32:2a:1026:C:H42	1.12	0.91
32:1a:1145:C:H42	32:1a:1156:G:H1	1.06	0.90
15:2T:55:ASN:H	15:2T:59:THR:HG22	1.35	0.90
15:1T:55:ASN:H	15:1T:59:THR:HG22	1.38	0.89
1:2A:1248:A:H2	1:2A:1286:A:H62	1.20	0.89
33:2b:92:TYR:CD1	33:2b:150:SER:C	2.51	0.89
1:1A:893:U:O4	1:1A:977:A:N6	2.06	0.88
32:2a:953:A:H4'	32:2a:954:G:H5''	1.56	0.88
33:2b:92:TYR:CD1	33:2b:151:GLY:HA2	2.08	0.88
6:2G:144:ILE:HG23	6:2G:148:MET:HE1	1.57	0.87
1:2A:786:U:OP2	59:2A:3601:HOH:O	1.92	0.86
1:1A:2330:G:N7	59:1A:4119:HOH:O	2.08	0.86
32:1a:77:G:N2	32:1a:87:C:N3	2.23	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1397:U:H3	32:1a:1464:G:H1	1.23	0.85
33:1b:69:LEU:HB3	33:1b:162:ILE:HG22	1.58	0.84
32:1a:953:A:H4'	32:1a:954:G:H5''	1.58	0.84
32:1a:402:G:H5'	35:1d:5:ILE:HD11	1.59	0.83
20:1Y:54:LYS:HA	20:1Y:56:PRO:HD3	1.59	0.83
32:2a:981:G:N2	32:2a:1021:C:N3	2.27	0.83
1:1A:869:G:OP1	59:1A:4101:HOH:O	1.97	0.83
29:17:24:THR:HG22	29:17:27:GLY:H	1.44	0.83
46:2o:54:ARG:HG2	46:2o:58:MET:HE2	1.61	0.83
32:1a:1145:C:N4	32:1a:1156:G:H1	1.77	0.82
33:2b:92:TYR:CG	33:2b:150:SER:C	2.56	0.82
4:1E:47:VAL:HG11	4:1E:86:PRO:HD2	1.61	0.82
33:2b:92:TYR:CE2	33:2b:151:GLY:CA	2.63	0.82
6:2G:33:ARG:HH11	6:2G:33:ARG:HB2	1.44	0.82
1:1A:1735:A:H62	1:1A:1744:A:H2	1.26	0.81
1:2A:655:A:OP1	11:2P:65:ARG:NH1	2.13	0.81
54:2x:49:G:H1	54:2x:65:C:N4	1.78	0.81
1:2A:1039:C:OP1	16:2U:53:ARG:NH2	2.14	0.81
15:2T:65:LYS:HE2	15:2T:67:SER:HB2	1.63	0.81
11:1P:25:SER:O	59:1P:301:HOH:O	1.99	0.81
33:2b:92:TYR:CD2	33:2b:150:SER:C	2.59	0.81
1:1A:2466:G:OP2	59:1A:4102:HOH:O	1.98	0.80
32:1a:156:A:H2	32:1a:343:G:H21	1.29	0.80
7:2H:8:PRO:HB3	7:2H:51:ARG:HG2	1.63	0.80
33:2b:92:TYR:CZ	33:2b:151:GLY:CA	2.65	0.80
33:2b:92:TYR:CD2	33:2b:151:GLY:HA3	2.16	0.80
8:1I:92:VAL:HG13	8:1I:120:ILE:HB	1.64	0.80
33:2b:92:TYR:CE1	33:2b:151:GLY:HA2	2.17	0.79
32:2a:1145:C:H42	32:2a:1156:G:H1	1.30	0.79
1:1A:1845:A:OP2	3:1D:54:ARG:NH2	2.15	0.79
32:2a:1233:A:HO2'	32:2a:1352:C:HO2'	1.21	0.79
40:2i:49:PRO:HG2	40:2i:81:ILE:HD11	1.64	0.79
1:2A:673:G:H4'	30:28:46:ARG:HH22	1.47	0.79
1:2A:1735:A:H62	1:2A:1744:A:H2	1.30	0.79
40:2i:21:PRO:HA	40:2i:59:PHE:HA	1.64	0.79
1:1A:786:U:OP2	59:1A:4103:HOH:O	2.00	0.79
2:2B:4:C:H42	2:2B:117:G:H1	1.30	0.79
1:1A:1316:G:OP2	59:1A:4104:HOH:O	2.00	0.79
40:1i:50:LEU:HB2	40:1i:81:ILE:HD11	1.63	0.79
1:1A:1694:C:OP1	59:1A:4105:HOH:O	2.01	0.79
50:2s:50:ALA:HB1	50:2s:57:HIS:HB3	1.64	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:1Y:92:ASN:HB2	20:1Y:94:LYS:H	1.47	0.78
1:1A:2100:U:OP1	23:11:21:ARG:NH2	2.15	0.78
32:1a:460:G:H2'	32:1a:461:G:H8	1.47	0.78
1:2A:1828:U:OP2	3:2D:274:ARG:NH2	2.16	0.78
1:2A:1310:A:OP2	59:2A:3602:HOH:O	2.01	0.78
32:1a:1298:G:H22	32:1a:1301:A:H5''	1.49	0.78
1:2A:1083:C:H42	1:2A:1162:G:H1	1.31	0.78
21:2Z:90:VAL:O	59:2Z:3101:HOH:O	2.01	0.78
1:2A:873:U:OP1	59:2A:3603:HOH:O	2.02	0.78
26:14:53:GLU:HB3	26:14:54:GLY:HA2	1.66	0.78
1:2A:554:G:N1	59:2A:3623:HOH:O	2.15	0.78
1:1A:838:G:O6	59:1A:4106:HOH:O	2.02	0.77
1:2A:1188:A:OP1	9:2N:25:ARG:NH2	2.18	0.77
1:2A:821:G:N3	59:2A:3648:HOH:O	2.18	0.77
32:2a:543:A:H4'	32:2a:544:U:H3'	1.67	0.77
41:2j:30:SER:H	41:2j:84:GLN:HE22	1.31	0.77
32:2a:900:G:H4'	36:2e:20:GLN:HA	1.67	0.77
32:2a:982:G:H2'	32:2a:983:A:H4'	1.67	0.77
1:1A:81:G:OP1	59:1A:4107:HOH:O	2.02	0.77
1:2A:2722:A:OP1	59:2A:3604:HOH:O	2.02	0.77
32:2a:506:C:H41	43:2l:53:ARG:HH22	1.33	0.77
32:2a:1112:C:N4	32:2a:1126:G:H1	1.81	0.77
32:1a:423:U:OP1	35:1d:13:ARG:NH2	2.19	0.76
42:2k:48:ILE:O	42:2k:50:TYR:N	2.17	0.76
1:2A:1377:G:OP1	59:2A:3605:HOH:O	2.03	0.76
32:2a:931:G:H5'	32:2a:943:A:H61	1.49	0.76
1:1A:1715:A:OP2	59:1A:4108:HOH:O	2.03	0.76
40:2i:121:ARG:NH1	40:2i:122:ALA:O	2.19	0.76
47:2p:1:MET:SD	47:2p:3:LYS:NZ	2.59	0.76
1:2A:2079:A:N7	59:2A:3650:HOH:O	2.18	0.76
8:2I:72:LEU:HD21	8:2I:107:VAL:HG11	1.66	0.76
22:20:11:ARG:O	22:20:14:ARG:NH2	2.19	0.76
32:2a:976:G:H1	32:2a:1026:C:N4	1.83	0.76
32:2a:446:A:H61	32:2a:466:G:H5'	1.50	0.76
32:2a:1173:A:OP1	34:2c:3:ASN:ND2	2.19	0.76
32:1a:661:U:H3	32:1a:697:G:H22	1.32	0.75
1:1A:2510:C:OP2	59:1A:4113:HOH:O	2.05	0.75
41:2j:44:VAL:HG11	41:2j:46:ARG:HH21	1.51	0.75
32:2a:516:A:O2'	32:2a:517:A:OP1	2.03	0.75
1:1A:2561:G:OP1	59:1A:4108:HOH:O	2.05	0.75
1:1A:1354:G:H4'	29:17:7:PRO:HB2	1.68	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2768:U:O4	1:1A:2770:A:N6	2.20	0.75
1:2A:186:C:OP2	59:2A:3606:HOH:O	2.04	0.75
33:2b:69:LEU:HB3	33:2b:162:ILE:HG22	1.66	0.75
38:2g:122:HIS:HA	38:2g:125:MET:HE2	1.68	0.75
1:1A:433:G:OP2	59:1A:4114:HOH:O	2.05	0.75
54:1x:47:U:H4'	54:1x:48:C:H5'	1.67	0.75
1:1A:1377:G:OP1	59:1A:4110:HOH:O	2.04	0.75
1:2A:2606:G:N7	59:2A:3656:HOH:O	2.20	0.75
32:2a:548:C:O2'	39:2h:91:ARG:NH2	2.19	0.74
32:1a:1171:C:OP1	41:1j:51:ARG:NH2	2.19	0.74
44:1m:58:GLU:O	44:1m:62:ASN:ND2	2.19	0.74
1:2A:2405:C:OP2	30:28:30:ARG:NH1	2.20	0.74
1:1A:238:G:OP2	30:18:13:ARG:NH2	2.19	0.74
1:1A:2698:U:O4	59:1A:4111:HOH:O	2.04	0.74
18:2W:14:PRO:HG2	18:2W:78:GLU:HG2	1.68	0.74
33:2b:92:TYR:CE1	33:2b:150:SER:C	2.65	0.74
1:1A:2364:G:N7	59:1A:4180:HOH:O	2.20	0.74
20:2Y:94:LYS:NZ	59:2Y:301:HOH:O	2.20	0.74
22:20:27:GLU:HG3	22:20:68:GLU:HA	1.69	0.74
1:1A:892:C:OP2	59:1A:4115:HOH:O	2.06	0.74
27:15:17:ASP:OD2	59:15:201:HOH:O	2.05	0.74
41:1j:49:VAL:HG23	45:1n:41:ARG:HD2	1.69	0.74
54:1x:75:C:OP1	59:1x:201:HOH:O	2.05	0.74
14:2S:84:GLN:HA	14:2S:111:GLU:HB2	1.68	0.74
1:1A:894:G:OP1	59:1A:4112:HOH:O	2.05	0.74
32:2a:428:A:OP2	59:2a:1902:HOH:O	2.06	0.74
32:2a:1147:G:H1	32:2a:1154:C:N4	1.86	0.74
44:2m:37:THR:HB	44:2m:55:ARG:HH12	1.52	0.74
17:1V:40:LEU:HB2	17:1V:46:VAL:HG13	1.70	0.74
32:1a:1480:A:H2	32:1a:1483:G:H1	1.33	0.74
33:1b:166:ASP:HB3	33:1b:169:LYS:HB2	1.70	0.74
2:2B:22:U:H3	2:2B:61:G:H1	1.34	0.74
1:2A:2694:C:OP1	15:2T:53:ARG:NH2	2.21	0.74
32:1a:557:A:OP2	59:1a:2001:HOH:O	2.06	0.73
33:1b:87:ARG:NH2	33:1b:220:ASP:OD1	2.21	0.73
50:1s:50:ALA:HB1	50:1s:57:HIS:HB3	1.70	0.73
32:1a:582:U:H2'	32:1a:583:C:H6	1.52	0.73
1:2A:1638:G:H2'	1:2A:1639:G:C8	2.23	0.73
1:2A:900:G:H2'	1:2A:901:G:H8	1.53	0.73
1:1A:1461:G:N2	1:1A:1628:C:O2	2.19	0.73
1:2A:550:A:OP1	59:2A:3607:HOH:O	2.05	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2517:U:OP1	4:2E:144:ARG:NH2	2.22	0.73
32:2a:937:A:HO2'	32:2a:962:C:HO2'	1.36	0.73
59:1A:4170:HOH:O	13:1R:3:HIS:NE2	2.21	0.73
3:1D:8:PRO:HB3	3:1D:14:ARG:HB2	1.68	0.73
32:2a:49:C:OP2	59:2a:1901:HOH:O	2.05	0.73
33:2b:92:TYR:CG	33:2b:150:SER:O	2.42	0.73
1:1A:2298:A:H62	1:1A:2355:U:H3	1.33	0.73
1:1A:2699:U:O4	59:1A:4109:HOH:O	2.04	0.73
1:1A:2718:G:N7	59:1A:4189:HOH:O	2.21	0.73
1:2A:807:A:N7	59:2A:3657:HOH:O	2.20	0.73
32:2a:984:A:OP2	32:2a:985:C:N4	2.22	0.73
32:1a:648:G:H22	32:1a:725:G:H1	1.35	0.73
1:2A:2456:G:OP1	5:2F:74:ARG:NH2	2.21	0.73
3:1D:69:ARG:NH2	3:1D:128:GLY:O	2.22	0.73
32:1a:465:U:OP1	59:1a:2002:HOH:O	2.06	0.73
1:2A:206:A:OP2	59:2A:3609:HOH:O	2.07	0.73
19:2X:60:ARG:HH22	29:27:47:ARG:HH22	1.34	0.73
1:1A:655:A:OP1	11:1P:65:ARG:NH1	2.21	0.73
32:1a:962:C:H42	32:1a:1203:G:H1	1.36	0.73
40:2i:17:VAL:HG21	40:2i:81:ILE:HG22	1.69	0.73
43:2l:75:HIS:HD2	43:2l:77:LEU:H	1.35	0.73
1:1A:1841:G:N7	59:1A:4201:HOH:O	2.22	0.72
40:1i:128:ARG:NH2	54:1x:33:U:OP2	2.21	0.72
32:2a:640:C:O2'	46:2o:28:GLN:NE2	2.16	0.72
20:2Y:44:ILE:H	20:2Y:44:ILE:HD13	1.52	0.72
34:2c:156:ARG:HH21	34:2c:161:GLU:HA	1.53	0.72
42:2k:72:ALA:HB1	42:2k:77:MET:HE3	1.70	0.72
12:1Q:32:TYR:OH	12:1Q:111:GLU:OE1	2.08	0.72
5:2F:157:VAL:HB	5:2F:194:MET:HG2	1.71	0.72
16:2U:49:HIS:HA	16:2U:52:ARG:HG2	1.69	0.72
32:2a:648:G:H22	32:2a:725:G:H1	1.37	0.72
44:2m:80:ARG:HH22	50:2s:69:HIS:HE1	1.36	0.72
5:1F:18:ARG:NH2	5:1F:127:GLU:OE2	2.23	0.72
12:1Q:64:ILE:HD12	21:1Z:178:GLU:HG3	1.71	0.72
1:2A:2310:G:H2'	1:2A:2311:G:H8	1.54	0.72
16:2U:76:TYR:OH	16:2U:92:ARG:NH1	2.23	0.72
33:2b:178:ARG:HH22	39:2h:68:ARG:HH12	1.38	0.72
34:1c:151:VAL:HG12	34:1c:200:ALA:HA	1.72	0.72
2:2B:16:G:H1	2:2B:68:C:H42	1.34	0.72
4:2E:47:VAL:HG11	4:2E:86:PRO:HD2	1.71	0.72
33:2b:188:ALA:HB1	33:2b:192:SER:HB2	1.71	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:957:C:OP1	12:2Q:8:LYS:NZ	2.22	0.72
44:1m:37:THR:O	44:1m:55:ARG:NH1	2.22	0.72
37:2f:89:MET:HE1	49:2r:72:ARG:HB3	1.70	0.72
41:1j:35:SER:HB3	41:1j:73:ASP:HB2	1.72	0.71
1:2A:1421:C:OP2	59:2A:3610:HOH:O	2.07	0.71
45:2n:26:ARG:HH11	45:2n:43:CYS:HB2	1.55	0.71
1:1A:1813:A:OP1	59:1A:4103:HOH:O	2.08	0.71
18:1W:14:PRO:HG2	18:1W:78:GLU:HG2	1.71	0.71
21:1Z:144:LEU:HD21	21:1Z:150:LEU:HD13	1.72	0.71
36:1e:8:GLU:OE1	36:1e:63:ARG:NH2	2.23	0.71
4:2E:132:HIS:NE2	59:2E:401:HOH:O	2.18	0.71
1:1A:785:G:OP1	59:1A:4120:HOH:O	2.08	0.71
1:2A:2600:A:OP1	59:2A:3608:HOH:O	2.06	0.71
1:2A:2691:C:OP2	4:2E:111:ARG:NH2	2.23	0.71
1:2A:1092:G:H1'	1:2A:1155:G:H22	1.54	0.71
32:2a:1128:C:H4'	32:2a:1129:A:H5'	1.71	0.71
48:2q:66:SER:OG	48:2q:67:LYS:N	2.22	0.71
48:2q:66:SER:O	48:2q:70:ARG:NH1	2.23	0.71
1:1A:474:A:N7	59:1A:4198:HOH:O	2.22	0.71
1:2A:2603:G:OP1	59:2A:3612:HOH:O	2.08	0.71
32:2a:937:A:O2'	32:2a:962:C:O2'	2.08	0.71
32:1a:847:G:N7	59:1a:2023:HOH:O	2.23	0.71
32:1a:973:C:H1'	45:1n:4:LYS:HE2	1.72	0.71
32:2a:542:G:O6	59:2a:1903:HOH:O	2.08	0.71
1:1A:1000:G:OP2	12:1Q:14:ARG:NH2	2.23	0.71
1:1A:1784:C:OP1	15:1T:96:ARG:NH1	2.22	0.71
1:1A:2730:G:OP1	59:1A:4116:HOH:O	2.07	0.71
36:1e:100:VAL:O	36:1e:107:ARG:NH2	2.24	0.71
1:2A:2067:G:H5'	27:25:19:ARG:HA	1.71	0.71
1:1A:1068:U:OP2	59:1A:4118:HOH:O	2.07	0.71
33:1b:185:ILE:HG23	33:1b:199:TYR:HB2	1.73	0.71
32:2a:466:G:O2'	32:2a:468:C:N4	2.21	0.71
41:2j:5:ARG:N	41:2j:73:ASP:OD1	2.24	0.71
35:1d:8:VAL:HG23	35:1d:11:LEU:HD22	1.73	0.70
32:2a:932:G:H21	32:2a:1209:A:H62	1.36	0.70
25:13:3:ARG:NH1	25:13:60:GLU:OE1	2.23	0.70
2:2B:48:A:H4'	14:2S:95:HIS:HD2	1.55	0.70
45:1n:43:CYS:HA	45:1n:46:GLU:HB2	1.74	0.70
32:2a:647:A:O3'	49:2r:64:ARG:NH2	2.24	0.70
5:1F:157:VAL:HB	5:1F:194:MET:HG2	1.72	0.70
32:1a:1052:C:OP2	59:1a:2003:HOH:O	2.08	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1739:U:O2'	3:2D:14:ARG:NH2	2.24	0.70
1:2A:2696:G:O6	59:2A:3611:HOH:O	2.07	0.70
32:2a:423:U:OP1	35:2d:13:ARG:NH2	2.23	0.70
26:14:58:ARG:HB2	50:1s:67:VAL:HB	1.74	0.70
3:2D:125:ILE:HB	37:2f:81:ILE:HD11	1.71	0.70
1:1A:1809:U:OP2	59:1A:4117:HOH:O	2.07	0.70
46:1o:54:ARG:HG2	46:1o:58:MET:HE2	1.72	0.70
39:2h:10:LEU:HD13	39:2h:83:ILE:HG12	1.73	0.70
1:1A:629:U:OP1	5:1F:102:PRO:HA	1.90	0.70
1:1A:1342:C:OP1	59:1A:4124:HOH:O	2.09	0.70
1:1A:1378:C:OP1	59:1A:4128:HOH:O	2.10	0.70
1:2A:661:A:H5''	11:2P:117:GLU:HG2	1.73	0.70
32:2a:420:G:H2'	32:2a:421:G:H8	1.56	0.70
14:1S:27:SER:HA	14:1S:88:ASP:HB3	1.73	0.70
1:2A:2226:G:H3'	1:2A:2227:G:C8	2.27	0.70
3:2D:69:ARG:NH2	3:2D:128:GLY:O	2.25	0.70
32:2a:543:A:OP1	36:2e:126:ARG:NH2	2.24	0.70
1:1A:2385:C:OP1	59:1A:4122:HOH:O	2.09	0.70
6:1G:15:VAL:HG22	6:1G:175:LEU:HB3	1.74	0.70
35:1d:9:CYS:SG	35:1d:22:LYS:NZ	2.65	0.70
1:2A:2078:A:OP2	59:2A:3614:HOH:O	2.09	0.70
32:2a:1204:G:O6	59:2a:1905:HOH:O	2.09	0.70
1:2A:1361:U:H2'	1:2A:1362:A:H8	1.55	0.69
48:2q:66:SER:HB3	48:2q:69:LYS:HB2	1.74	0.69
32:1a:636:U:O4	32:1a:736:G:O2'	2.09	0.69
1:2A:2488:C:O2	31:29:4:ARG:NH2	2.25	0.69
32:2a:488:C:OP1	59:2a:1904:HOH:O	2.08	0.69
1:1A:1853:G:OP1	3:1D:54:ARG:NH1	2.26	0.69
1:2A:1064:U:H3	1:2A:1187:A:H62	1.40	0.69
32:1a:199:U:H2'	32:1a:200:C:H6	1.56	0.69
1:2A:1470:G:N2	1:2A:1619:G:N7	2.40	0.69
42:1k:72:ALA:HB1	42:1k:77:MET:HE3	1.74	0.69
1:2A:183:A:N7	59:2A:3606:HOH:O	2.24	0.69
32:2a:1101:C:OP1	40:2i:104:ARG:NH1	2.25	0.69
1:1A:1229:C:OP2	59:1A:4127:HOH:O	2.10	0.69
20:1Y:102:CYS:SG	20:1Y:103:GLY:N	2.64	0.69
32:1a:378:A:H2'	32:1a:379:A:H8	1.58	0.69
32:2a:566:U:OP1	46:2o:64:ARG:NH1	2.26	0.69
35:2d:153:ARG:HH11	35:2d:181:MET:HE3	1.56	0.69
15:1T:41:ARG:NH2	32:1a:342:G:OP1	2.24	0.69
32:2a:393:A:OP2	59:2a:1906:HOH:O	2.10	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:2b:142:LEU:HG	33:2b:146:GLN:HE21	1.57	0.69
1:1A:1332:A:OP1	59:1A:4130:HOH:O	2.11	0.69
1:2A:8:U:H3	1:2A:2640:A:H2	1.39	0.69
1:2A:98:G:O2'	24:22:7:ARG:NH2	2.25	0.69
1:2A:836:C:OP2	59:2A:3620:HOH:O	2.11	0.69
1:2A:2510:C:OP2	59:2A:3615:HOH:O	2.10	0.69
4:2E:77:ILE:HD13	4:2E:195:LEU:HD22	1.75	0.69
32:2a:1116:G:H2'	32:2a:1117:G:H8	1.58	0.69
34:2c:186:PHE:HD1	34:2c:198:VAL:HB	1.58	0.69
1:1A:553:A:N1	59:1A:4233:HOH:O	2.25	0.69
1:1A:2230:G:N7	59:1A:4239:HOH:O	2.26	0.69
1:2A:2848:G:H5'	13:2R:46:GLY:HA2	1.73	0.69
32:2a:1038:A:N7	32:2a:1182:C:N4	2.41	0.69
32:2a:1292:G:H5'	44:2m:77:ASN:HD21	1.56	0.69
36:2e:91:LEU:HG	36:2e:118:ILE:HD11	1.75	0.69
38:2g:111:ARG:HB2	38:2g:119:ARG:HD2	1.73	0.69
1:1A:1648:A:OP1	59:1A:4123:HOH:O	2.09	0.69
32:1a:143:G:H1	32:1a:169:C:H42	1.38	0.69
32:1a:1041:G:OP1	34:1c:199:LYS:NZ	2.26	0.69
1:2A:1233:A:OP2	59:2A:3616:HOH:O	2.11	0.69
21:2Z:2:GLU:HG2	21:2Z:56:VAL:HB	1.75	0.69
33:2b:222:ILE:HD12	33:2b:223:ILE:HG23	1.74	0.69
1:1A:1000:G:O6	59:1A:4121:HOH:O	2.08	0.68
1:1A:1360:C:OP2	59:1A:4110:HOH:O	2.11	0.68
32:1a:1112:C:H42	32:1a:1126:G:H1	1.40	0.68
1:2A:1185:U:OP2	9:2N:63:THR:OG1	2.10	0.68
15:2T:41:ARG:NH2	32:2a:342:G:OP1	2.24	0.68
32:2a:1301:A:H61	32:2a:1343:G:H21	1.40	0.68
40:2i:9:ARG:HG2	40:2i:14:VAL:HG12	1.74	0.68
5:2F:184:TYR:CE2	5:2F:188:ARG:HD2	2.29	0.68
34:2c:120:VAL:HA	34:2c:123:GLN:HE21	1.57	0.68
1:1A:1086:C:H42	1:1A:1159:G:H1	1.38	0.68
40:2i:9:ARG:H	40:2i:79:LEU:HD23	1.58	0.68
1:1A:2670:G:O2'	7:1H:175:LYS:NZ	2.27	0.68
38:1g:50:ILE:HD11	38:1g:58:PRO:HA	1.75	0.68
1:1A:1808:U:OP1	59:1A:4125:HOH:O	2.10	0.68
1:1A:2502:U:OP2	59:1A:4129:HOH:O	2.10	0.68
19:1X:60:ARG:HH22	29:17:47:ARG:HH22	1.42	0.68
32:1a:889:U:OP2	43:1l:97:ARG:NH1	2.26	0.68
32:1a:1338:G:H2'	32:1a:1339:A:C8	2.29	0.68
32:1a:507:A:H61	43:1l:92:ASP:HB2	1.59	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:531:A:OP1	59:1a:2006:HOH:O	2.12	0.68
37:1f:89:MET:HE3	49:1r:76:LEU:HD23	1.74	0.68
1:2A:816:G:OP2	59:2A:3621:HOH:O	2.12	0.68
19:1X:31:HIS:CD2	19:1X:33:LYS:H	2.12	0.68
32:2a:1210:C:OP1	44:2m:115:LYS:N	2.26	0.68
54:2x:47:U:H4'	54:2x:48:C:H5'	1.76	0.68
1:2A:1512:G:HO2'	1:2A:1592:C:HO2'	1.31	0.68
32:2a:109:G:OP1	59:2a:1901:HOH:O	2.12	0.68
32:1a:1030:G:H5''	45:1n:4:LYS:HD3	1.75	0.68
9:2N:15:LEU:HB2	9:2N:135:PRO:HB2	1.76	0.68
11:2P:95:VAL:HA	11:2P:99:LEU:HD21	1.76	0.68
38:2g:113:GLU:HB2	38:2g:119:ARG:HG2	1.76	0.68
13:1R:67:LEU:HD13	13:1R:76:VAL:HG21	1.75	0.67
21:1Z:70:LEU:HG	21:1Z:91:LEU:HD21	1.74	0.67
1:2A:2360:G:OP1	59:2A:3619:HOH:O	2.11	0.67
7:2H:46:GLU:HB2	7:2H:49:VAL:HG12	1.76	0.67
1:1A:1312:U:OP1	59:1A:4135:HOH:O	2.13	0.67
1:1A:2586:C:OP2	59:1A:4126:HOH:O	2.10	0.67
1:2A:777:C:OP2	59:2A:3617:HOH:O	2.11	0.67
1:2A:2800:C:OP1	4:2E:61:ARG:NH2	2.27	0.67
1:1A:932:C:H2'	1:1A:933:A:H5''	1.76	0.67
1:1A:2327:C:O2'	6:1G:128:ARG:NH1	2.27	0.67
1:2A:1858:G:OP1	59:2A:3622:HOH:O	2.12	0.67
1:2A:2226:G:H5''	1:2A:2227:G:N7	2.09	0.67
7:2H:27:LYS:HA	7:2H:32:GLU:HB2	1.77	0.67
1:1A:1100:G:N2	1:1A:1149:C:O2	2.28	0.67
46:1o:5:LYS:H	46:1o:5:LYS:HE2	1.59	0.67
6:2G:135:LEU:HB2	6:2G:155:MET:HG2	1.75	0.67
12:2Q:109:VAL:HG13	12:2Q:113:GLN:HB3	1.75	0.67
32:2a:1088:A:H2'	32:2a:1089:G:H8	1.59	0.67
32:2a:1241:C:N4	32:2a:1242:C:O2	2.28	0.67
44:2m:91:ARG:HB2	44:2m:98:VAL:HG12	1.75	0.67
1:1A:1317:A:OP1	59:1A:4104:HOH:O	2.13	0.67
1:2A:610:U:OP2	59:2A:3624:HOH:O	2.13	0.67
1:2A:1026:A:OP1	59:2A:3618:HOH:O	2.11	0.67
1:2A:1154:C:H3'	1:2A:1155:G:C8	2.30	0.67
1:2A:1991:A:OP1	59:2A:3625:HOH:O	2.13	0.67
24:22:29:LYS:HG2	24:22:57:ILE:HD13	1.76	0.67
32:2a:927:A:H61	32:2a:1214:U:H3	1.40	0.67
2:1B:8:U:O3'	14:1S:25:ARG:NH2	2.22	0.67
34:1c:35:GLU:OE2	34:1c:59:ARG:NH2	2.20	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1e:151:LEU:O	39:1h:64:LYS:NZ	2.28	0.67
1:2A:1035:A:OP2	59:2A:3627:HOH:O	2.13	0.67
5:2F:53:THR:HG23	5:2F:55:GLY:H	1.60	0.67
1:2A:396:G:OP2	59:2A:3626:HOH:O	2.13	0.67
32:2a:36:G:O2'	43:2l:118:SER:O	2.07	0.67
32:2a:1379:A:OP1	59:2a:1907:HOH:O	2.12	0.67
32:1a:312:G:OP2	32:1a:347:G:O2'	2.13	0.67
32:1a:1060:G:N2	32:1a:1063:A:OP2	2.27	0.67
1:2A:423:G:N7	59:2A:3696:HOH:O	2.28	0.67
1:2A:2375:C:OP1	22:20:55:ARG:NH1	2.28	0.67
32:1a:525:G:N7	59:1a:2035:HOH:O	2.28	0.67
32:1a:1141:C:H5	32:1a:1163:G:H1	1.43	0.67
43:1l:70:ILE:HG12	43:1l:100:ILE:HD12	1.76	0.67
47:1p:20:VAL:HG23	47:1p:35:LYS:HA	1.77	0.67
1:2A:1068:U:OP2	59:2A:3630:HOH:O	2.13	0.67
1:2A:1109:C:H42	1:2A:1119:G:H1	1.40	0.67
1:2A:2509:C:OP2	59:2A:3615:HOH:O	2.13	0.67
46:2o:5:LYS:HZ2	46:2o:5:LYS:H	1.41	0.67
1:1A:2816:G:N1	1:1A:2901:G:O6	2.20	0.66
21:2Z:134:PRO:O	21:2Z:136:PHE:N	2.28	0.66
35:2d:173:TRP:HB3	35:2d:187:ARG:HE	1.60	0.66
1:1A:205:G:OP2	59:1A:4134:HOH:O	2.13	0.66
32:1a:130:C:O2'	59:1a:2005:HOH:O	2.12	0.66
32:1a:1091:G:O6	59:1a:2004:HOH:O	2.12	0.66
32:1a:1399:G:N7	59:1a:2038:HOH:O	2.28	0.66
33:1b:47:THR:HG22	33:1b:202:PRO:HB2	1.76	0.66
6:1G:161:THR:HG22	6:1G:163:ALA:H	1.59	0.66
17:1V:98:GLU:OE2	17:1V:100:ARG:NH1	2.29	0.66
32:1a:971:G:H1	32:1a:1028:C:H42	1.42	0.66
32:1a:1102:C:OP1	40:1i:83:ARG:NH2	2.28	0.66
51:1t:34:LYS:HG2	51:1t:80:ARG:HH12	1.59	0.66
1:2A:622:G:N2	1:2A:627:C:O3'	2.28	0.66
1:2A:2043:U:OP1	59:2A:3623:HOH:O	2.12	0.66
10:2O:80:ASP:OD1	15:2T:64:ARG:NH2	2.29	0.66
1:1A:1677:A:OP1	59:1A:4132:HOH:O	2.12	0.66
1:1A:1019:C:OP1	59:1A:4136:HOH:O	2.13	0.66
32:1a:204:A:C6	32:1a:217:C:H4'	2.31	0.66
32:2a:402:G:H5'	35:2d:5:ILE:HD11	1.77	0.66
11:1P:59:LEU:HD21	30:18:10:ALA:HA	1.76	0.66
34:1c:15:THR:HG22	34:1c:16:ARG:HG2	1.78	0.66
1:2A:1910:A:H2'	1:2A:1911:A:C8	2.30	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:2P:59:LEU:HD11	30:28:10:ALA:HB2	1.76	0.66
1:1A:2100:U:O3'	23:11:35:THR:OG1	2.14	0.66
1:1A:2510:C:OP1	59:1A:4133:HOH:O	2.12	0.66
1:1A:817:G:OP1	29:17:10:ARG:NH1	2.28	0.66
1:2A:181:U:OP2	59:2A:3629:HOH:O	2.13	0.66
2:2B:43:C:OP1	26:24:6:HIS:NE2	2.28	0.66
6:2G:13:GLU:O	6:2G:15:VAL:N	2.28	0.66
17:2V:1:MET:HA	17:2V:42:GLY:HA3	1.77	0.66
32:2a:251:G:OP1	48:2q:69:LYS:NZ	2.27	0.66
32:2a:1147:G:H1	32:2a:1154:C:H42	1.41	0.66
37:1f:10:LEU:HB2	37:1f:59:TYR:HB3	1.78	0.66
47:1p:53:VAL:HG22	47:1p:79:VAL:HG22	1.76	0.66
32:2a:499:G:OP2	59:2a:1908:HOH:O	2.12	0.66
1:1A:1381:A:OP2	19:1X:64:LYS:NZ	2.29	0.66
32:1a:1112:C:O2'	32:1a:1122:G:N7	2.28	0.66
32:1a:1112:C:N4	32:1a:1126:G:H1	1.93	0.66
32:1a:1121:G:H2'	32:1a:1123:C:H5''	1.76	0.66
32:1a:1127:G:H2'	32:1a:1128:C:H5''	1.77	0.66
7:2H:124:GLU:HB2	7:2H:132:ARG:HB3	1.77	0.65
1:1A:1314:A:N7	59:1A:4276:HOH:O	2.29	0.65
19:1X:31:HIS:HD2	19:1X:33:LYS:H	1.44	0.65
1:1A:2356:G:OP2	28:16:38:LYS:NZ	2.29	0.65
48:1q:67:LYS:O	48:1q:69:LYS:N	2.29	0.65
1:2A:2300:G:OP1	59:2A:3628:HOH:O	2.13	0.65
1:1A:481:C:H4'	59:1A:5612:HOH:O	1.97	0.65
11:1P:59:LEU:HD11	30:18:10:ALA:HB2	1.76	0.65
32:1a:447:A:H62	32:1a:465:U:H3	1.44	0.65
32:2a:1206:G:O2'	32:2a:1304:C:OP1	2.15	0.65
1:1A:183:A:OP1	11:1P:46:LYS:NZ	2.29	0.65
1:1A:1479:A:H61	1:1A:1604:A:H62	1.42	0.65
21:1Z:19:ARG:NH1	21:1Z:84:GLU:O	2.29	0.65
42:1k:99:GLN:O	59:1k:301:HOH:O	2.15	0.65
1:2A:1430:G:O2'	1:2A:1441:U:O2	2.13	0.65
32:2a:1287:G:N2	32:2a:1313:G:H1'	2.12	0.65
33:2b:88:ALA:HB2	33:2b:219:VAL:HG13	1.79	0.65
34:2c:43:LEU:HD22	34:2c:47:LEU:HD13	1.77	0.65
32:1a:1508:G:N7	59:1a:2044:HOH:O	2.30	0.65
41:1j:55:LYS:O	41:1j:57:LYS:N	2.29	0.65
1:1A:651:A:OP2	59:1A:4137:HOH:O	2.13	0.65
1:2A:2053:G:N7	59:2A:3701:HOH:O	2.30	0.65
1:1A:550:A:OP1	59:1A:4140:HOH:O	2.14	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:1D:237:GLU:OE2	59:1D:401:HOH:O	2.14	0.65
1:2A:829:A:OP2	59:2A:3608:HOH:O	2.13	0.65
1:2A:2284:A:H2'	1:2A:2285:A:C8	2.32	0.65
3:2D:184:LYS:HE3	3:2D:271:ILE:HD11	1.77	0.65
13:2R:2:ARG:NH1	13:2R:5:LYS:O	2.30	0.65
44:2m:60:VAL:HG23	44:2m:64:TRP:HE3	1.61	0.65
1:1A:2090:G:OP2	59:1A:4141:HOH:O	2.14	0.65
10:1O:35:VAL:HG21	10:1O:69:ILE:HD12	1.79	0.65
32:1a:1160:G:OP1	40:1i:93:ARG:NE	2.29	0.65
1:2A:1360:C:OP2	59:2A:3605:HOH:O	2.14	0.65
12:2Q:29:PHE:O	21:2Z:122:ARG:NH2	2.29	0.65
5:1F:30:PRO:HB3	11:1P:1:MET:HE1	1.79	0.65
32:1a:434:G:O2'	32:1a:479:U:O4	2.15	0.65
2:2B:43:C:O2	6:2G:95:ARG:NH1	2.30	0.65
6:2G:80:PHE:O	6:2G:82:LEU:N	2.23	0.65
33:2b:119:GLU:HG3	33:2b:142:LEU:HD11	1.78	0.65
51:2t:56:MET:HE2	51:2t:85:MET:HA	1.78	0.65
1:2A:2844:A:N3	59:2A:3699:HOH:O	2.29	0.64
32:2a:1112:C:H2'	32:2a:1122:G:N7	2.12	0.64
50:2s:27:GLU:HB2	50:2s:28:LYS:HD3	1.78	0.64
1:1A:2493:G:OP1	59:1A:4144:HOH:O	2.15	0.64
4:1E:127:ASP:OD2	59:1E:401:HOH:O	2.14	0.64
10:1O:35:VAL:HG21	10:1O:105:GLU:HG3	1.79	0.64
1:2A:2043:U:OP1	59:2A:3633:HOH:O	2.14	0.64
32:1a:954:G:N2	32:1a:1345:C:OP2	2.30	0.64
1:2A:2100:U:O3'	23:21:35:THR:OG1	2.16	0.64
32:2a:65:G:H4'	32:2a:66:U:H3'	1.78	0.64
32:2a:107:G:OP1	59:2a:1909:HOH:O	2.14	0.64
32:2a:460:G:H2'	32:2a:461:G:H8	1.63	0.64
32:2a:1273:G:H4'	40:2i:38:GLN:CD	2.22	0.64
1:1A:352:G:O6	20:1Y:19:LYS:N	2.30	0.64
1:1A:1991:A:OP1	59:1A:4143:HOH:O	2.15	0.64
32:1a:1100:G:H5''	40:1i:104:ARG:HH21	1.61	0.64
1:2A:1184:C:O3'	9:2N:25:ARG:NH1	2.30	0.64
34:2c:40:ARG:NH2	34:2c:55:VAL:O	2.30	0.64
32:1a:343:G:C2	32:1a:344:G:H1'	2.32	0.64
32:1a:1374:U:H2'	32:1a:1375:G:C8	2.32	0.64
33:1b:201:ILE:HG21	33:1b:214:ILE:HG21	1.79	0.64
32:2a:434:G:N1	32:2a:480:A:OP2	2.25	0.64
35:2d:61:LYS:NZ	35:2d:72:GLU:OE2	2.29	0.64
51:2t:103:GLY:O	59:2t:3101:HOH:O	2.15	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1358:U:OP1	59:2A:3635:HOH:O	2.15	0.64
10:2O:48:PRO:HB3	32:2a:1405:G:H5'	1.80	0.64
1:1A:2063:A:OP1	59:1A:4146:HOH:O	2.15	0.64
1:1A:2458:G:OP2	59:1A:4139:HOH:O	2.14	0.64
32:1a:372:G:H4'	47:1p:5:ARG:HE	1.63	0.64
1:2A:585:G:OP2	59:2A:3634:HOH:O	2.15	0.64
1:2A:2464:A:OP1	55:2z:3:LYS:NZ	2.25	0.64
32:2a:1298:G:N2	32:2a:1301:A:OP2	2.24	0.64
33:2b:102:LEU:HD23	33:2b:182:ILE:HD12	1.80	0.64
44:2m:37:THR:O	44:2m:55:ARG:NH2	2.31	0.64
1:1A:2338:A:H2'	1:1A:2339:A:C8	2.33	0.64
11:1P:50:ARG:HD3	30:18:7:HIS:CD2	2.33	0.64
1:2A:524:G:N1	1:2A:527:A:OP2	2.30	0.64
1:2A:1230:G:OP2	59:2A:3627:HOH:O	2.15	0.64
2:2B:44:G:OP1	6:2G:98:ARG:NH2	2.29	0.64
1:1A:921:G:H1	1:1A:947:C:H42	1.46	0.64
1:1A:1359:C:OP1	59:1A:4110:HOH:O	2.15	0.64
4:1E:111:ARG:HG3	4:1E:160:TYR:CD2	2.33	0.64
32:1a:207:G:H1	32:1a:213:C:H42	1.44	0.64
32:1a:274:G:OP2	48:1q:92:ARG:NH2	2.31	0.64
37:1f:100:ASN:HB2	49:1r:28:GLU:HA	1.80	0.64
7:2H:3:ARG:HH12	7:2H:6:ARG:H	1.46	0.64
33:2b:87:ARG:NH2	33:2b:220:ASP:OD1	2.25	0.64
1:1A:2482:C:OP2	59:1A:4145:HOH:O	2.15	0.64
32:2a:1435:G:OP1	51:2t:39:LYS:NZ	2.30	0.64
34:2c:181:ASN:HD22	34:2c:204:LEU:HB2	1.61	0.64
40:2i:79:LEU:HD22	40:2i:104:ARG:HB2	1.80	0.64
47:2p:34:GLU:OE2	47:2p:59:TRP:NE1	2.24	0.64
35:1d:188:LEU:HD23	35:1d:188:LEU:H	1.63	0.63
33:2b:92:TYR:CE2	33:2b:150:SER:C	2.76	0.63
36:2e:122:GLU:O	36:2e:126:ARG:NH1	2.31	0.63
41:2j:17:ASP:OD1	41:2j:70:ARG:NH1	2.29	0.63
1:1A:2044:G:H5'	1:1A:2628:C:H4'	1.79	0.63
32:1a:626:A:N3	39:1h:113:SER:OG	2.30	0.63
32:2a:1217:U:O2'	32:2a:1287:G:O5'	2.16	0.63
32:1a:143:G:N2	32:1a:169:C:N3	2.45	0.63
1:2A:2563:U:OP2	59:2A:3636:HOH:O	2.15	0.63
7:2H:42:ARG:NH1	7:2H:53:GLU:OE2	2.29	0.63
15:2T:85:LYS:NZ	15:2T:87:ASP:OD2	2.32	0.63
32:2a:1200:C:OP1	45:2n:12:ARG:NH2	2.30	0.63
34:2c:35:GLU:HA	34:2c:38:ARG:HD2	1.80	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:1E:143:ASN:HD22	4:1E:147:PRO:HD3	1.63	0.63
30:18:62:LEU:HB3	30:18:65:GLU:HG2	1.81	0.63
32:1a:249:U:OP2	59:1a:2009:HOH:O	2.15	0.63
32:1a:258:A:H2'	32:1a:259:A:C8	2.34	0.63
43:1l:79:GLU:HG2	43:1l:80:HIS:CD2	2.34	0.63
2:2B:31:C:H4'	6:2G:29:TRP:CH2	2.33	0.63
13:2R:95:THR:HG22	13:2R:116:LEU:HD23	1.80	0.63
21:2Z:92:SER:O	21:2Z:94:GLU:N	2.32	0.63
32:2a:1261:A:O2'	32:2a:1263:U:OP2	2.15	0.63
1:1A:138:A:H8	1:1A:1453:C:HO2'	1.47	0.63
32:1a:409:G:N7	35:1d:35:ARG:NH1	2.47	0.63
34:1c:134:ILE:HG23	34:1c:151:VAL:HG23	1.80	0.63
1:2A:900:G:H2'	1:2A:901:G:C8	2.34	0.63
12:1Q:110:THR:HG23	12:1Q:113:GLN:HB2	1.80	0.63
32:1a:900:G:H4'	36:1e:20:GLN:HA	1.81	0.63
32:1a:1106:A:O2'	41:1j:37:PRO:O	2.14	0.63
37:1f:36:ARG:NH2	37:1f:66:GLU:OE1	2.31	0.63
51:2t:57:ARG:HH22	51:2t:100:ILE:HD12	1.61	0.63
1:1A:1158:U:H2'	1:1A:1159:G:C8	2.34	0.63
4:1E:105:THR:OG1	4:1E:199:ARG:NH2	2.31	0.63
6:1G:16:ARG:HG2	6:1G:16:ARG:HH11	1.63	0.63
32:1a:597:C:H42	32:1a:611:G:H1	1.47	0.63
6:2G:33:ARG:HB2	6:2G:33:ARG:NH1	2.13	0.63
34:2c:30:ARG:HH21	45:2n:38:GLY:HA2	1.62	0.63
1:1A:184:A:H62	11:1P:38:GLN:HE22	1.47	0.63
10:1O:48:PRO:HB3	32:1a:1405:G:H5'	1.81	0.63
32:1a:1096:C:H42	32:1a:1169:G:H1	1.47	0.63
32:2a:881:G:OP1	59:2a:1910:HOH:O	2.15	0.63
1:1A:555:C:OP2	59:1A:4148:HOH:O	2.16	0.63
1:1A:1012:G:O6	59:1A:4131:HOH:O	2.12	0.63
32:1a:821:G:H1	32:1a:827:C:H42	1.44	0.63
1:2A:141:G:H4'	19:2X:35:THR:HG21	1.81	0.63
1:2A:2731:G:O6	59:2A:3632:HOH:O	2.14	0.63
6:2G:12:TYR:HA	6:2G:16:ARG:HG3	1.79	0.63
32:2a:1349:C:O2'	41:2j:60:ARG:NH2	2.31	0.63
1:1A:296:C:H2'	1:1A:297:G:H8	1.64	0.62
1:1A:1081:G:OP2	7:1H:59:ARG:NH1	2.31	0.62
1:2A:935:C:O2'	1:2A:936:A:O5'	2.16	0.62
8:2I:4:ILE:HG12	8:2I:18:VAL:HG22	1.81	0.62
32:2a:452:C:H2'	32:2a:453:C:H6	1.63	0.62
33:2b:40:HIS:HB3	33:2b:190:THR:HG21	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:541:C:OP1	27:15:16:ARG:NH2	2.32	0.62
1:2A:2733:A:OP1	59:2A:3637:HOH:O	2.16	0.62
32:2a:9:A:H5'	36:2e:101:ILE:HG22	1.80	0.62
32:2a:74:G:H1	32:2a:90:U:H3	1.46	0.62
33:2b:92:TYR:CE2	33:2b:152:PHE:N	2.66	0.62
1:1A:536:G:N7	59:1A:4165:HOH:O	2.31	0.62
1:1A:2323:U:H5'	6:1G:88:ILE:HD11	1.80	0.62
8:1I:3:VAL:HG12	8:1I:38:LEU:HA	1.81	0.62
8:1I:77:LEU:HB3	8:1I:142:VAL:HG13	1.79	0.62
28:16:13:CYS:SG	28:16:47:THR:HG21	2.39	0.62
1:2A:609:C:OP2	11:2P:21:ARG:NH2	2.33	0.62
28:26:13:CYS:SG	28:26:47:THR:HG21	2.39	0.62
32:2a:571:G:O3'	59:2a:1911:HOH:O	2.16	0.62
32:1a:378:A:H2'	32:1a:379:A:C8	2.35	0.62
1:2A:1115:A:N7	1:2A:1141:A:O2'	2.27	0.62
1:2A:2226:G:H8	1:2A:2227:G:N7	1.98	0.62
1:2A:2646:C:O2'	4:2E:48:GLN:NE2	2.31	0.62
32:2a:452:C:H2'	32:2a:453:C:C6	2.34	0.62
32:1a:1222:U:OP2	38:1g:116:ALA:N	2.23	0.62
32:1a:1375:G:H21	32:1a:1480:A:H8	1.46	0.62
49:1r:47:THR:HG23	49:1r:49:LYS:HG3	1.81	0.62
3:2D:242:ARG:HD3	3:2D:242:ARG:N	2.13	0.62
14:2S:35:ILE:HD13	14:2S:97:ARG:HH21	1.64	0.62
23:21:77:ALA:HA	23:21:80:LEU:HD13	1.82	0.62
35:2d:3:ARG:HB2	35:2d:3:ARG:HH11	1.64	0.62
35:2d:100:ARG:NH1	35:2d:137:SER:OG	2.32	0.62
33:1b:71:VAL:HA	33:1b:93:VAL:HG23	1.81	0.62
2:2B:75:G:H22	21:2Z:73:GLN:NE2	1.97	0.62
44:2m:98:VAL:HG23	44:2m:99:ARG:HG3	1.80	0.62
5:1F:116:ASP:OD1	5:1F:119:ARG:NH2	2.33	0.62
34:1c:152:ILE:HG23	34:1c:167:TRP:HB3	1.81	0.62
40:1i:79:LEU:HG	40:1i:83:ARG:HD2	1.81	0.62
1:2A:1576:C:H42	1:2A:1585:G:H1	1.47	0.62
36:2e:51:VAL:HG23	36:2e:52:PRO:HD3	1.81	0.62
1:1A:2844:A:N3	59:1A:4286:HOH:O	2.31	0.62
33:1b:19:HIS:NE2	33:1b:206:ASP:OD2	2.32	0.62
3:2D:202:LYS:NZ	32:2a:757:G:O3'	2.29	0.62
44:2m:47:ASP:N	44:2m:47:ASP:OD1	2.33	0.62
6:1G:77:ILE:HD12	6:1G:82:LEU:HD12	1.81	0.62
17:1V:76:LYS:HB2	17:1V:81:TYR:HB3	1.81	0.62
32:1a:638:G:OP2	59:1a:2010:HOH:O	2.16	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1057:G:O2'	32:1a:1084:A:N1	2.29	0.62
1:2A:2726:G:OP2	59:2A:3638:HOH:O	2.16	0.62
33:2b:47:THR:HG22	33:2b:51:LEU:HD22	1.82	0.62
34:2c:180:ALA:HB1	34:2c:203:PHE:HE1	1.64	0.62
18:1W:25:ARG:NH2	18:1W:74:ALA:O	2.32	0.62
32:1a:401:U:OP2	35:1d:3:ARG:NH2	2.31	0.62
32:1a:672:G:H2'	32:1a:673:C:H6	1.64	0.62
1:2A:596:C:OP1	59:2A:3639:HOH:O	2.16	0.62
33:2b:101:MET:HA	33:2b:108:ILE:HD12	1.80	0.62
35:2d:25:ARG:NH1	35:2d:30:LYS:O	2.31	0.62
3:1D:221:VAL:HG22	3:1D:226:MET:HE2	1.82	0.61
5:1F:53:THR:HG22	5:1F:55:GLY:H	1.65	0.61
2:2B:40:U:H2'	26:24:2:LYS:HE3	1.82	0.61
10:2O:7:TYR:HE1	10:2O:20:MET:HE3	1.64	0.61
32:2a:507:A:H61	43:2l:92:ASP:HB2	1.65	0.61
32:2a:661:U:H3	32:2a:697:G:H22	1.46	0.61
6:1G:109:VAL:HG13	26:14:33:VAL:HG11	1.82	0.61
35:1d:122:ARG:HA	35:1d:122:ARG:HE	1.66	0.61
16:2U:92:ARG:HA	16:2U:95:LEU:HB2	1.81	0.61
18:2W:4:LYS:HB2	18:2W:106:ILE:HG12	1.82	0.61
21:2Z:52:SER:OG	21:2Z:53:ILE:N	2.33	0.61
34:2c:164:ARG:NH1	34:2c:166:GLU:OE1	2.32	0.61
32:1a:544:U:O2'	32:1a:545:U:OP2	2.17	0.61
36:1e:7:GLU:OE2	36:1e:37:ARG:NH2	2.31	0.61
1:2A:1830:C:OP2	3:2D:183:ARG:NH2	2.33	0.61
1:2A:2302:U:H2'	1:2A:2303:C:C6	2.35	0.61
17:2V:76:LYS:HB2	17:2V:81:TYR:HB3	1.83	0.61
32:2a:964:A:H1'	50:2s:54:GLY:O	2.00	0.61
32:2a:1299:C:OP1	45:2n:17:LYS:HD2	2.01	0.61
1:2A:1685:U:H2'	1:2A:1686:C:H5''	1.82	0.61
1:2A:2278:A:H5''	1:2A:2279:A:H5'	1.81	0.61
6:2G:161:THR:HG22	6:2G:163:ALA:H	1.65	0.61
19:2X:31:HIS:CD2	19:2X:33:LYS:H	2.19	0.61
32:2a:1256:G:N2	32:2a:1257:A:N7	2.41	0.61
44:2m:58:GLU:O	44:2m:62:ASN:ND2	2.33	0.61
32:1a:1078:U:OP1	32:1a:1091:G:N2	2.30	0.61
14:2S:14:VAL:O	14:2S:18:ILE:HG12	2.01	0.61
1:1A:2858:U:H4'	1:1A:2877:A:C2	2.36	0.61
8:1I:72:LEU:O	8:1I:74:ASN:N	2.33	0.61
1:2A:1042:G:OP1	16:2U:92:ARG:HG2	2.01	0.61
1:2A:1400:G:OP1	3:2D:38:LYS:NZ	2.34	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1273:G:H2'	32:2a:1274:U:C6	2.36	0.61
32:2a:1456:C:OP2	59:2a:1913:HOH:O	2.16	0.61
1:1A:1232:U:H4'	17:1V:79:VAL:HG22	1.81	0.61
1:1A:1939:A:O2'	1:1A:1941:C:N4	2.34	0.61
10:1O:2:ILE:HD12	10:1O:6:THR:HG21	1.83	0.61
19:1X:57:LEU:HD11	19:1X:78:LYS:HE2	1.82	0.61
32:1a:825:U:C4	32:1a:826:C:H1'	2.36	0.61
1:2A:330:G:H21	1:2A:353:A:H62	1.49	0.61
1:2A:2805:G:H22	1:2A:2814:C:H1'	1.65	0.61
2:2B:50:G:OP1	14:2S:63:THR:N	2.33	0.61
1:2A:1311:G:O5'	18:2W:15:ARG:NH2	2.34	0.60
32:2a:859:G:OP1	43:2I:12:ARG:NH2	2.32	0.60
32:2a:1116:G:H1	32:2a:1124:C:H42	1.48	0.60
45:2n:34:TYR:O	45:2n:38:GLY:N	2.27	0.60
1:1A:2657:C:OP2	1:1A:2744:G:O2'	2.19	0.60
4:1E:54:GLN:HA	4:1E:54:GLN:HE21	1.64	0.60
32:1a:137:G:H2'	32:1a:138:A:H8	1.65	0.60
32:1a:181:C:H2'	32:1a:182:C:C6	2.36	0.60
32:1a:217:C:H2'	32:1a:218:U:H6	1.66	0.60
32:1a:434:G:OP1	59:1a:2011:HOH:O	2.16	0.60
50:1s:36:ARG:HB3	50:1s:72:GLY:HA3	1.83	0.60
1:2A:1638:G:H2'	1:2A:1639:G:H8	1.66	0.60
1:2A:2738:U:H4'	10:2O:1:MET:HE1	1.83	0.60
11:2P:94:GLU:HG3	11:2P:124:LYS:HD3	1.83	0.60
11:2P:100:LEU:HD12	11:2P:112:LEU:HD11	1.83	0.60
38:2g:70:LYS:HD3	38:2g:96:GLN:HB3	1.83	0.60
3:1D:148:GLU:HB2	3:1D:151:LYS:HD2	1.83	0.60
32:1a:954:G:OP2	32:1a:1340:U:O2'	2.16	0.60
42:1k:48:ILE:O	42:1k:50:TYR:N	2.34	0.60
1:2A:1129:A:N3	1:2A:1150:U:O2'	2.32	0.60
1:2A:2088:G:O2'	1:2A:2090:G:H5''	2.02	0.60
12:2Q:65:PHE:HB2	12:2Q:105:GLU:HB2	1.82	0.60
33:2b:19:HIS:HE1	33:2b:206:ASP:HB2	1.66	0.60
1:1A:1500:U:O2'	1:1A:1501:G:N7	2.31	0.60
32:1a:932:G:H21	32:1a:1209:A:H62	1.47	0.60
33:1b:54:THR:HG21	33:1b:201:ILE:HD11	1.81	0.60
39:1h:51:VAL:HG21	39:1h:60:ARG:HD2	1.83	0.60
54:1x:8:4SU:O5'	54:1x:8:4SU:H6	2.01	0.60
1:2A:2441:A:OP2	59:2A:3603:HOH:O	2.17	0.60
32:1a:460:G:H2'	32:1a:461:G:C8	2.34	0.60
42:1k:15:ALA:HA	42:1k:77:MET:HA	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:533:C:OP1	59:2A:3641:HOH:O	2.16	0.60
15:2T:64:ARG:HB2	15:2T:73:GLU:HG2	1.82	0.60
32:2a:936:A:N6	50:2s:77:THR:O	2.35	0.60
32:2a:1273:G:O3'	40:2i:38:GLN:NE2	2.35	0.60
1:1A:1697:G:OP1	13:1R:40:LYS:NZ	2.35	0.60
1:1A:1846:G:OP2	59:1A:4153:HOH:O	2.17	0.60
21:1Z:92:SER:O	21:1Z:94:GLU:N	2.35	0.60
32:1a:915:A:N6	32:1a:1327:U:O4	2.34	0.60
32:1a:1191:C:O2'	32:1a:1196:C:N4	2.32	0.60
38:1g:16:LEU:HD21	40:1i:45:ALA:HB2	1.83	0.60
44:1m:17:VAL:O	44:1m:20:THR:OG1	2.16	0.60
1:2A:1684:C:H5''	1:2A:2721:C:O2'	2.01	0.60
10:2O:2:ILE:HD12	10:2O:6:THR:HG21	1.83	0.60
1:1A:1039:C:OP1	16:1U:53:ARG:NH2	2.34	0.60
1:1A:1789:A:N3	59:1A:4298:HOH:O	2.32	0.60
1:2A:82:A:H5''	20:2Y:8:LYS:HE3	1.84	0.60
1:2A:624:G:O2'	1:2A:701:A:N6	2.35	0.60
32:2a:571:G:OP2	59:2a:1912:HOH:O	2.16	0.60
32:2a:646:G:H2'	32:2a:647:A:H8	1.67	0.60
32:2a:1259:C:HO2'	32:2a:1261:A:H8	1.48	0.60
43:2l:75:HIS:CD2	43:2l:77:LEU:H	2.18	0.60
54:2x:75:C:OP1	59:2x:3101:HOH:O	2.15	0.60
55:2z:6:TYR:CZ	55:2z:7:LEU:HD22	2.36	0.60
32:1a:487:C:OP2	43:1l:116:SER:OG	2.14	0.60
1:2A:775:G:C6	3:2D:208:LYS:HB2	2.36	0.60
2:2B:75:G:N2	21:2Z:87:ASP:OD1	2.35	0.60
32:2a:853:C:H1'	39:2h:15:ASN:HD21	1.67	0.60
32:2a:1480:A:H2	32:2a:1483:G:H1	1.50	0.60
1:1A:1323:A:OP1	13:1R:36:THR:HG23	2.02	0.60
1:1A:1760:G:N2	1:1A:1774:C:O2	2.33	0.60
23:11:77:ALA:HA	23:11:80:LEU:HD13	1.83	0.60
26:14:44:THR:O	26:14:46:GLN:N	2.35	0.60
32:2a:630:U:H2'	32:2a:631:C:C6	2.37	0.60
33:2b:90:MET:HG3	33:2b:91:PRO:HD2	1.84	0.60
34:2c:67:THR:HG23	34:2c:102:ASN:HB2	1.84	0.60
54:2x:23:C:H2'	54:2x:24:U:C6	2.37	0.60
1:1A:710:C:O2'	59:1A:4152:HOH:O	2.17	0.60
8:1I:48:GLU:HG2	8:1I:52:ARG:HH22	1.67	0.60
1:2A:1154:C:H3'	1:2A:1155:G:H8	1.66	0.60
1:1A:593:A:O2'	17:1V:78:LYS:NZ	2.35	0.59
1:1A:2622:U:C4	27:15:3:LYS:HG2	2.36	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:1P:95:VAL:HG22	11:1P:125:VAL:HB	1.84	0.59
13:1R:33:ARG:NH1	13:1R:115:GLU:OE2	2.34	0.59
15:1T:16:ARG:NH2	15:1T:83:ILE:O	2.35	0.59
32:1a:305:G:O2'	32:1a:591:A:N1	2.35	0.59
34:1c:52:LEU:HD23	34:1c:53:ALA:H	1.67	0.59
1:2A:1354:G:H4'	29:27:7:PRO:HB2	1.83	0.59
1:2A:1812:C:OP1	59:2A:3642:HOH:O	2.16	0.59
21:2Z:19:ARG:NH1	21:2Z:84:GLU:O	2.35	0.59
32:2a:1359:U:H2'	32:2a:1360:A:C8	2.36	0.59
1:1A:1038:G:OP1	16:1U:50:ARG:NH2	2.31	0.59
11:1P:138:LEU:HD23	11:1P:145:PRO:HB3	1.84	0.59
32:1a:954:G:H5'	32:1a:1340:U:O2'	2.01	0.59
37:1f:1:MET:HE3	37:1f:66:GLU:HG2	1.83	0.59
1:2A:361:G:OP2	59:2A:3640:HOH:O	2.16	0.59
12:2Q:52:VAL:HG22	21:2Z:183:LEU:HD11	1.83	0.59
8:1I:72:LEU:C	8:1I:74:ASN:H	2.11	0.59
32:1a:142:G:H2'	32:1a:143:G:C8	2.37	0.59
46:1o:25:THR:HG21	46:1o:70:LEU:HB2	1.84	0.59
46:1o:39:LEU:HD13	46:1o:56:LEU:HB2	1.84	0.59
1:2A:1039:C:O2'	1:2A:1041:A:OP1	2.21	0.59
33:2b:92:TYR:CZ	33:2b:150:SER:C	2.79	0.59
32:1a:94:C:H2'	32:1a:95:A:C8	2.37	0.59
32:1a:1296:C:OP2	50:1s:4:SER:OG	2.17	0.59
1:2A:555:C:OP1	1:2A:583:G:N1	2.34	0.59
2:2B:64:C:H2'	2:2B:65:C:C6	2.37	0.59
2:2B:114:C:H4'	14:2S:46:VAL:HG22	1.85	0.59
26:24:24:THR:OG1	26:24:25:TYR:N	2.32	0.59
40:2i:29:ASN:N	40:2i:63:ILE:O	2.30	0.59
1:1A:598:U:H2'	1:1A:599:G:C8	2.36	0.59
11:1P:88:LEU:HD11	11:1P:114:ILE:HD12	1.83	0.59
32:1a:752:A:OP2	59:1a:2014:HOH:O	2.17	0.59
44:1m:4:ILE:HG13	44:1m:57:ARG:HA	1.84	0.59
32:2a:1287:G:H22	32:2a:1313:G:H1'	1.68	0.59
35:2d:18:LYS:NZ	35:2d:31:CYS:SG	2.75	0.59
1:1A:404:C:O2'	59:1A:4155:HOH:O	2.17	0.59
1:1A:1303:C:OP2	59:1A:4151:HOH:O	2.16	0.59
1:1A:2650:A:OP2	59:1A:4157:HOH:O	2.17	0.59
24:12:32:LEU:HD22	24:12:36:ARG:HH11	1.67	0.59
32:1a:91:G:O2'	32:1a:92:G:OP2	2.17	0.59
1:2A:1002:U:OP2	12:2Q:14:ARG:NH1	2.35	0.59
1:2A:1231:G:H5'	17:2V:81:TYR:CE1	2.38	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:2Z:157:LEU:HD21	21:2Z:163:LEU:HD13	1.85	0.59
32:2a:669:G:N2	32:2a:670:U:O4	2.35	0.59
32:2a:868:G:O2'	32:2a:884:G:O6	2.19	0.59
40:2i:78:LYS:HD3	40:2i:101:PHE:HD2	1.67	0.59
45:2n:7:ILE:HG22	45:2n:23:ARG:HD3	1.84	0.59
1:2A:69:A:H5''	1:2A:71:A:C8	2.37	0.59
2:2B:62:C:H2'	2:2B:63:G:C8	2.38	0.59
33:2b:74:LYS:NZ	33:2b:206:ASP:OD1	2.36	0.59
35:2d:64:LEU:HB2	35:2d:198:VAL:HG11	1.85	0.59
47:2p:22:THR:HA	47:2p:33:ILE:HG13	1.83	0.59
1:1A:663:U:H2'	1:1A:664:C:C6	2.37	0.59
1:1A:1355:G:OP2	29:17:9:ARG:NH1	2.36	0.59
32:1a:1418:G:H2'	32:1a:1419:U:C6	2.38	0.59
33:1b:15:VAL:O	33:1b:16:HIS:HB3	2.02	0.59
43:1l:5:PRO:HG2	43:1l:10:LEU:HD21	1.84	0.59
1:2A:1992:A:OP2	3:2D:242:ARG:NH2	2.36	0.59
14:2S:99:LYS:NZ	14:2S:103:GLU:OE2	2.21	0.59
19:2X:53:LYS:HB3	19:2X:82:GLN:HB3	1.83	0.59
12:1Q:32:TYR:CE1	12:1Q:133:ARG:HG3	2.36	0.59
32:1a:232:G:OP1	48:1q:40:LYS:NZ	2.36	0.59
32:1a:1026:C:H2'	32:1a:1027:A:H5'	1.83	0.59
40:1i:3:GLN:OE1	40:1i:20:ARG:NH2	2.36	0.59
26:24:40:HIS:HB3	26:24:43:TYR:HB2	1.84	0.59
32:2a:6:U:H5''	32:2a:7:G:C5	2.38	0.59
32:2a:45:G:H1	32:2a:394:C:H42	1.50	0.59
33:2b:16:HIS:O	33:2b:18:GLY:N	2.35	0.59
40:2i:28:VAL:HG22	40:2i:63:ILE:HD12	1.84	0.59
1:1A:69:A:N7	19:1X:31:HIS:HE1	2.00	0.59
1:1A:1514:C:OP1	59:1A:4149:HOH:O	2.16	0.59
33:1b:168:THR:HG1	33:1b:192:SER:HG	1.47	0.59
1:2A:154:C:H42	1:2A:159:G:H1	1.51	0.59
1:2A:2297:A:H4'	1:2A:2298:A:O4'	2.02	0.59
2:2B:66:A:H61	2:2B:109:C:H5''	1.67	0.59
21:2Z:10:ARG:NH1	21:2Z:26:GLY:O	2.36	0.59
32:2a:573:C:H2'	32:2a:574:C:H6	1.68	0.59
32:2a:691:C:H2'	32:2a:692:C:C6	2.38	0.59
1:1A:1295:G:OP2	11:1P:21:ARG:NH1	2.35	0.58
8:1I:72:LEU:HD21	8:1I:107:VAL:HG11	1.85	0.58
12:1Q:52:VAL:O	12:1Q:56:ARG:HG3	2.03	0.58
26:14:63:TYR:N	26:14:64:GLY:HA2	2.18	0.58
32:1a:154:G:O2'	32:1a:156:A:N6	2.25	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:449:C:H5''	32:1a:450:C:C5	2.37	0.58
33:1b:21:ARG:C	33:1b:23:ARG:H	2.11	0.58
36:1e:110:LEU:HD13	36:1e:118:ILE:HG21	1.83	0.58
21:2Z:130:PRO:HB2	21:2Z:131:ARG:CZ	2.33	0.58
1:1A:1184:C:O3'	9:1N:25:ARG:NH1	2.36	0.58
1:1A:2383:G:N3	59:1A:4303:HOH:O	2.32	0.58
32:1a:741:U:H2'	32:1a:742:G:O4'	2.02	0.58
36:1e:50:GLU:HB2	36:1e:53:LEU:HD13	1.85	0.58
37:1f:25:ILE:HD12	37:1f:82:ARG:HH11	1.68	0.58
1:2A:1174:A:N6	1:2A:2502:U:OP1	2.36	0.58
32:2a:295:G:H2'	32:2a:296:A:C8	2.38	0.58
43:2l:28:LYS:HE3	43:2l:62:SER:HB2	1.84	0.58
32:1a:1169:G:H5'	40:1i:113:LYS:HZ3	1.69	0.58
37:1f:18:GLN:HA	37:1f:21:LEU:HD12	1.84	0.58
46:1o:56:LEU:O	46:1o:60:VAL:HG23	2.04	0.58
2:2B:15:A:OP2	2:2B:69:G:N2	2.34	0.58
8:2I:9:LEU:HD11	8:2I:35:LEU:HD13	1.85	0.58
23:21:3:LYS:HB2	23:21:61:ARG:HH11	1.68	0.58
1:1A:610:U:H2'	1:1A:611:C:C6	2.38	0.58
27:15:16:ARG:HG2	27:15:16:ARG:HH11	1.67	0.58
32:1a:142:G:H2'	32:1a:143:G:H8	1.68	0.58
32:1a:909:C:N3	32:1a:1369:G:O6	2.36	0.58
40:1i:5:TYR:HE1	40:1i:16:ARG:HB2	1.67	0.58
1:2A:1067:G:N2	1:2A:1068:U:O4	2.36	0.58
1:2A:2601:A:O3'	3:2D:239:ARG:NH2	2.36	0.58
32:2a:1077:G:O2'	32:2a:1091:G:N1	2.36	0.58
40:1i:127:LYS:O	40:1i:128:ARG:HG2	2.03	0.58
48:1q:66:SER:O	48:1q:70:ARG:NH1	2.36	0.58
6:2G:101:ILE:HD13	26:24:25:TYR:HB2	1.85	0.58
21:2Z:33:LEU:HD21	21:2Z:90:VAL:HG21	1.84	0.58
50:2s:36:ARG:HA	50:2s:71:LEU:HD23	1.85	0.58
1:1A:1868:C:O3'	59:1A:4158:HOH:O	2.17	0.58
14:1S:15:ARG:O	14:1S:19:LYS:HG2	2.04	0.58
43:1l:33:ARG:HH11	43:1l:62:SER:HB3	1.67	0.58
1:2A:2327:C:H2'	1:2A:2328:C:H6	1.68	0.58
32:2a:1221:A:H62	32:2a:1281:A:N6	2.01	0.58
9:1N:67:LEU:HD13	9:1N:87:LEU:HD13	1.86	0.58
32:1a:138:A:H5''	32:1a:139:G:H5'	1.86	0.58
32:1a:372:G:H5''	47:1p:5:ARG:HB2	1.85	0.58
1:2A:641:G:H5'	5:2F:205:ARG:HD2	1.84	0.58
1:2A:885:U:H2'	1:2A:886:C:C6	2.39	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:522:G:H5''	43:2l:114:LYS:HB2	1.85	0.58
40:2i:9:ARG:O	40:2i:104:ARG:HG3	2.03	0.58
1:1A:267:G:OP2	59:1A:4154:HOH:O	2.17	0.58
1:1A:2206:C:H2'	1:1A:2207:G:H8	1.69	0.58
1:1A:2330:G:H22	14:1S:3:ARG:HG2	1.68	0.58
10:1O:24:VAL:HA	10:1O:39:ILE:HG22	1.84	0.58
16:1U:76:TYR:OH	16:1U:92:ARG:NH1	2.35	0.58
34:1c:180:ALA:HB1	34:1c:203:PHE:HE1	1.68	0.58
1:2A:1292:A:OP1	5:2F:95:ARG:NH2	2.36	0.58
33:2b:162:ILE:HD11	33:2b:184:VAL:HG22	1.84	0.58
40:2i:128:ARG:NH2	54:2x:33:U:OP2	2.37	0.58
1:1A:1007:U:OP2	59:1A:4160:HOH:O	2.17	0.58
1:1A:2206:C:H2'	1:1A:2207:G:C8	2.39	0.58
1:2A:1682:C:OP2	59:2A:3647:HOH:O	2.17	0.58
32:2a:46:U:H2'	32:2a:47:G:C8	2.39	0.58
32:2a:548:C:OP1	59:2a:1914:HOH:O	2.17	0.58
33:2b:92:TYR:CD1	33:2b:151:GLY:HA3	2.36	0.58
1:2A:1066:A:H61	1:2A:1187:A:H61	1.50	0.58
1:2A:1854:G:N3	3:2D:254:THR:OG1	2.37	0.58
15:2T:56:GLY:O	15:2T:59:THR:HG23	2.04	0.58
32:2a:626:A:N3	39:2h:113:SER:OG	2.36	0.58
32:2a:1145:C:N4	32:2a:1156:G:H1	1.98	0.58
41:2j:19:SER:O	41:2j:23:ILE:N	2.35	0.58
1:1A:830:A:H5'	1:1A:831:G:OP1	2.03	0.57
32:1a:199:U:H2'	32:1a:200:C:C6	2.38	0.57
32:1a:677:G:H2'	32:1a:678:A:C8	2.39	0.57
1:2A:1070:G:C4	1:2A:1179:C:H1'	2.39	0.57
1:2A:1702:C:H2'	1:2A:1703:C:H6	1.69	0.57
19:2X:35:THR:HG22	19:2X:37:THR:H	1.67	0.57
32:2a:1491:A:H2'	32:2a:1492:C:C6	2.39	0.57
35:2d:8:VAL:HG12	35:2d:21:LEU:HD13	1.85	0.57
35:2d:61:LYS:HA	35:2d:203:VAL:HG22	1.85	0.57
36:2e:151:LEU:HD13	39:2h:77:GLU:HG2	1.84	0.57
1:1A:326:U:O4	59:1A:4156:HOH:O	2.17	0.57
1:1A:2797:C:OP1	4:1E:41:LYS:NZ	2.37	0.57
1:1A:2859:A:OP2	1:1A:2875:U:H5	1.88	0.57
5:1F:185:ASP:HA	5:1F:188:ARG:HD3	1.85	0.57
32:1a:1447:G:OP2	59:1a:2015:HOH:O	2.17	0.57
11:2P:95:VAL:HG12	11:2P:123:LEU:HD22	1.86	0.57
26:24:46:GLN:O	26:24:48:ARG:N	2.36	0.57
32:2a:929:G:N3	32:2a:948:C:O2'	2.32	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:2d:118:ARG:HG2	35:2d:136:PRO:HB3	1.85	0.57
38:2g:39:ALA:HA	38:2g:42:ILE:HD11	1.85	0.57
1:1A:670:A:H2'	1:1A:671:G:O4'	2.04	0.57
1:1A:1066:A:H62	1:1A:1185:U:H3	1.50	0.57
1:1A:2803:C:H2'	1:1A:2804:G:H8	1.68	0.57
32:1a:1254:G:H2'	32:1a:1255:G:O4'	2.04	0.57
32:1a:1259:C:O2'	32:1a:1261:A:H1'	2.05	0.57
1:2A:1823:C:OP1	59:2A:3645:HOH:O	2.17	0.57
11:2P:39:LYS:HA	11:2P:45:LEU:HG	1.86	0.57
33:2b:97:TRP:CZ2	33:2b:101:MET:HB2	2.39	0.57
47:2p:28:ARG:NH1	47:2p:29:ASP:OD1	2.37	0.57
49:2r:47:THR:HG23	49:2r:49:LYS:HG3	1.85	0.57
1:1A:1713:G:O2'	1:1A:2012:U:O4	2.17	0.57
1:1A:2017:C:H4'	1:1A:2018:G:OP1	2.04	0.57
1:1A:2033:G:OP1	18:1W:11:ARG:NH2	2.33	0.57
1:1A:2429:A:H2'	1:1A:2430:U:C6	2.38	0.57
32:1a:1108:U:H1'	32:1a:1109:U:H6	1.70	0.57
32:2a:1126:G:H2'	32:2a:1127:G:H8	1.69	0.57
32:2a:1298:G:N2	32:2a:1300:A:H3'	2.18	0.57
33:2b:56:ARG:HA	33:2b:56:ARG:HH11	1.69	0.57
4:1E:54:GLN:HB2	4:1E:76:ARG:HG3	1.85	0.57
7:1H:40:GLU:OE1	7:1H:61:HIS:NE2	2.31	0.57
32:1a:1287:G:N2	32:1a:1313:G:H1'	2.19	0.57
32:1a:1334:C:OP1	52:1u:3:LYS:NZ	2.25	0.57
32:2a:392:G:O2'	32:2a:394:C:OP1	2.15	0.57
46:2o:5:LYS:H	46:2o:5:LYS:NZ	2.02	0.57
1:1A:1603:C:OP2	1:1A:1604:A:O2'	2.18	0.57
2:1B:77:U:OP1	21:1Z:19:ARG:NH2	2.37	0.57
35:1d:164:ALA:C	35:1d:168:ARG:HH11	2.13	0.57
43:1l:53:ARG:HG3	43:1l:93:LEU:HD21	1.86	0.57
1:2A:704:C:H2'	1:2A:705:C:C6	2.40	0.57
15:2T:55:ASN:N	15:2T:59:THR:HG22	2.14	0.57
32:2a:712:A:H2'	32:2a:713:A:C8	2.38	0.57
32:2a:1237:G:OP1	41:2j:45:ARG:NH2	2.35	0.57
44:2m:60:VAL:HG23	44:2m:64:TRP:CE3	2.40	0.57
1:1A:2626:U:H2'	1:1A:2627:C:H6	1.70	0.57
15:1T:56:GLY:O	15:1T:59:THR:HG23	2.04	0.57
20:1Y:6:HIS:H	20:1Y:6:HIS:CD2	2.23	0.57
32:1a:812:A:H2'	32:1a:813:G:O4'	2.03	0.57
54:1x:17:C:H2'	54:1x:17(A):U:H6	1.70	0.57
54:1x:17:C:H5''	54:1x:61:C:H5''	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:2D:26:LYS:NZ	3:2D:30:GLU:OE1	2.31	0.57
32:2a:630:U:H2'	32:2a:631:C:H6	1.69	0.57
33:2b:71:VAL:HG23	33:2b:164:VAL:HA	1.87	0.57
8:1I:4:ILE:HG12	8:1I:18:VAL:HG22	1.87	0.57
12:1Q:55:VAL:HG12	12:1Q:64:ILE:HD13	1.86	0.57
32:1a:179:G:H2'	32:1a:180:A:H8	1.69	0.57
32:1a:1145:C:N3	32:1a:1156:G:N2	2.47	0.57
35:1d:8:VAL:HG22	35:1d:9:CYS:H	1.69	0.57
36:1e:86:ALA:N	59:1e:301:HOH:O	2.37	0.57
1:2A:948:C:H2'	1:2A:949:C:H6	1.70	0.57
1:2A:1052:C:H5''	9:2N:35:ARG:HH11	1.69	0.57
1:2A:2347:A:H61	22:20:43:THR:CG2	2.18	0.57
41:2j:35:SER:HB3	41:2j:73:ASP:HB2	1.85	0.57
1:1A:2563:U:OP1	59:1A:4162:HOH:O	2.18	0.57
32:1a:584:C:H42	32:1a:622:G:H1	1.52	0.57
33:1b:54:THR:HG23	33:1b:199:TYR:HB3	1.85	0.57
1:2A:30:C:OP1	59:2A:3646:HOH:O	2.17	0.57
32:2a:549:U:OP2	32:2a:550:G:O2'	2.23	0.57
32:2a:1222:U:N3	38:2g:30:ILE:O	2.34	0.57
32:2a:1233:A:H2'	32:2a:1234:A:C8	2.40	0.57
32:1a:1087:G:H4'	33:1b:111:ARG:NH1	2.20	0.56
41:1j:54:PHE:O	41:1j:56:HIS:N	2.36	0.56
1:2A:172:C:H2'	1:2A:173:U:C6	2.40	0.56
2:2B:90:A:C5	2:2B:91:C:H1'	2.40	0.56
4:1E:29:GLY:HA3	59:1E:404:HOH:O	2.04	0.56
34:1c:64:VAL:HG13	34:1c:99:VAL:HA	1.87	0.56
40:1i:17:VAL:HG21	40:1i:81:ILE:HG22	1.85	0.56
1:2A:493:G:N7	29:27:39:ARG:NH2	2.50	0.56
1:2A:1276:G:H2'	1:2A:1277:G:H8	1.70	0.56
32:2a:10:G:H2'	32:2a:11:A:H8	1.70	0.56
32:2a:646:G:H2'	32:2a:647:A:C8	2.39	0.56
32:2a:898:U:H2'	32:2a:899:U:C6	2.40	0.56
1:1A:1687:A:H2'	1:1A:1688:G:O4'	2.05	0.56
1:1A:2018:G:N7	59:1A:4297:HOH:O	2.32	0.56
10:1O:7:TYR:HE1	10:1O:20:MET:HE3	1.71	0.56
32:1a:657:G:H2'	32:1a:658:G:C8	2.41	0.56
32:1a:1328:A:N1	32:1a:1357:A:H5''	2.20	0.56
33:1b:32:ILE:HD13	33:1b:40:HIS:HB3	1.87	0.56
1:2A:137:G:H1'	1:2A:138:A:H2	1.68	0.56
1:2A:1066:A:H62	1:2A:1185:U:H3	1.53	0.56
1:2A:2238:A:OP2	59:2A:3643:HOH:O	2.16	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2375:C:H2'	1:2A:2376:G:O4'	2.06	0.56
12:2Q:12:GLN:HG2	12:2Q:73:PRO:HD2	1.86	0.56
32:2a:726:G:OP2	46:2o:35:ARG:NH2	2.37	0.56
32:2a:954:G:H5'	32:2a:1340:U:O2'	2.06	0.56
32:2a:1088:A:H2'	32:2a:1089:G:C8	2.39	0.56
32:2a:1102:C:H2'	32:2a:1103:G:C8	2.40	0.56
32:2a:1161:A:H5''	40:2i:102:LEU:HD22	1.86	0.56
47:2p:74:LEU:HD23	47:2p:79:VAL:HG21	1.87	0.56
52:2u:9:ARG:HA	52:2u:22:ARG:HB2	1.87	0.56
54:2x:61:C:H2'	54:2x:62:C:H6	1.70	0.56
1:1A:1387:A:OP2	59:1A:4142:HOH:O	2.18	0.56
1:1A:1826:U:H2'	1:1A:1827:C:C6	2.40	0.56
15:1T:35:LYS:HD3	15:1T:37:GLY:H	1.70	0.56
16:1U:85:LYS:HD3	16:1U:117:GLN:HA	1.86	0.56
42:1k:85:ARG:HD3	42:1k:113:PRO:HD3	1.87	0.56
1:2A:1039:C:OP2	16:2U:54:LYS:NZ	2.37	0.56
2:2B:31:C:H4'	6:2G:29:TRP:HH2	1.69	0.56
31:29:29:ASN:HD22	31:29:32:HIS:CE1	2.23	0.56
32:2a:846:C:H2'	32:2a:847:G:O4'	2.05	0.56
35:2d:100:ARG:NH2	35:2d:102:ASP:OD2	2.38	0.56
49:2r:25:THR:O	49:2r:25:THR:OG1	2.20	0.56
1:1A:638:G:OP1	59:1A:4159:HOH:O	2.17	0.56
6:1G:49:ASP:O	6:1G:51:ARG:N	2.29	0.56
20:1Y:92:ASN:N	20:1Y:93:GLY:HA2	2.21	0.56
32:1a:1101:C:H1'	32:1a:1161:A:C4	2.40	0.56
33:1b:82:ARG:NH1	33:1b:86:GLU:OE2	2.38	0.56
1:2A:1276:G:H2'	1:2A:1277:G:C8	2.40	0.56
5:2F:53:THR:HG22	5:2F:56:GLU:HG3	1.86	0.56
20:2Y:102:CYS:SG	20:2Y:103:GLY:N	2.79	0.56
32:2a:424:G:OP2	35:2d:10:ARG:NH1	2.38	0.56
32:2a:958:C:OP2	59:2a:1905:HOH:O	2.18	0.56
33:2b:98:LEU:HB2	33:2b:101:MET:HE3	1.87	0.56
34:2c:180:ALA:HA	34:2c:206:GLU:HA	1.87	0.56
1:1A:208:G:O2'	1:1A:221:A:N3	2.34	0.56
1:1A:1076:G:H21	31:19:36:GLN:HE22	1.53	0.56
3:1D:142:VAL:HG23	3:1D:193:VAL:HA	1.88	0.56
11:1P:100:LEU:HD12	11:1P:112:LEU:HD11	1.88	0.56
33:1b:195:ASP:O	39:1h:68:ARG:NH2	2.39	0.56
2:2B:55:U:O3'	6:2G:27:ASN:ND2	2.39	0.56
8:2I:4:ILE:HD11	8:2I:44:LEU:HD12	1.87	0.56
32:2a:556:A:OP1	59:2a:1915:HOH:O	2.17	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:1S:3:ARG:C	14:1S:3:ARG:HD3	2.31	0.56
32:1a:516:A:H2	32:1a:1188:G:H21	1.54	0.56
35:1d:105:VAL:HG13	35:1d:110:PHE:HB2	1.86	0.56
1:2A:2122:G:O6	1:2A:2209:C:N4	2.38	0.56
5:2F:29:ASN:H	5:2F:112:MET:HE1	1.70	0.56
28:26:14:THR:OG1	28:26:48:VAL:O	2.22	0.56
32:2a:703:C:O2'	49:2r:49:LYS:HB3	2.06	0.56
32:2a:951:G:P	41:2j:57:LYS:HZ3	2.28	0.56
40:2i:105:ASP:OD1	59:2i:5001:HOH:O	2.17	0.56
1:1A:1091:A:H3'	1:1A:1092:G:H5'	1.86	0.56
1:1A:2517:U:OP1	4:1E:144:ARG:NH2	2.37	0.56
2:1B:48:A:H4'	14:1S:95:HIS:HD2	1.70	0.56
36:1e:33:VAL:HG13	36:1e:112:LEU:HD12	1.88	0.56
50:1s:27:GLU:HB2	50:1s:28:LYS:HB3	1.88	0.56
1:2A:807:A:OP2	59:2A:3644:HOH:O	2.17	0.56
18:2W:71:VAL:HA	18:2W:107:LEU:HD12	1.87	0.56
32:2a:1220:A:OP2	59:2a:1918:HOH:O	2.18	0.56
1:1A:301:A:O2'	1:1A:302:C:OP1	2.20	0.56
1:1A:1409:G:P	23:11:3:LYS:HG3	2.46	0.56
5:1F:84:VAL:O	59:1F:401:HOH:O	2.18	0.56
1:2A:324:G:OP2	20:2Y:84:ARG:NH2	2.38	0.56
32:2a:719:C:H2'	32:2a:720:C:H6	1.69	0.56
39:2h:23:SER:HA	39:2h:63:LEU:HD22	1.88	0.56
1:1A:1536:G:O2'	3:1D:101:GLU:HB2	2.06	0.56
1:1A:2083:A:H62	55:1z:11:ARG:H	1.53	0.56
32:1a:962:C:N4	32:1a:1203:G:H1	2.01	0.56
1:2A:590:U:H5'	1:2A:989:A:N1	2.20	0.56
1:2A:2298:A:H62	1:2A:2355:U:H3	1.53	0.56
6:2G:17:PRO:HA	6:2G:20:ILE:HD12	1.87	0.56
32:2a:969:U:H4'	32:2a:970:U:OP2	2.04	0.56
32:2a:1294:G:H1	32:2a:1307:C:H42	1.54	0.56
1:1A:271:U:H4'	8:1I:50:ARG:HH12	1.71	0.55
1:1A:1934:A:N7	32:1a:1472:G:H5''	2.22	0.55
24:12:22:GLU:OE2	24:12:68:ARG:NH2	2.38	0.55
26:14:16:CYS:SG	26:14:17:GLY:N	2.79	0.55
32:1a:265:C:H2'	32:1a:266:A:C8	2.42	0.55
51:1t:16:HIS:O	51:1t:19:SER:OG	2.18	0.55
32:2a:59:C:O2'	32:2a:384:G:N7	2.33	0.55
33:2b:165:VAL:HG23	33:2b:166:ASP:H	1.71	0.55
44:2m:4:ILE:HG23	44:2m:5:ALA:H	1.71	0.55
1:1A:1090:A:H4'	1:1A:1091:A:H5''	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:19:2:LYS:NZ	31:19:31:LYS:O	2.34	0.55
32:1a:1164:G:H4'	32:1a:1165:A:H5'	1.88	0.55
32:1a:1203:G:OP1	32:1a:1302:C:N4	2.32	0.55
33:1b:119:GLU:OE1	33:1b:153:ARG:NH2	2.39	0.55
1:2A:2573:U:H1'	10:2O:23:ARG:HH11	1.71	0.55
32:2a:1303:C:H5''	32:2a:1304:C:H2'	1.87	0.55
1:1A:440:C:H2'	1:1A:441:A:C8	2.41	0.55
6:1G:50:ALA:O	6:1G:52:ILE:N	2.39	0.55
7:1H:3:ARG:HG2	7:1H:6:ARG:HG2	1.88	0.55
20:1Y:68:HIS:ND1	20:1Y:70:SER:HB3	2.21	0.55
32:1a:614:G:H2'	32:1a:615:G:C8	2.41	0.55
32:1a:720:C:H2'	32:1a:721:A:C8	2.40	0.55
46:1o:71:GLN:HG2	46:1o:78:TYR:CG	2.41	0.55
1:2A:2813:C:H2'	1:2A:2814:C:H6	1.71	0.55
3:2D:75:ILE:HG21	3:2D:99:ASP:HB2	1.88	0.55
11:2P:84:ASN:OD1	11:2P:117:GLU:HB2	2.06	0.55
18:2W:18:ARG:NH1	18:2W:76:VAL:O	2.40	0.55
32:2a:1154:C:H2'	32:2a:1155:G:C8	2.41	0.55
32:2a:1375:G:H21	32:2a:1480:A:H8	1.53	0.55
36:2e:36:ASP:C	36:2e:38:GLN:H	2.15	0.55
49:2r:30:ASP:C	49:2r:32:ARG:H	2.15	0.55
1:1A:1220:G:H21	1:1A:1221:A:H4'	1.71	0.55
32:1a:1194:U:H5''	32:1a:1195:A:H5'	1.89	0.55
40:1i:15:ALA:HB2	40:1i:65:VAL:HG23	1.88	0.55
1:2A:80:G:N1	1:2A:100:A:OP2	2.36	0.55
1:2A:2305:C:H5'	14:2S:10:ARG:HD2	1.89	0.55
1:2A:2785:C:OP1	4:2E:166:THR:OG1	2.24	0.55
5:2F:130:ALA:HB2	5:2F:142:TRP:HD1	1.71	0.55
32:2a:1255:G:H3'	32:2a:1256:G:H8	1.71	0.55
32:2a:1493:C:H2'	32:2a:1494:G:C8	2.41	0.55
45:2n:24:CYS:O	45:2n:28:GLY:N	2.40	0.55
1:1A:1450:U:H2'	1:1A:1451:U:C6	2.42	0.55
1:1A:1612:A:OP1	3:1D:211:ARG:NH1	2.39	0.55
1:1A:2117:U:H3	1:1A:2214:G:H1	1.53	0.55
1:1A:2339:A:H2'	1:1A:2340:G:C8	2.42	0.55
12:1Q:21:THR:HG21	12:1Q:101:ARG:HB2	1.88	0.55
32:1a:142:G:H1	32:1a:170:C:H42	1.54	0.55
32:1a:1194:U:H4'	32:1a:1195:A:C8	2.42	0.55
46:1o:8:LYS:O	46:1o:12:ILE:HG13	2.07	0.55
1:2A:2012:U:H2'	1:2A:2013:G:H5''	1.89	0.55
2:2B:75:G:H22	21:2Z:73:GLN:HE21	1.53	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:821:G:H1	32:2a:827:C:H42	1.54	0.55
32:2a:900:G:N3	32:2a:1381:A:H2	2.05	0.55
32:2a:1257:A:H2'	32:2a:1258:G:O4'	2.07	0.55
34:2c:153:VAL:HG22	34:2c:198:VAL:HG12	1.89	0.55
2:1B:33:G:H5'	6:1G:2:PRO:HD3	1.89	0.55
32:1a:204:A:C5	32:1a:217:C:H4'	2.42	0.55
32:1a:898:U:H2'	32:1a:899:U:C6	2.42	0.55
33:1b:212:GLN:O	33:1b:216:SER:OG	2.21	0.55
32:2a:1048:U:OP2	32:2a:1172:G:N2	2.37	0.55
33:2b:28:PHE:CD1	33:2b:190:THR:HA	2.42	0.55
33:2b:92:TYR:CD1	33:2b:150:SER:O	2.58	0.55
1:1A:1792:A:H2'	59:1A:5846:HOH:O	2.06	0.55
1:1A:2342:G:O2'	1:1A:2347:A:N1	2.33	0.55
21:1Z:24:LEU:HB2	21:1Z:41:LEU:HD23	1.88	0.55
32:1a:1488:U:H2'	32:1a:1489:G:C8	2.41	0.55
37:1f:10:LEU:HD23	37:1f:61:LEU:HD23	1.88	0.55
50:1s:3:ARG:NH1	50:1s:10:PHE:HB2	2.22	0.55
1:2A:239:A:C5	1:2A:240:G:H1'	2.42	0.55
1:2A:241:C:O2'	59:2A:3652:HOH:O	2.18	0.55
10:2O:115:VAL:HG13	10:2O:121:VAL:HG21	1.89	0.55
32:2a:741:U:H2'	32:2a:742:G:O4'	2.05	0.55
42:2k:82:VAL:HB	42:2k:108:ILE:HG12	1.89	0.55
1:1A:425:G:OP2	59:1A:4163:HOH:O	2.18	0.55
35:1d:57:ARG:NH2	36:1e:107:ARG:HD3	2.21	0.55
35:1d:107:ARG:HH22	35:1d:194:LEU:HD11	1.71	0.55
1:2A:754:C:H42	1:2A:769:G:H1	1.53	0.55
1:2A:1092:G:H1'	1:2A:1155:G:N2	2.21	0.55
35:2d:72:GLU:OE1	35:2d:207:TYR:OH	2.24	0.55
1:1A:239:A:C5	1:1A:240:G:H1'	2.42	0.55
1:1A:552:A:C2	1:1A:2064:C:H4'	2.41	0.55
32:1a:543:A:OP1	36:1e:126:ARG:NH2	2.40	0.55
32:1a:952:A:OP2	45:1n:41:ARG:NH1	2.38	0.55
35:1d:57:ARG:HH22	36:1e:107:ARG:HD3	1.72	0.55
39:1h:110:ALA:HB3	39:1h:121:ASP:HB3	1.89	0.55
47:1p:53:VAL:HG13	47:1p:79:VAL:HG13	1.89	0.55
1:2A:656:A:H2'	1:2A:657:A:C8	2.41	0.55
1:2A:1033:A:N7	59:2A:3715:HOH:O	2.34	0.55
6:2G:16:ARG:O	6:2G:20:ILE:HG13	2.07	0.55
11:2P:88:LEU:HD11	11:2P:114:ILE:HD12	1.88	0.55
13:2R:104:ARG:HG3	13:2R:111:LEU:HD21	1.88	0.55
32:2a:752:A:OP2	59:2a:1919:HOH:O	2.18	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:2d:36:ARG:HB3	35:2d:38:TYR:CE2	2.42	0.55
43:2l:24:VAL:HG23	43:2l:98:TYR:CE1	2.42	0.55
43:2l:79:GLU:HG2	43:2l:80:HIS:CD2	2.41	0.55
25:13:8:LEU:HD13	25:13:31:LEU:HD23	1.87	0.55
35:1d:28:SER:OG	35:1d:29:PRO:O	2.22	0.55
1:2A:504:A:N3	1:2A:506:G:H5''	2.22	0.55
1:2A:1073:A:H2'	1:2A:1074:A:C8	2.41	0.55
2:2B:98:G:H2'	2:2B:99:G:O4'	2.07	0.55
5:2F:110:LEU:HD11	5:2F:181:LEU:HG	1.89	0.55
32:2a:753:G:H4'	32:2a:1491:A:H4'	1.89	0.55
1:1A:2441:A:N3	1:1A:2441:A:H2'	2.22	0.54
42:1k:99:GLN:HG2	42:1k:105:VAL:HG21	1.88	0.54
1:2A:26:G:O2'	1:2A:27:A:OP2	2.24	0.54
1:2A:1061:G:H2'	1:2A:1062:G:O4'	2.06	0.54
1:2A:2619:G:N7	59:2A:3716:HOH:O	2.34	0.54
1:2A:2641:G:H2'	1:2A:2642:G:C8	2.42	0.54
32:2a:966:G:H2'	32:2a:967:C:O4'	2.08	0.54
33:2b:219:VAL:HG13	33:2b:222:ILE:HD11	1.88	0.54
44:2m:60:VAL:HG22	44:2m:66:LEU:HD11	1.88	0.54
49:2r:22:VAL:HG23	49:2r:55:ARG:O	2.08	0.54
1:1A:846:A:H8	1:1A:846:A:OP1	1.90	0.54
1:1A:1846:G:O6	3:1D:35:LYS:NZ	2.27	0.54
15:1T:55:ASN:N	15:1T:59:THR:HG22	2.16	0.54
24:12:22:GLU:HG2	24:12:64:LEU:HD11	1.89	0.54
26:14:46:GLN:O	26:14:48:ARG:N	2.40	0.54
32:1a:447:A:O2'	32:1a:448:A:OP2	2.22	0.54
43:1l:24:VAL:HB	43:1l:27:LEU:HD23	1.88	0.54
50:1s:31:ILE:HD12	50:1s:49:ILE:HG12	1.89	0.54
1:2A:33:C:H2'	1:2A:34:G:H5'	1.88	0.54
1:2A:2022:A:H2'	1:2A:2023:G:C8	2.42	0.54
2:2B:49:C:H2'	2:2B:50:G:C8	2.42	0.54
3:2D:148:GLU:HB2	3:2D:151:LYS:HD2	1.89	0.54
20:2Y:43:ASN:CG	20:2Y:65:ALA:HB3	2.32	0.54
32:2a:402:G:N2	35:2d:119:GLN:OE1	2.29	0.54
32:1a:796:C:O2	59:1a:2012:HOH:O	2.16	0.54
32:1a:1223:G:H2'	32:1a:1224:C:C6	2.43	0.54
40:1i:53:VAL:O	40:1i:55:ALA:N	2.40	0.54
45:1n:41:ARG:HG3	45:1n:42:ILE:N	2.22	0.54
1:2A:1110:U:O2	1:2A:1119:G:N2	2.41	0.54
1:2A:1295:G:OP2	11:2P:21:ARG:NH1	2.40	0.54
32:2a:544:U:H5'	32:2a:550:G:N2	2.22	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:741:G:OP1	1:1A:1425:G:O2'	2.25	0.54
1:1A:928:G:H1	1:1A:939:C:H42	1.56	0.54
1:1A:1210:U:H2'	1:1A:1211:C:C6	2.42	0.54
29:17:24:THR:O	29:17:28:ARG:HG3	2.08	0.54
1:2A:839:A:OP1	59:2A:3649:HOH:O	2.18	0.54
1:2A:1494:G:O2'	1:2A:1574:A:N1	2.38	0.54
7:2H:118:PRO:HG2	7:2H:121:ILE:HG13	1.90	0.54
32:2a:1287:G:H5'	52:2u:4:GLY:HA3	1.89	0.54
36:2e:143:ARG:NH1	39:2h:77:GLU:OE1	2.40	0.54
1:1A:534:C:OP1	59:1A:4165:HOH:O	2.18	0.54
1:1A:1847:G:OP1	3:1D:88:ARG:NH2	2.40	0.54
1:2A:671:G:H8	1:2A:671:G:O5'	1.90	0.54
1:2A:2735:C:OP2	4:2E:109:LYS:NZ	2.40	0.54
32:2a:657:G:H2'	32:2a:658:G:C8	2.42	0.54
1:1A:2316:A:H5''	6:1G:134:GLY:HA3	1.90	0.54
3:1D:108:PRO:HD2	3:1D:111:LEU:HG	1.90	0.54
38:1g:77:SER:OG	38:1g:86:GLN:NE2	2.40	0.54
1:2A:1015:C:OP2	59:2A:3651:HOH:O	2.18	0.54
1:2A:2821:G:H1	1:2A:2897:C:H42	1.54	0.54
32:2a:125:A:O2'	32:2a:126:C:O5'	2.23	0.54
32:2a:608:C:H2'	32:2a:609:G:H8	1.72	0.54
32:2a:1087:G:H4'	33:2b:111:ARG:NH1	2.21	0.54
32:2a:1393:G:H2'	32:2a:1394:C:C6	2.43	0.54
36:2e:52:PRO:HG2	36:2e:53:LEU:HD12	1.89	0.54
1:1A:235:G:H4'	1:1A:412:G:C5	2.43	0.54
1:1A:358:C:H4'	20:1Y:73:ARG:HD3	1.89	0.54
1:1A:703:U:H2'	1:1A:704:C:C6	2.43	0.54
1:1A:708:G:H5''	11:1P:16:ARG:HG3	1.89	0.54
1:1A:924:A:H2'	1:1A:925:G:H5'	1.88	0.54
32:1a:658:G:H2'	32:1a:659:A:C8	2.42	0.54
33:1b:109:SER:HA	33:1b:112:VAL:HG13	1.88	0.54
49:1r:26:LEU:HD21	49:1r:39:VAL:HG13	1.90	0.54
1:2A:560:A:H2'	1:2A:561:C:C6	2.43	0.54
1:2A:1923:C:H5'	3:2D:246:PRO:HD3	1.89	0.54
1:2A:2017:C:H4'	1:2A:2018:G:OP1	2.07	0.54
35:2d:187:ARG:NH2	35:2d:193:ASP:OD2	2.40	0.54
36:2e:110:LEU:HD13	36:2e:118:ILE:HG21	1.90	0.54
1:1A:274:C:H2'	1:1A:275:C:C6	2.43	0.54
1:1A:509:C:H2'	1:1A:510:C:C6	2.43	0.54
1:1A:1565:U:H2'	1:1A:1566:G:O4'	2.08	0.54
35:1d:32:ALA:HA	35:1d:35:ARG:HB2	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:6:G:H2'	1:2A:7:A:O4'	2.07	0.54
1:2A:629:U:OP1	5:2F:102:PRO:HA	2.07	0.54
1:2A:1048:G:O2'	1:2A:1055:A:N1	2.38	0.54
6:2G:63:ILE:HA	6:2G:143:GLU:HG3	1.88	0.54
15:2T:122:ASP:OD2	32:2a:1426:G:O2'	2.26	0.54
19:2X:31:HIS:HD2	19:2X:33:LYS:H	1.55	0.54
26:24:59:PHE:HA	26:24:61:ARG:N	2.23	0.54
32:2a:911:G:N2	32:2a:913:A:O4'	2.41	0.54
32:2a:966:G:H4'	32:2a:993:A:H61	1.73	0.54
32:2a:1443:C:H2'	32:2a:1444:C:O4'	2.08	0.54
43:2l:70:ILE:HD13	43:2l:77:LEU:HD12	1.89	0.54
1:1A:1026:A:OP1	59:1A:4164:HOH:O	2.18	0.54
32:1a:646:G:H2'	32:1a:647:A:C8	2.42	0.54
1:2A:323:A:P	20:2Y:86:ARG:HH21	2.31	0.54
1:2A:1381:A:OP2	19:2X:64:LYS:HE3	2.08	0.54
1:2A:1465:U:O2'	1:2A:1466:G:OP1	2.24	0.54
1:2A:2858:U:OP2	15:2T:95:ARG:NH1	2.38	0.54
14:2S:27:SER:HA	14:2S:88:ASP:HB3	1.90	0.54
19:2X:32:PRO:HA	19:2X:77:LYS:HB2	1.89	0.54
32:2a:111:G:OP2	59:2a:1922:HOH:O	2.19	0.54
32:2a:506:C:H41	43:2l:53:ARG:NH2	2.01	0.54
45:2n:43:CYS:HA	45:2n:46:GLU:HB2	1.89	0.54
51:2t:16:HIS:O	51:2t:19:SER:OG	2.23	0.54
1:1A:1056:G:OP1	16:1U:77:SER:OG	2.25	0.54
1:1A:1066:A:C8	1:1A:1066:A:H3'	2.43	0.54
1:1A:1218:A:H4'	1:1A:1219:U:OP1	2.07	0.54
1:1A:1920:G:N3	1:1A:1920:G:H2'	2.23	0.54
32:1a:501:G:N1	32:1a:517:A:OP2	2.38	0.54
32:1a:741:U:OP1	32:1a:806:C:O2'	2.23	0.54
44:1m:15:VAL:HG23	44:1m:43:THR:O	2.08	0.54
51:1t:66:ALA:HB1	51:1t:71:THR:HG21	1.90	0.54
1:2A:323:A:OP1	20:2Y:86:ARG:NH2	2.40	0.54
1:2A:2799:C:H1'	4:2E:62:PRO:HG3	1.89	0.54
1:2A:2830:A:H2'	1:2A:2831:G:C8	2.43	0.54
7:2H:144:VAL:O	7:2H:148:ILE:HG12	2.08	0.54
20:2Y:37:VAL:HG21	20:2Y:72:VAL:HG21	1.90	0.54
32:2a:645:G:H1	32:2a:728:C:H42	1.56	0.54
32:2a:1125:G:H3'	32:2a:1126:G:C8	2.43	0.54
1:1A:1070:G:C4	1:1A:1179:C:H1'	2.43	0.53
1:1A:1176:G:H21	9:1N:73:THR:HG21	1.74	0.53
1:1A:2095:U:H2'	1:1A:2096:U:C6	2.42	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2831:G:O2'	1:1A:2833:C:OP2	2.24	0.53
32:1a:672:G:H2'	32:1a:673:C:C6	2.43	0.53
1:2A:330:G:N1	1:2A:333:A:OP2	2.38	0.53
1:2A:1625:A:H2'	1:2A:1626:A:C8	2.43	0.53
2:2B:25:A:H2'	2:2B:26:A:C8	2.44	0.53
29:27:5:TRP:NE1	29:27:7:PRO:HG3	2.23	0.53
35:2d:153:ARG:NH1	35:2d:181:MET:HE3	2.23	0.53
1:1A:550:A:O2'	1:1A:2064:C:O2	2.25	0.53
1:1A:922:C:H2'	1:1A:923:U:O4'	2.08	0.53
1:1A:1017:A:H5'	1:1A:1232:U:H1'	1.90	0.53
1:1A:1510:C:H2'	1:1A:1511:G:C8	2.44	0.53
32:1a:641:G:N2	32:1a:733:C:O2	2.39	0.53
32:1a:1227:A:H2'	32:1a:1228:C:C6	2.43	0.53
40:1i:17:VAL:HG23	40:1i:63:ILE:HG12	1.90	0.53
1:2A:843:C:OP1	5:2F:60:SER:OG	2.25	0.53
1:2A:904:U:O2	1:2A:2279:A:H2'	2.09	0.53
1:2A:948:C:H2'	1:2A:949:C:C6	2.43	0.53
1:2A:2072:A:H5'	1:2A:2589:G:O4'	2.07	0.53
16:2U:104:GLN:OE1	16:2U:105:VAL:N	2.28	0.53
17:2V:40:LEU:HB2	17:2V:46:VAL:HG22	1.90	0.53
32:2a:10:G:H2'	32:2a:11:A:C8	2.43	0.53
45:2n:3:ARG:HH21	45:2n:4:LYS:HE3	1.71	0.53
1:1A:214:G:H21	1:1A:216:A:H62	1.55	0.53
32:1a:73:C:N3	32:1a:91:G:O6	2.41	0.53
32:1a:154:G:N2	32:1a:157:A:OP2	2.40	0.53
32:1a:1223:G:H2'	32:1a:1224:C:H6	1.73	0.53
1:2A:2327:C:H2'	1:2A:2328:C:C6	2.43	0.53
5:2F:29:ASN:H	5:2F:112:MET:CE	2.20	0.53
36:2e:68:GLU:HG2	36:2e:69:VAL:N	2.22	0.53
45:2n:16:PHE:HB3	45:2n:17:LYS:HZ3	1.74	0.53
1:1A:296:C:H2'	1:1A:297:G:C8	2.44	0.53
1:1A:1214:G:OP1	59:1A:4166:HOH:O	2.18	0.53
1:1A:2012:U:H2'	1:1A:2013:G:H5''	1.91	0.53
11:1P:63:PRO:HD3	30:18:27:THR:HG22	1.89	0.53
14:1S:10:ARG:O	14:1S:14:VAL:HG13	2.07	0.53
31:19:19:ARG:NH2	59:19:601:HOH:O	2.10	0.53
32:1a:838:A:H3'	32:1a:839:G:H8	1.72	0.53
32:1a:1232:A:H4'	40:1i:68:GLY:N	2.24	0.53
42:1k:20:TYR:HB2	42:1k:31:THR:HG23	1.90	0.53
47:1p:20:VAL:HG21	47:1p:32:TYR:CG	2.43	0.53
48:1q:86:GLU:O	48:1q:90:ILE:HG13	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:33:C:H41	1:2A:472:A:H61	1.57	0.53
1:2A:2568:G:H2'	1:2A:2569:C:H6	1.74	0.53
1:2A:2858:U:H4'	1:2A:2877:A:C2	2.43	0.53
8:2I:12:LEU:HD22	8:2I:19:VAL:HG21	1.89	0.53
32:2a:524:G:H2'	32:2a:525:G:H8	1.72	0.53
34:2c:117:ALA:HA	34:2c:186:PHE:CE1	2.43	0.53
5:1F:14:PRO:HD2	5:1F:127:GLU:OE1	2.09	0.53
32:1a:1135:A:OP1	41:1j:68:HIS:ND1	2.40	0.53
1:2A:50:A:OP2	1:2A:114:G:N1	2.27	0.53
1:2A:661:A:H2'	11:2P:117:GLU:OE2	2.09	0.53
1:2A:2670:G:O2'	7:2H:175:LYS:NZ	2.34	0.53
32:2a:61:A:N6	32:2a:104:C:N3	2.55	0.53
32:2a:648:G:P	49:2r:64:ARG:HH21	2.32	0.53
47:2p:21:VAL:HG22	47:2p:33:ILE:HD12	1.89	0.53
50:2s:28:LYS:HB2	50:2s:29:ARG:CB	2.39	0.53
1:1A:172:C:H2'	1:1A:173:U:C6	2.44	0.53
1:1A:2284:A:H2'	1:1A:2285:A:C8	2.43	0.53
32:1a:485:C:H1'	32:1a:533:C:H1'	1.89	0.53
43:1l:54:LYS:HD2	43:1l:54:LYS:N	2.24	0.53
1:2A:907:A:H2'	1:2A:908:G:O4'	2.09	0.53
1:2A:2314:G:O2'	6:2G:132:ASN:HB2	2.08	0.53
5:2F:140:LEU:HD21	5:2F:170:LEU:HD11	1.90	0.53
8:2I:126:TYR:HB2	8:2I:142:VAL:HG23	1.90	0.53
18:2W:86:LEU:HD22	18:2W:96:ILE:HD11	1.91	0.53
32:2a:262:G:O2'	48:2q:67:LYS:HB2	2.08	0.53
32:2a:1406:G:H2'	32:2a:1407:C:C6	2.44	0.53
1:1A:1091:A:H5'	1:1A:1092:G:C8	2.44	0.53
6:1G:115:ARG:HG3	6:1G:136:ARG:HH22	1.74	0.53
26:14:14:ILE:HD13	26:14:31:ILE:HB	1.90	0.53
44:1m:11:ARG:HD3	44:1m:46:LYS:HB3	1.91	0.53
1:2A:480:C:N3	1:2A:497:A:H2'	2.24	0.53
4:2E:9:VAL:HG13	4:2E:25:VAL:O	2.08	0.53
30:28:63:PRO:HG2	30:28:64:TYR:CD2	2.44	0.53
32:2a:923:G:N7	59:2a:1948:HOH:O	2.32	0.53
1:1A:1924:G:OP1	3:1D:241:PRO:HB2	2.09	0.53
1:1A:2315:G:H22	1:1A:2323:U:H3	1.55	0.53
1:1A:2347:A:H61	22:10:43:THR:CG2	2.22	0.53
12:1Q:60:ARG:H	12:1Q:60:ARG:NH1	2.07	0.53
32:1a:295:G:O6	59:1a:2013:HOH:O	2.17	0.53
32:1a:1359:U:H2'	32:1a:1360:A:C8	2.44	0.53
34:1c:39:ILE:HG22	34:1c:43:LEU:HD12	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1e:152:ARG:NH2	39:1h:107:LEU:O	2.42	0.53
38:1g:27:ILE:HD12	38:1g:40:ALA:HA	1.91	0.53
1:2A:842:C:H2'	1:2A:843:C:C6	2.44	0.53
5:2F:183:VAL:O	5:2F:187:VAL:HG23	2.09	0.53
32:2a:979:A:H2'	32:2a:980:G:C8	2.44	0.53
1:1A:84:C:H4'	1:1A:101:U:H1'	1.90	0.53
1:1A:302:C:H42	1:1A:384:G:H1	1.57	0.53
19:1X:60:ARG:NH2	29:17:47:ARG:HH22	2.07	0.53
32:1a:1051:G:N7	32:1a:1077:G:H2'	2.23	0.53
33:1b:98:LEU:HB2	33:1b:101:MET:HE3	1.91	0.53
35:1d:61:LYS:NZ	35:1d:72:GLU:OE2	2.36	0.53
47:1p:57:ARG:NH1	47:1p:79:VAL:O	2.41	0.53
6:2G:35:GLU:HG2	6:2G:36:LYS:HZ2	1.74	0.53
7:2H:164:TYR:HB2	7:2H:167:GLU:HB2	1.91	0.53
8:2I:130:TYR:HB3	8:2I:138:ILE:HB	1.91	0.53
36:2e:24:ARG:HB2	36:2e:24:ARG:HH11	1.74	0.53
50:2s:70:LYS:HB2	50:2s:73:GLU:HG2	1.91	0.53
1:1A:233:G:O6	30:18:8:LYS:NZ	2.30	0.53
1:1A:551:C:C5	1:1A:2791:U:H2'	2.44	0.53
1:1A:1337:U:H2'	1:1A:1338:C:C6	2.44	0.53
32:1a:215:C:H2'	32:1a:216:G:O4'	2.08	0.53
33:1b:167:PRO:HG3	33:1b:188:ALA:HB2	1.90	0.53
1:2A:1513:C:C5	1:2A:1592:C:H2'	2.44	0.53
1:2A:1873:C:H5'	3:2D:253:GLN:NE2	2.23	0.53
1:2A:2568:G:H2'	1:2A:2569:C:C6	2.44	0.53
5:2F:197:ASP:O	5:2F:200:GLU:HB2	2.09	0.53
11:2P:114:ILE:HG13	11:2P:125:VAL:HG21	1.91	0.53
11:2P:125:VAL:HG13	11:2P:138:LEU:HD21	1.91	0.53
32:2a:900:G:C6	32:2a:901:A:C6	2.96	0.53
35:2d:205:GLU:OE1	36:2e:100:VAL:HG12	2.09	0.53
49:2r:33:ASP:OD2	49:2r:36:ASN:HB2	2.09	0.53
1:1A:514:G:N7	18:1W:49:LYS:NZ	2.58	0.52
32:1a:508:G:H2'	32:1a:509:C:C6	2.44	0.52
32:1a:1284:U:OP2	44:1m:21:TYR:OH	2.28	0.52
40:1i:121:ARG:NH1	40:1i:122:ALA:O	2.42	0.52
1:2A:866:A:N3	1:2A:987:U:H4'	2.24	0.52
21:2Z:70:LEU:HG	21:2Z:91:LEU:HD21	1.91	0.52
32:2a:767:C:OP2	59:2a:1921:HOH:O	2.19	0.52
33:2b:145:LEU:O	33:2b:149:LEU:HB2	2.08	0.52
39:2h:77:GLU:HG3	39:2h:78:GLN:N	2.22	0.52
1:1A:957:C:OP1	12:1Q:8:LYS:NZ	2.40	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:1Z:153:SER:HB3	21:1Z:167:PRO:HB3	1.90	0.52
26:14:26:SER:OG	26:14:27:THR:N	2.43	0.52
36:1e:92:LYS:HB3	36:1e:119:LEU:HB2	1.91	0.52
37:1f:99:ALA:HB1	49:1r:23:LYS:HE3	1.90	0.52
1:2A:867:A:H2'	1:2A:990:G:H5''	1.90	0.52
1:2A:1685:U:C2'	1:2A:1686:C:H5''	2.38	0.52
5:2F:36:VAL:HG11	5:2F:183:VAL:HG11	1.92	0.52
32:2a:388:G:H2'	32:2a:389:A:C8	2.44	0.52
32:2a:1284:U:OP2	44:2m:21:TYR:OH	2.13	0.52
39:2h:113:SER:H	39:2h:134:ILE:HD13	1.74	0.52
32:1a:721:A:H2'	32:1a:722:C:C6	2.44	0.52
32:1a:931:G:H2'	32:1a:932:G:O4'	2.09	0.52
34:1c:114:PRO:HA	34:1c:185:GLY:HA3	1.91	0.52
39:1h:73:ASP:OD1	39:1h:75:ARG:HD3	2.09	0.52
1:2A:135:G:H2'	1:2A:137:G:N7	2.24	0.52
1:2A:309:C:H2'	1:2A:310:C:C6	2.44	0.52
1:2A:1073:A:N6	1:2A:1170:G:H2'	2.24	0.52
5:2F:143:ALA:HB1	5:2F:148:LEU:HB2	1.91	0.52
26:24:41:PRO:HG3	26:24:49:PHE:CE2	2.45	0.52
27:25:16:ARG:NH1	27:25:17:ASP:OD1	2.38	0.52
32:2a:810:C:H2'	32:2a:811:U:C6	2.44	0.52
36:2e:78:HIS:CD2	36:2e:142:LEU:HD23	2.44	0.52
1:1A:2330:G:N2	14:1S:3:ARG:HG2	2.24	0.52
32:1a:920:G:H21	40:1i:124:GLN:NE2	2.08	0.52
32:1a:950:C:O2'	41:1j:55:LYS:O	2.26	0.52
32:1a:1089:G:H5''	34:1c:172:ARG:HG2	1.90	0.52
40:1i:23:ASN:H	40:1i:23:ASN:HD22	1.57	0.52
1:2A:885:U:H2'	1:2A:886:C:H6	1.74	0.52
1:2A:2704:A:H2'	1:2A:2705:G:H8	1.74	0.52
33:2b:71:VAL:HA	33:2b:93:VAL:HG23	1.91	0.52
1:1A:2382:G:O6	59:1A:4150:HOH:O	2.16	0.52
14:1S:15:ARG:NE	14:1S:88:ASP:OD2	2.40	0.52
26:14:58:ARG:HH11	50:1s:68:GLY:H	1.55	0.52
32:1a:955:A:H2'	32:1a:956:A:H5''	1.91	0.52
33:1b:21:ARG:O	33:1b:23:ARG:N	2.37	0.52
35:1d:166:LYS:HA	35:1d:178:VAL:HG11	1.92	0.52
40:1i:21:PRO:HA	40:1i:59:PHE:HA	1.92	0.52
1:2A:601:G:H2'	1:2A:602:C:C6	2.45	0.52
1:2A:703:U:H2'	1:2A:704:C:C6	2.44	0.52
1:2A:2484:U:O2	1:2A:2484:U:H2'	2.08	0.52
4:2E:36:ARG:HG2	4:2E:47:VAL:HG12	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:2F:161:GLU:O	5:2F:165:ARG:HB2	2.09	0.52
8:2I:14:ASP:N	8:2I:17:GLN:OE1	2.37	0.52
11:2P:97:PRO:HD3	11:2P:126:VAL:O	2.08	0.52
29:27:24:THR:O	29:27:28:ARG:HG3	2.09	0.52
31:29:14:CYS:HA	31:29:27:CYS:HB2	1.91	0.52
32:2a:414:C:H2'	32:2a:415:C:C6	2.45	0.52
32:2a:1329:G:O2'	32:2a:1356:G:O6	2.27	0.52
32:2a:1418:G:H2'	32:2a:1419:U:C6	2.45	0.52
36:2e:36:ASP:O	36:2e:38:GLN:N	2.43	0.52
44:2m:20:THR:C	44:2m:22:ILE:H	2.17	0.52
1:1A:2052:A:C6	1:1A:2509:C:H1'	2.44	0.52
1:1A:2429:A:H2'	1:1A:2430:U:H6	1.75	0.52
1:1A:2719:G:H1'	13:1R:71:GLN:HE22	1.72	0.52
10:1O:80:ASP:OD1	15:1T:64:ARG:NH2	2.43	0.52
12:1Q:109:VAL:HG13	12:1Q:113:GLN:HB3	1.92	0.52
28:16:6:ARG:NE	28:16:24:GLU:OE1	2.35	0.52
46:1o:82:ILE:HD12	46:1o:88:ARG:HB2	1.92	0.52
1:2A:44:C:OP2	1:2A:203:G:H5'	2.10	0.52
1:2A:2719:G:H1'	13:2R:71:GLN:HE22	1.75	0.52
8:2I:48:GLU:HG2	8:2I:52:ARG:HH12	1.74	0.52
32:2a:516:A:H61	34:2c:193:TYR:HB2	1.75	0.52
1:1A:964:G:N2	1:1A:2280:A:OP2	2.43	0.52
1:1A:1288:G:O2'	11:1P:7:ARG:NH2	2.42	0.52
4:1E:14:ILE:HD11	4:1E:173:VAL:HG11	1.91	0.52
32:1a:372:G:H2'	32:1a:373:G:C8	2.45	0.52
32:1a:1078:U:P	32:1a:1091:G:H1	2.33	0.52
32:1a:1270:A:N3	32:1a:1334:C:O2'	2.34	0.52
33:1b:189:ASP:OD1	33:1b:189:ASP:N	2.43	0.52
35:1d:167:GLY:H	35:1d:168:ARG:CZ	2.21	0.52
43:1l:33:ARG:HD3	43:1l:62:SER:HB3	1.92	0.52
1:2A:780:A:O2'	1:2A:1681:G:H5'	2.10	0.52
1:2A:2095:U:H2'	1:2A:2096:U:C6	2.44	0.52
1:2A:2657:C:H2'	1:2A:2658:U:O4'	2.09	0.52
8:2I:114:LEU:HD11	8:2I:128:LEU:HD13	1.92	0.52
15:2T:60:THR:HG22	15:2T:77:PRO:HA	1.91	0.52
32:2a:459:G:H2'	32:2a:460:G:C8	2.44	0.52
32:2a:1316:G:OP2	59:2a:1920:HOH:O	2.18	0.52
33:2b:54:THR:O	33:2b:58:ILE:HG13	2.10	0.52
1:1A:173:U:H4'	1:1A:206:A:H4'	1.91	0.52
1:1A:1153:U:O2'	1:1A:1154:C:O5'	2.27	0.52
1:1A:1430:G:O2'	1:1A:1441:U:O2	2.21	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1649:C:OP2	59:1A:4123:HOH:O	2.19	0.52
1:1A:1828:U:H5'	3:1D:259:THR:HG23	1.91	0.52
1:1A:2107:U:H2'	1:1A:2108:G:C8	2.45	0.52
1:1A:2583:A:N7	4:1E:144:ARG:HD2	2.25	0.52
5:1F:140:LEU:HD21	5:1F:170:LEU:HD11	1.92	0.52
7:1H:154:PRO:HB3	7:1H:163:TYR:CE2	2.45	0.52
32:1a:1425:G:O2'	32:1a:1426:G:OP1	2.22	0.52
1:2A:928:G:H1	1:2A:939:C:H42	1.56	0.52
2:2B:95:C:H2'	2:2B:96:U:C6	2.44	0.52
4:2E:134:ILE:HA	4:2E:137:HIS:CD2	2.45	0.52
12:2Q:36:ALA:HB2	12:2Q:103:MET:SD	2.49	0.52
32:2a:1208:C:H2'	44:2m:103:THR:HB	1.91	0.52
32:2a:1258:G:H2'	32:2a:1259:C:H6	1.75	0.52
36:2e:92:LYS:HB3	36:2e:119:LEU:HB2	1.92	0.52
40:2i:4:TYR:O	40:2i:19:LEU:N	2.36	0.52
44:2m:51:ALA:O	44:2m:55:ARG:HB2	2.09	0.52
45:2n:17:LYS:CD	45:2n:17:LYS:H	2.23	0.52
48:2q:67:LYS:O	48:2q:70:ARG:NH1	2.42	0.52
1:1A:1093:A:OP2	1:1A:1154:C:N4	2.42	0.52
1:1A:2297:A:H4'	1:1A:2298:A:O4'	2.10	0.52
41:1j:26:ALA:O	41:1j:81:THR:OG1	2.27	0.52
41:1j:61:GLU:OE2	45:1n:49:HIS:NE2	2.39	0.52
50:1s:83:HIS:O	50:1s:85:LYS:N	2.43	0.52
1:2A:1232:U:H4'	17:2V:79:VAL:HG22	1.91	0.52
1:2A:1783:G:N1	1:2A:1786:G:OP2	2.42	0.52
1:2A:2282:G:H2'	1:2A:2283:U:H6	1.75	0.52
32:2a:160:C:H2'	32:2a:161:G:H8	1.74	0.52
32:2a:989:G:H2'	32:2a:990:G:H8	1.75	0.52
32:2a:1311:A:OP2	52:2u:7:ARG:NH1	2.36	0.52
33:2b:187:LEU:HB3	33:2b:201:ILE:HB	1.91	0.52
1:1A:2121:G:H1	1:1A:2210:U:H3	1.58	0.52
7:1H:98:LEU:HD13	7:1H:125:VAL:HG23	1.92	0.52
19:1X:35:THR:HG23	19:1X:37:THR:H	1.75	0.52
36:1e:75:THR:OG1	36:1e:76:ILE:N	2.41	0.52
2:2B:5:C:H42	2:2B:116:G:H1	1.58	0.52
32:2a:415:C:OP1	32:2a:497:C:O2'	2.26	0.52
33:2b:55:PHE:HD1	33:2b:58:ILE:HD12	1.74	0.52
1:1A:468:A:H1'	1:1A:1245:C:O4'	2.10	0.51
3:1D:68:LYS:HD2	3:1D:70:TRP:CZ2	2.45	0.51
15:1T:16:ARG:NH1	15:1T:18:ASP:OD1	2.43	0.51
34:1c:11:ARG:NH2	34:1c:177:THR:O	2.33	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:1m:20:THR:C	44:1m:22:ILE:H	2.18	0.51
1:2A:898:G:H2'	1:2A:899:G:C8	2.44	0.51
1:2A:1309:G:H2'	1:2A:2035:A:N6	2.25	0.51
5:2F:155:LEU:HD11	5:2F:176:LEU:HD12	1.91	0.51
8:2I:40:THR:O	8:2I:44:LEU:HB2	2.10	0.51
25:23:30:ARG:H	25:23:33:GLN:NE2	2.08	0.51
32:2a:1095:C:C2	34:2c:178:LEU:HD22	2.45	0.51
40:2i:127:LYS:O	40:2i:128:ARG:HG2	2.10	0.51
45:2n:32:SER:O	45:2n:40:CYS:HA	2.09	0.51
51:2t:10:LEU:HB3	51:2t:12:ALA:H	1.74	0.51
1:1A:552:A:N1	1:1A:2063:A:H2'	2.25	0.51
1:1A:1829:G:O2'	3:1D:181:GLU:OE2	2.25	0.51
11:1P:89:ALA:O	11:1P:121:LYS:NZ	2.39	0.51
32:1a:372:G:H2'	32:1a:373:G:H8	1.75	0.51
44:1m:80:ARG:NH2	50:1s:69:HIS:HE1	2.07	0.51
1:2A:237:C:O2	30:28:12:LYS:NZ	2.38	0.51
1:2A:647:G:H2'	1:2A:648:C:C6	2.45	0.51
1:2A:1291:A:OP1	5:2F:38:ARG:NH1	2.42	0.51
5:2F:129:PHE:CD2	5:2F:163:VAL:HG21	2.44	0.51
7:2H:69:ARG:HG3	7:2H:70:THR:N	2.25	0.51
10:2O:64:ARG:NH1	10:2O:81:ASP:OD1	2.42	0.51
14:2S:10:ARG:HG2	14:2S:13:ARG:NH2	2.26	0.51
32:2a:612:G:H2'	32:2a:613:G:C8	2.45	0.51
43:2l:39:VAL:HG11	43:2l:41:ARG:HH11	1.75	0.51
47:2p:58:TYR:O	47:2p:61:SER:OG	2.23	0.51
1:1A:775:G:C6	3:1D:208:LYS:HB2	2.46	0.51
1:1A:1064:U:O2'	1:1A:1066:A:H2	1.93	0.51
4:1E:28:ALA:HB3	4:1E:93:VAL:HG12	1.93	0.51
7:1H:144:VAL:O	7:1H:148:ILE:HG12	2.10	0.51
27:15:16:ARG:HD2	27:15:20:ARG:NH1	2.26	0.51
32:1a:61:A:OP1	32:1a:105:G:N2	2.41	0.51
1:2A:75:C:H42	1:2A:106:G:H1	1.57	0.51
1:2A:552:A:C2	1:2A:2064:C:H4'	2.46	0.51
1:2A:732:G:N2	1:2A:834:A:H61	2.09	0.51
1:2A:1911:A:OP2	59:2A:3653:HOH:O	2.19	0.51
16:2U:78:THR:O	16:2U:117:GLN:NE2	2.44	0.51
18:2W:18:ARG:HG3	18:2W:76:VAL:HB	1.91	0.51
1:1A:1540:A:H2'	1:1A:1541:A:C8	2.45	0.51
1:1A:1616:A:H2'	1:1A:1617:A:C8	2.45	0.51
32:1a:522:G:H5''	43:1l:114:LYS:HB2	1.92	0.51
37:1f:19:LEU:HD11	37:1f:59:TYR:CE1	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:1m:80:ARG:HH22	50:1s:69:HIS:HE1	1.58	0.51
1:2A:1084:G:H1	1:2A:1161:C:H42	1.58	0.51
1:2A:1240:C:H2'	1:2A:1241:G:H8	1.74	0.51
1:2A:1894:U:OP1	1:2A:2421:G:O2'	2.28	0.51
5:2F:117:ARG:HH12	11:2P:1:MET:N	2.09	0.51
22:20:18:ALA:HB3	22:20:20:ARG:HH21	1.75	0.51
23:21:3:LYS:HB2	23:21:61:ARG:NH1	2.25	0.51
32:2a:691:C:H2'	32:2a:692:C:H6	1.74	0.51
32:2a:1243:A:H5'	32:2a:1266:C:OP1	2.11	0.51
33:2b:19:HIS:CE1	33:2b:206:ASP:HB2	2.46	0.51
48:2q:95:TYR:HA	48:2q:98:LEU:HD12	1.92	0.51
1:1A:286:G:N7	1:1A:447:U:H2'	2.26	0.51
1:1A:2059:G:O6	59:1A:4167:HOH:O	2.18	0.51
3:1D:9:TYR:CZ	3:1D:13:ARG:HG2	2.46	0.51
21:1Z:110:GLY:HA3	21:1Z:174:VAL:HG11	1.90	0.51
32:1a:472:A:H2'	32:1a:473:C:O4'	2.10	0.51
32:1a:1043:C:C5	34:1c:2:GLY:HA3	2.45	0.51
32:1a:1172:G:H4'	34:1c:176:HIS:HE1	1.76	0.51
46:1o:55:GLY:HA2	46:1o:58:MET:HE3	1.91	0.51
1:2A:153:G:H1	1:2A:160:C:H42	1.58	0.51
1:2A:320:C:OP2	59:2A:3655:HOH:O	2.19	0.51
1:2A:1214:G:H1	1:2A:1224:C:H42	1.58	0.51
1:2A:1835:U:O2	3:2D:50:THR:HB	2.10	0.51
32:2a:954:G:P	45:2n:32:SER:H	2.33	0.51
33:2b:92:TYR:H	33:2b:151:GLY:HA3	1.76	0.51
50:2s:12:ASP:OD2	50:2s:38:SER:OG	2.26	0.51
1:1A:26:G:N2	1:1A:536:G:H1'	2.26	0.51
8:1I:40:THR:O	8:1I:44:LEU:HB2	2.10	0.51
32:1a:392:G:O2'	32:1a:394:C:OP1	2.19	0.51
1:2A:2310:G:H2'	1:2A:2311:G:C8	2.41	0.51
1:2A:2554:G:H21	1:2A:2657:C:H5''	1.74	0.51
3:2D:68:LYS:HD2	3:2D:70:TRP:CZ2	2.46	0.51
5:2F:20:LEU:HD13	5:2F:21:ALA:H	1.74	0.51
33:2b:50:GLU:O	33:2b:54:THR:OG1	2.20	0.51
34:2c:131:ARG:NH2	34:2c:166:GLU:OE2	2.44	0.51
50:2s:36:ARG:NH2	50:2s:72:GLY:O	2.44	0.51
10:1O:49:ARG:NH2	32:1a:1406:G:OP1	2.41	0.51
32:1a:695:G:H2'	32:1a:696:A:C8	2.46	0.51
32:1a:1265:G:O2'	59:1a:2016:HOH:O	2.19	0.51
32:1a:1329:G:C8	40:1i:107:ARG:HB3	2.45	0.51
35:1d:8:VAL:O	35:1d:10:ARG:N	2.39	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:1h:4:ASP:OD2	39:1h:85:ARG:NH1	2.41	0.51
41:1j:11:PHE:HE1	41:1j:67:THR:HG22	1.76	0.51
44:1m:84:ILE:HG13	44:1m:85:GLY:HA2	1.91	0.51
48:1q:59:ILE:HG22	48:1q:73:VAL:HA	1.93	0.51
1:2A:786:U:H2'	1:2A:787:G:C8	2.45	0.51
1:2A:1361:U:H2'	1:2A:1362:A:C8	2.40	0.51
1:2A:1445:G:H2'	1:2A:1446:G:C8	2.46	0.51
1:2A:1906:A:H2'	1:2A:1907:C:O4'	2.09	0.51
32:2a:571:G:N2	32:2a:738:C:OP2	2.36	0.51
32:2a:1127:G:N2	32:2a:1129:A:H62	2.08	0.51
32:2a:1241:C:C4	32:2a:1242:C:H1'	2.46	0.51
1:1A:1075:G:OP2	12:1Q:128:LYS:NZ	2.40	0.51
1:1A:1520:C:H2'	1:1A:1521:G:C8	2.45	0.51
1:1A:1828:U:H5'	3:1D:259:THR:CG2	2.41	0.51
2:1B:58:A:OP2	59:1B:301:HOH:O	2.20	0.51
14:1S:6:ALA:O	14:1S:10:ARG:HG3	2.09	0.51
21:1Z:158:PRO:HG2	21:1Z:161:VAL:HG11	1.93	0.51
37:1f:97:PHE:O	49:1r:31:LEU:HD23	2.11	0.51
1:2A:2658:U:H2'	1:2A:2659:C:C6	2.46	0.51
21:2Z:10:ARG:HB3	21:2Z:36:LYS:HB3	1.93	0.51
32:2a:425:U:H1'	32:2a:426:A:H5''	1.93	0.51
32:2a:1208:C:H4'	50:2s:80:TYR:OH	2.11	0.51
32:2a:1480:A:H2	32:2a:1483:G:N1	2.09	0.51
40:2i:17:VAL:HG23	40:2i:63:ILE:HG12	1.93	0.51
1:1A:1691:G:H5''	1:1A:1692:C:H5'	1.92	0.51
14:1S:15:ARG:HE	14:1S:88:ASP:CG	2.19	0.51
32:1a:1101:C:H1'	32:1a:1161:A:C5	2.46	0.51
32:1a:1219:C:O2'	32:1a:1282:G:N2	2.43	0.51
39:1h:75:ARG:HH11	39:1h:75:ARG:HB2	1.75	0.51
1:2A:309:C:H2'	1:2A:310:C:H6	1.74	0.51
1:2A:1735:A:OP2	1:2A:1744:A:N6	2.43	0.51
1:2A:2765:A:N3	31:29:15:LYS:NZ	2.52	0.51
12:2Q:57:HIS:HD2	12:2Q:117:ALA:HB2	1.76	0.51
32:2a:603:U:N3	35:2d:134:ASP:OD1	2.39	0.51
33:2b:16:HIS:CD2	33:2b:204:ASN:H	2.29	0.51
33:2b:167:PRO:HG3	33:2b:188:ALA:HB2	1.93	0.51
52:2u:5:ASP:O	52:2u:11:GLY:HA3	2.11	0.51
1:1A:877:G:O2'	11:1P:38:GLN:NE2	2.44	0.51
1:1A:893:U:OP2	59:1A:4168:HOH:O	2.18	0.51
1:1A:2783:C:H2'	1:1A:2784:C:C6	2.46	0.51
32:1a:711:G:N2	32:1a:714:G:OP2	2.43	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:1c:56:ASP:HB2	34:1c:67:THR:HB	1.92	0.51
1:2A:408:G:OP2	59:2A:3654:HOH:O	2.19	0.51
1:2A:2058:G:H2'	1:2A:2059:G:C8	2.46	0.51
2:2B:52:A:N3	2:2B:53:A:N6	2.58	0.51
17:2V:72:VAL:HG13	17:2V:85:LYS:HB3	1.93	0.51
32:2a:453:C:H2'	32:2a:454:G:O4'	2.11	0.51
32:2a:989:G:H2'	32:2a:990:G:C8	2.46	0.51
1:1A:286:G:O2'	1:1A:447:U:OP2	2.19	0.50
1:1A:593:A:OP2	59:1A:4171:HOH:O	2.20	0.50
1:1A:1354:G:O6	59:1A:4169:HOH:O	2.19	0.50
1:1A:1873:C:H5'	3:1D:253:GLN:NE2	2.26	0.50
7:1H:124:GLU:HB2	7:1H:132:ARG:HB3	1.92	0.50
32:1a:504:A:N1	32:1a:520:C:H1'	2.26	0.50
33:1b:231:GLU:H	33:1b:232:PRO:HD2	1.76	0.50
43:1l:84:LEU:HB3	43:1l:104:VAL:HG21	1.92	0.50
1:2A:1403:G:O2'	1:2A:1404:A:H5'	2.11	0.50
1:2A:2278:A:H5''	1:2A:2279:A:C5'	2.41	0.50
6:2G:96:ARG:O	6:2G:99:MET:HB3	2.11	0.50
11:2P:121:LYS:O	11:2P:123:LEU:N	2.45	0.50
16:2U:66:ASN:O	16:2U:70:ARG:HG3	2.11	0.50
33:2b:18:GLY:HA2	33:2b:42:ILE:HG13	1.92	0.50
33:2b:68:ILE:HG12	33:2b:161:ALA:HB3	1.92	0.50
44:2m:78:ILE:O	44:2m:82:MET:N	2.41	0.50
1:2A:483:G:C8	29:27:37:LYS:HG2	2.46	0.50
1:2A:516:A:H2'	1:2A:517:G:O4'	2.11	0.50
1:2A:1093:A:N1	1:2A:1157:G:O2'	2.40	0.50
1:2A:1675:G:H2'	1:2A:1676:C:C6	2.45	0.50
1:2A:2272:C:O2'	1:2A:2273:U:H5'	2.12	0.50
1:2A:2376:G:OP1	22:20:55:ARG:HG2	2.11	0.50
1:2A:2430:U:H5''	30:28:33:ASN:HB2	1.93	0.50
1:2A:2611:A:H2'	1:2A:2612:C:C6	2.46	0.50
7:2H:8:PRO:O	7:2H:69:ARG:NH1	2.44	0.50
11:2P:50:ARG:HD3	30:28:7:HIS:CD2	2.46	0.50
18:2W:79:GLY:HA3	18:2W:100:THR:HG22	1.93	0.50
32:2a:721:A:H2'	32:2a:722:C:C6	2.47	0.50
32:2a:980:G:N7	32:2a:981:G:H1'	2.26	0.50
32:2a:1276:G:H2'	32:2a:1277:G:C8	2.46	0.50
38:2g:51:GLN:O	38:2g:55:GLY:HA2	2.11	0.50
1:1A:216:A:H3'	1:1A:217:A:C5'	2.41	0.50
1:1A:1559:U:H2'	1:1A:1560:C:C6	2.46	0.50
1:1A:2831:G:OP2	59:1A:4170:HOH:O	2.19	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:1N:96:GLU:H	9:1N:96:GLU:CD	2.19	0.50
32:1a:57:U:H2'	32:1a:58:G:C8	2.46	0.50
32:1a:68:C:H2'	32:1a:69:G:H8	1.75	0.50
40:1i:26:VAL:HG22	40:1i:61:ALA:HB3	1.92	0.50
44:1m:3:ARG:HD2	44:1m:9:ILE:HG12	1.92	0.50
1:2A:898:G:H2'	1:2A:899:G:H8	1.75	0.50
1:2A:1856:G:H4'	3:2D:242:ARG:CZ	2.42	0.50
4:2E:52:LEU:O	4:2E:76:ARG:N	2.37	0.50
6:2G:33:ARG:NH1	6:2G:162:THR:OG1	2.45	0.50
9:2N:4:TYR:CD2	16:2U:100:VAL:HG11	2.46	0.50
19:2X:43:VAL:HG21	19:2X:81:VAL:HG11	1.93	0.50
20:2Y:44:ILE:H	20:2Y:44:ILE:CD1	2.21	0.50
21:2Z:134:PRO:C	21:2Z:136:PHE:H	2.20	0.50
33:2b:85:ALA:O	33:2b:89:GLY:N	2.45	0.50
39:2h:20:TYR:HA	39:2h:65:TYR:CZ	2.47	0.50
44:2m:15:VAL:HG12	44:2m:45:VAL:HG22	1.94	0.50
1:1A:2824:C:H5'	27:15:29:THR:HG21	1.94	0.50
3:1D:126:GLN:NE2	3:1D:127:VAL:H	2.09	0.50
6:1G:16:ARG:HG2	6:1G:16:ARG:NH1	2.22	0.50
26:14:69:LYS:HE2	50:1s:20:LEU:HD13	1.93	0.50
32:1a:733:C:H2'	32:1a:734:G:H8	1.76	0.50
32:1a:842:A:H2'	32:1a:843:A:C8	2.46	0.50
32:1a:1278:C:OP1	44:1m:44:ARG:NH2	2.44	0.50
1:2A:15:G:H2'	1:2A:16:G:H8	1.76	0.50
1:2A:1210:U:H2'	1:2A:1211:C:C6	2.46	0.50
2:2B:75:G:N1	59:2B:3101:HOH:O	2.25	0.50
5:2F:129:PHE:O	5:2F:132:VAL:HG13	2.11	0.50
12:2Q:32:TYR:CE1	12:2Q:133:ARG:HG3	2.47	0.50
12:2Q:110:THR:HG23	12:2Q:113:GLN:OE1	2.12	0.50
18:2W:46:PHE:O	18:2W:50:VAL:HG23	2.10	0.50
32:2a:1149:G:N2	32:2a:1152:A:OP2	2.44	0.50
32:2a:1178:U:O3'	59:2a:1924:HOH:O	2.19	0.50
32:2a:1270:A:H2'	32:2a:1271:A:C8	2.46	0.50
36:2e:50:GLU:HB3	36:2e:53:LEU:HD13	1.93	0.50
38:2g:47:CYS:O	38:2g:50:ILE:HG12	2.12	0.50
43:2l:24:VAL:HG21	43:2l:27:LEU:HD22	1.93	0.50
1:1A:2657:C:H2'	1:1A:2658:U:O4'	2.11	0.50
32:1a:521:G:H5''	43:1l:113:ARG:NH1	2.27	0.50
32:1a:909:C:O2	32:1a:1369:G:N1	2.43	0.50
33:1b:74:LYS:HD2	33:1b:166:ASP:HB2	1.93	0.50
34:1c:118:GLN:HA	34:1c:121:ALA:HB3	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:1d:166:LYS:H	35:1d:168:ARG:NH1	2.10	0.50
54:1x:55:PSU:H5'	54:1x:56:C:OP2	2.11	0.50
1:2A:922:C:H2'	1:2A:923:U:O4'	2.12	0.50
1:2A:2660:U:H2'	1:2A:2661:U:C6	2.47	0.50
6:2G:43:LEU:HD12	6:2G:45:GLU:HG3	1.93	0.50
6:2G:136:ARG:HD2	6:2G:136:ARG:C	2.36	0.50
32:2a:1457:C:H2'	32:2a:1458:G:H8	1.77	0.50
36:2e:19:MET:SD	36:2e:24:ARG:HG3	2.52	0.50
42:2k:81:ASP:OD1	42:2k:107:SER:OG	2.27	0.50
1:1A:322:A:N1	1:1A:345:A:O2'	2.40	0.50
1:1A:1765:G:N7	59:1A:4333:HOH:O	2.34	0.50
31:19:12:ASP:OD2	31:19:12:ASP:N	2.44	0.50
32:1a:77:G:C2	32:1a:87:C:N3	2.80	0.50
32:1a:370:A:O4'	32:1a:466:G:N2	2.45	0.50
43:1l:117:ARG:HB3	43:1l:122:THR:HB	1.94	0.50
1:2A:1302:C:H4'	5:2F:83:PHE:CD1	2.47	0.50
1:2A:2698:U:H2'	1:2A:2699:U:O4'	2.12	0.50
6:2G:35:GLU:HG2	6:2G:36:LYS:NZ	2.27	0.50
32:2a:646:G:O2'	32:2a:820:G:OP1	2.29	0.50
32:2a:1203:G:O3'	50:2s:77:THR:OG1	2.22	0.50
54:2x:23:C:H2'	54:2x:24:U:H6	1.75	0.50
1:1A:793:U:O2	1:1A:2035:A:H1'	2.11	0.50
1:1A:2107:U:H2'	1:1A:2108:G:H8	1.76	0.50
1:1A:2254:U:H2'	1:1A:2255:U:C6	2.47	0.50
11:1P:121:LYS:O	11:1P:123:LEU:N	2.44	0.50
18:1W:18:ARG:HG3	18:1W:76:VAL:HB	1.93	0.50
26:14:57:GLU:HB3	26:14:58:ARG:HG2	1.94	0.50
32:1a:110:A:H61	32:1a:309:A:H1'	1.76	0.50
32:1a:1268:A:H2'	32:1a:1269:A:H4'	1.93	0.50
34:1c:58:GLU:HB2	34:1c:65:ALA:HB3	1.93	0.50
54:1x:23:C:H2'	54:1x:24:U:C6	2.46	0.50
1:2A:921:G:O2'	21:2Z:151:HIS:HE1	1.95	0.50
1:2A:1278:C:H2'	1:2A:1279:U:H6	1.77	0.50
1:2A:1475:C:H2'	1:2A:1476:U:C6	2.47	0.50
1:2A:1826:U:H2'	1:2A:1827:C:C6	2.47	0.50
12:2Q:26:TYR:O	12:2Q:67:ARG:NH1	2.43	0.50
30:28:63:PRO:HG2	30:28:64:TYR:CE2	2.46	0.50
32:2a:993:A:H1'	50:2s:34:TRP:HB2	1.93	0.50
34:2c:20:SER:HB3	34:2c:22:TRP:NE1	2.27	0.50
34:2c:164:ARG:HG2	34:2c:165:THR:H	1.77	0.50
1:1A:222:C:H2'	1:1A:223:U:H6	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1066:A:H3'	1:1A:1066:A:H8	1.77	0.50
1:1A:1734:U:O2	1:1A:1746:A:H5'	2.11	0.50
1:1A:2800:C:OP1	4:1E:61:ARG:NH2	2.45	0.50
27:15:16:ARG:HG2	27:15:16:ARG:NH1	2.26	0.50
32:1a:8:G:H5'	32:1a:294:A:O4'	2.11	0.50
32:1a:952:A:H8	32:1a:952:A:OP1	1.94	0.50
32:1a:1287:G:H22	32:1a:1313:G:H1'	1.77	0.50
47:1p:20:VAL:HG21	47:1p:32:TYR:CD2	2.47	0.50
51:1t:87:LYS:O	51:1t:91:LEU:HG	2.11	0.50
1:2A:183:A:H5''	1:2A:184:A:O5'	2.11	0.50
1:2A:2315:G:N2	1:2A:2324:C:H5	2.10	0.50
32:2a:68:C:H2'	32:2a:69:G:C8	2.47	0.50
32:2a:836:G:O6	32:2a:847:G:H3'	2.12	0.50
32:2a:927:A:N6	32:2a:1214:U:H3	2.08	0.50
32:2a:1219:C:O3'	32:2a:1282:G:N2	2.43	0.50
34:2c:181:ASN:ND2	34:2c:204:LEU:HB2	2.27	0.50
34:2c:186:PHE:HB3	34:2c:198:VAL:HG23	1.94	0.50
35:2d:101:LEU:HD12	35:2d:138:TYR:HB3	1.92	0.50
46:2o:39:LEU:HD13	46:2o:56:LEU:HB2	1.94	0.50
1:1A:2828:G:O2'	59:1A:4147:HOH:O	2.15	0.50
2:1B:7:G:H5'	14:1S:29:PHE:CE2	2.46	0.50
12:1Q:59:ARG:HA	12:1Q:60:ARG:NH2	2.26	0.50
43:1l:33:ARG:HG2	43:1l:60:LEU:HG	1.94	0.50
46:1o:15:PHE:CZ	46:1o:84:LYS:HD2	2.46	0.50
1:2A:323:A:H1'	1:2A:342:C:H1'	1.92	0.50
1:2A:2218:U:H1'	1:2A:2219:A:C8	2.47	0.50
7:2H:44:VAL:HB	7:2H:51:ARG:H	1.77	0.50
32:2a:1045:U:H2'	32:2a:1046:C:C6	2.46	0.50
32:2a:1328:A:N1	32:2a:1357:A:H5''	2.26	0.50
32:2a:1330:U:H2'	32:2a:1331:A:H8	1.77	0.50
33:2b:16:HIS:HB2	33:2b:204:ASN:HB2	1.93	0.50
33:2b:92:TYR:CE2	33:2b:150:SER:N	2.80	0.50
39:2h:28:ALA:HB3	39:2h:57:PRO:HB2	1.94	0.50
41:2j:50:ILE:HD11	41:2j:57:LYS:NZ	2.27	0.50
1:1A:1098:C:H42	1:1A:1151:G:H1	1.59	0.49
23:11:4:VAL:HG22	23:11:11:ARG:HB3	1.93	0.49
32:1a:648:G:N2	32:1a:725:G:H1	2.06	0.49
33:1b:21:ARG:HB3	33:1b:38:GLY:O	2.12	0.49
1:2A:1015:C:H2'	1:2A:1016:G:O4'	2.11	0.49
1:2A:1090:A:H5''	1:2A:1092:G:O4'	2.12	0.49
1:2A:2353:C:O2'	1:2A:2385:C:OP1	2.24	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:2R:55:ALA:HB2	13:2R:79:LEU:HD13	1.93	0.49
32:2a:1329:G:C8	40:2i:107:ARG:HB2	2.46	0.49
32:2a:1350:C:O2'	41:2j:48:THR:HG21	2.12	0.49
1:1A:324:G:OP2	20:1Y:84:ARG:NH2	2.45	0.49
38:1g:62:PHE:HA	38:1g:124:LEU:HD22	1.94	0.49
1:2A:454:A:H3'	1:2A:455:A:H8	1.78	0.49
1:2A:2805:G:N2	1:2A:2814:C:H1'	2.28	0.49
7:2H:154:PRO:HB3	7:2H:163:TYR:CE2	2.47	0.49
8:2I:65:ALA:HB1	8:2I:136:VAL:HG11	1.94	0.49
38:2g:26:PHE:CE1	38:2g:30:ILE:HD11	2.47	0.49
46:2o:25:THR:HG21	46:2o:70:LEU:HB2	1.93	0.49
1:1A:206:A:C2	1:1A:223:U:H4'	2.47	0.49
1:1A:935:C:O2'	1:1A:936:A:O4'	2.30	0.49
13:1R:36:THR:HG22	13:1R:37:THR:H	1.76	0.49
18:1W:86:LEU:HD22	18:1W:96:ILE:HD11	1.94	0.49
20:1Y:11:ASP:OD2	20:1Y:97:ARG:NH2	2.44	0.49
32:1a:502:C:O2'	32:1a:514:G:N2	2.43	0.49
32:1a:1435:G:H2'	32:1a:1436:G:H8	1.77	0.49
1:2A:346:G:O2'	1:2A:1249:U:N3	2.44	0.49
1:2A:644:G:N3	1:2A:644:G:H5'	2.27	0.49
5:2F:21:ALA:HB3	5:2F:22:ALA:HA	1.93	0.49
32:2a:484:G:N2	32:2a:530:G:H1'	2.26	0.49
32:2a:538:C:H2'	32:2a:539:C:C6	2.47	0.49
35:2d:108:LEU:HD21	35:2d:183:GLY:HA3	1.93	0.49
47:2p:53:VAL:HG13	47:2p:79:VAL:HG22	1.94	0.49
3:1D:72:LYS:HE3	3:1D:75:ILE:HD12	1.93	0.49
14:1S:61:ASN:O	14:1S:65:VAL:HG23	2.13	0.49
32:1a:734:G:H1'	46:1o:22:THR:HG23	1.95	0.49
36:1e:100:VAL:HG22	36:1e:118:ILE:HG22	1.94	0.49
44:1m:78:ILE:HG22	44:1m:82:MET:HE2	1.93	0.49
45:1n:26:ARG:HH11	45:1n:43:CYS:HB2	1.76	0.49
1:2A:2480:A:H2'	1:2A:2481:G:O4'	2.12	0.49
1:2A:2622:U:C4	27:25:3:LYS:HG2	2.47	0.49
6:2G:16:ARG:NH2	6:2G:31:VAL:HG13	2.28	0.49
32:2a:420:G:H2'	32:2a:421:G:C8	2.43	0.49
32:2a:500:U:O2'	32:2a:503:C:N3	2.41	0.49
32:2a:599:C:H2'	32:2a:600:G:O4'	2.13	0.49
32:2a:909:C:H42	32:2a:1369:G:H1	1.60	0.49
32:2a:981:G:N2	32:2a:1021:C:C2	2.80	0.49
1:1A:1067:G:N2	1:1A:1068:U:O4	2.42	0.49
1:1A:1700:A:OP1	59:1A:4172:HOH:O	2.20	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1B:57:A:H1'	6:1G:29:TRP:HB2	1.93	0.49
3:1D:17:THR:O	3:1D:211:ARG:NH2	2.44	0.49
7:1H:7:LEU:HD12	7:1H:8:PRO:HD2	1.94	0.49
13:1R:51:LEU:HD22	13:1R:66:VAL:HG22	1.94	0.49
13:1R:55:ALA:HB2	13:1R:79:LEU:HD13	1.94	0.49
32:1a:77:G:N1	32:1a:87:C:N4	2.29	0.49
32:1a:476:G:H2'	32:1a:477:G:O4'	2.13	0.49
32:1a:1073:U:H2'	32:1a:1074:U:C6	2.46	0.49
32:1a:1328:A:N6	32:1a:1358:A:OP2	2.42	0.49
33:1b:62:ALA:HB2	33:1b:222:ILE:HG23	1.95	0.49
33:1b:87:ARG:NH1	33:1b:233:SER:OG	2.45	0.49
35:1d:155:LEU:HB3	35:1d:158:ILE:HG12	1.95	0.49
1:2A:853:U:OP2	11:2P:41:ARG:NH2	2.45	0.49
1:2A:895:A:H2	25:23:24:LYS:HB3	1.77	0.49
16:2U:97:ASP:OD1	16:2U:101:ARG:HD2	2.13	0.49
23:21:65:SER:OG	23:21:66:HIS:ND1	2.35	0.49
26:24:61:ARG:NH2	50:2s:9:VAL:HG21	2.28	0.49
32:2a:1158:A:H2'	32:2a:1159:G:C8	2.48	0.49
33:2b:118:LEU:HG	33:2b:142:LEU:HD13	1.94	0.49
34:2c:178:LEU:H	34:2c:178:LEU:HD13	1.77	0.49
1:1A:8:U:H3	1:1A:2640:A:H2	1.61	0.49
1:1A:1934:A:C5	32:1a:1472:G:H5''	2.47	0.49
1:1A:2205:G:H5'	1:1A:2206:C:OP2	2.12	0.49
1:1A:2880:C:OP1	59:1A:4174:HOH:O	2.20	0.49
15:1T:60:THR:HG22	15:1T:77:PRO:HA	1.93	0.49
16:1U:66:ASN:O	16:1U:70:ARG:HG3	2.12	0.49
19:1X:41:ASN:O	19:1X:45:THR:HG23	2.13	0.49
32:1a:295:G:H2'	32:1a:296:A:C8	2.47	0.49
32:1a:584:C:H4'	39:1h:128:GLY:O	2.13	0.49
33:1b:187:LEU:HA	33:1b:201:ILE:HB	1.94	0.49
41:1j:37:PRO:HA	41:1j:72:VAL:HG12	1.94	0.49
46:1o:84:LYS:O	46:1o:84:LYS:HD3	2.12	0.49
51:1t:56:MET:HE3	51:1t:88:VAL:HG21	1.94	0.49
54:1x:17:C:H2'	54:1x:17(A):U:H2'	1.94	0.49
1:2A:810:A:H5'	3:2D:210:GLY:CA	2.42	0.49
1:2A:1409:G:P	23:21:3:LYS:HG3	2.52	0.49
3:2D:227:ASN:O	3:2D:230:ASP:N	2.45	0.49
32:2a:979:A:H2'	32:2a:980:G:H8	1.78	0.49
32:2a:1097:C:O2'	45:2n:60:SER:O	2.25	0.49
38:2g:42:ILE:HD12	38:2g:43:PHE:H	1.77	0.49
47:2p:5:ARG:HH12	47:2p:28:ARG:HA	1.76	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2004:C:H4'	1:1A:2617:C:H4'	1.94	0.49
32:1a:440:G:H2'	32:1a:441:G:C8	2.48	0.49
32:1a:535:U:H2'	32:1a:536:U:C6	2.47	0.49
32:1a:1335:G:H2'	32:1a:1336:C:H6	1.76	0.49
32:1a:1435:G:H2'	32:1a:1436:G:C8	2.48	0.49
38:1g:91:VAL:HG13	38:1g:95:ARG:HD3	1.95	0.49
1:2A:745:A:H2'	1:2A:746:G:O4'	2.12	0.49
1:2A:1240:C:H2'	1:2A:1241:G:C8	2.48	0.49
1:2A:1765:G:H2'	1:2A:1768:G:O6	2.12	0.49
1:2A:2565:U:H2'	1:2A:2566:U:C6	2.46	0.49
7:2H:54:ARG:HB3	7:2H:65:HIS:CG	2.47	0.49
21:2Z:150:LEU:HD11	21:2Z:172:ALA:HB3	1.94	0.49
24:22:32:LEU:HD22	24:22:36:ARG:HH11	1.78	0.49
32:2a:976:G:N2	32:2a:1026:C:N3	2.51	0.49
32:2a:1091:G:H5'	34:2c:176:HIS:CD2	2.48	0.49
32:2a:1269:A:H2	32:2a:1335:G:N3	2.10	0.49
32:2a:1306:A:H4'	32:2a:1344:C:H4'	1.95	0.49
44:2m:73:GLU:O	44:2m:77:ASN:HB2	2.13	0.49
44:2m:102:ARG:HG2	44:2m:103:THR:N	2.26	0.49
1:1A:301:A:H2'	1:1A:302:C:C6	2.48	0.49
1:1A:330:G:H21	1:1A:353:A:H62	1.59	0.49
1:1A:2481:G:O6	1:1A:2487:A:O2'	2.19	0.49
2:1B:50:G:H5''	14:1S:61:ASN:HD22	1.77	0.49
31:19:27:CYS:SG	31:19:28:GLU:N	2.84	0.49
32:1a:835:C:H2'	32:1a:836:G:O4'	2.13	0.49
32:1a:902:C:O2'	32:1a:1480:A:N6	2.45	0.49
32:1a:963:C:H2'	32:1a:964:A:C8	2.48	0.49
33:1b:16:HIS:HD2	33:1b:203:GLY:HA3	1.78	0.49
1:2A:118:G:H4'	1:2A:148:A:H5'	1.93	0.49
1:2A:792:A:H2'	1:2A:2623:C:H5''	1.94	0.49
1:2A:861:C:H2'	1:2A:862:C:H6	1.78	0.49
1:2A:964:G:N2	1:2A:2280:A:OP2	2.46	0.49
1:2A:2518:C:H4'	55:2z:1:VAL:O	2.12	0.49
1:2A:2554:G:H2'	1:2A:2555:G:C8	2.47	0.49
2:2B:32:C:H42	2:2B:50:G:H1	1.60	0.49
8:2I:31:LEU:HD21	8:2I:38:LEU:HG	1.95	0.49
17:2V:31:ALA:O	17:2V:61:VAL:HG12	2.13	0.49
32:2a:914:C:H2'	32:2a:915:A:O4'	2.12	0.49
32:2a:1067:G:H5'	32:2a:1085:A:OP2	2.11	0.49
32:2a:1121:G:C6	32:2a:1123:C:H1'	2.47	0.49
33:2b:71:VAL:O	33:2b:165:VAL:HG22	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:2c:127:ARG:NH2	34:2c:192:THR:OG1	2.46	0.49
38:2g:42:ILE:HG22	38:2g:117:ALA:HB2	1.94	0.49
40:2i:53:VAL:O	40:2i:55:ALA:N	2.46	0.49
43:2l:24:VAL:HG23	43:2l:98:TYR:HE1	1.76	0.49
54:2x:61:C:H2'	54:2x:62:C:C6	2.46	0.49
1:1A:1231:G:H5''	17:1V:81:TYR:CE1	2.48	0.49
5:1F:129:PHE:CD1	5:1F:163:VAL:HG21	2.47	0.49
14:1S:10:ARG:HH21	14:1S:91:PRO:HB2	1.78	0.49
26:14:63:TYR:N	26:14:63:TYR:CD1	2.81	0.49
32:1a:90:U:C2'	32:1a:91:G:H5'	2.43	0.49
32:1a:964:A:H1'	50:1s:54:GLY:O	2.13	0.49
32:1a:1330:U:H4'	40:1i:120:ARG:HD2	1.94	0.49
35:1d:61:LYS:HD2	35:1d:207:TYR:OH	2.13	0.49
1:2A:345:A:OP2	5:2F:169:ASN:HB2	2.13	0.49
1:2A:610:U:H2'	1:2A:611:C:C6	2.47	0.49
1:2A:863:C:O2'	1:2A:885:U:H5''	2.13	0.49
1:2A:1333:U:O4	13:2R:106:GLY:HA3	2.13	0.49
1:2A:2389:A:H4'	14:2S:23:ARG:HH11	1.78	0.49
1:2A:2830:A:C2	1:2A:2831:G:C4	3.00	0.49
10:2O:49:ARG:NH1	32:2a:1406:G:OP1	2.46	0.49
32:2a:262:G:H5''	32:2a:264:C:H41	1.78	0.49
32:2a:1274:U:H2'	32:2a:1275:G:O4'	2.13	0.49
32:2a:1305:G:H4'	32:2a:1345:C:C2	2.48	0.49
32:2a:1355:U:H2'	32:2a:1356:G:O4'	2.12	0.49
35:2d:119:GLN:HG3	35:2d:123:HIS:CD2	2.48	0.49
44:2m:39:ILE:HD12	44:2m:56:LEU:HD13	1.94	0.49
1:1A:1222:C:H2'	1:1A:1223:C:C6	2.47	0.49
1:1A:2535:G:N7	59:1A:4346:HOH:O	2.35	0.49
6:1G:77:ILE:HG22	6:1G:80:PHE:H	1.78	0.49
19:1X:11:PRO:HB3	19:1X:92:LEU:HD11	1.95	0.49
26:14:33:VAL:HG12	26:14:34:GLU:H	1.78	0.49
32:1a:295:G:C6	32:1a:296:A:C6	3.01	0.49
32:1a:415:C:OP1	32:1a:497:C:O2'	2.25	0.49
32:1a:798:A:H2'	32:1a:800:A:H5''	1.94	0.49
32:1a:1056:U:O2'	33:1b:104:ASN:OD1	2.29	0.49
33:1b:220:ASP:O	33:1b:223:ILE:HG12	2.12	0.49
35:1d:100:ARG:NH1	35:1d:137:SER:OG	2.46	0.49
1:2A:2309:A:H2'	1:2A:2310:G:O4'	2.13	0.49
1:2A:2333:A:H2'	1:2A:2334:G:O4'	2.12	0.49
5:2F:101:LEU:HD12	5:2F:102:PRO:HD2	1.95	0.49
32:2a:98:G:N7	51:2t:14:LYS:NZ	2.57	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:841:U:O2'	32:2a:843:A:N7	2.36	0.49
35:2d:176:LEU:HA	35:2d:183:GLY:HA2	1.95	0.49
37:2f:10:LEU:HB2	37:2f:59:TYR:HB3	1.95	0.49
54:2x:19:G:C4	54:2x:57:A:C2	3.01	0.49
1:1A:2480:A:O3'	59:1A:4173:HOH:O	2.20	0.48
20:1Y:12:THR:HG1	20:1Y:26:LYS:HZ3	1.55	0.48
32:1a:17:A:O2'	36:1e:16:THR:HB	2.13	0.48
32:1a:265:C:H2'	32:1a:266:A:H8	1.77	0.48
32:1a:952:A:P	45:1n:41:ARG:HH12	2.35	0.48
33:1b:16:HIS:O	33:1b:18:GLY:N	2.45	0.48
34:1c:6:HIS:CD2	34:1c:8:ILE:HB	2.48	0.48
35:1d:107:ARG:HH12	35:1d:194:LEU:HG	1.78	0.48
44:1m:87:TYR:O	44:1m:91:ARG:HG2	2.13	0.48
1:2A:2328:C:H2'	1:2A:2329:G:H8	1.77	0.48
1:2A:2387:A:H8	1:2A:2387:A:OP1	1.96	0.48
3:2D:77:ALA:HA	3:2D:97:TYR:HA	1.95	0.48
10:2O:17:ARG:HG2	10:2O:47:ILE:HG23	1.95	0.48
32:2a:176:G:N2	32:2a:177:U:O4	2.40	0.48
49:2r:65:ILE:O	49:2r:69:THR:HG23	2.12	0.48
1:1A:810:A:H2	3:1D:219:PRO:HG3	1.78	0.48
3:1D:71:ASP:CB	3:1D:103:ARG:HH22	2.26	0.48
5:1F:62:ARG:HD3	59:1F:412:HOH:O	2.13	0.48
7:1H:159:GLU:HG3	7:1H:169:VAL:HG11	1.95	0.48
15:1T:65:LYS:HE2	15:1T:67:SER:HB2	1.95	0.48
1:2A:94:G:H4'	24:22:48:HIS:CD2	2.47	0.48
1:2A:555:C:H4'	1:2A:556:A:H5''	1.94	0.48
1:2A:1070:G:O2'	59:2A:3630:HOH:O	2.18	0.48
1:2A:1937:A:H2'	1:2A:1938:U:O4'	2.13	0.48
1:2A:2760:A:H5'	7:2H:4:ILE:HD12	1.94	0.48
2:2B:3:C:H2'	2:2B:4:C:C6	2.48	0.48
2:2B:55:U:H1'	6:2G:29:TRP:HE1	1.77	0.48
6:2G:50:ALA:O	6:2G:52:ILE:N	2.46	0.48
32:2a:57:U:H2'	32:2a:58:G:C8	2.48	0.48
32:2a:422:G:OP1	35:2d:36:ARG:NH1	2.44	0.48
32:2a:504:A:N1	32:2a:520:C:H1'	2.27	0.48
32:2a:955:A:O3'	32:2a:958:C:N4	2.46	0.48
32:2a:1219:C:O2'	32:2a:1282:G:N1	2.41	0.48
33:2b:144:ARG:HG2	33:2b:148:TYR:HE2	1.78	0.48
40:2i:4:TYR:CE2	40:2i:88:TYR:HA	2.48	0.48
41:2j:55:LYS:HE3	41:2j:56:HIS:CE1	2.47	0.48
42:2k:52:GLY:H	42:2k:55:LYS:HE3	1.77	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1185:U:OP1	9:1N:25:ARG:NH1	2.46	0.48
1:1A:1735:A:N6	1:1A:1744:A:H2	2.04	0.48
32:1a:134:G:N2	32:1a:220:C:O2	2.39	0.48
32:1a:453:C:H2'	32:1a:454:G:O4'	2.13	0.48
32:1a:524:G:H2'	32:1a:525:G:O4'	2.14	0.48
32:1a:1302:C:OP1	50:1s:70:LYS:NZ	2.46	0.48
37:1f:21:LEU:O	37:1f:24:GLU:HB3	2.12	0.48
38:1g:153:HIS:ND1	42:1k:58:PRO:HD2	2.28	0.48
44:1m:84:ILE:HD12	50:1s:74:PHE:HZ	1.78	0.48
49:1r:24:ALA:C	49:1r:26:LEU:H	2.19	0.48
51:1t:47:GLY:HA2	51:1t:48:LYS:C	2.38	0.48
1:2A:54:A:H2'	1:2A:55:C:O4'	2.13	0.48
1:2A:919:G:N2	1:2A:950:U:O2	2.46	0.48
1:2A:1000:G:H2'	1:2A:1001:A:H2'	1.94	0.48
1:2A:1322:G:O2'	13:2R:24:GLN:HG2	2.13	0.48
1:2A:1536:G:H2'	1:2A:1537:G:H8	1.79	0.48
1:2A:1873:C:H2'	1:2A:1874:C:C6	2.48	0.48
1:2A:2282:G:H2'	1:2A:2283:U:C6	2.48	0.48
4:2E:174:ASP:OD1	4:2E:175:VAL:N	2.45	0.48
14:2S:61:ASN:O	14:2S:65:VAL:HG23	2.13	0.48
32:2a:502:C:O2'	32:2a:514:G:N2	2.46	0.48
32:2a:573:C:H2'	32:2a:574:C:C6	2.48	0.48
32:2a:1038:A:N3	34:2c:156:ARG:HD2	2.29	0.48
32:2a:1315:A:H2'	32:2a:1316:G:O4'	2.13	0.48
33:2b:47:THR:O	33:2b:51:LEU:N	2.47	0.48
35:2d:13:ARG:HB2	35:2d:40:PRO:HD3	1.95	0.48
44:2m:13:LYS:HA	44:2m:44:ARG:HH21	1.79	0.48
16:1U:8:VAL:O	16:1U:12:ARG:HG3	2.13	0.48
32:1a:90:U:N3	32:1a:91:G:N7	2.62	0.48
44:1m:11:ARG:HB3	44:1m:11:ARG:HH11	1.78	0.48
44:1m:76:ALA:HA	44:1m:79:LYS:HB3	1.94	0.48
1:2A:26:G:N2	1:2A:536:G:H1'	2.29	0.48
1:2A:766:C:H2'	1:2A:767:C:C6	2.48	0.48
1:2A:955:A:N3	1:2A:2275:C:O2'	2.39	0.48
1:2A:993:C:H2'	1:2A:994:G:C8	2.49	0.48
1:2A:1759:U:H2'	1:2A:1760:G:H8	1.77	0.48
1:2A:1960:U:OP1	1:2A:2615:U:O2'	2.31	0.48
1:2A:2415:C:O3'	11:2P:77:ARG:NH2	2.47	0.48
1:2A:2588:A:H5'	27:25:3:LYS:HD2	1.95	0.48
3:2D:228:PRO:HD3	3:2D:235:GLY:N	2.29	0.48
6:2G:41:GLN:NE2	6:2G:154:GLY:O	2.45	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:2G:64:THR:HB	6:2G:94:LEU:HD11	1.95	0.48
6:2G:179:PRO:HG3	26:24:43:TYR:OH	2.14	0.48
7:2H:3:ARG:NH1	7:2H:6:ARG:H	2.10	0.48
7:2H:30:LYS:NZ	7:2H:81:GLU:O	2.33	0.48
32:2a:901:A:OP1	36:2e:21:ALA:HB2	2.14	0.48
40:2i:65:VAL:HG21	40:2i:73:GLN:HB3	1.95	0.48
46:2o:16:ALA:HB1	46:2o:21:ASP:HB3	1.95	0.48
1:1A:1643:C:H2'	1:1A:1644:C:H6	1.79	0.48
1:1A:2708:G:OP1	59:1A:4176:HOH:O	2.20	0.48
8:1I:106:GLY:HA2	8:1I:107:VAL:O	2.13	0.48
32:1a:924:A:H2'	32:1a:925:G:C8	2.48	0.48
40:1i:58:HIS:H	40:1i:58:HIS:CD2	2.30	0.48
1:2A:1330:G:N2	1:2A:1373:G:H5''	2.29	0.48
1:2A:1887:G:O2'	1:2A:1906:A:N6	2.42	0.48
25:23:12:PRO:HB2	25:23:20:LYS:HG2	1.95	0.48
32:2a:1105:U:C4	32:2a:1106:A:N7	2.81	0.48
42:2k:22:HIS:HB3	42:2k:29:ILE:HB	1.94	0.48
1:1A:714:G:H5'	1:1A:715:G:OP2	2.13	0.48
1:1A:740:U:OP1	3:1D:59:LYS:NZ	2.46	0.48
1:1A:942:C:H2'	1:1A:943:C:C6	2.49	0.48
6:1G:98:ARG:CZ	26:14:1:MET:HE3	2.43	0.48
11:1P:82:GLY:HA2	11:1P:113:LYS:O	2.14	0.48
32:1a:401:U:O2'	32:1a:482:U:H5'	2.14	0.48
32:1a:451:C:H2'	32:1a:452:C:C6	2.48	0.48
32:1a:582:U:H2'	32:1a:583:C:C6	2.42	0.48
32:1a:825:U:C5	32:1a:826:C:H1'	2.49	0.48
32:1a:953:A:H4'	32:1a:954:G:C5'	2.39	0.48
32:1a:1093:A:H8	32:1a:1093:A:O5'	1.96	0.48
32:1a:1335:G:H2'	32:1a:1336:C:C6	2.48	0.48
34:1c:115:LEU:H	34:1c:115:LEU:HD13	1.78	0.48
1:2A:661:A:H8	11:2P:117:GLU:HG3	1.78	0.48
1:2A:2205:G:H2'	1:2A:2206:C:C6	2.48	0.48
1:2A:2465:G:H1'	59:2A:3701:HOH:O	2.14	0.48
2:2B:72:G:O2'	2:2B:105:A:N6	2.47	0.48
3:2D:73:VAL:HG13	3:2D:120:GLY:HA3	1.95	0.48
20:2Y:44:ILE:HA	20:2Y:63:LYS:O	2.13	0.48
32:2a:524:G:H2'	32:2a:525:G:C8	2.49	0.48
32:2a:1166:G:H2'	32:2a:1167:G:H8	1.79	0.48
32:2a:1287:G:O2'	32:2a:1288:A:OP2	2.29	0.48
32:2a:1394:C:H2'	32:2a:1395:C:C6	2.49	0.48
1:1A:271:U:H4'	8:1I:50:ARG:NH1	2.28	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:312:A:N6	1:1A:374:G:O2'	2.43	0.48
1:1A:720:G:O2'	5:1F:74:ARG:HD3	2.13	0.48
1:1A:1833:A:O2'	3:1D:259:THR:HG21	2.14	0.48
1:1A:2405:C:OP2	30:18:30:ARG:NH1	2.46	0.48
1:1A:2518:C:H4'	55:1z:1:VAL:O	2.14	0.48
3:1D:145:VAL:HG12	3:1D:146:GLU:O	2.14	0.48
8:1I:93:THR:HG22	8:1I:119:PRO:HB3	1.95	0.48
21:1Z:180:VAL:O	21:1Z:183:LEU:HB2	2.14	0.48
24:12:29:LYS:HG2	24:12:57:ILE:HD13	1.95	0.48
48:1q:67:LYS:C	48:1q:69:LYS:H	2.22	0.48
1:2A:875:A:N7	1:2A:2259:C:H5'	2.28	0.48
1:2A:1673:G:H2'	1:2A:1674:U:C6	2.48	0.48
1:2A:1756:C:H2'	1:2A:1757:C:C6	2.48	0.48
1:2A:2854:G:H2'	1:2A:2855:G:C8	2.49	0.48
32:2a:1200:C:H2'	32:2a:1201:U:C6	2.48	0.48
35:2d:74:GLN:NE2	35:2d:137:SER:OG	2.47	0.48
37:2f:11:ASN:ND2	37:2f:84:ASN:OD1	2.44	0.48
43:2l:117:ARG:CZ	43:2l:117:ARG:HB2	2.42	0.48
50:2s:53:ASN:HB2	50:2s:77:THR:HA	1.94	0.48
32:1a:1382:C:C2	32:1a:1384:G:C5	3.02	0.48
1:2A:232:A:C2	1:2A:243:A:C4	3.02	0.48
1:2A:2384:G:H2'	1:2A:2385:C:C6	2.49	0.48
1:2A:2590:C:H4'	4:2E:134:ILE:HG12	1.95	0.48
11:2P:38:GLN:HG2	11:2P:45:LEU:N	2.29	0.48
12:2Q:58:PHE:CZ	12:2Q:109:VAL:HG21	2.49	0.48
21:2Z:100:VAL:HG21	21:2Z:134:PRO:HG2	1.96	0.48
32:2a:522:G:H2'	32:2a:523:A:H8	1.79	0.48
32:2a:677:G:H2'	32:2a:678:A:C8	2.48	0.48
32:2a:1325:G:H2'	32:2a:1326:C:C6	2.48	0.48
32:2a:1438:A:H2'	32:2a:1439:G:O4'	2.13	0.48
33:2b:13:ALA:HA	33:2b:15:VAL:N	2.29	0.48
35:2d:112:VAL:HG22	35:2d:116:GLN:OE1	2.14	0.48
1:1A:2759:G:O6	1:1A:2767:C:H5''	2.14	0.48
4:1E:73:GLU:H	4:1E:73:GLU:HG3	1.44	0.48
32:1a:5:U:O4	39:1h:105:ARG:HD3	2.14	0.48
32:1a:385:A:C6	32:1a:386:C:H1'	2.49	0.48
32:1a:1184:G:H21	45:1n:43:CYS:HB3	1.78	0.48
41:1j:38:ILE:HD11	41:1j:71:LEU:HD23	1.96	0.48
1:2A:1083:C:N4	1:2A:1162:G:H1	2.05	0.48
1:2A:1887:G:C6	1:2A:1888:G:C6	3.02	0.48
7:2H:90:LYS:NZ	7:2H:159:GLU:OE2	2.45	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:2O:77:ILE:HB	15:2T:74:ARG:HD3	1.96	0.48
14:2S:67:ARG:O	14:2S:71:ARG:HG3	2.14	0.48
30:28:62:LEU:HB3	30:28:65:GLU:HG2	1.95	0.48
32:2a:218:U:H2'	32:2a:219:U:C6	2.48	0.48
32:2a:1310:C:H3'	52:2u:7:ARG:HH22	1.78	0.48
34:2c:186:PHE:CD1	34:2c:198:VAL:HB	2.44	0.48
51:2t:18:GLN:O	51:2t:22:ARG:HG3	2.14	0.48
32:1a:1243:A:H3'	32:1a:1244:C:C6	2.49	0.48
36:1e:91:LEU:HG	36:1e:118:ILE:HD11	1.95	0.48
1:2A:1423:A:O2'	1:2A:1424:A:H5''	2.14	0.48
1:2A:1643:C:H2'	1:2A:1644:C:H6	1.79	0.48
1:2A:2080:A:O2'	5:2F:69:HIS:HD2	1.95	0.48
1:2A:2533:U:O2'	1:2A:2658:U:OP1	2.19	0.48
1:2A:2715:C:H2'	1:2A:2716:A:O4'	2.14	0.48
1:2A:2845:U:H2'	1:2A:2846:G:C8	2.48	0.48
11:2P:38:GLN:HG2	11:2P:45:LEU:H	1.79	0.48
30:28:60:LEU:HD23	30:28:60:LEU:HA	1.74	0.48
32:2a:184:G:H2'	32:2a:185:C:C6	2.49	0.48
32:2a:845:G:H8	32:2a:845:G:OP2	1.97	0.48
32:2a:953:A:H61	41:2j:48:THR:HG23	1.79	0.48
32:2a:981:G:H2'	32:2a:982:G:C8	2.48	0.48
32:2a:1106:A:H4'	41:2j:37:PRO:HD2	1.95	0.48
39:2h:35:ILE:HG12	39:2h:111:ILE:HD11	1.94	0.48
41:2j:50:ILE:HD11	41:2j:57:LYS:HZ2	1.78	0.48
1:1A:26:G:H22	1:1A:536:G:H1'	1.79	0.47
1:1A:661:A:H8	11:1P:117:GLU:HG3	1.79	0.47
1:1A:1223:C:H2'	1:1A:1224:C:H6	1.79	0.47
1:1A:1822:G:H5'	3:1D:205:VAL:HG13	1.96	0.47
1:1A:2575:A:C2	1:1A:2658:U:H4'	2.48	0.47
1:1A:2881:G:O2'	1:1A:2882:A:H5'	2.13	0.47
20:1Y:35:TYR:CE2	20:1Y:69:ALA:HB3	2.49	0.47
32:1a:155:A:N6	32:1a:341:C:OP2	2.46	0.47
33:1b:142:LEU:O	33:1b:146:GLN:HG3	2.14	0.47
33:1b:222:ILE:O	33:1b:226:ARG:HG2	2.14	0.47
36:1e:6:PHE:HB3	36:1e:34:VAL:HG22	1.94	0.47
1:2A:56:G:O2'	1:2A:71:A:N1	2.40	0.47
1:2A:363:A:H2'	1:2A:364:G:O4'	2.13	0.47
1:2A:1450:U:H2'	1:2A:1451:U:C6	2.48	0.47
1:2A:1890:G:H8	1:2A:1890:G:OP2	1.97	0.47
5:2F:150:GLY:HA2	5:2F:172:TRP:CE3	2.49	0.47
7:2H:13:LYS:HA	7:2H:14:GLY:HA2	1.51	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:2P:44:GLY:CA	11:2P:45:LEU:HB2	2.44	0.47
14:2S:34:HIS:ND1	14:2S:53:SER:OG	2.45	0.47
15:2T:23:ARG:HG3	15:2T:120:ARG:NH1	2.29	0.47
15:2T:27:THR:HB	15:2T:89:VAL:HG22	1.96	0.47
17:2V:80:GLN:NE2	59:2V:201:HOH:O	2.47	0.47
34:2c:156:ARG:NH2	34:2c:161:GLU:HA	2.25	0.47
41:2j:81:THR:HA	41:2j:84:GLN:OE1	2.13	0.47
44:2m:102:ARG:HG2	44:2m:104:ARG:H	1.78	0.47
1:1A:552:A:C2	1:1A:2063:A:H2'	2.48	0.47
18:1W:71:VAL:HA	18:1W:107:LEU:HD12	1.95	0.47
20:1Y:12:THR:OG1	20:1Y:26:LYS:NZ	2.30	0.47
26:14:40:HIS:O	26:14:43:TYR:N	2.46	0.47
32:1a:399:C:OP2	35:1d:74:GLN:NE2	2.41	0.47
32:1a:531:A:H5'	59:1a:2075:HOH:O	2.14	0.47
32:1a:613:G:H2'	32:1a:614:G:O4'	2.13	0.47
32:1a:1095:C:O2	34:1c:179:ARG:HG2	2.14	0.47
43:1l:34:ARG:NH2	59:1l:301:HOH:O	2.46	0.47
1:2A:508:A:O2'	20:2Y:49:VAL:O	2.25	0.47
1:2A:2077:G:OP2	59:2A:3614:HOH:O	2.20	0.47
1:2A:2347:A:H61	22:20:43:THR:HG22	1.79	0.47
1:2A:2386:G:O2'	1:2A:2388:A:N7	2.35	0.47
5:2F:126:VAL:HG21	5:2F:129:PHE:CZ	2.49	0.47
21:2Z:54:HIS:ND1	21:2Z:101:PRO:HG3	2.29	0.47
32:2a:503:C:H2'	32:2a:504:A:O4'	2.15	0.47
32:2a:1223:G:H2'	32:2a:1224:C:C6	2.48	0.47
54:2x:15:G:H2'	54:2x:59:A:N1	2.29	0.47
1:1A:905:G:O2'	1:1A:961:G:O6	2.28	0.47
1:1A:2358:C:O2'	28:16:21:TYR:OH	2.30	0.47
1:1A:2700:U:H4'	1:1A:2701:C:H5'	1.96	0.47
2:1B:90:A:N7	2:1B:91:C:H1'	2.29	0.47
6:1G:106:LEU:HD12	6:1G:110:ALA:HB3	1.95	0.47
8:1I:79:ILE:HB	8:1I:144:VAL:HG12	1.97	0.47
32:1a:355:U:H2'	32:1a:356:A:C8	2.49	0.47
32:1a:1281:A:H5''	32:1a:1281:A:N3	2.29	0.47
32:1a:1482:G:OP1	32:1a:1485:A:H4'	2.14	0.47
35:1d:108:LEU:HD11	35:1d:174:LEU:HD22	1.96	0.47
37:1f:80:ARG:NH1	37:1f:88:VAL:O	2.47	0.47
1:2A:2832:A:OP1	4:2E:113:PHE:HB2	2.14	0.47
2:2B:2:C:H2'	2:2B:3:C:H6	1.80	0.47
15:2T:39:ARG:NH2	32:2a:341:C:OP2	2.47	0.47
32:2a:166:A:H2'	32:2a:167:A:C8	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:972:A:C5	32:2a:1198:G:H4'	2.49	0.47
36:2e:5:ASP:N	36:2e:5:ASP:OD1	2.47	0.47
47:2p:40:ASP:HB3	47:2p:48:TRP:HB2	1.97	0.47
1:1A:209:A:N1	1:1A:253:A:O2'	2.43	0.47
1:1A:1153:U:O2'	1:1A:1154:C:H6	1.97	0.47
1:1A:2330:G:N2	14:1S:3:ARG:HA	2.29	0.47
4:1E:174:ASP:OD1	4:1E:175:VAL:N	2.47	0.47
8:1I:40:THR:OG1	8:1I:43:ASN:ND2	2.48	0.47
26:14:59:PHE:CD1	50:1s:64:GLU:HB3	2.50	0.47
47:1p:58:TYR:O	47:1p:62:VAL:HG23	2.13	0.47
1:2A:1553:A:H4'	1:2A:1555:A:C5	2.49	0.47
1:2A:2064:C:OP1	1:2A:2789:G:O2'	2.30	0.47
1:2A:2573:U:H1'	10:2O:23:ARG:HD3	1.97	0.47
4:2E:1:MET:HE3	4:2E:199:ARG:HD2	1.96	0.47
23:21:82:LEU:HA	23:21:85:LEU:HD12	1.97	0.47
32:2a:981:G:N1	32:2a:1021:C:N4	2.36	0.47
1:1A:10:G:H2'	1:1A:11:U:H5''	1.96	0.47
1:1A:1409:G:OP2	23:11:3:LYS:HG3	2.14	0.47
1:1A:2456:G:OP1	5:1F:74:ARG:NH2	2.47	0.47
4:1E:143:ASN:HD22	4:1E:147:PRO:CD	2.26	0.47
5:1F:13:SER:HA	5:1F:127:GLU:HG3	1.96	0.47
7:1H:13:LYS:HA	7:1H:14:GLY:HA2	1.59	0.47
7:1H:154:PRO:HB3	7:1H:163:TYR:CZ	2.49	0.47
8:1I:6:LEU:HG	8:1I:36:ALA:HA	1.96	0.47
10:1O:103:ALA:HB1	10:1O:105:GLU:HG2	1.96	0.47
20:1Y:28:LYS:HD2	20:1Y:40:GLU:HG3	1.96	0.47
32:1a:43:G:O2'	32:1a:606:A:N1	2.46	0.47
32:1a:491:C:H3'	32:1a:492:C:H2'	1.95	0.47
32:1a:746:C:H2'	32:1a:747:G:H8	1.79	0.47
41:1j:47:PHE:CZ	45:1n:37:PHE:HE2	2.32	0.47
49:1r:38:GLU:O	49:1r:41:LYS:HG2	2.14	0.47
54:1x:75:C:H2'	54:1x:76:A:C2	2.50	0.47
1:2A:1863:U:O2'	1:2A:1990:A:N1	2.40	0.47
1:2A:2813:C:H2'	1:2A:2814:C:C6	2.48	0.47
17:2V:4:ILE:HD12	17:2V:39:LEU:HB3	1.97	0.47
25:23:8:LEU:HD13	25:23:31:LEU:HD23	1.95	0.47
32:2a:153:G:H2'	32:2a:154:G:H8	1.79	0.47
32:2a:1133:U:O4	32:2a:1134:A:N6	2.47	0.47
32:2a:1198:G:H5''	45:2n:5:ALA:HB2	1.95	0.47
32:2a:1307:C:H2'	32:2a:1308:C:H5'	1.96	0.47
1:1A:1953:A:H2'	1:1A:1954:G:O4'	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:1F:102:PRO:HB2	5:1F:105:VAL:HG23	1.95	0.47
12:1Q:60:ARG:N	12:1Q:60:ARG:CZ	2.78	0.47
32:1a:643:U:H2'	32:1a:644:G:H8	1.80	0.47
32:1a:1030:G:O2'	32:1a:1197:G:O2'	2.30	0.47
32:1a:1298:G:H4'	45:1n:18:VAL:HG13	1.97	0.47
32:1a:1298:G:OP2	59:1a:2017:HOH:O	2.20	0.47
1:2A:1104:G:H3'	1:2A:1105:U:C6	2.50	0.47
1:2A:2331:A:N3	1:2A:2331:A:H2'	2.29	0.47
3:2D:61:LEU:HD12	3:2D:61:LEU:HA	1.80	0.47
6:2G:96:ARG:N	6:2G:99:MET:HE2	2.30	0.47
6:2G:116:ASP:OD2	44:2m:68:GLY:HA3	2.15	0.47
13:2R:87:TYR:OH	13:2R:117:VAL:O	2.30	0.47
32:2a:1328:A:O2'	38:2g:10:ARG:NH2	2.48	0.47
34:2c:12:LEU:HD23	34:2c:16:ARG:HB3	1.96	0.47
1:1A:485:A:H2'	1:1A:486:C:O4'	2.15	0.47
1:1A:1490:A:H5''	1:1A:1491:C:H5	1.80	0.47
1:1A:1528:G:O6	1:1A:1552:A:N6	2.47	0.47
1:1A:2478:C:OP2	59:1A:4182:HOH:O	2.20	0.47
1:1A:2678:C:N3	7:1H:110:SER:OG	2.42	0.47
3:1D:10:THR:OG1	3:1D:13:ARG:HB2	2.14	0.47
4:1E:144:ARG:HB3	4:1E:145:LYS:H	1.41	0.47
6:1G:3:LEU:HD13	26:14:25:TYR:CZ	2.49	0.47
7:1H:5:GLY:HA2	7:1H:69:ARG:HB3	1.96	0.47
15:1T:115:ARG:NH2	59:1T:3105:HOH:O	2.47	0.47
16:1U:108:GLU:O	16:1U:112:ARG:HG2	2.15	0.47
32:1a:100:C:H2'	32:1a:101:G:C8	2.49	0.47
32:1a:674:G:OP1	59:1a:2019:HOH:O	2.20	0.47
32:1a:836:G:O6	32:1a:847:G:H3'	2.15	0.47
32:1a:936:A:N3	32:1a:963:C:O2'	2.46	0.47
32:1a:1328:A:H5''	40:1i:120:ARG:HH12	1.80	0.47
33:1b:192:SER:O	33:1b:194:PRO:HD3	2.15	0.47
38:1g:42:ILE:HG23	38:1g:117:ALA:HA	1.97	0.47
47:1p:21:VAL:HG22	47:1p:33:ILE:HD12	1.96	0.47
1:2A:53:G:H2'	1:2A:54:A:H8	1.79	0.47
1:2A:483:G:O2'	1:2A:494:G:O6	2.28	0.47
1:2A:514:G:N7	18:2W:49:LYS:NZ	2.60	0.47
1:2A:610:U:H1'	5:2F:90:PHE:CG	2.49	0.47
1:2A:1136:G:N2	1:2A:1146:U:H1'	2.30	0.47
1:2A:1156:A:N3	1:2A:1157:G:H1'	2.30	0.47
1:2A:1475:C:H2'	1:2A:1476:U:H6	1.78	0.47
1:2A:1549:C:H2'	1:2A:1550:C:H6	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2548:U:H2'	1:2A:2549:C:C6	2.49	0.47
8:2I:77:LEU:HD11	8:2I:101:LEU:HB2	1.95	0.47
14:2S:10:ARG:NH2	14:2S:91:PRO:O	2.46	0.47
14:2S:26:LEU:HD22	14:2S:87:PHE:CE1	2.49	0.47
21:2Z:9:TYR:OH	21:2Z:61:LEU:HD23	2.15	0.47
22:20:19:LYS:HD2	22:20:19:LYS:N	2.29	0.47
32:2a:400:U:H2'	32:2a:401:U:H6	1.80	0.47
32:2a:526:G:P	35:2d:10:ARG:HH22	2.37	0.47
32:2a:930:U:H2'	32:2a:931:G:C8	2.49	0.47
32:2a:1118:U:H2'	32:2a:1120:C:N3	2.29	0.47
32:2a:1375:G:N2	32:2a:1480:A:H8	2.13	0.47
34:2c:45:LYS:HG3	34:2c:46:GLU:N	2.28	0.47
35:2d:105:VAL:HG13	35:2d:110:PHE:HB2	1.96	0.47
42:2k:98:LEU:O	42:2k:101:SER:OG	2.30	0.47
44:2m:15:VAL:HG11	44:2m:48:LEU:HD21	1.96	0.47
44:2m:92:HIS:CE1	44:2m:98:VAL:HG11	2.49	0.47
47:2p:56:ALA:HB1	47:2p:74:LEU:HD21	1.96	0.47
48:2q:6:LEU:O	48:2q:58:GLU:HA	2.15	0.47
11:1P:52:GLU:OE1	11:1P:55:ARG:NH1	2.39	0.47
21:1Z:7:ALA:O	21:1Z:62:PRO:HD3	2.14	0.47
41:1j:81:THR:C	41:1j:83:GLU:H	2.23	0.47
42:1k:99:GLN:HG3	42:1k:105:VAL:HG11	1.96	0.47
52:1u:5:ASP:O	52:1u:11:GLY:HA3	2.15	0.47
1:1A:1755:U:H2'	1:1A:1756:C:C6	2.50	0.47
1:1A:1992:A:C4	3:1D:241:PRO:HD3	2.50	0.47
1:1A:2257:G:H2'	1:1A:2258:A:C8	2.50	0.47
6:1G:116:ASP:OD1	44:1m:68:GLY:HA3	2.15	0.47
7:1H:167:GLU:HA	7:1H:168:PRO:HD3	1.77	0.47
14:1S:39:ILE:HB	14:1S:49:VAL:HG13	1.96	0.47
32:1a:643:U:H2'	32:1a:644:G:C8	2.49	0.47
32:1a:1132:C:H2'	32:1a:1133:U:H6	1.80	0.47
32:1a:1375:G:N2	32:1a:1480:A:H8	2.11	0.47
33:1b:28:PHE:CD1	33:1b:190:THR:HA	2.50	0.47
39:1h:7:ALA:HB2	39:1h:85:ARG:HD2	1.97	0.47
47:1p:23:ASP:OD1	47:1p:25:ARG:HG2	2.14	0.47
2:2B:24:G:N2	2:2B:27:C:N3	2.56	0.47
3:2D:108:PRO:HB2	3:2D:111:LEU:HB2	1.95	0.47
4:2E:24:THR:HG22	4:2E:186:GLY:O	2.15	0.47
32:2a:587:U:H2'	32:2a:588:G:H8	1.80	0.47
47:2p:8:ARG:HB3	47:2p:28:ARG:NH1	2.30	0.47
1:1A:26:G:C2	1:1A:536:G:N3	2.83	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1451:U:H2'	1:1A:1452:C:C6	2.50	0.47
1:1A:2404:A:H5''	11:1P:63:PRO:HB3	1.96	0.47
32:1a:1329:G:N2	32:1a:1356:G:H2'	2.30	0.47
1:2A:55:C:H2'	1:2A:56:G:O4'	2.14	0.47
1:2A:552:A:O2'	1:2A:553:A:H5'	2.15	0.47
1:2A:1820:C:H5''	1:2A:1821:A:OP1	2.15	0.47
1:2A:2421:G:C2	1:2A:2422:A:H1'	2.49	0.47
9:2N:94:HIS:HB3	9:2N:97:ARG:HD3	1.97	0.47
17:2V:43:GLU:N	17:2V:43:GLU:OE2	2.48	0.47
20:2Y:7:VAL:HG21	20:2Y:72:VAL:HG12	1.97	0.47
32:2a:470:G:O6	59:2a:1916:HOH:O	2.18	0.47
32:2a:1320:G:N3	54:2x:41:C:O2'	2.47	0.47
33:2b:16:HIS:HB3	33:2b:210:SER:HB3	1.96	0.47
33:2b:92:TYR:CZ	33:2b:150:SER:CA	2.98	0.47
37:2f:25:ILE:CD1	37:2f:82:ARG:HE	2.28	0.47
39:2h:19:VAL:HG23	39:2h:21:LYS:HD3	1.96	0.47
44:2m:3:ARG:N	44:2m:8:GLU:HA	2.30	0.47
1:1A:558:U:H2'	1:1A:559:C:C6	2.50	0.46
1:1A:1159:G:H2'	1:1A:1160:G:H8	1.80	0.46
1:1A:1766:A:O2'	1:1A:1768:G:N7	2.43	0.46
1:1A:2208:G:H4'	1:1A:2209:C:OP1	2.14	0.46
5:1F:53:THR:CG2	5:1F:55:GLY:H	2.27	0.46
6:1G:118:ARG:O	6:1G:181:ARG:HB3	2.16	0.46
24:12:70:GLN:HE21	24:12:70:GLN:C	2.23	0.46
32:1a:165:U:H1'	59:1a:2202:HOH:O	2.14	0.46
32:1a:480:A:H4'	32:1a:481:A:OP1	2.15	0.46
32:1a:658:G:H2'	32:1a:659:A:H8	1.81	0.46
40:1i:43:ALA:HA	40:1i:74:ILE:HD12	1.97	0.46
46:1o:74:ASP:OD2	46:1o:77:ARG:HG3	2.15	0.46
1:2A:241:C:OP2	30:28:5:LYS:NZ	2.28	0.46
1:2A:468:A:H5''	1:2A:469:C:OP1	2.15	0.46
1:2A:839:A:O2'	59:2A:3613:HOH:O	2.09	0.46
1:2A:947:C:H2'	1:2A:948:C:C6	2.49	0.46
1:2A:1104:G:H3'	1:2A:1105:U:H6	1.80	0.46
1:2A:1198:C:OP1	16:2U:92:ARG:NH1	2.48	0.46
1:2A:1676:C:H2'	59:2A:3662:HOH:O	2.14	0.46
1:2A:1756:C:H2'	1:2A:1757:C:H6	1.81	0.46
1:2A:2690:A:H4'	4:2E:165:VAL:HG11	1.97	0.46
20:2Y:13:VAL:HG12	20:2Y:74:PRO:HA	1.96	0.46
26:24:58:ARG:HB3	26:24:59:PHE:CD1	2.51	0.46
32:2a:541:G:N1	32:2a:542:G:C2	2.83	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1102:C:H2'	32:2a:1103:G:H8	1.79	0.46
35:2d:196:LEU:C	35:2d:198:VAL:H	2.23	0.46
38:2g:131:LYS:HG2	38:2g:132:GLY:H	1.80	0.46
39:2h:12:ARG:NH1	39:2h:27:PRO:HD3	2.30	0.46
44:2m:24:GLY:HA3	44:2m:66:LEU:HD23	1.95	0.46
54:2x:16:C:H5'	54:2x:59:A:N1	2.31	0.46
1:1A:777:C:OP2	59:1A:4184:HOH:O	2.21	0.46
1:1A:1989:G:OP1	59:1A:4177:HOH:O	2.20	0.46
59:1A:4116:HOH:O	15:1T:100:TYR:HB2	2.14	0.46
59:1A:4279:HOH:O	12:1Q:75:THR:HG23	2.15	0.46
13:1R:13:HIS:CE1	13:1R:16:HIS:HB2	2.50	0.46
32:1a:642:G:H2'	32:1a:643:U:C6	2.50	0.46
32:1a:979:A:N6	32:1a:980:G:O6	2.48	0.46
32:1a:1198:G:OP1	45:1n:2:ALA:N	2.48	0.46
37:1f:97:PHE:N	49:1r:30:ASP:OD1	2.48	0.46
46:1o:22:THR:O	46:1o:22:THR:OG1	2.31	0.46
1:2A:29:G:C5	1:2A:30:C:C4	3.02	0.46
1:2A:385:U:O2'	1:2A:386:G:H5'	2.15	0.46
1:2A:810:A:N1	1:2A:1819:A:O2'	2.39	0.46
1:2A:2027:C:O5'	1:2A:2027:C:H6	1.99	0.46
6:2G:48:GLU:O	6:2G:51:ARG:HG3	2.16	0.46
10:2O:23:ARG:HG3	10:2O:24:VAL:N	2.30	0.46
12:2Q:34:LEU:HB2	12:2Q:118:LEU:HD22	1.96	0.46
12:2Q:66:ILE:HG12	12:2Q:104:PHE:CE1	2.50	0.46
32:2a:698:G:H2'	32:2a:699:A:C8	2.49	0.46
40:2i:50:LEU:HD23	40:2i:51:ARG:HG3	1.96	0.46
3:1D:69:ARG:C	3:1D:71:ASP:H	2.23	0.46
4:1E:9:VAL:HG13	4:1E:25:VAL:O	2.15	0.46
26:14:58:ARG:O	26:14:61:ARG:N	2.47	0.46
32:1a:397:C:P	35:1d:73:ARG:HH11	2.39	0.46
32:1a:1100:G:H5''	40:1i:104:ARG:NH2	2.28	0.46
34:1c:29:TYR:CZ	45:1n:54:PRO:HG2	2.50	0.46
36:1e:122:GLU:O	36:1e:126:ARG:NH1	2.47	0.46
44:1m:74:VAL:O	44:1m:78:ILE:HG13	2.15	0.46
1:2A:200:G:H2'	1:2A:201:A:O4'	2.16	0.46
1:2A:670:A:H2'	1:2A:671:G:O4'	2.14	0.46
1:2A:1314:A:OP1	59:2A:3658:HOH:O	2.20	0.46
1:2A:1698:A:OP1	13:2R:8:ARG:NH1	2.47	0.46
1:2A:2037:U:H2'	1:2A:2038:U:C6	2.49	0.46
1:2A:2489:A:OP2	31:29:2:LYS:NZ	2.44	0.46
1:2A:2670:G:P	7:2H:158:HIS:HE2	2.38	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:2D:159:ALA:HB1	3:2D:198:ASN:HB3	1.97	0.46
8:2I:69:LYS:HG3	8:2I:138:ILE:HG12	1.98	0.46
32:2a:265:C:H2'	32:2a:266:A:C8	2.50	0.46
32:2a:1255:G:H5'	32:2a:1256:G:OP2	2.15	0.46
33:2b:48:MET:HA	33:2b:51:LEU:HB2	1.97	0.46
34:2c:47:LEU:HD21	34:2c:52:LEU:HG	1.96	0.46
39:2h:11:THR:HG23	39:2h:14:ARG:NH1	2.30	0.46
54:2x:55:PSU:H5'	54:2x:56:C:OP2	2.15	0.46
1:1A:864:G:H5'	1:1A:885:U:OP1	2.16	0.46
1:1A:1221:A:O2'	1:1A:1222:C:O4'	2.24	0.46
1:1A:1279:U:H2'	1:1A:1280:G:O4'	2.15	0.46
26:14:9:LEU:HD23	26:14:9:LEU:HA	1.78	0.46
28:16:11:LEU:HB3	28:16:49:HIS:HB3	1.98	0.46
32:1a:650:G:OP2	32:1a:709:G:N2	2.48	0.46
32:1a:1135:A:H5'	41:1j:13:HIS:CG	2.50	0.46
32:1a:1155:G:H2'	32:1a:1156:G:O4'	2.15	0.46
39:1h:51:VAL:HG12	39:1h:52:ASP:H	1.79	0.46
48:1q:45:HIS:NE2	48:1q:47:PRO:HG3	2.31	0.46
1:2A:251:C:H2'	1:2A:252:C:O4'	2.15	0.46
1:2A:982:G:OP2	30:28:52:LYS:NZ	2.43	0.46
1:2A:1346:A:H2	1:2A:1671:G:N3	2.14	0.46
1:2A:2461:A:O2'	54:2x:76:A:N6	2.49	0.46
4:2E:28:ALA:HB3	4:2E:93:VAL:HG12	1.97	0.46
32:2a:538:C:H2'	32:2a:539:C:H6	1.80	0.46
40:2i:107:ARG:HD3	59:2i:5001:HOH:O	2.15	0.46
45:2n:17:LYS:H	45:2n:17:LYS:CE	2.28	0.46
48:2q:56:VAL:O	48:2q:77:VAL:HB	2.16	0.46
1:1A:266:C:H3'	59:1A:4154:HOH:O	2.14	0.46
1:1A:351:U:H4'	20:1Y:68:HIS:CD2	2.51	0.46
1:1A:713:U:O2	30:18:2:PRO:HD2	2.16	0.46
1:1A:1821:A:H5'	3:1D:206:LEU:HD12	1.97	0.46
1:1A:2461:A:O2'	54:1x:76:A:N6	2.48	0.46
12:1Q:32:TYR:CZ	12:1Q:133:ARG:HG3	2.50	0.46
21:1Z:40:ASP:HB3	21:1Z:43:GLU:HB2	1.96	0.46
32:1a:1384:G:C2	32:1a:1385:C:H1'	2.51	0.46
35:1d:114:ARG:HA	35:1d:117:ALA:HB3	1.97	0.46
1:2A:263:G:H2'	1:2A:264:U:C6	2.50	0.46
2:2B:19:G:H2'	2:2B:20:C:O4'	2.15	0.46
6:2G:173:LEU:HB3	6:2G:178:PHE:CG	2.49	0.46
8:2I:102:SER:O	8:2I:106:GLY:N	2.42	0.46
31:29:17:ILE:HG12	31:29:26:ILE:HD11	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:673:C:OP2	42:2k:55:LYS:NZ	2.39	0.46
32:2a:719:C:H2'	32:2a:720:C:C6	2.50	0.46
32:2a:1490:U:H2'	32:2a:1491:A:C8	2.51	0.46
35:2d:173:TRP:CD2	35:2d:189:PRO:HB3	2.50	0.46
1:1A:517:G:H2'	1:1A:518:G:O4'	2.16	0.46
1:1A:1248:A:H2	1:1A:1286:A:H62	1.62	0.46
1:1A:1821:A:H3'	1:1A:1822:G:H8	1.81	0.46
1:1A:2811:A:H5''	1:1A:2812:G:C8	2.50	0.46
2:1B:48:A:H2'	2:1B:49:C:C6	2.51	0.46
12:1Q:60:ARG:H	12:1Q:60:ARG:CZ	2.28	0.46
32:1a:1120:C:H4'	32:1a:1121:G:C2	2.50	0.46
32:1a:1161:A:H2'	32:1a:1162:A:O4'	2.16	0.46
32:1a:1331:A:H5''	40:1i:121:ARG:HB2	1.98	0.46
33:1b:17:PHE:HA	33:1b:44:LEU:HD11	1.97	0.46
33:1b:145:LEU:HD11	33:1b:149:LEU:HD12	1.97	0.46
41:1j:38:ILE:HG13	41:1j:71:LEU:HB3	1.97	0.46
1:2A:105:U:H2'	1:2A:106:G:C8	2.51	0.46
1:2A:754:C:N4	1:2A:769:G:H1	2.13	0.46
1:2A:1072:A:C6	1:2A:1171:A:C4	3.04	0.46
8:2I:110:ASP:N	8:2I:130:TYR:OH	2.34	0.46
26:24:57:GLU:HA	26:24:58:ARG:HA	1.58	0.46
32:2a:23:G:H4'	32:2a:863:G:C8	2.51	0.46
32:2a:174:A:H2'	32:2a:175:U:C6	2.50	0.46
32:2a:1161:A:H2'	32:2a:1162:A:O4'	2.16	0.46
34:2c:54:ARG:H	34:2c:69:HIS:HB2	1.80	0.46
41:2j:49:VAL:HG13	45:2n:41:ARG:HD2	1.97	0.46
3:1D:26:LYS:HD3	3:1D:83:GLU:OE2	2.15	0.46
4:1E:116:VAL:HG13	4:1E:122:PHE:HB2	1.97	0.46
6:1G:137:GLU:HB3	6:1G:139:LEU:HD12	1.96	0.46
23:11:86:SER:N	23:11:89:GLU:OE2	2.34	0.46
32:1a:443:A:OP2	32:1a:470:G:N1	2.45	0.46
32:1a:972:A:N1	32:1a:1030:G:H4'	2.31	0.46
34:1c:22:TRP:CZ2	45:1n:54:PRO:HG3	2.51	0.46
36:1e:140:ARG:O	36:1e:143:ARG:NH2	2.49	0.46
38:1g:59:LEU:HD11	38:1g:63:LYS:HE2	1.97	0.46
54:1x:61:C:H2'	54:1x:62:C:H6	1.80	0.46
1:2A:209:A:O4'	1:2A:221:A:H1'	2.16	0.46
1:2A:319:C:O3'	20:2Y:95:LYS:NZ	2.48	0.46
1:2A:1439:U:H2'	1:2A:1440:A:O4'	2.16	0.46
1:2A:1845:A:H8	1:2A:1845:A:OP1	1.98	0.46
6:2G:98:ARG:NH2	26:24:1:MET:SD	2.89	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:2O:120:GLU:HB2	15:2T:68:TYR:HE2	1.79	0.46
11:2P:136:GLU:HG2	11:2P:137:LYS:N	2.31	0.46
21:2Z:10:ARG:NH1	21:2Z:26:GLY:H	2.13	0.46
24:22:64:LEU:O	24:22:68:ARG:HG2	2.15	0.46
30:28:23:VAL:HG11	30:28:47:LYS:HD3	1.98	0.46
32:2a:228:G:H1'	32:2a:258:A:N1	2.31	0.46
32:2a:251:G:H2'	32:2a:252:U:C6	2.51	0.46
32:2a:445:G:H4'	47:2p:41:PRO:HB2	1.96	0.46
32:2a:958:C:H1'	45:2n:19:ARG:HA	1.97	0.46
32:2a:1116:G:H1	32:2a:1124:C:N4	2.14	0.46
32:2a:1150:A:H3'	32:2a:1151:A:H8	1.80	0.46
33:2b:187:LEU:HD12	33:2b:201:ILE:HD12	1.98	0.46
1:1A:830:A:N6	3:1D:229:VAL:HG11	2.31	0.46
3:1D:27:THR:O	3:1D:27:THR:OG1	2.32	0.46
30:18:30:ARG:HA	30:18:30:ARG:HD3	1.45	0.46
32:1a:1184:G:N2	45:1n:43:CYS:HB3	2.30	0.46
32:1a:1300:A:H1'	50:1s:37:ARG:HH21	1.81	0.46
32:1a:1310:C:OP1	52:1u:21:TYR:OH	2.24	0.46
36:1e:78:HIS:NE2	36:1e:142:LEU:HA	2.30	0.46
44:1m:79:LYS:NZ	44:1m:83:ASP:OD2	2.38	0.46
48:1q:26:GLN:HE21	48:1q:37:LYS:HE2	1.81	0.46
1:2A:592:G:H2'	1:2A:2051:A:C5	2.51	0.46
1:2A:1108:G:H8	1:2A:1108:G:OP2	1.99	0.46
1:2A:1113:G:O2'	1:2A:1141:A:O2'	2.34	0.46
1:2A:2760:A:H3'	1:2A:2761:A:H8	1.81	0.46
6:2G:107:LEU:HA	6:2G:111:LEU:HD22	1.98	0.46
6:2G:115:ARG:H	6:2G:136:ARG:HH21	1.64	0.46
6:2G:179:PRO:HG3	26:24:43:TYR:CZ	2.51	0.46
12:2Q:97:VAL:HG21	12:2Q:103:MET:HE3	1.97	0.46
23:21:56:GLN:HA	23:21:56:GLN:HE21	1.81	0.46
26:24:62:ARG:O	26:24:64:GLY:N	2.44	0.46
32:2a:22:G:H2'	32:2a:23:G:C8	2.51	0.46
32:2a:811:U:H5''	32:2a:812:A:OP2	2.16	0.46
32:2a:819:U:H3	32:2a:829:G:H1	1.64	0.46
32:2a:1198:G:H2'	32:2a:1199:C:C6	2.50	0.46
32:2a:1254:G:H2'	32:2a:1255:G:O4'	2.16	0.46
32:2a:1395:C:H2'	32:2a:1396:A:C8	2.50	0.46
34:2c:195:VAL:HG12	34:2c:196:LEU:O	2.16	0.46
49:2r:24:ALA:C	49:2r:26:LEU:H	2.24	0.46
1:1A:214:G:N2	1:1A:216:A:H62	2.14	0.46
1:1A:1096:G:H4'	1:1A:2764:C:H4'	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1158:U:H2'	1:1A:1159:G:H8	1.80	0.46
1:1A:1520:C:H2'	1:1A:1521:G:H8	1.80	0.46
1:1A:1820:C:H2'	1:1A:1821:A:C5	2.50	0.46
1:1A:2210:U:H2'	1:1A:2211:G:H8	1.81	0.46
1:1A:2226:G:H5'	1:1A:2227:G:N7	2.31	0.46
3:1D:26:LYS:HE2	3:1D:28:GLU:O	2.16	0.46
16:1U:58:ARG:HA	16:1U:61:TRP:CE3	2.51	0.46
21:1Z:101:PRO:O	21:1Z:102:LEU:HD12	2.16	0.46
32:1a:487:C:H2'	32:1a:488:C:H6	1.81	0.46
32:1a:585:C:H2'	32:1a:586:A:C8	2.50	0.46
32:1a:889:U:H2'	32:1a:890:C:C6	2.50	0.46
33:1b:226:ARG:HG3	33:1b:227:GLY:H	1.81	0.46
34:1c:6:HIS:HD2	34:1c:8:ILE:H	1.64	0.46
34:1c:39:ILE:HD12	34:1c:57:ILE:HD13	1.98	0.46
48:1q:74:LEU:HD13	48:1q:75:ARG:HG2	1.97	0.46
1:2A:857:U:H2'	11:2P:21:ARG:HA	1.97	0.46
1:2A:1474:G:H2'	1:2A:1475:C:C6	2.51	0.46
1:2A:2706:C:H2'	1:2A:2707:U:C6	2.51	0.46
1:2A:2878:G:H2'	1:2A:2879:C:O4'	2.16	0.46
2:2B:16:G:H1	2:2B:68:C:N4	2.08	0.46
2:2B:54:G:H21	6:2G:29:TRP:HZ2	1.62	0.46
19:2X:12:VAL:HG22	19:2X:29:TRP:CE2	2.51	0.46
23:21:83:GLU:HA	23:21:84:GLY:HA2	1.72	0.46
32:2a:137:G:H2'	32:2a:138:A:H8	1.81	0.46
32:2a:360:A:H2'	32:2a:361:U:C6	2.50	0.46
32:2a:837:A:H2'	32:2a:838:A:O4'	2.16	0.46
32:2a:955:A:H1'	32:2a:959:U:H3	1.80	0.46
37:2f:61:LEU:HB3	37:2f:63:TYR:HE1	1.81	0.46
41:2j:46:ARG:NH1	45:2n:59:ALA:HB1	2.31	0.46
19:1X:35:THR:HG22	19:1X:38:GLU:H	1.81	0.46
32:1a:266:A:H2'	32:1a:267:C:C6	2.51	0.46
32:1a:455:A:O2'	32:1a:457:G:N7	2.45	0.46
32:1a:726:G:OP2	46:1o:35:ARG:NH2	2.49	0.46
45:1n:41:ARG:HG3	45:1n:42:ILE:HG13	1.96	0.46
1:2A:235:G:H4'	1:2A:412:G:C5	2.51	0.46
1:2A:1013:U:H4'	25:23:14:GLY:O	2.16	0.46
1:2A:2325:C:H2'	1:2A:2326:G:H8	1.81	0.46
32:2a:1134:A:HO2'	32:2a:1135:A:H8	1.63	0.46
32:2a:1305:G:H4'	32:2a:1345:C:N3	2.29	0.46
33:2b:127:ILE:C	33:2b:129:GLU:H	2.23	0.46
34:2c:39:ILE:O	34:2c:43:LEU:HB2	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:2j:30:SER:H	41:2j:84:GLN:NE2	2.09	0.46
46:2o:56:LEU:O	46:2o:60:VAL:HG23	2.16	0.46
49:2r:76:LEU:HD12	49:2r:76:LEU:HA	1.76	0.46
1:1A:671:G:H2'	1:1A:672:G:O4'	2.16	0.45
1:1A:1257:A:N3	1:1A:1283:G:O2'	2.37	0.45
1:1A:1343:C:N4	1:1A:1344:G:C6	2.84	0.45
1:1A:1757:C:OP2	59:1A:4179:HOH:O	2.20	0.45
1:1A:2043:U:O2'	1:1A:2628:C:H5'	2.16	0.45
1:1A:2523:C:H2'	1:1A:2524:G:O4'	2.16	0.45
1:1A:2568:G:H2'	1:1A:2569:C:C6	2.52	0.45
9:1N:114:ARG:HD2	59:1N:302:HOH:O	2.16	0.45
19:1X:57:LEU:CD1	19:1X:78:LYS:HB2	2.46	0.45
20:1Y:8:LYS:HD3	20:1Y:97:ARG:NH1	2.31	0.45
24:12:1:MET:HE3	24:12:5:GLU:HB3	1.97	0.45
32:1a:23:G:H4'	32:1a:863:G:C8	2.51	0.45
32:1a:57:U:H2'	32:1a:58:G:H8	1.81	0.45
32:1a:720:C:H2'	32:1a:721:A:H8	1.81	0.45
32:1a:993:A:H4'	50:1s:14:HIS:CE1	2.51	0.45
32:1a:1243:A:H3'	32:1a:1244:C:H6	1.82	0.45
39:1h:10:LEU:HD23	39:1h:83:ILE:HG12	1.98	0.45
41:1j:62:HIS:HB3	45:1n:59:ALA:HB3	1.98	0.45
52:1u:6:ARG:HE	52:1u:15:ARG:NE	2.14	0.45
1:2A:594:A:OP2	17:2V:78:LYS:HE2	2.16	0.45
1:2A:885:U:H1'	1:2A:1235:G:H1'	1.97	0.45
1:2A:2115:G:N2	1:2A:2217:C:H1'	2.31	0.45
4:2E:144:ARG:HB3	4:2E:145:LYS:H	1.49	0.45
6:2G:44:GLY:N	6:2G:88:ILE:O	2.50	0.45
20:2Y:9:LYS:HA	20:2Y:10:GLY:HA2	1.54	0.45
32:2a:176:G:H1'	32:2a:177:U:H5	1.81	0.45
32:2a:1125:G:H3'	32:2a:1126:G:H8	1.79	0.45
32:2a:1329:G:C5	40:2i:107:ARG:HD2	2.51	0.45
34:2c:186:PHE:CE2	34:2c:200:ALA:HB3	2.51	0.45
1:1A:62:A:O3'	19:1X:71:GLY:HA3	2.16	0.45
1:1A:800:C:H2'	1:1A:801:C:H6	1.80	0.45
20:1Y:13:VAL:HB	20:1Y:72:VAL:HG13	1.98	0.45
20:1Y:15:VAL:HG21	20:1Y:42:VAL:HG11	1.97	0.45
32:1a:584:C:H2'	32:1a:585:C:C6	2.52	0.45
32:1a:610:U:C2	32:1a:611:G:C8	3.04	0.45
32:1a:726:G:O6	59:1a:2018:HOH:O	2.20	0.45
32:1a:1349:C:H2'	32:1a:1350:C:H6	1.81	0.45
33:1b:55:PHE:HA	33:1b:58:ILE:HG12	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:1b:71:VAL:HB	33:1b:164:VAL:HG13	1.98	0.45
35:1d:20:TYR:HA	35:1d:26:CYS:SG	2.56	0.45
35:1d:173:TRP:CE3	35:1d:174:LEU:HG	2.51	0.45
1:2A:5:A:H2	1:2A:6:G:N7	2.14	0.45
1:2A:242:G:N7	30:28:5:LYS:HE2	2.31	0.45
1:2A:810:A:H5'	3:2D:210:GLY:HA3	1.98	0.45
1:2A:1459:G:N2	1:2A:1633:C:O2	2.46	0.45
1:2A:2049:U:H2'	1:2A:2050:G:O4'	2.16	0.45
21:2Z:153:SER:HB3	21:2Z:167:PRO:HB3	1.97	0.45
33:2b:92:TYR:CD2	33:2b:92:TYR:C	2.94	0.45
33:2b:115:LEU:HD13	33:2b:145:LEU:HB3	1.98	0.45
36:2e:139:LEU:HA	36:2e:142:LEU:HD12	1.97	0.45
1:1A:138:A:H8	1:1A:1453:C:O2'	1.96	0.45
1:1A:501:G:H4'	1:1A:526:A:N1	2.30	0.45
1:1A:1016:G:OP2	1:1A:1017:A:O2'	2.34	0.45
1:1A:1633:C:H2'	1:1A:1634:C:H6	1.81	0.45
1:1A:2249:G:N3	1:1A:2249:G:H2'	2.31	0.45
1:1A:2803:C:H2'	1:1A:2804:G:C8	2.50	0.45
3:1D:67:PHE:HB3	3:1D:153:ALA:H	1.81	0.45
13:1R:44:LEU:HD22	13:1R:48:VAL:HG23	1.97	0.45
20:1Y:56:PRO:C	20:1Y:58:GLY:H	2.24	0.45
32:1a:161:G:O2'	32:1a:162:G:H5'	2.17	0.45
32:1a:220:C:H2'	32:1a:221:C:C6	2.51	0.45
32:1a:458:A:O3'	47:1p:81:ARG:HA	2.17	0.45
32:1a:1395:C:H2'	32:1a:1396:A:C8	2.52	0.45
32:1a:1412:C:H2'	32:1a:1413:C:C6	2.52	0.45
37:1f:17:SER:O	37:1f:21:LEU:HG	2.17	0.45
1:2A:1200:A:H5''	16:2U:55:ARG:HD3	1.97	0.45
1:2A:1399:A:H2'	1:2A:1400:G:O4'	2.15	0.45
1:2A:2338:A:H2'	1:2A:2339:A:C8	2.51	0.45
1:2A:2358:C:H2'	1:2A:2359:U:C6	2.52	0.45
1:2A:2563:U:H2'	1:2A:2565:U:H5''	1.99	0.45
4:2E:119:ARG:HD2	4:2E:120:TRP:CE2	2.52	0.45
19:2X:21:PHE:HZ	19:2X:92:LEU:HD12	1.80	0.45
30:28:54:GLU:O	30:28:58:ILE:HG13	2.16	0.45
32:2a:981:G:C2	32:2a:1021:C:N3	2.84	0.45
39:2h:37:ARG:HE	39:2h:38:ILE:HD13	1.80	0.45
46:2o:24:SER:OG	46:2o:25:THR:N	2.48	0.45
50:2s:63:THR:HG23	50:2s:65:ASN:HD21	1.81	0.45
1:1A:346:G:C8	5:1F:171:PRO:HG3	2.51	0.45
1:1A:1200:A:OP1	16:1U:55:ARG:HD3	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1475:C:H2'	1:1A:1476:U:C6	2.51	0.45
1:1A:1735:A:OP2	59:1A:4185:HOH:O	2.21	0.45
1:1A:2375:C:H2'	1:1A:2376:G:O4'	2.16	0.45
6:1G:64:THR:HB	6:1G:94:LEU:HD21	1.98	0.45
6:1G:131:TYR:HB3	6:1G:159:VAL:HG13	1.98	0.45
35:1d:9:CYS:O	35:1d:13:ARG:HG3	2.16	0.45
35:1d:36:ARG:HB2	35:1d:38:TYR:CZ	2.51	0.45
44:1m:81:LEU:HD11	44:1m:88:ARG:HH21	1.82	0.45
44:1m:84:ILE:HD12	50:1s:74:PHE:CZ	2.52	0.45
48:1q:56:VAL:HB	48:1q:78:GLU:HB3	1.99	0.45
1:2A:53:G:O2'	1:2A:124:A:N1	2.43	0.45
1:2A:212:G:H2'	1:2A:213:A:O4'	2.16	0.45
1:2A:243:A:C6	1:2A:244:A:C5	3.04	0.45
1:2A:651:A:C6	1:2A:661:A:C8	3.05	0.45
1:2A:984:G:N3	1:2A:1235:G:H4'	2.32	0.45
1:2A:1309:G:H8	1:2A:1309:G:O5'	2.00	0.45
1:2A:1649:C:OP2	59:2A:3659:HOH:O	2.21	0.45
1:2A:2483:G:H2'	1:2A:2486:C:H42	1.82	0.45
2:2B:31:C:H42	2:2B:51:G:H1	1.64	0.45
8:2I:14:ASP:O	8:2I:17:GLN:HB3	2.15	0.45
8:2I:43:ASN:HD22	8:2I:43:ASN:C	2.23	0.45
11:2P:82:GLY:HA2	11:2P:113:LYS:O	2.17	0.45
14:2S:65:VAL:O	14:2S:68:GLN:HB2	2.16	0.45
24:22:1:MET:HE3	24:22:5:GLU:HB3	1.98	0.45
32:2a:1046:C:H3'	32:2a:1047:G:H2'	1.98	0.45
33:2b:13:ALA:HA	33:2b:15:VAL:H	1.81	0.45
37:2f:94:GLN:OE1	49:2r:32:ARG:HD2	2.16	0.45
38:2g:23:VAL:HG13	38:2g:43:PHE:CZ	2.51	0.45
44:2m:33:ALA:O	44:2m:37:THR:OG1	2.26	0.45
51:2t:39:LYS:HB2	51:2t:39:LYS:HE3	1.72	0.45
1:1A:909:A:H2'	1:1A:910:G:C8	2.51	0.45
1:1A:1369:G:C4	1:1A:1373:G:O6	2.69	0.45
1:1A:1386:U:OP1	1:1A:1442:U:N3	2.44	0.45
1:1A:1652:C:H4'	1:1A:1653:A:O5'	2.16	0.45
1:1A:2588:A:H5''	1:1A:2589:G:H5'	1.97	0.45
1:1A:2588:A:OP2	27:15:3:LYS:NZ	2.41	0.45
6:1G:128:ARG:HE	6:1G:128:ARG:HB2	1.65	0.45
20:1Y:20:TYR:CE1	20:1Y:43:ASN:HA	2.52	0.45
32:1a:164:C:C4	32:1a:165:U:C4	3.04	0.45
32:1a:205:G:C5	32:1a:216:G:C2	3.05	0.45
32:1a:326:C:O2	59:1a:2021:HOH:O	2.21	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:961:A:H5''	32:1a:962:C:OP2	2.16	0.45
32:1a:1026:C:C2'	32:1a:1027:A:H5'	2.46	0.45
33:1b:218:ALA:O	33:1b:222:ILE:HG13	2.17	0.45
39:1h:112:LEU:HA	39:1h:134:ILE:HG12	1.99	0.45
47:1p:71:ARG:O	47:1p:75:ARG:N	2.44	0.45
50:1s:40:ILE:HB	50:1s:67:VAL:O	2.16	0.45
1:2A:820:A:N3	1:2A:820:A:H2'	2.30	0.45
1:2A:1449:C:O2'	1:2A:1450:U:H5'	2.16	0.45
1:2A:2339:A:H2'	1:2A:2340:G:C8	2.52	0.45
2:2B:14:U:OP2	2:2B:70:C:O2'	2.30	0.45
3:2D:275:LYS:HA	3:2D:275:LYS:HD2	1.65	0.45
6:2G:98:ARG:H	6:2G:98:ARG:HG2	1.40	0.45
7:2H:71:LEU:HD22	7:2H:71:LEU:HA	1.84	0.45
7:2H:127:GLU:C	7:2H:129:THR:H	2.23	0.45
11:2P:65:ARG:HG3	30:28:25:MET:HG3	1.98	0.45
13:2R:21:TYR:OH	13:2R:43:GLU:HG2	2.16	0.45
32:2a:1300:A:OP1	50:2s:3:ARG:NH1	2.50	0.45
44:2m:80:ARG:NH2	50:2s:69:HIS:HE1	2.11	0.45
1:1A:761:G:C2	46:1o:56:LEU:HD21	2.50	0.45
1:1A:2626:U:H2'	1:1A:2627:C:C6	2.51	0.45
24:12:1:MET:N	24:12:52:ASP:OD2	2.46	0.45
24:12:32:LEU:HD12	24:12:57:ILE:HD12	1.98	0.45
24:12:53:LEU:HD23	24:12:53:LEU:HA	1.71	0.45
32:1a:986:C:N3	32:1a:1001:G:O6	2.50	0.45
32:1a:1286:G:OP2	59:1a:2020:HOH:O	2.20	0.45
32:1a:1412:C:H2'	32:1a:1413:C:H6	1.81	0.45
40:1i:79:LEU:HD22	40:1i:104:ARG:HB2	1.98	0.45
1:2A:211:A:N1	1:2A:433:G:O2'	2.45	0.45
1:2A:1051:C:C2	1:2A:1182:G:N2	2.84	0.45
1:2A:2685:G:H2'	1:2A:2686:A:C8	2.52	0.45
6:2G:56:ALA:N	6:2G:153:ARG:HH21	2.13	0.45
8:2I:45:LYS:O	8:2I:49:ALA:N	2.38	0.45
30:28:14:VAL:HG23	30:28:24:ALA:HB2	1.98	0.45
32:2a:870:A:N6	32:2a:884:G:O2'	2.50	0.45
33:2b:87:ARG:HE	33:2b:87:ARG:HB3	1.62	0.45
44:2m:13:LYS:O	44:2m:45:VAL:HG23	2.17	0.45
48:2q:59:ILE:HG22	48:2q:73:VAL:HA	1.99	0.45
1:1A:266:C:OP2	59:1A:4181:HOH:O	2.20	0.45
1:1A:604:G:H2'	1:1A:605:G:C8	2.52	0.45
1:1A:909:A:H2'	1:1A:910:G:H8	1.81	0.45
1:1A:956:A:H2'	12:1Q:9:TYR:OH	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1275:C:H2'	1:1A:1276:G:C8	2.52	0.45
1:1A:2319:G:O2'	1:1A:2321:A:N7	2.46	0.45
14:1S:84:GLN:HA	14:1S:111:GLU:HB2	1.98	0.45
32:1a:487:C:H2'	32:1a:488:C:C6	2.52	0.45
32:1a:703:C:O2'	49:1r:49:LYS:HB3	2.17	0.45
35:1d:53:ASP:HB3	35:1d:57:ARG:NH1	2.32	0.45
1:2A:275:C:H2'	1:2A:276:G:O4'	2.17	0.45
1:2A:910:G:C6	1:2A:911:C:N4	2.85	0.45
1:2A:1095:A:H2'	1:2A:1096:G:H8	1.82	0.45
1:2A:1873:C:H2'	1:2A:1874:C:H6	1.82	0.45
1:2A:1897:A:H2'	1:2A:1898:A:C8	2.50	0.45
1:2A:2224:U:H2'	1:2A:2225:C:C6	2.51	0.45
1:2A:2704:A:H2'	1:2A:2705:G:C8	2.52	0.45
19:2X:2:LYS:NZ	19:2X:38:GLU:OE2	2.49	0.45
32:2a:388:G:H2'	32:2a:389:A:H8	1.80	0.45
32:2a:983:A:O2'	32:2a:1021:C:H1'	2.16	0.45
32:2a:1132:C:O2'	32:2a:1262:A:N1	2.42	0.45
32:2a:1198:G:H5''	45:2n:5:ALA:CB	2.47	0.45
32:2a:1226:C:H2'	32:2a:1227:A:C8	2.52	0.45
34:2c:150:LYS:O	34:2c:201:TYR:N	2.45	0.45
36:2e:71:LEU:C	36:2e:72:GLN:HG2	2.41	0.45
49:2r:29:PHE:N	49:2r:29:PHE:CD1	2.85	0.45
1:1A:334:A:C6	1:1A:351:U:C4	3.04	0.45
1:1A:503:A:C6	1:1A:505:A:C6	3.04	0.45
1:1A:755:U:H2'	1:1A:756:G:C8	2.51	0.45
1:1A:1001:A:H5'	12:1Q:76:LYS:HG3	1.98	0.45
1:1A:2473:U:H1'	1:1A:2502:U:O4	2.17	0.45
1:1A:2829:A:OP2	13:1R:2:ARG:NH2	2.50	0.45
6:1G:72:ARG:NH1	6:1G:87:PRO:HG3	2.31	0.45
32:1a:324:C:H4'	32:1a:325:A:H5''	1.99	0.45
32:1a:569:G:N3	32:1a:857:C:H4'	2.31	0.45
33:1b:147:LYS:HB3	33:1b:147:LYS:HE3	1.75	0.45
35:1d:65:ARG:NH1	35:1d:70:ILE:O	2.48	0.45
1:2A:73:G:H4'	24:22:55:ARG:CZ	2.47	0.45
1:2A:769:G:H2'	1:2A:770:U:O4'	2.17	0.45
1:2A:903:C:OP2	22:20:77:ARG:NH2	2.50	0.45
1:2A:910:G:N2	1:2A:958:U:C2	2.84	0.45
1:2A:934:C:OP1	44:2m:93:ARG:NH1	2.48	0.45
1:2A:1003:A:N3	1:2A:2468:U:O2'	2.42	0.45
1:2A:1166:C:H2'	1:2A:1167:G:O4'	2.17	0.45
1:2A:1333:U:C2	1:2A:1372:C:O2	2.70	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1796:U:H2'	1:2A:1797:C:C6	2.52	0.45
3:2D:134:ARG:HD2	3:2D:135:PHE:CE1	2.52	0.45
9:2N:96:GLU:CD	9:2N:96:GLU:H	2.25	0.45
11:2P:8:PRO:HB2	11:2P:12:ALA:HB3	1.99	0.45
21:2Z:108:PRO:HG3	21:2Z:141:VAL:HB	1.98	0.45
26:24:16:CYS:SG	26:24:17:GLY:N	2.89	0.45
32:2a:1245:C:H2'	32:2a:1246:C:C6	2.52	0.45
33:2b:134:GLU:O	33:2b:138:LEU:HD23	2.17	0.45
34:2c:28:GLN:HG2	34:2c:31:HIS:HB2	1.99	0.45
45:2n:27:CYS:HB2	59:2n:601:HOH:O	2.15	0.45
45:2n:41:ARG:HG3	45:2n:42:ILE:HG13	1.99	0.45
1:1A:800:C:H2'	1:1A:801:C:C6	2.51	0.45
1:1A:1067:G:N7	9:1N:66:LYS:HE2	2.32	0.45
1:1A:1176:G:H21	9:1N:73:THR:CG2	2.29	0.45
1:1A:2578:G:H2'	1:1A:2579:C:C6	2.52	0.45
26:14:68:ARG:HA	26:14:68:ARG:HD2	1.73	0.45
30:18:62:LEU:HB3	30:18:65:GLU:CG	2.46	0.45
32:1a:675:G:H2'	32:1a:676:U:C6	2.52	0.45
33:1b:168:THR:OG1	33:1b:192:SER:OG	2.20	0.45
38:1g:50:ILE:HD11	38:1g:58:PRO:CA	2.44	0.45
52:1u:15:ARG:HH11	52:1u:15:ARG:HB2	1.81	0.45
1:2A:353:A:HO2'	1:2A:354:A:H8	1.65	0.45
1:2A:508:A:O4'	20:2Y:48:ALA:HB1	2.17	0.45
1:2A:623:C:O2'	5:2F:104:LYS:NZ	2.50	0.45
1:2A:972:G:H2'	1:2A:973:G:O4'	2.15	0.45
1:2A:1176:G:O6	1:2A:2061:C:H1'	2.16	0.45
1:2A:1604:A:H8	59:2A:4206:HOH:O	2.00	0.45
1:2A:2428:C:OP1	11:2P:65:ARG:NH2	2.50	0.45
1:2A:2854:G:H2'	1:2A:2855:G:H8	1.82	0.45
3:2D:13:ARG:HD2	3:2D:13:ARG:HA	1.71	0.45
4:2E:112:GLY:O	4:2E:159:HIS:HA	2.17	0.45
7:2H:159:GLU:HG3	7:2H:169:VAL:HG11	1.99	0.45
14:2S:87:PHE:CZ	14:2S:102:ALA:HB2	2.52	0.45
24:22:9:GLN:OE1	24:22:56:GLN:HG2	2.15	0.45
32:2a:1055:G:H2'	32:2a:1056:U:C6	2.52	0.45
32:2a:1112:C:N3	32:2a:1126:G:N2	2.52	0.45
32:2a:1134:A:O2'	32:2a:1135:A:H8	2.00	0.45
32:2a:1446:A:H2'	32:2a:1447:G:O4'	2.17	0.45
32:2a:1457:C:H2'	32:2a:1458:G:C8	2.52	0.45
32:2a:1488:U:H2'	32:2a:1489:G:C8	2.51	0.45
34:2c:18:TRP:HE1	45:2n:56:VAL:H	1.65	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:2d:117:ALA:O	35:2d:121:VAL:HG23	2.17	0.45
37:2f:82:ARG:HB3	37:2f:82:ARG:NH1	2.32	0.45
1:1A:2227:G:HO2'	1:1A:2228:A:P	2.40	0.45
1:1A:2802:A:H5''	1:1A:2803:C:H5'	1.99	0.45
4:1E:12:THR:HG22	4:1E:13:ARG:H	1.82	0.45
4:1E:145:LYS:NZ	59:1E:402:HOH:O	2.28	0.45
5:1F:64:ILE:HG21	5:1F:78:ILE:HG23	1.99	0.45
14:1S:18:ILE:HD13	14:1S:88:ASP:HA	1.99	0.45
28:16:6:ARG:NH1	28:16:26:ASN:HB2	2.32	0.45
29:17:12:ARG:NH2	29:17:44:PRO:HB3	2.32	0.45
32:1a:218:U:H2'	32:1a:219:U:C6	2.52	0.45
32:1a:246:A:H4'	32:1a:247:G:O5'	2.16	0.45
32:1a:254:G:H2'	32:1a:255:G:H8	1.82	0.45
32:1a:258:A:C6	32:1a:259:A:C6	3.04	0.45
32:1a:584:C:H2'	32:1a:585:C:H6	1.82	0.45
32:1a:1240:G:H2'	32:1a:1241:C:C6	2.52	0.45
32:1a:1302:C:O2'	50:1s:73:GLU:HB3	2.17	0.45
33:1b:178:ARG:NH2	39:1h:68:ARG:HH22	2.15	0.45
36:1e:85:GLY:C	36:1e:87:SER:H	2.22	0.45
37:1f:15:ASP:OD1	37:1f:18:GLN:N	2.37	0.45
38:1g:51:GLN:O	38:1g:55:GLY:HA2	2.17	0.45
1:2A:180:C:O2'	1:2A:848:A:N3	2.48	0.45
1:2A:338:G:H2'	1:2A:339:C:C6	2.52	0.45
1:2A:440:C:O2'	1:2A:441:A:H5'	2.17	0.45
1:2A:503:A:C6	1:2A:505:A:C6	3.05	0.45
1:2A:509:C:H2'	1:2A:510:C:C6	2.52	0.45
1:2A:2397:C:H2'	1:2A:2398:U:C6	2.52	0.45
1:2A:2637:C:H2'	1:2A:2638:G:O4'	2.17	0.45
4:2E:116:VAL:HG13	4:2E:122:PHE:HB2	1.98	0.45
11:2P:21:ARG:HA	11:2P:21:ARG:HD3	1.72	0.45
32:2a:982:G:C2'	32:2a:983:A:H4'	2.42	0.45
32:2a:1121:G:N1	32:2a:1123:C:H1'	2.32	0.45
42:2k:80:VAL:HG13	42:2k:103:LEU:HD12	1.98	0.45
51:2t:50:GLU:HG3	51:2t:100:ILE:HD13	1.99	0.45
1:1A:1066:A:H8	1:1A:1067:G:H5''	1.81	0.44
1:1A:1531:A:H2'	1:1A:1532:G:C8	2.52	0.44
1:1A:1633:C:H2'	1:1A:1634:C:C6	2.52	0.44
1:1A:2083:A:N6	55:1z:11:ARG:H	2.14	0.44
2:1B:33:G:C2	2:1B:50:G:C2	3.04	0.44
3:1D:89:SER:HB2	3:1D:201:HIS:CD2	2.52	0.44
6:1G:43:LEU:HD12	6:1G:43:LEU:HA	1.87	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:1g:48:LYS:O	38:1g:51:GLN:HB2	2.18	0.44
1:2A:29:G:H2'	1:2A:30:C:C6	2.51	0.44
1:2A:322:A:N1	1:2A:345:A:O2'	2.44	0.44
1:2A:1317:A:OP1	59:2A:3660:HOH:O	2.21	0.44
1:2A:1828:U:H5'	3:2D:259:THR:CG2	2.46	0.44
1:2A:2421:G:N2	1:2A:2422:A:H1'	2.32	0.44
3:2D:71:ASP:HB3	3:2D:103:ARG:NH2	2.32	0.44
12:2Q:59:ARG:HD3	12:2Q:60:ARG:HG2	1.99	0.44
14:2S:71:ARG:NE	14:2S:107:GLU:OE1	2.48	0.44
21:2Z:127:LYS:O	21:2Z:128:VAL:HG12	2.17	0.44
30:28:34:TRP:CE2	30:28:35:GLN:HB2	2.52	0.44
32:2a:459:G:H2'	32:2a:460:G:H8	1.82	0.44
1:1A:1262:C:H5''	1:1A:1262:C:H6	1.82	0.44
1:1A:1319:A:N3	1:1A:1342:C:H1'	2.32	0.44
1:1A:2206:C:O2'	1:1A:2207:G:H5'	2.17	0.44
1:1A:2881:G:OP2	59:1A:4188:HOH:O	2.21	0.44
4:1E:54:GLN:HE21	4:1E:54:GLN:CA	2.30	0.44
4:1E:116:VAL:HG11	4:1E:138:PRO:HB3	1.99	0.44
5:1F:172:TRP:CD1	5:1F:172:TRP:H	2.35	0.44
6:1G:11:TYR:HA	6:1G:15:VAL:HB	1.98	0.44
16:1U:46:ALA:O	16:1U:50:ARG:HB2	2.17	0.44
21:1Z:102:LEU:HD13	21:1Z:123:ASP:HA	1.99	0.44
32:1a:140:G:N2	32:1a:173:C:C2	2.85	0.44
32:1a:868:G:O2'	32:1a:884:G:O6	2.26	0.44
32:1a:1221:A:H4'	32:1a:1222:U:H5''	1.99	0.44
32:1a:1286:G:C6	32:1a:1287:G:N1	2.85	0.44
42:1k:87:THR:O	42:1k:87:THR:OG1	2.33	0.44
50:1s:63:THR:OG1	50:1s:64:GLU:N	2.50	0.44
1:2A:324:G:N2	1:2A:339:C:O2	2.42	0.44
1:2A:907:A:N3	2:2B:79:C:O2'	2.48	0.44
7:2H:126:PRO:HD2	7:2H:130:ARG:O	2.17	0.44
11:2P:101:VAL:HG12	11:2P:102:ARG:HD3	1.98	0.44
12:2Q:7:MET:HE2	12:2Q:7:MET:HB3	1.83	0.44
14:2S:11:LYS:O	14:2S:15:ARG:HG3	2.17	0.44
21:2Z:7:ALA:HB3	21:2Z:61:LEU:HD12	1.99	0.44
21:2Z:125:LEU:HB3	21:2Z:165:VAL:HG13	1.99	0.44
26:24:61:ARG:HD2	26:24:61:ARG:HA	1.70	0.44
32:2a:920:G:N2	40:2i:124:GLN:OE1	2.33	0.44
32:2a:925:G:H2'	32:2a:926:C:O4'	2.16	0.44
35:2d:173:TRP:CZ3	35:2d:193:ASP:HB3	2.52	0.44
36:2e:100:VAL:HG13	36:2e:107:ARG:HH21	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:2s:22:LEU:C	50:2s:27:GLU:HG3	2.41	0.44
50:2s:22:LEU:O	50:2s:27:GLU:HG3	2.17	0.44
1:1A:35:G:N3	1:1A:475:G:O2'	2.49	0.44
5:1F:65:TRP:CZ2	5:1F:75:HIS:HD2	2.35	0.44
14:1S:46:VAL:HG12	14:1S:48:LEU:HD12	1.99	0.44
17:1V:14:VAL:HB	17:1V:96:ILE:HG13	1.98	0.44
19:1X:12:VAL:HG22	19:1X:29:TRP:CE2	2.53	0.44
21:1Z:152:ALA:O	21:1Z:155:LEU:HB2	2.17	0.44
25:13:3:ARG:HB2	25:13:60:GLU:HG2	1.99	0.44
32:1a:304:C:H2'	32:1a:305:G:H8	1.83	0.44
32:1a:437:C:H2'	32:1a:438:C:C6	2.52	0.44
32:1a:994:A:H2'	32:1a:995:A:C8	2.53	0.44
34:1c:139:GLN:O	34:1c:143:GLU:HG3	2.17	0.44
34:1c:180:ALA:HB1	34:1c:203:PHE:CE1	2.50	0.44
35:1d:194:LEU:HD22	35:1d:194:LEU:HA	1.74	0.44
51:1t:10:LEU:HB3	51:1t:12:ALA:H	1.80	0.44
1:2A:27:A:O2'	1:2A:605:G:H5'	2.18	0.44
1:2A:105:U:H2'	1:2A:106:G:H8	1.81	0.44
1:2A:1076:G:H21	31:29:36:GLN:HE22	1.65	0.44
1:2A:1869:G:C8	1:2A:1948:A:H1'	2.52	0.44
1:2A:2752:A:C6	1:2A:2776:A:C8	3.05	0.44
6:2G:43:LEU:HB3	6:2G:44:GLY:H	1.56	0.44
14:2S:67:ARG:HG2	14:2S:71:ARG:NH2	2.33	0.44
16:2U:81:HIS:O	16:2U:84:LYS:HB3	2.17	0.44
25:23:5:LYS:NZ	25:23:34:GLU:OE2	2.43	0.44
32:2a:759:G:N2	32:2a:788:U:O4	2.51	0.44
32:2a:961:A:O2'	32:2a:1033:G:OP2	2.33	0.44
32:2a:1276:G:H2'	32:2a:1277:G:H8	1.83	0.44
32:2a:1354:G:C6	32:2a:1355:U:C4	3.05	0.44
33:2b:16:HIS:CG	33:2b:17:PHE:N	2.84	0.44
35:2d:135:LEU:HA	35:2d:136:PRO:HD2	1.84	0.44
48:2q:18:THR:HG23	48:2q:69:LYS:HD3	2.00	0.44
1:1A:852:C:O2	1:1A:2455:G:O2'	2.33	0.44
1:1A:1951:G:O2'	1:1A:1989:G:O6	2.28	0.44
1:1A:2395:G:OP2	22:10:55:ARG:NH1	2.51	0.44
2:1B:89:G:H2'	2:1B:90:A:C8	2.53	0.44
12:1Q:84:GLY:O	12:1Q:85:LYS:HB2	2.18	0.44
32:1a:77:G:H1	32:1a:87:C:H42	0.68	0.44
32:1a:295:G:O6	59:1a:2008:HOH:O	2.14	0.44
32:1a:837:A:OP2	32:1a:847:G:N1	2.44	0.44
32:1a:1140:A:H4'	32:1a:1141:C:O5'	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:1c:188:LEU:HD11	34:1c:195:VAL:HB	2.00	0.44
38:1g:110:GLN:HA	38:1g:110:GLN:HE21	1.82	0.44
39:1h:33:GLU:HG2	39:1h:48:TYR:OH	2.18	0.44
40:1i:50:LEU:HD12	40:1i:85:LEU:HD11	2.00	0.44
1:2A:80:G:N2	1:2A:100:A:OP2	2.45	0.44
1:2A:238:G:C6	1:2A:239:A:C6	3.06	0.44
1:2A:894:G:H2'	1:2A:895:A:C8	2.52	0.44
1:2A:1052:C:H5''	9:2N:35:ARG:NH1	2.33	0.44
1:2A:1056:G:OP2	16:2U:66:ASN:ND2	2.51	0.44
1:2A:1198:C:H2'	1:2A:1199:G:O4'	2.18	0.44
1:2A:1308:U:C4	1:2A:1309:G:C6	3.04	0.44
1:2A:2313:G:N1	1:2A:2326:G:C6	2.86	0.44
2:2B:80:U:H2'	2:2B:81:G:C8	2.52	0.44
4:2E:2:LYS:HA	4:2E:84:PHE:CD1	2.52	0.44
4:2E:181:LEU:HD12	4:2E:181:LEU:HA	1.80	0.44
5:2F:192:LEU:HD22	5:2F:194:MET:HG3	1.99	0.44
9:2N:104:LYS:HA	9:2N:107:LEU:HD12	1.98	0.44
12:2Q:27:VAL:HG12	12:2Q:29:PHE:H	1.82	0.44
14:2S:23:ARG:NH2	14:2S:84:GLN:HB3	2.33	0.44
16:2U:86:ALA:O	17:2V:49:THR:HG23	2.17	0.44
21:2Z:72:ARG:HA	21:2Z:72:ARG:HD3	1.86	0.44
21:2Z:110:GLY:HA3	21:2Z:174:VAL:HG11	1.98	0.44
32:2a:9:A:N6	35:2d:209:ARG:HB2	2.32	0.44
32:2a:1312:U:H4'	44:2m:23:TYR:CZ	2.52	0.44
32:2a:1359:U:H2'	32:2a:1360:A:H8	1.78	0.44
59:2a:1944:HOH:O	44:2m:104:ARG:NH2	2.50	0.44
37:2f:97:PHE:HB2	49:2r:32:ARG:HH21	1.82	0.44
40:2i:100:GLY:HA2	40:2i:102:LEU:HD12	1.99	0.44
45:2n:37:PHE:CE2	45:2n:53:LEU:HD13	2.52	0.44
49:2r:56:THR:HB	49:2r:58:LEU:HD23	1.99	0.44
1:1A:1844:G:H4'	3:1D:51:VAL:HG21	2.00	0.44
1:1A:2022:A:H2'	1:1A:2023:G:C8	2.52	0.44
11:1P:46:LYS:HE3	11:1P:46:LYS:HB3	1.68	0.44
22:10:27:GLU:HG3	22:10:68:GLU:HA	2.00	0.44
32:1a:604:C:H2'	32:1a:605:A:O4'	2.17	0.44
32:1a:676:U:H5'	32:1a:781:C:H5'	2.00	0.44
1:2A:250:A:H2'	1:2A:251:C:O4'	2.17	0.44
1:2A:1920:G:H2'	1:2A:1920:G:N3	2.33	0.44
1:2A:2381:G:C6	1:2A:2382:G:C6	3.05	0.44
6:2G:109:VAL:HG21	26:24:14:ILE:HD13	2.00	0.44
12:2Q:30:GLY:O	12:2Q:134:ARG:HD3	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:436:A:H3'	32:2a:437:C:H6	1.83	0.44
32:2a:554:G:H1'	32:2a:804:U:C4	2.52	0.44
32:2a:831:G:C2	32:2a:832:G:C8	3.06	0.44
32:2a:870:A:H2'	32:2a:871:C:C6	2.52	0.44
32:2a:900:G:H2'	32:2a:901:A:C8	2.52	0.44
32:2a:1258:G:H2'	32:2a:1259:C:C6	2.52	0.44
32:2a:1292:G:H5'	44:2m:77:ASN:ND2	2.30	0.44
32:2a:1370:G:H2'	32:2a:1371:C:C6	2.53	0.44
33:2b:125:PRO:HB2	33:2b:126:GLU:H	1.54	0.44
1:1A:222:C:H2'	1:1A:223:U:C6	2.52	0.44
1:1A:241:C:OP2	30:18:5:LYS:NZ	2.42	0.44
1:1A:820:A:H2'	1:1A:820:A:N3	2.33	0.44
1:1A:874:U:H4'	1:1A:877:G:N1	2.32	0.44
1:1A:1404:A:H5'	1:1A:1404:A:N3	2.33	0.44
1:1A:2085:C:H2'	1:1A:2086:C:C6	2.53	0.44
9:1N:67:LEU:HB3	9:1N:88:GLU:HG3	1.98	0.44
12:1Q:51:ARG:O	12:1Q:55:VAL:HG13	2.18	0.44
32:1a:1315:A:H2'	32:1a:1316:G:O4'	2.17	0.44
34:1c:36:ASP:O	34:1c:40:ARG:HG3	2.18	0.44
1:2A:62:A:O3'	19:2X:71:GLY:HA3	2.17	0.44
1:2A:91:C:H2'	1:2A:92:G:O4'	2.17	0.44
1:2A:1884:A:N1	1:2A:2108:G:O2'	2.47	0.44
2:2B:40:U:C2	2:2B:43:C:OP2	2.70	0.44
4:2E:59:VAL:HG21	4:2E:74:PRO:HB3	1.98	0.44
14:2S:15:ARG:HB3	14:2S:19:LYS:NZ	2.33	0.44
21:2Z:30:ASN:HA	21:2Z:89:PHE:HE1	1.82	0.44
22:20:56:ASP:CG	22:20:58:THR:HG1	2.26	0.44
32:2a:459:G:C2	32:2a:460:G:C4	3.06	0.44
32:2a:655:G:H1	32:2a:719:C:H42	1.65	0.44
32:2a:1115:C:H2'	32:2a:1116:G:H8	1.81	0.44
52:2u:9:ARG:O	52:2u:13:ILE:HG13	2.17	0.44
1:1A:491:A:P	29:17:34:ARG:HH21	2.41	0.44
1:1A:733:C:H5''	29:17:2:LYS:HE2	1.99	0.44
1:1A:842:C:H2'	1:1A:843:C:C6	2.53	0.44
1:1A:1674:U:H2'	1:1A:1675:G:C8	2.53	0.44
1:1A:1783:G:N7	59:1A:4359:HOH:O	2.36	0.44
1:1A:1820:C:H5''	1:1A:1821:A:OP1	2.18	0.44
1:1A:2720:G:OP2	59:1A:4192:HOH:O	2.21	0.44
1:1A:2811:A:N3	1:1A:2903:U:H1'	2.33	0.44
26:14:68:ARG:HA	26:14:68:ARG:HH21	1.83	0.44
32:1a:228:G:H1'	32:1a:258:A:N1	2.33	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1436:G:H5''	51:1t:31:SER:HB2	1.99	0.44
33:1b:102:LEU:HB3	33:1b:180:LEU:HD12	2.00	0.44
34:1c:35:GLU:O	34:1c:39:ILE:HG13	2.18	0.44
40:1i:106:ALA:O	40:1i:108:VAL:HG22	2.17	0.44
1:2A:1781:C:HO2'	1:2A:2870:G:HO2'	1.60	0.44
1:2A:2419:U:H2'	1:2A:2420:G:H8	1.83	0.44
10:2O:104:ARG:HH12	15:2T:43:GLN:HE22	1.66	0.44
11:2P:95:VAL:HG13	11:2P:125:VAL:HB	2.00	0.44
13:2R:38:VAL:HG22	13:2R:112:ALA:HB2	1.99	0.44
21:2Z:26:GLY:HA3	21:2Z:86:VAL:HG23	2.00	0.44
32:2a:255:G:H2'	32:2a:256:G:O4'	2.18	0.44
32:2a:386:C:H2'	32:2a:387:G:C8	2.53	0.44
32:2a:584:C:OP1	39:2h:97:VAL:HG12	2.18	0.44
32:2a:973:C:H4'	45:2n:8:GLU:OE2	2.17	0.44
32:2a:1109:U:H4'	32:2a:1263:U:H1'	2.00	0.44
32:2a:1115:C:H2'	32:2a:1116:G:C8	2.53	0.44
33:2b:62:ALA:HB2	33:2b:222:ILE:HG22	2.00	0.44
44:2m:70:LEU:O	44:2m:74:VAL:HG23	2.18	0.44
48:2q:62:SER:HB3	48:2q:72:ARG:HD3	1.99	0.44
1:1A:1494:G:O2'	1:1A:1574:A:N1	2.41	0.44
1:1A:2302:U:H2'	1:1A:2303:C:C6	2.53	0.44
1:1A:2855:G:H2'	1:1A:2856:U:O4'	2.18	0.44
6:1G:138:GLN:HE21	6:1G:153:ARG:HH21	1.65	0.44
7:1H:56:SER:OG	7:1H:58:GLU:HG2	2.18	0.44
8:1I:130:TYR:HB3	8:1I:138:ILE:HB	1.99	0.44
18:1W:79:GLY:HA3	18:1W:100:THR:HG22	1.98	0.44
32:1a:1096:C:N4	32:1a:1169:G:H1	2.13	0.44
32:1a:1111:C:H4'	32:1a:1131:U:O2	2.17	0.44
32:1a:1200:C:H2'	32:1a:1201:U:C6	2.52	0.44
32:1a:1382:C:C2	32:1a:1480:A:N6	2.86	0.44
35:1d:196:LEU:C	35:1d:198:VAL:H	2.25	0.44
36:1e:35:GLY:HA2	36:1e:40:ARG:O	2.17	0.44
38:1g:95:ARG:HE	38:1g:99:LEU:HD11	1.81	0.44
40:1i:7:THR:O	40:1i:83:ARG:NH1	2.37	0.44
40:1i:10:ARG:HA	40:1i:104:ARG:NH1	2.32	0.44
40:1i:70:LYS:O	40:1i:74:ILE:HG12	2.18	0.44
1:2A:154:C:N4	1:2A:159:G:H1	2.16	0.44
1:2A:1713:G:O2'	1:2A:2012:U:O4	2.33	0.44
1:2A:2044:G:H5'	1:2A:2628:C:H4'	1.98	0.44
1:2A:2303:C:O2'	1:2A:2304:C:H5'	2.17	0.44
1:2A:2638:G:N2	1:2A:2789:G:OP2	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2848:G:H5'	13:2R:46:GLY:CA	2.43	0.44
6:2G:36:LYS:HE2	6:2G:95:ARG:HH21	1.81	0.44
7:2H:88:LEU:HD23	7:2H:165:ALA:HA	2.00	0.44
15:2T:116:ALA:HB1	15:2T:121:ILE:HD11	1.99	0.44
32:2a:613:G:H2'	32:2a:614:G:O4'	2.18	0.44
32:2a:1034:C:H2'	32:2a:1035:U:C6	2.53	0.44
32:2a:1093:A:N6	32:2a:1094:A:N1	2.66	0.44
32:2a:1372:C:H2'	32:2a:1373:U:O4'	2.18	0.44
32:2a:1373:U:H2'	32:2a:1374:U:C6	2.53	0.44
34:2c:34:LEU:HD13	45:2n:25:VAL:HG21	2.00	0.44
36:2e:6:PHE:HB3	36:2e:34:VAL:HG22	2.00	0.44
37:2f:97:PHE:HB2	49:2r:32:ARG:NH2	2.33	0.44
40:2i:82:ALA:O	40:2i:86:VAL:HG23	2.18	0.44
1:1A:238:G:P	30:18:13:ARG:HH22	2.39	0.44
1:1A:732:G:OP2	1:1A:732:G:H4'	2.18	0.44
1:1A:894:G:H2'	1:1A:895:A:C8	2.53	0.44
1:1A:1992:A:OP2	3:1D:242:ARG:NH2	2.51	0.44
1:1A:2331:A:H2'	1:1A:2331:A:N3	2.33	0.44
8:1I:44:LEU:HD12	8:1I:44:LEU:HA	1.88	0.44
20:1Y:68:HIS:CE1	20:1Y:70:SER:HB3	2.52	0.44
21:1Z:14:LYS:HA	21:1Z:15:PRO:HD3	1.85	0.44
32:1a:70:G:H2'	32:1a:71:G:H8	1.83	0.44
32:1a:156:A:P	32:1a:156:A:H8	2.41	0.44
32:1a:426:A:OP2	35:1d:8:VAL:HG12	2.18	0.44
32:1a:433:U:H5''	35:1d:155:LEU:HD21	1.99	0.44
32:1a:474:C:H2'	32:1a:475:G:C8	2.53	0.44
32:1a:725:G:H2'	32:1a:726:G:C8	2.53	0.44
32:1a:1346:A:H4'	32:1a:1347:U:H2'	1.99	0.44
32:1a:1395:C:H2'	32:1a:1396:A:H8	1.83	0.44
38:1g:153:HIS:CE1	42:1k:58:PRO:HD2	2.52	0.44
41:1j:11:PHE:CE1	41:1j:67:THR:HG22	2.52	0.44
1:2A:635:G:H2'	1:2A:636:U:O2	2.18	0.44
1:2A:1967:U:H2'	1:2A:1968:C:C6	2.52	0.44
1:2A:2494:C:H2'	1:2A:2495:G:O4'	2.18	0.44
1:2A:2641:G:H2'	1:2A:2642:G:H8	1.83	0.44
6:2G:125:PHE:HB3	6:2G:166:ASP:CG	2.43	0.44
7:2H:11:VAL:HG13	7:2H:15:VAL:HG22	1.99	0.44
7:2H:27:LYS:HZ1	7:2H:32:GLU:HG3	1.82	0.44
11:2P:46:LYS:HE2	11:2P:46:LYS:HB3	1.87	0.44
24:22:31:GLU:O	24:22:35:LEU:HD23	2.18	0.44
32:2a:220:C:H2'	32:2a:221:C:C6	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:930:U:H2'	32:2a:931:G:H8	1.83	0.44
32:2a:1406:G:H2'	32:2a:1407:C:H6	1.81	0.44
34:2c:117:ALA:HA	34:2c:186:PHE:CD1	2.53	0.44
40:2i:89:ASN:HB3	40:2i:92:TYR:HB2	1.99	0.44
42:2k:62:GLN:HG3	42:2k:97:ALA:HB2	2.00	0.44
48:2q:63:ARG:HG2	48:2q:64:PRO:HD2	2.00	0.44
1:1A:28:U:H2'	1:1A:29:G:C8	2.53	0.43
1:1A:864:G:H4'	1:1A:884:C:O3'	2.18	0.43
1:1A:867:A:H2'	1:1A:990:G:H5''	2.00	0.43
2:1B:24:G:N7	2:1B:56:G:H2'	2.33	0.43
8:1I:46:ALA:O	8:1I:50:ARG:HG2	2.17	0.43
17:1V:1:MET:HB2	17:1V:43:GLU:OE2	2.18	0.43
18:1W:18:ARG:NH1	18:1W:76:VAL:O	2.51	0.43
32:1a:262:G:H4'	32:1a:263:C:C5	2.53	0.43
32:1a:352:A:N3	32:1a:364:U:O2'	2.38	0.43
32:1a:852:G:C6	32:1a:853:C:C4	3.06	0.43
32:1a:978:U:C2	32:1a:1025:G:C2	3.05	0.43
32:1a:1375:G:N2	32:1a:1480:A:C8	2.85	0.43
33:1b:170:GLU:O	33:1b:174:VAL:HG23	2.18	0.43
34:1c:19:GLU:O	34:1c:40:ARG:NH2	2.51	0.43
36:1e:84:PHE:CE2	36:1e:133:TYR:HD2	2.35	0.43
36:1e:90:VAL:O	36:1e:120:THR:HA	2.18	0.43
1:2A:82:A:N1	1:2A:96:G:O2'	2.45	0.43
1:2A:457:U:O5'	1:2A:457:U:H6	2.01	0.43
1:2A:861:C:H2'	1:2A:862:C:C6	2.53	0.43
1:2A:1098:C:H2'	1:2A:1099:A:H5'	2.00	0.43
1:2A:2325:C:H2'	1:2A:2326:G:C8	2.53	0.43
1:2A:2763:G:C6	7:2H:2:SER:HB2	2.53	0.43
5:2F:53:THR:CG2	5:2F:55:GLY:H	2.28	0.43
9:2N:43:THR:HA	9:2N:44:PRO:HD3	1.86	0.43
12:2Q:111:GLU:O	12:2Q:115:MET:HG2	2.18	0.43
21:2Z:99:TYR:HA	21:2Z:124:ILE:O	2.17	0.43
32:2a:21:U:H2'	32:2a:22:G:O4'	2.17	0.43
32:2a:523:A:H2'	32:2a:524:G:C8	2.53	0.43
32:2a:951:G:OP1	41:2j:57:LYS:NZ	2.51	0.43
32:2a:1272:G:H2'	32:2a:1273:G:H5'	1.99	0.43
32:2a:1503:G:OP1	42:2k:120:ARG:NH2	2.51	0.43
38:2g:24:THR:HA	38:2g:27:ILE:HD12	1.99	0.43
50:2s:3:ARG:HH22	50:2s:10:PHE:HB2	1.82	0.43
54:2x:35:A:C6	54:2x:36:U:C4	3.06	0.43
1:1A:353:A:HO2'	1:1A:354:A:H8	1.62	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:363:A:H2'	1:1A:364:G:O4'	2.18	0.43
1:1A:1220:G:H1'	1:1A:1221:A:C5'	2.48	0.43
1:1A:1685:U:H4'	1:1A:2710:C:H4'	2.00	0.43
1:1A:2327:C:HO2'	6:1G:128:ARG:NH1	2.16	0.43
1:1A:2604:U:H2'	1:1A:2605:C:C6	2.53	0.43
1:1A:2898:C:OP2	59:1A:4183:HOH:O	2.20	0.43
12:1Q:137:TYR:O	12:1Q:141:GLN:HG2	2.17	0.43
14:1S:59:LYS:HD2	14:1S:60:GLY:N	2.32	0.43
15:1T:54:ARG:HA	15:1T:59:THR:HG22	1.99	0.43
32:1a:77:G:H1'	32:1a:78:G:H8	1.82	0.43
32:1a:90:U:H2'	32:1a:91:G:H5'	1.99	0.43
36:1e:148:VAL:HG21	39:1h:107:LEU:HB3	2.00	0.43
39:1h:26:VAL:O	39:1h:59:LEU:N	2.49	0.43
45:1n:23:ARG:NH1	45:1n:30:ALA:HB2	2.33	0.43
1:2A:209:A:H5'	1:2A:221:A:O2'	2.19	0.43
1:2A:598:U:H2'	1:2A:599:G:C8	2.53	0.43
1:2A:955:A:N1	1:2A:2288:G:H1'	2.33	0.43
1:2A:1114:A:H4'	1:2A:1115:A:O5'	2.18	0.43
1:2A:1315:C:O2'	1:2A:1694:C:OP2	2.25	0.43
1:2A:1488:G:H1	1:2A:1594:C:H42	1.65	0.43
1:2A:1673:G:H2'	1:2A:1674:U:H6	1.82	0.43
1:2A:1833:A:O2'	3:2D:259:THR:HG21	2.18	0.43
1:2A:1958:A:C8	1:2A:1960:U:H2'	2.53	0.43
1:2A:2537:G:H2'	1:2A:2538:C:C6	2.53	0.43
11:2P:45:LEU:HD22	11:2P:45:LEU:HA	1.86	0.43
12:2Q:64:ILE:O	12:2Q:64:ILE:HG12	2.17	0.43
19:2X:31:HIS:CD2	19:2X:33:LYS:HB2	2.53	0.43
32:2a:45:G:H2'	32:2a:46:U:O4'	2.18	0.43
32:2a:899:U:O2	36:2e:19:MET:HB2	2.17	0.43
32:2a:1307:C:C2'	32:2a:1308:C:H5'	2.48	0.43
32:2a:1382:C:C2	32:2a:1480:A:N6	2.87	0.43
33:2b:222:ILE:H	33:2b:222:ILE:HG13	1.54	0.43
38:2g:111:ARG:HB3	38:2g:113:GLU:OE2	2.18	0.43
45:2n:4:LYS:HA	45:2n:7:ILE:HG12	2.00	0.43
47:2p:55:ARG:O	47:2p:58:TYR:HB3	2.17	0.43
49:2r:32:ARG:HA	49:2r:69:THR:HG21	2.00	0.43
1:1A:914:U:C4	1:1A:915:G:N7	2.86	0.43
1:1A:1474:G:H2'	1:1A:1475:C:C6	2.53	0.43
11:1P:63:PRO:C	30:18:13:ARG:HG2	2.44	0.43
34:1c:112:SER:OG	34:1c:115:LEU:HD11	2.18	0.43
34:1c:188:LEU:HD21	34:1c:195:VAL:HG11	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1e:12:LEU:HB3	36:1e:31:LEU:CB	2.48	0.43
1:2A:320:C:H2'	1:2A:321:G:O4'	2.19	0.43
1:2A:517:G:H2'	1:2A:518:G:O4'	2.19	0.43
1:2A:874:U:H4'	1:2A:877:G:N1	2.33	0.43
1:2A:1508:C:H4'	1:2A:2714:C:H5'	2.01	0.43
1:2A:1565:U:H2'	1:2A:1566:G:O4'	2.18	0.43
1:2A:1792:A:H2'	59:2A:4372:HOH:O	2.18	0.43
1:2A:2043:U:O2'	1:2A:2628:C:H5'	2.18	0.43
1:2A:2386:G:N2	1:2A:2389:A:OP2	2.41	0.43
1:2A:2419:U:H2'	1:2A:2420:G:C8	2.53	0.43
1:2A:2509:C:H3'	59:2A:3615:HOH:O	2.18	0.43
5:2F:149:ASP:OD1	5:2F:149:ASP:N	2.46	0.43
6:2G:15:VAL:HG22	6:2G:175:LEU:HB3	2.00	0.43
6:2G:43:LEU:HD12	6:2G:43:LEU:HA	1.79	0.43
6:2G:138:GLN:HG2	6:2G:144:ILE:HG21	1.98	0.43
8:2I:44:LEU:HD12	8:2I:44:LEU:HA	1.72	0.43
10:2O:68:GLU:HB3	10:2O:78:ARG:HB2	1.99	0.43
21:2Z:134:PRO:HG3	21:2Z:161:VAL:HG11	2.01	0.43
32:2a:71:G:H2'	32:2a:72:C:O4'	2.17	0.43
32:2a:294:A:C6	32:2a:295:G:C2	3.06	0.43
32:2a:659:A:O2'	42:2k:114:VAL:O	2.35	0.43
32:2a:1040:G:O3'	34:2c:197:GLY:HA3	2.18	0.43
47:2p:8:ARG:HB3	47:2p:28:ARG:HH12	1.83	0.43
47:2p:23:ASP:OD1	47:2p:25:ARG:NH1	2.51	0.43
1:1A:603:C:H2'	1:1A:604:G:C8	2.53	0.43
12:1Q:34:LEU:HD11	12:1Q:129:THR:HB	2.00	0.43
32:1a:904:G:H5''	32:1a:905:G:O5'	2.19	0.43
32:1a:909:C:H1'	32:1a:1370:G:N2	2.33	0.43
40:1i:38:GLN:HE21	40:1i:39:GLY:N	2.16	0.43
44:1m:84:ILE:HG13	44:1m:85:GLY:CA	2.49	0.43
1:2A:66:G:H2'	1:2A:67:C:O4'	2.19	0.43
1:2A:73:G:H4'	24:22:55:ARG:NH1	2.33	0.43
1:2A:491:A:N3	1:2A:729:C:H1'	2.33	0.43
1:2A:1361:U:C2	1:2A:1362:A:C8	3.06	0.43
1:2A:1741:G:N7	3:2D:14:ARG:NH2	2.66	0.43
1:2A:1808:U:H2'	1:2A:1814:A:N6	2.34	0.43
9:2N:120:LEU:HD22	9:2N:122:VAL:HG23	2.01	0.43
14:2S:48:LEU:HD23	14:2S:82:ILE:HD11	2.01	0.43
23:21:82:LEU:O	23:21:85:LEU:HD12	2.19	0.43
30:28:30:ARG:HD3	30:28:30:ARG:HA	1.51	0.43
32:2a:395:G:H2'	32:2a:396:C:C6	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:400:U:H2'	32:2a:401:U:C6	2.54	0.43
32:2a:905:G:H2'	32:2a:906:G:H8	1.83	0.43
32:2a:1298:G:H4'	45:2n:18:VAL:HG13	2.01	0.43
32:2a:1349:C:H2'	32:2a:1350:C:C6	2.53	0.43
42:2k:22:HIS:O	42:2k:28:THR:HA	2.18	0.43
44:2m:33:ALA:HB2	44:2m:64:TRP:CH2	2.54	0.43
49:2r:24:ALA:O	49:2r:26:LEU:N	2.48	0.43
1:1A:224:C:H2'	1:1A:225:C:C6	2.53	0.43
1:1A:661:A:OP1	11:1P:133:SER:OG	2.31	0.43
1:1A:1945:C:H4'	54:1x:13:C:O2'	2.18	0.43
2:1B:90:A:C5	2:1B:91:C:H1'	2.54	0.43
11:1P:3:LEU:HD12	11:1P:3:LEU:HA	1.78	0.43
11:1P:121:LYS:HG2	11:1P:122:PRO:HD2	1.99	0.43
15:1T:122:ASP:O	15:1T:126:ALA:N	2.52	0.43
20:1Y:65:ALA:HA	20:1Y:66:PRO:HD3	1.88	0.43
25:13:23:LEU:HD13	25:13:50:VAL:HG11	2.00	0.43
32:1a:703:C:OP2	32:1a:704:C:N4	2.43	0.43
51:1t:9:ASN:HD22	51:1t:10:LEU:H	1.65	0.43
1:2A:142:C:H2'	1:2A:143:C:H6	1.83	0.43
1:2A:310:C:H2'	1:2A:311:C:H6	1.84	0.43
1:2A:665:C:O2'	1:2A:2361:C:OP1	2.20	0.43
1:2A:822:G:H4'	1:2A:823:A:O5'	2.19	0.43
1:2A:1663:A:H5'	59:2A:3707:HOH:O	2.18	0.43
1:2A:1685:U:O2'	1:2A:2710:C:H4'	2.19	0.43
1:2A:2547:G:H2'	1:2A:2548:U:O4'	2.18	0.43
1:2A:2549:C:H2'	1:2A:2550:C:H6	1.84	0.43
1:2A:2785:C:H2'	1:2A:2786:C:H6	1.83	0.43
1:2A:2898:C:H2'	1:2A:2899:G:O4'	2.19	0.43
7:2H:27:LYS:NZ	7:2H:32:GLU:HG3	2.33	0.43
11:2P:83:VAL:HG23	11:2P:87:ASP:HB2	2.00	0.43
11:2P:101:VAL:HA	11:2P:106:LEU:O	2.19	0.43
16:2U:52:ARG:HA	16:2U:55:ARG:HG3	2.00	0.43
32:2a:11:A:OP2	36:2e:126:ARG:HD2	2.17	0.43
32:2a:143:G:H2'	32:2a:144:A:C8	2.52	0.43
32:2a:549:U:H3'	32:2a:550:G:H2'	1.99	0.43
37:2f:35:ALA:HA	37:2f:67:MET:HB3	2.01	0.43
45:2n:47:LEU:HA	45:2n:50:LYS:HB2	1.99	0.43
9:1N:131:GLN:CD	9:1N:131:GLN:H	2.27	0.43
12:1Q:97:VAL:HG21	12:1Q:103:MET:HE3	1.99	0.43
21:1Z:5:LEU:O	21:1Z:59:LEU:HA	2.19	0.43
32:1a:658:G:N2	32:1a:701:C:O2	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1233:A:H2'	32:1a:1234:A:C8	2.54	0.43
34:1c:32:LEU:HD22	34:1c:59:ARG:HH12	1.83	0.43
39:1h:23:SER:HA	39:1h:63:LEU:HD22	2.01	0.43
1:2A:25:G:C6	1:2A:26:G:N1	2.86	0.43
1:2A:509:C:H2'	1:2A:510:C:H6	1.84	0.43
1:2A:777:C:OP1	59:2A:3663:HOH:O	2.22	0.43
1:2A:806:G:H2'	1:2A:807:A:O4'	2.18	0.43
1:2A:856:U:OP1	59:2A:3661:HOH:O	2.21	0.43
1:2A:1095:A:H2'	1:2A:1096:G:C8	2.54	0.43
1:2A:2578:G:H2'	1:2A:2579:C:C6	2.53	0.43
1:2A:2582:C:H5''	1:2A:2583:A:H5''	2.01	0.43
9:2N:58:ASP:OD1	9:2N:58:ASP:N	2.45	0.43
18:2W:6:ILE:HA	18:2W:103:ILE:O	2.19	0.43
21:2Z:72:ARG:NH2	21:2Z:97:GLU:O	2.48	0.43
25:23:11:SER:HA	25:23:31:LEU:HD21	1.99	0.43
25:23:52:HIS:CD2	25:23:53:LEU:HG	2.53	0.43
32:2a:140:G:H2'	32:2a:141:G:O4'	2.19	0.43
32:2a:522:G:H2'	32:2a:523:A:C8	2.53	0.43
32:2a:523:A:OP2	43:2l:115:LYS:NZ	2.52	0.43
34:2c:36:ASP:OD1	34:2c:57:ILE:HG13	2.19	0.43
36:2e:93:PRO:HG3	39:2h:105:ARG:HG3	2.01	0.43
37:2f:10:LEU:HD23	37:2f:61:LEU:HD13	2.00	0.43
37:2f:82:ARG:HB3	37:2f:82:ARG:HH11	1.82	0.43
38:2g:47:CYS:HB3	38:2g:58:PRO:HB3	2.01	0.43
41:2j:89:ASP:O	41:2j:91:PRO:HD3	2.19	0.43
1:1A:195:A:H2'	1:1A:196:C:O4'	2.17	0.43
1:1A:482:A:H5''	59:1A:5612:HOH:O	2.17	0.43
1:1A:509:C:H2'	1:1A:510:C:H6	1.83	0.43
1:1A:717:C:H2'	1:1A:718:C:C6	2.53	0.43
1:1A:935:C:O2'	1:1A:936:A:O5'	2.37	0.43
1:1A:1223:C:H2'	1:1A:1224:C:C6	2.54	0.43
1:1A:1526:G:C6	1:1A:1527:U:N3	2.86	0.43
1:1A:1845:A:H8	1:1A:1845:A:OP1	2.01	0.43
1:1A:2296:C:OP2	28:16:6:ARG:NH1	2.51	0.43
1:1A:2323:U:O2'	6:1G:40:ASN:ND2	2.52	0.43
1:1A:2753:A:OP1	31:19:22:ARG:NH2	2.32	0.43
1:1A:2778:G:H2'	1:1A:2778:G:N3	2.33	0.43
14:1S:11:LYS:O	14:1S:15:ARG:HG3	2.17	0.43
14:1S:33:LYS:HB3	14:1S:34:HIS:CD2	2.54	0.43
14:1S:39:ILE:HD11	14:1S:110:LEU:HD21	2.01	0.43
14:1S:48:LEU:HD23	14:1S:82:ILE:HD11	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:1T:37:GLY:HA2	15:1T:38:ASN:HA	1.66	0.43
31:19:14:CYS:HA	31:19:27:CYS:HB2	1.99	0.43
32:1a:46:U:H2'	32:1a:47:G:C8	2.53	0.43
32:1a:767:C:OP1	32:1a:1493:C:O2'	2.35	0.43
32:1a:817:U:H2'	32:1a:818:C:C6	2.53	0.43
32:1a:1342:A:H8	32:1a:1342:A:O5'	2.02	0.43
32:1a:1491:A:H2'	32:1a:1492:C:C6	2.53	0.43
43:1l:53:ARG:HG3	43:1l:53:ARG:HH11	1.84	0.43
44:1m:96:LEU:C	44:1m:110:ARG:HG2	2.44	0.43
45:1n:11:LYS:HE2	45:1n:11:LYS:HB3	1.57	0.43
1:2A:398:G:O2'	1:2A:399:U:OP2	2.36	0.43
1:2A:1224:C:H2'	1:2A:1225:C:H6	1.82	0.43
1:2A:1402:U:H2'	1:2A:1403:G:O4'	2.18	0.43
3:2D:108:PRO:HD2	3:2D:111:LEU:HG	1.99	0.43
4:2E:128:SER:OG	4:2E:129:HIS:N	2.48	0.43
6:2G:19:LEU:HG	6:2G:175:LEU:HD22	2.00	0.43
30:28:32:LEU:O	30:28:36:LYS:HE3	2.19	0.43
32:2a:155:A:H1'	32:2a:340:A:N7	2.33	0.43
32:2a:531:A:H4'	32:2a:532:G:O5'	2.18	0.43
32:2a:729:C:H2'	32:2a:730:A:H8	1.83	0.43
32:2a:1208:C:H4'	50:2s:80:TYR:CZ	2.54	0.43
32:2a:1252:C:H2'	32:2a:1253:G:H8	1.82	0.43
45:2n:17:LYS:H	45:2n:17:LYS:HE2	1.84	0.43
1:1A:1220:G:H1'	1:1A:1221:A:H5'	2.00	0.43
1:1A:1714:A:H4'	1:1A:1715:A:O5'	2.18	0.43
1:1A:2473:U:H2'	1:1A:2474:C:C6	2.53	0.43
5:1F:143:ALA:HB1	5:1F:148:LEU:HB2	2.00	0.43
7:1H:60:ARG:HE	7:1H:60:ARG:HB3	1.47	0.43
8:1I:110:ASP:HA	8:1I:111:PRO:HD2	1.76	0.43
13:1R:111:LEU:N	59:1R:302:HOH:O	2.38	0.43
32:1a:50:U:O4	32:1a:358:G:N2	2.43	0.43
32:1a:916:A:C6	32:1a:917:G:C5	3.07	0.43
33:1b:172:ILE:H	33:1b:172:ILE:HG13	1.63	0.43
36:1e:5:ASP:OD1	36:1e:5:ASP:N	2.51	0.43
36:1e:85:GLY:O	36:1e:87:SER:N	2.46	0.43
47:1p:26:ARG:HG2	47:1p:27:LYS:N	2.34	0.43
50:1s:36:ARG:NH2	50:1s:77:THR:HG23	2.34	0.43
51:1t:59:ALA:O	51:1t:63:ILE:HG13	2.19	0.43
55:1z:8:PRO:O	55:1z:9:ARG:HB3	2.18	0.43
1:2A:724:C:H2'	1:2A:725:C:C6	2.54	0.43
1:2A:991:G:H2'	1:2A:992:G:H8	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1020:G:C2	1:2A:1035:A:C8	3.07	0.43
1:2A:2239:G:C5	1:2A:2240:C:C4	3.06	0.43
1:2A:2370:C:H2'	1:2A:2371:A:O4'	2.18	0.43
1:2A:2756:G:N2	7:2H:143:GLN:OE1	2.51	0.43
2:2B:61:G:C6	2:2B:62:C:C4	3.07	0.43
6:2G:3:LEU:HD23	6:2G:3:LEU:H	1.84	0.43
10:2O:24:VAL:HA	10:2O:39:ILE:HG22	2.00	0.43
24:22:65:ASN:OD1	24:22:69:ARG:NH1	2.42	0.43
32:2a:334:A:H2	32:2a:347:G:H22	1.67	0.43
32:2a:1280:C:OP2	38:2g:114:ARG:NH2	2.51	0.43
33:2b:193:ASP:HA	33:2b:194:PRO:HD2	1.90	0.43
50:2s:2:PRO:HB2	50:2s:3:ARG:H	1.62	0.43
51:2t:42:GLN:O	51:2t:45:GLN:HB3	2.18	0.43
9:1N:58:ASP:OD1	9:1N:58:ASP:N	2.42	0.43
20:1Y:19:LYS:HE2	20:1Y:20:TYR:CE1	2.54	0.43
20:1Y:81:LYS:HE2	20:1Y:81:LYS:HB3	1.71	0.43
22:10:10:THR:HB	22:10:11:ARG:H	1.34	0.43
23:11:18:ILE:HG12	23:11:37:ILE:HG23	2.01	0.43
23:11:23:LYS:HB3	23:11:29:GLY:HA3	2.01	0.43
24:12:2:LYS:H	24:12:2:LYS:HG2	1.62	0.43
30:18:61:LEU:O	30:18:63:PRO:HD3	2.18	0.43
32:1a:185:C:H42	32:1a:194:G:H1	1.67	0.43
32:1a:1056:U:H3	32:1a:1085:A:H61	1.67	0.43
33:1b:178:ARG:HB3	39:1h:72:PRO:HA	2.00	0.43
38:1g:41:ARG:O	38:1g:45:ASP:HB2	2.18	0.43
39:1h:121:ASP:OD2	39:1h:121:ASP:N	2.52	0.43
1:2A:335:G:H4'	1:2A:354:A:C2	2.54	0.43
1:2A:587:C:OP1	17:2V:82:ARG:NH2	2.43	0.43
1:2A:846:A:H8	1:2A:846:A:OP1	2.02	0.43
1:2A:955:A:C6	1:2A:956:A:C6	3.06	0.43
1:2A:1627:G:H2'	1:2A:1628:C:O4'	2.19	0.43
1:2A:1877:A:H4'	1:2A:1878:A:OP2	2.19	0.43
1:2A:2077:G:N2	27:25:5:PRO:HA	2.34	0.43
1:2A:2590:C:C4'	4:2E:134:ILE:HG12	2.49	0.43
1:2A:2700:U:P	1:2A:2731:G:H22	2.42	0.43
13:2R:1:MET:H1	13:2R:1:MET:HG2	1.69	0.43
22:20:82:ARG:HA	22:20:83:PRO:HD3	1.70	0.43
32:2a:48:C:H5''	32:2a:361:U:O2	2.18	0.43
32:2a:117:C:O2'	32:2a:286:C:O2	2.32	0.43
32:2a:153:G:H2'	32:2a:154:G:C8	2.53	0.43
32:2a:275:A:OP2	48:2q:95:TYR:OH	2.29	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:507:A:H61	43:2l:53:ARG:HH12	1.67	0.43
32:2a:962:C:H2'	32:2a:963:C:C6	2.54	0.43
32:2a:979:A:N6	32:2a:1022:C:H42	2.17	0.43
32:2a:1328:A:N6	32:2a:1358:A:OP2	2.50	0.43
36:2e:68:GLU:HG2	36:2e:70:PRO:HD3	2.00	0.43
36:2e:83:GLU:HA	36:2e:88:LYS:HA	2.01	0.43
54:2x:49:G:N2	54:2x:65:C:N3	2.52	0.43
1:1A:44:C:OP2	1:1A:203:G:H2'	2.19	0.43
1:1A:309:C:H2'	1:1A:310:C:C6	2.54	0.43
1:1A:1099:A:H62	1:1A:1150:U:H3	1.67	0.43
1:1A:1313:A:C2	1:1A:2034:A:C4	3.07	0.43
1:1A:1789:A:H1'	1:1A:2722:A:C2	2.54	0.43
2:1B:66:A:H61	2:1B:108:U:H2'	1.84	0.43
5:1F:116:ASP:O	5:1F:120:GLU:HG2	2.19	0.43
7:1H:7:LEU:HA	7:1H:8:PRO:HD3	1.91	0.43
7:1H:83:TYR:CE2	7:1H:138:LYS:HB2	2.53	0.43
11:1P:76:LYS:HB3	11:1P:76:LYS:HE2	1.52	0.43
25:13:7:LYS:HA	25:13:33:GLN:O	2.19	0.43
32:1a:41:C:H2'	32:1a:42:G:C8	2.54	0.43
32:1a:388:G:H2'	32:1a:389:A:C8	2.54	0.43
32:1a:414:C:H1'	32:1a:524:G:O2'	2.19	0.43
32:1a:493:A:H2'	32:1a:494:A:C8	2.54	0.43
32:1a:934:U:H2'	32:1a:935:U:O4'	2.19	0.43
32:1a:1150:A:H2'	32:1a:1151:A:C8	2.54	0.43
41:1j:13:HIS:HA	41:1j:16:LEU:HB3	2.01	0.43
47:1p:3:LYS:HD3	47:1p:65:GLN:O	2.19	0.43
55:1z:9:ARG:HA	55:1z:10:PRO:HD3	1.76	0.43
1:2A:1004:A:H5'	1:2A:2468:U:H4'	2.00	0.43
1:2A:2226:G:H3'	1:2A:2227:G:H8	1.77	0.43
2:2B:45:A:O2'	2:2B:46:A:OP1	2.36	0.43
5:2F:9:ILE:HA	5:2F:10:PRO:HD3	1.90	0.43
19:2X:31:HIS:HA	19:2X:32:PRO:HD3	1.91	0.43
21:2Z:91:LEU:HD13	21:2Z:91:LEU:HA	1.82	0.43
30:28:8:LYS:HB3	30:28:12:LYS:HE3	2.01	0.43
32:2a:674:G:C6	32:2a:675:G:C6	3.07	0.43
32:2a:1273:G:H2'	32:2a:1274:U:H6	1.80	0.43
32:2a:1310:C:OP1	52:2u:21:TYR:OH	2.28	0.43
1:1A:172:C:H2'	1:1A:173:U:H6	1.83	0.42
1:1A:315:C:C2	1:1A:372:G:C2	3.07	0.42
1:1A:359:C:O2'	20:1Y:35:TYR:OH	2.31	0.42
1:1A:663:U:H2'	1:1A:664:C:H6	1.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:943:C:H2'	1:1A:944:A:O4'	2.19	0.42
1:1A:1092:G:H1'	1:1A:1155:G:N2	2.34	0.42
1:1A:2376:G:N7	30:18:39:LYS:NZ	2.50	0.42
12:1Q:61:GLY:HA2	21:1Z:177:PRO:HB3	2.01	0.42
32:1a:77:G:H1'	32:1a:78:G:C8	2.54	0.42
32:1a:101:G:H2'	32:1a:102:G:O4'	2.19	0.42
32:1a:725:G:H2'	32:1a:726:G:O4'	2.18	0.42
1:2A:40:C:H2'	1:2A:41:G:H8	1.83	0.42
1:2A:345:A:H3'	5:2F:169:ASN:HD21	1.84	0.42
1:2A:830:A:O4'	3:2D:227:ASN:ND2	2.52	0.42
1:2A:920:G:H2'	1:2A:921:G:O4'	2.19	0.42
1:2A:1682:C:H2'	1:2A:1683:A:C8	2.54	0.42
1:2A:2342:G:O2'	1:2A:2347:A:N1	2.48	0.42
2:2B:2:C:H2'	2:2B:3:C:C6	2.53	0.42
7:2H:3:ARG:HH12	7:2H:6:ARG:N	2.14	0.42
7:2H:3:ARG:HB3	7:2H:3:ARG:HH11	1.84	0.42
15:2T:50:ILE:HA	15:2T:99:LEU:HD12	2.01	0.42
21:2Z:70:LEU:HD23	21:2Z:70:LEU:HA	1.80	0.42
21:2Z:102:LEU:HD11	21:2Z:124:ILE:HB	2.00	0.42
32:2a:37:C:OP1	43:2l:123:LYS:NZ	2.52	0.42
32:2a:601:G:H4'	47:2p:44:THR:O	2.19	0.42
32:2a:604:C:C2	35:2d:135:LEU:HG	2.53	0.42
32:2a:1040:G:H1	32:2a:1185:C:H42	1.67	0.42
32:2a:1260:U:H5''	32:2a:1261:A:H5'	2.01	0.42
34:2c:117:ALA:HB2	34:2c:186:PHE:CD2	2.54	0.42
35:2d:61:LYS:HE2	35:2d:206:PHE:CE2	2.54	0.42
36:2e:71:LEU:H	36:2e:71:LEU:HD22	1.84	0.42
41:2j:42:THR:HG23	41:2j:68:HIS:HA	2.01	0.42
44:2m:33:ALA:HB2	44:2m:64:TRP:CZ3	2.54	0.42
48:2q:19:VAL:HG23	48:2q:44:ALA:HB3	2.01	0.42
1:1A:469:C:H4'	5:1F:49:ALA:HB2	2.01	0.42
1:1A:2482:C:H2'	1:1A:2483:G:O4'	2.19	0.42
2:1B:28:C:H2'	2:1B:29:A:O4'	2.19	0.42
19:1X:57:LEU:HD12	19:1X:78:LYS:HB2	2.00	0.42
26:14:58:ARG:HD2	50:1s:65:ASN:O	2.19	0.42
27:15:16:ARG:NH1	27:15:17:ASP:OD1	2.49	0.42
32:1a:207:G:H1	32:1a:213:C:N4	2.11	0.42
32:1a:304:C:H2'	32:1a:305:G:C8	2.54	0.42
32:1a:430:U:H2'	32:1a:431:C:C6	2.54	0.42
32:1a:1145:C:C2	32:1a:1157:G:C2	3.07	0.42
32:1a:1156:G:H2'	32:1a:1157:G:H8	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:1f:61:LEU:HB3	37:1f:63:TYR:HE1	1.83	0.42
1:2A:786:U:H2'	1:2A:787:G:H8	1.83	0.42
1:2A:1789:A:H4'	1:2A:2727:C:O4'	2.19	0.42
1:2A:1973:A:N3	10:2O:22:ILE:HD12	2.34	0.42
1:2A:2323:U:O2'	6:2G:40:ASN:ND2	2.53	0.42
1:2A:2567:C:H2'	1:2A:2568:G:O4'	2.18	0.42
1:2A:2815:G:C6	1:2A:2816:G:C6	3.07	0.42
1:2A:2896:U:H2'	1:2A:2897:C:C6	2.54	0.42
4:2E:175:VAL:O	4:2E:177:PRO:HD3	2.19	0.42
9:2N:34:LEU:HD12	9:2N:34:LEU:HA	1.87	0.42
21:2Z:44:PHE:O	21:2Z:48:PHE:N	2.40	0.42
23:21:73:LEU:HD23	23:21:73:LEU:HA	1.85	0.42
32:2a:587:U:H2'	32:2a:588:G:C8	2.54	0.42
32:2a:675:G:H2'	32:2a:676:U:C6	2.54	0.42
32:2a:979:A:H61	32:2a:1022:C:N4	2.17	0.42
44:2m:40:ASN:HA	44:2m:41:PRO:HD2	1.82	0.42
1:1A:2093:G:N2	59:1A:4572:HOH:O	2.52	0.42
7:1H:44:VAL:HG12	7:1H:46:GLU:HG3	2.01	0.42
9:1N:62:VAL:HG22	9:1N:66:LYS:HD2	2.01	0.42
11:1P:100:LEU:HD23	11:1P:100:LEU:HA	1.80	0.42
13:1R:26:LYS:HE2	13:1R:70:LEU:O	2.18	0.42
32:1a:900:G:C6	32:1a:901:A:C6	3.08	0.42
32:1a:904:G:C6	32:1a:1483:G:C6	3.07	0.42
32:1a:936:A:C6	32:1a:937:A:N1	2.87	0.42
32:1a:1084:A:H4'	32:1a:1085:A:O5'	2.18	0.42
32:1a:1301:A:O2'	32:1a:1305:G:N7	2.48	0.42
32:1a:1489:G:H2'	32:1a:1490:U:O4'	2.18	0.42
39:1h:25:ASP:OD1	39:1h:60:ARG:HG3	2.19	0.42
45:1n:37:PHE:HB3	45:1n:39:LEU:HG	2.00	0.42
1:2A:323:A:H1'	1:2A:342:C:C1'	2.50	0.42
2:2B:75:G:O3'	21:2Z:10:ARG:NH2	2.52	0.42
4:2E:14:ILE:HG13	4:2E:21:VAL:HG13	2.00	0.42
4:2E:78:LEU:O	4:2E:79:ARG:HG2	2.18	0.42
5:2F:152:GLU:HA	5:2F:190:GLU:OE2	2.20	0.42
6:2G:106:LEU:O	6:2G:111:LEU:HD22	2.19	0.42
11:2P:62:LEU:O	30:28:13:ARG:NH1	2.52	0.42
32:2a:138:A:O3'	32:2a:139:G:H8	2.01	0.42
32:2a:196:G:H2'	32:2a:197:U:H6	1.83	0.42
32:2a:555:U:O4	32:2a:842:A:N6	2.52	0.42
32:2a:667:G:H2'	32:2a:668:A:C8	2.55	0.42
33:2b:63:MET:SD	33:2b:225:ALA:HB1	2.59	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:2t:47:GLY:HA2	51:2t:48:LYS:C	2.44	0.42
1:1A:230:G:C8	30:18:5:LYS:HG2	2.55	0.42
1:1A:1220:G:H1'	1:1A:1221:A:O5'	2.19	0.42
1:1A:2723:U:OP1	1:1A:2726:G:H4'	2.19	0.42
3:1D:38:LYS:HA	3:1D:38:LYS:HD2	1.81	0.42
13:1R:72:ASP:OD2	13:1R:75:LEU:HB2	2.19	0.42
20:1Y:52:SER:O	20:1Y:54:LYS:N	2.53	0.42
28:16:40:CYS:HA	28:16:41:PRO:HD3	1.79	0.42
34:1c:36:ASP:HA	34:1c:39:ILE:HD12	2.01	0.42
35:1d:187:ARG:NH1	35:1d:190:ASP:OD1	2.52	0.42
43:1l:54:LYS:HB3	43:1l:70:ILE:HB	2.01	0.42
54:1x:23:C:H2'	54:1x:24:U:H6	1.84	0.42
1:2A:104:C:H2'	1:2A:105:U:C6	2.54	0.42
1:2A:437:G:C5	11:2P:72:PRO:HB3	2.54	0.42
1:2A:1776:G:H2'	1:2A:1777:G:H8	1.84	0.42
1:2A:1857:C:OP2	3:2D:222:ARG:NH1	2.52	0.42
1:2A:1910:A:C6	1:2A:1911:A:C6	3.07	0.42
1:2A:2313:G:C2	1:2A:2314:G:C8	3.07	0.42
1:2A:2516:G:H2'	1:2A:2587:G:O6	2.19	0.42
3:2D:146:GLU:HB2	3:2D:189:CYS:HB3	2.01	0.42
6:2G:97:ASP:O	6:2G:101:ILE:HG13	2.19	0.42
14:2S:23:ARG:HE	14:2S:23:ARG:HB3	1.60	0.42
14:2S:84:GLN:CA	14:2S:111:GLU:HB2	2.43	0.42
31:29:3:VAL:HG12	31:29:37:GLY:C	2.44	0.42
32:2a:251:G:H2'	32:2a:252:U:H6	1.84	0.42
32:2a:1189:G:H2'	32:2a:1190:C:H6	1.84	0.42
32:2a:1248:G:N2	32:2a:1251:A:OP2	2.52	0.42
38:2g:117:ALA:HA	38:2g:120:ILE:HG13	2.00	0.42
38:2g:121:ALA:O	38:2g:125:MET:HG3	2.19	0.42
43:2l:109:GLY:HA3	43:2l:121:GLY:O	2.20	0.42
51:2t:61:SER:OG	51:2t:65:LYS:NZ	2.41	0.42
54:2x:17:C:H2'	54:2x:17(A):U:H6	1.84	0.42
1:1A:52:G:O2'	29:17:35:ARG:HD3	2.18	0.42
1:1A:230:G:O2'	1:1A:242:G:O6	2.29	0.42
1:1A:815:G:H5'	1:1A:1424:A:N6	2.35	0.42
1:1A:1065:A:N1	1:1A:1185:U:O2'	2.46	0.42
1:1A:1399:A:H2'	1:1A:1400:G:O4'	2.19	0.42
1:1A:1902:C:H2'	1:1A:1903:C:H6	1.83	0.42
1:1A:2111:G:H21	23:11:45:ASN:CG	2.26	0.42
1:1A:2217:C:OP2	59:1A:4193:HOH:O	2.22	0.42
1:1A:2347:A:H61	22:10:43:THR:HG22	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:1E:28:ALA:HB3	4:1E:93:VAL:CG1	2.50	0.42
5:1F:129:PHE:O	5:1F:132:VAL:HG13	2.20	0.42
8:1I:12:LEU:HD23	8:1I:12:LEU:HA	1.89	0.42
8:1I:127:VAL:HA	8:1I:140:LEU:O	2.19	0.42
21:1Z:146:ILE:HA	21:1Z:147:GLY:HA2	1.68	0.42
32:1a:963:C:H2'	32:1a:964:A:H8	1.83	0.42
32:1a:1104:U:H2'	32:1a:1105:U:H6	1.84	0.42
35:1d:158:ILE:O	35:1d:162:LEU:HD13	2.18	0.42
35:1d:171:GLY:C	35:1d:173:TRP:H	2.26	0.42
1:2A:10:G:H2'	1:2A:11:U:H5''	1.99	0.42
1:2A:1023:G:H2'	1:2A:1024:G:O4'	2.20	0.42
1:2A:1060:G:O2'	1:2A:1061:G:H5'	2.20	0.42
1:2A:1077:A:H2	1:2A:1167:G:H22	1.65	0.42
2:2B:95:C:H2'	2:2B:96:U:H6	1.83	0.42
5:2F:47:GLY:HA3	5:2F:95:ARG:O	2.20	0.42
6:2G:137:GLU:HG2	6:2G:152:LEU:HD23	2.01	0.42
9:2N:39:ARG:HA	9:2N:40:PRO:HD3	1.92	0.42
9:2N:69:GLN:O	9:2N:71:ILE:HG12	2.20	0.42
11:2P:121:LYS:HE2	11:2P:123:LEU:HD12	2.00	0.42
20:2Y:5:MET:HE2	20:2Y:5:MET:HB2	1.95	0.42
32:2a:547:A:N7	32:2a:551:G:H1'	2.34	0.42
32:2a:1236:C:H42	32:2a:1265:G:H1	1.67	0.42
32:2a:1286:G:O2'	32:2a:1315:A:N6	2.47	0.42
32:2a:1288:A:N6	32:2a:1313:G:O4'	2.52	0.42
32:2a:1344:C:H2'	32:2a:1345:C:H5''	2.02	0.42
35:2d:61:LYS:HE3	35:2d:61:LYS:HB3	1.93	0.42
35:2d:77:ASN:HD22	35:2d:77:ASN:HA	1.68	0.42
48:2q:27:PHE:CE2	48:2q:36:ILE:HD11	2.55	0.42
50:2s:41:VAL:HG22	50:2s:42:PRO:HD2	2.01	0.42
1:1A:671:G:O5'	1:1A:671:G:H8	2.02	0.42
1:1A:798:A:H3'	29:17:1:MET:HE1	2.02	0.42
1:1A:830:A:C8	1:1A:838:G:C5	3.08	0.42
1:1A:1463:G:H1'	1:1A:1627:G:N2	2.35	0.42
1:1A:2283:U:H5''	1:1A:2284:A:OP1	2.20	0.42
3:1D:71:ASP:HB3	3:1D:103:ARG:HH22	1.84	0.42
3:1D:264:LYS:HA	3:1D:265:PRO:HD3	1.93	0.42
5:1F:7:TYR:CD1	5:1F:24:LEU:HB2	2.54	0.42
26:14:48:ARG:O	26:14:50:VAL:N	2.53	0.42
27:15:55:ARG:HH12	27:15:57:VAL:HG13	1.84	0.42
32:1a:273:C:H2'	32:1a:274:G:H8	1.85	0.42
32:1a:388:G:H2'	32:1a:389:A:H8	1.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:698:G:H2'	32:1a:699:A:C8	2.55	0.42
32:1a:1047:G:H4'	32:1a:1048:U:OP1	2.20	0.42
32:1a:1298:G:N2	32:1a:1300:A:H3'	2.34	0.42
42:1k:44:SER:OG	42:1k:47:VAL:HG23	2.19	0.42
44:1m:11:ARG:HB2	44:1m:46:LYS:HB3	2.00	0.42
48:1q:37:LYS:HB2	48:1q:37:LYS:HE3	1.83	0.42
1:2A:227:U:H2'	1:2A:228:G:O4'	2.20	0.42
1:2A:1094:C:H1'	1:2A:1158:U:O2'	2.20	0.42
1:2A:2551:C:H2'	1:2A:2552:A:O4'	2.20	0.42
8:2I:15:VAL:C	8:2I:17:GLN:H	2.28	0.42
19:2X:50:LYS:O	19:2X:84:ALA:N	2.53	0.42
20:2Y:43:ASN:ND2	20:2Y:65:ALA:HB3	2.34	0.42
24:22:4:SER:HA	24:22:7:ARG:NH1	2.35	0.42
32:2a:732:C:H1'	32:2a:733:C:OP2	2.19	0.42
32:2a:863:G:O2'	32:2a:892:A:N1	2.39	0.42
32:2a:1236:C:OP1	41:2j:45:ARG:HG3	2.19	0.42
32:2a:1384:G:C2	32:2a:1385:C:H1'	2.54	0.42
43:2l:119:LYS:C	43:2l:121:GLY:H	2.27	0.42
45:2n:11:LYS:NZ	45:2n:11:LYS:HB2	2.35	0.42
1:1A:2086:C:H2'	1:1A:2087:C:C6	2.55	0.42
1:1A:2862:C:H2'	1:1A:2863:G:C8	2.54	0.42
6:1G:103:LEU:HA	6:1G:103:LEU:HD23	1.75	0.42
6:1G:146:TYR:O	6:1G:149:VAL:HG12	2.20	0.42
9:1N:131:GLN:O	9:1N:134:ARG:HG2	2.20	0.42
10:1O:68:GLU:HB3	10:1O:78:ARG:HB2	2.01	0.42
11:1P:85:LEU:HG	11:1P:115:LEU:O	2.20	0.42
20:1Y:38:ILE:HD13	20:1Y:66:PRO:HA	2.00	0.42
28:16:21:TYR:CE2	28:16:38:LYS:HG2	2.54	0.42
30:18:39:LYS:HA	30:18:42:ARG:NH1	2.35	0.42
32:1a:256:G:H2'	32:1a:257:U:C6	2.55	0.42
32:1a:267:C:H2'	32:1a:268:C:C6	2.55	0.42
32:1a:371:U:N3	32:1a:372:G:N7	2.68	0.42
32:1a:443:A:P	32:1a:470:G:H22	2.43	0.42
32:1a:820:G:H1	32:1a:828:U:H3	1.68	0.42
32:1a:1120:C:H5'	32:1a:1121:G:C5	2.55	0.42
32:1a:1434:G:O3'	51:1t:39:LYS:NZ	2.52	0.42
33:1b:71:VAL:O	33:1b:165:VAL:HG23	2.19	0.42
34:1c:52:LEU:HD23	34:1c:69:HIS:O	2.20	0.42
36:1e:37:ARG:NH1	36:1e:111:GLU:HG2	2.35	0.42
40:1i:96:LEU:H	40:1i:98:PRO:HD2	1.84	0.42
41:1j:65:LEU:HD13	45:1n:56:VAL:HG22	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:1p:1:MET:HE1	47:1p:3:LYS:HE2	2.00	0.42
1:2A:644:G:H8	1:2A:646:G:O6	2.02	0.42
1:2A:1056:G:C6	1:2A:1058:C:C4	3.08	0.42
1:2A:1089:G:H21	1:2A:1156:A:H2	1.68	0.42
1:2A:2273:U:H4'	1:2A:2339:A:C2	2.55	0.42
14:2S:15:ARG:O	14:2S:19:LYS:HG2	2.20	0.42
19:2X:36:LYS:HA	19:2X:39:ILE:HD12	2.00	0.42
21:2Z:98:MET:HE2	21:2Z:98:MET:HB2	1.99	0.42
25:23:7:LYS:HB2	25:23:34:GLU:HG2	2.02	0.42
32:2a:45:G:H1	32:2a:394:C:N4	2.16	0.42
32:2a:460:G:H2'	32:2a:461:G:C8	2.49	0.42
33:2b:115:LEU:HD12	33:2b:142:LEU:HD12	2.01	0.42
36:2e:42:GLY:HA2	36:2e:65:ASN:O	2.20	0.42
44:2m:15:VAL:O	44:2m:19:LEU:HD23	2.20	0.42
51:2t:43:LEU:O	51:2t:47:GLY:N	2.32	0.42
1:1A:330:G:N2	1:1A:332:G:H3'	2.34	0.42
1:1A:552:A:O2'	1:1A:553:A:H5'	2.20	0.42
1:1A:601:G:H2'	1:1A:602:C:C6	2.55	0.42
1:1A:1275:C:H2'	1:1A:1276:G:H8	1.83	0.42
1:1A:1639:G:H2'	1:1A:1640:G:O4'	2.20	0.42
1:1A:1869:G:C8	1:1A:1948:A:H1'	2.54	0.42
1:1A:2304:C:H2'	1:1A:2305:C:C6	2.55	0.42
1:1A:2388:A:H2'	1:1A:2389:A:C8	2.55	0.42
1:1A:2641:G:H2'	1:1A:2642:G:C8	2.54	0.42
1:1A:2888:C:OP2	59:1A:4190:HOH:O	2.21	0.42
2:1B:50:G:H5''	14:1S:61:ASN:ND2	2.34	0.42
2:1B:95:C:H2'	2:1B:96:U:C6	2.54	0.42
3:1D:213:ARG:HD2	3:1D:213:ARG:HA	1.74	0.42
5:1F:18:ARG:HG2	5:1F:19:GLU:H	1.85	0.42
5:1F:110:LEU:HD23	5:1F:110:LEU:HA	1.86	0.42
7:1H:130:ARG:HH12	7:1H:132:ARG:NH2	2.17	0.42
16:1U:17:ILE:HG23	16:1U:39:LEU:HD12	2.02	0.42
19:1X:53:LYS:HB3	19:1X:82:GLN:HB3	2.01	0.42
32:1a:341:C:O2	32:1a:341:C:H2'	2.20	0.42
32:1a:371:U:C2	32:1a:372:G:C8	3.08	0.42
32:1a:485:C:H2'	32:1a:486:G:C8	2.54	0.42
32:1a:817:U:H2'	32:1a:818:C:H6	1.84	0.42
32:1a:1359:U:OP1	38:1g:98:SER:HB3	2.20	0.42
36:1e:33:VAL:HG21	36:1e:109:ILE:HA	2.01	0.42
38:1g:103:TRP:CH2	38:1g:141:VAL:HG21	2.54	0.42
38:1g:121:ALA:O	38:1g:125:MET:HG3	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:1r:45:SER:OG	49:1r:47:THR:HG22	2.19	0.42
51:1t:33:ILE:HG23	51:1t:63:ILE:HG12	2.00	0.42
1:2A:303:C:H2'	1:2A:304:G:O4'	2.19	0.42
1:2A:494:G:N7	29:27:37:LYS:NZ	2.64	0.42
1:2A:713:U:O2	30:28:2:PRO:HD2	2.20	0.42
1:2A:909:A:H2'	1:2A:910:G:C8	2.54	0.42
1:2A:2505:G:O2'	12:2Q:80:GLU:HA	2.20	0.42
1:2A:2759:G:O6	1:2A:2767:C:H5''	2.20	0.42
9:2N:138:LEU:HB3	9:2N:140:VAL:HG13	2.02	0.42
20:2Y:54:LYS:O	20:2Y:56:PRO:HD3	2.20	0.42
32:2a:438:C:H2'	32:2a:439:C:H6	1.84	0.42
32:2a:886:A:H2'	32:2a:887:A:C8	2.54	0.42
32:2a:896:A:H2'	32:2a:897:A:O4'	2.20	0.42
34:2c:16:ARG:HD2	34:2c:16:ARG:HA	1.90	0.42
34:2c:68:VAL:HG12	34:2c:70:VAL:HG22	2.02	0.42
35:2d:3:ARG:HH12	35:2d:5:ILE:H	1.66	0.42
35:2d:73:ARG:HH11	35:2d:73:ARG:HB2	1.85	0.42
37:2f:76:ALA:O	37:2f:80:ARG:HG3	2.19	0.42
38:2g:69:VAL:HG21	38:2g:104:LEU:HD11	2.02	0.42
54:2x:50:U:H2'	54:2x:51:C:C6	2.54	0.42
1:1A:6:G:H2'	1:1A:7:A:O4'	2.19	0.42
7:1H:83:TYR:CZ	7:1H:138:LYS:HD2	2.54	0.42
10:1O:63:VAL:HG12	10:1O:106:LEU:HD11	2.02	0.42
16:1U:52:ARG:HB3	16:1U:52:ARG:HH11	1.85	0.42
18:1W:78:GLU:OE1	18:1W:99:ARG:NH1	2.52	0.42
32:1a:627:C:H5'	39:1h:31:PHE:CD1	2.55	0.42
32:1a:821:G:H1	32:1a:827:C:N4	2.16	0.42
32:1a:1053:U:H2'	32:1a:1054:C:C6	2.55	0.42
32:1a:1056:U:H2'	32:1a:1057:G:C8	2.55	0.42
1:2A:108:A:H4'	24:22:69:ARG:NH1	2.34	0.42
1:2A:530:G:O3'	1:2A:531:A:H8	2.02	0.42
1:2A:839:A:OP2	1:2A:2092:A:O2'	2.37	0.42
1:2A:865:A:C4	1:2A:1233:A:C2	3.08	0.42
1:2A:981:U:H2'	1:2A:982:G:O4'	2.19	0.42
1:2A:1101:G:H4'	1:2A:1131:A:H8	1.84	0.42
1:2A:1280:G:C6	1:2A:1281:G:N1	2.87	0.42
1:2A:1494:G:H1'	1:2A:1573:A:N1	2.34	0.42
1:2A:1652:C:H4'	1:2A:1653:A:O5'	2.19	0.42
2:2B:6:C:H42	2:2B:115:G:H1	1.67	0.42
2:2B:78:A:H2'	2:2B:79:C:O4'	2.20	0.42
8:2I:26:ALA:HA	8:2I:30:LEU:HB2	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:2I:57:ARG:O	8:2I:61:ARG:HG2	2.20	0.42
21:2Z:75:ASN:HB2	21:2Z:85:HIS:HB3	2.01	0.42
32:2a:196:G:H2'	32:2a:197:U:C6	2.55	0.42
32:2a:238:C:O2	59:2a:1923:HOH:O	2.19	0.42
32:2a:238:C:H2'	32:2a:239:A:H5'	2.02	0.42
32:2a:526:G:H5'	35:2d:41:GLY:HA3	2.02	0.42
37:2f:44:GLY:HA2	37:2f:59:TYR:CE1	2.54	0.42
38:2g:95:ARG:HE	38:2g:99:LEU:HD11	1.84	0.42
38:2g:110:GLN:HA	38:2g:110:GLN:HE21	1.84	0.42
39:2h:109:ILE:HD12	39:2h:111:ILE:HG22	2.02	0.42
43:2l:28:LYS:N	43:2l:29:GLY:HA2	2.35	0.42
1:1A:770:U:H2'	1:1A:771:G:O4'	2.20	0.42
1:1A:2842:G:H4'	1:1A:2843:G:OP2	2.19	0.42
7:1H:126:PRO:HB2	7:1H:127:GLU:H	1.63	0.42
12:1Q:68:ILE:HD13	12:1Q:103:MET:HE2	2.02	0.42
29:17:5:TRP:NE1	29:17:7:PRO:HG3	2.35	0.42
32:1a:729:C:OP1	32:1a:829:G:O2'	2.36	0.42
32:1a:802:G:HO2'	32:1a:804:U:H5	1.64	0.42
33:1b:55:PHE:HE1	33:1b:218:ALA:HA	1.84	0.42
35:1d:122:ARG:HA	35:1d:122:ARG:NE	2.34	0.42
37:1f:22:GLU:O	37:1f:26:ILE:HG13	2.20	0.42
45:1n:26:ARG:HD2	45:1n:47:LEU:HD11	2.02	0.42
48:1q:6:LEU:HD23	48:1q:23:VAL:HG21	2.01	0.42
1:2A:195:A:H2'	1:2A:196:C:O4'	2.20	0.42
1:2A:196:C:H2'	1:2A:197:C:C6	2.55	0.42
1:2A:264:U:H2'	1:2A:265:C:C6	2.55	0.42
1:2A:2083:A:N1	55:2z:11:ARG:HG2	2.35	0.42
1:2A:2503:U:H2'	1:2A:2504:U:H6	1.84	0.42
2:2B:54:G:N2	2:2B:55:U:O2	2.53	0.42
6:2G:125:PHE:O	6:2G:127:GLY:N	2.53	0.42
7:2H:11:VAL:HA	7:2H:12:PRO:HD2	1.85	0.42
9:2N:94:HIS:O	9:2N:97:ARG:HB2	2.20	0.42
16:2U:69:CYS:HB3	16:2U:74:LEU:O	2.20	0.42
17:2V:24:LYS:HA	17:2V:92:THR:OG1	2.20	0.42
21:2Z:8:TYR:HD1	21:2Z:62:PRO:HG3	1.84	0.42
24:22:1:MET:SD	24:22:56:GLN:NE2	2.93	0.42
32:2a:187:C:H2'	32:2a:188:C:O4'	2.20	0.42
32:2a:1086:C:H5''	33:2b:98:LEU:HD13	2.01	0.42
32:2a:1170:A:H2'	32:2a:1171:C:O4'	2.18	0.42
32:2a:1281:A:H2'	32:2a:1281:A:N3	2.35	0.42
32:2a:1394:C:H2'	32:2a:1395:C:H6	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:2e:103:GLY:O	36:2e:106:PRO:HD2	2.20	0.42
39:2h:29:SER:HB3	39:2h:32:LYS:HB2	2.02	0.42
42:2k:14:VAL:HG21	42:2k:34:ASP:HB3	2.02	0.42
50:2s:32:LYS:HA	50:2s:50:ALA:HB3	2.01	0.42
1:1A:152:C:OP2	23:11:92:LYS:NZ	2.53	0.41
1:1A:921:G:H2'	1:1A:922:C:O4'	2.20	0.41
1:1A:1187:A:C4	1:1A:1189:G:C8	3.08	0.41
1:1A:2227:G:O2'	1:1A:2228:A:OP1	2.35	0.41
1:1A:2590:C:H2'	1:1A:2591:U:O4'	2.19	0.41
1:1A:2712:C:H2'	1:1A:2713:U:H2'	2.02	0.41
5:1F:24:LEU:HB3	5:1F:115:ALA:HB2	2.02	0.41
11:1P:83:VAL:HG23	11:1P:87:ASP:HB2	2.02	0.41
18:1W:9:TYR:HA	18:1W:100:THR:HG23	2.02	0.41
19:1X:60:ARG:HH22	29:17:47:ARG:NH2	2.14	0.41
32:1a:838:A:H3'	32:1a:839:G:C8	2.53	0.41
32:1a:1237:G:C2	32:1a:1265:G:C2	3.08	0.41
32:1a:1306:A:O4'	32:1a:1344:C:H4'	2.20	0.41
33:1b:121:LEU:C	33:1b:123:ALA:H	2.28	0.41
35:1d:117:ALA:O	35:1d:121:VAL:HG23	2.19	0.41
52:1u:15:ARG:HB2	52:1u:15:ARG:NH1	2.35	0.41
1:2A:113:C:H2'	1:2A:114:G:O4'	2.20	0.41
1:2A:539:A:H1'	1:2A:603:C:H1'	2.01	0.41
1:2A:548:U:H2'	1:2A:549:U:C6	2.55	0.41
1:2A:894:G:N3	1:2A:977:A:H1'	2.35	0.41
1:2A:1316:G:OP2	59:2A:3660:HOH:O	2.22	0.41
1:2A:1726:U:N3	1:2A:1794:G:OP2	2.48	0.41
21:2Z:23:LYS:NZ	21:2Z:40:ASP:OD2	2.47	0.41
26:24:33:VAL:HG12	26:24:34:GLU:H	1.85	0.41
29:27:13:ALA:HB2	29:27:48:LYS:HE2	2.01	0.41
32:2a:879:A:O2'	32:2a:1491:A:OP1	2.31	0.41
32:2a:963:C:H2'	32:2a:964:A:C8	2.55	0.41
32:2a:1408:U:H1'	32:2a:1454:G:N2	2.35	0.41
32:2a:1493:C:H2'	32:2a:1494:G:H8	1.83	0.41
33:2b:16:HIS:C	33:2b:17:PHE:HD1	2.28	0.41
33:2b:215:LEU:O	33:2b:219:VAL:HG23	2.20	0.41
34:2c:5:ILE:HG21	41:2j:51:ARG:HH22	1.84	0.41
36:2e:72:GLN:O	36:2e:75:THR:HG22	2.20	0.41
38:2g:52:GLU:H	38:2g:52:GLU:CD	2.27	0.41
41:2j:23:ILE:HA	41:2j:23:ILE:HD13	1.80	0.41
42:2k:85:ARG:HA	42:2k:112:THR:OG1	2.20	0.41
1:1A:873:U:OP1	59:1A:4186:HOH:O	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1215:G:C2	1:1A:1224:C:C2	3.08	0.41
1:1A:1470:G:H2'	1:1A:1471:G:O4'	2.20	0.41
1:1A:1524:G:O2'	1:1A:1604:A:N1	2.50	0.41
1:1A:2324:C:H2'	1:1A:2325:C:H6	1.85	0.41
3:1D:4:LYS:HB3	3:1D:18:VAL:HG23	2.02	0.41
7:1H:11:VAL:HG21	7:1H:50:VAL:HG23	2.01	0.41
8:1I:92:VAL:HG11	8:1I:144:VAL:HG11	2.02	0.41
9:1N:85:ILE:HA	9:1N:86:PRO:HD3	1.87	0.41
12:1Q:58:PHE:O	12:1Q:60:ARG:N	2.50	0.41
18:1W:14:PRO:HG2	18:1W:78:GLU:CG	2.45	0.41
21:1Z:44:PHE:CZ	21:1Z:86:VAL:HG11	2.55	0.41
32:1a:104:C:O2'	47:1p:25:ARG:O	2.34	0.41
32:1a:722:C:H2'	32:1a:723:C:C6	2.56	0.41
32:1a:933:U:H1'	32:1a:1209:A:N6	2.36	0.41
32:1a:1325:G:O2'	40:1i:121:ARG:HD2	2.19	0.41
47:1p:51:VAL:HG11	47:1p:79:VAL:HG21	2.02	0.41
50:1s:3:ARG:HH12	50:1s:10:PHE:HB2	1.84	0.41
50:1s:17:GLU:O	50:1s:20:LEU:N	2.54	0.41
50:1s:43:GLU:OE1	50:1s:43:GLU:N	2.54	0.41
54:1x:61:C:H2'	54:1x:62:C:C6	2.54	0.41
1:2A:5:A:C2	1:2A:6:G:C8	3.08	0.41
1:2A:138:A:C8	1:2A:1453:C:O2'	2.70	0.41
1:2A:433:G:H2'	1:2A:434:G:C8	2.55	0.41
1:2A:552:A:C2	1:2A:2064:C:H5'	2.54	0.41
1:2A:775:G:H2'	1:2A:1805:U:H1'	2.01	0.41
1:2A:1116:G:H1'	1:2A:1134:G:C8	2.55	0.41
1:2A:1699:G:C6	13:2R:9:LYS:HB2	2.55	0.41
1:2A:1910:A:N1	1:2A:2245:G:H1'	2.35	0.41
1:2A:2124:C:O2	1:2A:2207:G:N1	2.50	0.41
1:2A:2851:G:H2'	1:2A:2852:G:O4'	2.19	0.41
6:2G:16:ARG:NH2	6:2G:33:ARG:HD2	2.35	0.41
12:2Q:29:PHE:HB2	12:2Q:105:GLU:OE2	2.19	0.41
12:2Q:38:GLU:HG3	12:2Q:127:ILE:HB	2.01	0.41
27:25:16:ARG:HG3	27:25:17:ASP:N	2.35	0.41
32:2a:101:G:H2'	32:2a:102:G:O4'	2.20	0.41
32:2a:317:A:C2	32:2a:329:G:C2	3.08	0.41
32:2a:821:G:H1	32:2a:827:C:N4	2.17	0.41
32:2a:1034:C:H2'	32:2a:1035:U:H6	1.85	0.41
32:2a:1117:G:C6	32:2a:1118:U:H1'	2.54	0.41
33:2b:92:TYR:CE2	33:2b:149:LEU:C	2.98	0.41
35:2d:201:GLN:OE1	36:2e:116:THR:OG1	2.39	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:301:A:HO2'	1:1A:302:C:P	2.43	0.41
1:1A:839:A:O2'	59:1A:4161:HOH:O	2.18	0.41
1:1A:857:U:O2'	11:1P:21:ARG:HD3	2.20	0.41
1:1A:1356:G:O2'	29:17:47:ARG:NH2	2.53	0.41
1:1A:2269:C:O2'	1:1A:2438:C:OP2	2.35	0.41
1:1A:2359:U:O4	1:1A:2393:G:N1	2.54	0.41
1:1A:2898:C:H2'	1:1A:2899:G:O4'	2.20	0.41
7:1H:69:ARG:HG3	7:1H:70:THR:N	2.34	0.41
16:1U:76:TYR:CZ	16:1U:80:ILE:HG13	2.54	0.41
16:1U:104:GLN:H	16:1U:104:GLN:HG3	1.60	0.41
17:1V:69:LYS:NZ	59:1V:301:HOH:O	2.46	0.41
20:1Y:9:LYS:HA	20:1Y:10:GLY:HA2	1.64	0.41
24:12:64:LEU:HD21	24:12:68:ARG:HE	1.85	0.41
30:18:28:GLY:O	30:18:36:LYS:NZ	2.43	0.41
32:1a:199:U:O4'	51:1t:102:GLY:HA2	2.19	0.41
32:1a:447:A:H4'	47:1p:72:ARG:CZ	2.50	0.41
32:1a:825:U:H6	32:1a:825:U:P	2.43	0.41
47:1p:51:VAL:HG11	47:1p:74:LEU:HD23	2.02	0.41
1:2A:5:A:H2	1:2A:6:G:C8	2.39	0.41
1:2A:440:C:H2'	1:2A:441:A:C8	2.55	0.41
1:2A:608:A:N1	1:2A:855:G:O2'	2.38	0.41
1:2A:766:C:H2'	1:2A:767:C:H6	1.85	0.41
1:2A:966:G:C6	1:2A:967:U:C4	3.09	0.41
1:2A:1366:A:H2'	1:2A:1367:A:O4'	2.21	0.41
4:2E:40:GLU:H	4:2E:40:GLU:HG2	1.56	0.41
18:2W:17:VAL:HG11	18:2W:103:ILE:HD11	2.02	0.41
20:2Y:52:SER:HB2	20:2Y:53:PRO:HD2	2.02	0.41
26:24:15:ILE:HB	26:24:32:TYR:CD1	2.55	0.41
32:2a:160:C:H2'	32:2a:161:G:C8	2.55	0.41
32:2a:693:G:H2'	32:2a:694:G:H8	1.84	0.41
32:2a:721:A:H2'	32:2a:722:C:H6	1.85	0.41
32:2a:839:G:HO2'	32:2a:852:G:HO2'	1.59	0.41
32:2a:1041:G:H2'	32:2a:1042:C:O4'	2.20	0.41
32:2a:1490:U:H2'	32:2a:1491:A:H8	1.85	0.41
33:2b:44:LEU:H	33:2b:44:LEU:HD22	1.86	0.41
34:2c:5:ILE:HG22	41:2j:51:ARG:HH12	1.85	0.41
34:2c:121:ALA:HB1	34:2c:189:ALA:HB2	2.01	0.41
35:2d:182:LYS:HB3	35:2d:183:GLY:H	1.69	0.41
36:2e:78:HIS:NE2	36:2e:142:LEU:HA	2.35	0.41
38:2g:72:ARG:HD3	38:2g:142:GLU:OE2	2.19	0.41
40:2i:23:ASN:OD1	40:2i:25:LYS:HG2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:2j:46:ARG:HG3	41:2j:64:GLU:CB	2.50	0.41
1:1A:75:C:OP1	24:12:59:ARG:HD3	2.21	0.41
1:1A:241:C:O2'	59:1A:4196:HOH:O	2.22	0.41
1:1A:645:A:OP2	11:1P:108:LYS:NZ	2.45	0.41
1:1A:904:U:O2	1:1A:2279:A:H2'	2.21	0.41
1:1A:921:G:H1	1:1A:947:C:N4	2.14	0.41
1:1A:1845:A:N1	59:1A:4356:HOH:O	2.36	0.41
1:1A:1937:A:H2'	1:1A:1938:U:O4'	2.20	0.41
1:1A:2325:C:H2'	1:1A:2326:G:H8	1.85	0.41
1:1A:2505:G:O2'	12:1Q:80:GLU:HA	2.21	0.41
4:1E:5:LEU:HD21	4:1E:79:ARG:HB3	2.03	0.41
7:1H:3:ARG:CG	7:1H:6:ARG:HG2	2.50	0.41
7:1H:8:PRO:O	7:1H:69:ARG:NH1	2.53	0.41
12:1Q:21:THR:HG21	12:1Q:101:ARG:N	2.34	0.41
15:1T:51:ARG:NH1	59:1T:3101:HOH:O	2.18	0.41
15:1T:101:PHE:N	59:1T:3102:HOH:O	2.35	0.41
23:11:82:LEU:HA	23:11:85:LEU:HD12	2.02	0.41
25:13:18:ASP:OD1	25:13:18:ASP:N	2.53	0.41
32:1a:41:C:H2'	32:1a:42:G:H8	1.86	0.41
32:1a:113:A:H4'	32:1a:114:A:C8	2.55	0.41
32:1a:671:A:N3	32:1a:672:G:H1'	2.34	0.41
32:1a:1270:A:N1	32:1a:1354:G:H1'	2.36	0.41
33:1b:21:ARG:C	33:1b:23:ARG:N	2.78	0.41
35:1d:22:LYS:HD2	35:1d:25:ARG:HD2	2.02	0.41
40:1i:49:PRO:HG3	40:1i:78:LYS:O	2.20	0.41
41:1j:47:PHE:N	41:1j:63:PHE:O	2.40	0.41
51:1t:29:LYS:O	51:1t:33:ILE:HG13	2.20	0.41
1:2A:310:C:H2'	1:2A:311:C:C6	2.55	0.41
1:2A:409:U:H2'	1:2A:411:C:H5	1.85	0.41
1:2A:1041:A:H4'	16:2U:91:ASP:OD2	2.20	0.41
1:2A:1194:G:H2'	1:2A:1195:C:C6	2.56	0.41
1:2A:1643:C:H2'	1:2A:1644:C:C6	2.55	0.41
1:2A:1821:A:C8	1:2A:1822:G:C8	3.09	0.41
1:2A:2072:A:OP2	1:2A:2072:A:H8	2.03	0.41
1:2A:2272:C:H1'	1:2A:2399:A:N3	2.36	0.41
1:2A:2367:C:O3'	22:20:20:ARG:HD2	2.21	0.41
1:2A:2416:G:C5'	11:2P:75:ILE:HD13	2.51	0.41
1:2A:2689:C:H2'	1:2A:2690:A:O4'	2.20	0.41
1:2A:2693:U:O2'	15:2T:58:ASN:ND2	2.53	0.41
14:2S:5:THR:O	14:2S:8:GLU:N	2.54	0.41
32:2a:367:G:H1'	32:2a:467:A:H1'	2.00	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:425:U:H3'	35:2d:9:CYS:SG	2.60	0.41
32:2a:459:G:C6	32:2a:460:G:C6	3.09	0.41
32:2a:1214:U:H2'	32:2a:1215:G:O4'	2.19	0.41
35:2d:121:VAL:O	35:2d:134:ASP:HA	2.20	0.41
36:2e:105:VAL:HB	36:2e:106:PRO:HD3	2.02	0.41
36:2e:110:LEU:O	36:2e:115:VAL:HG13	2.20	0.41
37:2f:21:LEU:O	37:2f:25:ILE:HG13	2.20	0.41
44:2m:87:TYR:O	44:2m:91:ARG:HG2	2.21	0.41
1:1A:82:A:OP2	20:1Y:8:LYS:NZ	2.39	0.41
1:1A:661:A:H5''	11:1P:117:GLU:HG2	2.03	0.41
1:1A:955:A:N3	1:1A:2275:C:O2'	2.48	0.41
1:1A:2210:U:H2'	1:1A:2211:G:C8	2.55	0.41
1:1A:2704:A:H2'	1:1A:2705:G:H8	1.86	0.41
6:1G:39:ILE:HD11	6:1G:102:PHE:CZ	2.56	0.41
8:1I:93:THR:H	8:1I:96:ASP:HB2	1.84	0.41
32:1a:50:U:O4	32:1a:361:U:H5	2.03	0.41
32:1a:296:A:H1'	32:1a:549:U:O2	2.21	0.41
32:1a:447:A:N7	32:1a:464:C:N4	2.68	0.41
32:1a:677:G:H2'	32:1a:678:A:H8	1.84	0.41
32:1a:855:C:H5''	39:1h:88:LYS:HD3	2.01	0.41
33:1b:92:TYR:CE1	33:1b:94:ASN:HB2	2.55	0.41
36:1e:12:LEU:HB3	36:1e:31:LEU:HB2	2.03	0.41
45:1n:4:LYS:HA	45:1n:7:ILE:HG12	2.01	0.41
46:1o:84:LYS:HD3	46:1o:84:LYS:C	2.46	0.41
1:2A:75:C:N4	1:2A:106:G:H1	2.19	0.41
1:2A:285:C:H1'	1:2A:289:G:H1'	2.01	0.41
1:2A:791:G:H2'	1:2A:792:A:H5'	2.03	0.41
1:2A:934:C:H2'	1:2A:935:C:C6	2.56	0.41
1:2A:1313:A:H2'	1:2A:1314:A:O4'	2.20	0.41
1:2A:1320:A:N1	1:2A:1340:C:O2'	2.48	0.41
1:2A:1677:A:OP1	59:2A:3662:HOH:O	2.21	0.41
1:2A:2107:U:H2'	1:2A:2108:G:C8	2.55	0.41
1:2A:2343:U:O2'	1:2A:2346:A:N3	2.41	0.41
1:2A:2485:C:H5''	1:2A:2486:C:OP2	2.20	0.41
2:2B:40:U:N3	2:2B:43:C:OP2	2.53	0.41
4:2E:9:VAL:HB	15:2T:3:ARG:HG2	2.02	0.41
4:2E:111:ARG:HA	13:2R:1:MET:SD	2.61	0.41
6:2G:80:PHE:C	6:2G:82:LEU:N	2.78	0.41
11:2P:126:VAL:HG12	11:2P:148:LEU:HD22	2.02	0.41
14:2S:77:ALA:HB1	14:2S:82:ILE:HB	2.03	0.41
17:2V:89:GLN:HA	17:2V:90:PRO:HD3	1.90	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:2Y:20:TYR:CE1	20:2Y:43:ASN:HA	2.56	0.41
26:24:14:ILE:CG2	26:24:22:ILE:HB	2.50	0.41
32:2a:386:C:O3'	47:2p:28:ARG:NH2	2.54	0.41
32:2a:448:A:C5	32:2a:449:C:C4	3.09	0.41
32:2a:489:G:H2'	32:2a:490:G:H8	1.86	0.41
32:2a:562:C:O2'	32:2a:712:A:O2'	2.31	0.41
32:2a:980:G:C5	32:2a:981:G:H1'	2.55	0.41
32:2a:1236:C:H2'	32:2a:1237:G:O4'	2.19	0.41
32:2a:1478:A:H5''	32:2a:1486:G:H5''	2.02	0.41
33:2b:25:ASN:HA	33:2b:26:PRO:HD3	1.78	0.41
35:2d:3:ARG:HB2	35:2d:3:ARG:NH1	2.32	0.41
35:2d:52:SER:O	35:2d:56:VAL:HG23	2.20	0.41
43:2l:27:LEU:HD13	43:2l:98:TYR:CE1	2.55	0.41
44:2m:16:ASP:N	44:2m:16:ASP:OD1	2.53	0.41
48:2q:81:ARG:HD2	48:2q:81:ARG:HA	1.90	0.41
1:1A:68:G:H5''	1:1A:109:U:O2	2.21	0.41
1:1A:291:G:C6	1:1A:292:C:C4	3.08	0.41
1:1A:765:C:O5'	1:1A:765:C:H6	2.03	0.41
1:1A:873:U:O2	1:1A:2257:G:H4'	2.21	0.41
1:1A:1222:C:H2'	1:1A:1223:C:H6	1.86	0.41
1:1A:1224:C:H2'	1:1A:1225:C:C6	2.55	0.41
1:1A:1311:G:O2'	1:1A:2033:G:O6	2.30	0.41
1:1A:1626:A:OP2	1:1A:1626:A:H8	2.04	0.41
1:1A:2694:C:O2	10:1O:70:LYS:NZ	2.26	0.41
17:1V:49:THR:O	17:1V:49:THR:HG22	2.21	0.41
18:1W:19:LEU:HB3	27:15:25:LEU:HD11	2.01	0.41
19:1X:35:THR:O	19:1X:38:GLU:HG2	2.21	0.41
25:13:26:LEU:O	25:13:35:ARG:NE	2.54	0.41
32:1a:344:G:C4	32:1a:345:A:C8	3.08	0.41
32:1a:1271:A:N1	32:1a:1354:G:O2'	2.49	0.41
33:1b:27:LYS:C	33:1b:29:ALA:H	2.29	0.41
34:1c:22:TRP:CH2	45:1n:54:PRO:HG3	2.55	0.41
38:1g:46:ALA:HB1	38:1g:121:ALA:HB2	2.03	0.41
1:2A:66:G:N2	1:2A:72:A:O5'	2.53	0.41
1:2A:184:A:C4	1:2A:851:G:C6	3.09	0.41
1:2A:364:G:H2'	1:2A:365:G:O4'	2.20	0.41
1:2A:706:G:H5'	5:2F:99:TYR:CE2	2.55	0.41
1:2A:1683:A:H4'	1:2A:2722:A:O2'	2.21	0.41
1:2A:2251:C:H2'	1:2A:2252:A:H8	1.86	0.41
1:2A:2503:U:H2'	1:2A:2504:U:C6	2.56	0.41
1:2A:2798:U:O2'	4:2E:65:GLY:HA3	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:2D:142:VAL:HG23	3:2D:193:VAL:HA	2.02	0.41
7:2H:7:LEU:O	7:2H:69:ARG:HD3	2.20	0.41
7:2H:118:PRO:O	7:2H:121:ILE:HB	2.20	0.41
16:2U:110:VAL:O	16:2U:113:ALA:HB3	2.21	0.41
18:2W:82:LEU:HB3	18:2W:84:ARG:NH1	2.36	0.41
20:2Y:23:ARG:HG2	20:2Y:42:VAL:HG22	2.03	0.41
32:2a:184:G:C6	32:2a:185:C:C4	3.09	0.41
32:2a:372:G:H5''	47:2p:5:ARG:HB2	2.02	0.41
32:2a:952:A:OP2	45:2n:41:ARG:NH1	2.54	0.41
32:2a:1269:A:N3	32:2a:1335:G:O2'	2.45	0.41
32:2a:1489:G:H2'	32:2a:1490:U:O4'	2.21	0.41
34:2c:39:ILE:HG22	34:2c:43:LEU:HD12	2.02	0.41
40:2i:96:LEU:HD23	40:2i:96:LEU:HA	1.93	0.41
1:1A:6:G:H2'	1:1A:7:A:C8	2.56	0.41
1:1A:1863:U:O2'	1:1A:1990:A:N1	2.47	0.41
59:1A:4570:HOH:O	28:16:2:ALA:N	2.54	0.41
4:1E:21:VAL:HA	4:1E:22:PRO:HD3	1.90	0.41
5:1F:93:LYS:HD3	5:1F:93:LYS:HA	1.96	0.41
7:1H:33:LEU:HD21	7:1H:136:ILE:HG13	2.03	0.41
7:1H:67:LEU:HG	7:1H:71:LEU:HD22	2.03	0.41
15:1T:127:ALA:C	15:1T:129:ARG:N	2.77	0.41
29:17:31:LEU:HD22	29:17:42:LEU:HB3	2.02	0.41
32:1a:100:C:H2'	32:1a:101:G:H8	1.86	0.41
32:1a:273:C:OP1	48:1q:41:LYS:HE3	2.21	0.41
32:1a:1087:G:O5'	33:1b:111:ARG:HD2	2.20	0.41
32:1a:1400:G:C6	32:1a:1460:G:C6	3.09	0.41
34:1c:87:LEU:O	34:1c:91:LEU:HB2	2.20	0.41
34:1c:111:LEU:HD21	34:1c:144:SER:O	2.21	0.41
46:1o:71:GLN:HG2	46:1o:78:TYR:CD1	2.56	0.41
1:2A:98:G:HO2'	24:22:7:ARG:HH22	1.64	0.41
1:2A:346:G:H1'	1:2A:1249:U:O2	2.20	0.41
1:2A:653:G:H1'	1:2A:663:U:O2'	2.20	0.41
1:2A:1717:U:O2'	1:2A:1719:U:H5	2.04	0.41
1:2A:1816:A:C4	1:2A:1959:A:C6	3.09	0.41
1:2A:2860:A:H2'	1:2A:2861:G:O4'	2.21	0.41
3:2D:10:THR:OG1	3:2D:13:ARG:HG2	2.21	0.41
7:2H:24:VAL:HG11	7:2H:43:VAL:HG11	2.03	0.41
12:2Q:54:MET:HE1	12:2Q:104:PHE:HB3	2.03	0.41
20:2Y:19:LYS:HE2	20:2Y:20:TYR:CE1	2.55	0.41
32:2a:662:U:H2'	32:2a:663:C:C6	2.56	0.41
32:2a:951:G:H3'	32:2a:952:A:H5''	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:2j:61:GLU:OE2	45:2n:49:HIS:NE2	2.52	0.41
1:1A:271:U:H4'	8:1I:50:ARG:HH22	1.86	0.41
1:1A:554:G:O4'	1:1A:554:G:N3	2.52	0.41
1:1A:623:C:OP1	5:1F:108:LYS:HE3	2.21	0.41
1:1A:1956:G:H1'	1:1A:1985:G:N2	2.36	0.41
1:1A:2282:G:OP1	22:10:18:ALA:HB1	2.21	0.41
12:1Q:14:ARG:HG2	12:1Q:41:TRP:HH2	1.85	0.41
12:1Q:69:PHE:HA	12:1Q:70:PRO:HD3	1.98	0.41
21:1Z:67:LEU:HA	21:1Z:68:PRO:HD3	1.92	0.41
21:1Z:155:LEU:HD12	21:1Z:155:LEU:HA	1.85	0.41
26:14:46:GLN:HB2	26:14:48:ARG:CZ	2.51	0.41
32:1a:198:G:O2'	51:1t:102:GLY:N	2.53	0.41
32:1a:798:A:N7	32:1a:800:A:C4	2.89	0.41
32:1a:1468:C:H2'	32:1a:1469:G:C8	2.56	0.41
38:1g:67:GLU:OE2	38:1g:70:LYS:NZ	2.53	0.41
41:1j:30:SER:O	41:1j:81:THR:HB	2.20	0.41
44:1m:40:ASN:HA	44:1m:41:PRO:HD2	1.85	0.41
51:1t:47:GLY:N	51:1t:48:LYS:HB2	2.36	0.41
1:2A:917:U:H5''	1:2A:918:A:OP1	2.20	0.41
1:2A:1041:A:H5'	16:2U:93:LYS:HD3	2.02	0.41
2:2B:32:C:N4	2:2B:50:G:H1	2.19	0.41
8:2I:61:ARG:HA	8:2I:61:ARG:HD3	1.89	0.41
12:2Q:73:PRO:HA	12:2Q:93:TYR:CD1	2.56	0.41
18:2W:34:ASN:ND2	27:25:39:MET:HG3	2.36	0.41
19:2X:21:PHE:CZ	19:2X:92:LEU:HD12	2.56	0.41
24:22:9:GLN:HE22	24:22:56:GLN:HB3	1.86	0.41
32:2a:36:G:H2'	32:2a:37:C:C6	2.56	0.41
32:2a:253:G:H2'	32:2a:254:G:C8	2.55	0.41
32:2a:293:G:O2'	32:2a:295:G:N7	2.51	0.41
32:2a:387:G:C6	32:2a:388:G:C5	3.09	0.41
32:2a:654:G:H2'	32:2a:655:G:O4'	2.21	0.41
32:2a:1125:G:H2'	32:2a:1126:G:O4'	2.20	0.41
32:2a:1198:G:H2'	32:2a:1199:C:H6	1.86	0.41
32:2a:1210:C:OP2	44:2m:111:LYS:HD3	2.21	0.41
32:2a:1296:C:H2'	32:2a:1297:U:C6	2.56	0.41
33:2b:92:TYR:CD2	33:2b:92:TYR:CB	2.85	0.41
41:2j:57:LYS:HD2	41:2j:60:ARG:HH21	1.85	0.41
1:1A:210:A:H5''	1:1A:447:U:OP1	2.21	0.41
1:1A:492:G:OP1	29:17:33:ARG:HD2	2.21	0.41
1:1A:885:U:H2'	1:1A:886:C:C6	2.55	0.41
1:1A:982:G:OP1	30:18:52:LYS:HD2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1047:G:H2'	1:1A:1048:G:O4'	2.21	0.41
1:1A:1726:U:H2'	1:1A:1727:G:O4'	2.21	0.41
1:1A:1925:G:O2'	1:1A:1949:A:N1	2.47	0.41
1:1A:1947:U:O2'	1:1A:1949:A:N7	2.45	0.41
1:1A:2103:A:H2'	1:1A:2104:G:O4'	2.20	0.41
1:1A:2356:G:H4'	1:1A:2357:A:H5''	2.02	0.41
1:1A:2503:U:H2'	1:1A:2504:U:C6	2.56	0.41
1:1A:2723:U:O2'	1:1A:2725:A:H5'	2.21	0.41
1:1A:2768:U:H1'	1:1A:2769:A:H5''	2.02	0.41
3:1D:33:LEU:HD23	3:1D:33:LEU:HA	1.95	0.41
3:1D:237:GLU:OE2	59:1D:402:HOH:O	2.22	0.41
5:1F:176:LEU:HA	5:1F:176:LEU:HD23	1.89	0.41
6:1G:43:LEU:HB3	6:1G:44:GLY:H	1.60	0.41
6:1G:125:PHE:O	6:1G:127:GLY:N	2.54	0.41
6:1G:142:PRO:HG2	6:1G:143:GLU:OE1	2.21	0.41
7:1H:4:ILE:O	7:1H:69:ARG:HG2	2.21	0.41
10:1O:80:ASP:CG	15:1T:71:GLY:HA3	2.46	0.41
11:1P:70:GLN:HE21	11:1P:70:GLN:HB3	1.68	0.41
14:1S:34:HIS:ND1	14:1S:53:SER:OG	2.42	0.41
15:1T:45:PHE:CE1	15:1T:65:LYS:HD3	2.55	0.41
25:13:39:ASP:OD2	25:13:44:ARG:NH2	2.53	0.41
26:14:14:ILE:HB	26:14:22:ILE:HB	2.02	0.41
32:1a:68:C:H2'	32:1a:69:G:C8	2.55	0.41
32:1a:695:G:H2'	32:1a:696:A:H8	1.85	0.41
32:1a:853:C:O2'	39:1h:14:ARG:HD2	2.21	0.41
32:1a:1121:G:C6	32:1a:1123:C:H1'	2.56	0.41
32:1a:1266:C:H3'	32:1a:1267:A:H8	1.86	0.41
32:1a:1303:C:H5''	32:1a:1304:C:H2'	2.03	0.41
32:1a:1362:G:N7	38:1g:2:ALA:HB3	2.36	0.41
33:1b:16:HIS:HB2	33:1b:210:SER:OG	2.20	0.41
36:1e:76:ILE:HD12	36:1e:142:LEU:HD21	2.03	0.41
38:1g:152:ALA:O	38:1g:155:ARG:NE	2.54	0.41
43:1l:124:LYS:HA	43:1l:125:PRO:HD3	1.81	0.41
48:1q:31:LEU:HD23	48:1q:32:TYR:CZ	2.56	0.41
52:1u:6:ARG:HE	52:1u:15:ARG:CZ	2.34	0.41
1:2A:33:C:H2'	1:2A:34:G:C5'	2.51	0.41
1:2A:69:A:N7	19:2X:31:HIS:HE1	2.19	0.41
1:2A:628:U:H4'	1:2A:704:C:H4'	2.02	0.41
1:2A:638:G:H5''	1:2A:639:A:OP1	2.20	0.41
1:2A:668:A:C2	1:2A:2380:A:H1'	2.55	0.41
1:2A:720:G:O2'	5:2F:74:ARG:HD3	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:821:G:C4	1:2A:840:G:C8	3.08	0.41
1:2A:979:C:O2'	1:2A:980:C:H5'	2.20	0.41
1:2A:998:G:H5''	12:2Q:13:GLN:HB3	2.03	0.41
1:2A:1777:G:H2'	1:2A:1778:G:H8	1.86	0.41
1:2A:2326:G:H2'	1:2A:2327:C:C6	2.56	0.41
1:2A:2367:C:H5'	22:20:24:LYS:HZ1	1.85	0.41
1:2A:2879:C:H2'	1:2A:2880:C:O4'	2.21	0.41
2:2B:55:U:C1'	6:2G:29:TRP:HE1	2.33	0.41
2:2B:84:C:H2'	2:2B:85:G:O4'	2.21	0.41
4:2E:37:ARG:HD2	4:2E:42:ASP:CG	2.46	0.41
5:2F:167:ALA:HB1	5:2F:173:VAL:HG11	2.02	0.41
5:2F:185:ASP:HA	5:2F:188:ARG:HD3	2.02	0.41
11:2P:48:PRO:O	30:28:57:ARG:NH2	2.50	0.41
12:2Q:141:GLN:NE2	21:2Z:74:VAL:O	2.51	0.41
13:2R:28:LEU:HD23	13:2R:28:LEU:HA	1.92	0.41
14:2S:33:LYS:HB3	14:2S:34:HIS:CD2	2.56	0.41
14:2S:110:LEU:HD12	14:2S:110:LEU:HA	1.94	0.41
18:2W:92:ARG:HD2	18:2W:93:ALA:N	2.36	0.41
19:2X:4:ALA:HB1	19:2X:42:ALA:HA	2.02	0.41
30:28:34:TRP:CG	30:28:35:GLN:N	2.89	0.41
32:2a:298:G:N3	32:2a:540:C:H4'	2.35	0.41
32:2a:410:A:C5	32:2a:427:A:C2	3.09	0.41
32:2a:438:C:H2'	32:2a:439:C:C6	2.55	0.41
32:2a:551:G:O6	43:2l:5:PRO:HD3	2.20	0.41
32:2a:723:C:OP1	46:2o:2:PRO:HD3	2.21	0.41
32:2a:775:G:O6	32:2a:776:A:N6	2.50	0.41
32:2a:898:U:H2'	32:2a:899:U:H6	1.82	0.41
32:2a:982:G:H3'	32:2a:982:G:N3	2.35	0.41
32:2a:1105:U:C2	32:2a:1106:A:C8	3.09	0.41
32:2a:1202:G:H21	50:2s:54:GLY:CA	2.33	0.41
32:2a:1468:C:H2'	32:2a:1469:G:C8	2.56	0.41
32:2a:1474:C:H2'	32:2a:1475:G:O4'	2.20	0.41
35:2d:179:GLU:C	35:2d:181:MET:H	2.29	0.41
38:2g:106:GLN:O	38:2g:110:GLN:HG2	2.21	0.41
44:2m:3:ARG:HH22	44:2m:11:ARG:NE	2.19	0.41
46:2o:39:LEU:HD23	46:2o:39:LEU:HA	1.91	0.41
47:2p:38:TYR:O	47:2p:49:LEU:HD12	2.21	0.41
47:2p:72:ARG:HG3	47:2p:73:LEU:N	2.34	0.41
50:2s:3:ARG:NH2	50:2s:10:PHE:HB2	2.36	0.41
50:2s:51:VAL:O	50:2s:57:HIS:HA	2.21	0.41
51:2t:53:LEU:O	51:2t:57:ARG:HG3	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:2x:22:G:H2'	54:2x:23:C:C6	2.56	0.41
1:1A:710:C:H2'	1:1A:711:C:H6	1.86	0.41
1:1A:931:C:H3'	1:1A:932:C:H5''	2.02	0.41
1:1A:1067:G:C5	1:1A:1184:C:C4	3.09	0.41
1:1A:1383:G:O2'	1:1A:1438:A:N1	2.40	0.41
1:1A:1731:C:H2'	1:1A:1732:C:H6	1.85	0.41
1:1A:2744:G:H3'	1:1A:2745:A:O4'	2.21	0.41
1:1A:2896:U:H2'	1:1A:2897:C:C6	2.55	0.41
3:1D:69:ARG:C	3:1D:71:ASP:N	2.78	0.41
3:1D:175:LEU:HD12	3:1D:185:VAL:HG21	2.03	0.41
4:1E:2:LYS:HA	4:1E:84:PHE:CG	2.57	0.41
11:1P:63:PRO:O	30:18:13:ARG:HG2	2.20	0.41
14:1S:59:LYS:H	14:1S:59:LYS:HE3	1.85	0.41
32:1a:139:G:N2	32:1a:174:A:H1'	2.36	0.41
32:1a:179:G:H2'	32:1a:180:A:C8	2.52	0.41
32:1a:566:U:OP2	32:1a:742:G:N1	2.37	0.41
32:1a:725:G:H2'	32:1a:726:G:H8	1.86	0.41
32:1a:859:G:P	43:1l:12:ARG:HH22	2.43	0.41
32:1a:1115:C:H2'	32:1a:1116:G:H8	1.85	0.41
34:1c:32:LEU:HD13	34:1c:59:ARG:HH12	1.85	0.41
34:1c:39:ILE:O	34:1c:43:LEU:HB2	2.21	0.41
34:1c:130:VAL:O	34:1c:134:ILE:HG13	2.21	0.41
1:2A:38:C:H2'	1:2A:39:C:C6	2.56	0.41
1:2A:732:G:H21	1:2A:834:A:H61	1.68	0.41
1:2A:794:G:O6	18:2W:90:ARG:NH1	2.54	0.41
1:2A:870:A:H1'	1:2A:2369:G:N7	2.35	0.41
1:2A:1732:C:H2'	1:2A:1733:G:O4'	2.21	0.41
3:2D:137:PRO:O	3:2D:140:THR:HG23	2.21	0.41
7:2H:97:ARG:HE	7:2H:104:GLU:CD	2.29	0.41
8:2I:140:LEU:HD23	8:2I:140:LEU:HA	1.83	0.41
9:2N:99:LEU:HD22	9:2N:99:LEU:HA	1.92	0.41
10:2O:122:LEU:HD13	15:2T:72:VAL:HG11	2.02	0.41
16:2U:29:SER:C	16:2U:30:LYS:HD3	2.46	0.41
21:2Z:128:VAL:HB	21:2Z:161:VAL:HA	2.02	0.41
32:2a:30:G:H5'	32:2a:292:U:OP1	2.21	0.41
32:2a:324:C:H4'	32:2a:325:A:H5'	2.03	0.41
32:2a:380:G:H2'	32:2a:381:C:C6	2.56	0.41
32:2a:591:A:H2'	32:2a:592:A:O4'	2.20	0.41
32:2a:826:C:O5'	32:2a:826:C:H6	2.04	0.41
32:2a:1172:G:H5'	34:2c:176:HIS:CE1	2.55	0.41
34:2c:6:HIS:HA	34:2c:7:PRO:HD3	1.82	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:2g:30:ILE:HG21	38:2g:42:ILE:HD13	2.02	0.41
44:2m:94:ARG:HB3	44:2m:96:LEU:HD23	2.01	0.41
1:1A:204:A:C4	1:1A:458:A:C2	3.09	0.40
1:1A:1461:G:O2'	1:1A:1462:C:OP2	2.33	0.40
1:1A:2124:C:O2	1:1A:2208:G:N2	2.55	0.40
1:1A:2543:G:O2'	1:1A:2668:A:N1	2.53	0.40
1:1A:2734:G:H2'	1:1A:2735:C:C6	2.56	0.40
15:1T:24:PRO:HA	15:1T:49:VAL:HG22	2.03	0.40
19:1X:31:HIS:HA	19:1X:32:PRO:HD3	1.92	0.40
28:16:34:LEU:HB2	28:16:51:GLU:HB2	2.03	0.40
32:1a:239:A:C2	32:1a:242:A:C8	3.09	0.40
32:1a:1062:G:H2'	32:1a:1063:A:C8	2.55	0.40
33:1b:68:ILE:HG12	33:1b:161:ALA:HB3	2.03	0.40
36:1e:103:GLY:O	36:1e:106:PRO:HD2	2.22	0.40
45:1n:37:PHE:CE1	45:1n:53:LEU:HD13	2.56	0.40
50:1s:30:LEU:HD12	50:1s:30:LEU:HA	1.86	0.40
50:1s:52:TYR:HB2	50:1s:57:HIS:CE1	2.56	0.40
1:2A:563:G:H2'	1:2A:564:C:C6	2.56	0.40
1:2A:861:C:C2	1:2A:1237:G:C2	3.09	0.40
1:2A:905:G:N2	1:2A:962:A:OP2	2.41	0.40
1:2A:1056:G:C5	1:2A:1058:C:C4	3.09	0.40
1:2A:1072:A:C2	1:2A:2499:A:H5'	2.56	0.40
1:2A:1411:A:H2'	1:2A:1412:A:O4'	2.22	0.40
1:2A:2347:A:H61	22:20:43:THR:HG21	1.85	0.40
1:2A:2668:A:O3'	7:2H:160:LYS:NZ	2.53	0.40
1:2A:2760:A:O2'	7:2H:63:SER:O	2.30	0.40
1:2A:2857:G:C8	15:2T:97:ALA:HB2	2.56	0.40
5:2F:164:ARG:O	5:2F:168:ARG:HG3	2.20	0.40
5:2F:188:ARG:HA	11:2P:3:LEU:HD23	2.01	0.40
25:23:18:ASP:OD1	25:23:18:ASP:N	2.54	0.40
32:2a:104:C:H2'	32:2a:105:G:O4'	2.21	0.40
32:2a:1052:C:O2'	32:2a:1174:C:H1'	2.21	0.40
36:2e:33:VAL:HG13	36:2e:112:LEU:HD12	2.01	0.40
42:2k:21:ILE:HB	42:2k:84:VAL:HG22	2.02	0.40
44:2m:10:PRO:HG3	44:2m:21:TYR:CD2	2.56	0.40
49:2r:29:PHE:N	49:2r:29:PHE:HD1	2.19	0.40
1:1A:25:G:C6	1:1A:26:G:C6	3.08	0.40
1:1A:115:A:C8	1:1A:116:A:C8	3.09	0.40
1:1A:603:C:H2'	1:1A:604:G:H8	1.87	0.40
1:1A:839:A:OP2	1:1A:2092:A:O2'	2.36	0.40
1:1A:908:G:H2'	1:1A:909:A:O4'	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1732:C:H2'	1:1A:1733:G:O4'	2.21	0.40
1:1A:2514:A:H4'	1:1A:2515:U:OP1	2.22	0.40
1:1A:2574:U:H4'	10:1O:28:SER:HA	2.03	0.40
2:1B:4:C:H2'	2:1B:5:C:O4'	2.21	0.40
2:1B:28:C:OP1	14:1S:31:SER:OG	2.38	0.40
2:1B:42:C:OP1	6:1G:67:LYS:NZ	2.48	0.40
6:1G:64:THR:HB	6:1G:94:LEU:HD11	2.03	0.40
7:1H:71:LEU:HD12	7:1H:71:LEU:HA	1.87	0.40
10:1O:7:TYR:CE1	10:1O:20:MET:HB2	2.57	0.40
11:1P:130:PHE:HB2	11:1P:135:LEU:HG	2.04	0.40
32:1a:751:A:H2'	32:1a:752:A:O4'	2.22	0.40
32:1a:953:A:N6	32:1a:1350:C:O4'	2.54	0.40
32:1a:1325:G:H2'	32:1a:1326:C:C6	2.56	0.40
39:1h:112:LEU:HB3	39:1h:133:LEU:HA	2.03	0.40
1:2A:223:U:H2'	1:2A:224:C:C6	2.57	0.40
1:2A:243:A:N6	1:2A:244:A:C6	2.89	0.40
1:2A:755:U:H2'	1:2A:756:G:C8	2.56	0.40
1:2A:1244:C:H5'	59:2A:3667:HOH:O	2.21	0.40
1:2A:1332:A:C5	1:2A:1333:U:C4	3.09	0.40
1:2A:1807:U:O2'	1:2A:1808:U:H5'	2.21	0.40
2:2B:20:C:N4	2:2B:21:G:C6	2.89	0.40
7:2H:89:ILE:O	7:2H:129:THR:HG22	2.21	0.40
8:2I:118:LYS:HA	8:2I:119:PRO:HD3	1.91	0.40
13:2R:56:LYS:NZ	13:2R:90:ARG:O	2.54	0.40
20:2Y:5:MET:HE1	20:2Y:32:PRO:HA	2.02	0.40
32:2a:407:A:O2'	32:2a:409:G:H5'	2.21	0.40
32:2a:582:U:H4'	39:2h:94:TYR:CG	2.56	0.40
32:2a:935:U:H2'	32:2a:937:A:OP2	2.20	0.40
33:2b:28:PHE:CD1	33:2b:31:TYR:HB2	2.57	0.40
33:2b:81:VAL:O	33:2b:85:ALA:N	2.46	0.40
35:2d:146:ILE:N	35:2d:146:ILE:HD12	2.36	0.40
50:2s:62:ILE:HA	50:2s:66:MET:SD	2.61	0.40
50:2s:63:THR:OG1	50:2s:64:GLU:N	2.53	0.40
1:1A:141:G:H1'	19:1X:37:THR:HG21	2.03	0.40
1:1A:210:A:OP2	59:1A:4194:HOH:O	2.22	0.40
1:1A:229:A:H5''	59:1A:5710:HOH:O	2.21	0.40
1:1A:818:C:H2'	1:1A:819:U:C6	2.56	0.40
1:1A:1086:C:N4	1:1A:1159:G:H1	2.13	0.40
1:1A:2244:U:H2'	1:1A:2245:G:C8	2.57	0.40
1:1A:2710:C:H2'	1:1A:2711:C:O4'	2.22	0.40
1:1A:2771:G:OP2	59:1A:4187:HOH:O	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:1G:181:ARG:HG3	6:1G:182:LYS:H	1.86	0.40
9:1N:99:LEU:HD23	9:1N:99:LEU:HA	1.93	0.40
25:13:15:TYR:CE2	25:13:53:LEU:HD21	2.56	0.40
32:1a:548:C:OP1	43:1l:15:ARG:NE	2.46	0.40
32:1a:825:U:H6	32:1a:825:U:OP2	2.05	0.40
32:1a:1067:G:C5	32:1a:1068:U:C4	3.09	0.40
32:1a:1120:C:H6	32:1a:1120:C:O5'	2.04	0.40
32:1a:1385:C:H2'	32:1a:1386:C:O4'	2.21	0.40
33:1b:169:LYS:HE2	33:1b:169:LYS:HB3	1.77	0.40
34:1c:110:ASN:O	34:1c:141:VAL:HG22	2.22	0.40
35:1d:120:LEU:HB3	35:1d:126:ILE:HD11	2.03	0.40
42:1k:38:ASN:HA	42:1k:39:PRO:HD3	1.82	0.40
47:1p:72:ARG:HD2	47:1p:73:LEU:HD23	2.03	0.40
49:1r:58:LEU:HD12	49:1r:62:GLU:HB3	2.02	0.40
1:2A:142:C:H2'	1:2A:143:C:C6	2.57	0.40
1:2A:602:C:H2'	1:2A:603:C:C6	2.57	0.40
1:2A:901:G:H2'	1:2A:902:C:C6	2.56	0.40
1:2A:991:G:H2'	1:2A:992:G:C8	2.56	0.40
1:2A:1003:A:N6	1:2A:1004:A:N1	2.70	0.40
1:2A:1101:G:H4'	1:2A:1131:A:C8	2.56	0.40
1:2A:1232:U:C4'	17:2V:79:VAL:HG22	2.51	0.40
1:2A:1634:C:H2'	1:2A:1635:U:C6	2.56	0.40
1:2A:2037:U:H2'	1:2A:2038:U:H6	1.86	0.40
1:2A:2752:A:C6	1:2A:2753:A:C6	3.10	0.40
2:2B:28:C:H2'	2:2B:29:A:O4'	2.21	0.40
2:2B:73:A:C4	2:2B:105:A:C2	3.09	0.40
4:2E:32:PRO:HD2	4:2E:50:GLY:O	2.20	0.40
6:2G:109:VAL:O	6:2G:113:ARG:HB2	2.22	0.40
10:2O:15:GLY:O	10:2O:47:ILE:HG12	2.21	0.40
10:2O:100:GLY:O	10:2O:119:PRO:HD2	2.21	0.40
11:2P:144:GLU:HA	11:2P:145:PRO:HD3	1.87	0.40
25:23:6:VAL:HG23	25:23:35:ARG:O	2.21	0.40
32:2a:544:U:H5'	32:2a:550:G:H22	1.87	0.40
32:2a:1272:G:C5	32:2a:1273:G:C8	3.09	0.40
32:2a:1309:C:H2'	32:2a:1310:C:C6	2.56	0.40
33:2b:164:VAL:N	33:2b:185:ILE:O	2.43	0.40
34:2c:125:GLU:HA	34:2c:191:THR:HG22	2.02	0.40
42:2k:58:PRO:HG3	42:2k:89:ALA:O	2.21	0.40
44:2m:44:ARG:HB2	44:2m:47:ASP:OD1	2.22	0.40
49:2r:70:ILE:O	49:2r:74:ARG:HG3	2.21	0.40
1:1A:235:G:H4'	1:1A:412:G:C6	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:830:A:C6	3:1D:229:VAL:HG11	2.56	0.40
1:1A:2059:G:H2'	1:1A:2060:C:O4'	2.22	0.40
1:1A:2536:G:C2	1:1A:2550:C:C2	3.09	0.40
6:1G:155:MET:HE2	6:1G:155:MET:HB3	2.00	0.40
8:1I:75:LEU:HD22	8:1I:105:HIS:ND1	2.37	0.40
10:1O:105:GLU:HG2	10:1O:105:GLU:H	1.53	0.40
16:1U:112:ARG:HG2	16:1U:112:ARG:H	1.74	0.40
26:14:8:LYS:HE2	26:14:8:LYS:HB3	1.91	0.40
32:1a:45:G:C2	32:1a:46:U:H1'	2.56	0.40
32:1a:141:G:N2	32:1a:172:C:C4	2.89	0.40
32:1a:192:G:C2	32:1a:193:G:C8	3.09	0.40
32:1a:1188:G:C6	32:1a:1189:G:C5	3.09	0.40
32:1a:1221:A:N3	32:1a:1280:C:N4	2.70	0.40
35:1d:31:CYS:O	35:1d:32:ALA:HB3	2.21	0.40
35:1d:61:LYS:HA	35:1d:203:VAL:HG22	2.02	0.40
37:1f:35:ALA:HA	37:1f:67:MET:HB3	2.04	0.40
1:2A:83:G:C5	1:2A:96:G:C2	3.10	0.40
1:2A:179:A:N1	59:2A:3736:HOH:O	2.37	0.40
1:2A:330:G:H21	1:2A:353:A:N6	2.15	0.40
1:2A:483:G:O2'	29:27:39:ARG:HD3	2.22	0.40
1:2A:639:A:C4	5:2F:180:GLY:HA3	2.57	0.40
1:2A:1409:G:OP2	23:21:3:LYS:HG3	2.21	0.40
1:2A:1415:C:N4	1:2A:1416:G:C6	2.89	0.40
1:2A:1480:G:H2'	1:2A:1481:G:O4'	2.22	0.40
1:2A:1829:G:O2'	3:2D:181:GLU:OE2	2.28	0.40
1:2A:1921:A:O2'	1:2A:1922:A:OP1	2.30	0.40
1:2A:2411:G:N2	1:2A:2428:C:C2	2.89	0.40
2:2B:78:A:C2	2:2B:100:A:C4	3.09	0.40
3:2D:72:LYS:CG	3:2D:103:ARG:HH21	2.35	0.40
3:2D:145:VAL:HG12	3:2D:146:GLU:O	2.21	0.40
3:2D:221:VAL:HG22	3:2D:226:MET:HE3	2.02	0.40
6:2G:23:PHE:HB2	6:2G:25:TYR:CZ	2.55	0.40
6:2G:49:ASP:C	6:2G:51:ARG:H	2.28	0.40
6:2G:108:ASN:HD22	26:24:37:SER:HB2	1.86	0.40
10:2O:1:MET:HE2	10:2O:1:MET:HB3	2.01	0.40
11:2P:98:GLU:O	11:2P:101:VAL:HG12	2.20	0.40
13:2R:70:LEU:HA	13:2R:70:LEU:HD23	1.80	0.40
32:2a:103:A:C6	32:2a:322:G:C6	3.09	0.40
32:2a:808:C:H2'	32:2a:809:G:H8	1.87	0.40
32:2a:953:A:N1	41:2j:48:THR:HG23	2.36	0.40
32:2a:1118:U:H2'	32:2a:1120:C:C2	2.57	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1120:C:H1'	32:2a:1121:G:N2	2.36	0.40
32:2a:1353:G:H5'	40:2i:12:GLU:HG3	2.04	0.40
34:2c:113:ALA:HB2	34:2c:202:ILE:HG13	2.03	0.40
41:2j:30:SER:HB3	41:2j:84:GLN:OE1	2.20	0.40
46:2o:8:LYS:O	46:2o:12:ILE:HG13	2.21	0.40
54:2x:50:U:OP1	59:2x:3102:HOH:O	2.22	0.40
1:1A:1159:G:H2'	1:1A:1160:G:C8	2.57	0.40
1:1A:1827:C:H4'	3:1D:257:LEU:O	2.21	0.40
1:1A:2114:G:C6	1:1A:2236:A:C8	3.10	0.40
1:1A:2330:G:H22	14:1S:3:ARG:CG	2.32	0.40
3:1D:68:LYS:O	3:1D:69:ARG:HB2	2.21	0.40
13:1R:70:LEU:O	13:1R:72:ASP:N	2.53	0.40
18:1W:88:ARG:HG3	18:1W:92:ARG:HH21	1.85	0.40
26:14:24:THR:OG1	26:14:25:TYR:N	2.52	0.40
30:18:23:VAL:CG2	30:18:47:LYS:HB3	2.52	0.40
32:1a:36:G:O2'	43:1l:118:SER:O	2.33	0.40
32:1a:164:C:H2'	32:1a:165:U:O4'	2.22	0.40
32:1a:335:C:H2'	32:1a:336:U:C6	2.56	0.40
32:1a:397:C:H2'	32:1a:398:G:C8	2.57	0.40
32:1a:969:U:H1'	32:1a:970:U:OP2	2.21	0.40
38:1g:12:LEU:HB2	38:1g:21:VAL:HG12	2.03	0.40
48:1q:53:LEU:HB3	48:1q:82:MET:SD	2.62	0.40
48:1q:81:ARG:HD2	48:1q:81:ARG:HA	1.92	0.40
50:1s:47:HIS:O	50:1s:62:ILE:HG13	2.22	0.40
52:1u:12:LYS:HB3	52:1u:22:ARG:HD2	2.04	0.40
1:2A:263:G:C2	1:2A:264:U:C2	3.10	0.40
1:2A:718:C:H2'	1:2A:719:C:C6	2.56	0.40
1:2A:830:A:C8	1:2A:838:G:C5	3.10	0.40
1:2A:1098:C:H42	1:2A:1151:G:H1	1.70	0.40
1:2A:1135:U:H2'	1:2A:1136:G:C8	2.56	0.40
1:2A:1556:A:H2'	1:2A:1557:G:C8	2.57	0.40
1:2A:1924:G:OP1	3:2D:241:PRO:HB2	2.21	0.40
1:2A:2080:A:O2'	5:2F:69:HIS:CD2	2.74	0.40
1:2A:2602:C:H2'	1:2A:2603:G:C8	2.56	0.40
1:2A:2669:C:H5''	7:2H:158:HIS:CD2	2.56	0.40
1:2A:2700:U:H4'	1:2A:2701:C:H5'	2.04	0.40
3:2D:132:PRO:HG3	3:2D:190:TYR:CE1	2.56	0.40
3:2D:264:LYS:HA	3:2D:265:PRO:HD3	1.92	0.40
21:2Z:35:ARG:HD2	21:2Z:35:ARG:HA	1.78	0.40
27:25:20:ARG:HG2	27:25:23:HIS:CE1	2.57	0.40
32:2a:46:U:H2'	32:2a:47:G:H8	1.85	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:585:C:H2'	32:2a:586:A:C8	2.56	0.40
32:2a:812:A:N6	32:2a:836:G:O2'	2.51	0.40
32:2a:911:G:C6	32:2a:1368:G:C6	3.09	0.40
32:2a:1054:C:H2'	32:2a:1055:G:H8	1.86	0.40
32:2a:1078:U:H2'	32:2a:1079:C:O4'	2.21	0.40
32:2a:1233:A:O2'	32:2a:1352:C:O2'	2.01	0.40
33:2b:127:ILE:O	33:2b:128:GLU:HB2	2.20	0.40
38:2g:99:LEU:HD23	38:2g:99:LEU:HA	1.92	0.40
39:2h:26:VAL:HA	39:2h:27:PRO:HD3	1.95	0.40
44:2m:65:LYS:H	44:2m:65:LYS:HG2	1.70	0.40
48:2q:37:LYS:HB2	48:2q:37:LYS:HE3	1.84	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	1D	273/276 (99%)	257 (94%)	16 (6%)	0	100	100
3	2D	273/276 (99%)	254 (93%)	17 (6%)	2 (1%)	18	47
4	1E	202/206 (98%)	194 (96%)	7 (4%)	1 (0%)	24	55
4	2E	202/206 (98%)	194 (96%)	7 (4%)	1 (0%)	24	55
5	1F	201/210 (96%)	189 (94%)	11 (6%)	1 (0%)	24	55
5	2F	201/210 (96%)	189 (94%)	10 (5%)	2 (1%)	12	38
6	1G	179/182 (98%)	158 (88%)	17 (10%)	4 (2%)	5	19
6	2G	179/182 (98%)	154 (86%)	20 (11%)	5 (3%)	4	14
7	1H	172/180 (96%)	162 (94%)	9 (5%)	1 (1%)	21	51
7	2H	172/180 (96%)	160 (93%)	10 (6%)	2 (1%)	10	34
8	1I	144/148 (97%)	121 (84%)	19 (13%)	4 (3%)	4	14

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	2I	144/148 (97%)	122 (85%)	20 (14%)	2 (1%)	9	30
9	1N	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
9	2N	138/140 (99%)	135 (98%)	2 (1%)	1 (1%)	18	47
10	1O	120/122 (98%)	114 (95%)	6 (5%)	0	100	100
10	2O	120/122 (98%)	114 (95%)	6 (5%)	0	100	100
11	1P	147/150 (98%)	140 (95%)	6 (4%)	1 (1%)	18	47
11	2P	147/150 (98%)	139 (95%)	8 (5%)	0	100	100
12	1Q	139/141 (99%)	130 (94%)	8 (6%)	1 (1%)	18	47
12	2Q	139/141 (99%)	127 (91%)	12 (9%)	0	100	100
13	1R	116/118 (98%)	107 (92%)	9 (8%)	0	100	100
13	2R	116/118 (98%)	107 (92%)	9 (8%)	0	100	100
14	1S	108/112 (96%)	100 (93%)	7 (6%)	1 (1%)	14	41
14	2S	108/112 (96%)	98 (91%)	9 (8%)	1 (1%)	14	41
15	1T	129/146 (88%)	124 (96%)	4 (3%)	1 (1%)	16	44
15	2T	129/146 (88%)	126 (98%)	3 (2%)	0	100	100
16	1U	114/118 (97%)	114 (100%)	0	0	100	100
16	2U	114/118 (97%)	113 (99%)	1 (1%)	0	100	100
17	1V	99/101 (98%)	96 (97%)	2 (2%)	1 (1%)	12	38
17	2V	99/101 (98%)	95 (96%)	3 (3%)	1 (1%)	12	38
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	36
19	2X	93/96 (97%)	90 (97%)	2 (2%)	1 (1%)	11	36
20	1Y	105/110 (96%)	94 (90%)	9 (9%)	2 (2%)	6	22
20	2Y	105/110 (96%)	97 (92%)	7 (7%)	1 (1%)	12	38
21	1Z	184/206 (89%)	167 (91%)	15 (8%)	2 (1%)	11	36
21	2Z	184/206 (89%)	163 (89%)	16 (9%)	5 (3%)	4	15
22	10	73/85 (86%)	72 (99%)	1 (1%)	0	100	100
22	20	73/85 (86%)	69 (94%)	4 (6%)	0	100	100
23	11	95/98 (97%)	94 (99%)	0	1 (1%)	11	36
23	21	95/98 (97%)	93 (98%)	1 (1%)	1 (1%)	11	36

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
24	12	68/72 (94%)	67 (98%)	1 (2%)	0	100	100
24	22	68/72 (94%)	65 (96%)	3 (4%)	0	100	100
25	13	57/60 (95%)	56 (98%)	1 (2%)	0	100	100
25	23	57/60 (95%)	54 (95%)	3 (5%)	0	100	100
26	14	67/71 (94%)	49 (73%)	10 (15%)	8 (12%)	0	1
26	24	67/71 (94%)	50 (75%)	10 (15%)	7 (10%)	0	1
27	15	57/60 (95%)	55 (96%)	2 (4%)	0	100	100
27	25	57/60 (95%)	55 (96%)	2 (4%)	0	100	100
28	16	51/54 (94%)	50 (98%)	1 (2%)	0	100	100
28	26	51/54 (94%)	50 (98%)	1 (2%)	0	100	100
29	17	46/49 (94%)	46 (100%)	0	0	100	100
29	27	46/49 (94%)	45 (98%)	1 (2%)	0	100	100
30	18	62/65 (95%)	59 (95%)	3 (5%)	0	100	100
30	28	62/65 (95%)	60 (97%)	2 (3%)	0	100	100
31	19	35/37 (95%)	35 (100%)	0	0	100	100
31	29	35/37 (95%)	35 (100%)	0	0	100	100
33	1b	229/256 (90%)	182 (80%)	36 (16%)	11 (5%)	2	6
33	2b	229/256 (90%)	187 (82%)	33 (14%)	9 (4%)	2	8
34	1c	204/239 (85%)	173 (85%)	28 (14%)	3 (2%)	8	28
34	2c	204/239 (85%)	166 (81%)	36 (18%)	2 (1%)	12	38
35	1d	206/209 (99%)	185 (90%)	20 (10%)	1 (0%)	24	55
35	2d	206/209 (99%)	188 (91%)	16 (8%)	2 (1%)	12	38
36	1e	146/162 (90%)	128 (88%)	15 (10%)	3 (2%)	5	20
36	2e	146/162 (90%)	130 (89%)	14 (10%)	2 (1%)	9	30
37	1f	98/101 (97%)	91 (93%)	7 (7%)	0	100	100
37	2f	98/101 (97%)	91 (93%)	7 (7%)	0	100	100
38	1g	153/156 (98%)	130 (85%)	23 (15%)	0	100	100
38	2g	153/156 (98%)	130 (85%)	23 (15%)	0	100	100
39	1h	135/138 (98%)	130 (96%)	5 (4%)	0	100	100
39	2h	135/138 (98%)	130 (96%)	4 (3%)	1 (1%)	18	47
40	1i	125/128 (98%)	106 (85%)	18 (14%)	1 (1%)	16	44

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
40	2i	125/128 (98%)	104 (83%)	19 (15%)	2 (2%)	7	27
41	1j	95/105 (90%)	82 (86%)	6 (6%)	7 (7%)	1	2
41	2j	94/105 (90%)	82 (87%)	9 (10%)	3 (3%)	3	11
42	1k	112/129 (87%)	100 (89%)	10 (9%)	2 (2%)	6	23
42	2k	112/129 (87%)	102 (91%)	8 (7%)	2 (2%)	6	23
43	1l	120/132 (91%)	115 (96%)	4 (3%)	1 (1%)	16	44
43	2l	120/132 (91%)	113 (94%)	7 (6%)	0	100	100
44	1m	116/126 (92%)	105 (90%)	8 (7%)	3 (3%)	4	15
44	2m	114/126 (90%)	100 (88%)	10 (9%)	4 (4%)	3	10
45	1n	58/61 (95%)	52 (90%)	5 (9%)	1 (2%)	7	25
45	2n	58/61 (95%)	53 (91%)	5 (9%)	0	100	100
46	1o	86/89 (97%)	80 (93%)	5 (6%)	1 (1%)	10	34
46	2o	86/89 (97%)	80 (93%)	4 (5%)	2 (2%)	5	18
47	1p	80/88 (91%)	65 (81%)	15 (19%)	0	100	100
47	2p	80/88 (91%)	65 (81%)	15 (19%)	0	100	100
48	1q	97/105 (92%)	88 (91%)	8 (8%)	1 (1%)	12	38
48	2q	97/105 (92%)	87 (90%)	10 (10%)	0	100	100
49	1r	66/88 (75%)	59 (89%)	6 (9%)	1 (2%)	8	28
49	2r	66/88 (75%)	62 (94%)	3 (4%)	1 (2%)	8	28
50	1s	82/93 (88%)	68 (83%)	14 (17%)	0	100	100
50	2s	81/93 (87%)	69 (85%)	11 (14%)	1 (1%)	10	34
51	1t	94/106 (89%)	80 (85%)	12 (13%)	2 (2%)	5	20
51	2t	94/106 (89%)	79 (84%)	13 (14%)	2 (2%)	5	20
52	1u	21/27 (78%)	20 (95%)	1 (5%)	0	100	100
52	2u	21/27 (78%)	20 (95%)	1 (5%)	0	100	100
55	1z	11/19 (58%)	10 (91%)	0	1 (9%)	0	1
55	2z	10/19 (53%)	10 (100%)	0	0	100	100
All	All	11431/12166 (94%)	10441 (91%)	856 (8%)	134 (1%)	10	34

All (134) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	1G	126	ASP

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Mol	Chain	Res	Type
8	1I	106	GLY
21	1Z	93	ASP
23	11	3	LYS
26	14	45	GLY
26	14	48	ARG
26	14	50	VAL
26	14	53	GLU
33	1b	16	HIS
33	1b	121	LEU
33	1b	125	PRO
34	1c	107	GLN
40	1i	54	ASP
41	1j	55	LYS
41	1j	56	HIS
42	1k	49	GLY
44	1m	4	ILE
45	1n	3	ARG
48	1q	68	ARG
6	2G	14	GLU
6	2G	47	LYS
6	2G	51	ARG
6	2G	126	ASP
7	2H	55	PRO
7	2H	126	PRO
8	2I	10	GLU
17	2V	79	VAL
21	2Z	93	ASP
21	2Z	128	VAL
21	2Z	135	GLU
26	24	45	GLY
26	24	62	ARG
26	24	68	ARG
33	2b	17	PHE
33	2b	93	VAL
33	2b	124	SER
40	2i	54	ASP
42	2k	49	GLY
44	2m	106	ASN
51	2t	99	LEU
5	1F	130	ALA
7	1H	126	PRO
12	1Q	58	PHE

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Mol	Chain	Res	Type
14	1S	60	GLY
17	1V	79	VAL
19	1X	94	GLY
33	1b	17	PHE
33	1b	95	GLN
33	1b	128	GLU
41	1j	31	GLY
43	1l	29	GLY
5	2F	130	ALA
6	2G	81	LYS
19	2X	94	GLY
20	2Y	54	LYS
26	24	54	GLY
33	2b	121	LEU
33	2b	125	PRO
36	2e	37	ARG
44	2m	4	ILE
44	2m	21	TYR
44	2m	107	ALA
6	1G	47	LYS
6	1G	51	ARG
8	1I	42	SER
8	1I	73	GLU
26	14	62	ARG
33	1b	22	LYS
33	1b	23	ARG
33	1b	231	GLU
41	1j	77	PRO
44	1m	106	ASN
51	1t	47	GLY
9	2N	2	LYS
23	21	3	LYS
26	24	47	GLN
40	2i	39	GLY
41	2j	77	PRO
41	2j	78	ASN
49	2r	25	THR
4	1E	52	LEU
20	1Y	53	PRO
20	1Y	54	LYS
26	14	49	PHE
33	1b	20	GLU

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Mol	Chain	Res	Type
44	1m	21	TYR
49	1r	25	THR
55	1z	9	ARG
4	2E	52	LEU
5	2F	18	ARG
8	2I	42	SER
26	24	63	TYR
34	2c	61	ALA
34	2c	187	ALA
35	2d	47	ARG
50	2s	30	LEU
51	2t	47	GLY
8	1I	107	VAL
21	1Z	101	PRO
26	14	46	GLN
26	14	47	GLN
33	1b	202	PRO
34	1c	3	ASN
41	1j	78	ASN
41	1j	82	ILE
3	2D	3	VAL
14	2S	84	GLN
21	2Z	101	PRO
21	2Z	127	LYS
33	2b	20	GLU
33	2b	202	PRO
33	2b	230	VAL
35	2d	45	GLN
46	2o	88	ARG
6	1G	50	ALA
34	1c	61	ALA
36	1e	69	VAL
41	1j	32	ALA
36	2e	69	VAL
46	2o	19	PRO
35	1d	8	VAL
3	2D	125	ILE
26	24	50	VAL
36	1e	85	GLY
42	1k	105	VAL
42	2k	105	VAL
46	1o	19	PRO

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Mol	Chain	Res	Type
33	2b	151	GLY
41	2j	82	ILE
11	1P	122	PRO
15	1T	37	GLY
36	1e	96	PRO
51	1t	102	GLY
39	2h	73	ASP

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	1D	215/218 (99%)	189 (88%)	26 (12%)	5	16
3	2D	216/218 (99%)	195 (90%)	21 (10%)	8	25
4	1E	164/166 (99%)	141 (86%)	23 (14%)	3	12
4	2E	164/166 (99%)	141 (86%)	23 (14%)	3	12
5	1F	160/166 (96%)	140 (88%)	20 (12%)	4	15
5	2F	159/166 (96%)	139 (87%)	20 (13%)	4	15
6	1G	143/156 (92%)	123 (86%)	20 (14%)	3	12
6	2G	142/156 (91%)	119 (84%)	23 (16%)	2	8
7	1H	144/148 (97%)	132 (92%)	12 (8%)	10	32
7	2H	144/148 (97%)	127 (88%)	17 (12%)	5	17
8	1I	110/124 (89%)	87 (79%)	23 (21%)	1	4
8	2I	104/124 (84%)	88 (85%)	16 (15%)	2	10
9	1N	118/119 (99%)	102 (86%)	16 (14%)	3	13
9	2N	118/119 (99%)	102 (86%)	16 (14%)	3	13
10	1O	100/100 (100%)	90 (90%)	10 (10%)	7	24
10	2O	100/100 (100%)	93 (93%)	7 (7%)	14	40
11	1P	116/116 (100%)	102 (88%)	14 (12%)	5	16
11	2P	115/116 (99%)	96 (84%)	19 (16%)	2	8

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
12	1Q	111/111 (100%)	102 (92%)	9 (8%)	11	33
12	2Q	111/111 (100%)	101 (91%)	10 (9%)	9	28
13	1R	101/101 (100%)	85 (84%)	16 (16%)	2	9
13	2R	101/101 (100%)	88 (87%)	13 (13%)	4	14
14	1S	87/88 (99%)	77 (88%)	10 (12%)	5	18
14	2S	85/88 (97%)	72 (85%)	13 (15%)	3	10
15	1T	115/127 (91%)	107 (93%)	8 (7%)	14	40
15	2T	113/127 (89%)	103 (91%)	10 (9%)	9	29
16	1U	93/94 (99%)	83 (89%)	10 (11%)	6	21
16	2U	93/94 (99%)	88 (95%)	5 (5%)	20	51
17	1V	80/82 (98%)	66 (82%)	14 (18%)	2	7
17	2V	80/82 (98%)	69 (86%)	11 (14%)	3	12
18	1W	90/92 (98%)	81 (90%)	9 (10%)	7	24
18	2W	90/92 (98%)	81 (90%)	9 (10%)	7	24
19	1X	77/78 (99%)	73 (95%)	4 (5%)	21	53
19	2X	77/78 (99%)	74 (96%)	3 (4%)	28	64
20	1Y	85/91 (93%)	78 (92%)	7 (8%)	10	33
20	2Y	85/91 (93%)	77 (91%)	8 (9%)	8	27
21	1Z	159/179 (89%)	140 (88%)	19 (12%)	5	17
21	2Z	156/179 (87%)	139 (89%)	17 (11%)	6	21
22	10	60/67 (90%)	56 (93%)	4 (7%)	15	42
22	20	60/67 (90%)	56 (93%)	4 (7%)	15	42
23	11	80/83 (96%)	72 (90%)	8 (10%)	7	24
23	21	80/83 (96%)	73 (91%)	7 (9%)	9	29
24	12	65/67 (97%)	62 (95%)	3 (5%)	24	58
24	22	65/67 (97%)	60 (92%)	5 (8%)	12	36
25	13	51/52 (98%)	44 (86%)	7 (14%)	3	13
25	23	50/52 (96%)	44 (88%)	6 (12%)	5	17
26	14	60/63 (95%)	49 (82%)	11 (18%)	2	6
26	24	53/63 (84%)	46 (87%)	7 (13%)	4	14
27	15	50/52 (96%)	45 (90%)	5 (10%)	7	24

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
27	25	50/52 (96%)	45 (90%)	5 (10%)	7	24
28	16	51/52 (98%)	46 (90%)	5 (10%)	7	25
28	26	50/52 (96%)	46 (92%)	4 (8%)	11	34
29	17	41/42 (98%)	38 (93%)	3 (7%)	13	38
29	27	41/42 (98%)	39 (95%)	2 (5%)	22	55
30	18	54/55 (98%)	50 (93%)	4 (7%)	13	37
30	28	54/55 (98%)	51 (94%)	3 (6%)	19	50
31	19	34/34 (100%)	33 (97%)	1 (3%)	37	73
31	29	34/34 (100%)	32 (94%)	2 (6%)	18	48
33	1b	177/220 (80%)	153 (86%)	24 (14%)	3	13
33	2b	158/220 (72%)	129 (82%)	29 (18%)	1	6
34	1c	127/188 (68%)	117 (92%)	10 (8%)	11	35
34	2c	108/188 (57%)	96 (89%)	12 (11%)	6	20
35	1d	161/181 (89%)	144 (89%)	17 (11%)	6	22
35	2d	164/181 (91%)	147 (90%)	17 (10%)	7	22
36	1e	113/123 (92%)	102 (90%)	11 (10%)	8	25
36	2e	106/123 (86%)	92 (87%)	14 (13%)	4	14
37	1f	83/90 (92%)	76 (92%)	7 (8%)	10	32
37	2f	86/90 (96%)	80 (93%)	6 (7%)	14	40
38	1g	111/127 (87%)	93 (84%)	18 (16%)	2	8
38	2g	107/127 (84%)	92 (86%)	15 (14%)	3	12
39	1h	114/119 (96%)	103 (90%)	11 (10%)	8	26
39	2h	111/119 (93%)	99 (89%)	12 (11%)	6	21
40	1i	89/99 (90%)	80 (90%)	9 (10%)	7	23
40	2i	80/99 (81%)	72 (90%)	8 (10%)	7	24
41	1j	60/92 (65%)	50 (83%)	10 (17%)	2	8
41	2j	62/92 (67%)	49 (79%)	13 (21%)	1	4
42	1k	82/99 (83%)	72 (88%)	10 (12%)	5	16
42	2k	82/99 (83%)	74 (90%)	8 (10%)	7	25
43	1l	95/109 (87%)	88 (93%)	7 (7%)	13	37
43	2l	94/109 (86%)	89 (95%)	5 (5%)	20	52

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
44	1m	90/101 (89%)	79 (88%)	11 (12%)	5	16
44	2m	87/101 (86%)	75 (86%)	12 (14%)	3	12
45	1n	47/50 (94%)	41 (87%)	6 (13%)	4	15
45	2n	43/50 (86%)	36 (84%)	7 (16%)	2	8
46	1o	75/80 (94%)	67 (89%)	8 (11%)	6	21
46	2o	78/80 (98%)	71 (91%)	7 (9%)	9	28
47	1p	67/74 (90%)	56 (84%)	11 (16%)	2	8
47	2p	68/74 (92%)	59 (87%)	9 (13%)	4	14
48	1q	91/97 (94%)	83 (91%)	8 (9%)	9	29
48	2q	94/97 (97%)	88 (94%)	6 (6%)	16	44
49	1r	59/77 (77%)	54 (92%)	5 (8%)	10	31
49	2r	59/77 (77%)	52 (88%)	7 (12%)	5	17
50	1s	65/80 (81%)	55 (85%)	10 (15%)	2	10
50	2s	67/80 (84%)	58 (87%)	9 (13%)	4	13
51	1t	66/82 (80%)	60 (91%)	6 (9%)	9	28
51	2t	71/82 (87%)	66 (93%)	5 (7%)	14	40
52	1u	16/22 (73%)	16 (100%)	0	100	100
52	2u	18/22 (82%)	17 (94%)	1 (6%)	19	50
55	1z	13/19 (68%)	11 (85%)	2 (15%)	2	10
55	2z	12/19 (63%)	11 (92%)	1 (8%)	10	32
All	All	9160/10104 (91%)	8129 (89%)	1031 (11%)	5	19

All (1031) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	1D	3	VAL
3	1D	14	ARG
3	1D	27	THR
3	1D	38	LYS
3	1D	61	LEU
3	1D	71	ASP
3	1D	94	LEU
3	1D	98	VAL
3	1D	99	ASP
3	1D	103	ARG

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Mol	Chain	Res	Type
3	1D	111	LEU
3	1D	113	VAL
3	1D	115	GLN
3	1D	138	VAL
3	1D	142	VAL
3	1D	155	LEU
3	1D	171	ASP
3	1D	173	VAL
3	1D	193	VAL
3	1D	211	ARG
3	1D	217	ARG
3	1D	221	VAL
3	1D	229	VAL
3	1D	257	LEU
3	1D	260	ARG
3	1D	275	LYS
4	1E	7	VAL
4	1E	9	VAL
4	1E	12	THR
4	1E	14	ILE
4	1E	21	VAL
4	1E	33	VAL
4	1E	40	GLU
4	1E	49	LEU
4	1E	54	GLN
4	1E	73	GLU
4	1E	75	VAL
4	1E	82	ARG
4	1E	111	ARG
4	1E	116	VAL
4	1E	119	ARG
4	1E	144	ARG
4	1E	154	LYS
4	1E	163	GLU
4	1E	167	VAL
4	1E	175	VAL
4	1E	181	LEU
4	1E	184	VAL
4	1E	188	VAL
5	1F	12	LEU
5	1F	20	LEU
5	1F	24	LEU

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Mol	Chain	Res	Type
5	1F	33	LEU
5	1F	53	THR
5	1F	57	VAL
5	1F	74	ARG
5	1F	88	VAL
5	1F	106	ARG
5	1F	110	LEU
5	1F	112	MET
5	1F	125	LEU
5	1F	132	VAL
5	1F	169	ASN
5	1F	170	LEU
5	1F	183	VAL
5	1F	191	ARG
5	1F	192	LEU
5	1F	195	ASP
5	1F	201	VAL
6	1G	4	ASP
6	1G	5	VAL
6	1G	7	LEU
6	1G	16	ARG
6	1G	31	VAL
6	1G	35	GLU
6	1G	43	LEU
6	1G	45	GLU
6	1G	60	LEU
6	1G	70	VAL
6	1G	82	LEU
6	1G	139	LEU
6	1G	140	ILE
6	1G	143	GLU
6	1G	148	MET
6	1G	159	VAL
6	1G	162	THR
6	1G	165	THR
6	1G	170	ARG
6	1G	181	ARG
7	1H	15	VAL
7	1H	43	VAL
7	1H	45	VAL
7	1H	49	VAL
7	1H	59	ARG

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Mol	Chain	Res	Type
7	1H	60	ARG
7	1H	69	ARG
7	1H	71	LEU
7	1H	127	GLU
7	1H	129	THR
7	1H	134	SER
7	1H	175	LYS
8	1I	9	LEU
8	1I	10	GLU
8	1I	20	ASP
8	1I	38	LEU
8	1I	43	ASN
8	1I	47	LEU
8	1I	50	ARG
8	1I	57	ARG
8	1I	60	GLU
8	1I	64	GLU
8	1I	66	GLU
8	1I	68	LEU
8	1I	75	LEU
8	1I	77	LEU
8	1I	87	LYS
8	1I	92	VAL
8	1I	101	LEU
8	1I	103	ARG
8	1I	109	ILE
8	1I	116	LEU
8	1I	127	VAL
8	1I	140	LEU
8	1I	142	VAL
9	1N	8	GLN
9	1N	14	VAL
9	1N	28	THR
9	1N	33	LEU
9	1N	34	LEU
9	1N	48	MET
9	1N	61	ARG
9	1N	73	THR
9	1N	87	LEU
9	1N	97	ARG
9	1N	99	LEU
9	1N	120	LEU

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Mol	Chain	Res	Type
9	1N	131	GLN
9	1N	133	GLN
9	1N	137	LYS
9	1N	138	LEU
10	1O	8	LEU
10	1O	10	VAL
10	1O	23	ARG
10	1O	24	VAL
10	1O	66	LYS
10	1O	69	ILE
10	1O	94	ARG
10	1O	98	VAL
10	1O	105	GLU
10	1O	113	LYS
11	1P	3	LEU
11	1P	55	ARG
11	1P	59	LEU
11	1P	70	GLN
11	1P	76	LYS
11	1P	83	VAL
11	1P	95	VAL
11	1P	98	GLU
11	1P	99	LEU
11	1P	106	LEU
11	1P	112	LEU
11	1P	125	VAL
11	1P	148	LEU
11	1P	149	GLU
12	1Q	1	MET
12	1Q	35	VAL
12	1Q	45	GLN
12	1Q	55	VAL
12	1Q	60	ARG
12	1Q	64	ILE
12	1Q	81	VAL
12	1Q	109	VAL
12	1Q	110	THR
13	1R	6	SER
13	1R	18	LEU
13	1R	28	LEU
13	1R	29	LEU
13	1R	33	ARG

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Mol	Chain	Res	Type
13	1R	36	THR
13	1R	44	LEU
13	1R	60	LEU
13	1R	65	LEU
13	1R	67	LEU
13	1R	75	LEU
13	1R	79	LEU
13	1R	91	GLN
13	1R	100	LEU
13	1R	111	LEU
13	1R	114	VAL
14	1S	3	ARG
14	1S	14	VAL
14	1S	20	ARG
14	1S	46	VAL
14	1S	49	VAL
14	1S	59	LYS
14	1S	61	ASN
14	1S	69	VAL
14	1S	85	VAL
14	1S	110	LEU
15	1T	6	LEU
15	1T	28	VAL
15	1T	34	VAL
15	1T	49	VAL
15	1T	78	LEU
15	1T	89	VAL
15	1T	108	ARG
15	1T	118	ARG
16	1U	8	VAL
16	1U	36	ARG
16	1U	52	ARG
16	1U	60	LEU
16	1U	74	LEU
16	1U	77	SER
16	1U	92	ARG
16	1U	95	LEU
16	1U	104	GLN
16	1U	108	GLU
17	1V	18	LEU
17	1V	21	ARG
17	1V	28	GLU

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Mol	Chain	Res	Type
17	1V	35	LEU
17	1V	38	LEU
17	1V	43	GLU
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	95	LEU
18	1W	1	MET
18	1W	11	ARG
18	1W	15	ARG
18	1W	17	VAL
18	1W	19	LEU
18	1W	23	LEU
18	1W	51	LEU
18	1W	100	THR
18	1W	107	LEU
19	1X	35	THR
19	1X	76	ARG
19	1X	88	LYS
19	1X	92	LEU
20	1Y	7	VAL
20	1Y	9	LYS
20	1Y	23	ARG
20	1Y	43	ASN
20	1Y	70	SER
20	1Y	72	VAL
20	1Y	90	LEU
21	1Z	11	GLU
21	1Z	18	LEU
21	1Z	31	ARG
21	1Z	33	LEU
21	1Z	42	VAL
21	1Z	61	LEU
21	1Z	70	LEU
21	1Z	86	VAL
21	1Z	91	LEU
21	1Z	107	THR
21	1Z	126	VAL

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Mol	Chain	Res	Type
21	1Z	131	ARG
21	1Z	146	ILE
21	1Z	150	LEU
21	1Z	155	LEU
21	1Z	161	VAL
21	1Z	162	GLU
21	1Z	170	THR
21	1Z	182	LYS
22	10	10	THR
22	10	20	ARG
22	10	49	LYS
22	10	63	VAL
23	11	21	ARG
23	11	35	THR
23	11	37	ILE
23	11	40	ARG
23	11	59	THR
23	11	78	LYS
23	11	89	GLU
23	11	95	LEU
24	12	19	VAL
24	12	53	LEU
24	12	70	GLN
25	13	3	ARG
25	13	6	VAL
25	13	8	LEU
25	13	23	LEU
25	13	31	LEU
25	13	54	VAL
25	13	56	VAL
26	14	8	LYS
26	14	33	VAL
26	14	34	GLU
26	14	47	GLN
26	14	48	ARG
26	14	49	PHE
26	14	56	VAL
26	14	60	GLN
26	14	61	ARG
26	14	63	TYR
26	14	68	ARG
27	15	6	VAL

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Mol	Chain	Res	Type
27	15	16	ARG
27	15	29	THR
27	15	40	LYS
27	15	57	VAL
28	16	4	GLU
28	16	6	ARG
28	16	14	THR
28	16	38	LYS
28	16	48	VAL
29	17	23	ARG
29	17	24	THR
29	17	43	THR
30	18	14	VAL
30	18	30	ARG
30	18	32	LEU
30	18	46	ARG
31	19	26	ILE
33	1b	7	VAL
33	1b	8	LYS
33	1b	10	LEU
33	1b	16	HIS
33	1b	17	PHE
33	1b	21	ARG
33	1b	39	ILE
33	1b	61	LEU
33	1b	67	THR
33	1b	76	GLN
33	1b	80	ILE
33	1b	93	VAL
33	1b	96	ARG
33	1b	112	VAL
33	1b	127	ILE
33	1b	156	LYS
33	1b	169	LYS
33	1b	185	ILE
33	1b	187	LEU
33	1b	189	ASP
33	1b	190	THR
33	1b	208	ILE
33	1b	215	LEU
33	1b	221	LEU
34	1c	15	THR

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Mol	Chain	Res	Type
34	1c	47	LEU
34	1c	52	LEU
34	1c	59	ARG
34	1c	64	VAL
34	1c	70	VAL
34	1c	115	LEU
34	1c	131	ARG
34	1c	150	LYS
34	1c	204	LEU
35	1d	5	ILE
35	1d	15	GLU
35	1d	28	SER
35	1d	45	GLN
35	1d	49	ARG
35	1d	58	LEU
35	1d	73	ARG
35	1d	101	LEU
35	1d	107	ARG
35	1d	122	ARG
35	1d	141	ARG
35	1d	160	GLN
35	1d	162	LEU
35	1d	168	ARG
35	1d	178	VAL
35	1d	188	LEU
35	1d	194	LEU
36	1e	18	ARG
36	1e	31	LEU
36	1e	41	VAL
36	1e	47	LYS
36	1e	51	VAL
36	1e	67	VAL
36	1e	73	ASN
36	1e	75	THR
36	1e	79	GLU
36	1e	83	GLU
36	1e	91	LEU
37	1f	40	VAL
37	1f	43	LEU
37	1f	69	GLU
37	1f	72	VAL
37	1f	74	ASP

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Mol	Chain	Res	Type
37	1f	75	LEU
37	1f	89	MET
38	1g	6	ARG
38	1g	8	GLU
38	1g	13	GLN
38	1g	15	ASP
38	1g	16	LEU
38	1g	21	VAL
38	1g	45	ASP
38	1g	50	ILE
38	1g	52	GLU
38	1g	56	GLN
38	1g	57	GLU
38	1g	61	VAL
38	1g	75	VAL
38	1g	98	SER
38	1g	104	LEU
38	1g	110	GLN
38	1g	113	GLU
38	1g	131	LYS
39	1h	21	LYS
39	1h	26	VAL
39	1h	51	VAL
39	1h	63	LEU
39	1h	64	LYS
39	1h	69	ARG
39	1h	75	ARG
39	1h	78	GLN
39	1h	86	ILE
39	1h	91	ARG
39	1h	137	VAL
40	1i	23	ASN
40	1i	27	THR
40	1i	42	ARG
40	1i	81	ILE
40	1i	86	VAL
40	1i	102	LEU
40	1i	108	VAL
40	1i	113	LYS
40	1i	127	LYS
41	1j	30	SER
41	1j	43	ARG

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Mol	Chain	Res	Type
41	1j	48	THR
41	1j	49	VAL
41	1j	84	GLN
41	1j	85	LEU
41	1j	92	THR
41	1j	94	VAL
41	1j	95	GLU
41	1j	98	ILE
42	1k	14	VAL
42	1k	18	ARG
42	1k	31	THR
42	1k	48	ILE
42	1k	78	GLN
42	1k	84	VAL
42	1k	87	THR
42	1k	106	LYS
42	1k	109	VAL
42	1k	114	VAL
43	1l	27	LEU
43	1l	33	ARG
43	1l	54	LYS
43	1l	60	LEU
43	1l	67	THR
43	1l	70	ILE
43	1l	83	VAL
44	1m	4	ILE
44	1m	11	ARG
44	1m	19	LEU
44	1m	56	LEU
44	1m	69	GLU
44	1m	70	LEU
44	1m	98	VAL
44	1m	102	ARG
44	1m	109	THR
44	1m	110	ARG
44	1m	117	VAL
45	1n	8	GLU
45	1n	11	LYS
45	1n	18	VAL
45	1n	22	THR
45	1n	33	VAL
45	1n	46	GLU

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Mol	Chain	Res	Type
46	1o	3	ILE
46	1o	5	LYS
46	1o	22	THR
46	1o	26	GLU
46	1o	39	LEU
46	1o	71	GLN
46	1o	83	GLU
46	1o	87	ILE
47	1p	1	MET
47	1p	2	VAL
47	1p	5	ARG
47	1p	11	SER
47	1p	19	ILE
47	1p	20	VAL
47	1p	45	THR
47	1p	47	ASP
47	1p	54	GLU
47	1p	62	VAL
47	1p	67	THR
48	1q	9	VAL
48	1q	43	LEU
48	1q	49	GLU
48	1q	60	ILE
48	1q	74	LEU
48	1q	79	SER
48	1q	89	LEU
48	1q	98	LEU
49	1r	26	LEU
49	1r	37	VAL
49	1r	38	GLU
49	1r	68	LYS
49	1r	76	LEU
50	1s	3	ARG
50	1s	5	LEU
50	1s	22	LEU
50	1s	28	LYS
50	1s	37	ARG
50	1s	63	THR
50	1s	65	ASN
50	1s	77	THR
50	1s	81	ARG
50	1s	83	HIS

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Mol	Chain	Res	Type
51	1t	9	ASN
51	1t	24	LEU
51	1t	60	GLU
51	1t	62	LEU
51	1t	81	LYS
51	1t	84	LEU
55	1z	1	VAL
55	1z	3	LYS
3	2D	39	LYS
3	2D	54	ARG
3	2D	61	LEU
3	2D	94	LEU
3	2D	106	ILE
3	2D	113	VAL
3	2D	134	ARG
3	2D	138	VAL
3	2D	141	VAL
3	2D	142	VAL
3	2D	154	LYS
3	2D	164	GLN
3	2D	173	VAL
3	2D	193	VAL
3	2D	217	ARG
3	2D	221	VAL
3	2D	229	VAL
3	2D	242	ARG
3	2D	257	LEU
3	2D	260	ARG
3	2D	276	LYS
4	2E	9	VAL
4	2E	12	THR
4	2E	14	ILE
4	2E	21	VAL
4	2E	33	VAL
4	2E	34	VAL
4	2E	40	GLU
4	2E	49	LEU
4	2E	52	LEU
4	2E	75	VAL
4	2E	82	ARG
4	2E	111	ARG
4	2E	116	VAL

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Mol	Chain	Res	Type
4	2E	119	ARG
4	2E	134	ILE
4	2E	144	ARG
4	2E	154	LYS
4	2E	163	GLU
4	2E	175	VAL
4	2E	181	LEU
4	2E	184	VAL
4	2E	188	VAL
4	2E	202	LYS
5	2F	15	SER
5	2F	20	LEU
5	2F	24	LEU
5	2F	33	LEU
5	2F	53	THR
5	2F	57	VAL
5	2F	74	ARG
5	2F	88	VAL
5	2F	106	ARG
5	2F	132	VAL
5	2F	135	LYS
5	2F	153	SER
5	2F	169	ASN
5	2F	170	LEU
5	2F	183	VAL
5	2F	191	ARG
5	2F	192	LEU
5	2F	196	LEU
5	2F	197	ASP
5	2F	201	VAL
6	2G	5	VAL
6	2G	9	ARG
6	2G	13	GLU
6	2G	28	VAL
6	2G	31	VAL
6	2G	33	ARG
6	2G	35	GLU
6	2G	43	LEU
6	2G	60	LEU
6	2G	70	VAL
6	2G	98	ARG
6	2G	111	LEU

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Mol	Chain	Res	Type
6	2G	113	ARG
6	2G	136	ARG
6	2G	139	LEU
6	2G	140	ILE
6	2G	143	GLU
6	2G	148	MET
6	2G	153	ARG
6	2G	159	VAL
6	2G	162	THR
6	2G	165	THR
6	2G	170	ARG
7	2H	3	ARG
7	2H	15	VAL
7	2H	27	LYS
7	2H	32	GLU
7	2H	33	LEU
7	2H	41	MET
7	2H	42	ARG
7	2H	45	VAL
7	2H	49	VAL
7	2H	69	ARG
7	2H	71	LEU
7	2H	98	LEU
7	2H	129	THR
7	2H	134	SER
7	2H	136	ILE
7	2H	139	GLN
7	2H	171	LEU
8	2I	15	VAL
8	2I	38	LEU
8	2I	43	ASN
8	2I	47	LEU
8	2I	61	ARG
8	2I	68	LEU
8	2I	75	LEU
8	2I	76	THR
8	2I	77	LEU
8	2I	102	SER
8	2I	114	LEU
8	2I	116	LEU
8	2I	117	GLU
8	2I	127	VAL

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Mol	Chain	Res	Type
8	2I	140	LEU
8	2I	142	VAL
9	2N	14	VAL
9	2N	33	LEU
9	2N	34	LEU
9	2N	43	THR
9	2N	48	MET
9	2N	59	LYS
9	2N	61	ARG
9	2N	62	VAL
9	2N	63	THR
9	2N	87	LEU
9	2N	97	ARG
9	2N	99	LEU
9	2N	120	LEU
9	2N	131	GLN
9	2N	133	GLN
9	2N	137	LYS
10	2O	8	LEU
10	2O	10	VAL
10	2O	23	ARG
10	2O	24	VAL
10	2O	69	ILE
10	2O	94	ARG
10	2O	98	VAL
11	2P	3	LEU
11	2P	15	ARG
11	2P	21	ARG
11	2P	45	LEU
11	2P	55	ARG
11	2P	59	LEU
11	2P	65	ARG
11	2P	83	VAL
11	2P	96	THR
11	2P	99	LEU
11	2P	101	VAL
11	2P	106	LEU
11	2P	112	LEU
11	2P	121	LYS
11	2P	123	LEU
11	2P	125	VAL
11	2P	133	SER

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Mol	Chain	Res	Type
11	2P	136	GLU
11	2P	148	LEU
12	2Q	5	ARG
12	2Q	21	THR
12	2Q	22	LYS
12	2Q	35	VAL
12	2Q	38	GLU
12	2Q	45	GLN
12	2Q	64	ILE
12	2Q	81	VAL
12	2Q	109	VAL
12	2Q	110	THR
13	2R	1	MET
13	2R	6	SER
13	2R	18	LEU
13	2R	28	LEU
13	2R	29	LEU
13	2R	44	LEU
13	2R	60	LEU
13	2R	65	LEU
13	2R	75	LEU
13	2R	79	LEU
13	2R	100	LEU
13	2R	111	LEU
13	2R	114	VAL
14	2S	4	LEU
14	2S	14	VAL
14	2S	23	ARG
14	2S	35	ILE
14	2S	44	LYS
14	2S	46	VAL
14	2S	50	SER
14	2S	67	ARG
14	2S	69	VAL
14	2S	75	GLU
14	2S	83	LYS
14	2S	85	VAL
14	2S	110	LEU
15	2T	6	LEU
15	2T	8	LYS
15	2T	28	VAL
15	2T	34	VAL

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Mol	Chain	Res	Type
15	2T	49	VAL
15	2T	78	LEU
15	2T	89	VAL
15	2T	96	ARG
15	2T	98	LYS
15	2T	118	ARG
16	2U	60	LEU
16	2U	74	LEU
16	2U	92	ARG
16	2U	104	GLN
16	2U	108	GLU
17	2V	18	LEU
17	2V	21	ARG
17	2V	35	LEU
17	2V	46	VAL
17	2V	51	VAL
17	2V	52	VAL
17	2V	61	VAL
17	2V	62	LEU
17	2V	72	VAL
17	2V	79	VAL
17	2V	95	LEU
18	2W	1	MET
18	2W	11	ARG
18	2W	15	ARG
18	2W	17	VAL
18	2W	23	LEU
18	2W	27	LYS
18	2W	51	LEU
18	2W	100	THR
18	2W	107	LEU
19	2X	57	LEU
19	2X	76	ARG
19	2X	92	LEU
20	2Y	7	VAL
20	2Y	8	LYS
20	2Y	9	LYS
20	2Y	44	ILE
20	2Y	70	SER
20	2Y	72	VAL
20	2Y	92	ASN
20	2Y	101	LYS

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Mol	Chain	Res	Type
21	2Z	33	LEU
21	2Z	42	VAL
21	2Z	70	LEU
21	2Z	73	GLN
21	2Z	74	VAL
21	2Z	76	LEU
21	2Z	86	VAL
21	2Z	91	LEU
21	2Z	107	THR
21	2Z	126	VAL
21	2Z	131	ARG
21	2Z	135	GLU
21	2Z	136	PHE
21	2Z	150	LEU
21	2Z	161	VAL
21	2Z	175	VAL
21	2Z	185	GLU
22	20	10	THR
22	20	19	LYS
22	20	20	ARG
22	20	63	VAL
23	21	4	VAL
23	21	21	ARG
23	21	35	THR
23	21	40	ARG
23	21	56	GLN
23	21	59	THR
23	21	95	LEU
24	22	19	VAL
24	22	35	LEU
24	22	53	LEU
24	22	64	LEU
24	22	70	GLN
25	23	3	ARG
25	23	6	VAL
25	23	8	LEU
25	23	31	LEU
25	23	54	VAL
25	23	56	VAL
26	24	33	VAL
26	24	52	THR
26	24	58	ARG

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Mol	Chain	Res	Type
26	24	61	ARG
26	24	63	TYR
26	24	68	ARG
26	24	69	LYS
27	25	6	VAL
27	25	16	ARG
27	25	29	THR
27	25	40	LYS
27	25	57	VAL
28	26	14	THR
28	26	28	ARG
28	26	38	LYS
28	26	48	VAL
29	27	1	MET
29	27	46	VAL
30	28	14	VAL
30	28	26	LYS
30	28	32	LEU
31	29	17	ILE
31	29	26	ILE
33	2b	7	VAL
33	2b	8	LYS
33	2b	17	PHE
33	2b	19	HIS
33	2b	20	GLU
33	2b	35	GLU
33	2b	44	LEU
33	2b	48	MET
33	2b	51	LEU
33	2b	56	ARG
33	2b	60	ASP
33	2b	61	LEU
33	2b	63	MET
33	2b	67	THR
33	2b	71	VAL
33	2b	81	VAL
33	2b	90	MET
33	2b	93	VAL
33	2b	117	GLU
33	2b	126	GLU
33	2b	128	GLU
33	2b	154	LEU

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Mol	Chain	Res	Type
33	2b	160	ASP
33	2b	179	LYS
33	2b	185	ILE
33	2b	187	LEU
33	2b	191	ASP
33	2b	222	ILE
33	2b	224	GLN
34	2c	3	ASN
34	2c	5	ILE
34	2c	14	ILE
34	2c	16	ARG
34	2c	47	LEU
34	2c	52	LEU
34	2c	59	ARG
34	2c	70	VAL
34	2c	125	GLU
34	2c	152	ILE
34	2c	178	LEU
34	2c	182	ILE
35	2d	3	ARG
35	2d	5	ILE
35	2d	8	VAL
35	2d	26	CYS
35	2d	34	GLU
35	2d	38	TYR
35	2d	49	ARG
35	2d	58	LEU
35	2d	73	ARG
35	2d	96	LEU
35	2d	108	LEU
35	2d	135	LEU
35	2d	157	LEU
35	2d	170	VAL
35	2d	178	VAL
35	2d	187	ARG
35	2d	194	LEU
36	2e	24	ARG
36	2e	27	ARG
36	2e	31	LEU
36	2e	40	ARG
36	2e	41	VAL
36	2e	47	LYS

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Mol	Chain	Res	Type
36	2e	50	GLU
36	2e	51	VAL
36	2e	68	GLU
36	2e	83	GLU
36	2e	91	LEU
36	2e	115	VAL
36	2e	121	LYS
36	2e	152	ARG
37	2f	28	ARG
37	2f	40	VAL
37	2f	43	LEU
37	2f	69	GLU
37	2f	72	VAL
37	2f	75	LEU
38	2g	8	GLU
38	2g	11	GLN
38	2g	15	ASP
38	2g	16	LEU
38	2g	21	VAL
38	2g	42	ILE
38	2g	57	GLU
38	2g	61	VAL
38	2g	75	VAL
38	2g	98	SER
38	2g	104	LEU
38	2g	110	GLN
38	2g	114	ARG
38	2g	120	ILE
38	2g	129	GLU
39	2h	10	LEU
39	2h	26	VAL
39	2h	51	VAL
39	2h	63	LEU
39	2h	69	ARG
39	2h	78	GLN
39	2h	84	ARG
39	2h	91	ARG
39	2h	111	ILE
39	2h	112	LEU
39	2h	120	THR
39	2h	137	VAL
40	2i	3	GLN

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Mol	Chain	Res	Type
40	2i	38	GLN
40	2i	50	LEU
40	2i	81	ILE
40	2i	89	ASN
40	2i	102	LEU
40	2i	104	ARG
40	2i	124	GLN
41	2j	8	LEU
41	2j	16	LEU
41	2j	21	GLN
41	2j	23	ILE
41	2j	46	ARG
41	2j	48	THR
41	2j	49	VAL
41	2j	57	LYS
41	2j	68	HIS
41	2j	84	GLN
41	2j	92	THR
41	2j	94	VAL
41	2j	95	GLU
42	2k	18	ARG
42	2k	48	ILE
42	2k	70	LYS
42	2k	75	TYR
42	2k	78	GLN
42	2k	103	LEU
42	2k	109	VAL
42	2k	114	VAL
43	2l	33	ARG
43	2l	83	VAL
43	2l	104	VAL
43	2l	115	LYS
43	2l	123	LYS
44	2m	47	ASP
44	2m	49	THR
44	2m	52	GLU
44	2m	55	ARG
44	2m	65	LYS
44	2m	81	LEU
44	2m	82	MET
44	2m	90	LEU
44	2m	102	ARG

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Mol	Chain	Res	Type
44	2m	106	ASN
44	2m	109	THR
44	2m	110	ARG
45	2n	11	LYS
45	2n	17	LYS
45	2n	18	VAL
45	2n	27	CYS
45	2n	32	SER
45	2n	33	VAL
45	2n	46	GLU
46	2o	3	ILE
46	2o	5	LYS
46	2o	24	SER
46	2o	26	GLU
46	2o	39	LEU
46	2o	83	GLU
46	2o	87	ILE
47	2p	1	MET
47	2p	2	VAL
47	2p	5	ARG
47	2p	11	SER
47	2p	54	GLU
47	2p	62	VAL
47	2p	67	THR
47	2p	72	ARG
47	2p	74	LEU
48	2q	6	LEU
48	2q	43	LEU
48	2q	49	GLU
48	2q	60	ILE
48	2q	74	LEU
48	2q	79	SER
49	2r	25	THR
49	2r	26	LEU
49	2r	29	PHE
49	2r	37	VAL
49	2r	38	GLU
49	2r	65	ILE
49	2r	76	LEU
50	2s	3	ARG
50	2s	27	GLU
50	2s	28	LYS

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Mol	Chain	Res	Type
50	2s	30	LEU
50	2s	41	VAL
50	2s	63	THR
50	2s	65	ASN
50	2s	77	THR
50	2s	83	HIS
51	2t	10	LEU
51	2t	24	LEU
51	2t	62	LEU
51	2t	71	THR
51	2t	84	LEU
52	2u	10	ARG
55	2z	7	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (158) such sidechains are listed below:

Mol	Chain	Res	Type
3	1D	126	GLN
3	1D	253	GLN
4	1E	54	GLN
4	1E	85	ASN
4	1E	143	ASN
5	1F	8	GLN
5	1F	133	ASN
5	1F	169	ASN
5	1F	203	GLN
6	1G	40	ASN
6	1G	79	ASN
8	1I	43	ASN
8	1I	139	GLN
9	1N	8	GLN
9	1N	56	ASN
10	1O	5	GLN
11	1P	38	GLN
11	1P	70	GLN
12	1Q	45	GLN
13	1R	50	HIS
13	1R	71	GLN
14	1S	95	HIS
15	1T	43	GLN
15	1T	84	GLN
15	1T	123	GLN

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Mol	Chain	Res	Type
16	1U	72	HIS
19	1X	31	HIS
20	1Y	6	HIS
20	1Y	92	ASN
21	1Z	151	HIS
24	12	38	GLN
24	12	70	GLN
25	13	32	GLN
26	14	60	GLN
28	16	20	ASN
30	18	35	GLN
31	19	36	GLN
33	1b	16	HIS
33	1b	94	ASN
33	1b	110	GLN
34	1c	6	HIS
34	1c	170	GLN
34	1c	176	HIS
35	1d	43	HIS
35	1d	45	GLN
35	1d	77	ASN
35	1d	123	HIS
35	1d	160	GLN
36	1e	38	GLN
36	1e	141	GLN
37	1f	100	ASN
38	1g	13	GLN
38	1g	86	GLN
38	1g	97	GLN
38	1g	110	GLN
39	1h	82	HIS
40	1i	31	GLN
40	1i	38	GLN
40	1i	58	HIS
40	1i	73	GLN
40	1i	87	GLN
40	1i	89	ASN
40	1i	124	GLN
41	1j	56	HIS
42	1k	78	GLN
42	1k	93	GLN
43	1l	78	GLN

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Mol	Chain	Res	Type
43	1l	99	HIS
48	1q	16	GLN
48	1q	26	GLN
50	1s	14	HIS
50	1s	23	ASN
50	1s	47	HIS
50	1s	56	GLN
50	1s	69	HIS
51	1t	9	ASN
51	1t	16	HIS
51	1t	26	ASN
51	1t	45	GLN
3	2D	87	ASN
3	2D	253	GLN
5	2F	69	HIS
5	2F	133	ASN
5	2F	169	ASN
5	2F	203	GLN
6	2G	40	ASN
6	2G	108	ASN
8	2I	43	ASN
9	2N	8	GLN
9	2N	94	HIS
9	2N	133	GLN
12	2Q	45	GLN
13	2R	31	HIS
13	2R	50	HIS
13	2R	71	GLN
14	2S	68	GLN
14	2S	95	HIS
15	2T	43	GLN
15	2T	58	ASN
15	2T	123	GLN
16	2U	94	ASN
17	2V	64	HIS
19	2X	31	HIS
20	2Y	43	ASN
20	2Y	92	ASN
21	2Z	50	GLN
21	2Z	73	GLN
21	2Z	151	HIS
23	21	56	GLN

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Mol	Chain	Res	Type
24	22	38	GLN
25	23	33	GLN
28	26	20	ASN
28	26	32	ASN
30	28	35	GLN
31	29	36	GLN
33	2b	19	HIS
33	2b	45	GLN
33	2b	146	GLN
34	2c	3	ASN
34	2c	6	HIS
34	2c	98	ASN
34	2c	123	GLN
34	2c	136	GLN
34	2c	176	HIS
34	2c	181	ASN
35	2d	74	GLN
35	2d	77	ASN
35	2d	123	HIS
35	2d	125	HIS
35	2d	201	GLN
38	2g	28	ASN
38	2g	97	GLN
38	2g	110	GLN
38	2g	122	HIS
38	2g	148	ASN
40	2i	3	GLN
40	2i	38	GLN
41	2j	21	GLN
41	2j	56	HIS
41	2j	84	GLN
42	2k	22	HIS
42	2k	78	GLN
42	2k	93	GLN
42	2k	104	GLN
43	2l	75	HIS
43	2l	78	GLN
43	2l	99	HIS
44	2m	40	ASN
44	2m	62	ASN
44	2m	77	ASN
46	2o	28	GLN

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Mol	Chain	Res	Type
47	2p	16	HIS
48	2q	16	GLN
50	2s	56	GLN
50	2s	69	HIS
50	2s	83	HIS
51	2t	18	GLN
51	2t	90	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1A	2737/2915 (93%)	384 (14%)	21 (0%)
1	2A	2781/2915 (95%)	469 (16%)	21 (0%)
2	1B	119/121 (98%)	10 (8%)	0
2	2B	119/121 (98%)	24 (20%)	2 (1%)
32	1a	1472/1521 (96%)	263 (17%)	0
32	2a	1479/1521 (97%)	283 (19%)	0
53	1v	4/24 (16%)	1 (25%)	0
53	2v	4/24 (16%)	1 (25%)	0
54	1x	75/77 (97%)	17 (22%)	0
54	2x	75/77 (97%)	15 (20%)	0
All	All	8865/9316 (95%)	1467 (16%)	44 (0%)

All (1467) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1A	11	U
1	1A	33	C
1	1A	44	C
1	1A	53	G
1	1A	62	A
1	1A	69	A
1	1A	72	A
1	1A	73	G
1	1A	82	A
1	1A	91	C
1	1A	115	A
1	1A	116	A
1	1A	117	U
1	1A	122	G
1	1A	135	G

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Mol	Chain	Res	Type
1	1A	137	G
1	1A	148	A
1	1A	160	C
1	1A	169	A
1	1A	170	A
1	1A	184	A
1	1A	187	A
1	1A	193	G
1	1A	203	G
1	1A	204	A
1	1A	210	A
1	1A	214	G
1	1A	216	A
1	1A	217	A
1	1A	221	A
1	1A	236	G
1	1A	268	G
1	1A	271	U
1	1A	272	G
1	1A	273	U
1	1A	274	C
1	1A	287	U
1	1A	288	G
1	1A	294	C
1	1A	295	U
1	1A	302	C
1	1A	334	A
1	1A	347	A
1	1A	352	G
1	1A	353	A
1	1A	375	G
1	1A	386	G
1	1A	388	G
1	1A	398	G
1	1A	406	U
1	1A	412	G
1	1A	422	G
1	1A	431	U
1	1A	433	G
1	1A	437	G
1	1A	438	A
1	1A	447	U

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Mol	Chain	Res	Type
1	1A	454	A
1	1A	467	G
1	1A	468	A
1	1A	469	C
1	1A	473	U
1	1A	476	C
1	1A	482	A
1	1A	495	A
1	1A	500	U
1	1A	506	G
1	1A	528	U
1	1A	529	A
1	1A	533	C
1	1A	554	G
1	1A	555	C
1	1A	556	A
1	1A	557	G
1	1A	572	G
1	1A	585	G
1	1A	595	G
1	1A	597	A
1	1A	624	G
1	1A	625	A
1	1A	626	G
1	1A	629	U
1	1A	638	G
1	1A	640	G
1	1A	658	C
1	1A	661	A
1	1A	669	C
1	1A	670	A
1	1A	681	G
1	1A	682	G
1	1A	696	C
1	1A	700	A
1	1A	714	G
1	1A	715	G
1	1A	732	G
1	1A	763	G
1	1A	765	C
1	1A	776	C
1	1A	785	G

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Mol	Chain	Res	Type
1	1A	797	A
1	1A	803	U
1	1A	810	A
1	1A	821	G
1	1A	822	G
1	1A	828	A
1	1A	830	A
1	1A	831	G
1	1A	836	C
1	1A	838	G
1	1A	851	G
1	1A	857	U
1	1A	858	C
1	1A	873	U
1	1A	874	U
1	1A	876	G
1	1A	901	G
1	1A	905	G
1	1A	912	A
1	1A	915	G
1	1A	925	G
1	1A	931	C
1	1A	932	C
1	1A	933	A
1	1A	934	C
1	1A	935	C
1	1A	936	A
1	1A	937	G
1	1A	938	C
1	1A	939	C
1	1A	941	A
1	1A	942	C
1	1A	952	U
1	1A	955	A
1	1A	976	G
1	1A	985	A
1	1A	989	A
1	1A	990	G
1	1A	1002	U
1	1A	1003	A
1	1A	1005	C
1	1A	1018	G

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Mol	Chain	Res	Type
1	1A	1019	C
1	1A	1028	A
1	1A	1041	A
1	1A	1057	U
1	1A	1058	C
1	1A	1067	G
1	1A	1071	U
1	1A	1078	U
1	1A	1083	C
1	1A	1086	C
1	1A	1090	A
1	1A	1091	A
1	1A	1092	G
1	1A	1150	U
1	1A	1154	C
1	1A	1156	A
1	1A	1159	G
1	1A	1173	A
1	1A	1174	A
1	1A	1175	U
1	1A	1179	C
1	1A	1180	G
1	1A	1183	G
1	1A	1194	G
1	1A	1200	A
1	1A	1215	G
1	1A	1217	G
1	1A	1218	A
1	1A	1219	U
1	1A	1220	G
1	1A	1221	A
1	1A	1264	A
1	1A	1265	C
1	1A	1285	U
1	1A	1286	A
1	1A	1293	G
1	1A	1298	A
1	1A	1301	G
1	1A	1316	G
1	1A	1317	A
1	1A	1318	U
1	1A	1345	U

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Mol	Chain	Res	Type
1	1A	1346	A
1	1A	1348	G
1	1A	1397	U
1	1A	1404	A
1	1A	1405	A
1	1A	1410	A
1	1A	1418	A
1	1A	1429	A
1	1A	1430	G
1	1A	1461	G
1	1A	1462	C
1	1A	1465	U
1	1A	1466	G
1	1A	1473	C
1	1A	1482	C
1	1A	1490	A
1	1A	1496	G
1	1A	1501	G
1	1A	1505	G
1	1A	1511	G
1	1A	1513	C
1	1A	1524	G
1	1A	1528	G
1	1A	1535	A
1	1A	1538	C
1	1A	1541	A
1	1A	1553	A
1	1A	1554	C
1	1A	1555	A
1	1A	1570	G
1	1A	1578	C
1	1A	1588	A
1	1A	1589	C
1	1A	1604	A
1	1A	1605	G
1	1A	1612	A
1	1A	1615	A
1	1A	1624	U
1	1A	1627	G
1	1A	1630	C
1	1A	1631	A
1	1A	1632	A

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Mol	Chain	Res	Type
1	1A	1653	A
1	1A	1654	A
1	1A	1655	A
1	1A	1694	C
1	1A	1700	A
1	1A	1704	C
1	1A	1720	G
1	1A	1746	A
1	1A	1747	A
1	1A	1766	A
1	1A	1767	U
1	1A	1776	G
1	1A	1793	G
1	1A	1794	G
1	1A	1799	G
1	1A	1803	A
1	1A	1810	A
1	1A	1821	A
1	1A	1830	C
1	1A	1831	G
1	1A	1846	G
1	1A	1859	A
1	1A	1869	G
1	1A	1877	A
1	1A	1899	G
1	1A	1910	A
1	1A	1917	G
1	1A	1921	A
1	1A	1927	G
1	1A	1934	A
1	1A	1940	A
1	1A	1948	A
1	1A	1950	G
1	1A	1951	G
1	1A	1958	A
1	1A	1959	A
1	1A	1976	U
1	1A	1984	U
1	1A	1988	C
1	1A	1991	A
1	1A	1992	A
1	1A	1993	A

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Mol	Chain	Res	Type
1	1A	2013	G
1	1A	2014	U
1	1A	2018	G
1	1A	2041	A
1	1A	2044	G
1	1A	2052	A
1	1A	2053	G
1	1A	2054	A
1	1A	2064	C
1	1A	2076	C
1	1A	2077	G
1	1A	2081	A
1	1A	2082	G
1	1A	2083	A
1	1A	2090	G
1	1A	2101	G
1	1A	2114	G
1	1A	2205	G
1	1A	2206	C
1	1A	2207	G
1	1A	2209	C
1	1A	2212	G
1	1A	2213	G
1	1A	2219	A
1	1A	2226	G
1	1A	2227	G
1	1A	2228	A
1	1A	2229	U
1	1A	2236	A
1	1A	2249	G
1	1A	2250	G
1	1A	2251	C
1	1A	2279	A
1	1A	2280	A
1	1A	2284	A
1	1A	2286	C
1	1A	2294	C
1	1A	2298	A
1	1A	2316	A
1	1A	2331	A
1	1A	2336	G
1	1A	2338	A

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Mol	Chain	Res	Type
1	1A	2345	G
1	1A	2347	A
1	1A	2354	C
1	1A	2358	C
1	1A	2361	C
1	1A	2365	G
1	1A	2394	G
1	1A	2396	C
1	1A	2416	G
1	1A	2417	U
1	1A	2418	G
1	1A	2433	A
1	1A	2434	U
1	1A	2436	A
1	1A	2440	G
1	1A	2441	A
1	1A	2442	U
1	1A	2446	A
1	1A	2450	A
1	1A	2452	C
1	1A	2459	A
1	1A	2487	A
1	1A	2489	A
1	1A	2501	G
1	1A	2513	G
1	1A	2516	G
1	1A	2517	U
1	1A	2529	A
1	1A	2540	G
1	1A	2565	U
1	1A	2577	A
1	1A	2578	G
1	1A	2584	C
1	1A	2593	G
1	1A	2613	A
1	1A	2620	U
1	1A	2621	C
1	1A	2622	U
1	1A	2623	C
1	1A	2634	G
1	1A	2639	C
1	1A	2640	A

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Mol	Chain	Res	Type
1	1A	2641	G
1	1A	2665	A
1	1A	2690	A
1	1A	2700	U
1	1A	2701	C
1	1A	2702	C
1	1A	2713	U
1	1A	2718	G
1	1A	2724	A
1	1A	2725	A
1	1A	2726	G
1	1A	2738	U
1	1A	2745	A
1	1A	2769	A
1	1A	2770	A
1	1A	2776	A
1	1A	2777	A
1	1A	2778	G
1	1A	2790	A
1	1A	2802	A
1	1A	2806	C
1	1A	2812	G
1	1A	2829	A
1	1A	2830	A
1	1A	2844	A
1	1A	2867	C
1	1A	2881	G
1	1A	2882	A
1	1A	2889	C
1	1A	2900	A
1	1A	2902	G
1	1A	2903	U
1	1A	2905	U
2	1B	2	C
2	1B	13	A
2	1B	25	A
2	1B	56	G
2	1B	65	C
2	1B	67	G
2	1B	73	A
2	1B	85	G
2	1B	106	G

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Mol	Chain	Res	Type
2	1B	110	G
32	1a	6	U
32	1a	10	G
32	1a	33	A
32	1a	40	G
32	1a	44	C
32	1a	45	G
32	1a	48	C
32	1a	49	C
32	1a	51	A
32	1a	52	A
32	1a	62	G
32	1a	65	G
32	1a	66	U
32	1a	74	G
32	1a	76	G
32	1a	77	G
32	1a	78	G
32	1a	89	G
32	1a	91	G
32	1a	92	G
32	1a	95	A
32	1a	110	A
32	1a	115	C
32	1a	126	C
32	1a	132	C
32	1a	133	G
32	1a	139	G
32	1a	146	A
32	1a	149	C
32	1a	150	C
32	1a	156	A
32	1a	161	G
32	1a	162	G
32	1a	168	U
32	1a	169	C
32	1a	177	U
32	1a	189	U
32	1a	202	A
32	1a	204	A
32	1a	206	G
32	1a	208	C

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Mol	Chain	Res	Type
32	1a	210	U
32	1a	211	U
32	1a	212	G
32	1a	219	U
32	1a	243	G
32	1a	246	A
32	1a	247	G
32	1a	254	G
32	1a	258	A
32	1a	262	G
32	1a	263	C
32	1a	264	C
32	1a	277	G
32	1a	285	G
32	1a	297	G
32	1a	313	G
32	1a	317	A
32	1a	324	C
32	1a	325	A
32	1a	326	C
32	1a	339	U
32	1a	342	G
32	1a	343	G
32	1a	344	G
32	1a	348	C
32	1a	349	A
32	1a	350	G
32	1a	351	C
32	1a	363	U
32	1a	368	C
32	1a	369	A
32	1a	380	G
32	1a	386	C
32	1a	393	A
32	1a	394	C
32	1a	402	G
32	1a	408	A
32	1a	409	G
32	1a	419	G
32	1a	420	G
32	1a	425	U
32	1a	431	C

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Mol	Chain	Res	Type
32	1a	435	A
32	1a	437	C
32	1a	447	A
32	1a	449	C
32	1a	455	A
32	1a	456	C
32	1a	457	G
32	1a	470	G
32	1a	481	A
32	1a	482	U
32	1a	489	G
32	1a	493	A
32	1a	494	A
32	1a	495	C
32	1a	502	C
32	1a	511	G
32	1a	516	A
32	1a	517	A
32	1a	531	A
32	1a	543	A
32	1a	545	U
32	1a	556	A
32	1a	557	A
32	1a	560	G
32	1a	561	G
32	1a	574	C
32	1a	576	G
32	1a	602	C
32	1a	614	G
32	1a	625	U
32	1a	637	A
32	1a	649	A
32	1a	671	A
32	1a	672	G
32	1a	677	G
32	1a	701	C
32	1a	707	U
32	1a	731	C
32	1a	733	C
32	1a	739	G
32	1a	743	A
32	1a	757	G

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Mol	Chain	Res	Type
32	1a	761	A
32	1a	776	A
32	1a	777	U
32	1a	778	A
32	1a	799	A
32	1a	800	A
32	1a	801	C
32	1a	812	A
32	1a	813	G
32	1a	820	G
32	1a	824	C
32	1a	825	U
32	1a	826	C
32	1a	829	G
32	1a	837	A
32	1a	838	A
32	1a	848	U
32	1a	850	A
32	1a	851	A
32	1a	880	G
32	1a	892	A
32	1a	904	G
32	1a	905	G
32	1a	909	C
32	1a	912	C
32	1a	913	A
32	1a	914	C
32	1a	938	U
32	1a	939	U
32	1a	946	A
32	1a	947	A
32	1a	949	G
32	1a	950	C
32	1a	952	A
32	1a	953	A
32	1a	954	G
32	1a	955	A
32	1a	970	U
32	1a	971	G
32	1a	972	A
32	1a	977	C
32	1a	980	G

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Mol	Chain	Res	Type
32	1a	982	G
32	1a	983	A
32	1a	984	A
32	1a	987	C
32	1a	988	G
32	1a	989	G
32	1a	990	G
32	1a	995	A
32	1a	999	U
32	1a	1025	G
32	1a	1026	C
32	1a	1027	A
32	1a	1034	C
32	1a	1036	G
32	1a	1037	C
32	1a	1047	G
32	1a	1048	U
32	1a	1049	C
32	1a	1064	G
32	1a	1069	U
32	1a	1077	G
32	1a	1078	U
32	1a	1084	A
32	1a	1091	G
32	1a	1094	A
32	1a	1106	A
32	1a	1107	G
32	1a	1115	C
32	1a	1116	G
32	1a	1117	G
32	1a	1119	U
32	1a	1120	C
32	1a	1122	G
32	1a	1135	A
32	1a	1142	U
32	1a	1143	G
32	1a	1149	G
32	1a	1164	G
32	1a	1165	A
32	1a	1166	G
32	1a	1175	G
32	1a	1178	U

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Mol	Chain	Res	Type
32	1a	1179	G
32	1a	1184	G
32	1a	1194	U
32	1a	1195	A
32	1a	1196	C
32	1a	1209	A
32	1a	1220	A
32	1a	1222	U
32	1a	1238	A
32	1a	1239	U
32	1a	1240	G
32	1a	1252	C
32	1a	1255	G
32	1a	1260	U
32	1a	1261	A
32	1a	1262	A
32	1a	1268	A
32	1a	1269	A
32	1a	1281	A
32	1a	1282	G
32	1a	1284	U
32	1a	1287	G
32	1a	1294	G
32	1a	1301	A
32	1a	1304	C
32	1a	1320	G
32	1a	1322	A
32	1a	1329	G
32	1a	1335	G
32	1a	1342	A
32	1a	1345	C
32	1a	1353	G
32	1a	1360	A
32	1a	1361	C
32	1a	1362	G
32	1a	1364	U
32	1a	1379	A
32	1a	1380	C
32	1a	1392	C
32	1a	1402	G
32	1a	1424	G
32	1a	1425	G

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Mol	Chain	Res	Type
32	1a	1426	G
32	1a	1432	A
32	1a	1433	C
32	1a	1465	G
32	1a	1475	G
32	1a	1480	A
32	1a	1481	A
32	1a	1482	G
32	1a	1484	U
32	1a	1495	G
32	1a	1507	G
32	1a	1508	G
53	1v	15	A
54	1x	6	G
54	1x	9	G
54	1x	13	C
54	1x	16	C
54	1x	17	C
54	1x	17(A)	U
54	1x	20	U
54	1x	21	A
54	1x	31	G
54	1x	42	G
54	1x	47	U
54	1x	54	5MU
54	1x	55	PSU
54	1x	56	C
54	1x	65	C
54	1x	70	G
54	1x	76	A
1	2A	7	A
1	2A	11	U
1	2A	12	A
1	2A	13	A
1	2A	14	G
1	2A	34	G
1	2A	44	C
1	2A	53	G
1	2A	59	G
1	2A	69	A
1	2A	72	A
1	2A	73	G

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Mol	Chain	Res	Type
1	2A	81	G
1	2A	82	A
1	2A	88	U
1	2A	93	G
1	2A	98	G
1	2A	99	G
1	2A	115	A
1	2A	116	A
1	2A	117	U
1	2A	128	G
1	2A	137	G
1	2A	138	A
1	2A	154	C
1	2A	155	U
1	2A	160	C
1	2A	169	A
1	2A	170	A
1	2A	184	A
1	2A	187	A
1	2A	193	G
1	2A	201	A
1	2A	203	G
1	2A	204	A
1	2A	209	A
1	2A	210	A
1	2A	212	G
1	2A	217	A
1	2A	223	U
1	2A	224	C
1	2A	225	C
1	2A	236	G
1	2A	238	G
1	2A	252	C
1	2A	253	A
1	2A	268	G
1	2A	270	U
1	2A	271	U
1	2A	272	G
1	2A	274	C
1	2A	287	U
1	2A	288	G
1	2A	301	A

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Mol	Chain	Res	Type
1	2A	334	A
1	2A	347	A
1	2A	350	G
1	2A	352	G
1	2A	353	A
1	2A	355	A
1	2A	357	C
1	2A	358	C
1	2A	361	G
1	2A	365	G
1	2A	375	G
1	2A	385	U
1	2A	386	G
1	2A	389	G
1	2A	412	G
1	2A	422	G
1	2A	431	U
1	2A	433	G
1	2A	437	G
1	2A	438	A
1	2A	441	A
1	2A	453	U
1	2A	454	A
1	2A	460	U
1	2A	468	A
1	2A	469	C
1	2A	471	G
1	2A	479	A
1	2A	480	C
1	2A	481	C
1	2A	482	A
1	2A	495	A
1	2A	506	G
1	2A	528	U
1	2A	529	A
1	2A	533	C
1	2A	552	A
1	2A	554	G
1	2A	555	C
1	2A	556	A
1	2A	557	G
1	2A	573	G

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Mol	Chain	Res	Type
1	2A	585	G
1	2A	590	U
1	2A	595	G
1	2A	596	C
1	2A	597	A
1	2A	608	A
1	2A	615	G
1	2A	625	A
1	2A	626	G
1	2A	629	U
1	2A	637	U
1	2A	638	G
1	2A	639	A
1	2A	640	G
1	2A	651	A
1	2A	658	C
1	2A	661	A
1	2A	669	C
1	2A	670	A
1	2A	673	G
1	2A	678	A
1	2A	679	G
1	2A	697	G
1	2A	732	G
1	2A	763	G
1	2A	772	G
1	2A	776	C
1	2A	811	G
1	2A	817	G
1	2A	821	G
1	2A	822	G
1	2A	828	A
1	2A	829	A
1	2A	830	A
1	2A	831	G
1	2A	838	G
1	2A	848	A
1	2A	851	G
1	2A	858	C
1	2A	865	A
1	2A	873	U
1	2A	874	U

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Mol	Chain	Res	Type
1	2A	903	C
1	2A	905	G
1	2A	906	U
1	2A	912	A
1	2A	915	G
1	2A	918	A
1	2A	924	A
1	2A	925	G
1	2A	926	G
1	2A	928	G
1	2A	930	C
1	2A	932	C
1	2A	933	A
1	2A	934	C
1	2A	935	C
1	2A	936	A
1	2A	938	C
1	2A	941	A
1	2A	942	C
1	2A	945	A
1	2A	946	A
1	2A	955	A
1	2A	956	A
1	2A	960	C
1	2A	962	A
1	2A	975	G
1	2A	976	G
1	2A	980	C
1	2A	982	G
1	2A	985	A
1	2A	989	A
1	2A	990	G
1	2A	997	A
1	2A	1003	A
1	2A	1005	C
1	2A	1018	G
1	2A	1019	C
1	2A	1025	A
1	2A	1028	A
1	2A	1041	A
1	2A	1050	C
1	2A	1057	U

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Mol	Chain	Res	Type
1	2A	1058	C
1	2A	1066	A
1	2A	1067	G
1	2A	1070	G
1	2A	1078	U
1	2A	1088	C
1	2A	1090	A
1	2A	1091	A
1	2A	1092	G
1	2A	1093	A
1	2A	1103	G
1	2A	1104	G
1	2A	1105	U
1	2A	1106	U
1	2A	1107	G
1	2A	1108	G
1	2A	1109	C
1	2A	1110	U
1	2A	1115	A
1	2A	1118	A
1	2A	1120	C
1	2A	1121	C
1	2A	1126	U
1	2A	1128	U
1	2A	1132	G
1	2A	1133	A
1	2A	1136	G
1	2A	1142	U
1	2A	1152	G
1	2A	1156	A
1	2A	1157	G
1	2A	1158	U
1	2A	1159	G
1	2A	1167	G
1	2A	1175	U
1	2A	1179	C
1	2A	1180	G
1	2A	1183	G
1	2A	1187	A
1	2A	1216	G
1	2A	1249	U
1	2A	1264	A

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Mol	Chain	Res	Type
1	2A	1265	C
1	2A	1266	C
1	2A	1276	G
1	2A	1281	G
1	2A	1284	G
1	2A	1295	G
1	2A	1297	G
1	2A	1298	A
1	2A	1301	G
1	2A	1316	G
1	2A	1317	A
1	2A	1318	U
1	2A	1345	U
1	2A	1346	A
1	2A	1348	G
1	2A	1350	C
1	2A	1359	C
1	2A	1374	U
1	2A	1387	A
1	2A	1399	A
1	2A	1400	G
1	2A	1404	A
1	2A	1405	A
1	2A	1410	A
1	2A	1413	G
1	2A	1415	C
1	2A	1429	A
1	2A	1430	G
1	2A	1431	C
1	2A	1448	C
1	2A	1461	G
1	2A	1462	C
1	2A	1465	U
1	2A	1466	G
1	2A	1472	A
1	2A	1473	C
1	2A	1486	G
1	2A	1490	A
1	2A	1495	A
1	2A	1496	G
1	2A	1501	G
1	2A	1502	G

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Mol	Chain	Res	Type
1	2A	1507	G
1	2A	1513	C
1	2A	1517	A
1	2A	1524	G
1	2A	1528	G
1	2A	1534	U
1	2A	1535	A
1	2A	1538	C
1	2A	1542	U
1	2A	1554	C
1	2A	1555	A
1	2A	1570	G
1	2A	1589	C
1	2A	1604	A
1	2A	1605	G
1	2A	1612	A
1	2A	1615	A
1	2A	1624	U
1	2A	1626	A
1	2A	1630	C
1	2A	1631	A
1	2A	1653	A
1	2A	1654	A
1	2A	1655	A
1	2A	1663	A
1	2A	1667	G
1	2A	1686	C
1	2A	1687	A
1	2A	1694	C
1	2A	1715	A
1	2A	1720	G
1	2A	1746	A
1	2A	1765	G
1	2A	1766	A
1	2A	1786	G
1	2A	1792	A
1	2A	1793	G
1	2A	1794	G
1	2A	1803	A
1	2A	1810	A
1	2A	1812	C
1	2A	1821	A

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Mol	Chain	Res	Type
1	2A	1830	C
1	2A	1831	G
1	2A	1846	G
1	2A	1859	A
1	2A	1869	G
1	2A	1877	A
1	2A	1889	A
1	2A	1898	A
1	2A	1899	G
1	2A	1921	A
1	2A	1927	G
1	2A	1934	A
1	2A	1935	C
1	2A	1950	G
1	2A	1951	G
1	2A	1952	U
1	2A	1955	C
1	2A	1958	A
1	2A	1962	C
1	2A	1976	U
1	2A	1984	U
1	2A	1985	G
1	2A	1988	C
1	2A	1991	A
1	2A	1992	A
1	2A	1993	A
1	2A	2014	U
1	2A	2018	G
1	2A	2041	A
1	2A	2044	G
1	2A	2052	A
1	2A	2054	A
1	2A	2057	C
1	2A	2064	C
1	2A	2067	G
1	2A	2076	C
1	2A	2077	G
1	2A	2081	A
1	2A	2082	G
1	2A	2083	A
1	2A	2090	G
1	2A	2120	U

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Mol	Chain	Res	Type
1	2A	2206	C
1	2A	2209	C
1	2A	2210	U
1	2A	2213	G
1	2A	2219	A
1	2A	2226	G
1	2A	2227	G
1	2A	2228	A
1	2A	2236	A
1	2A	2246	G
1	2A	2250	G
1	2A	2278	A
1	2A	2279	A
1	2A	2280	A
1	2A	2286	C
1	2A	2289	A
1	2A	2290	G
1	2A	2294	C
1	2A	2298	A
1	2A	2299	A
1	2A	2300	G
1	2A	2304	C
1	2A	2308	C
1	2A	2316	A
1	2A	2318	G
1	2A	2319	G
1	2A	2322	A
1	2A	2323	U
1	2A	2329	G
1	2A	2330	G
1	2A	2331	A
1	2A	2336	G
1	2A	2345	G
1	2A	2347	A
1	2A	2354	C
1	2A	2358	C
1	2A	2361	C
1	2A	2377	A
1	2A	2390	G
1	2A	2394	G
1	2A	2396	C
1	2A	2398	U

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Mol	Chain	Res	Type
1	2A	2413	C
1	2A	2417	U
1	2A	2418	G
1	2A	2421	G
1	2A	2430	U
1	2A	2433	A
1	2A	2436	A
1	2A	2439	G
1	2A	2440	G
1	2A	2441	A
1	2A	2446	A
1	2A	2450	A
1	2A	2451	C
1	2A	2452	C
1	2A	2456	G
1	2A	2459	A
1	2A	2476	C
1	2A	2480	A
1	2A	2485	C
1	2A	2487	A
1	2A	2497	G
1	2A	2501	G
1	2A	2508	A
1	2A	2513	G
1	2A	2516	G
1	2A	2517	U
1	2A	2529	A
1	2A	2531	C
1	2A	2540	G
1	2A	2554	G
1	2A	2565	U
1	2A	2566	U
1	2A	2577	A
1	2A	2578	G
1	2A	2585	G
1	2A	2590	C
1	2A	2613	A
1	2A	2620	U
1	2A	2622	U
1	2A	2623	C
1	2A	2640	A
1	2A	2641	G

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Mol	Chain	Res	Type
1	2A	2657	C
1	2A	2665	A
1	2A	2700	U
1	2A	2701	C
1	2A	2714	C
1	2A	2724	A
1	2A	2725	A
1	2A	2726	G
1	2A	2738	U
1	2A	2745	A
1	2A	2756	G
1	2A	2763	G
1	2A	2769	A
1	2A	2776	A
1	2A	2777	A
1	2A	2778	G
1	2A	2790	A
1	2A	2795	G
1	2A	2801	C
1	2A	2805	G
1	2A	2812	G
1	2A	2817	U
1	2A	2827	G
1	2A	2829	A
1	2A	2830	A
1	2A	2842	G
1	2A	2843	G
1	2A	2845	U
1	2A	2869	A
1	2A	2881	G
1	2A	2884	C
1	2A	2888	C
1	2A	2889	C
1	2A	2900	A
1	2A	2902	G
1	2A	2903	U
1	2A	2905	U
2	2B	2	C
2	2B	7	G
2	2B	9	G
2	2B	13	A
2	2B	16	G

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Mol	Chain	Res	Type
2	2B	28	C
2	2B	34	U
2	2B	43	C
2	2B	45	A
2	2B	46	A
2	2B	52	A
2	2B	53	A
2	2B	56	G
2	2B	58	A
2	2B	59	A
2	2B	63	G
2	2B	67	G
2	2B	73	A
2	2B	85	G
2	2B	90	A
2	2B	110	G
2	2B	116	G
2	2B	119	G
2	2B	120	A
32	2a	6	U
32	2a	10	G
32	2a	15	U
32	2a	16	G
32	2a	23	G
32	2a	33	A
32	2a	39	G
32	2a	40	G
32	2a	48	C
32	2a	49	C
32	2a	51	A
32	2a	52	A
32	2a	66	U
32	2a	67	G
32	2a	74	G
32	2a	79	G
32	2a	84	A
32	2a	85	C
32	2a	91	G
32	2a	95	A
32	2a	110	A
32	2a	115	C
32	2a	123	U

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Mol	Chain	Res	Type
32	2a	124	G
32	2a	126	C
32	2a	138	A
32	2a	141	G
32	2a	151	G
32	2a	158	C
32	2a	169	C
32	2a	177	U
32	2a	202	A
32	2a	204	A
32	2a	211	U
32	2a	212	G
32	2a	213	C
32	2a	243	G
32	2a	247	G
32	2a	262	G
32	2a	263	C
32	2a	277	G
32	2a	285	G
32	2a	297	G
32	2a	317	A
32	2a	324	C
32	2a	326	C
32	2a	328	G
32	2a	340	A
32	2a	346	G
32	2a	347	G
32	2a	348	C
32	2a	349	A
32	2a	350	G
32	2a	363	U
32	2a	365	C
32	2a	368	C
32	2a	380	G
32	2a	394	C
32	2a	400	U
32	2a	402	G
32	2a	408	A
32	2a	418	C
32	2a	425	U
32	2a	426	A
32	2a	435	A

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Mol	Chain	Res	Type
32	2a	437	C
32	2a	447	A
32	2a	455	A
32	2a	456	C
32	2a	457	G
32	2a	463	A
32	2a	466	G
32	2a	470	G
32	2a	481	A
32	2a	482	U
32	2a	489	G
32	2a	495	C
32	2a	496	U
32	2a	497	C
32	2a	502	C
32	2a	505	G
32	2a	511	G
32	2a	515	U
32	2a	516	A
32	2a	517	A
32	2a	529	C
32	2a	531	A
32	2a	543	A
32	2a	545	U
32	2a	546	C
32	2a	552	G
32	2a	556	A
32	2a	557	A
32	2a	560	G
32	2a	561	G
32	2a	575	U
32	2a	576	G
32	2a	580	C
32	2a	581	G
32	2a	591	A
32	2a	610	U
32	2a	614	G
32	2a	636	U
32	2a	637	A
32	2a	641	G
32	2a	649	A
32	2a	658	G

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Mol	Chain	Res	Type
32	2a	671	A
32	2a	672	G
32	2a	677	G
32	2a	679	A
32	2a	686	A
32	2a	696	A
32	2a	705	G
32	2a	707	U
32	2a	708	G
32	2a	715	G
32	2a	733	C
32	2a	737	A
32	2a	738	C
32	2a	739	G
32	2a	744	G
32	2a	754	C
32	2a	758	G
32	2a	761	A
32	2a	777	U
32	2a	778	A
32	2a	783	G
32	2a	800	A
32	2a	801	C
32	2a	805	G
32	2a	811	U
32	2a	812	A
32	2a	813	G
32	2a	824	C
32	2a	825	U
32	2a	826	C
32	2a	827	C
32	2a	831	G
32	2a	836	G
32	2a	837	A
32	2a	852	G
32	2a	880	G
32	2a	892	A
32	2a	904	G
32	2a	905	G
32	2a	909	C
32	2a	912	C
32	2a	913	A

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Mol	Chain	Res	Type
32	2a	916	A
32	2a	920	G
32	2a	938	U
32	2a	939	U
32	2a	946	A
32	2a	947	A
32	2a	949	G
32	2a	952	A
32	2a	953	A
32	2a	954	G
32	2a	955	A
32	2a	956	A
32	2a	963	C
32	2a	967	C
32	2a	970	U
32	2a	971	G
32	2a	977	C
32	2a	979	A
32	2a	981	G
32	2a	983	A
32	2a	984	A
32	2a	986	C
32	2a	988	G
32	2a	1000	G
32	2a	1001	G
32	2a	1002	G
32	2a	1028	C
32	2a	1033	G
32	2a	1036	G
32	2a	1037	C
32	2a	1038	A
32	2a	1039	U
32	2a	1048	U
32	2a	1049	C
32	2a	1064	G
32	2a	1077	G
32	2a	1078	U
32	2a	1084	A
32	2a	1093	A
32	2a	1096	C
32	2a	1099	C
32	2a	1101	C

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Mol	Chain	Res	Type
32	2a	1104	U
32	2a	1105	U
32	2a	1107	G
32	2a	1110	G
32	2a	1112	C
32	2a	1113	A
32	2a	1117	G
32	2a	1118	U
32	2a	1119	U
32	2a	1120	C
32	2a	1121	G
32	2a	1122	G
32	2a	1123	C
32	2a	1129	A
32	2a	1140	A
32	2a	1141	C
32	2a	1142	U
32	2a	1146	C
32	2a	1149	G
32	2a	1158	A
32	2a	1165	A
32	2a	1168	G
32	2a	1172	G
32	2a	1173	A
32	2a	1178	U
32	2a	1184	G
32	2a	1191	C
32	2a	1193	U
32	2a	1194	U
32	2a	1196	C
32	2a	1210	C
32	2a	1218	A
32	2a	1220	A
32	2a	1222	U
32	2a	1223	G
32	2a	1228	C
32	2a	1238	A
32	2a	1239	U
32	2a	1240	G
32	2a	1242	C
32	2a	1243	A
32	2a	1244	C

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Mol	Chain	Res	Type
32	2a	1255	G
32	2a	1260	U
32	2a	1262	A
32	2a	1263	U
32	2a	1264	C
32	2a	1268	A
32	2a	1269	A
32	2a	1281	A
32	2a	1285	C
32	2a	1287	G
32	2a	1293	G
32	2a	1301	A
32	2a	1302	C
32	2a	1304	C
32	2a	1305	G
32	2a	1307	C
32	2a	1308	C
32	2a	1320	G
32	2a	1328	A
32	2a	1329	G
32	2a	1335	G
32	2a	1341	C
32	2a	1342	A
32	2a	1345	C
32	2a	1347	U
32	2a	1353	G
32	2a	1359	U
32	2a	1380	C
32	2a	1381	A
32	2a	1402	G
32	2a	1425	G
32	2a	1426	G
32	2a	1427	A
32	2a	1430	C
32	2a	1431	U
32	2a	1432	A
32	2a	1433	C
32	2a	1434	G
32	2a	1469	G
32	2a	1480	A
32	2a	1481	A
32	2a	1482	G

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Mol	Chain	Res	Type
32	2a	1483	G
32	2a	1484	U
32	2a	1495	G
32	2a	1498	G
32	2a	1507	G
32	2a	1508	G
32	2a	1509	A
32	2a	1510	U
53	2v	15	A
54	2x	6	G
54	2x	9	G
54	2x	13	C
54	2x	16	C
54	2x	17	C
54	2x	17(A)	U
54	2x	21	A
54	2x	31	G
54	2x	42	G
54	2x	47	U
54	2x	55	PSU
54	2x	56	C
54	2x	65	C
54	2x	70	G
54	2x	76	A

All (44) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1A	183	A
1	1A	184	A
1	1A	270	U
1	1A	301	A
1	1A	516	A
1	1A	792	A
1	1A	873	U
1	1A	1018	G
1	1A	1047	G
1	1A	1153	U
1	1A	1218	A
1	1A	1220	G
1	1A	1285	U
1	1A	1425	G

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Mol	Chain	Res	Type
1	1A	1653	A
1	1A	2013	G
1	1A	2208	G
1	1A	2417	U
1	1A	2441	A
1	1A	2700	U
1	1A	2768	U
1	2A	183	A
1	2A	184	A
1	2A	203	G
1	2A	357	C
1	2A	516	A
1	2A	810	A
1	2A	902	C
1	2A	945	A
1	2A	1114	A
1	2A	1238	A
1	2A	1425	G
1	2A	1465	U
1	2A	1604	A
1	2A	1934	A
1	2A	2013	G
1	2A	2328	C
1	2A	2417	U
1	2A	2450	A
1	2A	2700	U
1	2A	2762	A
1	2A	2768	U
2	2B	42	C
2	2B	45	A

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

8 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
54	PSU	1x	55	54	18,21,22	1.37	1 (5%)	21,30,33	1.97	3 (14%)
54	5MC	2x	32	54	19,22,23	1.60	3 (15%)	26,32,35	1.18	3 (11%)
54	PSU	2x	55	54	18,21,22	1.40	2 (11%)	21,30,33	1.91	4 (19%)
54	4SU	2x	8	54	18,21,22	1.98	6 (33%)	25,30,33	1.23	4 (16%)
54	5MU	1x	54	54	19,22,23	1.49	5 (26%)	27,32,35	1.77	5 (18%)
54	5MU	2x	54	54	19,22,23	1.38	5 (26%)	27,32,35	1.93	7 (25%)
54	4SU	1x	8	54	18,21,22	2.19	5 (27%)	25,30,33	1.38	4 (16%)
54	5MC	1x	32	54	19,22,23	1.64	3 (15%)	26,32,35	1.19	2 (7%)

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
54	PSU	1x	55	54	-	2/7/25/26	0/2/2/2
54	5MC	2x	32	54	-	0/7/25/26	0/2/2/2
54	PSU	2x	55	54	-	2/7/25/26	0/2/2/2
54	4SU	2x	8	54	-	1/7/25/26	0/2/2/2
54	5MU	1x	54	54	-	2/7/25/26	0/2/2/2
54	5MU	2x	54	54	-	2/7/25/26	0/2/2/2
54	4SU	1x	8	54	-	0/7/25/26	0/2/2/2
54	5MC	1x	32	54	-	0/7/25/26	0/2/2/2

All (30) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
54	1x	32	5MC	C5-C4	5.71	1.48	1.44
54	2x	32	5MC	C5-C4	5.59	1.48	1.44
54	1x	8	4SU	C4-N3	-5.25	1.32	1.37
54	1x	8	4SU	C4-S4	-4.91	1.60	1.68
54	2x	8	4SU	C4-N3	-4.49	1.33	1.37
54	2x	8	4SU	C4-S4	-4.19	1.61	1.68
54	2x	55	PSU	C6-C5	4.11	1.39	1.35
54	1x	8	4SU	C5-C4	-3.50	1.38	1.42
54	1x	55	PSU	C6-C5	3.50	1.39	1.35
54	1x	8	4SU	C2-N3	-3.21	1.32	1.38
54	1x	54	5MU	C6-C5	3.19	1.39	1.34
54	2x	8	4SU	C2-N3	-3.17	1.32	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
54	2x	8	4SU	C5-C4	-2.92	1.39	1.42
54	1x	32	5MC	C6-C5	2.90	1.39	1.34
54	2x	32	5MC	C6-C5	2.88	1.39	1.34
54	2x	54	5MU	C6-C5	2.87	1.39	1.34
54	1x	54	5MU	C4-N3	-2.76	1.33	1.38
54	1x	54	5MU	C4-C5	2.45	1.48	1.44
54	2x	54	5MU	C4-N3	-2.34	1.34	1.38
54	2x	54	5MU	C4-C5	2.33	1.48	1.44
54	1x	32	5MC	C6-N1	-2.32	1.34	1.38
54	1x	54	5MU	C2-N3	-2.30	1.34	1.38
54	1x	54	5MU	C2-N1	2.25	1.42	1.38
54	1x	8	4SU	O2-C2	2.25	1.27	1.23
54	2x	54	5MU	C2-N1	2.24	1.42	1.38
54	2x	55	PSU	C4-N3	-2.23	1.34	1.38
54	2x	32	5MC	C6-N1	-2.16	1.34	1.38
54	2x	8	4SU	O2-C2	2.12	1.26	1.23
54	2x	8	4SU	C6-C5	2.07	1.39	1.35
54	2x	54	5MU	C6-N1	-2.03	1.34	1.38

All (32) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
54	1x	55	PSU	N1-C2-N3	5.98	121.47	115.17
54	2x	55	PSU	N1-C2-N3	5.85	121.34	115.17
54	1x	55	PSU	O2-C2-N1	-4.83	117.81	122.79
54	2x	54	5MU	N3-C2-N1	4.65	120.95	114.89
54	2x	54	5MU	C4-N3-C2	-4.36	121.62	127.34
54	1x	54	5MU	N3-C2-N1	4.28	120.47	114.89
54	1x	54	5MU	C4-N3-C2	-4.13	121.93	127.34
54	1x	8	4SU	C6-C5-C4	-4.06	116.44	119.95
54	2x	54	5MU	O4-C4-C5	-4.04	120.29	124.92
54	1x	54	5MU	C5-C4-N3	3.96	118.77	115.32
54	2x	55	PSU	C4-N3-C2	-3.94	120.95	126.37
54	1x	54	5MU	C5-C6-N1	-3.80	119.19	123.31
54	2x	54	5MU	C5-C4-N3	3.62	118.47	115.32
54	1x	8	4SU	C5-C4-N3	3.59	118.09	114.75
54	1x	32	5MC	C5-C6-N1	-3.55	119.46	123.31
54	1x	55	PSU	C4-N3-C2	-3.24	121.91	126.37
54	1x	54	5MU	O4-C4-C5	-3.14	121.32	124.92
54	1x	32	5MC	C5-C4-N3	-3.14	118.54	121.75
54	2x	32	5MC	C5-C6-N1	-3.09	119.95	123.31
54	2x	32	5MC	C5-C4-N3	-2.95	118.73	121.75

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
54	2x	8	4SU	C5-C4-N3	2.76	117.32	114.75
54	2x	32	5MC	O2-C2-N3	-2.60	118.24	122.33
54	2x	8	4SU	C1'-N1-C2	2.58	122.23	117.59
54	2x	54	5MU	C5-C6-N1	-2.55	120.54	123.31
54	2x	55	PSU	O2-C2-N1	-2.46	120.25	122.79
54	2x	8	4SU	C6-C5-C4	-2.44	117.84	119.95
54	2x	54	5MU	O2-C2-N1	-2.37	119.72	122.80
54	2x	8	4SU	O2-C2-N1	2.17	125.62	122.80
54	1x	8	4SU	S4-C4-N3	-2.14	117.96	120.20
54	2x	54	5MU	C5M-C5-C4	2.11	121.04	118.78
54	2x	55	PSU	C6-C5-C4	-2.09	116.77	118.17
54	1x	8	4SU	C1'-N1-C2	2.07	121.30	117.59

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
54	1x	55	PSU	O4'-C4'-C5'-O5'
54	2x	55	PSU	O4'-C4'-C5'-O5'
54	1x	55	PSU	C3'-C4'-C5'-O5'
54	2x	55	PSU	C3'-C4'-C5'-O5'
54	1x	54	5MU	C3'-C4'-C5'-O5'
54	2x	54	5MU	C3'-C4'-C5'-O5'
54	1x	54	5MU	O4'-C4'-C5'-O5'
54	2x	54	5MU	O4'-C4'-C5'-O5'
54	2x	8	4SU	C2'-C1'-N1-C2

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
54	1x	55	PSU	1	0
54	2x	55	PSU	1	0
54	1x	8	4SU	1	0

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2436 ligands modelled in this entry, 2434 are monoatomic - leaving 2 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
58	SF4	1d	501	35	0,12,12	-	-	-		
58	SF4	2d	501	35	0,12,12	-	-	-		

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
58	SF4	1d	501	35	-	-	0/6/5/5
58	SF4	2d	501	35	-	-	0/6/5/5

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	1A	2746/2915 (94%)	-0.42	29 (1%) 78 70	20, 42, 84, 108	0
1	2A	2790/2915 (95%)	-0.35	14 (0%) 87 82	24, 46, 91, 108	0
2	1B	120/121 (99%)	0.02	2 (1%) 69 60	35, 63, 80, 89	0
2	2B	120/121 (99%)	0.49	4 (3%) 49 39	41, 68, 82, 91	0
3	1D	275/276 (99%)	-0.21	0 100 100	21, 40, 56, 78	0
3	2D	275/276 (99%)	-0.20	3 (1%) 78 70	22, 42, 59, 78	0
4	1E	204/206 (99%)	-0.14	0 100 100	21, 44, 65, 84	0
4	2E	204/206 (99%)	-0.05	0 100 100	23, 47, 67, 85	0
5	1F	203/210 (96%)	0.08	0 100 100	22, 50, 74, 88	0
5	2F	203/210 (96%)	0.10	2 (0%) 79 72	23, 54, 77, 90	0
6	1G	181/182 (99%)	0.56	8 (4%) 39 31	50, 67, 79, 91	0
6	2G	181/182 (99%)	1.04	14 (7%) 19 14	54, 71, 81, 92	0
7	1H	174/180 (96%)	0.58	3 (1%) 69 60	48, 63, 75, 85	0
7	2H	174/180 (96%)	0.80	9 (5%) 33 25	52, 68, 79, 86	0
8	1I	146/148 (98%)	0.45	4 (2%) 56 46	46, 74, 84, 90	0
8	2I	146/148 (98%)	0.48	3 (2%) 63 54	48, 74, 84, 90	0
9	1N	140/140 (100%)	0.06	0 100 100	29, 47, 65, 76	0
9	2N	140/140 (100%)	0.10	1 (0%) 84 77	33, 50, 68, 78	0
10	1O	122/122 (100%)	-0.13	1 (0%) 82 75	32, 44, 61, 74	0
10	2O	122/122 (100%)	-0.06	0 100 100	34, 47, 62, 74	0
11	1P	149/150 (99%)	0.17	0 100 100	22, 53, 74, 81	0
11	2P	149/150 (99%)	0.18	1 (0%) 84 77	24, 56, 76, 83	0
12	1Q	141/141 (100%)	0.22	4 (2%) 55 45	32, 48, 61, 79	0
12	2Q	141/141 (100%)	0.26	2 (1%) 73 64	35, 51, 64, 78	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
13	1R	118/118 (100%)	0.03	0 100 100	27, 39, 50, 64	0
13	2R	118/118 (100%)	-0.15	0 100 100	30, 42, 54, 66	0
14	1S	110/112 (98%)	0.37	4 (3%) 46 37	43, 61, 71, 77	0
14	2S	110/112 (98%)	1.00	12 (10%) 10 8	48, 63, 76, 79	0
15	1T	131/146 (89%)	0.13	3 (2%) 61 51	37, 49, 72, 84	0
15	2T	131/146 (89%)	0.10	3 (2%) 61 51	40, 50, 73, 83	0
16	1U	116/118 (98%)	-0.02	1 (0%) 81 74	27, 39, 56, 74	0
16	2U	116/118 (98%)	0.04	0 100 100	29, 43, 61, 74	0
17	1V	101/101 (100%)	-0.00	0 100 100	28, 47, 65, 75	0
17	2V	101/101 (100%)	0.09	0 100 100	32, 53, 69, 76	0
18	1W	112/113 (99%)	-0.30	0 100 100	27, 36, 55, 89	0
18	2W	112/113 (99%)	-0.13	1 (0%) 81 74	28, 39, 57, 90	0
19	1X	95/96 (98%)	0.14	2 (2%) 63 54	26, 46, 66, 81	0
19	2X	95/96 (98%)	0.36	4 (4%) 40 32	29, 49, 68, 81	0
20	1Y	107/110 (97%)	0.48	2 (1%) 66 57	42, 59, 76, 86	0
20	2Y	107/110 (97%)	0.66	4 (3%) 45 36	47, 62, 79, 88	0
21	1Z	186/206 (90%)	0.37	1 (0%) 87 82	48, 66, 79, 89	0
21	2Z	186/206 (90%)	0.76	7 (3%) 44 35	53, 69, 81, 91	0
22	10	75/85 (88%)	-0.32	0 100 100	18, 36, 48, 61	0
22	20	75/85 (88%)	0.60	3 (4%) 42 33	46, 62, 73, 80	0
23	11	97/98 (98%)	0.10	1 (1%) 79 72	28, 48, 72, 77	0
23	21	97/98 (98%)	0.18	0 100 100	31, 51, 72, 75	0
24	12	70/72 (97%)	0.45	3 (4%) 40 31	43, 56, 70, 74	0
24	22	70/72 (97%)	0.39	1 (1%) 73 64	46, 60, 73, 74	0
25	13	59/60 (98%)	0.15	1 (1%) 69 60	32, 44, 64, 77	0
25	23	59/60 (98%)	0.12	0 100 100	35, 48, 66, 77	0
26	14	69/71 (97%)	0.52	8 (11%) 9 7	47, 71, 93, 97	0
26	24	69/71 (97%)	1.22	9 (13%) 7 6	56, 89, 96, 98	0
27	15	59/60 (98%)	-0.65	0 100 100	16, 28, 46, 72	0
27	25	59/60 (98%)	-0.13	0 100 100	29, 49, 66, 75	0
28	16	53/54 (98%)	-0.53	0 100 100	24, 38, 54, 63	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
28	26	53/54 (98%)	0.09	0 100 100	41, 58, 74, 79	0
29	17	48/49 (97%)	-0.12	2 (4%) 40 32	24, 32, 64, 78	0
29	27	48/49 (97%)	-0.05	1 (2%) 63 54	27, 34, 66, 77	0
30	18	64/65 (98%)	0.04	0 100 100	32, 39, 49, 60	0
30	28	64/65 (98%)	0.14	0 100 100	35, 43, 54, 62	0
31	19	37/37 (100%)	0.40	1 (2%) 56 46	38, 49, 66, 70	0
31	29	37/37 (100%)	0.83	2 (5%) 31 24	44, 52, 67, 72	0
32	1a	1477/1521 (97%)	0.09	21 (1%) 73 64	32, 70, 96, 113	0
32	2a	1483/1521 (97%)	0.27	26 (1%) 67 58	44, 77, 98, 111	0
33	1b	231/256 (90%)	0.86	19 (8%) 17 13	66, 81, 93, 101	0
33	2b	231/256 (90%)	0.99	20 (8%) 16 11	68, 86, 96, 102	0
34	1c	206/239 (86%)	0.85	13 (6%) 26 19	65, 81, 88, 95	0
34	2c	206/239 (86%)	1.15	25 (12%) 8 6	69, 82, 89, 93	0
35	1d	208/209 (99%)	0.83	11 (5%) 32 24	51, 75, 88, 96	0
35	2d	208/209 (99%)	0.69	7 (3%) 48 39	58, 72, 85, 90	0
36	1e	148/162 (91%)	0.27	2 (1%) 73 64	45, 67, 77, 84	0
36	2e	148/162 (91%)	0.57	2 (1%) 73 64	56, 74, 83, 89	0
37	1f	100/101 (99%)	0.46	2 (2%) 65 56	57, 72, 80, 88	0
37	2f	100/101 (99%)	0.30	1 (1%) 79 72	58, 73, 83, 87	0
38	1g	155/156 (99%)	0.73	16 (10%) 12 9	67, 77, 91, 95	0
38	2g	155/156 (99%)	0.81	18 (11%) 9 7	67, 78, 90, 93	0
39	1h	137/138 (99%)	0.52	0 100 100	53, 69, 77, 85	0
39	2h	137/138 (99%)	0.62	4 (2%) 53 43	65, 76, 83, 89	0
40	1i	127/128 (99%)	1.20	22 (17%) 4 3	64, 83, 91, 95	0
40	2i	127/128 (99%)	1.79	43 (33%) 1 1	65, 84, 92, 98	0
41	1j	97/105 (92%)	1.52	29 (29%) 1 1	67, 85, 93, 97	0
41	2j	96/105 (91%)	1.61	28 (29%) 1 1	69, 86, 94, 97	0
42	1k	114/129 (88%)	0.32	2 (1%) 67 58	43, 67, 80, 88	0
42	2k	114/129 (88%)	0.44	3 (2%) 57 47	56, 76, 86, 91	0
43	1l	122/132 (92%)	0.40	5 (4%) 41 33	43, 61, 72, 79	0
43	2l	122/132 (92%)	0.54	3 (2%) 58 48	52, 67, 75, 81	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
44	1m	118/126 (93%)	0.75	6 (5%) 33 25	59, 77, 85, 94	0
44	2m	116/126 (92%)	1.26	13 (11%) 10 7	66, 80, 86, 93	0
45	1n	60/61 (98%)	1.11	9 (15%) 5 4	62, 73, 83, 84	0
45	2n	60/61 (98%)	2.03	32 (53%) 0 0	76, 84, 90, 92	0
46	1o	88/89 (98%)	0.32	1 (1%) 78 70	47, 64, 80, 90	0
46	2o	88/89 (98%)	0.50	0 100 100	58, 72, 83, 86	0
47	1p	82/88 (93%)	1.15	10 (12%) 8 6	61, 76, 87, 94	0
47	2p	82/88 (93%)	0.74	3 (3%) 45 36	57, 70, 82, 90	0
48	1q	99/105 (94%)	0.57	0 100 100	47, 67, 78, 82	0
48	2q	99/105 (94%)	0.57	0 100 100	56, 72, 80, 87	0
49	1r	68/88 (77%)	0.32	1 (1%) 72 63	54, 68, 81, 87	0
49	2r	68/88 (77%)	0.42	2 (2%) 53 43	61, 72, 82, 92	0
50	1s	84/93 (90%)	1.04	7 (8%) 17 12	66, 78, 86, 97	0
50	2s	83/93 (89%)	1.67	32 (38%) 1 0	73, 89, 96, 103	0
51	1t	96/106 (90%)	0.92	10 (10%) 11 8	58, 73, 81, 88	0
51	2t	96/106 (90%)	0.63	7 (7%) 21 15	57, 71, 81, 86	0
52	1u	23/27 (85%)	1.48	8 (34%) 1 0	68, 75, 80, 84	0
52	2u	23/27 (85%)	1.92	9 (39%) 1 0	69, 76, 83, 85	0
53	1v	5/24 (20%)	0.84	1 (20%) 3 2	63, 66, 85, 92	0
53	2v	5/24 (20%)	0.66	0 100 100	66, 69, 85, 93	0
54	1x	72/77 (93%)	-0.03	0 100 100	32, 66, 81, 96	0
54	2x	72/77 (93%)	0.11	0 100 100	34, 69, 83, 97	0
55	1z	13/19 (68%)	0.67	0 100 100	26, 36, 52, 56	0
55	2z	12/19 (63%)	0.44	1 (8%) 17 12	28, 39, 53, 55	0
All	All	20521/21482 (95%)	0.18	654 (3%) 50 40	16, 61, 89, 113	0

All (654) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
7	1H	2	SER	6.7
32	1a	980	G	6.6
32	1a	981	G	6.2
20	1Y	1	MET	4.8
38	1g	79	ARG	4.8

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Mol	Chain	Res	Type	RSRZ
52	2u	6	ARG	4.8
40	2i	15	ALA	4.6
45	1n	2	ALA	4.6
31	29	37	GLY	4.5
33	1b	214	ILE	4.5
41	2j	63	PHE	4.5
32	2a	981	G	4.4
40	2i	29	ASN	4.4
45	2n	2	ALA	4.4
45	2n	25	VAL	4.4
40	1i	2	GLU	4.4
38	2g	16	LEU	4.4
40	2i	67	GLY	4.4
52	2u	14	TRP	4.3
26	24	49	PHE	4.3
1	1A	2815	G	4.3
44	2m	102	ARG	4.3
38	1g	80	VAL	4.3
29	17	48	LYS	4.3
40	1i	15	ALA	4.3
38	2g	78	ARG	4.1
45	2n	33	VAL	4.1
33	2b	152	PHE	4.1
6	2G	28	VAL	4.1
45	2n	17	LYS	4.0
15	2T	131	ALA	4.0
36	2e	20	GLN	4.0
34	1c	2	GLY	3.9
32	2a	980	G	3.9
40	2i	42	ARG	3.9
40	2i	102	LEU	3.8
45	2n	21	TYR	3.8
1	1A	1149	C	3.8
45	2n	3	ARG	3.7
50	2s	71	LEU	3.7
52	2u	11	GLY	3.7
23	11	2	SER	3.6
41	1j	31	GLY	3.6
50	2s	16	LEU	3.6
33	2b	187	LEU	3.6
33	2b	97	TRP	3.6
32	1a	979	A	3.6

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Mol	Chain	Res	Type	RSRZ
32	2a	1265	G	3.5
51	1t	103	GLY	3.5
45	2n	18	VAL	3.5
40	2i	66	ARG	3.5
34	1c	28	GLN	3.5
20	2Y	1	MET	3.5
44	2m	75	ALA	3.5
34	2c	186	PHE	3.5
50	2s	9	VAL	3.5
38	2g	83	ALA	3.5
45	2n	49	HIS	3.5
32	1a	982	G	3.4
31	29	5	ALA	3.4
50	2s	12	ASP	3.4
41	2j	76	ASN	3.4
50	1s	9	VAL	3.4
40	2i	10	ARG	3.4
33	1b	237	ALA	3.4
41	1j	98	ILE	3.4
1	1A	2813	C	3.3
38	1g	83	ALA	3.3
43	2l	18	VAL	3.3
6	1G	51	ARG	3.3
12	1Q	60	ARG	3.3
41	1j	5	ARG	3.3
33	2b	134	GLU	3.3
45	2n	11	LYS	3.3
1	1A	1554	C	3.3
41	1j	62	HIS	3.3
26	24	56	VAL	3.3
34	1c	207	VAL	3.3
40	2i	16	ARG	3.3
8	1I	10	GLU	3.3
47	1p	19	ILE	3.3
51	1t	69	GLY	3.3
1	1A	8	U	3.2
40	2i	21	PRO	3.2
15	1T	130	ALA	3.2
40	2i	41	VAL	3.2
40	2i	65	VAL	3.2
22	20	10	THR	3.2
1	1A	33	C	3.2

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Mol	Chain	Res	Type	RSRZ
34	1c	184	TYR	3.2
38	2g	38	LEU	3.2
45	2n	37	PHE	3.2
41	1j	63	PHE	3.2
47	2p	82	GLN	3.2
33	2b	92	TYR	3.1
38	1g	78	ARG	3.1
40	2i	9	ARG	3.1
33	1b	70	PHE	3.1
50	2s	67	VAL	3.1
32	1a	1268	A	3.1
50	2s	2	PRO	3.1
51	2t	25	ARG	3.1
40	2i	36	TYR	3.1
32	2a	1268	A	3.1
40	2i	11	LYS	3.1
44	2m	90	LEU	3.1
50	2s	40	ILE	3.0
51	1t	10	LEU	3.0
26	14	57	GLU	3.0
45	1n	13	THR	3.0
15	2T	130	ALA	3.0
47	1p	80	PHE	3.0
1	2A	1582	C	3.0
33	2b	99	GLY	3.0
41	1j	10	GLY	3.0
41	2j	87	THR	3.0
41	2j	72	VAL	3.0
43	1l	18	VAL	3.0
52	2u	3	LYS	3.0
41	2j	40	LEU	3.0
41	2j	49	VAL	3.0
50	2s	70	LYS	2.9
19	1X	95	LEU	2.9
35	1d	101	LEU	2.9
16	1U	117	GLN	2.9
39	2h	131	GLY	2.9
1	1A	836	C	2.9
40	2i	61	ALA	2.9
26	14	59	PHE	2.9
40	2i	17	VAL	2.9
40	2i	19	LEU	2.9

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Mol	Chain	Res	Type	RSRZ
6	1G	2	PRO	2.9
41	2j	32	ALA	2.9
44	2m	118	ALA	2.9
43	1l	89	ARG	2.9
52	1u	15	ARG	2.9
40	1i	19	LEU	2.9
5	2F	208	GLY	2.9
50	2s	52	TYR	2.9
51	1t	21	LYS	2.9
33	1b	7	VAL	2.9
34	2c	116	VAL	2.9
40	2i	14	VAL	2.9
41	1j	100	THR	2.9
41	2j	77	PRO	2.8
19	2X	69	TYR	2.8
15	1T	131	ALA	2.8
33	2b	21	ARG	2.8
38	1g	81	GLY	2.8
40	1i	12	GLU	2.8
35	1d	104	VAL	2.8
40	2i	5	TYR	2.8
52	2u	9	ARG	2.8
40	2i	13	ALA	2.8
38	1g	42	ILE	2.8
32	2a	1184	G	2.8
40	2i	2	GLU	2.8
41	2j	5	ARG	2.8
40	2i	119	ALA	2.8
45	2n	10	ALA	2.8
45	2n	16	PHE	2.8
21	2Z	5	LEU	2.8
32	1a	1239	U	2.8
35	2d	154	ASN	2.8
50	2s	66	MET	2.8
1	1A	2814	C	2.8
7	1H	3	ARG	2.7
19	2X	68	ARG	2.7
40	2i	109	VAL	2.7
32	2a	979	A	2.7
45	2n	34	TYR	2.7
41	2j	55	LYS	2.7
41	1j	76	ASN	2.7

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Mol	Chain	Res	Type	RSRZ
38	1g	5	ARG	2.7
45	2n	35	ARG	2.7
1	1A	2206	C	2.7
41	1j	72	VAL	2.7
20	2Y	94	LYS	2.7
38	2g	84	ASN	2.7
52	2u	17	THR	2.7
34	2c	155	GLY	2.7
38	2g	32	ARG	2.7
40	2i	37	PHE	2.7
1	1A	2205	G	2.7
3	2D	2	ALA	2.7
40	1i	13	ALA	2.7
41	1j	32	ALA	2.7
50	2s	31	ILE	2.7
45	1n	17	LYS	2.7
26	24	52	THR	2.7
42	1k	36	ASP	2.7
40	2i	126	SER	2.7
41	1j	85	LEU	2.7
50	2s	15	LEU	2.7
3	2D	153	ALA	2.6
8	1I	29	TYR	2.6
8	2I	11	ASN	2.6
32	2a	1207	A	2.6
45	1n	7	ILE	2.6
45	2n	7	ILE	2.6
26	14	49	PHE	2.6
38	1g	156	TRP	2.6
14	2S	7	TYR	2.6
38	2g	5	ARG	2.6
1	1A	2904	C	2.6
14	2S	58	LEU	2.6
41	2j	65	LEU	2.6
1	1A	1934	A	2.6
50	2s	69	HIS	2.6
47	2p	59	TRP	2.6
44	1m	59	TYR	2.6
1	1A	2901	G	2.6
1	2A	2902	G	2.6
40	1i	56	LEU	2.6
6	1G	35	GLU	2.6

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Mol	Chain	Res	Type	RSRZ
6	1G	48	GLU	2.6
50	1s	56	GLN	2.6
34	2c	129	ALA	2.6
45	1n	59	ALA	2.6
1	1A	2806	C	2.6
35	1d	102	ASP	2.6
34	1c	179	ARG	2.6
33	1b	22	LYS	2.6
14	2S	90	GLY	2.6
41	1j	39	PRO	2.6
6	2G	175	LEU	2.6
35	1d	155	LEU	2.6
41	2j	44	VAL	2.6
50	2s	51	VAL	2.6
33	2b	237	ALA	2.6
34	2c	128	PHE	2.6
51	1t	12	ALA	2.6
40	1i	105	ASP	2.6
1	1A	270	U	2.5
12	1Q	59	ARG	2.5
50	1s	29	ARG	2.5
6	2G	53	LEU	2.5
40	1i	67	GLY	2.5
20	2Y	5	MET	2.5
41	1j	75	ILE	2.5
44	2m	60	VAL	2.5
40	1i	64	THR	2.5
51	2t	9	ASN	2.5
24	12	69	ARG	2.5
50	1s	13	ASP	2.5
1	2A	2812	G	2.5
1	2A	2801	C	2.5
41	1j	77	PRO	2.5
38	2g	82	GLY	2.5
45	2n	44	LEU	2.5
50	1s	16	LEU	2.5
40	2i	125	TYR	2.5
41	1j	34	VAL	2.5
41	2j	75	ILE	2.5
41	1j	64	GLU	2.5
41	2j	100	THR	2.5
29	17	45	ALA	2.5

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Mol	Chain	Res	Type	RSRZ
38	1g	2	ALA	2.5
40	1i	106	ALA	2.5
41	1j	27	ALA	2.5
35	1d	154	ASN	2.5
50	2s	13	ASP	2.5
32	2a	1510	U	2.5
41	1j	71	LEU	2.5
8	1I	90	GLY	2.5
33	1b	97	TRP	2.5
37	2f	6	VAL	2.5
40	2i	62	TYR	2.5
52	1u	18	TYR	2.5
52	1u	21	TYR	2.5
50	2s	3	ARG	2.5
20	1Y	92	ASN	2.5
24	12	15	LYS	2.5
38	1g	84	ASN	2.5
50	2s	53	ASN	2.5
51	2t	74	LYS	2.5
33	2b	138	LEU	2.5
38	2g	85	TYR	2.5
42	1k	25	TYR	2.5
45	2n	36	PHE	2.5
1	1A	2209	C	2.5
50	1s	85	LYS	2.5
32	1a	1121	G	2.5
32	2a	982	G	2.5
8	2I	96	ASP	2.4
33	1b	215	LEU	2.4
33	1b	222	ILE	2.4
7	2H	52	VAL	2.4
38	1g	77	SER	2.4
50	2s	35	SER	2.4
32	1a	209	U	2.4
26	24	57	GLU	2.4
40	2i	107	ARG	2.4
44	1m	94	ARG	2.4
41	1j	33	GLN	2.4
52	1u	3	LYS	2.4
40	2i	7	THR	2.4
32	1a	158	C	2.4
38	2g	37	ASN	2.4

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Mol	Chain	Res	Type	RSRZ
33	1b	187	LEU	2.4
38	1g	12	LEU	2.4
32	2a	1509	A	2.4
53	1v	14	A	2.4
1	1A	1220	G	2.4
1	2A	2815	G	2.4
1	2A	2901	G	2.4
6	2G	160	VAL	2.4
18	2W	112	GLY	2.4
21	2Z	175	VAL	2.4
37	1f	88	VAL	2.4
50	2s	8	GLY	2.4
34	2c	154	SER	2.4
35	1d	153	ARG	2.4
5	2F	130	ALA	2.4
44	1m	2	ALA	2.4
34	1c	201	TYR	2.4
26	24	45	GLY	2.4
32	1a	1432	A	2.4
32	1a	1509	A	2.4
12	2Q	59	ARG	2.4
19	1X	65	ARG	2.4
29	27	48	LYS	2.4
38	2g	36	LYS	2.4
41	1j	70	ARG	2.4
44	2m	104	ARG	2.4
2	2B	23	G	2.4
44	2m	67	GLU	2.4
45	2n	61	TRP	2.4
32	1a	211	U	2.4
26	14	63	TYR	2.4
50	2s	14	HIS	2.4
39	2h	2	LEU	2.4
41	2j	8	LEU	2.4
6	1G	88	ILE	2.4
44	2m	78	ILE	2.4
50	2s	49	ILE	2.4
35	1d	180	GLY	2.4
51	2t	69	GLY	2.4
51	2t	10	LEU	2.4
40	2i	63	ILE	2.4
45	2n	42	ILE	2.4

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Mol	Chain	Res	Type	RSRZ
26	14	50	VAL	2.3
40	2i	53	VAL	2.3
11	2P	116	GLY	2.3
41	2j	52	GLY	2.3
32	2a	957	C	2.3
14	2S	34	HIS	2.3
40	2i	99	LEU	2.3
34	2c	124	ILE	2.3
40	2i	81	ILE	2.3
14	1S	93	LYS	2.3
40	1i	127	LYS	2.3
40	2i	98	PRO	2.3
51	2t	21	LYS	2.3
1	1A	2902	G	2.3
32	1a	614	G	2.3
34	2c	179	ARG	2.3
35	2d	118	ARG	2.3
50	2s	11	VAL	2.3
7	2H	174	GLY	2.3
36	1e	22	GLY	2.3
41	1j	69	ASN	2.3
44	2m	100	GLY	2.3
40	2i	33	PHE	2.3
41	1j	47	PHE	2.3
34	2c	180	ALA	2.3
45	2n	20	ALA	2.3
45	2n	6	LEU	2.3
40	1i	7	THR	2.3
50	2s	80	TYR	2.3
51	1t	55	ILE	2.3
1	2A	1071	U	2.3
51	2t	23	ARG	2.3
26	24	50	VAL	2.3
34	1c	185	GLY	2.3
52	2u	16	GLY	2.3
41	2j	78	ASN	2.3
24	12	12	GLU	2.3
38	1g	39	ALA	2.3
40	2i	105	ASP	2.3
40	2i	56	LEU	2.3
6	1G	182	LYS	2.3
50	2s	33	THR	2.3

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Mol	Chain	Res	Type	RSRZ
14	1S	92	TYR	2.3
20	2Y	2	ARG	2.3
39	2h	122	ARG	2.3
1	2A	1121	C	2.3
40	1i	109	VAL	2.3
41	2j	34	VAL	2.3
45	1n	33	VAL	2.3
47	1p	41	PRO	2.3
41	2j	10	GLY	2.3
14	2S	61	ASN	2.3
33	1b	28	PHE	2.3
34	1c	10	PHE	2.3
34	2c	53	ALA	2.3
21	2Z	125	LEU	2.3
31	19	12	ASP	2.3
33	1b	11	LEU	2.3
34	2c	107	GLN	2.3
47	1p	68	ASP	2.3
1	2A	1579	G	2.3
47	1p	16	HIS	2.3
52	2u	13	ILE	2.3
50	2s	34	TRP	2.3
45	2n	32	SER	2.3
6	2G	149	VAL	2.3
7	2H	45	VAL	2.3
14	2S	65	VAL	2.3
33	1b	165	VAL	2.3
40	1i	6	GLY	2.3
1	1A	1098	C	2.2
6	2G	137	GLU	2.2
33	1b	188	ALA	2.2
34	2c	137	ALA	2.2
50	2s	73	GLU	2.2
35	1d	162	LEU	2.2
49	2r	66	LEU	2.2
43	2l	126	LYS	2.2
34	2c	6	HIS	2.2
41	2j	9	ARG	2.2
51	1t	8	ARG	2.2
7	1H	133	VAL	2.2
26	14	56	VAL	2.2
26	24	67	TYR	2.2

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Mol	Chain	Res	Type	RSRZ
40	1i	126	SER	2.2
47	1p	51	VAL	2.2
52	2u	23	PRO	2.2
33	2b	151	GLY	2.2
34	2c	159	GLY	2.2
40	1i	68	GLY	2.2
22	20	69	PHE	2.2
32	1a	978	U	2.2
26	14	53	GLU	2.2
41	2j	18	ALA	2.2
26	24	9	LEU	2.2
38	1g	38	LEU	2.2
49	2r	46	GLU	2.2
1	2A	1120	C	2.2
41	2j	80	LYS	2.2
42	2k	117	ASN	2.2
45	2n	15	LYS	2.2
6	2G	39	ILE	2.2
33	1b	201	ILE	2.2
41	1j	4	ILE	2.2
33	2b	137	ARG	2.2
34	2c	62	ASP	2.2
34	2c	172	ARG	2.2
35	1d	118	ARG	2.2
44	1m	102	ARG	2.2
55	2z	11	ARG	2.2
6	2G	31	VAL	2.2
47	1p	66	PRO	2.2
7	2H	2	SER	2.2
50	2s	4	SER	2.2
15	2T	69	GLY	2.2
1	2A	1216	G	2.2
2	2B	118	G	2.2
14	2S	32	LEU	2.2
32	1a	65	G	2.2
33	2b	171	ALA	2.2
36	2e	94	ALA	2.2
41	2j	33	GLN	2.2
44	2m	101	GLN	2.2
45	2n	57	ARG	2.2
47	1p	82	GLN	2.2
2	2B	88	C	2.2

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Mol	Chain	Res	Type	RSRZ
32	2a	1231	C	2.2
34	1c	7	PRO	2.2
40	2i	123	PRO	2.2
50	1s	76	PRO	2.2
45	2n	22	THR	2.2
6	2G	42	GLY	2.2
33	2b	236	TYR	2.2
43	2l	64	TYR	2.2
50	2s	74	PHE	2.2
10	1O	91	LEU	2.2
33	2b	44	LEU	2.2
8	2I	146	ALA	2.2
41	2j	6	ILE	2.2
44	1m	4	ILE	2.2
1	1A	2905	U	2.2
45	2n	41	ARG	2.2
51	1t	80	ARG	2.2
32	2a	949	G	2.2
7	2H	112	PRO	2.2
21	2Z	167	PRO	2.2
32	2a	1238	A	2.2
33	1b	136	VAL	2.2
35	1d	7	PRO	2.2
38	2g	80	VAL	2.2
41	2j	41	PRO	2.2
1	1A	934	C	2.2
32	2a	1236	C	2.2
47	2p	69	THR	2.2
34	2c	167	TRP	2.2
33	2b	31	TYR	2.2
6	2G	76	SER	2.2
7	2H	71	LEU	2.2
40	2i	48	GLU	2.2
26	24	31	ILE	2.1
52	1u	6	ARG	2.1
1	1A	1071	U	2.1
51	1t	9	ASN	2.1
7	2H	115	VAL	2.1
14	2S	28	VAL	2.1
25	13	2	PRO	2.1
40	1i	41	VAL	2.1
41	1j	86	MET	2.1

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Mol	Chain	Res	Type	RSRZ
1	1A	9	G	2.1
12	2Q	22	LYS	2.1
1	1A	571	A	2.1
1	1A	2802	A	2.1
2	2B	119	G	2.1
15	1T	37	GLY	2.1
32	1a	516	A	2.1
32	2a	1206	G	2.1
32	2a	1469	G	2.1
40	2i	64	THR	2.1
52	1u	2	GLY	2.1
38	2g	156	TRP	2.1
32	1a	64	C	2.1
32	2a	1021	C	2.1
34	2c	52	LEU	2.1
21	2Z	164	ALA	2.1
34	2c	160	ALA	2.1
38	1g	7	ALA	2.1
6	1G	54	GLU	2.1
41	1j	66	ARG	2.1
42	2k	126	ARG	2.1
34	2c	39	ILE	2.1
9	2N	5	VAL	2.1
34	2c	64	VAL	2.1
34	2c	198	VAL	2.1
50	2s	76	PRO	2.1
40	2i	91	ASP	2.1
21	1Z	69	THR	2.1
41	2j	93	GLY	2.1
35	2d	155	LEU	2.1
14	2S	37	ALA	2.1
32	2a	1232	A	2.1
52	1u	10	ARG	2.1
1	1A	2812	G	2.1
1	2A	638	G	2.1
32	2a	1164	G	2.1
1	1A	669	C	2.1
2	1B	12	C	2.1
2	1B	88	C	2.1
32	1a	160	C	2.1
41	1j	30	SER	2.1
6	2G	15	VAL	2.1

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Mol	Chain	Res	Type	RSRZ
19	2X	33	LYS	2.1
21	2Z	1	MET	2.1
40	2i	108	VAL	2.1
43	1l	91	LYS	2.1
44	2m	98	VAL	2.1
45	1n	15	LYS	2.1
45	2n	4	LYS	2.1
50	2s	41	VAL	2.1
40	1i	49	PRO	2.1
32	2a	1109	U	2.1
8	1I	6	LEU	2.1
12	1Q	33	GLY	2.1
36	1e	85	GLY	2.1
45	2n	38	GLY	2.1
14	2S	29	PHE	2.1
21	2Z	87	ASP	2.1
22	20	44	ARG	2.1
6	2G	50	ALA	2.1
33	2b	162	ILE	2.1
34	2c	168	ALA	2.1
34	2c	189	ALA	2.1
44	2m	18	ALA	2.1
38	2g	154	TYR	2.1
32	2a	1165	A	2.1
33	2b	150	SER	2.1
1	1A	2805	G	2.1
1	2A	33	C	2.1
1	2A	1132	G	2.1
19	2X	1	MET	2.1
24	22	1	MET	2.1
33	2b	197	VAL	2.1
40	1i	28	VAL	2.1
41	1j	24	VAL	2.1
44	1m	27	LYS	2.1
35	1d	188	LEU	2.1
1	1A	1465	U	2.1
32	1a	1023	U	2.1
34	1c	81	GLY	2.1
35	2d	87	GLY	2.1
14	1S	13	ARG	2.1
26	14	55	ARG	2.1
41	1j	46	ARG	2.1

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Mol	Chain	Res	Type	RSRZ
41	2j	67	THR	2.1
34	1c	206	GLU	2.1
39	2h	99	GLU	2.1
37	1f	54	LYS	2.0
45	2n	9	LYS	2.0
50	2s	18	LYS	2.0
34	1c	6	HIS	2.0
38	2g	21	VAL	2.0
44	2m	97	PRO	2.0
33	1b	61	LEU	2.0
38	2g	12	LEU	2.0
45	2n	39	LEU	2.0
14	2S	20	ARG	2.0
32	1a	176	G	2.0
32	2a	1000	G	2.0
32	2a	1025	G	2.0
40	2i	68	GLY	2.0
51	1t	86	ARG	2.0
47	1p	22	THR	2.0
7	2H	145	ALA	2.0
33	1b	225	ALA	2.0
45	2n	30	ALA	2.0
34	2c	44	GLU	2.0
35	2d	163	GLU	2.0
41	2j	61	GLU	2.0
52	1u	14	TRP	2.0
33	1b	236	TYR	2.0
34	1c	23	TYR	2.0
12	1Q	1	MET	2.0
14	2S	68	GLN	2.0
35	2d	170	VAL	2.0
38	2g	9	VAL	2.0
50	2s	38	SER	2.0
40	1i	98	PRO	2.0
41	1j	90	LEU	2.0
46	1o	56	LEU	2.0
14	1S	10	ARG	2.0
45	2n	12	ARG	2.0
6	1G	42	GLY	2.0
6	2G	102	PHE	2.0
38	1g	82	GLY	2.0
40	1i	33	PHE	2.0

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Mol	Chain	Res	Type	RSRZ
42	2k	90	GLY	2.0
32	1a	208	C	2.0
32	2a	1049	C	2.0
6	2G	71	THR	2.0
45	1n	5	ALA	2.0
45	1n	20	ALA	2.0
32	2a	999	U	2.0
38	2g	33	ASP	2.0
43	1l	92	ASP	2.0
3	2D	38	LYS	2.0
33	2b	129	GLU	2.0
35	2d	156	GLU	2.0
43	1l	126	LYS	2.0
33	2b	101	MET	2.0
47	1p	38	TYR	2.0
7	2H	79	VAL	2.0
33	1b	229	VAL	2.0
40	1i	17	VAL	2.0
49	1r	86	VAL	2.0

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

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
54	PSU	2x	55	20/21	0.78	0.13	54,68,77,91	0
54	5MU	2x	54	21/22	0.89	0.10	68,73,80,91	0
54	5MC	2x	32	21/22	0.90	0.13	61,75,84,88	0
54	5MU	1x	54	21/22	0.91	0.09	55,62,73,81	0
54	4SU	2x	8	20/21	0.92	0.09	73,78,85,87	0
54	PSU	1x	55	20/21	0.93	0.09	51,64,77,80	0
54	4SU	1x	8	20/21	0.93	0.09	58,63,74,74	0
54	5MC	1x	32	21/22	0.95	0.10	40,61,68,75	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
56	MG	1H	203	1/1	0.45	0.51	95,95,95,95	0
56	MG	2x	3005	1/1	0.50	0.26	80,80,80,80	0
56	MG	1A	4030	1/1	0.56	0.26	77,77,77,77	0
56	MG	1A	3545	1/1	0.57	0.22	61,61,61,61	0
56	MG	1A	3353	1/1	0.58	0.29	63,63,63,63	0
56	MG	1B	213	1/1	0.58	0.22	68,68,68,68	0
56	MG	2a	1741	1/1	0.59	0.28	89,89,89,89	0
56	MG	1A	3409	1/1	0.60	0.15	51,51,51,51	0
56	MG	2A	3452	1/1	0.60	0.30	69,69,69,69	0
56	MG	1A	3535	1/1	0.61	0.14	57,57,57,57	0
56	MG	2A	3513	1/1	0.61	0.13	66,66,66,66	0
56	MG	1A	3346	1/1	0.62	0.20	76,76,76,76	0
56	MG	2A	3496	1/1	0.63	0.31	66,66,66,66	0
56	MG	1A	3918	1/1	0.63	0.54	47,47,47,47	0
56	MG	1x	101	1/1	0.64	0.33	89,89,89,89	0
56	MG	1a	1902	1/1	0.64	0.22	92,92,92,92	0
56	MG	1A	3523	1/1	0.67	0.24	77,77,77,77	0
56	MG	2a	1758	1/1	0.67	0.16	59,59,59,59	0
56	MG	1A	3336	1/1	0.67	0.14	62,62,62,62	0
56	MG	1a	1783	1/1	0.68	0.19	78,78,78,78	0
56	MG	1A	3389	1/1	0.69	0.17	50,50,50,50	0
56	MG	2a	1733	1/1	0.69	0.21	67,67,67,67	0
56	MG	1B	227	1/1	0.69	0.15	70,70,70,70	0
56	MG	1A	3317	1/1	0.69	0.16	56,56,56,56	0
56	MG	1A	3538	1/1	0.69	0.15	67,67,67,67	0
56	MG	1A	3540	1/1	0.70	0.13	69,69,69,69	0
56	MG	1a	1786	1/1	0.70	0.14	71,71,71,71	0
56	MG	1a	1812	1/1	0.70	0.26	66,66,66,66	0
56	MG	2a	1810	1/1	0.71	0.25	84,84,84,84	0
56	MG	1A	3280	1/1	0.71	0.18	76,76,76,76	0
56	MG	1A	3942	1/1	0.72	0.12	53,53,53,53	0
56	MG	2a	1813	1/1	0.72	0.26	72,72,72,72	0
56	MG	2a	1817	1/1	0.72	0.37	84,84,84,84	0
56	MG	2e	202	1/1	0.72	0.22	74,74,74,74	0
56	MG	1A	3322	1/1	0.72	0.16	55,55,55,55	0
56	MG	1A	3436	1/1	0.73	0.13	66,66,66,66	0
56	MG	1A	3521	1/1	0.73	0.11	51,51,51,51	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2B	3008	1/1	0.73	0.20	69,69,69,69	0
56	MG	1A	3363	1/1	0.73	0.16	65,65,65,65	0
56	MG	2a	1739	1/1	0.73	0.18	73,73,73,73	0
56	MG	1A	3534	1/1	0.73	0.12	64,64,64,64	0
56	MG	1a	1811	1/1	0.74	0.14	90,90,90,90	0
56	MG	1A	3891	1/1	0.74	0.28	65,65,65,65	0
56	MG	1a	1889	1/1	0.74	0.22	68,68,68,68	0
56	MG	2A	3554	1/1	0.74	0.27	70,70,70,70	0
56	MG	1A	3407	1/1	0.74	0.14	67,67,67,67	0
56	MG	1A	3564	1/1	0.74	0.18	72,72,72,72	0
56	MG	2A	3365	1/1	0.74	0.16	49,49,49,49	0
56	MG	1a	1755	1/1	0.75	0.18	68,68,68,68	0
56	MG	1A	4037	1/1	0.75	0.14	54,54,54,54	0
56	MG	2a	1740	1/1	0.75	0.18	101,101,101,101	0
56	MG	2A	3406	1/1	0.75	0.14	58,58,58,58	0
56	MG	2a	1744	1/1	0.75	0.27	63,63,63,63	0
56	MG	1A	3368	1/1	0.75	0.14	53,53,53,53	0
56	MG	1A	3463	1/1	0.75	0.23	54,54,54,54	0
56	MG	1A	3483	1/1	0.75	0.20	75,75,75,75	0
56	MG	10	105	1/1	0.75	0.19	61,61,61,61	0
56	MG	1a	1688	1/1	0.75	0.15	72,72,72,72	0
56	MG	2a	1612	1/1	0.75	0.23	67,67,67,67	0
56	MG	1A	3519	1/1	0.76	0.13	62,62,62,62	0
56	MG	1A	3471	1/1	0.76	0.18	58,58,58,58	0
56	MG	2a	1789	1/1	0.76	0.18	88,88,88,88	0
56	MG	1A	3893	1/1	0.76	0.22	53,53,53,53	0
56	MG	1A	3311	1/1	0.76	0.17	67,67,67,67	0
56	MG	1A	3486	1/1	0.76	0.14	70,70,70,70	0
56	MG	1N	201	1/1	0.76	0.32	73,73,73,73	0
56	MG	1A	3994	1/1	0.76	0.38	33,33,33,33	0
56	MG	1A	3871	1/1	0.77	0.20	45,45,45,45	0
56	MG	1A	3303	1/1	0.77	0.21	43,43,43,43	0
56	MG	1A	4059	1/1	0.77	0.14	52,52,52,52	0
56	MG	1A	3461	1/1	0.77	0.10	57,57,57,57	0
56	MG	1A	3294	1/1	0.77	0.11	64,64,64,64	0
56	MG	1A	3745	1/1	0.77	0.20	69,69,69,69	0
56	MG	1a	1869	1/1	0.77	0.21	66,66,66,66	0
56	MG	1A	3991	1/1	0.77	0.24	94,94,94,94	0
56	MG	1A	3816	1/1	0.77	0.15	56,56,56,56	0
56	MG	1a	1605	1/1	0.77	0.20	83,83,83,83	0
56	MG	2A	3331	1/1	0.78	0.13	58,58,58,58	0
56	MG	2A	3356	1/1	0.78	0.16	41,41,41,41	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1a	1804	1/1	0.78	0.13	66,66,66,66	0
56	MG	1a	1807	1/1	0.78	0.16	74,74,74,74	0
56	MG	2A	3413	1/1	0.78	0.16	63,63,63,63	0
56	MG	1T	205	1/1	0.78	0.14	76,76,76,76	0
56	MG	1A	3554	1/1	0.78	0.13	61,61,61,61	0
56	MG	1a	1764	1/1	0.78	0.27	85,85,85,85	0
56	MG	1a	1766	1/1	0.78	0.16	82,82,82,82	0
56	MG	1A	3319	1/1	0.78	0.13	50,50,50,50	0
56	MG	2Z	3001	1/1	0.78	0.19	73,73,73,73	0
56	MG	1a	1621	1/1	0.78	0.23	68,68,68,68	0
56	MG	1A	3458	1/1	0.79	0.10	71,71,71,71	0
56	MG	1a	1872	1/1	0.79	0.14	50,50,50,50	0
56	MG	1A	4064	1/1	0.79	0.16	69,69,69,69	0
56	MG	1A	3890	1/1	0.79	0.18	63,63,63,63	0
56	MG	1A	3415	1/1	0.79	0.15	58,58,58,58	0
56	MG	2A	3107	1/1	0.79	0.17	54,54,54,54	0
56	MG	2a	1617	1/1	0.79	0.15	67,67,67,67	0
56	MG	2a	1694	1/1	0.79	0.17	61,61,61,61	0
56	MG	2A	3201	1/1	0.79	0.14	62,62,62,62	0
56	MG	2A	3268	1/1	0.79	0.28	75,75,75,75	0
56	MG	1a	1666	1/1	0.79	0.12	61,61,61,61	0
56	MG	1A	3400	1/1	0.79	0.17	69,69,69,69	0
56	MG	1a	1737	1/1	0.79	0.20	70,70,70,70	0
56	MG	1A	3506	1/1	0.79	0.17	57,57,57,57	0
56	MG	1a	1819	1/1	0.79	0.11	59,59,59,59	0
56	MG	2a	1808	1/1	0.79	0.18	73,73,73,73	0
56	MG	2A	3437	1/1	0.79	0.18	56,56,56,56	0
56	MG	1a	1840	1/1	0.79	0.14	57,57,57,57	0
56	MG	2A	3480	1/1	0.79	0.22	74,74,74,74	0
56	MG	2A	3489	1/1	0.79	0.29	60,60,60,60	0
56	MG	2A	3492	1/1	0.79	0.12	43,43,43,43	0
56	MG	1a	1864	1/1	0.80	0.31	61,61,61,61	0
56	MG	1a	1754	1/1	0.80	0.17	60,60,60,60	0
56	MG	1A	3865	1/1	0.80	0.16	60,60,60,60	0
56	MG	1A	3274	1/1	0.80	0.16	57,57,57,57	0
56	MG	1a	1894	1/1	0.80	0.20	72,72,72,72	0
56	MG	1A	3398	1/1	0.80	0.26	58,58,58,58	0
56	MG	1a	1700	1/1	0.80	0.18	62,62,62,62	0
56	MG	2a	1791	1/1	0.80	0.32	71,71,71,71	0
56	MG	2A	3095	1/1	0.80	0.16	54,54,54,54	0
56	MG	1A	3459	1/1	0.80	0.12	44,44,44,44	0
56	MG	2a	1621	1/1	0.80	0.22	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2a	1632	1/1	0.80	0.22	76,76,76,76	0
56	MG	2a	1666	1/1	0.80	0.20	65,65,65,65	0
56	MG	2A	3108	1/1	0.80	0.31	59,59,59,59	0
56	MG	2a	1629	1/1	0.81	0.22	72,72,72,72	0
56	MG	1A	3125	1/1	0.81	0.22	56,56,56,56	0
56	MG	10	101	1/1	0.81	0.18	64,64,64,64	0
56	MG	2a	1667	1/1	0.81	0.23	69,69,69,69	0
56	MG	1A	3376	1/1	0.81	0.19	55,55,55,55	0
56	MG	18	103	1/1	0.81	0.20	59,59,59,59	0
56	MG	1A	3873	1/1	0.81	0.15	48,48,48,48	0
56	MG	1m	202	1/1	0.81	0.25	71,71,71,71	0
56	MG	1a	1790	1/1	0.81	0.21	68,68,68,68	0
56	MG	1a	1792	1/1	0.81	0.15	63,63,63,63	0
56	MG	1A	3344	1/1	0.81	0.19	73,73,73,73	0
56	MG	2a	1774	1/1	0.81	0.13	69,69,69,69	0
56	MG	2A	3514	1/1	0.81	0.18	53,53,53,53	0
56	MG	2A	3545	1/1	0.81	0.24	69,69,69,69	0
56	MG	2a	1800	1/1	0.81	0.35	73,73,73,73	0
56	MG	1A	3069	1/1	0.81	0.14	58,58,58,58	0
56	MG	1A	3301	1/1	0.81	0.18	85,85,85,85	0
56	MG	1a	1697	1/1	0.81	0.21	67,67,67,67	0
56	MG	1A	3356	1/1	0.81	0.18	56,56,56,56	0
56	MG	1A	3531	1/1	0.81	0.12	68,68,68,68	0
56	MG	1A	3279	1/1	0.81	0.18	53,53,53,53	0
56	MG	1a	1875	1/1	0.82	0.17	61,61,61,61	0
56	MG	1a	1887	1/1	0.82	0.19	64,64,64,64	0
56	MG	2A	3409	1/1	0.82	0.12	68,68,68,68	0
56	MG	2a	1642	1/1	0.82	0.24	87,87,87,87	0
56	MG	1a	1789	1/1	0.82	0.10	62,62,62,62	0
56	MG	2A	3435	1/1	0.82	0.14	59,59,59,59	0
56	MG	1A	3566	1/1	0.82	0.11	64,64,64,64	0
56	MG	2a	1715	1/1	0.82	0.29	82,82,82,82	0
56	MG	2a	1728	1/1	0.82	0.12	75,75,75,75	0
56	MG	1a	1900	1/1	0.82	0.20	68,68,68,68	0
56	MG	2A	3468	1/1	0.82	0.17	57,57,57,57	0
56	MG	2A	3476	1/1	0.82	0.21	72,72,72,72	0
56	MG	1A	3307	1/1	0.82	0.14	61,61,61,61	0
56	MG	1A	3109	1/1	0.82	0.09	60,60,60,60	0
56	MG	1a	1749	1/1	0.82	0.11	72,72,72,72	0
56	MG	1A	4028	1/1	0.82	0.20	87,87,87,87	0
56	MG	1A	3412	1/1	0.82	0.17	77,77,77,77	0
56	MG	1A	3505	1/1	0.82	0.14	58,58,58,58	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2A	3113	1/1	0.82	0.19	44,44,44,44	0
56	MG	1a	1658	1/1	0.82	0.12	69,69,69,69	0
56	MG	2A	3212	1/1	0.82	0.25	64,64,64,64	0
56	MG	1a	1780	1/1	0.82	0.17	62,62,62,62	0
56	MG	1R	205	1/1	0.82	0.25	55,55,55,55	0
56	MG	2a	1616	1/1	0.82	0.19	61,61,61,61	0
56	MG	1T	204	1/1	0.82	0.15	68,68,68,68	0
56	MG	1a	1761	1/1	0.83	0.16	77,77,77,77	0
56	MG	2A	3339	1/1	0.83	0.18	78,78,78,78	0
56	MG	1A	3468	1/1	0.83	0.33	64,64,64,64	0
56	MG	2a	1627	1/1	0.83	0.40	68,68,68,68	0
56	MG	1A	3877	1/1	0.83	0.13	41,41,41,41	0
56	MG	2A	3373	1/1	0.83	0.13	41,41,41,41	0
56	MG	2A	3381	1/1	0.83	0.13	52,52,52,52	0
56	MG	1a	1886	1/1	0.83	0.16	60,60,60,60	0
56	MG	1A	4019	1/1	0.83	0.14	59,59,59,59	0
56	MG	1A	3624	1/1	0.83	0.12	50,50,50,50	0
56	MG	1a	1668	1/1	0.83	0.12	81,81,81,81	0
56	MG	1A	3312	1/1	0.83	0.17	59,59,59,59	0
56	MG	2a	1732	1/1	0.83	0.25	75,75,75,75	0
56	MG	1A	3473	1/1	0.83	0.35	47,47,47,47	0
56	MG	1b	3001	1/1	0.83	0.21	63,63,63,63	0
56	MG	1U	205	1/1	0.83	0.29	30,30,30,30	0
56	MG	1a	1716	1/1	0.83	0.15	77,77,77,77	0
56	MG	1x	105	1/1	0.83	0.27	65,65,65,65	0
56	MG	2a	1755	1/1	0.83	0.23	82,82,82,82	0
56	MG	1a	1805	1/1	0.83	0.16	77,77,77,77	0
56	MG	1A	3912	1/1	0.83	0.12	55,55,55,55	0
56	MG	2a	1776	1/1	0.83	0.16	54,54,54,54	0
56	MG	2a	1781	1/1	0.83	0.32	68,68,68,68	0
56	MG	10	103	1/1	0.83	0.19	59,59,59,59	0
56	MG	1a	1750	1/1	0.83	0.15	73,73,73,73	0
56	MG	2a	1799	1/1	0.83	0.34	56,56,56,56	0
56	MG	2A	3544	1/1	0.83	0.11	48,48,48,48	0
56	MG	1A	3510	1/1	0.83	0.34	62,62,62,62	0
56	MG	1A	3266	1/1	0.83	0.10	57,57,57,57	0
56	MG	2A	3252	1/1	0.83	0.14	58,58,58,58	0
56	MG	1a	1756	1/1	0.83	0.22	74,74,74,74	0
56	MG	2e	201	1/1	0.83	0.17	71,71,71,71	0
56	MG	2A	3291	1/1	0.83	0.10	48,48,48,48	0
56	MG	2a	1614	1/1	0.83	0.17	55,55,55,55	0
56	MG	2A	3055	1/1	0.84	0.16	57,57,57,57	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2A	3092	1/1	0.84	0.19	52,52,52,52	0
56	MG	1A	3621	1/1	0.84	0.19	79,79,79,79	0
56	MG	1T	201	1/1	0.84	0.17	57,57,57,57	0
56	MG	1A	3934	1/1	0.84	0.09	52,52,52,52	0
56	MG	1A	3385	1/1	0.84	0.23	56,56,56,56	0
56	MG	2A	3172	1/1	0.84	0.20	58,58,58,58	0
56	MG	1A	3972	1/1	0.84	0.34	80,80,80,80	0
56	MG	1A	3720	1/1	0.84	0.25	67,67,67,67	0
56	MG	2a	1628	1/1	0.84	0.26	66,66,66,66	0
56	MG	1A	3465	1/1	0.84	0.13	49,49,49,49	0
56	MG	1a	1797	1/1	0.84	0.10	54,54,54,54	0
56	MG	2a	1639	1/1	0.84	0.23	80,80,80,80	0
56	MG	2A	3275	1/1	0.84	0.15	45,45,45,45	0
56	MG	1A	3997	1/1	0.84	0.12	48,48,48,48	0
56	MG	2A	3311	1/1	0.84	0.14	32,32,32,32	0
56	MG	1A	4002	1/1	0.84	0.21	70,70,70,70	0
56	MG	2a	1710	1/1	0.84	0.14	71,71,71,71	0
56	MG	1a	1602	1/1	0.84	0.25	81,81,81,81	0
56	MG	1A	3796	1/1	0.84	0.23	59,59,59,59	0
56	MG	2a	1729	1/1	0.84	0.12	58,58,58,58	0
56	MG	1A	3365	1/1	0.84	0.10	57,57,57,57	0
56	MG	1a	1624	1/1	0.84	0.18	64,64,64,64	0
56	MG	1A	3432	1/1	0.84	0.27	52,52,52,52	0
56	MG	1A	4036	1/1	0.84	0.18	61,61,61,61	0
56	MG	1A	3287	1/1	0.84	0.21	43,43,43,43	0
56	MG	1A	4039	1/1	0.84	0.27	81,81,81,81	0
56	MG	1A	3442	1/1	0.84	0.25	64,64,64,64	0
56	MG	1a	1880	1/1	0.84	0.19	68,68,68,68	0
56	MG	1A	3451	1/1	0.84	0.11	52,52,52,52	0
56	MG	1A	4066	1/1	0.84	0.12	51,51,51,51	0
56	MG	2A	3472	1/1	0.84	0.17	53,53,53,53	0
56	MG	2a	1785	1/1	0.84	0.17	68,68,68,68	0
56	MG	1A	3452	1/1	0.84	0.25	69,69,69,69	0
56	MG	1B	220	1/1	0.84	0.12	52,52,52,52	0
56	MG	1A	3087	1/1	0.84	0.28	52,52,52,52	0
56	MG	1A	3380	1/1	0.84	0.17	49,49,49,49	0
56	MG	2A	3494	1/1	0.84	0.20	54,54,54,54	0
56	MG	1A	3382	1/1	0.84	0.37	59,59,59,59	0
56	MG	1m	201	1/1	0.84	0.28	73,73,73,73	0
56	MG	1N	202	1/1	0.84	0.23	49,49,49,49	0
56	MG	2A	3528	1/1	0.84	0.11	60,60,60,60	0
56	MG	1P	205	1/1	0.84	0.28	75,75,75,75	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1Q	3004	1/1	0.84	0.25	51,51,51,51	0
56	MG	1a	1616	1/1	0.85	0.32	63,63,63,63	0
56	MG	2B	3009	1/1	0.85	0.34	58,58,58,58	0
56	MG	1A	3501	1/1	0.85	0.13	66,66,66,66	0
56	MG	2a	1607	1/1	0.85	0.24	54,54,54,54	0
56	MG	1B	214	1/1	0.85	0.11	69,69,69,69	0
56	MG	2a	1613	1/1	0.85	0.14	63,63,63,63	0
56	MG	1A	3551	1/1	0.85	0.12	85,85,85,85	0
56	MG	2A	3188	1/1	0.85	0.11	54,54,54,54	0
56	MG	1B	224	1/1	0.85	0.09	58,58,58,58	0
56	MG	1A	3992	1/1	0.85	0.14	70,70,70,70	0
56	MG	2A	3219	1/1	0.85	0.14	61,61,61,61	0
56	MG	1A	3329	1/1	0.85	0.10	52,52,52,52	0
56	MG	1A	3308	1/1	0.85	0.14	40,40,40,40	0
56	MG	2A	3273	1/1	0.85	0.19	70,70,70,70	0
56	MG	1a	1698	1/1	0.85	0.12	64,64,64,64	0
56	MG	1a	1843	1/1	0.85	0.12	69,69,69,69	0
56	MG	2a	1662	1/1	0.85	0.12	83,83,83,83	0
56	MG	1a	1851	1/1	0.85	0.21	64,64,64,64	0
56	MG	1A	3009	1/1	0.85	0.10	47,47,47,47	0
56	MG	1A	4008	1/1	0.85	0.16	68,68,68,68	0
56	MG	1a	1717	1/1	0.85	0.13	73,73,73,73	0
56	MG	1a	1718	1/1	0.85	0.15	67,67,67,67	0
56	MG	1a	1878	1/1	0.85	0.28	64,64,64,64	0
56	MG	1A	4014	1/1	0.85	0.21	47,47,47,47	0
56	MG	1A	3614	1/1	0.85	0.11	58,58,58,58	0
56	MG	1A	3413	1/1	0.85	0.15	53,53,53,53	0
56	MG	1A	3006	1/1	0.85	0.13	48,48,48,48	0
56	MG	1A	3643	1/1	0.85	0.12	34,34,34,34	0
56	MG	1A	3649	1/1	0.85	0.14	54,54,54,54	0
56	MG	1a	1901	1/1	0.85	0.26	65,65,65,65	0
56	MG	2a	1751	1/1	0.85	0.26	55,55,55,55	0
56	MG	1Z	302	1/1	0.85	0.11	56,56,56,56	0
56	MG	1A	4038	1/1	0.85	0.16	63,63,63,63	0
56	MG	2a	1760	1/1	0.85	0.20	59,59,59,59	0
56	MG	1h	3003	1/1	0.85	0.21	70,70,70,70	0
56	MG	1A	3694	1/1	0.85	0.11	76,76,76,76	0
56	MG	2A	3483	1/1	0.85	0.11	43,43,43,43	0
56	MG	1a	1774	1/1	0.85	0.12	75,75,75,75	0
56	MG	1r	101	1/1	0.85	0.14	65,65,65,65	0
56	MG	1A	3710	1/1	0.85	0.09	25,25,25,25	0
56	MG	10	106	1/1	0.85	0.16	72,72,72,72	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1x	108	1/1	0.85	0.16	59,59,59,59	0
56	MG	2a	1806	1/1	0.85	0.14	57,57,57,57	0
56	MG	2A	3012	1/1	0.85	0.09	57,57,57,57	0
56	MG	2A	3525	1/1	0.85	0.12	40,40,40,40	0
56	MG	2A	3040	1/1	0.85	0.25	60,60,60,60	0
56	MG	1A	3544	1/1	0.85	0.35	67,67,67,67	0
56	MG	1A	3732	1/1	0.85	0.15	67,67,67,67	0
56	MG	1B	206	1/1	0.85	0.14	38,38,38,38	0
56	MG	2e	203	1/1	0.85	0.11	78,78,78,78	0
56	MG	2B	3002	1/1	0.85	0.13	65,65,65,65	0
56	MG	1a	1611	1/1	0.86	0.13	76,76,76,76	0
56	MG	2A	3313	1/1	0.86	0.21	57,57,57,57	0
56	MG	1a	1612	1/1	0.86	0.20	58,58,58,58	0
56	MG	1A	3750	1/1	0.86	0.13	41,41,41,41	0
56	MG	1A	3441	1/1	0.86	0.12	59,59,59,59	0
56	MG	1A	3361	1/1	0.86	0.19	53,53,53,53	0
56	MG	1A	3828	1/1	0.86	0.11	22,22,22,22	0
56	MG	1A	3836	1/1	0.86	0.15	57,57,57,57	0
56	MG	2a	1633	1/1	0.86	0.23	86,86,86,86	0
56	MG	1r	103	1/1	0.86	0.13	51,51,51,51	0
56	MG	1u	8001	1/1	0.86	0.14	69,69,69,69	0
56	MG	1A	3861	1/1	0.86	0.12	34,34,34,34	0
56	MG	2A	3429	1/1	0.86	0.11	58,58,58,58	0
56	MG	2A	3430	1/1	0.86	0.13	59,59,59,59	0
56	MG	1A	3082	1/1	0.86	0.18	65,65,65,65	0
56	MG	1A	4013	1/1	0.86	0.15	55,55,55,55	0
56	MG	2A	3445	1/1	0.86	0.20	56,56,56,56	0
56	MG	2a	1717	1/1	0.86	0.14	57,57,57,57	0
56	MG	2a	1726	1/1	0.86	0.32	59,59,59,59	0
56	MG	1A	3532	1/1	0.86	0.08	54,54,54,54	0
56	MG	1Q	3007	1/1	0.86	0.11	60,60,60,60	0
56	MG	2A	3470	1/1	0.86	0.26	67,67,67,67	0
56	MG	2A	3048	1/1	0.86	0.12	43,43,43,43	0
56	MG	2a	1734	1/1	0.86	0.20	69,69,69,69	0
56	MG	1A	3031	1/1	0.86	0.20	60,60,60,60	0
56	MG	2A	3060	1/1	0.86	0.12	50,50,50,50	0
56	MG	2A	3081	1/1	0.86	0.21	60,60,60,60	0
56	MG	1A	3455	1/1	0.86	0.13	59,59,59,59	0
56	MG	1A	3880	1/1	0.86	0.20	76,76,76,76	0
56	MG	2A	3098	1/1	0.86	0.29	50,50,50,50	0
56	MG	1a	1849	1/1	0.86	0.09	59,59,59,59	0
56	MG	2A	3504	1/1	0.86	0.17	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2a	1763	1/1	0.86	0.12	57,57,57,57	0
56	MG	2a	1766	1/1	0.86	0.15	83,83,83,83	0
56	MG	1A	3496	1/1	0.86	0.16	57,57,57,57	0
56	MG	1A	3347	1/1	0.86	0.14	47,47,47,47	0
56	MG	1A	3431	1/1	0.86	0.12	64,64,64,64	0
56	MG	1A	3906	1/1	0.86	0.23	67,67,67,67	0
56	MG	2a	1788	1/1	0.86	0.23	68,68,68,68	0
56	MG	2A	3529	1/1	0.86	0.11	43,43,43,43	0
56	MG	2A	3192	1/1	0.86	0.12	49,49,49,49	0
56	MG	2a	1796	1/1	0.86	0.20	73,73,73,73	0
56	MG	1A	4050	1/1	0.86	0.25	55,55,55,55	0
56	MG	2A	3546	1/1	0.86	0.15	48,48,48,48	0
56	MG	2A	3210	1/1	0.86	0.19	52,52,52,52	0
56	MG	1A	3136	1/1	0.86	0.28	39,39,39,39	0
56	MG	1A	3103	1/1	0.86	0.12	53,53,53,53	0
56	MG	2a	1811	1/1	0.86	0.13	66,66,66,66	0
56	MG	1A	3744	1/1	0.86	0.11	59,59,59,59	0
56	MG	1A	3438	1/1	0.86	0.09	54,54,54,54	0
56	MG	20	8001	1/1	0.86	0.15	67,67,67,67	0
56	MG	1a	1767	1/1	0.86	0.09	63,63,63,63	0
56	MG	1a	1773	1/1	0.86	0.11	65,65,65,65	0
56	MG	1A	3971	1/1	0.86	0.16	82,82,82,82	0
56	MG	1A	3978	1/1	0.87	0.16	67,67,67,67	0
56	MG	2A	3307	1/1	0.87	0.14	63,63,63,63	0
56	MG	1A	3193	1/1	0.87	0.17	50,50,50,50	0
56	MG	1A	3528	1/1	0.87	0.21	64,64,64,64	0
56	MG	1A	3349	1/1	0.87	0.11	46,46,46,46	0
56	MG	2a	1624	1/1	0.87	0.21	62,62,62,62	0
56	MG	1l	201	1/1	0.87	0.15	74,74,74,74	0
56	MG	2A	3343	1/1	0.87	0.15	53,53,53,53	0
56	MG	1A	3482	1/1	0.87	0.17	55,55,55,55	0
56	MG	1a	1639	1/1	0.87	0.26	76,76,76,76	0
56	MG	1a	1641	1/1	0.87	0.29	64,64,64,64	0
56	MG	2a	1638	1/1	0.87	0.10	59,59,59,59	0
56	MG	1A	3226	1/1	0.87	0.08	31,31,31,31	0
56	MG	2A	3388	1/1	0.87	0.20	57,57,57,57	0
56	MG	2A	3401	1/1	0.87	0.24	60,60,60,60	0
56	MG	1A	3682	1/1	0.87	0.09	37,37,37,37	0
56	MG	1A	3328	1/1	0.87	0.11	78,78,78,78	0
56	MG	2a	1678	1/1	0.87	0.11	58,58,58,58	0
56	MG	1A	3700	1/1	0.87	0.12	31,31,31,31	0
56	MG	2a	1705	1/1	0.87	0.25	68,68,68,68	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2a	1706	1/1	0.87	0.21	58,58,58,58	0
56	MG	1a	1693	1/1	0.87	0.15	55,55,55,55	0
56	MG	2A	3005	1/1	0.87	0.17	59,59,59,59	0
56	MG	1a	1810	1/1	0.87	0.24	69,69,69,69	0
56	MG	2A	3036	1/1	0.87	0.19	61,61,61,61	0
56	MG	1A	3490	1/1	0.87	0.24	56,56,56,56	0
56	MG	2A	3447	1/1	0.87	0.09	57,57,57,57	0
56	MG	1A	3423	1/1	0.87	0.13	59,59,59,59	0
56	MG	2A	3453	1/1	0.87	0.12	67,67,67,67	0
56	MG	2A	3460	1/1	0.87	0.13	44,44,44,44	0
56	MG	2A	3463	1/1	0.87	0.15	57,57,57,57	0
56	MG	2A	3054	1/1	0.87	0.17	44,44,44,44	0
56	MG	1A	3896	1/1	0.87	0.13	47,47,47,47	0
56	MG	1a	1822	1/1	0.87	0.14	76,76,76,76	0
56	MG	1a	1834	1/1	0.87	0.21	48,48,48,48	0
56	MG	2A	3088	1/1	0.87	0.09	46,46,46,46	0
56	MG	1a	1703	1/1	0.87	0.17	66,66,66,66	0
56	MG	2A	3486	1/1	0.87	0.25	70,70,70,70	0
56	MG	1A	3285	1/1	0.87	0.14	47,47,47,47	0
56	MG	1A	3460	1/1	0.87	0.14	61,61,61,61	0
56	MG	2a	1769	1/1	0.87	0.13	56,56,56,56	0
56	MG	2A	3106	1/1	0.87	0.16	58,58,58,58	0
56	MG	1A	3236	1/1	0.87	0.12	50,50,50,50	0
56	MG	1A	3922	1/1	0.87	0.21	52,52,52,52	0
56	MG	1a	1744	1/1	0.87	0.13	53,53,53,53	0
56	MG	1A	3928	1/1	0.87	0.16	57,57,57,57	0
56	MG	1A	3148	1/1	0.87	0.22	43,43,43,43	0
56	MG	1A	3561	1/1	0.87	0.13	55,55,55,55	0
56	MG	2A	3198	1/1	0.87	0.10	51,51,51,51	0
56	MG	1A	3406	1/1	0.87	0.13	49,49,49,49	0
56	MG	1A	4077	1/1	0.87	0.14	62,62,62,62	0
56	MG	2a	1804	1/1	0.87	0.19	60,60,60,60	0
56	MG	17	106	1/1	0.87	0.10	40,40,40,40	0
56	MG	1A	4079	1/1	0.87	0.15	49,49,49,49	0
56	MG	2A	3223	1/1	0.87	0.08	82,82,82,82	0
56	MG	2A	3226	1/1	0.87	0.17	72,72,72,72	0
56	MG	2A	3250	1/1	0.87	0.22	70,70,70,70	0
56	MG	1a	1890	1/1	0.87	0.23	66,66,66,66	0
56	MG	1B	201	1/1	0.87	0.32	72,72,72,72	0
56	MG	1a	1897	1/1	0.87	0.24	53,53,53,53	0
56	MG	2a	1610	1/1	0.87	0.25	60,60,60,60	0
56	MG	2l	203	1/1	0.87	0.11	55,55,55,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3178	1/1	0.87	0.15	48,48,48,48	0
56	MG	1a	1609	1/1	0.88	0.28	56,56,56,56	0
56	MG	2A	3261	1/1	0.88	0.18	66,66,66,66	0
56	MG	2a	1606	1/1	0.88	0.13	78,78,78,78	0
56	MG	1A	3201	1/1	0.88	0.20	49,49,49,49	0
56	MG	2a	1608	1/1	0.88	0.18	67,67,67,67	0
56	MG	1a	1776	1/1	0.88	0.13	54,54,54,54	0
56	MG	1A	3351	1/1	0.88	0.16	47,47,47,47	0
56	MG	2A	3281	1/1	0.88	0.12	41,41,41,41	0
56	MG	1h	3001	1/1	0.88	0.17	70,70,70,70	0
56	MG	2A	3297	1/1	0.88	0.24	49,49,49,49	0
56	MG	1A	3137	1/1	0.88	0.10	58,58,58,58	0
56	MG	1k	201	1/1	0.88	0.10	68,68,68,68	0
56	MG	1a	1784	1/1	0.88	0.10	95,95,95,95	0
56	MG	2A	3314	1/1	0.88	0.12	49,49,49,49	0
56	MG	1B	209	1/1	0.88	0.29	66,66,66,66	0
56	MG	1a	1788	1/1	0.88	0.14	71,71,71,71	0
56	MG	2a	1631	1/1	0.88	0.29	51,51,51,51	0
56	MG	2A	3342	1/1	0.88	0.22	56,56,56,56	0
56	MG	1A	3965	1/1	0.88	0.10	39,39,39,39	0
56	MG	2a	1635	1/1	0.88	0.07	88,88,88,88	0
56	MG	1A	3772	1/1	0.88	0.20	51,51,51,51	0
56	MG	2A	3361	1/1	0.88	0.11	53,53,53,53	0
56	MG	1a	1791	1/1	0.88	0.19	71,71,71,71	0
56	MG	2a	1643	1/1	0.88	0.21	69,69,69,69	0
56	MG	1A	3780	1/1	0.88	0.12	23,23,23,23	0
56	MG	2A	3377	1/1	0.88	0.11	39,39,39,39	0
56	MG	1A	3790	1/1	0.88	0.15	38,38,38,38	0
56	MG	2a	1672	1/1	0.88	0.30	57,57,57,57	0
56	MG	1a	1800	1/1	0.88	0.11	67,67,67,67	0
56	MG	2A	3393	1/1	0.88	0.15	44,44,44,44	0
56	MG	2a	1695	1/1	0.88	0.16	58,58,58,58	0
56	MG	2a	1703	1/1	0.88	0.20	57,57,57,57	0
56	MG	1a	1659	1/1	0.88	0.17	68,68,68,68	0
56	MG	1A	3292	1/1	0.88	0.26	76,76,76,76	0
56	MG	1A	3110	1/1	0.88	0.10	52,52,52,52	0
56	MG	2A	3411	1/1	0.88	0.24	65,65,65,65	0
56	MG	1a	1809	1/1	0.88	0.16	75,75,75,75	0
56	MG	1a	1671	1/1	0.88	0.24	54,54,54,54	0
56	MG	2A	3051	1/1	0.88	0.42	62,62,62,62	0
56	MG	1A	3325	1/1	0.88	0.12	59,59,59,59	0
56	MG	1A	3578	1/1	0.88	0.16	47,47,47,47	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2A	3438	1/1	0.88	0.10	39,39,39,39	0
56	MG	1a	1817	1/1	0.88	0.12	71,71,71,71	0
56	MG	2A	3065	1/1	0.88	0.19	56,56,56,56	0
56	MG	2A	3449	1/1	0.88	0.13	52,52,52,52	0
56	MG	2A	3078	1/1	0.88	0.16	51,51,51,51	0
56	MG	1A	3300	1/1	0.88	0.12	28,28,28,28	0
56	MG	2a	1747	1/1	0.88	0.11	45,45,45,45	0
56	MG	2a	1748	1/1	0.88	0.17	50,50,50,50	0
56	MG	2a	1749	1/1	0.88	0.23	66,66,66,66	0
56	MG	2A	3459	1/1	0.88	0.17	46,46,46,46	0
56	MG	1A	3049	1/1	0.88	0.10	60,60,60,60	0
56	MG	1A	3866	1/1	0.88	0.11	53,53,53,53	0
56	MG	1a	1839	1/1	0.88	0.13	70,70,70,70	0
56	MG	2A	3097	1/1	0.88	0.20	51,51,51,51	0
56	MG	1A	3272	1/1	0.88	0.12	60,60,60,60	0
56	MG	2A	3102	1/1	0.88	0.15	53,53,53,53	0
56	MG	1A	3343	1/1	0.88	0.12	54,54,54,54	0
56	MG	1A	3874	1/1	0.88	0.09	33,33,33,33	0
56	MG	2A	3485	1/1	0.88	0.13	48,48,48,48	0
56	MG	1A	3187	1/1	0.88	0.09	42,42,42,42	0
56	MG	1T	206	1/1	0.88	0.12	69,69,69,69	0
56	MG	2A	3142	1/1	0.88	0.30	53,53,53,53	0
56	MG	2A	3165	1/1	0.88	0.07	35,35,35,35	0
56	MG	1a	1742	1/1	0.88	0.18	69,69,69,69	0
56	MG	2A	3184	1/1	0.88	0.11	43,43,43,43	0
56	MG	1A	4033	1/1	0.88	0.11	71,71,71,71	0
56	MG	1A	3652	1/1	0.88	0.14	48,48,48,48	0
56	MG	1A	3345	1/1	0.88	0.11	51,51,51,51	0
56	MG	1A	3477	1/1	0.88	0.09	56,56,56,56	0
56	MG	2A	3205	1/1	0.88	0.13	46,46,46,46	0
56	MG	1A	3481	1/1	0.88	0.11	56,56,56,56	0
56	MG	1A	3189	1/1	0.88	0.17	37,37,37,37	0
56	MG	2a	1814	1/1	0.88	0.15	79,79,79,79	0
56	MG	1A	3079	1/1	0.88	0.15	46,46,46,46	0
56	MG	1A	3722	1/1	0.88	0.12	62,62,62,62	0
56	MG	1A	3727	1/1	0.88	0.18	43,43,43,43	0
56	MG	2A	3249	1/1	0.88	0.24	53,53,53,53	0
56	MG	1A	3448	1/1	0.88	0.10	58,58,58,58	0
56	MG	2p	101	1/1	0.88	0.24	62,62,62,62	0
56	MG	2x	3004	1/1	0.88	0.19	76,76,76,76	0
56	MG	2G	3001	1/1	0.88	0.07	49,49,49,49	0
56	MG	2B	3003	1/1	0.89	0.15	60,60,60,60	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2B	3005	1/1	0.89	0.21	51,51,51,51	0
56	MG	1B	222	1/1	0.89	0.12	62,62,62,62	0
56	MG	1a	1863	1/1	0.89	0.10	64,64,64,64	0
56	MG	2A	3211	1/1	0.89	0.11	58,58,58,58	0
56	MG	1a	1690	1/1	0.89	0.18	78,78,78,78	0
56	MG	1a	1865	1/1	0.89	0.11	55,55,55,55	0
56	MG	1A	3479	1/1	0.89	0.13	75,75,75,75	0
56	MG	1A	3480	1/1	0.89	0.10	47,47,47,47	0
56	MG	2A	3228	1/1	0.89	0.11	52,52,52,52	0
56	MG	2A	3240	1/1	0.89	0.10	46,46,46,46	0
56	MG	2A	3245	1/1	0.89	0.12	23,23,23,23	0
56	MG	1G	3002	1/1	0.89	0.12	48,48,48,48	0
56	MG	1A	3829	1/1	0.89	0.15	49,49,49,49	0
56	MG	1A	3524	1/1	0.89	0.28	63,63,63,63	0
56	MG	1a	1710	1/1	0.89	0.18	59,59,59,59	0
56	MG	2A	3266	1/1	0.89	0.17	76,76,76,76	0
56	MG	1A	3238	1/1	0.89	0.16	63,63,63,63	0
56	MG	1O	201	1/1	0.89	0.12	47,47,47,47	0
56	MG	1A	3342	1/1	0.89	0.11	49,49,49,49	0
56	MG	1A	4000	1/1	0.89	0.10	50,50,50,50	0
56	MG	2a	1630	1/1	0.89	0.08	60,60,60,60	0
56	MG	1a	1895	1/1	0.89	0.14	47,47,47,47	0
56	MG	1A	4001	1/1	0.89	0.11	49,49,49,49	0
56	MG	1a	1743	1/1	0.89	0.09	73,73,73,73	0
56	MG	1A	3124	1/1	0.89	0.19	49,49,49,49	0
56	MG	1A	3868	1/1	0.89	0.16	65,65,65,65	0
56	MG	1A	3484	1/1	0.89	0.11	54,54,54,54	0
56	MG	1c	3001	1/1	0.89	0.19	64,64,64,64	0
56	MG	1A	3160	1/1	0.89	0.18	53,53,53,53	0
56	MG	2a	1645	1/1	0.89	0.29	57,57,57,57	0
56	MG	1A	3306	1/1	0.89	0.12	47,47,47,47	0
56	MG	1A	3493	1/1	0.89	0.15	54,54,54,54	0
56	MG	1A	3466	1/1	0.89	0.13	57,57,57,57	0
56	MG	2a	1671	1/1	0.89	0.24	53,53,53,53	0
56	MG	2A	3360	1/1	0.89	0.17	41,41,41,41	0
56	MG	1A	3500	1/1	0.89	0.17	60,60,60,60	0
56	MG	1a	1765	1/1	0.89	0.17	69,69,69,69	0
56	MG	2A	3369	1/1	0.89	0.25	45,45,45,45	0
56	MG	1o	3001	1/1	0.89	0.13	64,64,64,64	0
56	MG	1q	3303	1/1	0.89	0.15	60,60,60,60	0
56	MG	2A	3379	1/1	0.89	0.22	64,64,64,64	0
56	MG	1A	3288	1/1	0.89	0.10	82,82,82,82	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3552	1/1	0.89	0.14	53,53,53,53	0
56	MG	2a	1716	1/1	0.89	0.09	53,53,53,53	0
56	MG	1A	3737	1/1	0.89	0.14	60,60,60,60	0
56	MG	11	103	1/1	0.89	0.11	50,50,50,50	0
56	MG	13	101	1/1	0.89	0.20	46,46,46,46	0
56	MG	2A	3408	1/1	0.89	0.14	46,46,46,46	0
56	MG	1a	1779	1/1	0.89	0.15	47,47,47,47	0
56	MG	13	102	1/1	0.89	0.22	72,72,72,72	0
56	MG	2A	3007	1/1	0.89	0.11	57,57,57,57	0
56	MG	15	104	1/1	0.89	0.13	54,54,54,54	0
56	MG	1A	3229	1/1	0.89	0.10	57,57,57,57	0
56	MG	1A	3457	1/1	0.89	0.08	52,52,52,52	0
56	MG	2A	3045	1/1	0.89	0.09	38,38,38,38	0
56	MG	1A	3476	1/1	0.89	0.08	61,61,61,61	0
56	MG	1A	4060	1/1	0.89	0.22	56,56,56,56	0
56	MG	1a	1608	1/1	0.89	0.21	73,73,73,73	0
56	MG	1A	4062	1/1	0.89	0.11	62,62,62,62	0
56	MG	1A	3920	1/1	0.89	0.24	87,87,87,87	0
56	MG	1A	3756	1/1	0.89	0.13	43,43,43,43	0
56	MG	1a	1615	1/1	0.89	0.12	66,66,66,66	0
56	MG	1a	1802	1/1	0.89	0.09	56,56,56,56	0
56	MG	2A	3085	1/1	0.89	0.07	31,31,31,31	0
56	MG	1A	3565	1/1	0.89	0.12	67,67,67,67	0
56	MG	1a	1617	1/1	0.89	0.09	60,60,60,60	0
56	MG	1a	1806	1/1	0.89	0.17	79,79,79,79	0
56	MG	1A	3777	1/1	0.89	0.14	41,41,41,41	0
56	MG	2a	1784	1/1	0.89	0.18	71,71,71,71	0
56	MG	1A	3940	1/1	0.89	0.10	48,48,48,48	0
56	MG	2A	3101	1/1	0.89	0.18	52,52,52,52	0
56	MG	1B	205	1/1	0.89	0.14	57,57,57,57	0
56	MG	2A	3104	1/1	0.89	0.12	52,52,52,52	0
56	MG	2a	1794	1/1	0.89	0.16	68,68,68,68	0
56	MG	1A	3511	1/1	0.89	0.17	47,47,47,47	0
56	MG	2A	3490	1/1	0.89	0.14	48,48,48,48	0
56	MG	1a	1642	1/1	0.89	0.20	95,95,95,95	0
56	MG	2a	1802	1/1	0.89	0.23	68,68,68,68	0
56	MG	1a	1645	1/1	0.89	0.12	59,59,59,59	0
56	MG	1a	1646	1/1	0.89	0.10	60,60,60,60	0
56	MG	2A	3498	1/1	0.89	0.13	63,63,63,63	0
56	MG	2A	3125	1/1	0.89	0.30	55,55,55,55	0
56	MG	2A	3129	1/1	0.89	0.07	43,43,43,43	0
56	MG	1A	3944	1/1	0.89	0.29	50,50,50,50	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1a	1830	1/1	0.89	0.15	59,59,59,59	0
56	MG	2a	1816	1/1	0.89	0.14	52,52,52,52	0
56	MG	1a	1832	1/1	0.89	0.19	65,65,65,65	0
56	MG	2A	3173	1/1	0.89	0.16	54,54,54,54	0
56	MG	1A	3956	1/1	0.89	0.11	17,17,17,17	0
56	MG	1A	3107	1/1	0.89	0.14	53,53,53,53	0
56	MG	1A	3590	1/1	0.89	0.18	40,40,40,40	0
56	MG	2l	204	1/1	0.89	0.07	43,43,43,43	0
56	MG	1B	221	1/1	0.89	0.10	57,57,57,57	0
56	MG	2B	3001	1/1	0.89	0.15	57,57,57,57	0
56	MG	1a	1679	1/1	0.89	0.17	54,54,54,54	0
56	MG	1A	3498	1/1	0.90	0.25	44,44,44,44	0
56	MG	2A	3548	1/1	0.90	0.15	53,53,53,53	0
56	MG	1A	3394	1/1	0.90	0.16	60,60,60,60	0
56	MG	1A	3567	1/1	0.90	0.20	47,47,47,47	0
56	MG	1W	3001	1/1	0.90	0.18	43,43,43,43	0
56	MG	1a	1893	1/1	0.90	0.24	71,71,71,71	0
56	MG	1A	4003	1/1	0.90	0.11	53,53,53,53	0
56	MG	1A	3838	1/1	0.90	0.09	28,28,28,28	0
56	MG	1a	1896	1/1	0.90	0.15	72,72,72,72	0
56	MG	2B	3010	1/1	0.90	0.19	55,55,55,55	0
56	MG	1A	3854	1/1	0.90	0.11	35,35,35,35	0
56	MG	2N	8001	1/1	0.90	0.08	56,56,56,56	0
56	MG	1A	3855	1/1	0.90	0.12	51,51,51,51	0
56	MG	1A	3856	1/1	0.90	0.12	48,48,48,48	0
56	MG	28	8001	1/1	0.90	0.26	58,58,58,58	0
56	MG	1A	3039	1/1	0.90	0.12	51,51,51,51	0
56	MG	1A	3019	1/1	0.90	0.22	46,46,46,46	0
56	MG	2A	3259	1/1	0.90	0.09	36,36,36,36	0
56	MG	1A	3598	1/1	0.90	0.08	48,48,48,48	0
56	MG	2A	3264	1/1	0.90	0.09	36,36,36,36	0
56	MG	1e	201	1/1	0.90	0.16	75,75,75,75	0
56	MG	1A	3195	1/1	0.90	0.11	38,38,38,38	0
56	MG	17	102	1/1	0.90	0.13	40,40,40,40	0
56	MG	1A	3129	1/1	0.90	0.09	41,41,41,41	0
56	MG	2a	1620	1/1	0.90	0.32	66,66,66,66	0
56	MG	2A	3278	1/1	0.90	0.13	52,52,52,52	0
56	MG	2a	1623	1/1	0.90	0.28	63,63,63,63	0
56	MG	18	102	1/1	0.90	0.16	48,48,48,48	0
56	MG	2A	3284	1/1	0.90	0.09	45,45,45,45	0
56	MG	1A	3318	1/1	0.90	0.12	53,53,53,53	0
56	MG	1A	3215	1/1	0.90	0.11	50,50,50,50	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3646	1/1	0.90	0.12	49,49,49,49	0
56	MG	1A	3219	1/1	0.90	0.12	62,62,62,62	0
56	MG	1A	3884	1/1	0.90	0.13	47,47,47,47	0
56	MG	1A	3089	1/1	0.90	0.08	50,50,50,50	0
56	MG	2A	3323	1/1	0.90	0.21	56,56,56,56	0
56	MG	2A	3325	1/1	0.90	0.12	70,70,70,70	0
56	MG	1A	3655	1/1	0.90	0.14	36,36,36,36	0
56	MG	1A	3417	1/1	0.90	0.20	44,44,44,44	0
56	MG	1A	3062	1/1	0.90	0.09	50,50,50,50	0
56	MG	2a	1644	1/1	0.90	0.11	47,47,47,47	0
56	MG	1A	3898	1/1	0.90	0.09	50,50,50,50	0
56	MG	2A	3348	1/1	0.90	0.16	49,49,49,49	0
56	MG	1A	3902	1/1	0.90	0.13	70,70,70,70	0
56	MG	1a	1796	1/1	0.90	0.15	54,54,54,54	0
56	MG	2A	3008	1/1	0.90	0.16	58,58,58,58	0
56	MG	1A	3903	1/1	0.90	0.15	50,50,50,50	0
56	MG	2A	3366	1/1	0.90	0.10	51,51,51,51	0
56	MG	2a	1684	1/1	0.90	0.25	60,60,60,60	0
56	MG	2a	1687	1/1	0.90	0.18	62,62,62,62	0
56	MG	2A	3016	1/1	0.90	0.08	58,58,58,58	0
56	MG	2A	3370	1/1	0.90	0.13	49,49,49,49	0
56	MG	2a	1698	1/1	0.90	0.26	57,57,57,57	0
56	MG	2A	3019	1/1	0.90	0.17	45,45,45,45	0
56	MG	2a	1704	1/1	0.90	0.30	57,57,57,57	0
56	MG	2A	3023	1/1	0.90	0.16	49,49,49,49	0
56	MG	1a	1798	1/1	0.90	0.13	52,52,52,52	0
56	MG	1a	1637	1/1	0.90	0.20	51,51,51,51	0
56	MG	2a	1712	1/1	0.90	0.15	67,67,67,67	0
56	MG	1a	1801	1/1	0.90	0.13	58,58,58,58	0
56	MG	1A	3904	1/1	0.90	0.15	64,64,64,64	0
56	MG	2A	3050	1/1	0.90	0.19	47,47,47,47	0
56	MG	2A	3404	1/1	0.90	0.19	55,55,55,55	0
56	MG	1A	3430	1/1	0.90	0.09	58,58,58,58	0
56	MG	2A	3407	1/1	0.90	0.26	68,68,68,68	0
56	MG	1B	210	1/1	0.90	0.15	50,50,50,50	0
56	MG	1a	1644	1/1	0.90	0.21	60,60,60,60	0
56	MG	1A	3702	1/1	0.90	0.14	48,48,48,48	0
56	MG	2a	1736	1/1	0.90	0.15	74,74,74,74	0
56	MG	1A	3005	1/1	0.90	0.22	57,57,57,57	0
56	MG	2A	3428	1/1	0.90	0.25	58,58,58,58	0
56	MG	1a	1652	1/1	0.90	0.12	63,63,63,63	0
56	MG	1A	3332	1/1	0.90	0.17	54,54,54,54	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2A	3083	1/1	0.90	0.15	51,51,51,51	0
56	MG	1A	3375	1/1	0.90	0.16	62,62,62,62	0
56	MG	1a	1813	1/1	0.90	0.17	56,56,56,56	0
56	MG	2A	3089	1/1	0.90	0.09	47,47,47,47	0
56	MG	2a	1753	1/1	0.90	0.08	63,63,63,63	0
56	MG	1a	1664	1/1	0.90	0.10	50,50,50,50	0
56	MG	1A	3536	1/1	0.90	0.15	45,45,45,45	0
56	MG	1A	3078	1/1	0.90	0.19	56,56,56,56	0
56	MG	1A	3378	1/1	0.90	0.12	36,36,36,36	0
56	MG	1A	3542	1/1	0.90	0.17	53,53,53,53	0
56	MG	1a	1686	1/1	0.90	0.14	48,48,48,48	0
56	MG	1a	1836	1/1	0.90	0.13	52,52,52,52	0
56	MG	2A	3464	1/1	0.90	0.15	59,59,59,59	0
56	MG	2a	1780	1/1	0.90	0.15	64,64,64,64	0
56	MG	1A	3338	1/1	0.90	0.21	61,61,61,61	0
56	MG	1A	3247	1/1	0.90	0.16	62,62,62,62	0
56	MG	1A	3034	1/1	0.90	0.16	57,57,57,57	0
56	MG	2A	3475	1/1	0.90	0.12	53,53,53,53	0
56	MG	1a	1844	1/1	0.90	0.13	53,53,53,53	0
56	MG	1a	1847	1/1	0.90	0.15	45,45,45,45	0
56	MG	2A	3481	1/1	0.90	0.19	83,83,83,83	0
56	MG	1N	203	1/1	0.90	0.14	47,47,47,47	0
56	MG	2A	3132	1/1	0.90	0.09	52,52,52,52	0
56	MG	1A	3488	1/1	0.90	0.12	43,43,43,43	0
56	MG	2A	3487	1/1	0.90	0.09	67,67,67,67	0
56	MG	2A	3488	1/1	0.90	0.15	57,57,57,57	0
56	MG	2A	3163	1/1	0.90	0.20	52,52,52,52	0
56	MG	1A	3112	1/1	0.90	0.10	45,45,45,45	0
56	MG	1A	3558	1/1	0.90	0.10	65,65,65,65	0
56	MG	1a	1707	1/1	0.90	0.16	65,65,65,65	0
56	MG	2A	3175	1/1	0.90	0.19	30,30,30,30	0
56	MG	1A	3559	1/1	0.90	0.12	47,47,47,47	0
56	MG	2A	3499	1/1	0.90	0.17	56,56,56,56	0
56	MG	1a	1713	1/1	0.90	0.13	54,54,54,54	0
56	MG	1A	3453	1/1	0.90	0.11	48,48,48,48	0
56	MG	2A	3194	1/1	0.90	0.28	48,48,48,48	0
56	MG	2A	3196	1/1	0.90	0.31	51,51,51,51	0
56	MG	1A	3390	1/1	0.90	0.10	56,56,56,56	0
56	MG	1A	3821	1/1	0.90	0.12	59,59,59,59	0
56	MG	2A	3536	1/1	0.90	0.14	37,37,37,37	0
56	MG	2A	3202	1/1	0.90	0.13	47,47,47,47	0
56	MG	2A	3204	1/1	0.90	0.08	46,46,46,46	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2A	3096	1/1	0.91	0.10	43,43,43,43	0
56	MG	1A	3416	1/1	0.91	0.15	56,56,56,56	0
56	MG	1A	3985	1/1	0.91	0.08	22,22,22,22	0
56	MG	17	101	1/1	0.91	0.26	35,35,35,35	0
56	MG	1A	3003	1/1	0.91	0.16	41,41,41,41	0
56	MG	17	104	1/1	0.91	0.10	31,31,31,31	0
56	MG	1A	3420	1/1	0.91	0.15	72,72,72,72	0
56	MG	2A	3495	1/1	0.91	0.11	44,44,44,44	0
56	MG	1A	3041	1/1	0.91	0.14	50,50,50,50	0
56	MG	1A	3282	1/1	0.91	0.20	36,36,36,36	0
56	MG	19	104	1/1	0.91	0.11	46,46,46,46	0
56	MG	2A	3123	1/1	0.91	0.08	53,53,53,53	0
56	MG	1A	3366	1/1	0.91	0.10	48,48,48,48	0
56	MG	2A	3126	1/1	0.91	0.07	44,44,44,44	0
56	MG	2A	3515	1/1	0.91	0.12	53,53,53,53	0
56	MG	2A	3516	1/1	0.91	0.10	30,30,30,30	0
56	MG	2A	3522	1/1	0.91	0.10	50,50,50,50	0
56	MG	2A	3523	1/1	0.91	0.13	57,57,57,57	0
56	MG	1A	3023	1/1	0.91	0.07	47,47,47,47	0
56	MG	1A	3433	1/1	0.91	0.10	53,53,53,53	0
56	MG	2A	3137	1/1	0.91	0.20	63,63,63,63	0
56	MG	1A	3823	1/1	0.91	0.10	62,62,62,62	0
56	MG	2A	3538	1/1	0.91	0.15	56,56,56,56	0
56	MG	2A	3540	1/1	0.91	0.16	45,45,45,45	0
56	MG	2A	3143	1/1	0.91	0.24	49,49,49,49	0
56	MG	2A	3157	1/1	0.91	0.10	40,40,40,40	0
56	MG	1A	4004	1/1	0.91	0.14	53,53,53,53	0
56	MG	1a	1814	1/1	0.91	0.17	61,61,61,61	0
56	MG	2A	3549	1/1	0.91	0.12	49,49,49,49	0
56	MG	2A	3169	1/1	0.91	0.10	54,54,54,54	0
56	MG	2A	3555	1/1	0.91	0.11	50,50,50,50	0
56	MG	1a	1815	1/1	0.91	0.08	72,72,72,72	0
56	MG	1a	1816	1/1	0.91	0.07	56,56,56,56	0
56	MG	1A	3563	1/1	0.91	0.14	62,62,62,62	0
56	MG	2A	3176	1/1	0.91	0.21	37,37,37,37	0
56	MG	2A	3179	1/1	0.91	0.12	47,47,47,47	0
56	MG	1a	1818	1/1	0.91	0.12	69,69,69,69	0
56	MG	2A	3185	1/1	0.91	0.09	46,46,46,46	0
56	MG	2E	303	1/1	0.91	0.18	42,42,42,42	0
56	MG	1A	3435	1/1	0.91	0.07	71,71,71,71	0
56	MG	1a	1820	1/1	0.91	0.10	50,50,50,50	0
56	MG	1A	3831	1/1	0.91	0.09	42,42,42,42	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3832	1/1	0.91	0.07	36,36,36,36	0
56	MG	1a	1620	1/1	0.91	0.11	72,72,72,72	0
56	MG	1A	3372	1/1	0.91	0.13	52,52,52,52	0
56	MG	1a	1623	1/1	0.91	0.24	71,71,71,71	0
56	MG	1A	3437	1/1	0.91	0.09	51,51,51,51	0
56	MG	1A	4031	1/1	0.91	0.22	64,64,64,64	0
56	MG	1A	3848	1/1	0.91	0.12	69,69,69,69	0
56	MG	1A	3849	1/1	0.91	0.11	55,55,55,55	0
56	MG	1a	1845	1/1	0.91	0.07	70,70,70,70	0
56	MG	2A	3215	1/1	0.91	0.11	43,43,43,43	0
56	MG	1A	3373	1/1	0.91	0.17	58,58,58,58	0
56	MG	1A	3570	1/1	0.91	0.09	32,32,32,32	0
56	MG	1A	3134	1/1	0.91	0.19	35,35,35,35	0
56	MG	1a	1859	1/1	0.91	0.10	65,65,65,65	0
56	MG	2A	3239	1/1	0.91	0.18	59,59,59,59	0
56	MG	2a	1626	1/1	0.91	0.17	55,55,55,55	0
56	MG	1a	1861	1/1	0.91	0.10	48,48,48,48	0
56	MG	1A	4047	1/1	0.91	0.12	44,44,44,44	0
56	MG	1A	3331	1/1	0.91	0.09	39,39,39,39	0
56	MG	1a	1654	1/1	0.91	0.07	72,72,72,72	0
56	MG	1A	3052	1/1	0.91	0.15	49,49,49,49	0
56	MG	2A	3258	1/1	0.91	0.14	52,52,52,52	0
56	MG	1A	3450	1/1	0.91	0.06	54,54,54,54	0
56	MG	1a	1663	1/1	0.91	0.12	64,64,64,64	0
56	MG	2a	1637	1/1	0.91	0.20	71,71,71,71	0
56	MG	1A	3095	1/1	0.91	0.07	60,60,60,60	0
56	MG	1A	3869	1/1	0.91	0.10	81,81,81,81	0
56	MG	1a	1667	1/1	0.91	0.28	51,51,51,51	0
56	MG	1A	3002	1/1	0.91	0.10	48,48,48,48	0
56	MG	1A	4073	1/1	0.91	0.26	47,47,47,47	0
56	MG	2A	3277	1/1	0.91	0.12	42,42,42,42	0
56	MG	1a	1677	1/1	0.91	0.15	45,45,45,45	0
56	MG	1A	4076	1/1	0.91	0.14	36,36,36,36	0
56	MG	1a	1680	1/1	0.91	0.16	45,45,45,45	0
56	MG	2A	3287	1/1	0.91	0.12	55,55,55,55	0
56	MG	1A	3872	1/1	0.91	0.09	28,28,28,28	0
56	MG	2a	1676	1/1	0.91	0.26	60,60,60,60	0
56	MG	1A	3638	1/1	0.91	0.16	56,56,56,56	0
56	MG	2a	1681	1/1	0.91	0.14	53,53,53,53	0
56	MG	2A	3300	1/1	0.91	0.18	50,50,50,50	0
56	MG	1A	3235	1/1	0.91	0.08	36,36,36,36	0
56	MG	1A	3156	1/1	0.91	0.17	40,40,40,40	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3647	1/1	0.91	0.11	41,41,41,41	0
56	MG	1A	3881	1/1	0.91	0.13	43,43,43,43	0
56	MG	2a	1700	1/1	0.91	0.16	55,55,55,55	0
56	MG	2a	1701	1/1	0.91	0.27	46,46,46,46	0
56	MG	2A	3318	1/1	0.91	0.13	58,58,58,58	0
56	MG	1a	1699	1/1	0.91	0.14	68,68,68,68	0
56	MG	1A	3518	1/1	0.91	0.08	57,57,57,57	0
56	MG	1A	3885	1/1	0.91	0.16	51,51,51,51	0
56	MG	2a	1708	1/1	0.91	0.20	59,59,59,59	0
56	MG	1A	3159	1/1	0.91	0.24	69,69,69,69	0
56	MG	1A	3065	1/1	0.91	0.24	53,53,53,53	0
56	MG	2a	1714	1/1	0.91	0.33	65,65,65,65	0
56	MG	1A	3662	1/1	0.91	0.10	22,22,22,22	0
56	MG	1A	3255	1/1	0.91	0.19	61,61,61,61	0
56	MG	2A	3352	1/1	0.91	0.10	62,62,62,62	0
56	MG	2a	1725	1/1	0.91	0.15	58,58,58,58	0
56	MG	1A	3692	1/1	0.91	0.15	61,61,61,61	0
56	MG	1A	3693	1/1	0.91	0.08	25,25,25,25	0
56	MG	1a	1734	1/1	0.91	0.27	54,54,54,54	0
56	MG	2A	3363	1/1	0.91	0.19	52,52,52,52	0
56	MG	2A	3364	1/1	0.91	0.13	42,42,42,42	0
56	MG	1D	304	1/1	0.91	0.14	44,44,44,44	0
56	MG	1a	1740	1/1	0.91	0.21	46,46,46,46	0
56	MG	2a	1737	1/1	0.91	0.11	74,74,74,74	0
56	MG	1A	3264	1/1	0.91	0.11	51,51,51,51	0
56	MG	1t	3001	1/1	0.91	0.21	53,53,53,53	0
56	MG	1A	3402	1/1	0.91	0.13	51,51,51,51	0
56	MG	2a	1742	1/1	0.91	0.21	71,71,71,71	0
56	MG	2a	1743	1/1	0.91	0.22	35,35,35,35	0
56	MG	2A	3375	1/1	0.91	0.13	57,57,57,57	0
56	MG	1A	3529	1/1	0.91	0.13	46,46,46,46	0
56	MG	1a	1748	1/1	0.91	0.12	56,56,56,56	0
56	MG	1A	3462	1/1	0.91	0.10	62,62,62,62	0
56	MG	2A	3003	1/1	0.91	0.11	44,44,44,44	0
56	MG	2A	3390	1/1	0.91	0.10	55,55,55,55	0
56	MG	1A	3913	1/1	0.91	0.09	73,73,73,73	0
56	MG	1N	205	1/1	0.91	0.06	42,42,42,42	0
56	MG	1A	3713	1/1	0.91	0.10	48,48,48,48	0
56	MG	1O	203	1/1	0.91	0.10	60,60,60,60	0
56	MG	1a	1760	1/1	0.91	0.08	48,48,48,48	0
56	MG	2a	1768	1/1	0.91	0.17	70,70,70,70	0
56	MG	2A	3018	1/1	0.91	0.10	50,50,50,50	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2a	1771	1/1	0.91	0.22	50,50,50,50	0
56	MG	1A	3714	1/1	0.91	0.08	54,54,54,54	0
56	MG	1P	206	1/1	0.91	0.17	44,44,44,44	0
56	MG	2a	1777	1/1	0.91	0.17	66,66,66,66	0
56	MG	2A	3032	1/1	0.91	0.07	59,59,59,59	0
56	MG	1A	3715	1/1	0.91	0.20	57,57,57,57	0
56	MG	1A	3924	1/1	0.91	0.12	23,23,23,23	0
56	MG	1A	3927	1/1	0.91	0.18	61,61,61,61	0
56	MG	1a	1770	1/1	0.91	0.09	60,60,60,60	0
56	MG	1A	3717	1/1	0.91	0.15	48,48,48,48	0
56	MG	1A	3032	1/1	0.91	0.07	66,66,66,66	0
56	MG	2A	3439	1/1	0.91	0.08	65,65,65,65	0
56	MG	2A	3442	1/1	0.91	0.14	60,60,60,60	0
56	MG	1A	3935	1/1	0.91	0.09	69,69,69,69	0
56	MG	1A	3936	1/1	0.91	0.09	37,37,37,37	0
56	MG	1A	3533	1/1	0.91	0.09	57,57,57,57	0
56	MG	2A	3450	1/1	0.91	0.12	52,52,52,52	0
56	MG	1A	3350	1/1	0.91	0.24	67,67,67,67	0
56	MG	2A	3070	1/1	0.91	0.18	53,53,53,53	0
56	MG	2A	3076	1/1	0.91	0.09	42,42,42,42	0
56	MG	1A	3070	1/1	0.91	0.16	52,52,52,52	0
56	MG	1A	3950	1/1	0.91	0.14	68,68,68,68	0
56	MG	2A	3082	1/1	0.91	0.16	55,55,55,55	0
56	MG	1A	3952	1/1	0.91	0.12	66,66,66,66	0
56	MG	2A	3084	1/1	0.91	0.12	39,39,39,39	0
56	MG	1A	3011	1/1	0.91	0.14	49,49,49,49	0
56	MG	1A	3355	1/1	0.91	0.10	54,54,54,54	0
56	MG	1l	101	1/1	0.91	0.33	75,75,75,75	0
56	MG	2A	3477	1/1	0.91	0.09	52,52,52,52	0
56	MG	2A	3091	1/1	0.91	0.13	52,52,52,52	0
56	MG	1A	3275	1/1	0.91	0.16	58,58,58,58	0
56	MG	2q	3002	1/1	0.91	0.18	59,59,59,59	0
56	MG	2x	3002	1/1	0.91	0.15	57,57,57,57	0
56	MG	2A	3093	1/1	0.91	0.21	52,52,52,52	0
56	MG	1A	3475	1/1	0.91	0.23	50,50,50,50	0
56	MG	1A	3742	1/1	0.92	0.15	37,37,37,37	0
56	MG	2A	3518	1/1	0.92	0.12	58,58,58,58	0
56	MG	1a	1891	1/1	0.92	0.07	52,52,52,52	0
56	MG	1A	3090	1/1	0.92	0.07	36,36,36,36	0
56	MG	1A	3608	1/1	0.92	0.09	32,32,32,32	0
56	MG	1A	3478	1/1	0.92	0.21	50,50,50,50	0
56	MG	1l	102	1/1	0.92	0.12	58,58,58,58	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2A	3532	1/1	0.92	0.24	43,43,43,43	0
56	MG	1A	4035	1/1	0.92	0.17	57,57,57,57	0
56	MG	1A	3286	1/1	0.92	0.17	63,63,63,63	0
56	MG	1A	3897	1/1	0.92	0.12	46,46,46,46	0
56	MG	1A	3758	1/1	0.92	0.07	28,28,28,28	0
56	MG	1a	1904	1/1	0.92	0.11	60,60,60,60	0
56	MG	1A	3899	1/1	0.92	0.07	80,80,80,80	0
56	MG	2A	3547	1/1	0.92	0.11	51,51,51,51	0
56	MG	2A	3216	1/1	0.92	0.08	44,44,44,44	0
56	MG	1A	3764	1/1	0.92	0.06	41,41,41,41	0
56	MG	1d	502	1/1	0.92	0.16	60,60,60,60	0
56	MG	2A	3225	1/1	0.92	0.10	50,50,50,50	0
56	MG	2A	3559	1/1	0.92	0.17	58,58,58,58	0
56	MG	1A	3015	1/1	0.92	0.10	52,52,52,52	0
56	MG	1A	4055	1/1	0.92	0.36	53,53,53,53	0
56	MG	2A	3229	1/1	0.92	0.13	64,64,64,64	0
56	MG	1a	1763	1/1	0.92	0.08	57,57,57,57	0
56	MG	1A	3022	1/1	0.92	0.07	46,46,46,46	0
56	MG	1A	3905	1/1	0.92	0.20	43,43,43,43	0
56	MG	19	101	1/1	0.92	0.11	55,55,55,55	0
56	MG	2E	302	1/1	0.92	0.18	45,45,45,45	0
56	MG	1A	3639	1/1	0.92	0.20	57,57,57,57	0
56	MG	1A	3042	1/1	0.92	0.14	44,44,44,44	0
56	MG	1o	3002	1/1	0.92	0.09	57,57,57,57	0
56	MG	1q	3301	1/1	0.92	0.19	49,49,49,49	0
56	MG	1a	1772	1/1	0.92	0.09	83,83,83,83	0
56	MG	25	502	1/1	0.92	0.28	52,52,52,52	0
56	MG	1a	1604	1/1	0.92	0.26	63,63,63,63	0
56	MG	2a	1601	1/1	0.92	0.23	54,54,54,54	0
56	MG	2a	1602	1/1	0.92	0.07	41,41,41,41	0
56	MG	1A	4065	1/1	0.92	0.08	42,42,42,42	0
56	MG	1a	1775	1/1	0.92	0.11	55,55,55,55	0
56	MG	2A	3270	1/1	0.92	0.11	27,27,27,27	0
56	MG	2A	3272	1/1	0.92	0.14	44,44,44,44	0
56	MG	1a	1607	1/1	0.92	0.12	62,62,62,62	0
56	MG	2A	3274	1/1	0.92	0.07	46,46,46,46	0
56	MG	1a	1778	1/1	0.92	0.08	70,70,70,70	0
56	MG	1A	3792	1/1	0.92	0.11	26,26,26,26	0
56	MG	1x	106	1/1	0.92	0.24	46,46,46,46	0
56	MG	1A	3414	1/1	0.92	0.15	55,55,55,55	0
56	MG	2A	3002	1/1	0.92	0.14	47,47,47,47	0
56	MG	1a	1782	1/1	0.92	0.22	61,61,61,61	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	4074	1/1	0.92	0.22	37,37,37,37	0
56	MG	1A	3454	1/1	0.92	0.15	42,42,42,42	0
56	MG	1A	3485	1/1	0.92	0.25	58,58,58,58	0
56	MG	2A	3301	1/1	0.92	0.11	43,43,43,43	0
56	MG	1A	3315	1/1	0.92	0.12	50,50,50,50	0
56	MG	1A	3827	1/1	0.92	0.17	44,44,44,44	0
56	MG	1A	3456	1/1	0.92	0.10	52,52,52,52	0
56	MG	1A	3932	1/1	0.92	0.10	58,58,58,58	0
56	MG	1A	3341	1/1	0.92	0.13	49,49,49,49	0
56	MG	2A	3024	1/1	0.92	0.08	46,46,46,46	0
56	MG	2A	3030	1/1	0.92	0.11	45,45,45,45	0
56	MG	2A	3329	1/1	0.92	0.08	36,36,36,36	0
56	MG	2A	3031	1/1	0.92	0.16	49,49,49,49	0
56	MG	2a	1640	1/1	0.92	0.07	81,81,81,81	0
56	MG	2A	3334	1/1	0.92	0.17	57,57,57,57	0
56	MG	1a	1795	1/1	0.92	0.12	56,56,56,56	0
56	MG	1A	3677	1/1	0.92	0.07	16,16,16,16	0
56	MG	1a	1630	1/1	0.92	0.10	59,59,59,59	0
56	MG	2a	1651	1/1	0.92	0.28	56,56,56,56	0
56	MG	2a	1658	1/1	0.92	0.15	53,53,53,53	0
56	MG	2A	3042	1/1	0.92	0.21	50,50,50,50	0
56	MG	2a	1664	1/1	0.92	0.28	51,51,51,51	0
56	MG	2A	3043	1/1	0.92	0.18	46,46,46,46	0
56	MG	2A	3354	1/1	0.92	0.13	49,49,49,49	0
56	MG	1a	1631	1/1	0.92	0.13	45,45,45,45	0
56	MG	2A	3357	1/1	0.92	0.13	55,55,55,55	0
56	MG	1a	1636	1/1	0.92	0.26	66,66,66,66	0
56	MG	1A	3680	1/1	0.92	0.07	45,45,45,45	0
56	MG	1A	3492	1/1	0.92	0.12	59,59,59,59	0
56	MG	1a	1803	1/1	0.92	0.10	57,57,57,57	0
56	MG	1A	3690	1/1	0.92	0.12	15,15,15,15	0
56	MG	2a	1691	1/1	0.92	0.21	55,55,55,55	0
56	MG	2A	3057	1/1	0.92	0.23	54,54,54,54	0
56	MG	2A	3367	1/1	0.92	0.12	41,41,41,41	0
56	MG	2A	3059	1/1	0.92	0.10	64,64,64,64	0
56	MG	1A	3943	1/1	0.92	0.10	54,54,54,54	0
56	MG	2A	3371	1/1	0.92	0.21	61,61,61,61	0
56	MG	2A	3062	1/1	0.92	0.10	43,43,43,43	0
56	MG	1A	3839	1/1	0.92	0.12	28,28,28,28	0
56	MG	2A	3067	1/1	0.92	0.25	56,56,56,56	0
56	MG	1A	3845	1/1	0.92	0.13	53,53,53,53	0
56	MG	1A	3951	1/1	0.92	0.11	40,40,40,40	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2A	3077	1/1	0.92	0.19	54,54,54,54	0
56	MG	2a	1711	1/1	0.92	0.21	61,61,61,61	0
56	MG	1a	1648	1/1	0.92	0.39	60,60,60,60	0
56	MG	1a	1649	1/1	0.92	0.09	49,49,49,49	0
56	MG	2A	3396	1/1	0.92	0.17	64,64,64,64	0
56	MG	1D	303	1/1	0.92	0.14	37,37,37,37	0
56	MG	1A	3847	1/1	0.92	0.47	40,40,40,40	0
56	MG	2a	1723	1/1	0.92	0.36	67,67,67,67	0
56	MG	1D	305	1/1	0.92	0.11	46,46,46,46	0
56	MG	1E	308	1/1	0.92	0.14	28,28,28,28	0
56	MG	1A	3954	1/1	0.92	0.12	42,42,42,42	0
56	MG	1H	202	1/1	0.92	0.09	53,53,53,53	0
56	MG	1A	3384	1/1	0.92	0.15	48,48,48,48	0
56	MG	1A	3359	1/1	0.92	0.09	43,43,43,43	0
56	MG	2A	3414	1/1	0.92	0.19	67,67,67,67	0
56	MG	2A	3419	1/1	0.92	0.11	45,45,45,45	0
56	MG	2A	3420	1/1	0.92	0.14	54,54,54,54	0
56	MG	2a	1738	1/1	0.92	0.07	58,58,58,58	0
56	MG	2A	3421	1/1	0.92	0.16	61,61,61,61	0
56	MG	1A	3422	1/1	0.92	0.11	63,63,63,63	0
56	MG	2A	3094	1/1	0.92	0.17	45,45,45,45	0
56	MG	1A	3698	1/1	0.92	0.10	26,26,26,26	0
56	MG	1a	1823	1/1	0.92	0.16	54,54,54,54	0
56	MG	1a	1672	1/1	0.92	0.08	53,53,53,53	0
56	MG	1A	3973	1/1	0.92	0.06	29,29,29,29	0
56	MG	1a	1678	1/1	0.92	0.14	54,54,54,54	0
56	MG	2A	3440	1/1	0.92	0.18	56,56,56,56	0
56	MG	1A	3387	1/1	0.92	0.18	33,33,33,33	0
56	MG	2a	1752	1/1	0.92	0.11	59,59,59,59	0
56	MG	2A	3443	1/1	0.92	0.16	53,53,53,53	0
56	MG	1A	3108	1/1	0.92	0.09	51,51,51,51	0
56	MG	1A	3502	1/1	0.92	0.14	61,61,61,61	0
56	MG	1a	1687	1/1	0.92	0.07	51,51,51,51	0
56	MG	1A	3503	1/1	0.92	0.08	56,56,56,56	0
56	MG	2A	3109	1/1	0.92	0.16	57,57,57,57	0
56	MG	1A	3298	1/1	0.92	0.13	46,46,46,46	0
56	MG	2A	3458	1/1	0.92	0.17	64,64,64,64	0
56	MG	2A	3115	1/1	0.92	0.15	49,49,49,49	0
56	MG	2A	3118	1/1	0.92	0.13	37,37,37,37	0
56	MG	1A	3391	1/1	0.92	0.07	44,44,44,44	0
56	MG	1a	1694	1/1	0.92	0.06	45,45,45,45	0
56	MG	1a	1695	1/1	0.92	0.11	40,40,40,40	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2A	3128	1/1	0.92	0.10	46,46,46,46	0
56	MG	1a	1855	1/1	0.92	0.18	58,58,58,58	0
56	MG	2A	3474	1/1	0.92	0.12	63,63,63,63	0
56	MG	2A	3131	1/1	0.92	0.13	46,46,46,46	0
56	MG	1R	202	1/1	0.92	0.22	64,64,64,64	0
56	MG	1a	1860	1/1	0.92	0.09	49,49,49,49	0
56	MG	2a	1792	1/1	0.92	0.14	44,44,44,44	0
56	MG	2A	3139	1/1	0.92	0.10	40,40,40,40	0
56	MG	1A	3716	1/1	0.92	0.07	52,52,52,52	0
56	MG	1a	1862	1/1	0.92	0.11	58,58,58,58	0
56	MG	1A	3393	1/1	0.92	0.08	54,54,54,54	0
56	MG	1T	203	1/1	0.92	0.17	50,50,50,50	0
56	MG	1A	3196	1/1	0.92	0.17	54,54,54,54	0
56	MG	1A	3397	1/1	0.92	0.11	46,46,46,46	0
56	MG	2A	3171	1/1	0.92	0.11	40,40,40,40	0
56	MG	1A	3725	1/1	0.92	0.13	56,56,56,56	0
56	MG	1A	3063	1/1	0.92	0.08	41,41,41,41	0
56	MG	2A	3493	1/1	0.92	0.23	57,57,57,57	0
56	MG	1a	1876	1/1	0.92	0.13	47,47,47,47	0
56	MG	1U	206	1/1	0.92	0.19	46,46,46,46	0
56	MG	1A	3177	1/1	0.92	0.07	52,52,52,52	0
56	MG	2A	3497	1/1	0.92	0.16	62,62,62,62	0
56	MG	2A	3181	1/1	0.92	0.17	38,38,38,38	0
56	MG	2A	3183	1/1	0.92	0.14	44,44,44,44	0
56	MG	2k	3001	1/1	0.92	0.08	60,60,60,60	0
56	MG	2l	202	1/1	0.92	0.13	69,69,69,69	0
56	MG	2A	3502	1/1	0.92	0.08	47,47,47,47	0
56	MG	2A	3503	1/1	0.92	0.18	50,50,50,50	0
56	MG	1A	3882	1/1	0.92	0.11	49,49,49,49	0
56	MG	2A	3509	1/1	0.92	0.12	44,44,44,44	0
56	MG	1a	1730	1/1	0.92	0.16	49,49,49,49	0
56	MG	1A	3370	1/1	0.92	0.12	43,43,43,43	0
56	MG	2A	3191	1/1	0.92	0.18	51,51,51,51	0
56	MG	2A	3133	1/1	0.93	0.07	33,33,33,33	0
56	MG	2A	3135	1/1	0.93	0.17	46,46,46,46	0
56	MG	1A	3879	1/1	0.93	0.11	48,48,48,48	0
56	MG	2A	3491	1/1	0.93	0.15	53,53,53,53	0
56	MG	1A	3513	1/1	0.93	0.11	58,58,58,58	0
56	MG	1A	3316	1/1	0.93	0.11	48,48,48,48	0
56	MG	1A	3245	1/1	0.93	0.14	25,25,25,25	0
56	MG	2A	3148	1/1	0.93	0.17	54,54,54,54	0
56	MG	1A	3520	1/1	0.93	0.11	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2A	3162	1/1	0.93	0.17	42,42,42,42	0
56	MG	1a	1647	1/1	0.93	0.08	45,45,45,45	0
56	MG	1A	3092	1/1	0.93	0.27	47,47,47,47	0
56	MG	2A	3501	1/1	0.93	0.12	52,52,52,52	0
56	MG	2A	3167	1/1	0.93	0.09	40,40,40,40	0
56	MG	1A	4069	1/1	0.93	0.18	38,38,38,38	0
56	MG	1A	3888	1/1	0.93	0.23	87,87,87,87	0
56	MG	1A	3522	1/1	0.93	0.09	73,73,73,73	0
56	MG	1A	3064	1/1	0.93	0.09	57,57,57,57	0
56	MG	1a	1856	1/1	0.93	0.11	68,68,68,68	0
56	MG	1a	1857	1/1	0.93	0.14	47,47,47,47	0
56	MG	1A	3320	1/1	0.93	0.08	52,52,52,52	0
56	MG	1a	1661	1/1	0.93	0.12	58,58,58,58	0
56	MG	2A	3182	1/1	0.93	0.07	47,47,47,47	0
56	MG	1A	3703	1/1	0.93	0.09	29,29,29,29	0
56	MG	1A	4096	1/1	0.93	0.16	69,69,69,69	0
56	MG	1A	3527	1/1	0.93	0.16	68,68,68,68	0
56	MG	2A	3186	1/1	0.93	0.17	35,35,35,35	0
56	MG	2A	3531	1/1	0.93	0.06	47,47,47,47	0
56	MG	1A	3257	1/1	0.93	0.23	55,55,55,55	0
56	MG	2A	3534	1/1	0.93	0.21	45,45,45,45	0
56	MG	2A	3189	1/1	0.93	0.15	45,45,45,45	0
56	MG	1A	3258	1/1	0.93	0.19	43,43,43,43	0
56	MG	1a	1867	1/1	0.93	0.12	56,56,56,56	0
56	MG	2A	3542	1/1	0.93	0.07	41,41,41,41	0
56	MG	1A	3327	1/1	0.93	0.09	64,64,64,64	0
56	MG	1a	1870	1/1	0.93	0.13	58,58,58,58	0
56	MG	1A	3263	1/1	0.93	0.09	31,31,31,31	0
56	MG	1a	1675	1/1	0.93	0.18	59,59,59,59	0
56	MG	1A	3012	1/1	0.93	0.23	46,46,46,46	0
56	MG	2A	3203	1/1	0.93	0.09	19,19,19,19	0
56	MG	1a	1877	1/1	0.93	0.16	65,65,65,65	0
56	MG	1A	3163	1/1	0.93	0.11	38,38,38,38	0
56	MG	1A	3171	1/1	0.93	0.17	45,45,45,45	0
56	MG	1A	3335	1/1	0.93	0.11	46,46,46,46	0
56	MG	1A	3464	1/1	0.93	0.11	25,25,25,25	0
56	MG	2A	3214	1/1	0.93	0.08	42,42,42,42	0
56	MG	1a	1888	1/1	0.93	0.15	46,46,46,46	0
56	MG	1A	3914	1/1	0.93	0.11	51,51,51,51	0
56	MG	1A	3172	1/1	0.93	0.19	56,56,56,56	0
56	MG	2A	3220	1/1	0.93	0.09	43,43,43,43	0
56	MG	2D	301	1/1	0.93	0.11	50,50,50,50	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2D	304	1/1	0.93	0.15	27,27,27,27	0
56	MG	2D	305	1/1	0.93	0.11	27,27,27,27	0
56	MG	1A	3919	1/1	0.93	0.17	48,48,48,48	0
56	MG	1a	1692	1/1	0.93	0.22	61,61,61,61	0
56	MG	2E	304	1/1	0.93	0.07	58,58,58,58	0
56	MG	1A	3068	1/1	0.93	0.13	53,53,53,53	0
56	MG	1A	3047	1/1	0.93	0.12	40,40,40,40	0
56	MG	2Q	3001	1/1	0.93	0.13	39,39,39,39	0
56	MG	1D	307	1/1	0.93	0.12	43,43,43,43	0
56	MG	1D	313	1/1	0.93	0.09	39,39,39,39	0
56	MG	1E	305	1/1	0.93	0.13	45,45,45,45	0
56	MG	2A	3241	1/1	0.93	0.14	35,35,35,35	0
56	MG	2A	3242	1/1	0.93	0.18	53,53,53,53	0
56	MG	1E	307	1/1	0.93	0.19	64,64,64,64	0
56	MG	2a	1603	1/1	0.93	0.15	50,50,50,50	0
56	MG	2A	3246	1/1	0.93	0.13	56,56,56,56	0
56	MG	1A	3923	1/1	0.93	0.08	46,46,46,46	0
56	MG	1a	1702	1/1	0.93	0.19	43,43,43,43	0
56	MG	1F	302	1/1	0.93	0.10	42,42,42,42	0
56	MG	1b	3002	1/1	0.93	0.07	82,82,82,82	0
56	MG	1G	3001	1/1	0.93	0.11	45,45,45,45	0
56	MG	2A	3260	1/1	0.93	0.13	63,63,63,63	0
56	MG	1A	3470	1/1	0.93	0.26	43,43,43,43	0
56	MG	1A	3184	1/1	0.93	0.25	35,35,35,35	0
56	MG	2a	1618	1/1	0.93	0.10	74,74,74,74	0
56	MG	2A	3265	1/1	0.93	0.08	49,49,49,49	0
56	MG	1A	3017	1/1	0.93	0.28	53,53,53,53	0
56	MG	1A	3930	1/1	0.93	0.09	28,28,28,28	0
56	MG	2A	3269	1/1	0.93	0.10	52,52,52,52	0
56	MG	1A	3408	1/1	0.93	0.07	43,43,43,43	0
56	MG	1a	1721	1/1	0.93	0.24	36,36,36,36	0
56	MG	1a	1727	1/1	0.93	0.22	66,66,66,66	0
56	MG	1a	1728	1/1	0.93	0.16	49,49,49,49	0
56	MG	1a	1729	1/1	0.93	0.21	38,38,38,38	0
56	MG	1A	3933	1/1	0.93	0.09	42,42,42,42	0
56	MG	1a	1731	1/1	0.93	0.17	42,42,42,42	0
56	MG	1A	3556	1/1	0.93	0.15	67,67,67,67	0
56	MG	1a	1735	1/1	0.93	0.19	43,43,43,43	0
56	MG	1A	3762	1/1	0.93	0.09	60,60,60,60	0
56	MG	2A	3289	1/1	0.93	0.18	49,49,49,49	0
56	MG	1a	1738	1/1	0.93	0.16	53,53,53,53	0
56	MG	1A	3557	1/1	0.93	0.10	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3937	1/1	0.93	0.08	51,51,51,51	0
56	MG	1A	3938	1/1	0.93	0.07	34,34,34,34	0
56	MG	1Q	3003	1/1	0.93	0.14	59,59,59,59	0
56	MG	2A	3309	1/1	0.93	0.08	39,39,39,39	0
56	MG	2a	1647	1/1	0.93	0.10	64,64,64,64	0
56	MG	1a	1747	1/1	0.93	0.12	43,43,43,43	0
56	MG	2a	1657	1/1	0.93	0.21	61,61,61,61	0
56	MG	1x	109	1/1	0.93	0.17	78,78,78,78	0
56	MG	1x	110	1/1	0.93	0.07	53,53,53,53	0
56	MG	1A	3077	1/1	0.93	0.07	59,59,59,59	0
56	MG	2A	3319	1/1	0.93	0.09	55,55,55,55	0
56	MG	1A	3410	1/1	0.93	0.17	47,47,47,47	0
56	MG	2A	3004	1/1	0.93	0.10	55,55,55,55	0
56	MG	1A	3018	1/1	0.93	0.12	46,46,46,46	0
56	MG	2a	1674	1/1	0.93	0.12	50,50,50,50	0
56	MG	2A	3006	1/1	0.93	0.07	54,54,54,54	0
56	MG	1A	3122	1/1	0.93	0.14	44,44,44,44	0
56	MG	2a	1679	1/1	0.93	0.20	52,52,52,52	0
56	MG	1A	3946	1/1	0.93	0.15	29,29,29,29	0
56	MG	1A	3055	1/1	0.93	0.17	41,41,41,41	0
56	MG	2a	1686	1/1	0.93	0.14	49,49,49,49	0
56	MG	2A	3014	1/1	0.93	0.20	59,59,59,59	0
56	MG	2a	1688	1/1	0.93	0.15	49,49,49,49	0
56	MG	2A	3345	1/1	0.93	0.17	51,51,51,51	0
56	MG	2a	1693	1/1	0.93	0.20	67,67,67,67	0
56	MG	2A	3015	1/1	0.93	0.13	57,57,57,57	0
56	MG	1a	1757	1/1	0.93	0.08	50,50,50,50	0
56	MG	2a	1697	1/1	0.93	0.12	60,60,60,60	0
56	MG	2A	3353	1/1	0.93	0.11	59,59,59,59	0
56	MG	2A	3017	1/1	0.93	0.05	66,66,66,66	0
56	MG	1a	1758	1/1	0.93	0.09	50,50,50,50	0
56	MG	1a	1759	1/1	0.93	0.16	58,58,58,58	0
56	MG	2A	3359	1/1	0.93	0.10	49,49,49,49	0
56	MG	1A	3795	1/1	0.93	0.10	37,37,37,37	0
56	MG	1A	3060	1/1	0.93	0.11	46,46,46,46	0
56	MG	2A	3026	1/1	0.93	0.20	54,54,54,54	0
56	MG	2A	3029	1/1	0.93	0.22	54,54,54,54	0
56	MG	1A	3812	1/1	0.93	0.10	59,59,59,59	0
56	MG	1U	202	1/1	0.93	0.21	56,56,56,56	0
56	MG	1U	204	1/1	0.93	0.36	33,33,33,33	0
56	MG	2A	3368	1/1	0.93	0.09	43,43,43,43	0
56	MG	2A	3035	1/1	0.93	0.13	57,57,57,57	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3955	1/1	0.93	0.14	46,46,46,46	0
56	MG	2a	1721	1/1	0.93	0.18	49,49,49,49	0
56	MG	1A	3293	1/1	0.93	0.13	50,50,50,50	0
56	MG	2a	1724	1/1	0.93	0.24	64,64,64,64	0
56	MG	1a	1769	1/1	0.93	0.12	58,58,58,58	0
56	MG	1A	3205	1/1	0.93	0.17	40,40,40,40	0
56	MG	1A	3970	1/1	0.93	0.12	28,28,28,28	0
56	MG	1A	3297	1/1	0.93	0.12	41,41,41,41	0
56	MG	1A	3213	1/1	0.93	0.08	63,63,63,63	0
56	MG	1A	3580	1/1	0.93	0.09	22,22,22,22	0
56	MG	1A	3974	1/1	0.93	0.09	46,46,46,46	0
56	MG	2A	3391	1/1	0.93	0.14	47,47,47,47	0
56	MG	1A	3977	1/1	0.93	0.16	54,54,54,54	0
56	MG	2A	3394	1/1	0.93	0.08	57,57,57,57	0
56	MG	2A	3395	1/1	0.93	0.14	51,51,51,51	0
56	MG	1A	3126	1/1	0.93	0.11	44,44,44,44	0
56	MG	1A	3981	1/1	0.93	0.09	43,43,43,43	0
56	MG	1l	104	1/1	0.93	0.07	59,59,59,59	0
56	MG	2A	3061	1/1	0.93	0.08	44,44,44,44	0
56	MG	1A	3358	1/1	0.93	0.08	55,55,55,55	0
56	MG	2a	1745	1/1	0.93	0.19	54,54,54,54	0
56	MG	1A	3987	1/1	0.93	0.07	54,54,54,54	0
56	MG	1A	3083	1/1	0.93	0.16	48,48,48,48	0
56	MG	2A	3068	1/1	0.93	0.15	50,50,50,50	0
56	MG	1a	1787	1/1	0.93	0.10	61,61,61,61	0
56	MG	1A	3613	1/1	0.93	0.07	30,30,30,30	0
56	MG	2A	3416	1/1	0.93	0.15	50,50,50,50	0
56	MG	2A	3418	1/1	0.93	0.11	56,56,56,56	0
56	MG	2a	1757	1/1	0.93	0.12	60,60,60,60	0
56	MG	1A	3837	1/1	0.93	0.07	44,44,44,44	0
56	MG	2a	1759	1/1	0.93	0.12	68,68,68,68	0
56	MG	1A	3225	1/1	0.93	0.15	49,49,49,49	0
56	MG	2A	3079	1/1	0.93	0.09	45,45,45,45	0
56	MG	2a	1765	1/1	0.93	0.15	52,52,52,52	0
56	MG	2A	3424	1/1	0.93	0.10	44,44,44,44	0
56	MG	2A	3426	1/1	0.93	0.08	43,43,43,43	0
56	MG	1A	3305	1/1	0.93	0.26	52,52,52,52	0
56	MG	2a	1770	1/1	0.93	0.07	63,63,63,63	0
56	MG	1A	3622	1/1	0.93	0.11	61,61,61,61	0
56	MG	1a	1794	1/1	0.93	0.12	60,60,60,60	0
56	MG	2A	3432	1/1	0.93	0.19	48,48,48,48	0
56	MG	2A	3433	1/1	0.93	0.17	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2a	1778	1/1	0.93	0.13	69,69,69,69	0
56	MG	1A	3495	1/1	0.93	0.09	61,61,61,61	0
56	MG	1A	3625	1/1	0.93	0.08	43,43,43,43	0
56	MG	19	103	1/1	0.93	0.07	40,40,40,40	0
56	MG	1A	3635	1/1	0.93	0.09	83,83,83,83	0
56	MG	2a	1786	1/1	0.93	0.12	71,71,71,71	0
56	MG	1a	1601	1/1	0.93	0.20	62,62,62,62	0
56	MG	2A	3441	1/1	0.93	0.09	43,43,43,43	0
56	MG	1A	4005	1/1	0.93	0.15	65,65,65,65	0
56	MG	1A	3851	1/1	0.93	0.10	52,52,52,52	0
56	MG	1A	3086	1/1	0.93	0.09	39,39,39,39	0
56	MG	2a	1795	1/1	0.93	0.09	53,53,53,53	0
56	MG	1A	3228	1/1	0.93	0.16	33,33,33,33	0
56	MG	1A	3641	1/1	0.93	0.10	36,36,36,36	0
56	MG	1A	4024	1/1	0.93	0.11	61,61,61,61	0
56	MG	1A	3857	1/1	0.93	0.16	51,51,51,51	0
56	MG	2A	3099	1/1	0.93	0.12	57,57,57,57	0
56	MG	1A	4029	1/1	0.93	0.09	61,61,61,61	0
56	MG	1a	1614	1/1	0.93	0.08	74,74,74,74	0
56	MG	1A	3858	1/1	0.93	0.16	44,44,44,44	0
56	MG	1A	3367	1/1	0.93	0.08	53,53,53,53	0
56	MG	1A	3061	1/1	0.93	0.11	51,51,51,51	0
56	MG	1A	3439	1/1	0.93	0.07	64,64,64,64	0
56	MG	2a	1815	1/1	0.93	0.11	56,56,56,56	0
56	MG	1A	3310	1/1	0.93	0.23	51,51,51,51	0
56	MG	1a	1622	1/1	0.93	0.16	59,59,59,59	0
56	MG	1A	3026	1/1	0.93	0.19	49,49,49,49	0
56	MG	1A	3447	1/1	0.93	0.07	47,47,47,47	0
56	MG	2A	3120	1/1	0.93	0.09	33,33,33,33	0
56	MG	1A	3508	1/1	0.93	0.12	52,52,52,52	0
56	MG	2l	201	1/1	0.93	0.12	66,66,66,66	0
56	MG	2A	3479	1/1	0.93	0.10	56,56,56,56	0
56	MG	1A	4046	1/1	0.93	0.19	50,50,50,50	0
56	MG	1a	1821	1/1	0.93	0.17	64,64,64,64	0
56	MG	2A	3482	1/1	0.93	0.21	59,59,59,59	0
56	MG	1a	1634	1/1	0.93	0.09	41,41,41,41	0
56	MG	2t	3001	1/1	0.93	0.18	53,53,53,53	0
56	MG	1A	3028	1/1	0.93	0.11	52,52,52,52	0
56	MG	1A	3679	1/1	0.93	0.14	41,41,41,41	0
56	MG	1A	3149	1/1	0.93	0.05	35,35,35,35	0
56	MG	2A	3512	1/1	0.94	0.16	32,32,32,32	0
56	MG	1A	3844	1/1	0.94	0.11	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1Q	3002	1/1	0.94	0.16	36,36,36,36	0
56	MG	1a	1719	1/1	0.94	0.21	53,53,53,53	0
56	MG	1A	3650	1/1	0.94	0.09	30,30,30,30	0
56	MG	2A	3207	1/1	0.94	0.16	41,41,41,41	0
56	MG	2A	3520	1/1	0.94	0.11	25,25,25,25	0
56	MG	2A	3209	1/1	0.94	0.09	49,49,49,49	0
56	MG	1a	1722	1/1	0.94	0.09	65,65,65,65	0
56	MG	1A	3472	1/1	0.94	0.17	46,46,46,46	0
56	MG	2A	3526	1/1	0.94	0.10	46,46,46,46	0
56	MG	1e	203	1/1	0.94	0.10	61,61,61,61	0
56	MG	1f	3001	1/1	0.94	0.18	56,56,56,56	0
56	MG	1A	3362	1/1	0.94	0.19	41,41,41,41	0
56	MG	1A	3659	1/1	0.94	0.08	25,25,25,25	0
56	MG	2A	3533	1/1	0.94	0.16	28,28,28,28	0
56	MG	2A	3217	1/1	0.94	0.16	46,46,46,46	0
56	MG	2A	3218	1/1	0.94	0.05	37,37,37,37	0
56	MG	1A	3980	1/1	0.94	0.07	33,33,33,33	0
56	MG	2A	3539	1/1	0.94	0.07	29,29,29,29	0
56	MG	1A	3104	1/1	0.94	0.07	52,52,52,52	0
56	MG	2A	3541	1/1	0.94	0.09	31,31,31,31	0
56	MG	2A	3221	1/1	0.94	0.17	30,30,30,30	0
56	MG	1A	3670	1/1	0.94	0.10	19,19,19,19	0
56	MG	2A	3224	1/1	0.94	0.06	37,37,37,37	0
56	MG	1A	3364	1/1	0.94	0.07	41,41,41,41	0
56	MG	1a	1736	1/1	0.94	0.18	59,59,59,59	0
56	MG	2A	3227	1/1	0.94	0.08	59,59,59,59	0
56	MG	1A	3130	1/1	0.94	0.20	35,35,35,35	0
56	MG	1A	3131	1/1	0.94	0.19	50,50,50,50	0
56	MG	2A	3233	1/1	0.94	0.18	58,58,58,58	0
56	MG	1a	1739	1/1	0.94	0.10	54,54,54,54	0
56	MG	1A	3283	1/1	0.94	0.08	47,47,47,47	0
56	MG	1A	3687	1/1	0.94	0.08	53,53,53,53	0
56	MG	1A	3689	1/1	0.94	0.10	34,34,34,34	0
56	MG	1A	3284	1/1	0.94	0.16	41,41,41,41	0
56	MG	1A	3369	1/1	0.94	0.11	38,38,38,38	0
56	MG	1x	103	1/1	0.94	0.19	68,68,68,68	0
56	MG	1X	3001	1/1	0.94	0.14	43,43,43,43	0
56	MG	1Y	201	1/1	0.94	0.17	39,39,39,39	0
56	MG	2A	3253	1/1	0.94	0.16	29,29,29,29	0
56	MG	2A	3255	1/1	0.94	0.08	42,42,42,42	0
56	MG	2D	306	1/1	0.94	0.12	55,55,55,55	0
56	MG	1x	107	1/1	0.94	0.08	50,50,50,50	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3543	1/1	0.94	0.09	41,41,41,41	0
56	MG	1a	1751	1/1	0.94	0.22	60,60,60,60	0
56	MG	1A	3024	1/1	0.94	0.15	48,48,48,48	0
56	MG	2A	3001	1/1	0.94	0.08	39,39,39,39	0
56	MG	1A	3232	1/1	0.94	0.40	39,39,39,39	0
56	MG	2Y	201	1/1	0.94	0.07	58,58,58,58	0
56	MG	1A	4007	1/1	0.94	0.09	68,68,68,68	0
56	MG	1A	3549	1/1	0.94	0.13	64,64,64,64	0
56	MG	1A	4010	1/1	0.94	0.13	37,37,37,37	0
56	MG	1A	4012	1/1	0.94	0.12	42,42,42,42	0
56	MG	1A	3550	1/1	0.94	0.11	81,81,81,81	0
56	MG	1A	3233	1/1	0.94	0.15	42,42,42,42	0
56	MG	1A	3704	1/1	0.94	0.04	26,26,26,26	0
56	MG	1A	4020	1/1	0.94	0.09	30,30,30,30	0
56	MG	1A	4022	1/1	0.94	0.14	64,64,64,64	0
56	MG	16	103	1/1	0.94	0.06	36,36,36,36	0
56	MG	2a	1609	1/1	0.94	0.29	60,60,60,60	0
56	MG	1A	3020	1/1	0.94	0.07	47,47,47,47	0
56	MG	1A	4026	1/1	0.94	0.14	45,45,45,45	0
56	MG	2A	3285	1/1	0.94	0.07	48,48,48,48	0
56	MG	1A	3066	1/1	0.94	0.13	56,56,56,56	0
56	MG	1A	3333	1/1	0.94	0.11	53,53,53,53	0
56	MG	18	101	1/1	0.94	0.07	30,30,30,30	0
56	MG	2A	3025	1/1	0.94	0.19	45,45,45,45	0
56	MG	2a	1619	1/1	0.94	0.21	53,53,53,53	0
56	MG	1A	3142	1/1	0.94	0.15	62,62,62,62	0
56	MG	2A	3027	1/1	0.94	0.08	53,53,53,53	0
56	MG	2A	3306	1/1	0.94	0.09	32,32,32,32	0
56	MG	1A	3381	1/1	0.94	0.14	38,38,38,38	0
56	MG	2A	3308	1/1	0.94	0.08	44,44,44,44	0
56	MG	1A	4032	1/1	0.94	0.07	35,35,35,35	0
56	MG	2A	3310	1/1	0.94	0.12	55,55,55,55	0
56	MG	1a	1777	1/1	0.94	0.09	64,64,64,64	0
56	MG	2A	3312	1/1	0.94	0.07	27,27,27,27	0
56	MG	1A	3886	1/1	0.94	0.20	65,65,65,65	0
56	MG	2A	3033	1/1	0.94	0.14	57,57,57,57	0
56	MG	2A	3315	1/1	0.94	0.16	50,50,50,50	0
56	MG	2a	1634	1/1	0.94	0.07	94,94,94,94	0
56	MG	1A	4034	1/1	0.94	0.10	50,50,50,50	0
56	MG	1A	3887	1/1	0.94	0.07	44,44,44,44	0
56	MG	2A	3321	1/1	0.94	0.08	32,32,32,32	0
56	MG	2A	3039	1/1	0.94	0.23	45,45,45,45	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1a	1781	1/1	0.94	0.10	48,48,48,48	0
56	MG	2A	3326	1/1	0.94	0.22	50,50,50,50	0
56	MG	2A	3327	1/1	0.94	0.07	56,56,56,56	0
56	MG	1A	3239	1/1	0.94	0.16	25,25,25,25	0
56	MG	1A	3494	1/1	0.94	0.18	63,63,63,63	0
56	MG	2a	1646	1/1	0.94	0.18	70,70,70,70	0
56	MG	1A	3445	1/1	0.94	0.11	55,55,55,55	0
56	MG	2a	1648	1/1	0.94	0.12	68,68,68,68	0
56	MG	2a	1649	1/1	0.94	0.17	51,51,51,51	0
56	MG	1a	1785	1/1	0.94	0.08	66,66,66,66	0
56	MG	2a	1656	1/1	0.94	0.10	50,50,50,50	0
56	MG	1a	1606	1/1	0.94	0.12	62,62,62,62	0
56	MG	1A	3723	1/1	0.94	0.08	51,51,51,51	0
56	MG	1A	3894	1/1	0.94	0.06	49,49,49,49	0
56	MG	2A	3347	1/1	0.94	0.23	60,60,60,60	0
56	MG	1A	3383	1/1	0.94	0.19	43,43,43,43	0
56	MG	2A	3351	1/1	0.94	0.10	52,52,52,52	0
56	MG	2a	1669	1/1	0.94	0.07	43,43,43,43	0
56	MG	2A	3056	1/1	0.94	0.06	37,37,37,37	0
56	MG	1A	4049	1/1	0.94	0.20	18,18,18,18	0
56	MG	2a	1673	1/1	0.94	0.29	52,52,52,52	0
56	MG	1A	3295	1/1	0.94	0.10	50,50,50,50	0
56	MG	2a	1675	1/1	0.94	0.17	59,59,59,59	0
56	MG	1A	3729	1/1	0.94	0.08	43,43,43,43	0
56	MG	1A	3731	1/1	0.94	0.14	58,58,58,58	0
56	MG	1A	3900	1/1	0.94	0.10	49,49,49,49	0
56	MG	1A	4061	1/1	0.94	0.13	48,48,48,48	0
56	MG	1a	1618	1/1	0.94	0.07	58,58,58,58	0
56	MG	2A	3362	1/1	0.94	0.22	62,62,62,62	0
56	MG	1a	1619	1/1	0.94	0.08	82,82,82,82	0
56	MG	1A	3339	1/1	0.94	0.18	73,73,73,73	0
56	MG	2A	3073	1/1	0.94	0.10	43,43,43,43	0
56	MG	2a	1692	1/1	0.94	0.10	67,67,67,67	0
56	MG	1A	3192	1/1	0.94	0.21	47,47,47,47	0
56	MG	1A	3035	1/1	0.94	0.26	59,59,59,59	0
56	MG	1A	3571	1/1	0.94	0.11	42,42,42,42	0
56	MG	1A	3577	1/1	0.94	0.10	32,32,32,32	0
56	MG	1a	1626	1/1	0.94	0.12	62,62,62,62	0
56	MG	1A	3909	1/1	0.94	0.14	54,54,54,54	0
56	MG	1A	3911	1/1	0.94	0.09	46,46,46,46	0
56	MG	2a	1702	1/1	0.94	0.11	64,64,64,64	0
56	MG	1a	1632	1/1	0.94	0.20	47,47,47,47	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3748	1/1	0.94	0.09	64,64,64,64	0
56	MG	2A	3086	1/1	0.94	0.07	36,36,36,36	0
56	MG	2A	3087	1/1	0.94	0.16	49,49,49,49	0
56	MG	2A	3387	1/1	0.94	0.10	37,37,37,37	0
56	MG	2a	1709	1/1	0.94	0.16	64,64,64,64	0
56	MG	1a	1635	1/1	0.94	0.22	66,66,66,66	0
56	MG	1A	3251	1/1	0.94	0.12	58,58,58,58	0
56	MG	1A	3754	1/1	0.94	0.11	61,61,61,61	0
56	MG	2a	1713	1/1	0.94	0.10	60,60,60,60	0
56	MG	1A	4080	1/1	0.94	0.24	45,45,45,45	0
56	MG	1a	1640	1/1	0.94	0.07	57,57,57,57	0
56	MG	1A	4086	1/1	0.94	0.07	51,51,51,51	0
56	MG	1A	3579	1/1	0.94	0.06	51,51,51,51	0
56	MG	2a	1718	1/1	0.94	0.20	53,53,53,53	0
56	MG	1a	1643	1/1	0.94	0.13	47,47,47,47	0
56	MG	1A	3194	1/1	0.94	0.14	50,50,50,50	0
56	MG	1B	202	1/1	0.94	0.20	56,56,56,56	0
56	MG	1A	3582	1/1	0.94	0.14	45,45,45,45	0
56	MG	1A	3027	1/1	0.94	0.09	42,42,42,42	0
56	MG	1A	3594	1/1	0.94	0.12	36,36,36,36	0
56	MG	2A	3410	1/1	0.94	0.12	56,56,56,56	0
56	MG	1a	1825	1/1	0.94	0.14	64,64,64,64	0
56	MG	2A	3105	1/1	0.94	0.16	29,29,29,29	0
56	MG	1A	3596	1/1	0.94	0.12	45,45,45,45	0
56	MG	2A	3415	1/1	0.94	0.16	47,47,47,47	0
56	MG	1A	3779	1/1	0.94	0.11	36,36,36,36	0
56	MG	1A	3507	1/1	0.94	0.10	40,40,40,40	0
56	MG	1a	1657	1/1	0.94	0.09	25,25,25,25	0
56	MG	2A	3112	1/1	0.94	0.12	40,40,40,40	0
56	MG	1A	3150	1/1	0.94	0.07	39,39,39,39	0
56	MG	2A	3422	1/1	0.94	0.23	53,53,53,53	0
56	MG	2A	3114	1/1	0.94	0.23	45,45,45,45	0
56	MG	1A	3260	1/1	0.94	0.17	50,50,50,50	0
56	MG	2A	3427	1/1	0.94	0.07	43,43,43,43	0
56	MG	1a	1660	1/1	0.94	0.14	57,57,57,57	0
56	MG	1A	3010	1/1	0.94	0.21	46,46,46,46	0
56	MG	2A	3122	1/1	0.94	0.12	54,54,54,54	0
56	MG	2A	3431	1/1	0.94	0.08	59,59,59,59	0
56	MG	1A	3619	1/1	0.94	0.09	24,24,24,24	0
56	MG	1B	225	1/1	0.94	0.10	51,51,51,51	0
56	MG	1a	1665	1/1	0.94	0.15	54,54,54,54	0
56	MG	2A	3127	1/1	0.94	0.25	45,45,45,45	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1B	226	1/1	0.94	0.09	47,47,47,47	0
56	MG	1A	3802	1/1	0.94	0.08	36,36,36,36	0
56	MG	1A	3013	1/1	0.94	0.09	50,50,50,50	0
56	MG	1a	1670	1/1	0.94	0.16	60,60,60,60	0
56	MG	1A	3514	1/1	0.94	0.24	46,46,46,46	0
56	MG	2A	3134	1/1	0.94	0.11	40,40,40,40	0
56	MG	2A	3444	1/1	0.94	0.07	58,58,58,58	0
56	MG	1A	3817	1/1	0.94	0.08	49,49,49,49	0
56	MG	2A	3446	1/1	0.94	0.08	52,52,52,52	0
56	MG	2A	3136	1/1	0.94	0.06	44,44,44,44	0
56	MG	1a	1673	1/1	0.94	0.11	51,51,51,51	0
56	MG	1D	306	1/1	0.94	0.14	50,50,50,50	0
56	MG	2A	3451	1/1	0.94	0.07	53,53,53,53	0
56	MG	2A	3141	1/1	0.94	0.14	37,37,37,37	0
56	MG	1A	3819	1/1	0.94	0.12	80,80,80,80	0
56	MG	1D	311	1/1	0.94	0.14	58,58,58,58	0
56	MG	2a	1783	1/1	0.94	0.13	59,59,59,59	0
56	MG	2A	3144	1/1	0.94	0.04	43,43,43,43	0
56	MG	1A	3265	1/1	0.94	0.18	52,52,52,52	0
56	MG	2A	3150	1/1	0.94	0.17	39,39,39,39	0
56	MG	2A	3153	1/1	0.94	0.08	45,45,45,45	0
56	MG	2A	3154	1/1	0.94	0.11	39,39,39,39	0
56	MG	1A	3044	1/1	0.94	0.31	38,38,38,38	0
56	MG	2A	3159	1/1	0.94	0.31	71,71,71,71	0
56	MG	2a	1793	1/1	0.94	0.17	58,58,58,58	0
56	MG	2A	3473	1/1	0.94	0.08	42,42,42,42	0
56	MG	1a	1683	1/1	0.94	0.20	51,51,51,51	0
56	MG	1A	3826	1/1	0.94	0.11	42,42,42,42	0
56	MG	2a	1797	1/1	0.94	0.11	57,57,57,57	0
56	MG	2A	3164	1/1	0.94	0.10	37,37,37,37	0
56	MG	1A	3271	1/1	0.94	0.10	36,36,36,36	0
56	MG	2a	1801	1/1	0.94	0.08	63,63,63,63	0
56	MG	1a	1873	1/1	0.94	0.19	52,52,52,52	0
56	MG	1A	3947	1/1	0.94	0.14	32,32,32,32	0
56	MG	1a	1689	1/1	0.94	0.06	61,61,61,61	0
56	MG	1F	307	1/1	0.94	0.10	41,41,41,41	0
56	MG	2a	1809	1/1	0.94	0.27	64,64,64,64	0
56	MG	1A	3948	1/1	0.94	0.17	56,56,56,56	0
56	MG	1A	3949	1/1	0.94	0.26	37,37,37,37	0
56	MG	1a	1883	1/1	0.94	0.22	47,47,47,47	0
56	MG	2A	3177	1/1	0.94	0.12	40,40,40,40	0
56	MG	1a	1885	1/1	0.94	0.20	49,49,49,49	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1G	3003	1/1	0.94	0.07	45,45,45,45	0
56	MG	1A	3313	1/1	0.94	0.06	50,50,50,50	0
56	MG	1a	1696	1/1	0.94	0.12	59,59,59,59	0
56	MG	1A	3357	1/1	0.94	0.10	54,54,54,54	0
56	MG	1A	3162	1/1	0.94	0.17	35,35,35,35	0
56	MG	1A	3411	1/1	0.94	0.11	47,47,47,47	0
56	MG	2A	3187	1/1	0.94	0.19	40,40,40,40	0
56	MG	1A	3835	1/1	0.94	0.06	57,57,57,57	0
56	MG	1A	3644	1/1	0.94	0.09	60,60,60,60	0
56	MG	1A	3217	1/1	0.94	0.07	43,43,43,43	0
56	MG	2n	502	1/1	0.94	0.26	56,56,56,56	0
56	MG	1O	202	1/1	0.94	0.08	52,52,52,52	0
56	MG	2q	3001	1/1	0.94	0.14	54,54,54,54	0
56	MG	1A	3360	1/1	0.94	0.21	48,48,48,48	0
56	MG	1P	204	1/1	0.94	0.31	34,34,34,34	0
56	MG	2x	3001	1/1	0.94	0.14	57,57,57,57	0
56	MG	2A	3197	1/1	0.94	0.15	47,47,47,47	0
56	MG	2x	3003	1/1	0.94	0.15	48,48,48,48	0
56	MG	1a	1715	1/1	0.94	0.09	47,47,47,47	0
56	MG	1A	3046	1/1	0.94	0.08	51,51,51,51	0
57	ZN	24	501	1/1	0.94	0.07	114,114,114,114	0
56	MG	1A	3114	1/1	0.95	0.12	36,36,36,36	0
56	MG	1e	202	1/1	0.95	0.12	81,81,81,81	0
56	MG	1E	306	1/1	0.95	0.05	51,51,51,51	0
56	MG	2A	3524	1/1	0.95	0.06	46,46,46,46	0
56	MG	1A	3586	1/1	0.95	0.13	55,55,55,55	0
56	MG	1a	1701	1/1	0.95	0.18	60,60,60,60	0
56	MG	2A	3527	1/1	0.95	0.07	37,37,37,37	0
56	MG	1A	3588	1/1	0.95	0.10	14,14,14,14	0
56	MG	1A	3761	1/1	0.95	0.14	47,47,47,47	0
56	MG	2A	3530	1/1	0.95	0.07	46,46,46,46	0
56	MG	1a	1705	1/1	0.95	0.09	38,38,38,38	0
56	MG	1F	306	1/1	0.95	0.09	49,49,49,49	0
56	MG	1A	3216	1/1	0.95	0.09	41,41,41,41	0
56	MG	1a	1711	1/1	0.95	0.09	60,60,60,60	0
56	MG	1A	3115	1/1	0.95	0.12	48,48,48,48	0
56	MG	1A	3767	1/1	0.95	0.10	71,71,71,71	0
56	MG	1A	3769	1/1	0.95	0.09	44,44,44,44	0
56	MG	2A	3232	1/1	0.95	0.10	47,47,47,47	0
56	MG	1A	3440	1/1	0.95	0.10	45,45,45,45	0
56	MG	2A	3236	1/1	0.95	0.14	55,55,55,55	0
56	MG	1A	3941	1/1	0.95	0.11	50,50,50,50	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3774	1/1	0.95	0.17	63,63,63,63	0
56	MG	1A	3377	1/1	0.95	0.18	43,43,43,43	0
56	MG	1A	3604	1/1	0.95	0.07	30,30,30,30	0
56	MG	1A	3606	1/1	0.95	0.12	58,58,58,58	0
56	MG	1x	104	1/1	0.95	0.10	40,40,40,40	0
56	MG	2A	3551	1/1	0.95	0.09	32,32,32,32	0
56	MG	1N	206	1/1	0.95	0.08	37,37,37,37	0
56	MG	1A	3782	1/1	0.95	0.06	27,27,27,27	0
56	MG	1A	3789	1/1	0.95	0.11	21,21,21,21	0
56	MG	1A	3058	1/1	0.95	0.10	63,63,63,63	0
56	MG	2A	3254	1/1	0.95	0.17	55,55,55,55	0
56	MG	1a	1732	1/1	0.95	0.33	42,42,42,42	0
56	MG	1P	201	1/1	0.95	0.14	56,56,56,56	0
56	MG	2B	3007	1/1	0.95	0.08	48,48,48,48	0
56	MG	1A	3444	1/1	0.95	0.13	63,63,63,63	0
56	MG	1A	3123	1/1	0.95	0.18	43,43,43,43	0
56	MG	1A	3334	1/1	0.95	0.17	37,37,37,37	0
56	MG	1A	3033	1/1	0.95	0.07	39,39,39,39	0
56	MG	2D	302	1/1	0.95	0.12	48,48,48,48	0
56	MG	1A	3804	1/1	0.95	0.10	58,58,58,58	0
56	MG	1A	3805	1/1	0.95	0.08	21,21,21,21	0
56	MG	2A	3267	1/1	0.95	0.12	50,50,50,50	0
56	MG	2E	301	1/1	0.95	0.09	30,30,30,30	0
56	MG	1A	3959	1/1	0.95	0.09	27,27,27,27	0
56	MG	1R	201	1/1	0.95	0.20	55,55,55,55	0
56	MG	1A	3964	1/1	0.95	0.08	20,20,20,20	0
56	MG	2F	301	1/1	0.95	0.06	39,39,39,39	0
56	MG	1a	1745	1/1	0.95	0.12	50,50,50,50	0
56	MG	1A	3449	1/1	0.95	0.07	54,54,54,54	0
56	MG	2O	3001	1/1	0.95	0.15	49,49,49,49	0
56	MG	1R	206	1/1	0.95	0.09	37,37,37,37	0
56	MG	2Q	3002	1/1	0.95	0.14	44,44,44,44	0
56	MG	2Q	3004	1/1	0.95	0.15	38,38,38,38	0
56	MG	2U	202	1/1	0.95	0.20	48,48,48,48	0
56	MG	1A	3967	1/1	0.95	0.12	51,51,51,51	0
56	MG	2Y	203	1/1	0.95	0.10	41,41,41,41	0
56	MG	2A	3276	1/1	0.95	0.06	58,58,58,58	0
56	MG	1A	3623	1/1	0.95	0.05	61,61,61,61	0
56	MG	1A	3164	1/1	0.95	0.17	20,20,20,20	0
56	MG	2A	3021	1/1	0.95	0.17	42,42,42,42	0
56	MG	2A	3282	1/1	0.95	0.06	39,39,39,39	0
56	MG	1a	1753	1/1	0.95	0.24	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3337	1/1	0.95	0.05	39,39,39,39	0
56	MG	2a	1605	1/1	0.95	0.12	66,66,66,66	0
56	MG	2A	3286	1/1	0.95	0.09	32,32,32,32	0
56	MG	1A	3820	1/1	0.95	0.13	45,45,45,45	0
56	MG	1A	3626	1/1	0.95	0.06	27,27,27,27	0
56	MG	1A	3627	1/1	0.95	0.07	50,50,50,50	0
56	MG	2A	3295	1/1	0.95	0.08	32,32,32,32	0
56	MG	2a	1611	1/1	0.95	0.07	68,68,68,68	0
56	MG	2A	3296	1/1	0.95	0.12	40,40,40,40	0
56	MG	2A	3028	1/1	0.95	0.11	45,45,45,45	0
56	MG	2A	3298	1/1	0.95	0.09	31,31,31,31	0
56	MG	2A	3299	1/1	0.95	0.14	65,65,65,65	0
56	MG	1A	3630	1/1	0.95	0.14	47,47,47,47	0
56	MG	1A	3979	1/1	0.95	0.15	32,32,32,32	0
56	MG	1A	3632	1/1	0.95	0.06	27,27,27,27	0
56	MG	1W	3002	1/1	0.95	0.17	40,40,40,40	0
56	MG	1A	3515	1/1	0.95	0.10	57,57,57,57	0
56	MG	1A	3982	1/1	0.95	0.13	40,40,40,40	0
56	MG	1A	3072	1/1	0.95	0.14	44,44,44,44	0
56	MG	1A	3093	1/1	0.95	0.17	54,54,54,54	0
56	MG	1A	3990	1/1	0.95	0.12	47,47,47,47	0
56	MG	1a	1768	1/1	0.95	0.08	56,56,56,56	0
56	MG	10	104	1/1	0.95	0.10	46,46,46,46	0
56	MG	1A	3173	1/1	0.95	0.13	44,44,44,44	0
56	MG	2A	3317	1/1	0.95	0.07	37,37,37,37	0
56	MG	1a	1771	1/1	0.95	0.10	52,52,52,52	0
56	MG	1A	3833	1/1	0.95	0.07	36,36,36,36	0
56	MG	1A	3834	1/1	0.95	0.09	51,51,51,51	0
56	MG	2A	3053	1/1	0.95	0.07	47,47,47,47	0
56	MG	1A	3996	1/1	0.95	0.31	32,32,32,32	0
56	MG	1A	3642	1/1	0.95	0.08	39,39,39,39	0
56	MG	1A	3999	1/1	0.95	0.08	27,27,27,27	0
56	MG	1A	3127	1/1	0.95	0.18	39,39,39,39	0
56	MG	2A	3058	1/1	0.95	0.12	46,46,46,46	0
56	MG	2A	3332	1/1	0.95	0.08	48,48,48,48	0
56	MG	1A	3073	1/1	0.95	0.12	49,49,49,49	0
56	MG	2A	3338	1/1	0.95	0.07	53,53,53,53	0
56	MG	15	102	1/1	0.95	0.05	45,45,45,45	0
56	MG	15	103	1/1	0.95	0.18	33,33,33,33	0
56	MG	1A	3392	1/1	0.95	0.11	44,44,44,44	0
56	MG	2A	3063	1/1	0.95	0.15	47,47,47,47	0
56	MG	2A	3346	1/1	0.95	0.10	44,44,44,44	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2a	1653	1/1	0.95	0.18	60,60,60,60	0
56	MG	2A	3064	1/1	0.95	0.23	33,33,33,33	0
56	MG	1A	3179	1/1	0.95	0.17	38,38,38,38	0
56	MG	2A	3066	1/1	0.95	0.23	59,59,59,59	0
56	MG	2a	1659	1/1	0.95	0.15	60,60,60,60	0
56	MG	2a	1660	1/1	0.95	0.12	62,62,62,62	0
56	MG	1A	3840	1/1	0.95	0.10	59,59,59,59	0
56	MG	1A	3180	1/1	0.95	0.08	39,39,39,39	0
56	MG	1A	4006	1/1	0.95	0.18	51,51,51,51	0
56	MG	1A	3395	1/1	0.95	0.05	61,61,61,61	0
56	MG	2a	1668	1/1	0.95	0.19	42,42,42,42	0
56	MG	2A	3074	1/1	0.95	0.15	50,50,50,50	0
56	MG	2a	1670	1/1	0.95	0.12	60,60,60,60	0
56	MG	1A	3242	1/1	0.95	0.13	30,30,30,30	0
56	MG	1A	4009	1/1	0.95	0.17	40,40,40,40	0
56	MG	1A	3099	1/1	0.95	0.20	53,53,53,53	0
56	MG	1A	3657	1/1	0.95	0.09	48,48,48,48	0
56	MG	1A	3399	1/1	0.95	0.10	39,39,39,39	0
56	MG	1A	3186	1/1	0.95	0.23	36,36,36,36	0
56	MG	1a	1793	1/1	0.95	0.09	29,29,29,29	0
56	MG	1A	4018	1/1	0.95	0.08	49,49,49,49	0
56	MG	1A	3664	1/1	0.95	0.07	37,37,37,37	0
56	MG	1A	3668	1/1	0.95	0.13	31,31,31,31	0
56	MG	1A	3302	1/1	0.95	0.14	28,28,28,28	0
56	MG	1A	3249	1/1	0.95	0.08	43,43,43,43	0
56	MG	1a	1799	1/1	0.95	0.09	39,39,39,39	0
56	MG	2a	1689	1/1	0.95	0.08	43,43,43,43	0
56	MG	2a	1690	1/1	0.95	0.28	55,55,55,55	0
56	MG	1A	3859	1/1	0.95	0.20	41,41,41,41	0
56	MG	1A	4027	1/1	0.95	0.07	50,50,50,50	0
56	MG	2A	3376	1/1	0.95	0.11	48,48,48,48	0
56	MG	1A	3860	1/1	0.95	0.09	59,59,59,59	0
56	MG	1a	1610	1/1	0.95	0.07	48,48,48,48	0
56	MG	2a	1696	1/1	0.95	0.13	43,43,43,43	0
56	MG	2A	3380	1/1	0.95	0.07	37,37,37,37	0
56	MG	1A	3678	1/1	0.95	0.13	44,44,44,44	0
56	MG	2A	3382	1/1	0.95	0.20	47,47,47,47	0
56	MG	1A	3352	1/1	0.95	0.12	37,37,37,37	0
56	MG	1a	1613	1/1	0.95	0.13	44,44,44,44	0
56	MG	1A	3250	1/1	0.95	0.20	52,52,52,52	0
56	MG	1A	3867	1/1	0.95	0.17	48,48,48,48	0
56	MG	1A	3021	1/1	0.95	0.10	43,43,43,43	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3685	1/1	0.95	0.11	31,31,31,31	0
56	MG	2A	3103	1/1	0.95	0.18	50,50,50,50	0
56	MG	1A	3870	1/1	0.95	0.06	47,47,47,47	0
56	MG	2A	3397	1/1	0.95	0.06	27,27,27,27	0
56	MG	2A	3400	1/1	0.95	0.12	34,34,34,34	0
56	MG	1A	3253	1/1	0.95	0.18	54,54,54,54	0
56	MG	2A	3402	1/1	0.95	0.09	44,44,44,44	0
56	MG	2A	3403	1/1	0.95	0.23	53,53,53,53	0
56	MG	1A	3188	1/1	0.95	0.09	50,50,50,50	0
56	MG	1A	3474	1/1	0.95	0.08	49,49,49,49	0
56	MG	1A	3029	1/1	0.95	0.28	40,40,40,40	0
56	MG	1A	4040	1/1	0.95	0.12	51,51,51,51	0
56	MG	2a	1719	1/1	0.95	0.23	63,63,63,63	0
56	MG	2a	1720	1/1	0.95	0.20	60,60,60,60	0
56	MG	2A	3110	1/1	0.95	0.26	44,44,44,44	0
56	MG	2a	1722	1/1	0.95	0.23	47,47,47,47	0
56	MG	1A	3105	1/1	0.95	0.05	43,43,43,43	0
56	MG	1A	3878	1/1	0.95	0.07	20,20,20,20	0
56	MG	2A	3412	1/1	0.95	0.09	53,53,53,53	0
56	MG	1A	4048	1/1	0.95	0.19	41,41,41,41	0
56	MG	1A	3037	1/1	0.95	0.09	50,50,50,50	0
56	MG	2A	3117	1/1	0.95	0.09	41,41,41,41	0
56	MG	2a	1730	1/1	0.95	0.12	66,66,66,66	0
56	MG	1A	3262	1/1	0.95	0.34	43,43,43,43	0
56	MG	2A	3417	1/1	0.95	0.06	42,42,42,42	0
56	MG	1a	1633	1/1	0.95	0.10	51,51,51,51	0
56	MG	1A	4051	1/1	0.95	0.06	45,45,45,45	0
56	MG	1a	1826	1/1	0.95	0.10	47,47,47,47	0
56	MG	2A	3124	1/1	0.95	0.17	48,48,48,48	0
56	MG	1a	1828	1/1	0.95	0.08	45,45,45,45	0
56	MG	1A	3699	1/1	0.95	0.09	49,49,49,49	0
56	MG	1A	3140	1/1	0.95	0.33	38,38,38,38	0
56	MG	1A	3701	1/1	0.95	0.09	28,28,28,28	0
56	MG	1A	3553	1/1	0.95	0.16	50,50,50,50	0
56	MG	2A	3130	1/1	0.95	0.08	43,43,43,43	0
56	MG	1a	1837	1/1	0.95	0.11	46,46,46,46	0
56	MG	2a	1746	1/1	0.95	0.10	46,46,46,46	0
56	MG	1A	3141	1/1	0.95	0.21	37,37,37,37	0
56	MG	1A	4063	1/1	0.95	0.09	38,38,38,38	0
56	MG	1a	1842	1/1	0.95	0.15	39,39,39,39	0
56	MG	2a	1750	1/1	0.95	0.24	54,54,54,54	0
56	MG	1A	3418	1/1	0.95	0.08	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3707	1/1	0.95	0.08	50,50,50,50	0
56	MG	1A	3889	1/1	0.95	0.08	46,46,46,46	0
56	MG	2A	3138	1/1	0.95	0.09	36,36,36,36	0
56	MG	1A	3419	1/1	0.95	0.08	47,47,47,47	0
56	MG	1A	4072	1/1	0.95	0.07	70,70,70,70	0
56	MG	1a	1850	1/1	0.95	0.15	47,47,47,47	0
56	MG	1A	3712	1/1	0.95	0.11	29,29,29,29	0
56	MG	2a	1762	1/1	0.95	0.08	70,70,70,70	0
56	MG	1A	3014	1/1	0.95	0.13	46,46,46,46	0
56	MG	2a	1764	1/1	0.95	0.14	52,52,52,52	0
56	MG	1A	3050	1/1	0.95	0.06	62,62,62,62	0
56	MG	1A	3560	1/1	0.95	0.12	37,37,37,37	0
56	MG	2A	3151	1/1	0.95	0.10	40,40,40,40	0
56	MG	2A	3448	1/1	0.95	0.17	53,53,53,53	0
56	MG	1A	4078	1/1	0.95	0.05	23,23,23,23	0
56	MG	1a	1655	1/1	0.95	0.09	50,50,50,50	0
56	MG	2a	1772	1/1	0.95	0.26	63,63,63,63	0
56	MG	1A	3267	1/1	0.95	0.19	51,51,51,51	0
56	MG	2A	3158	1/1	0.95	0.14	39,39,39,39	0
56	MG	1A	3562	1/1	0.95	0.08	63,63,63,63	0
56	MG	2A	3455	1/1	0.95	0.09	45,45,45,45	0
56	MG	2A	3457	1/1	0.95	0.10	68,68,68,68	0
56	MG	1A	4081	1/1	0.95	0.39	27,27,27,27	0
56	MG	1A	4084	1/1	0.95	0.15	36,36,36,36	0
56	MG	1A	3719	1/1	0.95	0.07	34,34,34,34	0
56	MG	2A	3461	1/1	0.95	0.09	64,64,64,64	0
56	MG	1a	1866	1/1	0.95	0.11	55,55,55,55	0
56	MG	2a	1787	1/1	0.95	0.21	67,67,67,67	0
56	MG	1a	1662	1/1	0.95	0.10	61,61,61,61	0
56	MG	2A	3465	1/1	0.95	0.19	52,52,52,52	0
56	MG	2a	1790	1/1	0.95	0.10	72,72,72,72	0
56	MG	1A	3424	1/1	0.95	0.08	45,45,45,45	0
56	MG	1A	3487	1/1	0.95	0.08	41,41,41,41	0
56	MG	1a	1871	1/1	0.95	0.07	50,50,50,50	0
56	MG	1A	3426	1/1	0.95	0.16	56,56,56,56	0
56	MG	1B	204	1/1	0.95	0.20	59,59,59,59	0
56	MG	1A	3489	1/1	0.95	0.06	41,41,41,41	0
56	MG	1A	3040	1/1	0.95	0.12	34,34,34,34	0
56	MG	2a	1798	1/1	0.95	0.10	69,69,69,69	0
56	MG	2A	3178	1/1	0.95	0.19	52,52,52,52	0
56	MG	1B	208	1/1	0.95	0.04	30,30,30,30	0
56	MG	1A	3568	1/1	0.95	0.14	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3908	1/1	0.95	0.15	49,49,49,49	0
56	MG	1B	212	1/1	0.95	0.18	50,50,50,50	0
56	MG	2a	1805	1/1	0.95	0.11	52,52,52,52	0
56	MG	1A	3730	1/1	0.95	0.12	59,59,59,59	0
56	MG	2a	1807	1/1	0.95	0.09	46,46,46,46	0
56	MG	1a	1676	1/1	0.95	0.14	49,49,49,49	0
56	MG	1A	3910	1/1	0.95	0.09	37,37,37,37	0
56	MG	1A	3212	1/1	0.95	0.11	50,50,50,50	0
56	MG	1A	3324	1/1	0.95	0.07	62,62,62,62	0
56	MG	1A	3576	1/1	0.95	0.12	45,45,45,45	0
56	MG	2A	3190	1/1	0.95	0.21	44,44,44,44	0
56	MG	1a	1682	1/1	0.95	0.19	48,48,48,48	0
56	MG	1a	1892	1/1	0.95	0.09	49,49,49,49	0
56	MG	2A	3193	1/1	0.95	0.06	50,50,50,50	0
56	MG	2d	502	1/1	0.95	0.22	48,48,48,48	0
56	MG	1A	3738	1/1	0.95	0.06	46,46,46,46	0
56	MG	1a	1684	1/1	0.95	0.14	52,52,52,52	0
56	MG	1A	3916	1/1	0.95	0.19	49,49,49,49	0
56	MG	1A	3007	1/1	0.95	0.32	43,43,43,43	0
56	MG	2A	3200	1/1	0.95	0.07	41,41,41,41	0
56	MG	1A	3743	1/1	0.95	0.08	69,69,69,69	0
56	MG	1a	1898	1/1	0.95	0.09	47,47,47,47	0
56	MG	1D	301	1/1	0.95	0.08	31,31,31,31	0
56	MG	1A	3371	1/1	0.95	0.12	46,46,46,46	0
56	MG	1A	3921	1/1	0.95	0.08	52,52,52,52	0
56	MG	2A	3506	1/1	0.95	0.06	37,37,37,37	0
56	MG	2A	3508	1/1	0.95	0.09	45,45,45,45	0
56	MG	1a	1903	1/1	0.95	0.15	72,72,72,72	0
56	MG	1A	3214	1/1	0.95	0.14	63,63,63,63	0
56	MG	1A	3747	1/1	0.95	0.14	64,64,64,64	0
56	MG	1A	3497	1/1	0.95	0.16	36,36,36,36	0
56	MG	1A	3581	1/1	0.95	0.13	51,51,51,51	0
56	MG	2A	3213	1/1	0.95	0.07	53,53,53,53	0
56	MG	1A	3753	1/1	0.95	0.08	21,21,21,21	0
56	MG	2A	3303	1/1	0.96	0.05	30,30,30,30	0
56	MG	2D	303	1/1	0.96	0.10	46,46,46,46	0
56	MG	2A	3304	1/1	0.96	0.05	40,40,40,40	0
56	MG	1A	3254	1/1	0.96	0.14	29,29,29,29	0
56	MG	1A	3569	1/1	0.96	0.09	36,36,36,36	0
56	MG	1A	3491	1/1	0.96	0.07	45,45,45,45	0
56	MG	1A	3056	1/1	0.96	0.27	57,57,57,57	0
56	MG	1A	3572	1/1	0.96	0.08	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1a	1603	1/1	0.96	0.06	56,56,56,56	0
56	MG	1A	3573	1/1	0.96	0.12	38,38,38,38	0
56	MG	2F	303	1/1	0.96	0.12	50,50,50,50	0
56	MG	1A	3574	1/1	0.96	0.12	29,29,29,29	0
56	MG	2A	3069	1/1	0.96	0.22	52,52,52,52	0
56	MG	1A	3427	1/1	0.96	0.09	44,44,44,44	0
56	MG	2O	3002	1/1	0.96	0.04	36,36,36,36	0
56	MG	2A	3072	1/1	0.96	0.23	40,40,40,40	0
56	MG	1A	3197	1/1	0.96	0.12	44,44,44,44	0
56	MG	1A	3724	1/1	0.96	0.10	50,50,50,50	0
56	MG	2A	3320	1/1	0.96	0.18	46,46,46,46	0
56	MG	2W	201	1/1	0.96	0.06	42,42,42,42	0
56	MG	2A	3075	1/1	0.96	0.08	26,26,26,26	0
56	MG	1A	4042	1/1	0.96	0.17	32,32,32,32	0
56	MG	1A	4045	1/1	0.96	0.34	34,34,34,34	0
56	MG	1A	3200	1/1	0.96	0.15	28,28,28,28	0
56	MG	1A	3314	1/1	0.96	0.09	52,52,52,52	0
56	MG	1A	3259	1/1	0.96	0.14	52,52,52,52	0
56	MG	1A	3434	1/1	0.96	0.15	47,47,47,47	0
56	MG	1A	3016	1/1	0.96	0.17	41,41,41,41	0
56	MG	1A	3895	1/1	0.96	0.07	57,57,57,57	0
56	MG	2a	1604	1/1	0.96	0.27	47,47,47,47	0
56	MG	1A	4052	1/1	0.96	0.20	43,43,43,43	0
56	MG	1A	3261	1/1	0.96	0.11	43,43,43,43	0
56	MG	2A	3341	1/1	0.96	0.13	54,54,54,54	0
56	MG	1A	4058	1/1	0.96	0.10	56,56,56,56	0
56	MG	1A	3733	1/1	0.96	0.05	44,44,44,44	0
56	MG	1A	3074	1/1	0.96	0.19	34,34,34,34	0
56	MG	2A	3090	1/1	0.96	0.15	33,33,33,33	0
56	MG	1A	3207	1/1	0.96	0.20	47,47,47,47	0
56	MG	1A	3504	1/1	0.96	0.09	64,64,64,64	0
56	MG	1A	3208	1/1	0.96	0.20	51,51,51,51	0
56	MG	1a	1625	1/1	0.96	0.06	51,51,51,51	0
56	MG	1A	3597	1/1	0.96	0.15	36,36,36,36	0
56	MG	1a	1629	1/1	0.96	0.13	33,33,33,33	0
56	MG	1A	3209	1/1	0.96	0.07	45,45,45,45	0
56	MG	1A	3600	1/1	0.96	0.08	50,50,50,50	0
56	MG	2A	3358	1/1	0.96	0.11	47,47,47,47	0
56	MG	1A	4067	1/1	0.96	0.14	37,37,37,37	0
56	MG	1A	3601	1/1	0.96	0.06	24,24,24,24	0
56	MG	2a	1625	1/1	0.96	0.22	42,42,42,42	0
56	MG	1A	3602	1/1	0.96	0.05	46,46,46,46	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3751	1/1	0.96	0.06	20,20,20,20	0
56	MG	1a	1824	1/1	0.96	0.14	52,52,52,52	0
56	MG	1A	3752	1/1	0.96	0.16	25,25,25,25	0
56	MG	1A	3323	1/1	0.96	0.11	40,40,40,40	0
56	MG	1a	1827	1/1	0.96	0.10	55,55,55,55	0
56	MG	1A	3210	1/1	0.96	0.09	45,45,45,45	0
56	MG	1A	3509	1/1	0.96	0.23	43,43,43,43	0
56	MG	1A	3757	1/1	0.96	0.19	33,33,33,33	0
56	MG	1A	3609	1/1	0.96	0.07	26,26,26,26	0
56	MG	1A	3917	1/1	0.96	0.14	58,58,58,58	0
56	MG	2A	3372	1/1	0.96	0.10	58,58,58,58	0
56	MG	1A	3612	1/1	0.96	0.11	37,37,37,37	0
56	MG	1A	4085	1/1	0.96	0.06	46,46,46,46	0
56	MG	2A	3116	1/1	0.96	0.06	33,33,33,33	0
56	MG	1A	3443	1/1	0.96	0.14	50,50,50,50	0
56	MG	2A	3378	1/1	0.96	0.10	34,34,34,34	0
56	MG	1A	4093	1/1	0.96	0.27	39,39,39,39	0
56	MG	2A	3119	1/1	0.96	0.07	25,25,25,25	0
56	MG	1A	3379	1/1	0.96	0.11	41,41,41,41	0
56	MG	2A	3121	1/1	0.96	0.11	35,35,35,35	0
56	MG	2A	3386	1/1	0.96	0.12	68,68,68,68	0
56	MG	2a	1650	1/1	0.96	0.05	70,70,70,70	0
56	MG	1A	3616	1/1	0.96	0.08	32,32,32,32	0
56	MG	2a	1652	1/1	0.96	0.07	45,45,45,45	0
56	MG	1a	1651	1/1	0.96	0.06	52,52,52,52	0
56	MG	2A	3389	1/1	0.96	0.13	52,52,52,52	0
56	MG	1a	1846	1/1	0.96	0.12	55,55,55,55	0
56	MG	1A	3768	1/1	0.96	0.09	39,39,39,39	0
56	MG	1B	203	1/1	0.96	0.13	53,53,53,53	0
56	MG	1A	3512	1/1	0.96	0.28	34,34,34,34	0
56	MG	2a	1661	1/1	0.96	0.14	58,58,58,58	0
56	MG	1A	3770	1/1	0.96	0.09	26,26,26,26	0
56	MG	2a	1663	1/1	0.96	0.10	51,51,51,51	0
56	MG	1A	3926	1/1	0.96	0.09	52,52,52,52	0
56	MG	2a	1665	1/1	0.96	0.17	41,41,41,41	0
56	MG	1B	207	1/1	0.96	0.12	43,43,43,43	0
56	MG	1A	3211	1/1	0.96	0.08	43,43,43,43	0
56	MG	1A	3446	1/1	0.96	0.07	43,43,43,43	0
56	MG	1A	3929	1/1	0.96	0.17	47,47,47,47	0
56	MG	1B	211	1/1	0.96	0.04	46,46,46,46	0
56	MG	1A	3775	1/1	0.96	0.07	14,14,14,14	0
56	MG	2A	3405	1/1	0.96	0.07	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3931	1/1	0.96	0.07	42,42,42,42	0
56	MG	1A	3776	1/1	0.96	0.10	42,42,42,42	0
56	MG	1B	219	1/1	0.96	0.07	25,25,25,25	0
56	MG	1A	3326	1/1	0.96	0.06	62,62,62,62	0
56	MG	1a	1669	1/1	0.96	0.16	45,45,45,45	0
56	MG	1A	3516	1/1	0.96	0.06	54,54,54,54	0
56	MG	1A	3517	1/1	0.96	0.05	55,55,55,55	0
56	MG	1A	3075	1/1	0.96	0.24	57,57,57,57	0
56	MG	2A	3146	1/1	0.96	0.15	32,32,32,32	0
56	MG	1A	3111	1/1	0.96	0.12	35,35,35,35	0
56	MG	2A	3149	1/1	0.96	0.11	39,39,39,39	0
56	MG	1A	3165	1/1	0.96	0.09	35,35,35,35	0
56	MG	1A	3939	1/1	0.96	0.14	30,30,30,30	0
56	MG	1A	3168	1/1	0.96	0.10	38,38,38,38	0
56	MG	1A	3793	1/1	0.96	0.15	50,50,50,50	0
56	MG	2A	3156	1/1	0.96	0.14	28,28,28,28	0
56	MG	1A	3634	1/1	0.96	0.06	32,32,32,32	0
56	MG	1A	3169	1/1	0.96	0.27	48,48,48,48	0
56	MG	1a	1882	1/1	0.96	0.07	40,40,40,40	0
56	MG	2A	3160	1/1	0.96	0.12	52,52,52,52	0
56	MG	1A	3801	1/1	0.96	0.05	15,15,15,15	0
56	MG	1A	3636	1/1	0.96	0.09	35,35,35,35	0
56	MG	1D	308	1/1	0.96	0.14	16,16,16,16	0
56	MG	1D	309	1/1	0.96	0.07	31,31,31,31	0
56	MG	1A	3388	1/1	0.96	0.07	60,60,60,60	0
56	MG	1D	312	1/1	0.96	0.08	44,44,44,44	0
56	MG	2A	3434	1/1	0.96	0.09	49,49,49,49	0
56	MG	2A	3170	1/1	0.96	0.06	40,40,40,40	0
56	MG	2a	1707	1/1	0.96	0.05	58,58,58,58	0
56	MG	1A	3170	1/1	0.96	0.10	23,23,23,23	0
56	MG	1A	3135	1/1	0.96	0.20	36,36,36,36	0
56	MG	1a	1691	1/1	0.96	0.09	59,59,59,59	0
56	MG	1A	3815	1/1	0.96	0.05	52,52,52,52	0
56	MG	1A	3025	1/1	0.96	0.07	44,44,44,44	0
56	MG	1A	3043	1/1	0.96	0.07	36,36,36,36	0
56	MG	1F	301	1/1	0.96	0.16	36,36,36,36	0
56	MG	1A	3953	1/1	0.96	0.12	44,44,44,44	0
56	MG	2A	3180	1/1	0.96	0.24	34,34,34,34	0
56	MG	1F	304	1/1	0.96	0.20	19,19,19,19	0
56	MG	1F	305	1/1	0.96	0.09	48,48,48,48	0
56	MG	1A	3174	1/1	0.96	0.05	47,47,47,47	0
56	MG	1A	3138	1/1	0.96	0.09	32,32,32,32	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3230	1/1	0.96	0.13	28,28,28,28	0
56	MG	1A	3822	1/1	0.96	0.05	48,48,48,48	0
56	MG	1A	3961	1/1	0.96	0.07	54,54,54,54	0
56	MG	1A	3962	1/1	0.96	0.06	42,42,42,42	0
56	MG	1A	3396	1/1	0.96	0.13	39,39,39,39	0
56	MG	1a	1708	1/1	0.96	0.13	40,40,40,40	0
56	MG	2a	1727	1/1	0.96	0.09	45,45,45,45	0
56	MG	1d	503	1/1	0.96	0.09	56,56,56,56	0
56	MG	1A	3825	1/1	0.96	0.10	13,13,13,13	0
56	MG	1A	3966	1/1	0.96	0.09	56,56,56,56	0
56	MG	1a	1712	1/1	0.96	0.13	53,53,53,53	0
56	MG	1A	3139	1/1	0.96	0.14	21,21,21,21	0
56	MG	1a	1714	1/1	0.96	0.30	56,56,56,56	0
56	MG	1A	3651	1/1	0.96	0.07	23,23,23,23	0
56	MG	2A	3466	1/1	0.96	0.06	45,45,45,45	0
56	MG	2A	3467	1/1	0.96	0.09	39,39,39,39	0
56	MG	2A	3199	1/1	0.96	0.10	42,42,42,42	0
56	MG	2A	3469	1/1	0.96	0.10	60,60,60,60	0
56	MG	1A	3289	1/1	0.96	0.07	32,32,32,32	0
56	MG	1A	3290	1/1	0.96	0.06	55,55,55,55	0
56	MG	1A	3830	1/1	0.96	0.06	38,38,38,38	0
56	MG	1A	3656	1/1	0.96	0.14	46,46,46,46	0
56	MG	1a	1720	1/1	0.96	0.17	40,40,40,40	0
56	MG	1A	3975	1/1	0.96	0.12	50,50,50,50	0
56	MG	1P	203	1/1	0.96	0.14	52,52,52,52	0
56	MG	1a	1723	1/1	0.96	0.19	48,48,48,48	0
56	MG	1q	3304	1/1	0.96	0.11	47,47,47,47	0
56	MG	1a	1724	1/1	0.96	0.04	47,47,47,47	0
56	MG	1r	102	1/1	0.96	0.05	47,47,47,47	0
56	MG	1a	1725	1/1	0.96	0.19	59,59,59,59	0
56	MG	1a	1726	1/1	0.96	0.15	53,53,53,53	0
56	MG	1A	3539	1/1	0.96	0.08	56,56,56,56	0
56	MG	1A	3291	1/1	0.96	0.08	33,33,33,33	0
56	MG	1A	3541	1/1	0.96	0.12	44,44,44,44	0
56	MG	1A	3401	1/1	0.96	0.10	46,46,46,46	0
56	MG	1A	3053	1/1	0.96	0.24	41,41,41,41	0
56	MG	1A	3403	1/1	0.96	0.06	38,38,38,38	0
56	MG	1Q	3006	1/1	0.96	0.16	37,37,37,37	0
56	MG	1A	3674	1/1	0.96	0.10	37,37,37,37	0
56	MG	1A	3986	1/1	0.96	0.07	38,38,38,38	0
56	MG	1A	3404	1/1	0.96	0.05	38,38,38,38	0
56	MG	2a	1767	1/1	0.96	0.09	57,57,57,57	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3988	1/1	0.96	0.18	37,37,37,37	0
56	MG	1A	3546	1/1	0.96	0.10	62,62,62,62	0
56	MG	1A	3841	1/1	0.96	0.10	17,17,17,17	0
56	MG	1T	202	1/1	0.96	0.08	38,38,38,38	0
56	MG	2A	3500	1/1	0.96	0.21	53,53,53,53	0
56	MG	1A	3547	1/1	0.96	0.08	56,56,56,56	0
56	MG	1A	3405	1/1	0.96	0.11	36,36,36,36	0
56	MG	1A	3995	1/1	0.96	0.17	16,16,16,16	0
56	MG	2A	3237	1/1	0.96	0.07	46,46,46,46	0
56	MG	2A	3505	1/1	0.96	0.07	42,42,42,42	0
56	MG	1A	3681	1/1	0.96	0.08	43,43,43,43	0
56	MG	2A	3009	1/1	0.96	0.22	45,45,45,45	0
56	MG	2A	3011	1/1	0.96	0.26	50,50,50,50	0
56	MG	2A	3510	1/1	0.96	0.11	49,49,49,49	0
56	MG	2A	3511	1/1	0.96	0.20	45,45,45,45	0
56	MG	1A	3234	1/1	0.96	0.10	52,52,52,52	0
56	MG	2A	3013	1/1	0.96	0.13	52,52,52,52	0
56	MG	1A	3998	1/1	0.96	0.07	47,47,47,47	0
56	MG	1A	3118	1/1	0.96	0.06	33,33,33,33	0
56	MG	1A	3348	1/1	0.96	0.09	20,20,20,20	0
56	MG	2A	3517	1/1	0.96	0.05	36,36,36,36	0
56	MG	1A	3852	1/1	0.96	0.09	41,41,41,41	0
56	MG	1A	3853	1/1	0.96	0.08	44,44,44,44	0
56	MG	1W	3003	1/1	0.96	0.10	43,43,43,43	0
56	MG	1W	3004	1/1	0.96	0.14	34,34,34,34	0
56	MG	2A	3257	1/1	0.96	0.07	35,35,35,35	0
56	MG	2A	3022	1/1	0.96	0.05	42,42,42,42	0
56	MG	1W	3005	1/1	0.96	0.15	32,32,32,32	0
56	MG	1A	3183	1/1	0.96	0.24	43,43,43,43	0
56	MG	1A	3296	1/1	0.96	0.09	42,42,42,42	0
56	MG	1Z	301	1/1	0.96	0.07	44,44,44,44	0
56	MG	1A	3555	1/1	0.96	0.12	47,47,47,47	0
56	MG	1A	3080	1/1	0.96	0.11	38,38,38,38	0
56	MG	1A	3143	1/1	0.96	0.15	41,41,41,41	0
56	MG	1A	3697	1/1	0.96	0.05	23,23,23,23	0
56	MG	1A	3240	1/1	0.96	0.09	37,37,37,37	0
56	MG	2A	3535	1/1	0.96	0.05	51,51,51,51	0
56	MG	1A	3144	1/1	0.96	0.14	34,34,34,34	0
56	MG	1A	3864	1/1	0.96	0.10	53,53,53,53	0
56	MG	2a	1812	1/1	0.96	0.20	42,42,42,42	0
56	MG	1A	3102	1/1	0.96	0.08	51,51,51,51	0
56	MG	1A	3081	1/1	0.96	0.07	57,57,57,57	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2A	3038	1/1	0.96	0.21	46,46,46,46	0
56	MG	1A	4017	1/1	0.96	0.07	42,42,42,42	0
56	MG	1A	3304	1/1	0.96	0.07	72,72,72,72	0
56	MG	1A	3048	1/1	0.96	0.19	43,43,43,43	0
56	MG	1A	3154	1/1	0.96	0.18	34,34,34,34	0
56	MG	1A	4021	1/1	0.96	0.04	18,18,18,18	0
56	MG	2A	3283	1/1	0.96	0.09	57,57,57,57	0
56	MG	2f	3001	1/1	0.96	0.09	54,54,54,54	0
56	MG	2A	3046	1/1	0.96	0.11	38,38,38,38	0
56	MG	2A	3047	1/1	0.96	0.17	48,48,48,48	0
56	MG	2A	3552	1/1	0.96	0.07	47,47,47,47	0
56	MG	1A	3706	1/1	0.96	0.18	68,68,68,68	0
56	MG	16	101	1/1	0.96	0.10	42,42,42,42	0
56	MG	1A	4023	1/1	0.96	0.12	39,39,39,39	0
56	MG	1A	3071	1/1	0.96	0.06	41,41,41,41	0
56	MG	1A	4025	1/1	0.96	0.09	30,30,30,30	0
56	MG	1A	3709	1/1	0.96	0.09	15,15,15,15	0
56	MG	2B	3004	1/1	0.96	0.17	45,45,45,45	0
56	MG	17	105	1/1	0.96	0.10	44,44,44,44	0
56	MG	1A	3158	1/1	0.96	0.08	38,38,38,38	0
56	MG	1A	3711	1/1	0.96	0.16	63,63,63,63	0
56	MG	1A	3876	1/1	0.96	0.06	26,26,26,26	0
56	MG	1A	3309	1/1	0.96	0.06	48,48,48,48	0
56	MG	2A	3302	1/1	0.96	0.09	48,48,48,48	0
56	MG	1A	4070	1/1	0.97	0.05	25,25,25,25	0
56	MG	1A	3863	1/1	0.97	0.17	45,45,45,45	0
56	MG	1A	3960	1/1	0.97	0.11	47,47,47,47	0
56	MG	1A	3666	1/1	0.97	0.04	28,28,28,28	0
56	MG	2A	3052	1/1	0.97	0.11	37,37,37,37	0
56	MG	10	102	1/1	0.97	0.06	51,51,51,51	0
56	MG	1A	4075	1/1	0.97	0.08	36,36,36,36	0
56	MG	1A	3204	1/1	0.97	0.08	36,36,36,36	0
56	MG	1A	3669	1/1	0.97	0.05	17,17,17,17	0
56	MG	1A	3340	1/1	0.97	0.06	43,43,43,43	0
56	MG	1A	3760	1/1	0.97	0.11	36,36,36,36	0
56	MG	1a	1709	1/1	0.97	0.11	66,66,66,66	0
56	MG	1a	1848	1/1	0.97	0.12	45,45,45,45	0
56	MG	2a	1636	1/1	0.97	0.05	92,92,92,92	0
56	MG	1A	3113	1/1	0.97	0.09	27,27,27,27	0
56	MG	1A	3675	1/1	0.97	0.11	21,21,21,21	0
56	MG	1A	4083	1/1	0.97	0.09	34,34,34,34	0
56	MG	1A	3676	1/1	0.97	0.06	22,22,22,22	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3273	1/1	0.97	0.03	16,16,16,16	0
56	MG	1A	3599	1/1	0.97	0.10	47,47,47,47	0
56	MG	2A	3231	1/1	0.97	0.07	42,42,42,42	0
56	MG	1a	1858	1/1	0.97	0.11	35,35,35,35	0
56	MG	1A	4087	1/1	0.97	0.05	37,37,37,37	0
56	MG	2A	3235	1/1	0.97	0.26	54,54,54,54	0
56	MG	1A	4088	1/1	0.97	0.29	35,35,35,35	0
56	MG	1A	4089	1/1	0.97	0.14	34,34,34,34	0
56	MG	2A	3238	1/1	0.97	0.06	45,45,45,45	0
56	MG	2A	3071	1/1	0.97	0.11	42,42,42,42	0
56	MG	1A	4090	1/1	0.97	0.22	38,38,38,38	0
56	MG	1A	4091	1/1	0.97	0.06	45,45,45,45	0
56	MG	2a	1655	1/1	0.97	0.16	60,60,60,60	0
56	MG	1A	3206	1/1	0.97	0.07	37,37,37,37	0
56	MG	2A	3243	1/1	0.97	0.07	27,27,27,27	0
56	MG	2A	3244	1/1	0.97	0.09	55,55,55,55	0
56	MG	17	103	1/1	0.97	0.09	49,49,49,49	0
56	MG	1A	4094	1/1	0.97	0.11	27,27,27,27	0
56	MG	2A	3247	1/1	0.97	0.13	47,47,47,47	0
56	MG	1A	3875	1/1	0.97	0.04	19,19,19,19	0
56	MG	1a	1868	1/1	0.97	0.04	41,41,41,41	0
56	MG	1A	3157	1/1	0.97	0.06	40,40,40,40	0
56	MG	2A	3080	1/1	0.97	0.09	41,41,41,41	0
56	MG	2A	3456	1/1	0.97	0.06	31,31,31,31	0
56	MG	1A	3771	1/1	0.97	0.07	11,11,11,11	0
56	MG	1A	3276	1/1	0.97	0.16	37,37,37,37	0
56	MG	1A	3421	1/1	0.97	0.08	52,52,52,52	0
56	MG	18	104	1/1	0.97	0.09	41,41,41,41	0
56	MG	1a	1874	1/1	0.97	0.09	48,48,48,48	0
56	MG	1A	3605	1/1	0.97	0.06	42,42,42,42	0
56	MG	1A	3686	1/1	0.97	0.04	36,36,36,36	0
56	MG	2A	3263	1/1	0.97	0.16	41,41,41,41	0
56	MG	1A	3983	1/1	0.97	0.11	53,53,53,53	0
56	MG	1a	1733	1/1	0.97	0.08	41,41,41,41	0
56	MG	1A	3278	1/1	0.97	0.04	28,28,28,28	0
56	MG	1a	1881	1/1	0.97	0.08	40,40,40,40	0
56	MG	1A	3883	1/1	0.97	0.13	45,45,45,45	0
56	MG	2a	1682	1/1	0.97	0.17	48,48,48,48	0
56	MG	1A	3778	1/1	0.97	0.06	30,30,30,30	0
56	MG	2a	1685	1/1	0.97	0.13	53,53,53,53	0
56	MG	1A	3688	1/1	0.97	0.07	21,21,21,21	0
56	MG	2A	3271	1/1	0.97	0.11	42,42,42,42	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3989	1/1	0.97	0.12	38,38,38,38	0
56	MG	1A	3059	1/1	0.97	0.09	43,43,43,43	0
56	MG	1A	3781	1/1	0.97	0.06	19,19,19,19	0
56	MG	2A	3478	1/1	0.97	0.04	42,42,42,42	0
56	MG	1a	1741	1/1	0.97	0.27	58,58,58,58	0
56	MG	1A	3067	1/1	0.97	0.17	48,48,48,48	0
56	MG	1A	3993	1/1	0.97	0.19	30,30,30,30	0
56	MG	1A	3785	1/1	0.97	0.06	21,21,21,21	0
56	MG	2A	3279	1/1	0.97	0.04	55,55,55,55	0
56	MG	2A	3280	1/1	0.97	0.06	46,46,46,46	0
56	MG	1A	3787	1/1	0.97	0.11	33,33,33,33	0
56	MG	2a	1699	1/1	0.97	0.12	71,71,71,71	0
56	MG	1A	3611	1/1	0.97	0.11	31,31,31,31	0
56	MG	1A	3425	1/1	0.97	0.07	62,62,62,62	0
56	MG	1A	3281	1/1	0.97	0.09	53,53,53,53	0
56	MG	1A	3695	1/1	0.97	0.10	29,29,29,29	0
56	MG	1A	3794	1/1	0.97	0.05	57,57,57,57	0
56	MG	1a	1752	1/1	0.97	0.35	60,60,60,60	0
56	MG	2A	3288	1/1	0.97	0.05	35,35,35,35	0
56	MG	1D	302	1/1	0.97	0.12	63,63,63,63	0
56	MG	2A	3290	1/1	0.97	0.12	40,40,40,40	0
56	MG	2A	3111	1/1	0.97	0.12	36,36,36,36	0
56	MG	2A	3292	1/1	0.97	0.11	43,43,43,43	0
56	MG	2A	3294	1/1	0.97	0.08	41,41,41,41	0
56	MG	1A	3696	1/1	0.97	0.06	34,34,34,34	0
56	MG	1A	3243	1/1	0.97	0.15	51,51,51,51	0
56	MG	1A	3800	1/1	0.97	0.04	25,25,25,25	0
56	MG	1a	1906	1/1	0.97	0.06	75,75,75,75	0
56	MG	1a	1907	1/1	0.97	0.13	37,37,37,37	0
56	MG	1A	3429	1/1	0.97	0.07	45,45,45,45	0
56	MG	1A	3901	1/1	0.97	0.05	40,40,40,40	0
56	MG	1A	3618	1/1	0.97	0.06	39,39,39,39	0
56	MG	1A	3181	1/1	0.97	0.05	41,41,41,41	0
56	MG	1D	310	1/1	0.97	0.15	31,31,31,31	0
56	MG	1a	1762	1/1	0.97	0.07	59,59,59,59	0
56	MG	1A	3182	1/1	0.97	0.15	33,33,33,33	0
56	MG	1a	1627	1/1	0.97	0.04	36,36,36,36	0
56	MG	1A	3808	1/1	0.97	0.07	31,31,31,31	0
56	MG	1A	3809	1/1	0.97	0.05	43,43,43,43	0
56	MG	1E	301	1/1	0.97	0.08	14,14,14,14	0
56	MG	1A	4011	1/1	0.97	0.12	48,48,48,48	0
56	MG	1A	3810	1/1	0.97	0.04	43,43,43,43	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3036	1/1	0.97	0.06	41,41,41,41	0
56	MG	2a	1731	1/1	0.97	0.06	68,68,68,68	0
56	MG	1A	3813	1/1	0.97	0.06	37,37,37,37	0
56	MG	2A	3521	1/1	0.97	0.10	38,38,38,38	0
56	MG	2A	3316	1/1	0.97	0.10	33,33,33,33	0
56	MG	1n	502	1/1	0.97	0.05	55,55,55,55	0
56	MG	1A	4016	1/1	0.97	0.08	26,26,26,26	0
56	MG	1A	3814	1/1	0.97	0.11	35,35,35,35	0
56	MG	1a	1638	1/1	0.97	0.04	56,56,56,56	0
56	MG	1q	3302	1/1	0.97	0.18	53,53,53,53	0
56	MG	2A	3322	1/1	0.97	0.23	41,41,41,41	0
56	MG	1F	303	1/1	0.97	0.11	35,35,35,35	0
56	MG	2A	3324	1/1	0.97	0.09	24,24,24,24	0
56	MG	1A	3354	1/1	0.97	0.10	56,56,56,56	0
56	MG	1A	3120	1/1	0.97	0.07	28,28,28,28	0
56	MG	2A	3140	1/1	0.97	0.16	35,35,35,35	0
56	MG	2A	3328	1/1	0.97	0.08	47,47,47,47	0
56	MG	1A	3705	1/1	0.97	0.05	16,16,16,16	0
56	MG	1A	3088	1/1	0.97	0.09	47,47,47,47	0
56	MG	1A	3321	1/1	0.97	0.06	28,28,28,28	0
56	MG	1A	3708	1/1	0.97	0.06	46,46,46,46	0
56	MG	2A	3337	1/1	0.97	0.09	59,59,59,59	0
56	MG	2A	3145	1/1	0.97	0.16	33,33,33,33	0
56	MG	2a	1754	1/1	0.97	0.13	44,44,44,44	0
56	MG	1A	3252	1/1	0.97	0.07	29,29,29,29	0
56	MG	2A	3340	1/1	0.97	0.05	58,58,58,58	0
56	MG	2A	3147	1/1	0.97	0.09	33,33,33,33	0
56	MG	1A	3628	1/1	0.97	0.04	26,26,26,26	0
56	MG	1A	3629	1/1	0.97	0.08	40,40,40,40	0
56	MG	1A	3054	1/1	0.97	0.16	50,50,50,50	0
56	MG	1A	3631	1/1	0.97	0.11	43,43,43,43	0
56	MG	2A	3550	1/1	0.97	0.08	51,51,51,51	0
56	MG	2A	3152	1/1	0.97	0.13	30,30,30,30	0
56	MG	1A	3106	1/1	0.97	0.12	57,57,57,57	0
56	MG	2A	3553	1/1	0.97	0.12	42,42,42,42	0
56	MG	1a	1653	1/1	0.97	0.24	54,54,54,54	0
56	MG	1N	204	1/1	0.97	0.15	36,36,36,36	0
56	MG	2A	3557	1/1	0.97	0.06	52,52,52,52	0
56	MG	1A	3925	1/1	0.97	0.06	50,50,50,50	0
56	MG	1A	3633	1/1	0.97	0.06	21,21,21,21	0
56	MG	2a	1773	1/1	0.97	0.10	53,53,53,53	0
56	MG	2A	3355	1/1	0.97	0.07	22,22,22,22	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3166	1/1	0.97	0.14	29,29,29,29	0
56	MG	1A	3256	1/1	0.97	0.15	37,37,37,37	0
56	MG	1A	3190	1/1	0.97	0.09	55,55,55,55	0
56	MG	2a	1779	1/1	0.97	0.09	39,39,39,39	0
56	MG	2B	3006	1/1	0.97	0.13	40,40,40,40	0
56	MG	1A	3222	1/1	0.97	0.14	21,21,21,21	0
56	MG	2a	1782	1/1	0.97	0.17	46,46,46,46	0
56	MG	1A	3721	1/1	0.97	0.07	51,51,51,51	0
56	MG	1A	3224	1/1	0.97	0.07	37,37,37,37	0
56	MG	2A	3166	1/1	0.97	0.07	40,40,40,40	0
56	MG	1A	3640	1/1	0.97	0.10	42,42,42,42	0
56	MG	2A	3168	1/1	0.97	0.11	43,43,43,43	0
56	MG	1A	3530	1/1	0.97	0.04	41,41,41,41	0
56	MG	1Q	3001	1/1	0.97	0.16	31,31,31,31	0
56	MG	1A	3330	1/1	0.97	0.10	56,56,56,56	0
56	MG	1A	3575	1/1	0.97	0.06	62,62,62,62	0
56	MG	1A	4044	1/1	0.97	0.06	27,27,27,27	0
56	MG	2A	3174	1/1	0.97	0.15	32,32,32,32	0
56	MG	1A	3008	1/1	0.97	0.07	53,53,53,53	0
56	MG	1A	3645	1/1	0.97	0.10	44,44,44,44	0
56	MG	1A	3842	1/1	0.97	0.06	47,47,47,47	0
56	MG	2F	302	1/1	0.97	0.07	36,36,36,36	0
56	MG	2A	3374	1/1	0.97	0.07	41,41,41,41	0
56	MG	1A	3051	1/1	0.97	0.09	47,47,47,47	0
56	MG	1a	1674	1/1	0.97	0.16	46,46,46,46	0
56	MG	2A	3020	1/1	0.97	0.15	44,44,44,44	0
56	MG	1A	3057	1/1	0.97	0.12	49,49,49,49	0
56	MG	1A	3648	1/1	0.97	0.07	24,24,24,24	0
56	MG	1A	3094	1/1	0.97	0.04	42,42,42,42	0
56	MG	2Q	3003	1/1	0.97	0.06	37,37,37,37	0
56	MG	1A	3038	1/1	0.97	0.13	51,51,51,51	0
56	MG	2Q	3005	1/1	0.97	0.06	46,46,46,46	0
56	MG	2U	201	1/1	0.97	0.06	30,30,30,30	0
56	MG	1A	4053	1/1	0.97	0.08	29,29,29,29	0
56	MG	2A	3385	1/1	0.97	0.05	42,42,42,42	0
56	MG	1A	3945	1/1	0.97	0.20	36,36,36,36	0
56	MG	1A	3537	1/1	0.97	0.07	43,43,43,43	0
56	MG	1A	3097	1/1	0.97	0.06	55,55,55,55	0
56	MG	1U	201	1/1	0.97	0.05	33,33,33,33	0
56	MG	1a	1685	1/1	0.97	0.07	37,37,37,37	0
56	MG	1A	3654	1/1	0.97	0.06	20,20,20,20	0
56	MG	1A	3132	1/1	0.97	0.07	39,39,39,39	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3746	1/1	0.97	0.06	38,38,38,38	0
56	MG	2A	3034	1/1	0.97	0.10	44,44,44,44	0
56	MG	2A	3195	1/1	0.97	0.17	38,38,38,38	0
56	MG	1A	3587	1/1	0.97	0.06	38,38,38,38	0
56	MG	2A	3398	1/1	0.97	0.10	45,45,45,45	0
56	MG	2A	3399	1/1	0.97	0.04	58,58,58,58	0
56	MG	1V	201	1/1	0.97	0.19	39,39,39,39	0
56	MG	2A	3037	1/1	0.97	0.15	44,44,44,44	0
56	MG	1A	3374	1/1	0.97	0.07	48,48,48,48	0
56	MG	1A	3176	1/1	0.97	0.06	38,38,38,38	0
56	MG	1A	3660	1/1	0.97	0.06	30,30,30,30	0
56	MG	2A	3041	1/1	0.97	0.08	28,28,28,28	0
56	MG	1A	3591	1/1	0.97	0.11	52,52,52,52	0
56	MG	1A	4068	1/1	0.97	0.08	36,36,36,36	0
56	MG	2A	3044	1/1	0.97	0.12	32,32,32,32	0
56	MG	2A	3206	1/1	0.97	0.23	55,55,55,55	0
56	MG	1a	1831	1/1	0.97	0.12	32,32,32,32	0
56	MG	2A	3208	1/1	0.97	0.10	43,43,43,43	0
56	MG	1A	3593	1/1	0.97	0.06	38,38,38,38	0
56	MG	2a	1622	1/1	0.97	0.06	53,53,53,53	0
56	MG	1A	3663	1/1	0.98	0.06	20,20,20,20	0
56	MG	1U	203	1/1	0.98	0.06	42,42,42,42	0
56	MG	1A	3045	1/1	0.98	0.23	42,42,42,42	0
56	MG	1A	3227	1/1	0.98	0.07	27,27,27,27	0
56	MG	1A	3004	1/1	0.98	0.07	49,49,49,49	0
56	MG	1a	1656	1/1	0.98	0.04	56,56,56,56	0
56	MG	1A	3803	1/1	0.98	0.09	53,53,53,53	0
56	MG	2A	3155	1/1	0.98	0.12	33,33,33,33	0
56	MG	1A	3202	1/1	0.98	0.15	33,33,33,33	0
56	MG	1A	3615	1/1	0.98	0.04	16,16,16,16	0
56	MG	2A	3556	1/1	0.98	0.19	40,40,40,40	0
56	MG	1A	3806	1/1	0.98	0.04	65,65,65,65	0
56	MG	2A	3558	1/1	0.98	0.06	40,40,40,40	0
56	MG	1A	3672	1/1	0.98	0.05	17,17,17,17	0
56	MG	1A	3673	1/1	0.98	0.08	32,32,32,32	0
56	MG	2A	3161	1/1	0.98	0.05	37,37,37,37	0
56	MG	1A	3203	1/1	0.98	0.05	19,19,19,19	0
56	MG	1B	215	1/1	0.98	0.04	36,36,36,36	0
56	MG	2A	3423	1/1	0.98	0.06	65,65,65,65	0
56	MG	1B	216	1/1	0.98	0.07	33,33,33,33	0
56	MG	2A	3425	1/1	0.98	0.09	46,46,46,46	0
56	MG	1B	217	1/1	0.98	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
56	MG	1A	3299	1/1	0.98	0.12	16,16,16,16	0
56	MG	1a	1879	1/1	0.98	0.05	43,43,43,43	0
56	MG	1A	3734	1/1	0.98	0.04	45,45,45,45	0
56	MG	2A	3293	1/1	0.98	0.13	36,36,36,36	0
56	MG	1A	3736	1/1	0.98	0.08	34,34,34,34	0
56	MG	1A	3084	1/1	0.98	0.17	32,32,32,32	0
56	MG	1B	223	1/1	0.98	0.17	48,48,48,48	0
56	MG	1A	3620	1/1	0.98	0.08	7,7,7,7	0
56	MG	1A	3085	1/1	0.98	0.06	28,28,28,28	0
56	MG	2A	3436	1/1	0.98	0.09	32,32,32,32	0
56	MG	1A	3957	1/1	0.98	0.05	20,20,20,20	0
56	MG	1A	3098	1/1	0.98	0.07	44,44,44,44	0
56	MG	1A	3525	1/1	0.98	0.11	54,54,54,54	0
56	MG	1A	3526	1/1	0.98	0.28	41,41,41,41	0
56	MG	1A	3116	1/1	0.98	0.06	21,21,21,21	0
56	MG	1A	3892	1/1	0.98	0.12	44,44,44,44	0
56	MG	1A	3683	1/1	0.98	0.15	48,48,48,48	0
56	MG	1a	1681	1/1	0.98	0.11	52,52,52,52	0
56	MG	1A	4041	1/1	0.98	0.10	12,12,12,12	0
56	MG	1A	3268	1/1	0.98	0.08	51,51,51,51	0
56	MG	1A	4043	1/1	0.98	0.03	24,24,24,24	0
56	MG	16	104	1/1	0.98	0.04	43,43,43,43	0
56	MG	1a	1899	1/1	0.98	0.05	43,43,43,43	0
56	MG	2a	1735	1/1	0.98	0.07	51,51,51,51	0
56	MG	1A	3269	1/1	0.98	0.10	17,17,17,17	0
56	MG	1A	3968	1/1	0.98	0.07	21,21,21,21	0
56	MG	1A	3969	1/1	0.98	0.04	40,40,40,40	0
56	MG	1A	3117	1/1	0.98	0.09	29,29,29,29	0
56	MG	2A	3454	1/1	0.98	0.08	61,61,61,61	0
56	MG	1A	3237	1/1	0.98	0.09	27,27,27,27	0
56	MG	1a	1905	1/1	0.98	0.06	52,52,52,52	0
56	MG	1A	3091	1/1	0.98	0.11	46,46,46,46	0
56	MG	1E	304	1/1	0.98	0.03	44,44,44,44	0
56	MG	1A	3145	1/1	0.98	0.09	29,29,29,29	0
56	MG	1A	3691	1/1	0.98	0.06	8,8,8,8	0
56	MG	1A	3146	1/1	0.98	0.05	39,39,39,39	0
56	MG	1A	3976	1/1	0.98	0.14	46,46,46,46	0
56	MG	1A	4054	1/1	0.98	0.06	40,40,40,40	0
56	MG	1A	3241	1/1	0.98	0.19	30,30,30,30	0
56	MG	1A	4056	1/1	0.98	0.09	30,30,30,30	0
56	MG	1A	4057	1/1	0.98	0.14	40,40,40,40	0
56	MG	1A	3759	1/1	0.98	0.09	41,41,41,41	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2A	3330	1/1	0.98	0.07	37,37,37,37	0
56	MG	1A	3277	1/1	0.98	0.08	33,33,33,33	0
56	MG	2a	1756	1/1	0.98	0.13	47,47,47,47	0
56	MG	1h	3002	1/1	0.98	0.05	63,63,63,63	0
56	MG	1A	3147	1/1	0.98	0.07	33,33,33,33	0
56	MG	1a	1704	1/1	0.98	0.08	40,40,40,40	0
56	MG	1A	3119	1/1	0.98	0.04	31,31,31,31	0
56	MG	2a	1615	1/1	0.98	0.06	56,56,56,56	0
56	MG	1a	1706	1/1	0.98	0.07	53,53,53,53	0
56	MG	1a	1808	1/1	0.98	0.07	57,57,57,57	0
56	MG	1A	3907	1/1	0.98	0.08	15,15,15,15	0
56	MG	1A	3763	1/1	0.98	0.04	41,41,41,41	0
56	MG	1H	201	1/1	0.98	0.16	49,49,49,49	0
56	MG	1A	3984	1/1	0.98	0.09	51,51,51,51	0
56	MG	1A	3637	1/1	0.98	0.10	31,31,31,31	0
56	MG	1A	3244	1/1	0.98	0.07	14,14,14,14	0
56	MG	2A	3484	1/1	0.98	0.07	53,53,53,53	0
56	MG	2A	3100	1/1	0.98	0.10	38,38,38,38	0
56	MG	1A	3583	1/1	0.98	0.15	47,47,47,47	0
56	MG	1A	3386	1/1	0.98	0.06	34,34,34,34	0
56	MG	2a	1775	1/1	0.98	0.17	42,42,42,42	0
56	MG	1A	3499	1/1	0.98	0.07	42,42,42,42	0
56	MG	1A	3101	1/1	0.98	0.11	46,46,46,46	0
56	MG	1A	4071	1/1	0.98	0.06	40,40,40,40	0
56	MG	1N	207	1/1	0.98	0.03	19,19,19,19	0
56	MG	1N	208	1/1	0.98	0.04	47,47,47,47	0
56	MG	1x	102	1/1	0.98	0.14	42,42,42,42	0
56	MG	1A	3915	1/1	0.98	0.04	13,13,13,13	0
56	MG	1A	3246	1/1	0.98	0.06	23,23,23,23	0
56	MG	1A	3121	1/1	0.98	0.06	30,30,30,30	0
56	MG	2A	3230	1/1	0.98	0.10	45,45,45,45	0
56	MG	1A	3592	1/1	0.98	0.10	35,35,35,35	0
56	MG	1P	202	1/1	0.98	0.05	41,41,41,41	0
56	MG	1A	3850	1/1	0.98	0.16	43,43,43,43	0
56	MG	2a	1641	1/1	0.98	0.03	64,64,64,64	0
56	MG	2A	3234	1/1	0.98	0.20	55,55,55,55	0
56	MG	1A	3152	1/1	0.98	0.12	29,29,29,29	0
56	MG	1a	1829	1/1	0.98	0.14	37,37,37,37	0
56	MG	1A	3153	1/1	0.98	0.11	36,36,36,36	0
56	MG	1a	1628	1/1	0.98	0.06	35,35,35,35	0
56	MG	1A	3428	1/1	0.98	0.09	36,36,36,36	0
56	MG	2A	3507	1/1	0.98	0.06	63,63,63,63	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1a	1833	1/1	0.98	0.04	51,51,51,51	0
56	MG	1A	3548	1/1	0.98	0.04	44,44,44,44	0
56	MG	1a	1835	1/1	0.98	0.06	54,54,54,54	0
56	MG	1A	3218	1/1	0.98	0.22	28,28,28,28	0
56	MG	1A	3467	1/1	0.98	0.06	50,50,50,50	0
56	MG	2a	1654	1/1	0.98	0.05	49,49,49,49	0
56	MG	2a	1803	1/1	0.98	0.05	60,60,60,60	0
56	MG	1A	3030	1/1	0.98	0.06	38,38,38,38	0
56	MG	2A	3010	1/1	0.98	0.08	46,46,46,46	0
56	MG	1Q	3005	1/1	0.98	0.06	38,38,38,38	0
56	MG	2A	3248	1/1	0.98	0.15	45,45,45,45	0
56	MG	1a	1841	1/1	0.98	0.07	37,37,37,37	0
56	MG	1A	3783	1/1	0.98	0.07	22,22,22,22	0
56	MG	2A	3519	1/1	0.98	0.08	44,44,44,44	0
56	MG	2A	3383	1/1	0.98	0.09	49,49,49,49	0
56	MG	2A	3384	1/1	0.98	0.05	33,33,33,33	0
56	MG	2A	3251	1/1	0.98	0.12	40,40,40,40	0
56	MG	1A	3653	1/1	0.98	0.09	25,25,25,25	0
56	MG	1A	3786	1/1	0.98	0.06	31,31,31,31	0
56	MG	1A	3469	1/1	0.98	0.04	16,16,16,16	0
56	MG	1R	203	1/1	0.98	0.06	24,24,24,24	0
56	MG	2A	3256	1/1	0.98	0.06	36,36,36,36	0
56	MG	1R	204	1/1	0.98	0.10	58,58,58,58	0
56	MG	2A	3392	1/1	0.98	0.07	24,24,24,24	0
56	MG	1A	3862	1/1	0.98	0.04	45,45,45,45	0
56	MG	1A	3788	1/1	0.98	0.07	27,27,27,27	0
56	MG	1A	3220	1/1	0.98	0.07	30,30,30,30	0
56	MG	1A	3221	1/1	0.98	0.04	36,36,36,36	0
56	MG	2A	3262	1/1	0.98	0.10	35,35,35,35	0
56	MG	2a	1677	1/1	0.98	0.07	55,55,55,55	0
56	MG	1a	1853	1/1	0.98	0.04	31,31,31,31	0
56	MG	1a	1854	1/1	0.98	0.09	41,41,41,41	0
56	MG	2a	1680	1/1	0.98	0.07	49,49,49,49	0
56	MG	1A	3791	1/1	0.98	0.08	19,19,19,19	0
56	MG	1a	1746	1/1	0.98	0.09	54,54,54,54	0
56	MG	2a	1683	1/1	0.98	0.07	43,43,43,43	0
56	MG	1A	3175	1/1	0.98	0.15	21,21,21,21	0
56	MG	1A	3223	1/1	0.98	0.06	24,24,24,24	0
56	MG	1A	3155	1/1	0.98	0.15	27,27,27,27	0
56	MG	2A	3543	1/1	0.98	0.04	47,47,47,47	0
56	MG	1A	3199	1/1	0.98	0.12	36,36,36,36	0
57	ZN	1n	501	1/1	0.98	0.04	84,84,84,84	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1a	1650	1/1	0.98	0.06	42,42,42,42	0
57	ZN	26	501	1/1	0.98	0.04	62,62,62,62	0
57	ZN	2n	501	1/1	0.98	0.06	93,93,93,93	0
58	SF4	1d	501	8/8	0.98	0.05	56,73,76,77	0
58	SF4	2d	501	8/8	0.98	0.04	56,71,81,82	0
56	MG	1A	3797	1/1	0.99	0.07	15,15,15,15	0
56	MG	1A	3798	1/1	0.99	0.07	23,23,23,23	0
56	MG	1A	3843	1/1	0.99	0.04	29,29,29,29	0
56	MG	1A	3799	1/1	0.99	0.06	39,39,39,39	0
56	MG	1A	3161	1/1	0.99	0.13	27,27,27,27	0
56	MG	1A	3100	1/1	0.99	0.05	34,34,34,34	0
56	MG	1A	3191	1/1	0.99	0.08	37,37,37,37	0
56	MG	1A	3726	1/1	0.99	0.04	23,23,23,23	0
56	MG	1A	3671	1/1	0.99	0.03	16,16,16,16	0
56	MG	1A	4082	1/1	0.99	0.04	44,44,44,44	0
56	MG	1A	3603	1/1	0.99	0.07	45,45,45,45	0
56	MG	1A	3765	1/1	0.99	0.03	36,36,36,36	0
56	MG	1A	3807	1/1	0.99	0.04	47,47,47,47	0
56	MG	1A	3766	1/1	0.99	0.07	43,43,43,43	0
56	MG	1E	302	1/1	0.99	0.04	55,55,55,55	0
56	MG	1E	303	1/1	0.99	0.06	14,14,14,14	0
56	MG	1A	3584	1/1	0.99	0.05	33,33,33,33	0
56	MG	1A	3585	1/1	0.99	0.05	20,20,20,20	0
56	MG	1A	3811	1/1	0.99	0.06	34,34,34,34	0
56	MG	1A	3076	1/1	0.99	0.09	40,40,40,40	0
56	MG	1A	3270	1/1	0.99	0.16	41,41,41,41	0
56	MG	2A	3462	1/1	0.99	0.05	44,44,44,44	0
56	MG	2A	3333	1/1	0.99	0.05	45,45,45,45	0
56	MG	1A	4092	1/1	0.99	0.22	33,33,33,33	0
56	MG	2A	3336	1/1	0.99	0.05	38,38,38,38	0
56	MG	1A	3001	1/1	0.99	0.15	30,30,30,30	0
56	MG	1A	3735	1/1	0.99	0.05	32,32,32,32	0
56	MG	1A	4095	1/1	0.99	0.06	32,32,32,32	0
56	MG	2A	3049	1/1	0.99	0.07	35,35,35,35	0
56	MG	1A	3610	1/1	0.99	0.09	27,27,27,27	0
56	MG	2A	3537	1/1	0.99	0.02	45,45,45,45	0
56	MG	2A	3471	1/1	0.99	0.05	40,40,40,40	0
56	MG	2A	3222	1/1	0.99	0.05	34,34,34,34	0
56	MG	1A	3096	1/1	0.99	0.04	46,46,46,46	0
56	MG	2A	3344	1/1	0.99	0.04	43,43,43,43	0
56	MG	1a	1884	1/1	0.99	0.09	44,44,44,44	0
56	MG	1A	3818	1/1	0.99	0.06	19,19,19,19	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3231	1/1	0.99	0.07	42,42,42,42	0
56	MG	1A	3739	1/1	0.99	0.05	16,16,16,16	0
56	MG	2A	3349	1/1	0.99	0.03	63,63,63,63	0
56	MG	2A	3350	1/1	0.99	0.05	55,55,55,55	0
56	MG	1A	3740	1/1	0.99	0.08	23,23,23,23	0
56	MG	1A	3151	1/1	0.99	0.20	26,26,26,26	0
56	MG	1A	3185	1/1	0.99	0.16	29,29,29,29	0
56	MG	1A	3824	1/1	0.99	0.06	19,19,19,19	0
56	MG	1A	3167	1/1	0.99	0.06	35,35,35,35	0
56	MG	1A	3963	1/1	0.99	0.02	33,33,33,33	0
56	MG	1a	1838	1/1	0.99	0.02	34,34,34,34	0
56	MG	1A	3684	1/1	0.99	0.07	21,21,21,21	0
56	MG	1A	3658	1/1	0.99	0.05	36,36,36,36	0
56	MG	1A	3784	1/1	0.99	0.05	27,27,27,27	0
56	MG	1A	3595	1/1	0.99	0.07	27,27,27,27	0
56	MG	1A	3617	1/1	0.99	0.09	38,38,38,38	0
56	MG	2a	1761	1/1	0.99	0.03	45,45,45,45	0
56	MG	1A	4015	1/1	0.99	0.03	29,29,29,29	0
56	MG	1A	3749	1/1	0.99	0.04	48,48,48,48	0
56	MG	1B	218	1/1	0.99	0.05	43,43,43,43	0
56	MG	1A	3661	1/1	0.99	0.03	16,16,16,16	0
56	MG	1A	3248	1/1	0.99	0.08	42,42,42,42	0
56	MG	1A	3198	1/1	0.99	0.07	46,46,46,46	0
56	MG	1A	3718	1/1	0.99	0.02	8,8,8,8	0
56	MG	2A	3305	1/1	0.99	0.06	41,41,41,41	0
57	ZN	1Y	202	1/1	0.99	0.05	65,65,65,65	0
57	ZN	14	501	1/1	0.99	0.02	75,75,75,75	0
57	ZN	15	101	1/1	0.99	0.04	48,48,48,48	0
57	ZN	16	102	1/1	0.99	0.10	57,57,57,57	0
56	MG	1A	3133	1/1	0.99	0.06	28,28,28,28	0
57	ZN	2Y	202	1/1	0.99	0.03	80,80,80,80	0
56	MG	1a	1852	1/1	0.99	0.05	51,51,51,51	0
57	ZN	25	501	1/1	0.99	0.04	47,47,47,47	0
56	MG	1A	3755	1/1	0.99	0.06	51,51,51,51	0
57	ZN	29	501	1/1	0.99	0.03	58,58,58,58	0
56	MG	1A	3665	1/1	0.99	0.05	40,40,40,40	0
56	MG	1A	3128	1/1	0.99	0.09	27,27,27,27	0
56	MG	1A	3667	1/1	0.99	0.12	19,19,19,19	0
56	MG	1A	3728	1/1	1.00	0.01	17,17,17,17	0
56	MG	1A	3773	1/1	1.00	0.02	49,49,49,49	0
56	MG	1A	3958	1/1	1.00	0.05	18,18,18,18	0
56	MG	1A	3741	1/1	1.00	0.06	13,13,13,13	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3589	1/1	1.00	0.06	31,31,31,31	0
56	MG	2A	3335	1/1	1.00	0.02	38,38,38,38	0
56	MG	1A	3846	1/1	1.00	0.06	21,21,21,21	0
56	MG	1A	3607	1/1	1.00	0.05	27,27,27,27	0
57	ZN	19	102	1/1	1.00	0.04	46,46,46,46	0

6.5 Other polymers [i](#)

There are no such residues in this entry.