



Full wwPDB EM Validation Report ⓘ

Jun 23, 2026 – 10:48 AM JST

PDB ID : 6LSS / pdb_00006lss
EMDB ID : EMD-0964
Title : Cryo-EM structure of a pre-60S ribosomal subunit - state preA
Authors : Liang, X.; Zuo, M.; Zhang, Y.; Li, N.; Ma, C.; Dong, M.; Gao, N.
Deposited on : 2020-01-20
Resolution : 3.23 Å(reported)

This is a Full wwPDB EM 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/EMValidationReportHelp>

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:

EMDB validation analysis : 0.0.1.dev132
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

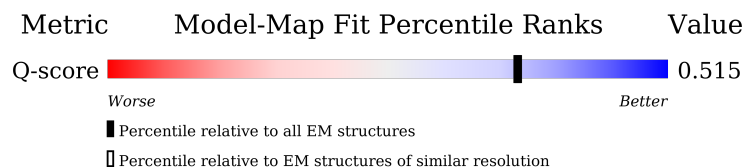
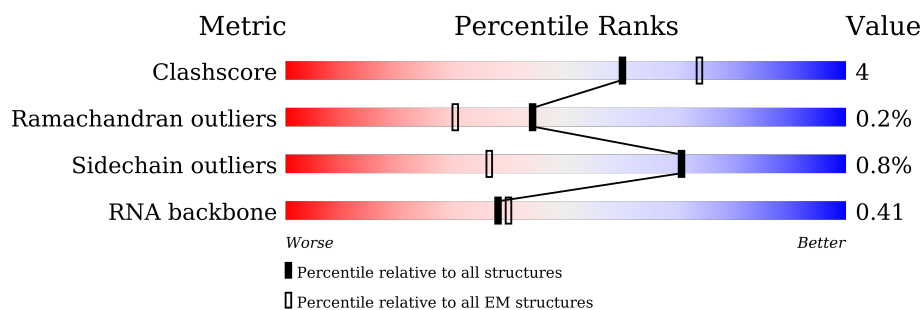
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.23 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.



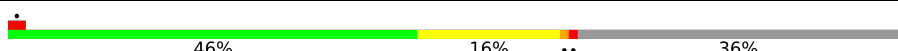
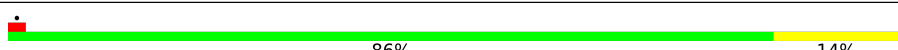
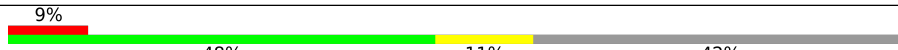
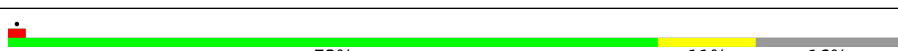
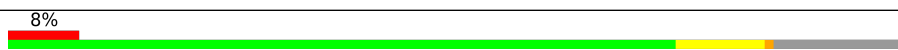
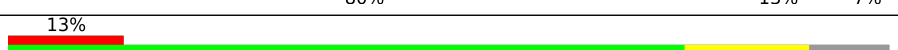
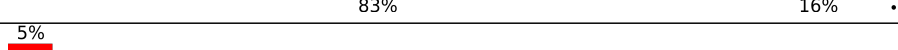
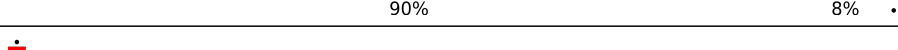
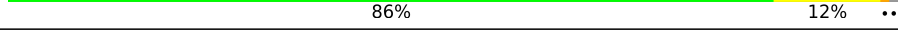
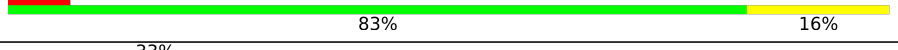
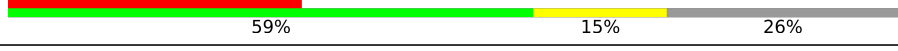
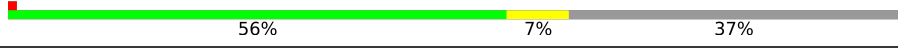
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14612 (2.73 - 3.73)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the 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 EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	1	731	 97%
2	2	5070	 6% 43% 21% 31%
3	4	634	 20% 82% 16%

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Mol	Chain	Length	Quality of chain
4	5	120	
5	6	245	
6	7	163	
7	8	156	
8	9	134	
9	B	403	
10	C	159	
11	D	427	
12	E	115	
13	F	117	
14	G	266	
15	H	123	
16	I	192	
17	K	105	
18	L	148	
19	M	97	
20	N	178	
21	O	70	
22	P	51	
23	Q	211	
24	R	203	
25	S	215	
26	U	204	
27	V	203	
28	W	106	

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Mol	Chain	Length	Quality of chain
29	X	92	
30	Y	184	
31	Z	188	
32	a	196	
33	b	176	
34	c	160	
35	d	128	
36	e	140	
37	g	156	
38	h	145	
39	i	136	
40	j	125	
41	k	135	
42	l	137	
43	m	257	
44	n	110	
45	o	288	
46	p	248	
47	r	297	
48	z	129	

2 Entry composition

There are 50 unique types of molecules in this entry. The entry contains 140545 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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 protein called Nucleolar GTP-binding protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	19	Total	C	N	O	S	0	0
			148	88	23	35	2		

- Molecule 2 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	3474	Total	C	N	O	P	0	0
			74611	33280	13653	24205	3473		

- Molecule 3 is a protein called Nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	4	620	Total	C	N	O	S	0	0
			5093	3198	935	933	27		

- Molecule 4 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	5	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		

- Molecule 5 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	6	244	Total	C	N	O	S	0	0
			1852	1149	318	372	13		

- Molecule 6 is a protein called Probable ribosome biogenesis protein RLP24.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	7	135	Total	C	N	O	S	0	0
			1159	737	225	187	10		

- Molecule 7 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	8	156	Total	C	N	O	P	0	0
			3315	1481	585	1094	155		

- Molecule 8 is a protein called Zinc finger protein 593.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	9	86	Total	C	N	O	S	0	0
			711	433	154	121	3		

- Molecule 9 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	B	402	Total	C	N	O	S	1	0
			3244	2065	609	556	14		

- Molecule 10 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	C	93	Total	C	N	O	S	0	0
			764	476	167	117	4		

- Molecule 11 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	D	358	Total	C	N	O	S	0	0
			2853	1797	570	473	13		

- Molecule 12 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	E	98	Total	C	N	O	S	0	0
			764	485	135	138	6		

- Molecule 13 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	F	109	Total	C	N	O	S	0	0
			868	544	179	139	6		

- Molecule 14 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	G	241	Total	C	N	O	S	1	0
			1935	1233	374	324	4		

- Molecule 15 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	H	122	Total	C	N	O	S	0	0
			1015	641	205	168	1		

- Molecule 16 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	I	190	Total	C	N	O	S	0	0
			1518	956	284	272	6		

- Molecule 17 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	K	102	Total	C	N	O	S	0	0
			832	521	177	129	5		

- Molecule 18 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	L	147	Total	C	N	O	S	0	0
			1162	736	237	186	3		

- Molecule 19 is a protein called 60S ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	M	86	Total	C	N	O	S	0	0
			705	434	155	111	5		

- Molecule 20 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	N	165	Total	C	N	O	S	0	0
			1319	836	245	233	5		

- Molecule 21 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	O	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

- Molecule 22 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	P	50	Total	C	N	O	S	0	0
			444	281	98	64	1		

- Molecule 23 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	Q	210	Total	C	N	O	S	0	0
			1701	1064	352	281	4		

- Molecule 24 is a protein called Translation machinery-associated protein 16.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	R	150	Total	C	N	O	S	0	0
			1272	793	244	230	5		

- Molecule 25 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	S	135	Total	C	N	O	S	0	0
			1111	713	213	178	7		

- Molecule 26 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	U	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		

- Molecule 27 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	V	201	Total	C	N	O	S	0	0
			1650	1063	321	261	5		

- Molecule 28 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	W	101	Total	C	N	O	S	0	0
			827	517	170	134	6		

- Molecule 29 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	X	91	Total	C	N	O	S	0	0
			708	445	136	120	7		

- Molecule 30 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Y	153	Total	C	N	O	S	0	0
			1242	776	241	216	9		

- Molecule 31 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Z	187	Total	C	N	O	S	0	0
			1513	944	314	250	5		

- Molecule 32 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	a	148	Total	C	N	O	S	0	0
			1239	772	266	192	9		

- Molecule 33 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	b	176	Total	C	N	O	S	0	0
			1461	930	284	236	11		

- Molecule 34 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	c	155	Total	C	N	O	S	0	0
			1264	801	248	210	5		

- Molecule 35 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	d	101	Total	C	N	O	S	0	0
			825	529	144	150	2		

- Molecule 36 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	e	131	Total	C	N	O	S	0	0
			979	618	184	172	5		

- Molecule 37 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	g	118	Total	C	N	O	S	0	0
			967	618	181	167	1		

- Molecule 38 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	h	134	Total	C	N	O	S	0	0
			1115	700	226	186	3		

- Molecule 39 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	i	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 40 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	j	107	Total	C	N	O	S	0	0
			888	560	171	155	2		

- Molecule 41 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	k	128	Total	C	N	O	S	0	0
			1053	667	216	165	5		

- Molecule 42 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	l	125	Total	C	N	O	S	0	0
			1002	622	207	168	5		

- Molecule 43 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	m	248	Total	C	N	O	S	0	0
			1898	1189	389	314	6		

- Molecule 44 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	n	109	Total	C	N	O	S	0	0
			876	555	174	144	3		

- Molecule 45 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	o	235	Total	C	N	O	S	0	0
			1897	1217	360	316	4		

- Molecule 46 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	p	225	Total	C	N	O	S	1	0
			1878	1207	361	301	9		

- Molecule 47 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	r	293	Total	C	N	O	S	0	0
			2382	1507	434	427	14		

- Molecule 48 is a protein called Protein LLP homolog.

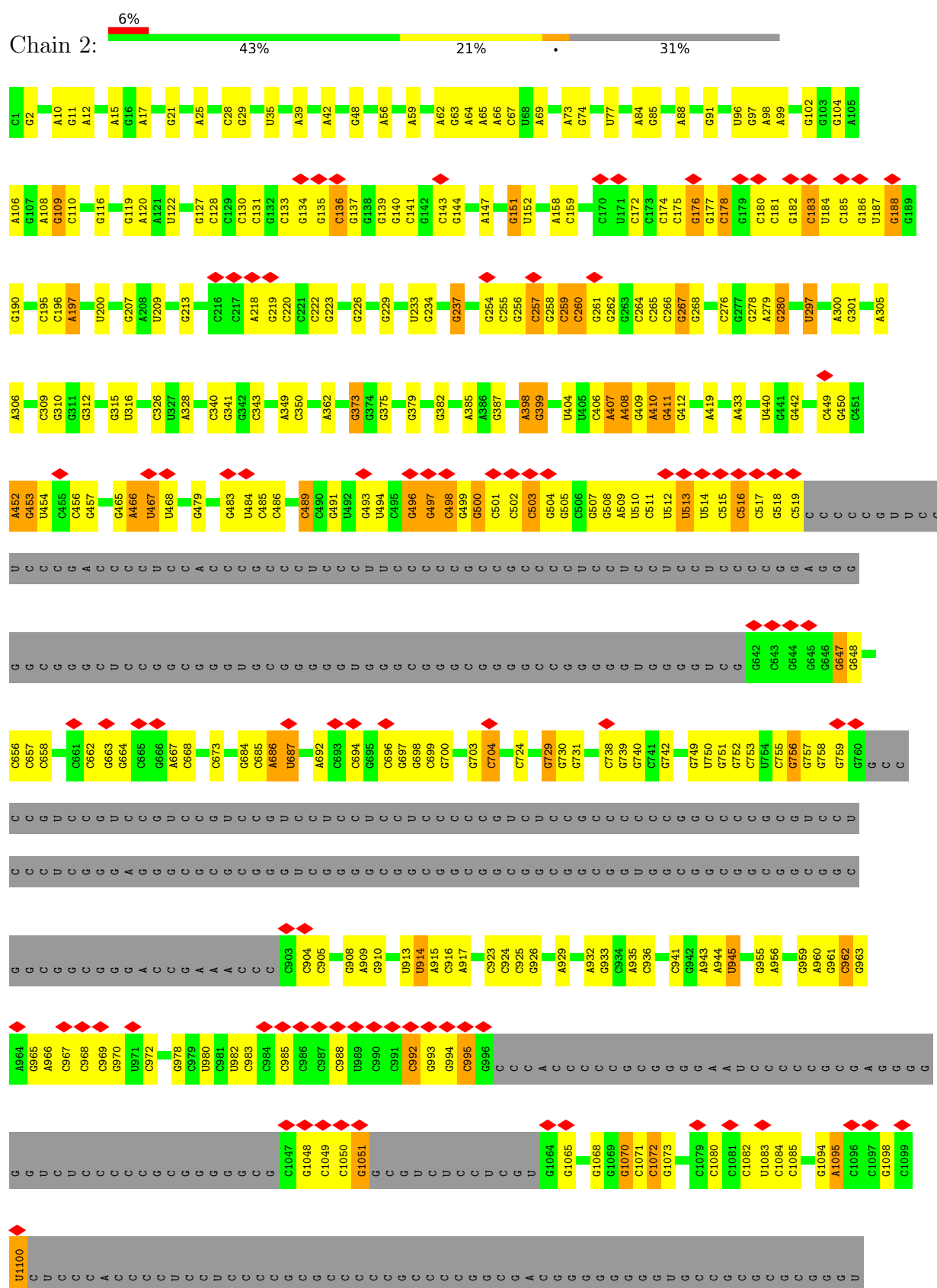
Mol	Chain	Residues	Atoms					AltConf	Trace
48	z	34	Total	C	N	O	S	0	0
			284	179	61	43	1		

- Molecule 49 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
49	2	229	Total 229	Mg 229	0
49	4	1	Total 1	Mg 1	0
49	5	3	Total 3	Mg 3	0
49	8	5	Total 5	Mg 5	0
49	9	1	Total 1	Mg 1	0
49	B	2	Total 2	Mg 2	0
49	D	1	Total 1	Mg 1	0
49	F	1	Total 1	Mg 1	0
49	L	1	Total 1	Mg 1	0
49	M	1	Total 1	Mg 1	0
49	R	1	Total 1	Mg 1	0
49	k	1	Total 1	Mg 1	0
49	m	1	Total 1	Mg 1	0
49	n	1	Total 1	Mg 1	0
49	p	1	Total 1	Mg 1	0

- Molecule 50 is water.

Mol	Chain	Residues	Atoms		AltConf
50	2	13	Total 13	O 13	0
50	k	1	Total 1	O 1	0
50	o	1	Total 1	O 1	0
50	p	1	Total 1	O 1	0

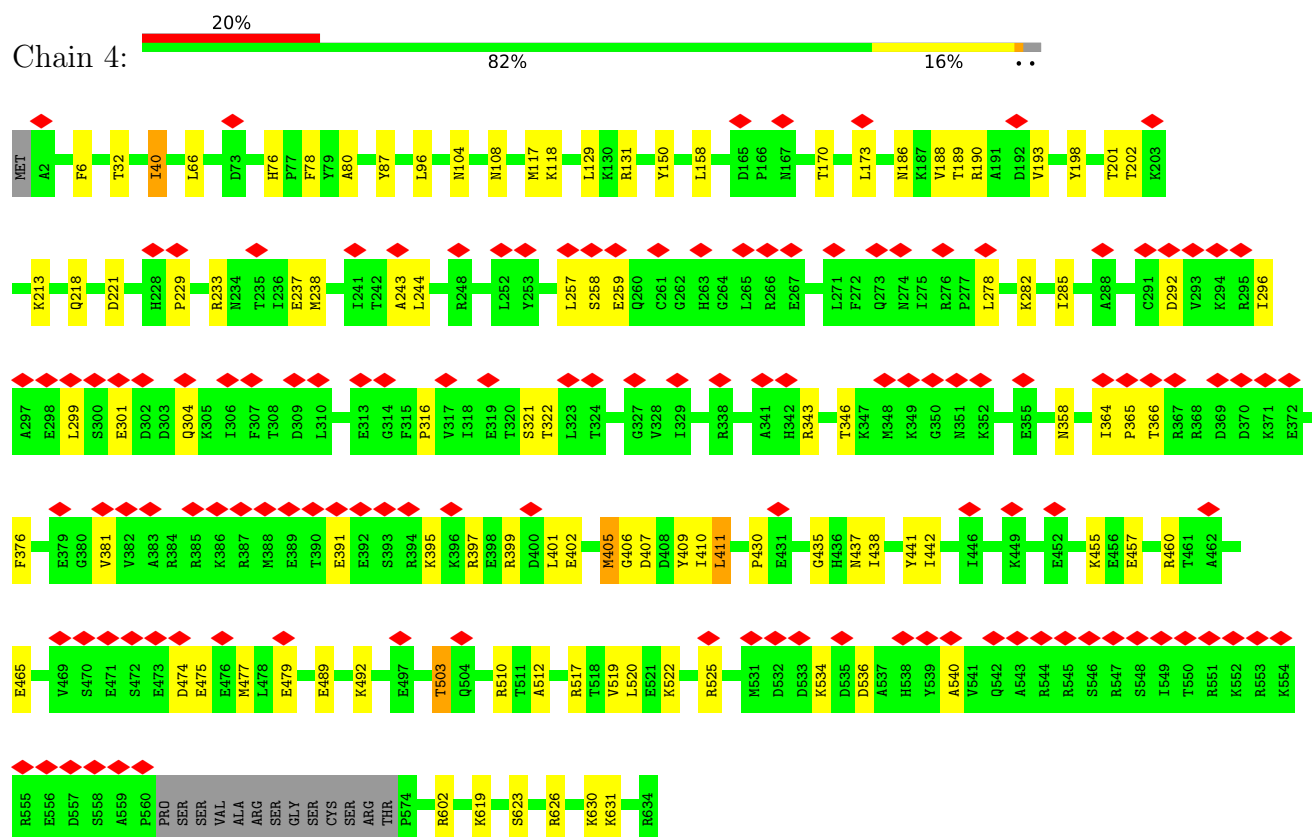




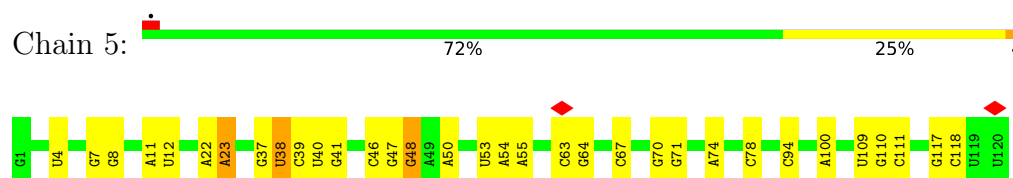




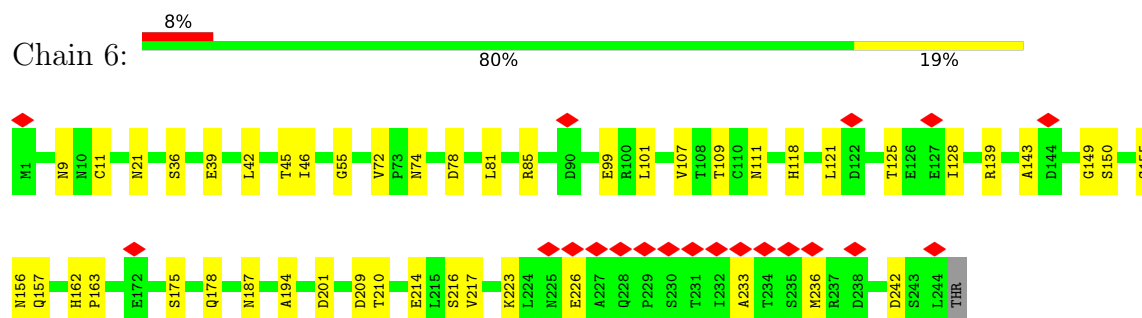
- Molecule 3: Nucleolar GTP-binding protein 1



- Molecule 4: 5S rRNA



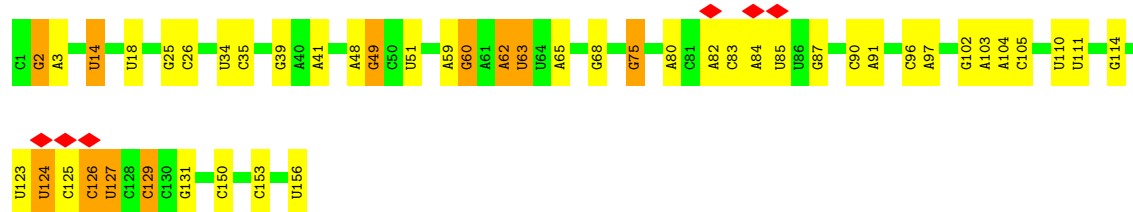
- Molecule 5: Eukaryotic translation initiation factor 6



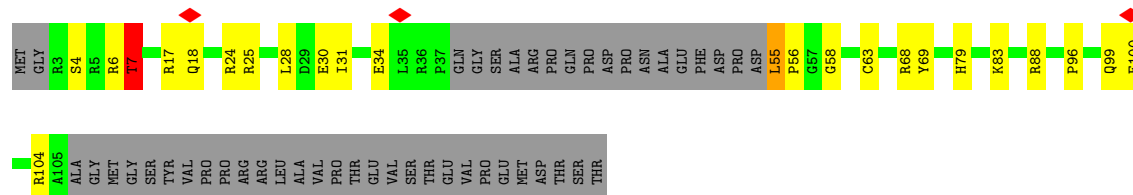
- Molecule 6: Probable ribosome biogenesis protein RLP24



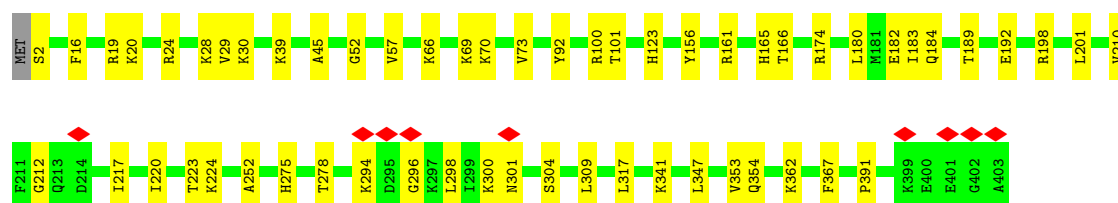
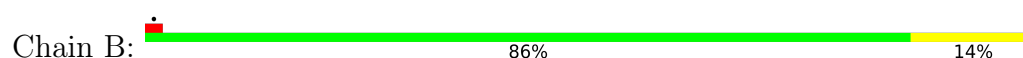
- Molecule 7: 28S rRNA



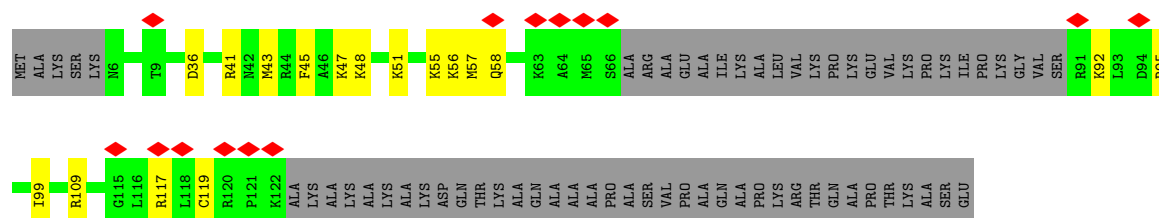
- Molecule 8: Zinc finger protein 593



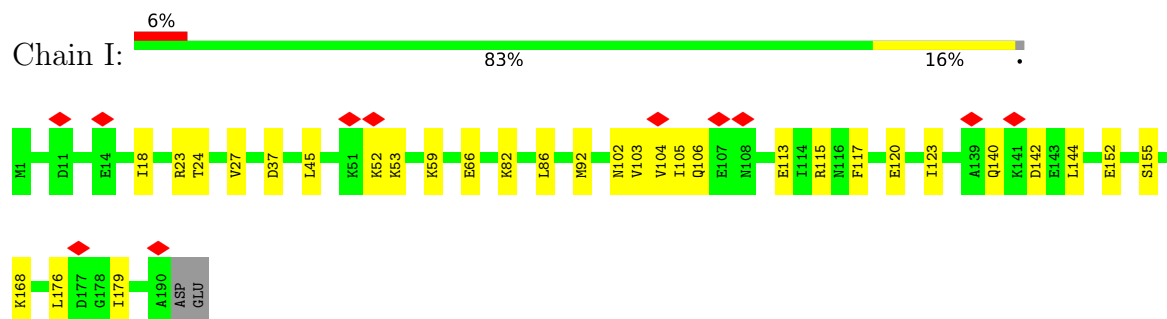
- Molecule 9: 60S ribosomal protein L3



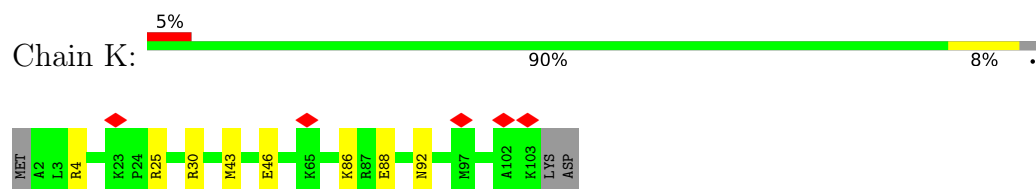
- Molecule 10: 60S ribosomal protein L29



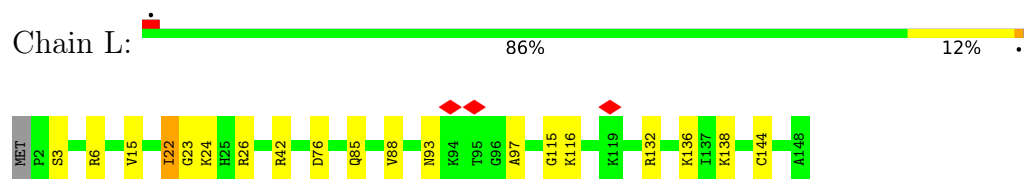
- Molecule 16: 60S ribosomal protein L9



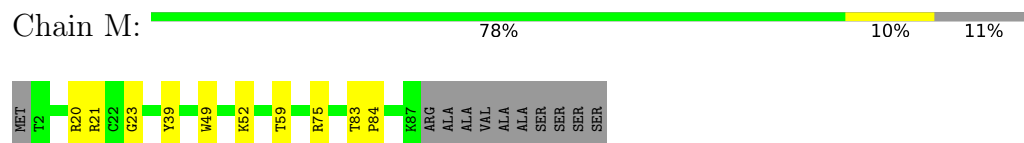
- Molecule 17: 60S ribosomal protein L36



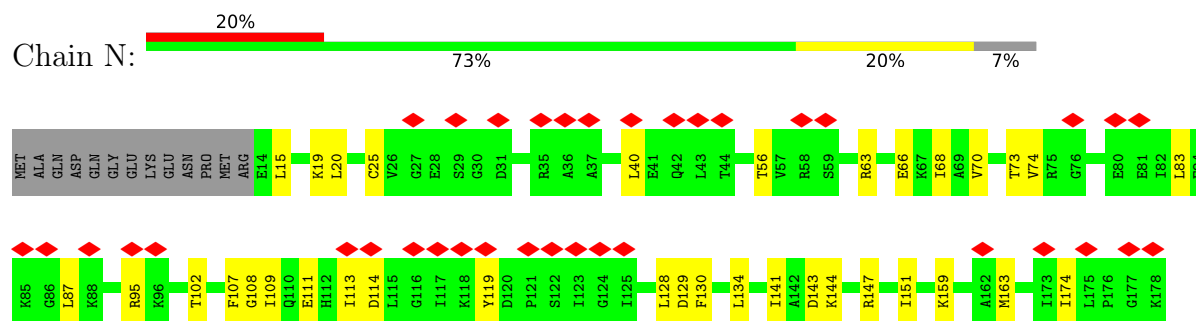
- Molecule 18: 60S ribosomal protein L27a



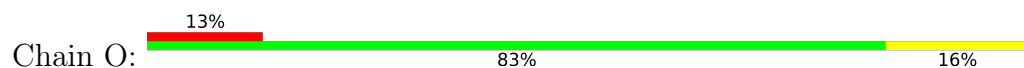
- Molecule 19: 60S ribosomal protein L37

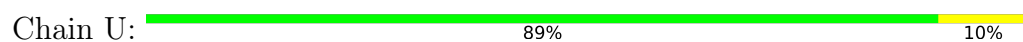


- Molecule 20: 60S ribosomal protein L11



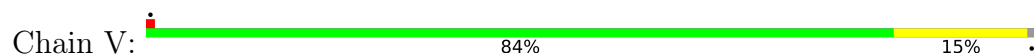
- Molecule 21: 60S ribosomal protein L38



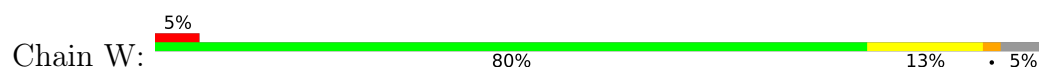




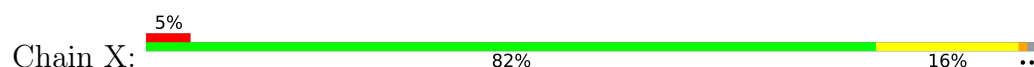
- Molecule 27: 60S ribosomal protein L13a



- Molecule 28: 60S ribosomal protein L36a



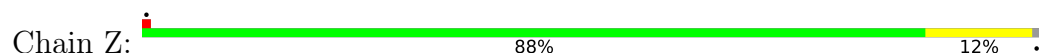
- Molecule 29: 60S ribosomal protein L37a



- Molecule 30: 60S ribosomal protein L17

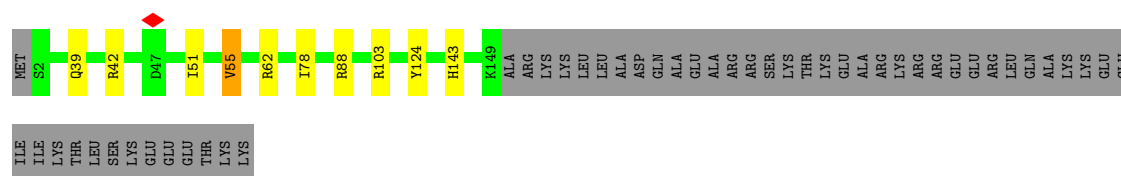


- Molecule 31: 60S ribosomal protein L18

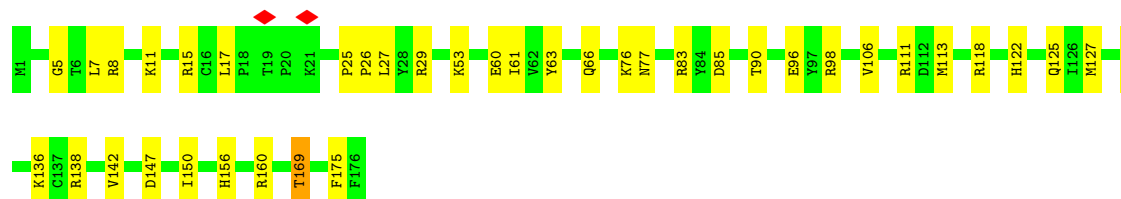
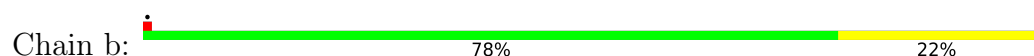


- Molecule 32: 60S ribosomal protein L19

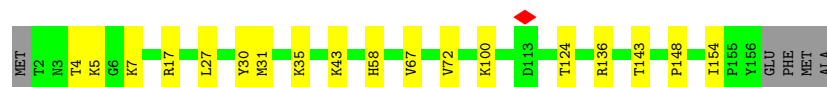
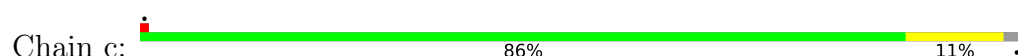




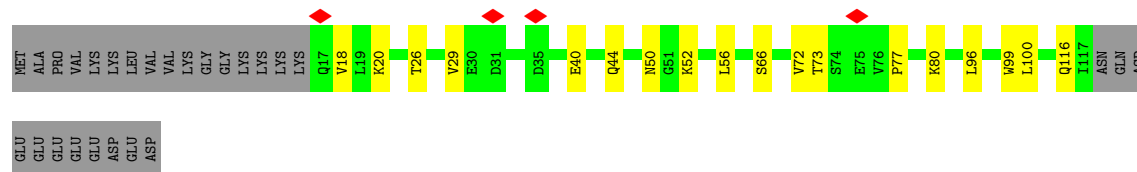
- Molecule 33: 60S ribosomal protein L18a



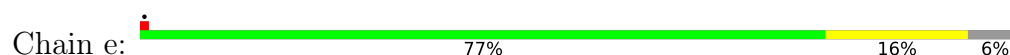
- Molecule 34: 60S ribosomal protein L21



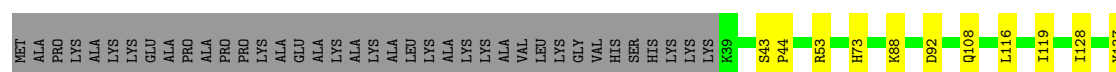
- Molecule 35: 60S ribosomal protein L22



- Molecule 36: 60S ribosomal protein L23

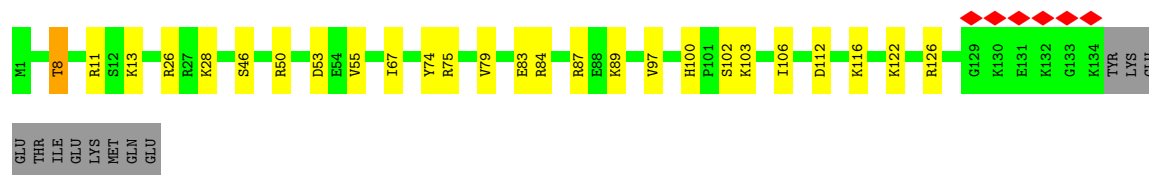
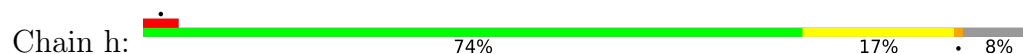


- Molecule 37: 60S ribosomal protein L23a

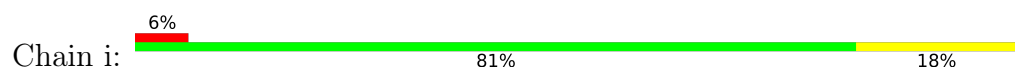




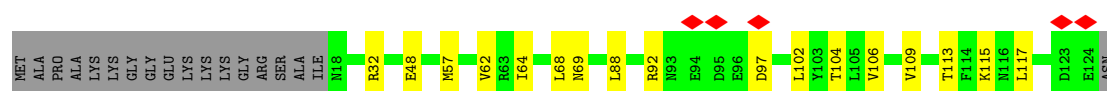
- Molecule 38: 60S ribosomal protein L26



- Molecule 39: 60S ribosomal protein L27



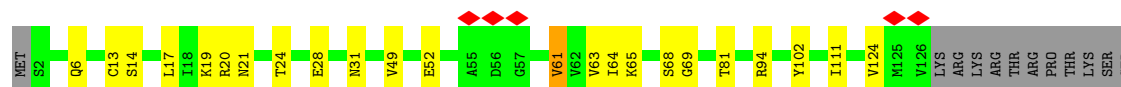
- Molecule 40: 60S ribosomal protein L31



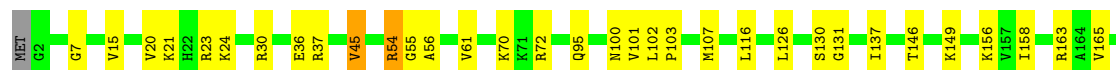
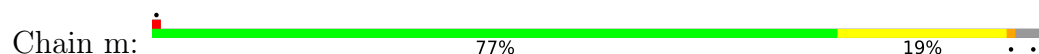
- Molecule 41: 60S ribosomal protein L32



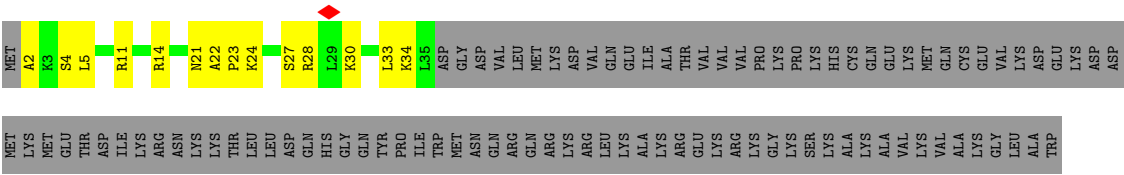
- Molecule 42: 60S ribosomal protein L28



- Molecule 43: 60S ribosomal protein L8



● Molecule 48: Protein LLP homolog



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	10277	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	64	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.377	Depositor
Minimum map value	-0.158	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.012	Depositor
Recommended contour level	0.065	Depositor
Map size (Å)	507.84, 507.84, 507.84	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.058, 1.058, 1.058	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 2MG, MHG, B8H, UR3, B9B, 7MG, OMU, BGH, B8K, E6G, P7G, E7G, 6MZ, A2M, B8T, 5MU, 5MC, OMG, I4U, OMC, PSU, M7A, MG, 1MA, B9H, P4U, B8Q, B8W

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	1	0.21	0/148	0.36	0/196
2	2	0.39	1/81090 (0.0%)	0.47	2/126417 (0.0%)
3	4	0.33	0/5177	0.75	8/6942 (0.1%)
4	5	0.35	0/2858	0.44	0/4455
5	6	0.36	0/1877	0.65	1/2554 (0.0%)
6	7	0.52	0/1181	0.88	5/1563 (0.3%)
7	8	0.42	0/3679	0.42	0/5732
8	9	0.38	0/723	0.79	3/961 (0.3%)
9	B	0.42	0/3315	0.65	0/4435
10	C	0.31	0/777	0.62	0/1026
11	D	0.44	0/2907	0.68	1/3905 (0.0%)
12	E	0.31	0/774	0.52	0/1038
13	F	0.41	0/878	0.63	0/1170
14	G	0.36	0/1971	0.64	0/2651
15	H	0.36	0/1023	0.55	0/1351
16	I	0.35	0/1537	0.64	0/2066
17	K	0.30	0/843	0.56	0/1115
18	L	0.44	0/1191	0.57	0/1591
19	M	0.45	0/720	0.65	0/952
20	N	0.31	0/1341	0.69	2/1793 (0.1%)
21	O	0.34	0/575	0.57	0/761
22	P	0.45	0/454	0.64	0/599
23	Q	0.39	0/1732	0.67	0/2315
24	R	0.28	0/1293	0.70	0/1725
25	S	0.36	0/1133	0.58	0/1516
26	U	0.44	0/1746	0.60	0/2338
27	V	0.41	0/1682	0.61	1/2250 (0.0%)
28	W	0.35	0/840	0.63	0/1107
29	X	0.39	0/718	0.58	0/953
30	Y	0.42	0/1268	0.62	1/1701 (0.1%)
31	Z	0.40	0/1537	0.61	0/2052

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	a	0.39	0/1255	0.60	1/1662 (0.1%)
33	b	0.39	0/1501	0.54	0/2013
34	c	0.37	0/1291	0.58	0/1725
35	d	0.36	0/839	0.72	0/1126
36	e	0.40	0/993	0.64	0/1332
37	g	0.36	0/984	0.52	0/1323
38	h	0.40	0/1132	0.65	0/1504
39	i	0.35	0/1130	0.60	0/1507
40	j	0.40	0/903	0.64	0/1216
41	k	0.46	0/1071	0.60	0/1429
42	l	0.40	0/1017	0.63	0/1364
43	m	0.43	0/1936	0.70	1/2596 (0.0%)
44	n	0.46	0/895	0.71	3/1198 (0.3%)
45	o	0.36	0/1935	0.66	1/2596 (0.0%)
46	p	0.41	0/1916	0.61	0/2553
47	r	0.32	0/2428	0.60	0/3252
48	z	0.41	0/286	0.59	0/372
All	All	0.39	1/148500 (0.0%)	0.54	30/217998 (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
3	4	0	4
9	B	0	2
23	Q	0	1
24	R	0	1
43	m	0	1
44	n	0	1
45	o	0	1
All	All	0	11

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	2	1534	A2M	O3'-P	5.38	1.61	1.56

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	n	106	TYR	N-CA-C	7.25	125.83	109.81
20	N	119	TYR	CA-C-N	7.16	139.68	122.36
20	N	119	TYR	C-N-CA	7.16	139.68	122.36
44	n	105	LEU	CA-C-N	7.00	138.89	121.80
44	n	105	LEU	C-N-CA	7.00	138.89	121.80
3	4	503	THR	CA-C-N	6.83	133.99	121.70
3	4	503	THR	C-N-CA	6.83	133.99	121.70
32	a	78	ILE	N-CA-C	-6.70	106.26	112.96
45	o	280	GLY	O-C-N	6.22	125.33	121.85
6	7	65	VAL	CA-C-N	6.14	133.27	121.54
6	7	65	VAL	C-N-CA	6.14	133.27	121.54
5	6	226	GLU	N-CA-C	6.00	117.49	111.07
6	7	114	LYS	N-CA-C	-6.00	104.81	113.21
6	7	62	GLU	CB-CA-C	5.88	122.12	110.42
8	9	7	THR	N-CA-C	5.76	117.55	111.28
3	4	229	PRO	CA-C-N	5.56	132.16	121.54
3	4	229	PRO	C-N-CA	5.56	132.16	121.54
3	4	391	GLU	CA-C-N	5.39	131.84	121.54
3	4	391	GLU	C-N-CA	5.39	131.84	121.54
43	m	7	GLY	N-CA-C	-5.37	107.27	114.25
11	D	320	LYS	N-CA-C	-5.33	108.03	114.75
8	9	4	SER	CA-C-N	5.17	131.43	121.54
8	9	4	SER	C-N-CA	5.17	131.43	121.54
2	2	914	U	P-O3'-C3'	5.09	127.84	120.20
6	7	114	LYS	O-C-N	5.09	126.58	121.85
2	2	914	U	C2'-C3'-O3'	5.07	117.10	109.50
3	4	406	GLY	CA-C-N	5.04	131.16	121.54
3	4	406	GLY	C-N-CA	5.04	131.16	121.54
30	Y	134	GLY	N-CA-C	-5.04	108.29	115.64
27	V	110	PRO	N-CA-C	5.00	116.80	110.70

There are no chirality outliers.

All (11) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	4	198	TYR	Peptide
3	4	365	PRO	Peptide
3	4	40	ILE	Peptide
3	4	503	THR	Peptide
9	B	16	PHE	Peptide
9	B	296	GLY	Peptide
23	Q	154	VAL	Peptide
24	R	163	ALA	Peptide

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Mol	Chain	Res	Type	Group
43	m	54	ARG	Peptide
44	n	106	TYR	Peptide
45	o	98	GLY	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	1	148	0	135	1	0
2	2	74611	0	37473	390	0
3	4	5093	0	5239	77	0
4	5	2558	0	1296	12	0
5	6	1852	0	1828	34	0
6	7	1159	0	1224	39	0
7	8	3315	0	1685	22	0
8	9	711	0	724	26	0
9	B	3244	0	3389	54	0
10	C	764	0	822	12	0
11	D	2853	0	3028	36	0
12	E	764	0	804	6	0
13	F	868	0	963	13	0
14	G	1935	0	2087	24	0
15	H	1015	0	1148	16	0
16	I	1518	0	1601	21	0
17	K	832	0	917	7	0
18	L	1162	0	1213	15	0
19	M	705	0	741	8	0
20	N	1319	0	1358	23	0
21	O	569	0	637	6	0
22	P	444	0	483	11	0
23	Q	1701	0	1818	23	0
24	R	1272	0	1291	21	0
25	S	1111	0	1174	10	0
26	U	1701	0	1749	19	0
27	V	1650	0	1794	21	0
28	W	827	0	895	13	0
29	X	708	0	760	11	0
30	Y	1242	0	1268	16	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
31	Z	1513	0	1628	13	0
32	a	1239	0	1362	8	0
33	b	1461	0	1502	32	0
34	c	1264	0	1337	17	0
35	d	825	0	850	12	0
36	e	979	0	1039	17	0
37	g	967	0	1040	11	0
38	h	1115	0	1205	17	0
39	i	1107	0	1182	16	0
40	j	888	0	930	8	0
41	k	1053	0	1147	7	0
42	l	1002	0	1068	14	0
43	m	1898	0	1993	33	0
44	n	876	0	912	7	0
45	o	1897	0	2046	39	0
46	p	1878	0	2009	18	0
47	r	2382	0	2410	32	0
48	z	284	0	333	30	0
49	2	229	0	0	0	0
49	4	1	0	0	0	0
49	5	3	0	0	0	0
49	8	5	0	0	0	0
49	9	1	0	0	0	0
49	B	2	0	0	0	0
49	D	1	0	0	0	0
49	F	1	0	0	0	0
49	L	1	0	0	0	0
49	M	1	0	0	0	0
49	R	1	0	0	0	0
49	k	1	0	0	0	0
49	m	1	0	0	0	0
49	n	1	0	0	0	0
49	p	1	0	0	0	0
50	2	13	0	0	0	0
50	k	1	0	0	0	0
50	o	1	0	0	0	0
50	p	1	0	0	0	0
All	All	140545	0	103537	1029	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 4.

All (1029) 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)
2:2:1860:B8H:C5	2:2:1860:B8H:C4	1.81	1.59
2:2:4296:B8H:C5	2:2:4296:B8H:C4	1.80	1.55
9:B:39:LYS:HE2	48:z:30:LYS:NZ	1.50	1.24
2:2:2380:B8W:O4'	2:2:2380:B8W:C1'	1.65	1.23
2:2:4690:B8K:O4'	2:2:4690:B8K:C4'	1.67	1.20
2:2:4129:B8W:O4'	2:2:4129:B8W:C1'	1.65	1.20
2:2:3897:B8K:O4'	2:2:3897:B8K:C4'	1.68	1.18
2:2:4185:B8W:O4'	2:2:4185:B8W:C1'	1.65	1.17
2:2:4529:B8W:O4'	2:2:4529:B8W:C1'	1.66	1.16
2:2:4472:B8W:O4'	2:2:4472:B8W:C1'	1.65	1.13
2:2:3899:BGH:O4'	2:2:3899:BGH:C4'	1.66	1.12
9:B:39:LYS:CE	48:z:30:LYS:NZ	2.17	1.06
6:7:57:LYS:HD2	6:7:64:THR:HG22	1.38	1.05
6:7:63:LEU:HD21	6:7:104:GLN:HG2	1.46	0.93
2:2:4745:G:H1	2:2:4955:A:N6	1.66	0.93
6:7:57:LYS:HD2	6:7:64:THR:CG2	1.98	0.93
6:7:53:LYS:NZ	6:7:62:GLU:OE1	2.00	0.93
9:B:39:LYS:HE2	48:z:30:LYS:HZ1	1.09	0.92
2:2:4745:G:H1	2:2:4955:A:H61	0.94	0.90
3:4:381:VAL:HB	5:6:45:THR:HG21	1.55	0.89
2:2:4468:U:HO2'	48:z:2:ALA:N	1.74	0.86
3:4:411:LEU:HD23	3:4:411:LEU:H	1.39	0.86
2:2:2858:A:OP1	8:9:7:THR:O	1.95	0.85
48:z:34:LYS:HE2	48:z:34:LYS:HA	1.58	0.85
6:7:63:LEU:CD2	6:7:104:GLN:HG2	2.05	0.84
6:7:109:MET:HE2	9:B:391:PRO:HB3	1.61	0.81
9:B:212:GLY:CA	48:z:33:LEU:HD21	2.13	0.78
3:4:401:LEU:O	3:4:405:MET:HG2	1.82	0.77
3:4:405:MET:HA	3:4:405:MET:HE2	1.66	0.77
48:z:23:PRO:O	48:z:27:SER:OG	2.03	0.76
11:D:334:THR:HG1	46:p:51:TYR:HH	1.26	0.75
6:7:68:SER:OG	6:7:100:LYS:HB2	1.85	0.75
9:B:39:LYS:CD	48:z:30:LYS:NZ	2.50	0.75
3:4:381:VAL:HB	5:6:45:THR:CG2	2.17	0.74
24:R:140:LEU:O	24:R:144:ARG:HB2	1.88	0.73
3:4:405:MET:HA	3:4:405:MET:CE	2.19	0.71
31:Z:85:THR:HG22	31:Z:104:ARG:HB2	1.73	0.71
2:2:1445:U:H3	2:2:2102:G:H1	1.38	0.70
9:B:39:LYS:CE	48:z:30:LYS:HZ3	2.02	0.70
16:I:140:GLN:HG3	16:I:142:ASP:H	1.56	0.70
2:2:685:C:P	45:o:99:ASP:O	2.50	0.70
2:2:1094:G:O6	2:2:1201:U:C4	2.45	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:6:157:GLN:HE21	5:6:201:ASP:HB2	1.57	0.70
3:4:411:LEU:HD23	3:4:411:LEU:N	2.06	0.69
30:Y:131:ARG:HG3	30:Y:137:ASN:HD22	1.56	0.69
47:r:211:LEU:HB3	47:r:219:TYR:HB2	1.74	0.69
26:U:165:THR:O	26:U:169:ARG:HB2	1.93	0.68
3:4:411:LEU:H	3:4:411:LEU:CD2	2.07	0.68
9:B:212:GLY:HA3	48:z:33:LEU:HD21	1.75	0.68
2:2:1098:G:H1	2:2:1197:C:H42	1.42	0.67
9:B:210:VAL:O	48:z:33:LEU:HD13	1.94	0.67
6:7:23:ARG:HH21	8:9:25:ARG:HH22	1.42	0.67
3:4:437:ASN:HD21	6:7:3:ILE:H	1.42	0.67
2:2:1252:C:H41	2:2:1259:G:H21	1.42	0.67
38:h:83:GLU:HG3	38:h:84:ARG:HD3	1.75	0.67
2:2:5041:G:OP2	6:7:61:LYS:HE3	1.95	0.66
4:5:74:A:N3	33:b:53:LYS:NZ	2.43	0.66
2:2:489:C:H42	2:2:664:G:H1	1.42	0.65
2:2:3944:G:H22	2:2:4069:U:H3	1.44	0.65
3:4:626:ARG:HH21	3:4:631:LYS:HE2	1.60	0.65
6:7:111:ARG:NH2	6:7:111:ARG:HB3	2.12	0.65
9:B:354:GLN:O	48:z:21:ASN:ND2	2.30	0.65
8:9:55:LEU:HD23	8:9:55:LEU:N	2.12	0.65
8:9:6:ARG:HG2	8:9:6:ARG:HH21	1.62	0.65
5:6:109:THR:HG23	5:6:149:GLY:HA2	1.78	0.64
12:E:28:VAL:HG21	12:E:37:MET:HG3	1.78	0.64
7:8:127:U:O4	7:8:129:C:N4	2.31	0.64
9:B:57:VAL:HG22	9:B:367:PHE:HB3	1.80	0.64
9:B:39:LYS:HE2	48:z:30:LYS:HZ2	1.59	0.63
9:B:161:ARG:HE	9:B:184:GLN:HE21	1.47	0.63
14:G:99:ALA:HB1	14:G:136:LEU:HD11	1.80	0.63
2:2:1508:A:OP1	11:D:110:ARG:NH1	2.32	0.63
2:2:2337:C:H4'	42:l:19:LYS:HB2	1.80	0.63
3:4:602:ARG:HD2	30:Y:123:PRO:HB2	1.81	0.63
5:6:42:LEU:HD13	5:6:46:ILE:HD11	1.81	0.63
11:D:245:HIS:ND1	42:l:13:CYS:SG	2.72	0.62
39:i:22:LYS:NZ	39:i:132:GLN:O	2.32	0.62
8:9:31:ILE:HA	8:9:34:GLU:HG2	1.81	0.62
45:o:46:ARG:HH11	45:o:66:LYS:HG2	1.64	0.62
3:4:475:GLU:O	3:4:479:GLU:HB2	1.99	0.62
7:8:83:C:N3	38:h:50:ARG:NH2	2.47	0.62
9:B:39:LYS:HD3	48:z:30:LYS:NZ	2.14	0.62
11:D:92:PHE:O	11:D:100:ARG:NH1	2.32	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:496:G:N7	2:2:498:C:N4	2.47	0.62
25:S:3:PHE:H	33:b:175:PHE:HZ	1.48	0.62
2:2:1521:C:OP1	11:D:100:ARG:NH2	2.32	0.62
42:l:28:GLU:OE2	42:l:31:ASN:ND2	2.33	0.62
3:4:381:VAL:CB	5:6:45:THR:HG21	2.27	0.61
9:B:39:LYS:HD3	48:z:30:LYS:HZ3	1.65	0.61
3:4:170:THR:HG22	3:4:218:GLN:HE21	1.64	0.61
9:B:198:ARG:HA	9:B:201:LEU:HD13	1.81	0.61
2:2:1301:C:OP2	2:2:1303:A:N6	2.33	0.61
2:2:2888:G:N7	8:9:83:LYS:NZ	2.47	0.61
7:8:96:C:H5''	15:H:66:LYS:HD2	1.83	0.61
2:2:2380:B8W:N2	2:2:2425:U:OP1	2.33	0.61
3:4:244:LEU:HB3	3:4:278:LEU:HD21	1.83	0.61
2:2:1095:A:N1	2:2:1200:G:O6	2.33	0.61
2:2:1364:U:OP2	23:Q:36:ARG:NH1	2.34	0.61
11:D:133:LEU:HD13	42:l:6:GLN:HE21	1.66	0.61
42:l:49:VAL:HG23	42:l:64:ILE:HG22	1.83	0.61
36:e:90:ARG:NH1	36:e:124:GLU:OE1	2.34	0.60
2:2:4678:G:N7	48:z:11:ARG:NH2	2.49	0.60
6:7:69:PHE:HD1	6:7:100:LYS:NZ	1.99	0.60
13:F:15:THR:O	13:F:19:LYS:NZ	2.35	0.60
2:2:2885:A:OP1	8:9:68:ARG:NH1	2.35	0.60
30:Y:12:THR:HG23	30:Y:13:LYS:HG3	1.84	0.60
45:o:178:PRO:HB3	45:o:258:LEU:HD21	1.83	0.60
2:2:280:G:H5''	26:U:14:LYS:HE2	1.83	0.60
47:r:55:VAL:HG12	47:r:60:ILE:HG12	1.83	0.60
3:4:411:LEU:O	9:B:69:LYS:NZ	2.26	0.60
5:6:36:SER:HA	5:6:39:GLU:HG2	1.84	0.60
6:7:108:ILE:HD12	9:B:391:PRO:HD2	1.82	0.59
2:2:497:G:H21	2:2:498:C:H41	1.51	0.59
7:8:62:A:OP1	15:H:52:LYS:NZ	2.34	0.59
44:n:33:VAL:HG23	44:n:38:GLU:HB2	1.83	0.59
2:2:968:C:H5'	45:o:110:ARG:HE	1.68	0.59
3:4:104:ASN:O	3:4:108:ASN:ND2	2.35	0.59
2:2:2306:G:OP1	41:k:128:ARG:NH2	2.36	0.59
2:2:2382:A:N1	2:2:2829:U:O2'	2.35	0.59
1:1:164:ILE:HD13	3:4:278:LEU:HD12	1.84	0.59
2:2:1718:C:OP2	46:p:200:ARG:NH2	2.36	0.59
3:4:358:ASN:ND2	5:6:163:PRO:O	2.35	0.59
2:2:186:G:H1'	2:2:1366:G:H21	1.68	0.59
31:Z:67:ILE:HD11	31:Z:95:VAL:HG13	1.85	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:2431:A:OP1	22:P:41:ARG:NH1	2.33	0.59
3:4:442:ILE:HD13	6:7:89:THR:HG21	1.85	0.58
27:V:121:PRO:HA	27:V:124:LEU:HD12	1.85	0.58
33:b:29:ARG:HB2	34:c:148:PRO:HB2	1.85	0.58
2:2:2621:A:OP1	35:d:80:LYS:NZ	2.35	0.58
2:2:4478:G:O2'	2:2:4602:A:N1	2.35	0.58
2:2:5061:A:H5''	9:B:123:HIS:HE1	1.67	0.58
41:k:84:GLU:OE2	42:l:20:ARG:NH1	2.35	0.58
2:2:1552:G:O2'	2:2:1574:B9B:N2	2.37	0.58
2:2:1256:G:OP2	2:2:1257:A:N6	2.37	0.58
19:M:20:ARG:NH2	19:M:39:TYR:OH	2.37	0.58
2:2:1273:G:OP1	10:C:117:ARG:NH1	2.37	0.58
45:o:161:ARG:HB3	45:o:271:LEU:HD23	1.86	0.58
48:z:5:LEU:O	48:z:14:ARG:NH2	2.37	0.58
42:l:14:SER:HB3	42:l:17:LEU:HD13	1.85	0.58
2:2:508:G:H21	18:L:85:GLN:HE22	1.52	0.58
20:N:147:ARG:HH11	47:r:27:LYS:HE2	1.69	0.58
6:7:63:LEU:HD21	6:7:104:GLN:CG	2.27	0.57
6:7:69:PHE:CD1	6:7:100:LYS:NZ	2.72	0.57
2:2:2611:A:H5'	2:2:2688:G:H4'	1.86	0.57
2:2:4939:C:OP1	45:o:187:ARG:NH1	2.37	0.57
16:I:105:ILE:O	16:I:106:GLN:NE2	2.36	0.57
40:j:64:ILE:HG23	40:j:68:LEU:HD23	1.86	0.57
2:2:2088:A:OP2	31:Z:37:ARG:NH1	2.37	0.57
5:6:99:GLU:HG3	5:6:101:LEU:H	1.69	0.57
39:i:41:ALA:HB2	39:i:77:TYR:HE1	1.69	0.57
2:2:4741:C:OP1	2:2:4900:C:N4	2.37	0.57
37:g:88:LYS:O	37:g:92:ASP:HB2	2.05	0.57
2:2:452:A:H4'	2:2:453:G:H5'	1.87	0.57
10:C:48:LYS:O	10:C:51:LYS:NZ	2.38	0.57
2:2:1922:G:OP1	33:b:160:ARG:NH2	2.38	0.57
7:8:75:G:OP2	38:h:74:TYR:OH	2.22	0.57
2:2:1895:G:O2'	2:2:1907:A:N3	2.35	0.57
47:r:125:VAL:HG21	47:r:199:ILE:HG21	1.87	0.57
47:r:223:PHE:HB3	47:r:226:TYR:HB2	1.86	0.57
2:2:3589:G:N2	2:2:3590:G:N7	2.50	0.57
2:2:3928:A:OP1	26:U:90:ASN:ND2	2.38	0.57
3:4:366:THR:HG21	5:6:178:GLN:HA	1.85	0.57
3:4:381:VAL:CG2	5:6:45:THR:HG21	2.34	0.57
29:X:8:VAL:O	29:X:27:LYS:NZ	2.38	0.57
44:n:56:ASN:OD1	44:n:66:LYS:NZ	2.35	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:o:190:HIS:HD2	45:o:192:LYS:H	1.53	0.57
2:2:1094:G:N1	2:2:1201:U:N3	2.53	0.57
2:2:1823:G:H4'	47:r:45:ASN:HB2	1.87	0.57
7:8:51:U:OP2	22:P:21:ARG:NH2	2.38	0.57
33:b:77:ASN:HD22	33:b:98:ARG:HG2	1.69	0.57
2:2:704:C:N4	2:2:1290:G:O6	2.38	0.56
2:2:3620:G:OP1	2:2:3622:C:N4	2.38	0.56
2:2:4084:G:O6	43:m:72:ARG:NH2	2.37	0.56
48:z:34:LYS:HA	48:z:34:LYS:CE	2.32	0.56
2:2:1321:G:N2	2:2:3876:A:O4'	2.38	0.56
3:4:376:PHE:HB3	5:6:21:ASN:HD22	1.70	0.56
6:7:63:LEU:HD23	6:7:63:LEU:O	2.05	0.56
2:2:4589:A:N1	2:2:4621:C:O2'	2.38	0.56
2:2:4751:G:N7	44:n:52:LYS:NZ	2.52	0.56
2:2:5025:C:O2	2:2:5028:G:N2	2.38	0.56
9:B:39:LYS:CD	48:z:30:LYS:HZ2	2.18	0.56
9:B:73:VAL:O	36:e:89:ARG:NH2	2.39	0.56
11:D:318:PRO:HB2	11:D:325:MET:HE2	1.87	0.56
11:D:321:ASN:HB3	11:D:324:ILE:HB	1.86	0.56
33:b:5:GLY:O	33:b:111:ARG:NH1	2.38	0.56
43:m:30:ARG:NH2	43:m:36:GLU:OE1	2.38	0.56
23:Q:80:GLU:OE2	23:Q:102:ARG:NH1	2.38	0.56
29:X:26:VAL:HG21	43:m:180:LEU:HD11	1.88	0.56
2:2:5001:U:H4'	9:B:317:LEU:HB3	1.87	0.56
21:O:30:ASP:OD1	21:O:31:ASN:ND2	2.39	0.56
2:2:1433:A:N6	2:2:1451:G:O2'	2.39	0.56
2:2:2860:C:OP1	8:9:17:ARG:NH2	2.38	0.56
2:2:4334:U:H5''	34:c:7:LYS:HD2	1.86	0.56
2:2:4596:C:OP1	5:6:9:ASN:ND2	2.39	0.56
5:6:150:SER:HA	5:6:194:ALA:HB3	1.87	0.56
15:H:122:LYS:HE3	23:Q:125:ILE:HD11	1.86	0.56
40:j:113:THR:OG1	40:j:115:LYS:NZ	2.39	0.56
2:2:5039:U:OP1	6:7:111:ARG:NH2	2.38	0.56
20:N:108:GLY:HA2	20:N:129:ASP:HA	1.87	0.56
45:o:50:LEU:HD12	45:o:51:VAL:HG22	1.88	0.56
2:2:280:G:OP1	26:U:47:LYS:NZ	2.37	0.56
2:2:2521:G:H4'	13:F:26:PRO:HD2	1.88	0.56
36:e:30:ASP:HB3	36:e:32:THR:HG22	1.88	0.56
11:D:342:ARG:O	11:D:346:ASN:ND2	2.39	0.56
6:7:53:LYS:O	6:7:57:LYS:HG2	2.06	0.56
24:R:104:ARG:HH11	33:b:136:LYS:HE3	1.71	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:C:99:ILE:O	10:C:109:ARG:NH1	2.39	0.55
2:2:2483:G:H22	2:2:2484:A:H62	1.54	0.55
2:2:4261:C:OP1	20:N:19:LYS:NZ	2.38	0.55
2:2:4457:U:OP1	36:e:50:ASN:ND2	2.39	0.55
2:2:223:G:N2	11:D:223:ASN:O	2.38	0.55
2:2:1646:A:OP2	11:D:80:ARG:NH1	2.39	0.55
2:2:2557:G:H1	2:2:2570:U:H3	1.55	0.55
3:4:285:ILE:HG23	3:4:316:PRO:HG2	1.88	0.55
2:2:4940:C:OP1	45:o:156:ARG:NH2	2.36	0.55
33:b:83:ARG:NH1	33:b:125:GLN:OE1	2.38	0.55
2:2:139:G:H2'	2:2:140:G:H8	1.72	0.55
2:2:4471:U:OP1	16:I:168:LYS:NZ	2.39	0.55
8:9:56:PRO:HD2	8:9:69:TYR:CB	2.37	0.55
2:2:151:G:OP2	26:U:4:TYR:OH	2.23	0.55
9:B:57:VAL:HG12	9:B:73:VAL:HG22	1.88	0.55
9:B:100:ARG:NH1	9:B:101:THR:O	2.39	0.55
17:K:88:GLU:O	17:K:92:ASN:ND2	2.40	0.55
25:S:50:MET:HE2	25:S:55:MET:HE2	1.88	0.55
2:2:12:A:H4'	37:g:53:ARG:HD2	1.88	0.55
2:2:1280:C:OP2	45:o:52:ARG:NH2	2.40	0.55
2:2:4517:A:OP2	9:B:2:SER:OG	2.24	0.55
18:L:3:SER:HA	18:L:6:ARG:HE	1.72	0.55
2:2:729:2MG:N2	33:b:66:GLN:O	2.38	0.55
2:2:1280:C:H5'	45:o:52:ARG:HH22	1.72	0.55
6:7:69:PHE:HD1	6:7:100:LYS:HZ2	1.50	0.55
28:W:45:GLN:NE2	28:W:52:THR:OG1	2.40	0.55
2:2:2479:G:H2'	2:2:2480:G:H8	1.71	0.55
2:2:4394:A:H3'	2:2:4395:U:H2'	1.88	0.55
2:2:4881:U:OP2	25:S:121:ARG:NH1	2.40	0.54
3:4:233:ARG:HB2	3:4:238:MET:HE2	1.88	0.54
5:6:157:GLN:HB3	5:6:223:LYS:HE2	1.89	0.54
2:2:4672:A:OP1	36:e:15:ARG:NH2	2.40	0.54
6:7:63:LEU:HB3	6:7:107:PHE:CD2	2.43	0.54
11:D:209:ILE:HB	11:D:229:LEU:HD13	1.89	0.54
35:d:20:LYS:H	35:d:73:THR:HA	1.73	0.54
39:i:115:LYS:NZ	39:i:119:GLU:OE2	2.39	0.54
45:o:264:ILE:HD11	45:o:267:LEU:HD22	1.89	0.54
2:2:4688:C:O2'	16:I:155:SER:OG	2.26	0.54
3:4:186:ASN:HD21	3:4:193:VAL:H	1.56	0.54
2:2:35:U:OP2	26:U:83:LYS:NZ	2.37	0.54
2:2:2667:C:OP2	32:a:103:ARG:NH1	2.41	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:4980:C:N3	30:Y:69:ARG:NH2	2.54	0.54
2:2:2666:U:OP2	32:a:124:TYR:OH	2.24	0.54
2:2:4322:G:N2	2:2:4325:A:OP2	2.35	0.54
2:2:5047:C:O2'	2:2:5050:C:OP2	2.26	0.54
2:2:5066:U:OP1	30:Y:43:LYS:NZ	2.36	0.54
39:i:90:PRO:O	39:i:117:LYS:NZ	2.36	0.54
46:p:182:TYR:HB3	46:p:200:ARG:HG3	1.89	0.54
2:2:4732:G:N2	2:2:4733:C:O2	2.41	0.54
2:2:4985:U:O2	9:B:174:ARG:NH1	2.38	0.54
29:X:29:ILE:HG21	43:m:177:LYS:HB2	1.89	0.54
33:b:83:ARG:NH2	34:c:154:ILE:O	2.40	0.54
2:2:1480:C:O2'	2:2:1482:G:OP2	2.26	0.53
2:2:1697:G:N2	2:2:2084:C:OP1	2.41	0.53
6:7:57:LYS:HD2	6:7:64:THR:HG23	1.88	0.53
15:H:117:ARG:NH2	23:Q:127:PHE:O	2.41	0.53
2:2:178:C:H42	2:2:259:C:H42	1.54	0.53
2:2:350:C:OP2	11:D:199:ARG:NH2	2.41	0.53
2:2:373:OMG:HM21	2:2:1645:C:H4'	1.91	0.53
27:V:130:LYS:HB2	27:V:133:ARG:HG2	1.90	0.53
38:h:67:ILE:O	38:h:84:ARG:NH2	2.42	0.53
39:i:36:ARG:NH1	39:i:38:TYR:OH	2.42	0.53
2:2:685:C:OP1	45:o:99:ASP:O	2.27	0.53
2:2:1100:U:O2	2:2:1195:G:O6	2.27	0.53
2:2:4096:C:N4	2:2:4113:U:O2	2.38	0.53
3:4:244:LEU:O	3:4:282:LYS:NZ	2.41	0.53
8:9:6:ARG:HG2	8:9:6:ARG:NH2	2.24	0.53
14:G:234:ARG:NH2	17:K:46:GLU:OE1	2.41	0.53
2:2:260:C:H2'	2:2:261:G:H8	1.73	0.53
2:2:1872:G:O2'	2:2:4219:A:N3	2.36	0.53
2:2:2478:C:O2	2:2:2591:A:O2'	2.26	0.53
3:4:117:MET:HE2	3:4:129:LEU:HB3	1.90	0.53
11:D:340:ILE:HG21	45:o:50:LEU:HD13	1.90	0.53
2:2:2562:G:N2	2:2:2565:A:OP2	2.42	0.53
2:2:2755:A:OP2	39:i:51:ARG:NH1	2.41	0.53
2:2:2418:A:N1	2:2:2429:A:O2'	2.42	0.53
2:2:4688:C:HO2'	16:I:155:SER:HG	1.53	0.53
14:G:211:ASP:OD1	14:G:211:ASP:N	2.41	0.53
34:c:43:LYS:O	34:c:58:HIS:ND1	2.31	0.53
2:2:2280:G:N2	2:2:2281:U:O4	2.42	0.53
3:4:460:ARG:NH1	3:4:465:GLU:OE1	2.42	0.53
23:Q:111:GLN:HA	23:Q:114:VAL:HG22	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:Z:151:HIS:ND1	31:Z:164:LYS:O	2.41	0.53
42:l:52:GLU:HB3	42:l:61:VAL:HG13	1.91	0.53
46:p:102:SER:O	46:p:106:ARG:HB2	2.09	0.53
6:7:23:ARG:HE	8:9:25:ARG:HH12	1.56	0.52
2:2:4418:G:H2'	2:2:4421:C:H41	1.73	0.52
10:C:43:MET:HG2	10:C:47:LYS:HE2	1.92	0.52
14:G:180:PRO:HG3	14:G:219:VAL:HG13	1.90	0.52
17:K:25:ARG:NH1	23:Q:100:PRO:O	2.42	0.52
44:n:108:SER:O	45:o:141:ARG:NH1	2.43	0.52
48:z:4:SER:OG	48:z:5:LEU:N	2.42	0.52
2:2:1569:U:O4	29:X:2:ALA:N	2.42	0.52
2:2:1825:A:O2'	10:C:43:MET:SD	2.67	0.52
2:2:2488:C:N4	7:8:126:C:OP2	2.42	0.52
2:2:4645:C:OP2	32:a:62:ARG:NH2	2.42	0.52
4:5:38:U:N3	4:5:41:G:OP2	2.35	0.52
8:9:28:LEU:H	8:9:31:ILE:HD11	1.74	0.52
2:2:1517:2MG:HN2	11:D:103:ALA:HA	1.74	0.52
2:2:2487:G:O2'	2:2:2489:C:OP1	2.26	0.52
5:6:55:GLY:HA2	9:B:70:LYS:HE3	1.90	0.52
2:2:1915:C:OP2	27:V:94:ARG:NH2	2.42	0.52
2:2:2343:G:OP2	11:D:109:ARG:NH1	2.42	0.52
2:2:4149:C:OP1	39:i:59:LYS:N	2.42	0.52
9:B:217:ILE:HD12	9:B:347:LEU:HB3	1.90	0.52
13:F:11:LEU:O	13:F:18:ASN:ND2	2.42	0.52
36:e:82:ILE:HG13	36:e:83:ARG:HG2	1.91	0.52
47:r:23:ARG:NH2	47:r:23:ARG:O	2.42	0.52
11:D:35:ASP:OD1	11:D:35:ASP:N	2.41	0.52
40:j:57:MET:HG2	40:j:88:LEU:HD13	1.92	0.52
2:2:305:A:OP2	26:U:15:GLN:NE2	2.42	0.52
2:2:1578:U:H4'	29:X:17:ARG:HH22	1.73	0.52
3:4:457:GLU:OE1	6:7:102:LYS:NZ	2.37	0.52
27:V:46:ASN:O	27:V:50:ASN:ND2	2.43	0.52
39:i:70:SER:OG	39:i:71:PHE:N	2.42	0.52
47:r:181:PRO:HD2	47:r:195:HIS:HD2	1.75	0.52
2:2:4208:U:OP2	34:c:4:THR:OG1	2.20	0.52
22:P:10:LYS:NZ	37:g:128:ILE:O	2.42	0.52
2:2:181:C:OP2	2:2:183:C:N4	2.42	0.52
6:7:56:ARG:HB3	6:7:62:GLU:OE2	2.10	0.52
31:Z:70:MET:HE1	31:Z:137:VAL:HB	1.92	0.52
43:m:131:GLY:H	43:m:169:VAL:HG13	1.75	0.52
2:2:188:G:O2'	2:2:190:G:OP2	2.27	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:1070:G:OP2	45:o:65:ARG:NH1	2.44	0.51
3:4:441:TYR:OH	6:7:97:GLU:OE2	2.27	0.51
20:N:15:LEU:HD11	20:N:134:LEU:HB3	1.92	0.51
45:o:214:ASP:O	45:o:218:LYS:HB2	2.10	0.51
2:2:4468:U:O2'	48:z:2:ALA:N	2.41	0.51
3:4:66:LEU:HD23	3:4:96:LEU:HD12	1.90	0.51
18:L:138:LYS:HZ3	18:L:144:CYS:H	1.57	0.51
2:2:3688:U:OP2	43:m:198:ARG:NH1	2.43	0.51
3:4:399:ARG:NH2	3:4:402:GLU:OE1	2.44	0.51
6:7:63:LEU:HD23	6:7:63:LEU:H	1.74	0.51
2:2:749:G:N2	2:2:750:U:O4	2.42	0.51
3:4:87:TYR:O	3:4:150:TYR:OH	2.27	0.51
7:8:124:U:OP1	7:8:126:C:N4	2.43	0.51
43:m:101:VAL:HG22	43:m:165:VAL:HG22	1.92	0.51
2:2:2448:G:O2'	43:m:21:LYS:NZ	2.43	0.51
2:2:2758:G:O2'	2:2:2765:A:N3	2.41	0.51
3:4:343:ARG:NH1	5:6:242:ASP:OD1	2.44	0.51
12:E:17:ARG:NH1	12:E:101:ASP:O	2.44	0.51
16:I:113:GLU:OE1	16:I:115:ARG:NH2	2.43	0.51
20:N:83:LEU:O	20:N:87:LEU:HB2	2.10	0.51
2:2:4623:OMG:OP1	9:B:19:ARG:NH2	2.44	0.51
22:P:28:ARG:NH1	22:P:36:ARG:O	2.43	0.51
3:4:522:LYS:HA	3:4:525:ARG:HB2	1.93	0.51
9:B:52:GLY:HA2	9:B:341[A]:LYS:HE3	1.92	0.51
2:2:2579:G:N2	2:2:2582:A:OP2	2.36	0.51
2:2:4606:G:OP1	3:4:190:ARG:NH2	2.44	0.51
12:E:55:LEU:HD11	13:F:92:LYS:HG3	1.93	0.51
23:Q:16:LYS:O	23:Q:21:ARG:NH1	2.39	0.51
30:Y:17:SER:HB2	30:Y:97:ASN:HD22	1.76	0.51
48:z:34:LYS:HE2	48:z:34:LYS:CA	2.37	0.51
2:2:757:G:H4'	16:I:52:LYS:HZ3	1.76	0.51
2:2:945:U:OP1	11:D:342:ARG:NH2	2.44	0.51
8:9:100:GLU:OE1	8:9:104:ARG:NH2	2.44	0.51
2:2:513:U:O2'	2:2:516:C:N4	2.44	0.51
11:D:12:SER:HA	11:D:155:GLU:HG3	1.92	0.51
41:k:114:ARG:HA	41:k:117:GLN:HE21	1.76	0.51
42:l:68:SER:OG	42:l:69:GLY:N	2.43	0.51
2:2:1734:G:O2'	2:2:1793:A:N6	2.38	0.50
2:2:2641:A:OP1	13:F:21:ARG:NH2	2.44	0.50
2:2:3838:U:H5'	8:9:17:ARG:HD2	1.94	0.50
8:9:55:LEU:N	8:9:55:LEU:CD2	2.73	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:d:18:VAL:HG21	35:d:77:PRO:HA	1.93	0.50
36:e:82:ILE:HG12	36:e:103:GLY:HA2	1.93	0.50
43:m:137:ILE:HD11	43:m:149:LYS:HB2	1.93	0.50
2:2:174:C:O2'	15:H:103:LYS:NZ	2.44	0.50
2:2:399:G:H4'	30:Y:18:ARG:HB3	1.94	0.50
2:2:1656:U:OP2	18:L:26:ARG:NH2	2.44	0.50
3:4:401:LEU:O	3:4:405:MET:CG	2.54	0.50
31:Z:172:ARG:HA	31:Z:176:ARG:HG3	1.92	0.50
2:2:4407:G:OP1	3:4:131:ARG:NH2	2.44	0.50
3:4:201:THR:OG1	3:4:202:THR:N	2.44	0.50
6:7:109:MET:HE2	9:B:391:PRO:CB	2.38	0.50
18:L:76:ASP:N	18:L:76:ASP:OD1	2.40	0.50
29:X:51:ALA:HB3	29:X:54:ILE:HD12	1.92	0.50
40:j:32:ARG:HB3	40:j:48:GLU:HG3	1.94	0.50
42:l:65:LYS:O	42:l:102:TYR:OH	2.24	0.50
2:2:1797:E7G:OP1	46:p:104:LYS:NZ	2.45	0.50
2:2:2562:G:H22	2:2:2565:A:H5''	1.76	0.50
2:2:4875:G:H2'	33:b:169:THR:HG22	1.93	0.50
14:G:160:ASP:OD1	14:G:160:ASP:N	2.45	0.50
25:S:62:LEU:HD21	25:S:82:ILE:HD11	1.93	0.50
36:e:106:VAL:HG12	36:e:112:MET:HA	1.92	0.50
2:2:1328:G:O2'	2:2:2349:A:OP1	2.29	0.50
2:2:4088:C:OP1	43:m:37:ARG:NH1	2.45	0.50
2:2:4238:G:H2'	2:2:4239:A:H8	1.75	0.50
4:5:55:A:O2'	20:N:151:ILE:O	2.26	0.50
9:B:353:VAL:HG11	48:z:22:ALA:HB2	1.93	0.50
26:U:68:ARG:NH1	26:U:124:ASP:O	2.45	0.50
38:h:26:ARG:NH1	38:h:75:ARG:O	2.44	0.50
2:2:1245:C:H2'	2:2:1246:G:H8	1.77	0.50
32:a:39:GLN:H	32:a:42:ARG:HG3	1.77	0.50
47:r:75:VAL:O	47:r:112:ARG:NH1	2.45	0.50
2:2:4092:G:H3'	2:2:4093:G:H21	1.77	0.50
30:Y:7:ASP:OD1	30:Y:7:ASP:N	2.42	0.50
2:2:2295:C:O2'	11:D:45:ARG:NH2	2.45	0.50
2:2:3899:BGH:O4'	2:2:3899:BGH:C5'	2.53	0.50
16:I:103:VAL:HG21	16:I:144:LEU:HD22	1.94	0.50
21:O:31:ASN:HB3	21:O:48:THR:HG22	1.94	0.50
28:W:45:GLN:HE22	28:W:52:THR:H	1.60	0.50
2:2:2493:G:H21	7:8:126:C:H3'	1.76	0.49
5:6:155:SER:OG	5:6:156:ASN:N	2.45	0.49
2:2:375:G:OP2	19:M:52:LYS:NZ	2.39	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:6:216:SER:HB2	5:6:236:MET:HE1	1.94	0.49
2:2:109:G:OP2	23:Q:74:ARG:NH2	2.45	0.49
2:2:328:A:OP2	17:K:30:ARG:NH1	2.43	0.49
2:2:1445:U:O4	2:2:2100:A:N6	2.35	0.49
2:2:1730:U:H4'	34:c:100:LYS:HB2	1.93	0.49
2:2:2556:G:H1'	39:i:112:ARG:HH12	1.77	0.49
2:2:2614:C:O2'	2:2:2808:G:OP1	2.28	0.49
38:h:46:SER:O	38:h:122:LYS:NZ	2.45	0.49
43:m:103:PRO:HA	43:m:163:ARG:HA	1.94	0.49
2:2:2601:A:OP2	13:F:40:LYS:NZ	2.46	0.49
3:4:364:ILE:HG22	3:4:366:THR:H	1.77	0.49
4:5:12:U:O3'	4:5:109:U:O2'	2.26	0.49
2:2:1957:U:O2'	2:2:1962:A:O2'	2.26	0.49
8:9:18:GLN:HA	8:9:24:ARG:HE	1.78	0.49
33:b:85:ASP:OD1	33:b:85:ASP:N	2.44	0.49
2:2:2781:G:O2'	22:P:3:SER:O	2.29	0.49
2:2:4076:G:OP1	14:G:73:ARG:NE	2.46	0.49
2:2:4414:A:H2'	2:2:4422:A:C6	2.47	0.49
2:2:4448:G:H22	2:2:4502:C:H5	1.61	0.49
3:4:430:PRO:HB3	9:B:309:LEU:HD13	1.95	0.49
9:B:39:LYS:CE	48:z:30:LYS:HZ1	1.96	0.49
14:G:223:ARG:HG3	14:G:227:ASN:HB2	1.94	0.49
16:I:59:LYS:HE3	16:I:66:GLU:HG3	1.94	0.49
23:Q:25:TRP:NE1	26:U:199:GLN:OE1	2.38	0.49
23:Q:64:VAL:HA	23:Q:67:HIS:CD2	2.48	0.49
35:d:26:THR:HA	35:d:29:VAL:HG12	1.93	0.49
45:o:133:PHE:O	45:o:138:ARG:NH2	2.45	0.49
2:2:1068:G:O6	45:o:43:HIS:NE2	2.42	0.49
2:2:2529:A:O2'	2:2:2531:C:OP2	2.31	0.49
2:2:407:A:O2'	2:2:410:A:OP1	2.25	0.49
4:5:117:G:OP1	47:r:253:TYR:OH	2.31	0.49
37:g:140:LEU:HD11	37:g:149:VAL:HG21	1.93	0.49
43:m:181:LYS:HB2	43:m:184:ARG:HG3	1.94	0.49
44:n:35:ALA:HB3	44:n:38:GLU:HG3	1.95	0.49
47:r:265:ARG:HH12	47:r:267:ASN:HB2	1.77	0.49
2:2:1396:G:H5''	18:L:132:ARG:HH12	1.78	0.49
28:W:23:VAL:HG12	28:W:70:LEU:HG	1.95	0.49
36:e:82:ILE:HB	36:e:121:VAL:HG13	1.94	0.49
37:g:146:ALA:HA	37:g:149:VAL:HG22	1.95	0.49
2:2:85:G:O2'	2:2:97:G:O6	2.24	0.49
2:2:2034:G:O2'	33:b:118:ARG:NH2	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:2652:G:N2	29:X:59:SER:O	2.45	0.49
3:4:522:LYS:HA	3:4:525:ARG:HD3	1.95	0.49
8:9:56:PRO:HD2	8:9:69:TYR:HB3	1.95	0.49
27:V:196:LEU:HD23	27:V:202:LEU:HG	1.95	0.49
45:o:172:LEU:HD23	45:o:188:ARG:HB3	1.95	0.49
45:o:225:PRO:O	45:o:227:HIS:ND1	2.38	0.49
2:2:1701:A:N7	2:2:1703:C:N4	2.61	0.48
3:4:405:MET:CB	3:4:409:TYR:HB2	2.43	0.48
8:9:55:LEU:HG	8:9:58:GLY:O	2.13	0.48
9:B:39:LYS:CD	48:z:30:LYS:HZ3	2.16	0.48
11:D:341:LEU:HD21	45:o:56:ARG:HG3	1.95	0.48
20:N:107:PHE:O	20:N:130:PHE:N	2.42	0.48
2:2:195:C:OP2	38:h:28:LYS:NZ	2.43	0.48
2:2:2742:G:OP1	43:m:24:LYS:NZ	2.40	0.48
9:B:189:THR:HG23	9:B:192:GLU:H	1.77	0.48
20:N:95:ARG:NH1	20:N:174:ILE:O	2.46	0.48
45:o:145:THR:O	45:o:148:THR:OG1	2.30	0.48
45:o:190:HIS:CD2	45:o:192:LYS:H	2.31	0.48
2:2:4318:C:O2'	28:W:18:HIS:ND1	2.40	0.48
8:9:55:LEU:HD12	8:9:69:TYR:CE2	2.48	0.48
23:Q:205:GLN:HB3	23:Q:209:LYS:HG2	1.96	0.48
24:R:108:SER:O	24:R:108:SER:OG	2.27	0.48
24:R:105:ARG:NH1	33:b:138:ARG:O	2.45	0.48
34:c:143:THR:HG23	46:p:80:ASN:HA	1.96	0.48
12:E:29:LEU:HD11	12:E:87:LYS:HE3	1.96	0.48
20:N:40:LEU:HD12	20:N:70:VAL:HG23	1.94	0.48
2:2:382:G:N1	2:2:385:A:OP2	2.40	0.48
2:2:4673:U:OP2	36:e:15:ARG:NH1	2.44	0.48
7:8:63:U:O2'	15:H:52:LYS:NZ	2.41	0.48
2:2:1292:C:H3'	2:2:1293:G:H21	1.78	0.48
2:2:4220:6MZ:H8	2:2:4220:6MZ:OP1	2.14	0.48
28:W:71:GLU:OE2	28:W:78:ARG:NH2	2.46	0.48
30:Y:118:GLN:HE22	30:Y:120:ASN:HD21	1.60	0.48
41:k:81:ASN:N	41:k:81:ASN:OD1	2.44	0.48
43:m:246:LEU:O	43:m:249:THR:OG1	2.31	0.48
2:2:88:A:N7	31:Z:173:LYS:NZ	2.60	0.48
4:5:12:U:OP2	4:5:67:C:O2'	2.31	0.48
24:R:115:GLN:HB3	24:R:119:ARG:HH21	1.78	0.48
46:p:105:VAL:HG13	46:p:136:VAL:HG12	1.94	0.48
3:4:619:LYS:O	3:4:623:SER:HB2	2.14	0.48
8:9:25:ARG:NH2	36:e:99:GLU:OE2	2.47	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:D:110:ARG:O	11:D:113:ARG:NH1	2.46	0.48
2:2:2521:G:H2'	2:2:2522:7MG:H82	1.96	0.48
2:2:3641:U:OP2	2:2:3646:A:N6	2.39	0.48
18:L:85:GLN:HA	18:L:88:VAL:HG12	1.95	0.48
47:r:182:GLY:HA2	47:r:194:VAL:HB	1.96	0.48
3:4:405:MET:HB3	3:4:409:TYR:HB2	1.95	0.47
14:G:161:VAL:HG11	14:G:200:THR:HG23	1.95	0.47
14:G:224:THR:HA	14:G:228:ASP:HB2	1.96	0.47
2:2:699:C:H2'	2:2:700:G:C8	2.49	0.47
2:2:4377:G:O6	18:L:42:ARG:NH2	2.46	0.47
20:N:159:LYS:HE3	20:N:163:MET:HE3	1.96	0.47
43:m:95:GLN:O	43:m:100:ASN:ND2	2.47	0.47
2:2:442:G:OP1	44:n:68:ARG:NH1	2.40	0.47
2:2:2092:G:O2'	2:2:2262:G:N2	2.46	0.47
7:8:97:A:H5'	15:H:62:ASN:HD22	1.79	0.47
20:N:114:ASP:N	20:N:114:ASP:OD1	2.48	0.47
2:2:4093:G:H2'	2:2:4094:G:C8	2.49	0.47
2:2:4277:G:H5''	34:c:17:ARG:HG2	1.97	0.47
11:D:12:SER:HB3	11:D:18:SER:HB3	1.95	0.47
35:d:66:SER:O	35:d:66:SER:OG	2.29	0.47
14:G:167:VAL:HG12	14:G:170:LEU:HD12	1.96	0.47
27:V:54:TYR:OH	27:V:73:PHE:O	2.33	0.47
47:r:65:ALA:HB2	47:r:74:ILE:HD13	1.97	0.47
2:2:4238:G:H2'	2:2:4239:A:C8	2.48	0.47
2:2:5018:C:H2'	2:2:5019:A:H8	1.80	0.47
11:D:5:ARG:NH1	11:D:24:LEU:O	2.47	0.47
24:R:91:GLN:HE22	24:R:94:LEU:HD22	1.79	0.47
26:U:31:ARG:NH1	26:U:124:ASP:OD1	2.47	0.47
33:b:85:ASP:HA	33:b:90:THR:HA	1.96	0.47
2:2:197:A:N3	2:2:222:C:O2'	2.47	0.47
2:2:500:G:OP2	2:2:503:C:O2'	2.31	0.47
2:2:685:C:OP2	45:o:99:ASP:O	2.32	0.47
2:2:1405:C:N4	2:2:1413:C:O2	2.47	0.47
2:2:2372:U:O2'	40:j:69:ASN:ND2	2.48	0.47
2:2:3717:A:OP2	2:2:3735:G:N2	2.45	0.47
2:2:4314:C:O2'	10:C:36:ASP:OD1	2.30	0.47
2:2:4740:G:H1'	2:2:4742:G:H5''	1.97	0.47
3:4:257:LEU:HB2	3:4:299:LEU:HD11	1.97	0.47
3:4:364:ILE:O	3:4:366:THR:OG1	2.31	0.47
3:4:395:LYS:HG2	3:4:397:ARG:H	1.79	0.47
33:b:17:LEU:HD21	34:c:136:ARG:HH11	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:b:147:ASP:HB3	33:b:150:ILE:HB	1.96	0.47
41:k:67:LYS:O	41:k:75:ARG:NH2	2.48	0.47
2:2:4626:A:OP2	9:B:224:LYS:NZ	2.33	0.47
3:4:173:LEU:HD12	3:4:221:ASP:HA	1.97	0.47
23:Q:124:LEU:HD21	23:Q:126:LEU:HD13	1.96	0.47
2:2:2886:U:OP2	8:9:68:ARG:NH2	2.45	0.47
3:4:366:THR:HG23	5:6:175:SER:HA	1.97	0.47
16:I:59:LYS:HA	16:I:59:LYS:HD2	1.71	0.47
30:Y:36:ILE:HD11	30:Y:48:LEU:HG	1.96	0.47
47:r:79:TYR:HB2	47:r:82:GLU:HG3	1.97	0.47
47:r:84:PRO:HD3	47:r:92:LEU:HD11	1.95	0.47
2:2:4448:G:H1	2:2:4502:C:H41	1.63	0.47
2:2:4935:C:H2'	2:2:4936:G:C8	2.50	0.47
3:4:258:SER:OG	3:4:259:GLU:N	2.48	0.47
9:B:223:THR:HB	9:B:275:HIS:H	1.80	0.47
16:I:18:ILE:HG22	16:I:27:VAL:HG13	1.97	0.47
18:L:93:ASN:HD21	18:L:97:ALA:HB3	1.80	0.47
43:m:229:ALA:HB3	43:m:234:LYS:HB3	1.96	0.47
2:2:1320:U:OP1	2:2:1854:G:O2'	2.33	0.46
20:N:129:ASP:N	20:N:129:ASP:OD1	2.48	0.46
41:k:100:ALA:O	41:k:108:ARG:NH2	2.48	0.46
2:2:1646:A:O2'	19:M:49:TRP:O	2.33	0.46
2:2:1913:C:O2'	27:V:87:MET:O	2.32	0.46
16:I:53:LYS:HD2	16:I:53:LYS:HA	1.75	0.46
45:o:256:GLN:O	45:o:260:LYS:NZ	2.45	0.46
2:2:992:C:H41	2:2:995:C:H4'	1.81	0.46
9:B:212:GLY:N	48:z:33:LEU:HD21	2.29	0.46
2:2:2049:G:O2'	2:2:3884:U:O2'	2.28	0.46
2:2:4882:U:OP1	25:S:117:LYS:NZ	2.48	0.46
45:o:157:HIS:HB3	45:o:160:LYS:HD2	1.96	0.46
2:2:1824:G:OP1	34:c:35:LYS:NZ	2.40	0.46
2:2:2300:A:H62	11:D:143:ARG:HH21	1.64	0.46
2:2:4940:C:H5'	2:2:4941:G:H5''	1.95	0.46
5:6:214:GLU:HA	5:6:217:VAL:HG22	1.97	0.46
10:C:55:LYS:HD2	10:C:58:GLN:HE21	1.80	0.46
43:m:225:ILE:HG12	43:m:234:LYS:HA	1.97	0.46
2:2:1628:C:H5''	43:m:15:VAL:HG21	1.97	0.46
2:2:4940:C:O2'	45:o:246:ARG:NH2	2.40	0.46
6:7:68:SER:HG	6:7:100:LYS:HB2	1.77	0.46
14:G:165:GLU:HA	14:G:168:VAL:HG22	1.96	0.46
30:Y:64:ASN:HD22	30:Y:80:GLN:NE2	2.13	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:I:82:LYS:O	16:I:86:LEU:HB2	2.15	0.46
33:b:60:GLU:HB3	34:c:136:ARG:HH12	1.80	0.46
38:h:53:ASP:OD1	38:h:53:ASP:N	2.47	0.46
43:m:56:ALA:HB2	43:m:130:SER:HB3	1.97	0.46
2:2:1516:G:O2'	23:Q:18:TRP:NE1	2.47	0.46
3:4:188:VAL:HG12	3:4:189:THR:H	1.80	0.46
3:4:477:MET:HE1	6:7:120:LYS:HG3	1.98	0.46
20:N:20:LEU:HD12	20:N:74:VAL:HB	1.96	0.46
23:Q:130:LYS:HG2	23:Q:132:SER:H	1.81	0.46
24:R:33:LYS:HA	24:R:36:LYS:HE2	1.97	0.46
25:S:126:GLU:OE2	27:V:184:ASN:ND2	2.43	0.46
35:d:40:GLU:O	35:d:44:GLN:HB2	2.15	0.46
39:i:66:SER:HB2	39:i:122:TYR:HE2	1.81	0.46
40:j:97:ASP:OD1	40:j:97:ASP:N	2.49	0.46
46:p:214:SER:OG	46:p:215:SER:N	2.49	0.46
2:2:257:C:H2'	2:2:258:G:C8	2.51	0.46
2:2:1094:G:C6	2:2:1201:U:N3	2.84	0.46
2:2:2580:U:OP1	39:i:36:ARG:NH2	2.38	0.46
12:E:31:TYR:HA	12:E:34:THR:HG22	1.96	0.46
17:K:4:ARG:HE	17:K:4:ARG:HB3	1.52	0.46
36:e:61:VAL:O	36:e:79:ALA:N	2.49	0.46
2:2:139:G:H2'	2:2:140:G:C8	2.51	0.46
2:2:300:A:H2'	2:2:301:G:H8	1.81	0.46
2:2:962:C:H5''	2:2:963:G:C8	2.51	0.46
2:2:1883:OMG:HM22	2:2:2070:U:H3	1.81	0.46
14:G:31:LEU:HD11	39:i:123:LYS:HA	1.98	0.46
24:R:147:ASP:OD1	24:R:147:ASP:N	2.46	0.46
2:2:136:C:N4	15:H:77:LYS:O	2.48	0.45
16:I:24:THR:OG1	16:I:37:ASP:OD2	2.33	0.45
29:X:26:VAL:HG12	29:X:30:GLU:HG3	1.98	0.45
44:n:106:TYR:HB2	45:o:193:PHE:HD1	1.80	0.45
47:r:231:VAL:HA	47:r:235:MET:HE2	1.98	0.45
2:2:4910:G:N2	27:V:106:ASP:O	2.47	0.45
25:S:15:VAL:HG22	25:S:50:MET:HE1	1.98	0.45
38:h:8:THR:HG21	38:h:13:LYS:HD2	1.98	0.45
39:i:88:ASP:OD1	39:i:88:ASP:N	2.45	0.45
2:2:2580:U:O2'	39:i:79:HIS:ND1	2.48	0.45
2:2:4541:G:N2	2:2:4544:A:OP2	2.40	0.45
2:2:4774:C:O2'	2:2:4775:C:O4'	2.34	0.45
5:6:143:ALA:HB3	5:6:162:HIS:HE1	1.82	0.45
14:G:140:VAL:O	14:G:144:THR:OG1	2.30	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:S:101:LYS:HB2	27:V:200:GLY:HA3	1.97	0.45
46:p:70[B]:ARG:HG2	46:p:74:MET:HE3	1.99	0.45
2:2:662:C:H2'	2:2:663:G:C8	2.52	0.45
2:2:1211:G:O2'	46:p:70[B]:ARG:NH1	2.49	0.45
2:2:3861:A:H2'	2:2:3862:A:H8	1.81	0.45
11:D:211:TYR:HE1	11:D:229:LEU:HB3	1.82	0.45
14:G:95:LEU:HD11	14:G:222:ILE:HD11	1.99	0.45
21:O:33:LYS:HG2	21:O:46:VAL:HG22	1.99	0.45
25:S:16:SER:OG	25:S:17:PHE:N	2.50	0.45
33:b:15:ARG:HB3	33:b:27:LEU:HD23	1.96	0.45
2:2:2789:A:H2	22:P:45:ARG:HH22	1.63	0.45
3:4:76:HIS:O	3:4:80:ALA:HB2	2.16	0.45
16:I:102:ASN:HB2	16:I:115:ARG:HB3	1.99	0.45
27:V:8:VAL:HG12	27:V:117:ARG:HG3	1.96	0.45
11:D:140:LYS:O	11:D:204:ARG:NH1	2.50	0.45
11:D:142:HIS:CE1	11:D:204:ARG:HH22	2.35	0.45
28:W:33:LEU:HA	28:W:38:LYS:HG2	1.98	0.45
37:g:141:ALA:HB3	37:g:144:TYR:HD2	1.81	0.45
3:4:292:ASP:OD1	3:4:292:ASP:N	2.50	0.45
14:G:158:ALA:HB2	14:G:190:LEU:HD12	1.99	0.45
16:I:23:ARG:HA	16:I:45:LEU:HD12	1.99	0.45
35:d:50:ASN:O	35:d:52:LYS:NZ	2.38	0.45
2:2:62:A:N3	2:2:77:U:O2'	2.42	0.45
2:2:229:G:OP1	38:h:11:ARG:NH1	2.47	0.45
2:2:362:A:N6	22:P:37:TYR:O	2.37	0.45
2:2:1595:G:H1'	2:2:1597:G:H21	1.80	0.45
2:2:1864:G:N7	24:R:22:ARG:NH1	2.65	0.45
2:2:4967:A:H2'	2:2:4968:A:C8	2.52	0.45
16:I:92:MET:HE2	16:I:179:ILE:HG22	1.99	0.45
16:I:117:PHE:O	16:I:120:GLU:HG2	2.17	0.45
19:M:21:ARG:NH2	19:M:39:TYR:O	2.48	0.45
43:m:207:VAL:HG13	43:m:208:GLU:HG3	1.99	0.45
3:4:517:ARG:NH1	3:4:534:LYS:O	2.44	0.45
5:6:111:ASN:ND2	5:6:155:SER:O	2.38	0.45
5:6:209:ASP:OD1	5:6:209:ASP:N	2.45	0.45
2:2:175:C:H2'	2:2:176:G:C8	2.52	0.45
2:2:1457:G:O2'	31:Z:75:ARG:NH2	2.50	0.45
2:2:4088:C:H2'	2:2:4089:G:C8	2.52	0.45
5:6:85:ARG:HE	6:7:80:LYS:HG3	1.81	0.45
13:F:33:LEU:HD23	13:F:33:LEU:HA	1.89	0.45
20:N:128:LEU:HD13	20:N:130:PHE:HE1	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:Q:163:LYS:NZ	23:Q:164:GLU:O	2.42	0.45
27:V:193:THR:HG22	27:V:197:LYS:HE3	1.99	0.45
40:j:117:LEU:HD23	40:j:117:LEU:HA	1.82	0.45
2:2:755:C:H2'	2:2:756:G:C8	2.52	0.44
2:2:1333:A:H2'	2:2:1334:A:C8	2.52	0.44
2:2:4449:A:H5'	3:4:118:LYS:HD2	1.98	0.44
4:5:39:C:N3	20:N:73:THR:OG1	2.37	0.44
42:l:94:ARG:HB2	42:l:111:ILE:HD11	1.99	0.44
20:N:141:ILE:HA	20:N:144:LYS:HG3	2.00	0.44
33:b:76:LYS:HD2	33:b:131:GLU:HG3	1.99	0.44
2:2:980:U:H5'	45:o:42:PRO:HA	1.99	0.44
2:2:2809:G:O2'	2:2:4644:G:OP1	2.27	0.44
29:X:38:THR:HA	29:X:45:THR:HA	1.98	0.44
39:i:54:THR:HG23	39:i:57:MET:HE3	1.98	0.44
45:o:150:LEU:HB3	45:o:194:VAL:HG13	1.99	0.44
2:2:1050:C:H3'	2:2:1051:G:H3'	1.99	0.44
2:2:2419:C:OP1	30:Y:23:ARG:NH2	2.51	0.44
2:2:3717:A:H2'	2:2:3718:A2M:C8	2.47	0.44
3:4:489:GLU:HA	3:4:492:LYS:HE3	1.99	0.44
5:6:107:VAL:HG22	5:6:118:HIS:HB2	1.98	0.44
6:7:63:LEU:CD2	6:7:63:LEU:N	2.81	0.44
9:B:165:HIS:HB3	9:B:180:LEU:HD23	1.99	0.44
11:D:14:LYS:HD2	11:D:173:LYS:HZ3	1.83	0.44
29:X:47:MET:HA	29:X:57:CYS:HA	1.98	0.44
23:Q:162:LYS:HE3	23:Q:162:LYS:HB2	1.80	0.44
31:Z:159:PRO:HA	31:Z:160:HIS:HA	1.80	0.44
2:2:1419:G:C2	18:L:116:LYS:HD3	2.52	0.44
2:2:1442:C:O2'	2:2:1443:A:N7	2.49	0.44
2:2:2556:G:H2'	2:2:2557:G:C8	2.52	0.44
2:2:4302:U:H4'	34:c:5:LYS:HD3	1.99	0.44
14:G:132:ARG:HA	14:G:133:PRO:HD3	1.89	0.44
2:2:2812:A:H5'	32:a:88:ARG:HD2	2.00	0.44
3:4:536:ASP:O	3:4:540:ALA:CB	2.66	0.44
7:8:102:G:OP2	7:8:104:A:O2'	2.30	0.44
14:G:157:ILE:HB	14:G:183:ILE:HD13	1.99	0.44
33:b:11:LYS:HE3	33:b:11:LYS:HB2	1.84	0.44
37:g:43:SER:HA	37:g:44:PRO:HD3	1.86	0.44
42:l:21:ASN:OD1	42:l:21:ASN:N	2.51	0.44
2:2:4258:C:H5'	20:N:68:ILE:HD11	1.98	0.44
2:2:4286:C:H5'	28:W:99:ARG:HH22	1.82	0.44
2:2:4678:G:OP1	48:z:14:ARG:NH1	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:6:121:LEU:O	5:6:139:ARG:NH1	2.51	0.44
21:O:22:SER:HA	21:O:65:ALA:HB3	2.00	0.44
43:m:72:ARG:HA	43:m:72:ARG:HD3	1.80	0.44
2:2:408:A:O2'	2:2:411:G:OP2	2.29	0.44
2:2:724:C:H1'	11:D:343:GLN:HG2	2.00	0.44
2:2:4363:A:H5''	28:W:36:GLN:HG2	2.00	0.44
6:7:69:PHE:C	6:7:71:PHE:H	2.25	0.44
6:7:111:ARG:HB3	6:7:111:ARG:CZ	2.47	0.44
27:V:6:VAL:HG12	27:V:32:LYS:HB2	2.00	0.44
48:z:24:LYS:O	48:z:28:ARG:HD2	2.17	0.44
2:2:1174:G:N2	2:2:1187:G:N7	2.66	0.43
2:2:1613:A:H5'	43:m:183:GLY:HA2	1.99	0.43
2:2:1812:C:H5''	10:C:56:LYS:HD3	1.99	0.43
41:k:117:GLN:H	41:k:117:GLN:HG2	1.59	0.43
47:r:221:LYS:HB3	47:r:221:LYS:HE2	1.83	0.43
2:2:2364:OMG:HM23	2:2:2364:OMG:H1'	1.90	0.43
2:2:3861:A:H2'	2:2:3862:A:C8	2.53	0.43
2:2:4346:U:O2'	28:W:80:LYS:O	2.34	0.43
3:4:233:ARG:HB3	3:4:237:GLU:HB3	2.00	0.43
14:G:107:LYS:HD3	14:G:107:LYS:HA	1.77	0.43
24:R:89:LEU:HD23	24:R:89:LEU:HA	1.86	0.43
34:c:30:TYR:O	47:r:41:LYS:NZ	2.41	0.43
38:h:112:ASP:O	38:h:116:LYS:HB2	2.18	0.43
2:2:158:A:N1	2:2:276:C:O2'	2.41	0.43
2:2:1968:G:H3'	2:2:1969:G:H8	1.82	0.43
11:D:204:ARG:NH2	11:D:205:ARG:O	2.51	0.43
15:H:82:ASP:OD1	15:H:82:ASP:N	2.51	0.43
33:b:113:MET:HE3	33:b:113:MET:HB3	1.83	0.43
34:c:31:MET:HE2	34:c:31:MET:HB3	1.85	0.43
34:c:100:LYS:HB3	34:c:100:LYS:HE2	1.87	0.43
35:d:44:GLN:HG3	35:d:56:LEU:HD21	2.01	0.43
37:g:73:HIS:HB2	37:g:116:LEU:HD23	2.00	0.43
47:r:164:LYS:NZ	47:r:168:ASP:OD1	2.37	0.43
2:2:468:U:N3	2:2:684:G:N7	2.66	0.43
2:2:4128:A:H1'	14:G:35:ARG:HB2	1.99	0.43
2:2:4637:OMG:HM23	2:2:4637:OMG:H1'	1.86	0.43
9:B:24:ARG:HD3	9:B:28:LYS:H	1.83	0.43
18:L:22:ILE:HB	18:L:23:GLY:H	1.63	0.43
24:R:129:LEU:HD23	24:R:129:LEU:HA	1.86	0.43
33:b:7:LEU:HD12	33:b:106:VAL:HG12	2.01	0.43
43:m:102:LEU:HG	43:m:107:MET:HE3	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:729:2MG:OP1	33:b:63:TYR:OH	2.32	0.43
2:2:2651:C:O2'	2:2:2653:C:OP1	2.29	0.43
2:2:3838:U:OP1	8:9:17:ARG:NH1	2.41	0.43
18:L:24:LYS:HD3	18:L:26:ARG:NH2	2.34	0.43
23:Q:56:ARG:NH1	23:Q:74:ARG:O	2.47	0.43
27:V:8:VAL:HA	27:V:34:VAL:HG22	2.01	0.43
36:e:16:ILE:HD11	36:e:57:VAL:H	1.82	0.43
47:r:271:MET:HE3	47:r:271:MET:HB2	1.85	0.43
2:2:2406:G:N7	22:P:2:SER:N	2.66	0.43
3:4:536:ASP:O	3:4:540:ALA:HB2	2.19	0.43
5:6:11:CYS:O	5:6:187:ASN:ND2	2.44	0.43
13:F:41:ALA:HB3	13:F:52:ARG:HB3	2.01	0.43
18:L:115:GLY:O	18:L:136:LYS:NZ	2.36	0.43
23:Q:55:ILE:O	23:Q:97:SER:OG	2.34	0.43
26:U:96:ARG:HH12	26:U:104:GLU:HG2	1.83	0.43
27:V:47:PHE:HZ	27:V:144:GLU:HG3	1.83	0.43
34:c:67:VAL:HA	34:c:72:VAL:HG12	2.00	0.43
2:2:2420:A:OP2	30:Y:127:ARG:NH1	2.51	0.43
2:2:2694:G:OP2	2:2:2696:A:N6	2.51	0.43
2:2:3745:U:HO2'	43:m:243:THR:H	1.67	0.43
5:6:78:ASP:OD2	6:7:2:ARG:NH1	2.43	0.43
8:9:88:ARG:HA	8:9:88:ARG:HD3	1.81	0.43
30:Y:128:ARG:HB3	30:Y:136:ILE:HD11	1.99	0.43
31:Z:66:MET:HE1	31:Z:100:VAL:HG22	2.01	0.43
36:e:69:LYS:HA	36:e:69:LYS:HD3	1.86	0.43
46:p:155:TYR:OH	46:p:188:GLU:OE2	2.33	0.43
2:2:1443:A:H2'	2:2:1444:G:C8	2.53	0.43
2:2:1702:C:H5'	11:D:308:LYS:HB3	2.01	0.43
2:2:2635:U:H4'	32:a:55:VAL:HG11	2.01	0.43
2:2:4524:G:C2	9:B:252:ALA:HB1	2.54	0.43
3:4:455:LYS:HD2	3:4:455:LYS:HA	1.80	0.43
3:4:520:LEU:O	35:d:99:TRP:NE1	2.39	0.43
6:7:57:LYS:HB3	6:7:64:THR:CG2	2.48	0.43
7:8:26:C:O2'	11:D:53:ALA:O	2.34	0.43
7:8:41:A:O2'	19:M:59:THR:OG1	2.31	0.43
11:D:143:ARG:HA	11:D:143:ARG:HD2	1.84	0.43
13:F:85:LYS:HE2	13:F:85:LYS:HB3	1.83	0.43
28:W:98:LYS:H	28:W:98:LYS:HG2	1.62	0.43
35:d:96:LEU:HB3	35:d:100:LEU:HD12	2.00	0.43
46:p:70[A]:ARG:HG2	46:p:74:MET:HE3	2.00	0.43
2:2:106:A:OP1	23:Q:39:ARG:NH1	2.49	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:1363:C:OP2	23:Q:36:ARG:NH2	2.52	0.43
2:2:2520:C:H2'	2:2:2521:G:C8	2.54	0.43
2:2:4736:C:H2'	2:2:4737:G:H8	1.84	0.43
9:B:165:HIS:ND1	9:B:166:THR:O	2.52	0.43
20:N:63:ARG:N	20:N:66:GLU:OE2	2.48	0.43
21:O:10:ASP:HA	21:O:13:LEU:HG	2.01	0.43
28:W:4:VAL:O	28:W:94:GLY:N	2.46	0.43
45:o:178:PRO:HB2	45:o:181:LEU:HB2	2.01	0.43
45:o:245:GLN:HA	45:o:248:ILE:HG12	1.99	0.43
2:2:2436:U:OP1	37:g:137:TYR:OH	2.34	0.43
2:2:2468:U:O2'	2:2:2506:G:N2	2.51	0.43
2:2:3717:A:H2'	2:2:3718:A2M:H8	2.00	0.43
2:2:4543:G:H2'	2:2:4544:A:C8	2.54	0.43
2:2:4764:A:OP1	33:b:156:HIS:ND1	2.44	0.43
17:K:43:MET:HE2	17:K:43:MET:HB2	1.71	0.43
24:R:51:VAL:HG12	24:R:153:LEU:HD21	1.99	0.43
33:b:53:LYS:HB2	33:b:53:LYS:HE3	1.82	0.43
47:r:94:ASN:H	47:r:97:ALA:HB3	1.83	0.43
2:2:750:U:H2'	2:2:751:G:C8	2.54	0.42
2:2:1094:G:O6	2:2:1201:U:O4	2.36	0.42
2:2:1833:G:N2	2:2:1835:G:O4'	2.52	0.42
2:2:1907:A:H4'	46:p:223:LYS:HE3	2.01	0.42
43:m:20:VAL:HG12	43:m:23:ARG:HD2	2.01	0.42
2:2:4163:U:H5'	2:2:4164:C:H5''	2.01	0.42
13:F:71:LYS:HA	13:F:71:LYS:HD3	1.93	0.42
18:L:24:LYS:HB2	18:L:24:LYS:HE3	1.62	0.42
27:V:31:ARG:HD2	27:V:31:ARG:HA	1.83	0.42
45:o:221:LYS:HD2	45:o:221:LYS:HA	1.77	0.42
2:2:1188:C:H2'	2:2:1189:G:C8	2.55	0.42
2:2:3680:U:OP1	43:m:54:ARG:NH2	2.44	0.42
39:i:95:VAL:HG11	39:i:113:GLU:HG3	2.01	0.42
2:2:404:U:O3'	38:h:87:ARG:NH1	2.52	0.42
2:2:1084:C:H2'	2:2:1085:C:H6	1.84	0.42
2:2:2520:C:H2'	2:2:2521:G:H8	1.84	0.42
2:2:4474:A:OP2	2:2:4476:C:N4	2.52	0.42
33:b:25:PRO:HA	33:b:26:PRO:HD3	1.91	0.42
2:2:74:G:O6	23:Q:103:ARG:NH2	2.48	0.42
2:2:147:A:OP1	14:G:197:LYS:NZ	2.41	0.42
2:2:1080:C:H1'	2:2:1220:G:H22	1.84	0.42
2:2:1738:A:OP1	24:R:37:LYS:NZ	2.42	0.42
2:2:2765:A:H2'	2:2:2766:A:C8	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:M:83:THR:HA	19:M:84:PRO:HD3	1.92	0.42
22:P:24:PRO:HB2	22:P:27:ILE:HG12	2.00	0.42
23:Q:155:MET:HA	23:Q:156:PRO:HD3	1.82	0.42
47:r:107:ARG:HG3	47:r:248:ARG:HD2	2.02	0.42
2:2:1072:C:H2'	2:2:1073:G:C8	2.54	0.42
2:2:3867:A2M:HM'3	2:2:3867:A2M:H1'	1.85	0.42
3:4:395:LYS:HB3	3:4:395:LYS:HE2	1.78	0.42
9:B:294:LYS:HZ3	9:B:298:LEU:HD21	1.85	0.42
9:B:300:LYS:O	9:B:304:SER:HB3	2.19	0.42
15:H:52:LYS:HA	15:H:52:LYS:HD3	1.80	0.42
38:h:100:HIS:ND1	38:h:102:SER:OG	2.46	0.42
45:o:223:ARG:HA	45:o:224:LYS:HA	1.73	0.42
47:r:265:ARG:HD2	47:r:265:ARG:HA	1.85	0.42
2:2:63:G:OP1	26:U:169:ARG:NH1	2.52	0.42
2:2:908:G:H2'	2:2:909:A:H8	1.84	0.42
2:2:1398:A:H4'	2:2:1399:G:H5'	2.02	0.42
5:6:125:THR:HA	5:6:128:ILE:HG22	2.00	0.42
11:D:317:ASN:HD22	11:D:320:LYS:HE2	1.84	0.42
14:G:137[A]:ARG:HD2	14:G:146:LEU:HD11	2.02	0.42
26:U:165:THR:O	26:U:169:ARG:CB	2.66	0.42
2:2:2752:G:H3'	2:2:2753:G:H8	1.85	0.42
2:2:4568:A:O2'	2:2:4981:G:N7	2.47	0.42
4:5:23:A:N3	4:5:118:C:O2'	2.40	0.42
7:8:49:G:H4'	15:H:35:LYS:HE2	2.02	0.42
8:9:63:CYS:SG	8:9:79:HIS:NE2	2.91	0.42
33:b:127:MET:HE2	33:b:127:MET:HB3	1.91	0.42
43:m:146:THR:N	43:m:158:ILE:O	2.52	0.42
46:p:222:LYS:HB3	46:p:231:GLY:HA2	2.01	0.42
48:z:34:LYS:CE	48:z:34:LYS:CA	2.98	0.42
2:2:29:G:H5''	26:U:172:ARG:HG2	2.02	0.42
2:2:2406:G:O2'	22:P:48:LYS:NZ	2.50	0.42
2:2:2457:G:OP1	26:U:65:ARG:NH1	2.52	0.42
15:H:71:LYS:HD3	15:H:71:LYS:HA	1.77	0.42
16:I:105:ILE:HD12	16:I:105:ILE:HA	1.91	0.42
18:L:24:LYS:HD3	18:L:26:ARG:CZ	2.50	0.42
20:N:143:ASP:OD1	20:N:143:ASP:N	2.53	0.42
35:d:116:GLN:HE21	35:d:116:GLN:HB3	1.65	0.42
2:2:297:U:O2'	26:U:179:LYS:O	2.37	0.42
2:2:466:A:N3	2:2:467:U:H1'	2.34	0.42
2:2:3924:C:H5''	28:W:57:ARG:HH12	1.84	0.42
2:2:4088:C:H2'	2:2:4089:G:H8	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:5053:U:H5'	2:2:5054:C:C4	2.55	0.42
3:4:296:ILE:O	3:4:304:GLN:NE2	2.53	0.42
4:5:94:C:H4'	33:b:122:HIS:HB2	2.01	0.42
10:C:57:MET:HE3	10:C:57:MET:HB2	1.85	0.42
30:Y:17:SER:HB3	30:Y:98:ALA:HB2	2.01	0.42
36:e:82:ILE:HD13	36:e:104:VAL:HG13	2.02	0.42
2:2:2740:U:O2'	2:2:2742:G:N2	2.53	0.41
3:4:213:LYS:HA	3:4:213:LYS:HD3	1.68	0.41
8:9:68:ARG:HE	8:9:68:ARG:HB3	1.69	0.41
12:E:38:ILE:HG21	12:E:63:TYR:HB3	2.02	0.41
20:N:56:THR:HB	20:N:63:ARG:HA	2.02	0.41
23:Q:130:LYS:HD3	23:Q:132:SER:HB2	2.02	0.41
27:V:180:GLN:O	27:V:184:ASN:HB2	2.20	0.41
38:h:103:LYS:HA	38:h:103:LYS:HD3	1.85	0.41
40:j:92:ARG:HA	40:j:102:LEU:HD12	2.02	0.41
45:o:91:THR:OG1	45:o:107:VAL:O	2.29	0.41
2:2:67:C:OP2	2:2:312:G:N2	2.48	0.41
2:2:2040:A:H4'	2:2:2041:A:H5''	2.02	0.41
2:2:2309:G:O2'	7:8:18:U:O2	2.39	0.41
2:2:4323:A:H5'	47:r:178:LYS:HD3	2.02	0.41
3:4:6:PHE:HB3	3:4:158:LEU:HG	2.02	0.41
7:8:14:OMU:H1'	7:8:14:OMU:HM23	1.52	0.41
11:D:66:SER:O	11:D:66:SER:OG	2.37	0.41
14:G:161:VAL:HG23	14:G:164:ILE:HA	2.02	0.41
24:R:158:MET:HE3	24:R:158:MET:HB2	1.86	0.41
25:S:96:GLU:OE1	25:S:100:ARG:NH2	2.51	0.41
46:p:187:MET:HB2	46:p:187:MET:HE3	1.82	0.41
2:2:267:G:H2'	2:2:268:G:H8	1.84	0.41
7:8:2:G:N2	7:8:3:A:N7	2.68	0.41
13:F:19:LYS:HD3	13:F:19:LYS:HA	1.85	0.41
29:X:30:GLU:HA	29:X:33:GLN:HG2	2.02	0.41
43:m:116:LEU:HB2	43:m:126:LEU:HB2	2.02	0.41
47:r:173:ILE:O	47:r:175:HIS:ND1	2.34	0.41
47:r:265:ARG:HH21	47:r:269:PRO:HG3	1.85	0.41
2:2:99:A:H5''	26:U:184:ILE:HD13	2.02	0.41
2:2:1213:G:H5''	2:2:1214:C:H5''	2.01	0.41
2:2:2063:G:H2'	2:2:2064:G:C8	2.56	0.41
2:2:4528:G:O2'	2:2:4529:B8W:O5'	2.38	0.41
9:B:66:LYS:HB3	9:B:66:LYS:HE2	1.95	0.41
15:H:103:LYS:HB2	15:H:103:LYS:HE3	1.89	0.41
2:2:196:C:H4'	38:h:126:ARG:HG3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:4411:G:N2	2:2:4431:U:O2	2.54	0.41
24:R:130:GLU:HG2	24:R:158:MET:HG2	2.02	0.41
26:U:104:GLU:HA	26:U:160:GLU:HG3	2.02	0.41
27:V:133:ARG:HA	27:V:133:ARG:HD3	1.80	0.41
28:W:71:GLU:HB2	28:W:80:LYS:HG3	2.03	0.41
30:Y:69:ARG:HA	30:Y:80:GLN:HA	2.03	0.41
42:l:19:LYS:HG2	42:l:24:THR:HG23	2.02	0.41
42:l:61:VAL:HA	42:l:81:THR:HA	2.02	0.41
47:r:10:LYS:HE3	47:r:10:LYS:HB2	1.94	0.41
2:2:2764:A:H2'	2:2:2765:A:H8	1.86	0.41
2:2:4239:A:H2'	2:2:4240:G:C8	2.56	0.41
2:2:4412:C:H2'	2:2:4413:C:H6	1.85	0.41
2:2:5018:C:H2'	2:2:5019:A:C8	2.55	0.41
4:5:8:G:O6	47:r:21:ARG:NH2	2.52	0.41
7:8:60:G:O6	7:8:96:C:O2'	2.33	0.41
7:8:131:G:H5''	37:g:108:GLN:HE21	1.86	0.41
9:B:92:TYR:OH	9:B:182:GLU:OE2	2.33	0.41
10:C:92:LYS:HA	10:C:95:ARG:HD3	2.03	0.41
24:R:102:GLN:HA	24:R:103:GLY:HA2	1.74	0.41
46:p:216:PRO:HD3	46:p:247:MET:HE2	2.02	0.41
2:2:180:C:N4	2:2:181:C:N3	2.69	0.41
4:5:48:G:OP1	47:r:226:TYR:OH	2.34	0.41
9:B:45:ALA:HB3	9:B:183:ILE:HG23	2.03	0.41
14:G:205:THR:HG22	14:G:206:GLN:H	1.86	0.41
15:H:73:TYR:HB3	15:H:79:LYS:HG2	2.03	0.41
19:M:21:ARG:O	19:M:23:GLY:N	2.53	0.41
2:2:1100:U:O2	2:2:1195:G:C6	2.74	0.41
2:2:4105:A:H1'	2:2:4106:G:C2	2.56	0.41
2:2:4912:G:N2	9:B:156:TYR:OH	2.54	0.41
9:B:362:LYS:HB3	9:B:362:LYS:HE3	1.85	0.41
2:2:343:C:O2'	19:M:75:ARG:NH2	2.45	0.41
2:2:685:C:H4'	2:2:686:A:C4	2.56	0.41
2:2:687:U:O2'	45:o:95:PRO:O	2.35	0.41
2:2:750:U:H2'	2:2:751:G:H8	1.86	0.41
2:2:4242:U:H3	2:2:4281:A:H2	1.68	0.41
2:2:4271:A:OP1	2:2:4272:G:N2	2.54	0.41
2:2:4478:G:N2	2:2:4608:G:O2'	2.54	0.41
2:2:4546:A:N7	43:m:215:ASN:ND2	2.69	0.41
2:2:4586:G:OP2	27:V:74:ARG:NH1	2.54	0.41
3:4:78:PHE:HE1	3:4:243:ALA:HA	1.86	0.41
3:4:630:LYS:HA	3:4:630:LYS:HD2	1.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:6:72:VAL:HG21	5:6:81:LEU:HD13	2.03	0.41
6:7:63:LEU:CD2	6:7:63:LEU:H	2.32	0.41
6:7:106:LYS:HD2	6:7:106:LYS:HA	1.92	0.41
10:C:119:CYS:HB2	45:o:72:LYS:HB2	2.03	0.41
14:G:252:LYS:HA	14:G:252:LYS:HD2	1.87	0.41
20:N:111:GLU:HG2	20:N:113:ILE:H	1.86	0.41
22:P:33:ASN:ND2	22:P:35:ILE:O	2.53	0.41
24:R:26:GLN:HG2	24:R:29:ARG:NH2	2.36	0.41
24:R:74:ALA:O	24:R:78:ILE:HG13	2.21	0.41
26:U:73:ARG:HA	26:U:74:PRO:HD3	1.90	0.41
31:Z:154:LYS:HD3	31:Z:154:LYS:HA	1.97	0.41
36:e:129:TRP:HB2	36:e:132:ILE:HG12	2.02	0.41
43:m:70:LYS:HD2	43:m:72:ARG:HH21	1.86	0.41
47:r:81:HIS:HA	47:r:92:LEU:HD21	2.02	0.41
47:r:88:VAL:HG12	47:r:239:MET:HE3	2.03	0.41
2:2:1094:G:C6	2:2:1201:U:C4	3.08	0.41
2:2:1444:G:H2'	2:2:1445:U:H6	1.86	0.41
2:2:2480:G:H2'	2:2:2481:G:C8	2.56	0.41
2:2:4717:A:H4'	9:B:20:LYS:HD3	2.03	0.41
2:2:4717:A:OP2	9:B:30:LYS:NZ	2.43	0.41
2:2:4761:G:H2'	2:2:4762:A:H8	1.86	0.41
3:4:343:ARG:O	3:4:346:THR:OG1	2.28	0.41
5:6:74:ASN:HD21	5:6:99:GLU:H	1.69	0.41
15:H:86:LYS:HD2	15:H:92:ARG:HH12	1.86	0.41
24:R:17:ILE:HD13	24:R:17:ILE:HA	1.92	0.41
31:Z:50:ARG:HB3	31:Z:83:VAL:HG21	2.03	0.41
38:h:89:LYS:HB2	38:h:89:LYS:HE3	1.86	0.41
2:2:102:G:O2'	2:2:1381:U:O2'	2.33	0.40
2:2:309:C:H5''	2:2:310:G:H5'	2.03	0.40
2:2:4251:A:H61	20:N:25:CYS:H	1.68	0.40
2:2:4593:C:OP2	48:z:2:ALA:N	2.54	0.40
6:7:6:CYS:HB3	6:7:11:GLY:H	1.86	0.40
17:K:86:LYS:HA	17:K:86:LYS:HD3	1.88	0.40
33:b:96:GLU:HB3	33:b:142:VAL:HG21	2.03	0.40
34:c:27:LEU:HD12	47:r:33:ARG:HH21	1.85	0.40
37:g:147:LEU:HD12	37:g:147:LEU:HA	1.94	0.40
45:o:94:LYS:HE2	45:o:94:LYS:HB3	1.91	0.40
46:p:124:LYS:HB3	46:p:124:LYS:HE2	1.85	0.40
2:2:419:A:N3	2:2:1332:C:O2'	2.43	0.40
2:2:3710:G:N2	2:2:3711:A:N7	2.56	0.40
2:2:4618:G:H5''	36:e:15:ARG:HB2	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:4689:U:O2'	16:I:152:GLU:OE2	2.31	0.40
3:4:40:ILE:HA	3:4:40:ILE:HD12	1.81	0.40
3:4:321:SER:OG	3:4:322:THR:N	2.54	0.40
9:B:29:VAL:HA	9:B:220:ILE:HD13	2.02	0.40
9:B:301:ASN:OD1	9:B:301:ASN:N	2.54	0.40
27:V:128:ARG:HA	27:V:128:ARG:HD2	1.92	0.40
31:Z:122:THR:OG1	31:Z:124:ASP:OD1	2.37	0.40
35:d:52:LYS:HE2	35:d:52:LYS:HB2	1.92	0.40
43:m:221:LYS:HE3	43:m:221:LYS:HB3	1.91	0.40
2:2:697:G:H2'	2:2:698:G:H8	1.86	0.40
2:2:2624:G:OP1	3:4:510:ARG:HG2	2.21	0.40
2:2:3596:A:H4'	32:a:143:HIS:HB3	2.03	0.40
2:2:3662:A:OP2	43:m:156:LYS:NZ	2.40	0.40
2:2:4861:G:H2'	2:2:4862:G:H8	1.86	0.40
3:4:430:PRO:HB2	3:4:438:ILE:HD12	2.03	0.40
3:4:474:ASP:OD1	3:4:474:ASP:N	2.53	0.40
3:4:512:ALA:HB1	32:a:51:ILE:HD13	2.03	0.40
4:5:46:C:H2'	4:5:47:G:H8	1.86	0.40
5:6:210:THR:HG23	5:6:214:GLU:HG3	2.04	0.40
5:6:233:ALA:HA	5:6:236:MET:HG2	2.04	0.40
16:I:115:ARG:HD3	16:I:123:ILE:HG23	2.04	0.40
24:R:63:ASP:OD1	24:R:63:ASP:N	2.54	0.40
24:R:77:LEU:HD12	24:R:77:LEU:HA	1.93	0.40
2:2:515:C:N4	2:2:647:G:H22	2.20	0.40
2:2:1238:A:O3'	46:p:48:LYS:NZ	2.53	0.40
2:2:1560:A:H2'	2:2:1561:G:H8	1.86	0.40
2:2:1573:G:OP1	2:2:2667:C:O2'	2.35	0.40
2:2:3887:OMC:HM22	2:2:3888:G:H5'	2.03	0.40
7:8:65:A:O2'	15:H:10:ARG:NH2	2.54	0.40
8:9:30:GLU:HG2	8:9:96:PRO:HB2	2.03	0.40
10:C:41:ARG:HH21	10:C:45:PHE:HE2	1.68	0.40
13:F:57:ARG:HE	13:F:57:ARG:HB3	1.62	0.40
21:O:12:LEU:HB3	21:O:16:ARG:HH21	1.85	0.40
27:V:79:ILE:O	27:V:83:THR:HG23	2.22	0.40
43:m:45:VAL:HA	43:m:61:VAL:HA	2.04	0.40
2:2:10:A:H2'	2:2:11:G:C8	2.56	0.40
2:2:2402:G:O2'	13:F:10:ARG:O	2.39	0.40
2:2:3848:U:H2'	2:2:3849:A:C8	2.57	0.40
2:2:4635:A:H3'	2:2:4636:PSU:H4'	2.04	0.40
7:8:90:C:H2'	7:8:91:A:C8	2.56	0.40
20:N:109:ILE:HG22	20:N:128:LEU:HB2	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:b:8:ARG:HB3	33:b:66:GLN:HE21	1.86	0.40
33:b:61:ILE:HD13	33:b:61:ILE:HA	1.96	0.40
38:h:55:VAL:HG23	38:h:106:ILE:HA	2.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

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	
1	1	17/731 (2%)	17 (100%)	0	0	100	100
3	4	616/634 (97%)	535 (87%)	78 (13%)	3 (0%)	24	56
5	6	242/245 (99%)	224 (93%)	18 (7%)	0	100	100
6	7	133/163 (82%)	124 (93%)	7 (5%)	2 (2%)	8	34
8	9	82/134 (61%)	71 (87%)	10 (12%)	1 (1%)	10	38
9	B	401/403 (100%)	368 (92%)	33 (8%)	0	100	100
10	C	89/159 (56%)	85 (96%)	4 (4%)	0	100	100
11	D	356/427 (83%)	330 (93%)	26 (7%)	0	100	100
12	E	96/115 (84%)	89 (93%)	7 (7%)	0	100	100
13	F	107/117 (92%)	105 (98%)	2 (2%)	0	100	100
14	G	240/266 (90%)	221 (92%)	19 (8%)	0	100	100
15	H	120/123 (98%)	113 (94%)	7 (6%)	0	100	100
16	I	188/192 (98%)	167 (89%)	21 (11%)	0	100	100
17	K	100/105 (95%)	95 (95%)	5 (5%)	0	100	100
18	L	145/148 (98%)	134 (92%)	10 (7%)	1 (1%)	18	50
19	M	84/97 (87%)	80 (95%)	4 (5%)	0	100	100
20	N	163/178 (92%)	144 (88%)	19 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
21	O	67/70 (96%)	64 (96%)	3 (4%)	0	100	100
22	P	48/51 (94%)	46 (96%)	2 (4%)	0	100	100
23	Q	208/211 (99%)	190 (91%)	18 (9%)	0	100	100
24	R	148/203 (73%)	137 (93%)	11 (7%)	0	100	100
25	S	133/215 (62%)	122 (92%)	11 (8%)	0	100	100
26	U	201/204 (98%)	189 (94%)	11 (6%)	1 (0%)	24	56
27	V	199/203 (98%)	193 (97%)	6 (3%)	0	100	100
28	W	99/106 (93%)	89 (90%)	10 (10%)	0	100	100
29	X	89/92 (97%)	83 (93%)	6 (7%)	0	100	100
30	Y	151/184 (82%)	140 (93%)	11 (7%)	0	100	100
31	Z	185/188 (98%)	176 (95%)	9 (5%)	0	100	100
32	a	146/196 (74%)	138 (94%)	8 (6%)	0	100	100
33	b	174/176 (99%)	166 (95%)	8 (5%)	0	100	100
34	c	153/160 (96%)	144 (94%)	9 (6%)	0	100	100
35	d	99/128 (77%)	88 (89%)	11 (11%)	0	100	100
36	e	129/140 (92%)	118 (92%)	11 (8%)	0	100	100
37	g	116/156 (74%)	109 (94%)	7 (6%)	0	100	100
38	h	132/145 (91%)	130 (98%)	2 (2%)	0	100	100
39	i	133/136 (98%)	122 (92%)	11 (8%)	0	100	100
40	j	105/125 (84%)	97 (92%)	8 (8%)	0	100	100
41	k	126/135 (93%)	115 (91%)	11 (9%)	0	100	100
42	l	123/137 (90%)	111 (90%)	12 (10%)	0	100	100
43	m	246/257 (96%)	216 (88%)	29 (12%)	1 (0%)	30	60
44	n	107/110 (97%)	97 (91%)	8 (8%)	2 (2%)	6	30
45	o	231/288 (80%)	210 (91%)	21 (9%)	0	100	100
46	p	224/248 (90%)	210 (94%)	14 (6%)	0	100	100
47	r	291/297 (98%)	269 (92%)	22 (8%)	0	100	100
48	z	32/129 (25%)	30 (94%)	2 (6%)	0	100	100
All	All	7274/8927 (82%)	6701 (92%)	562 (8%)	11 (0%)	44	72

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	7	66	ASP
6	7	70	GLU
44	n	106	TYR
3	4	301	GLU
8	9	99	GLN
3	4	407	ASP
18	L	22	ILE
43	m	55	GLY
3	4	435	GLY
26	U	83	LYS
44	n	107	PRO

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

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	
1	1	17/654 (3%)	17 (100%)	0	100	100
3	4	562/574 (98%)	557 (99%)	5 (1%)	70	79
5	6	212/213 (100%)	212 (100%)	0	100	100
6	7	126/149 (85%)	122 (97%)	4 (3%)	34	62
8	9	74/114 (65%)	72 (97%)	2 (3%)	39	65
9	B	349/349 (100%)	348 (100%)	1 (0%)	86	87
10	C	78/126 (62%)	78 (100%)	0	100	100
11	D	298/348 (86%)	295 (99%)	3 (1%)	68	78
12	E	83/97 (86%)	81 (98%)	2 (2%)	43	67
13	F	94/100 (94%)	94 (100%)	0	100	100
14	G	204/223 (92%)	204 (100%)	0	100	100
15	H	109/110 (99%)	108 (99%)	1 (1%)	70	79
16	I	169/171 (99%)	167 (99%)	2 (1%)	63	76
17	K	86/89 (97%)	86 (100%)	0	100	100
18	L	120/121 (99%)	119 (99%)	1 (1%)	73	80
19	M	73/80 (91%)	73 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
20	N	138/149 (93%)	137 (99%)	1 (1%)	76	81
21	O	64/65 (98%)	64 (100%)	0	100	100
22	P	47/48 (98%)	47 (100%)	0	100	100
23	Q	176/177 (99%)	174 (99%)	2 (1%)	65	77
24	R	138/184 (75%)	138 (100%)	0	100	100
25	S	115/161 (71%)	114 (99%)	1 (1%)	70	79
26	U	171/172 (99%)	170 (99%)	1 (1%)	78	83
27	V	173/174 (99%)	172 (99%)	1 (1%)	78	83
28	W	89/94 (95%)	87 (98%)	2 (2%)	45	68
29	X	74/75 (99%)	72 (97%)	2 (3%)	39	65
30	Y	134/163 (82%)	133 (99%)	1 (1%)	76	81
31	Z	164/165 (99%)	164 (100%)	0	100	100
32	a	133/175 (76%)	132 (99%)	1 (1%)	73	80
33	b	157/157 (100%)	156 (99%)	1 (1%)	78	83
34	c	136/140 (97%)	135 (99%)	1 (1%)	76	81
35	d	91/115 (79%)	90 (99%)	1 (1%)	65	77
36	e	101/107 (94%)	100 (99%)	1 (1%)	68	78
37	g	106/133 (80%)	105 (99%)	1 (1%)	70	79
38	h	124/135 (92%)	121 (98%)	3 (2%)	43	67
39	i	117/118 (99%)	116 (99%)	1 (1%)	70	79
40	j	98/110 (89%)	94 (96%)	4 (4%)	27	57
41	k	114/121 (94%)	114 (100%)	0	100	100
42	l	109/121 (90%)	106 (97%)	3 (3%)	38	64
43	m	190/199 (96%)	189 (100%)	1 (0%)	81	84
44	n	88/89 (99%)	87 (99%)	1 (1%)	65	77
45	o	208/252 (82%)	207 (100%)	1 (0%)	81	84
46	p	195/215 (91%)	195 (100%)	0	100	100
47	r	246/250 (98%)	245 (100%)	1 (0%)	84	85
48	z	30/115 (26%)	30 (100%)	0	100	100
All	All	6380/7697 (83%)	6327 (99%)	53 (1%)	70	80

All (53) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	4	32	THR
3	4	405	MET
3	4	410	ILE
3	4	411	LEU
3	4	519	VAL
6	7	62	GLU
6	7	63	LEU
6	7	65	VAL
6	7	70	GLU
8	9	7	THR
8	9	55	LEU
9	B	278	THR
11	D	27	VAL
11	D	154	VAL
11	D	333	LYS
12	E	11	LEU
12	E	28	VAL
15	H	104	THR
16	I	104	VAL
16	I	176	LEU
18	L	15	VAL
20	N	102	THR
23	Q	63	THR
23	Q	70	VAL
25	S	38	VAL
26	U	89	VAL
27	V	34	VAL
28	W	4	VAL
28	W	23	VAL
29	X	59	SER
29	X	63	THR
30	Y	36	ILE
32	a	55	VAL
33	b	169	THR
34	c	124	THR
35	d	72	VAL
36	e	81	VAL
37	g	119	ILE
38	h	8	THR
38	h	79	VAL
38	h	97	VAL
39	i	74	VAL
40	j	62	VAL

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Mol	Chain	Res	Type
40	j	104	THR
40	j	106	VAL
40	j	109	VAL
42	l	61	VAL
42	l	63	VAL
42	l	124	VAL
43	m	45	VAL
44	n	33	VAL
45	o	121	VAL
47	r	275	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (120) such sidechains are listed below:

Mol	Chain	Res	Type
3	4	27	GLN
3	4	59	HIS
3	4	108	ASN
3	4	144	GLN
3	4	157	HIS
3	4	167	ASN
3	4	218	GLN
3	4	354	ASN
3	4	437	ASN
3	4	601	ASN
5	6	21	ASN
5	6	79	GLN
5	6	145	GLN
5	6	162	HIS
5	6	170	GLN
6	7	24	ASN
6	7	87	ASN
6	7	104	GLN
6	7	115	ASN
9	B	184	GLN
9	B	213	GLN
9	B	302	ASN
10	C	58	GLN
10	C	61	ASN
11	D	50	GLN
11	D	142	HIS
11	D	178	ASN
11	D	299	GLN

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Mol	Chain	Res	Type
11	D	317	ASN
11	D	329	ASN
12	E	19	GLN
12	E	50	ASN
14	G	43	GLN
14	G	208	ASN
14	G	225	ASN
15	H	62	ASN
15	H	96	ASN
15	H	107	GLN
16	I	156	ASN
17	K	92	ASN
18	L	60	HIS
18	L	66	ASN
18	L	85	GLN
18	L	89	ASN
18	L	120	GLN
19	M	66	HIS
20	N	46	GLN
21	O	28	ASN
21	O	31	ASN
22	P	4	HIS
23	Q	19	GLN
23	Q	104	ASN
23	Q	111	GLN
23	Q	149	GLN
23	Q	175	ASN
23	Q	205	GLN
24	R	56	GLN
24	R	91	GLN
24	R	102	GLN
25	S	34	ASN
26	U	145	ASN
26	U	196	ASN
27	V	42	ASN
27	V	63	ASN
27	V	150	GLN
27	V	167	HIS
27	V	173	GLN
27	V	180	GLN
28	W	45	GLN
28	W	51	GLN

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Mol	Chain	Res	Type
29	X	72	ASN
30	Y	21	ASN
30	Y	54	GLN
30	Y	56	GLN
30	Y	80	GLN
30	Y	97	ASN
30	Y	118	GLN
30	Y	137	ASN
31	Z	7	HIS
31	Z	44	ASN
31	Z	93	GLN
32	a	34	ASN
32	a	40	GLN
32	a	86	ASN
32	a	141	HIS
33	b	66	GLN
33	b	77	ASN
34	c	66	ASN
34	c	144	ASN
35	d	94	ASN
35	d	116	GLN
36	e	101	ASN
37	g	108	GLN
37	g	111	GLN
37	g	151	ASN
38	h	96	HIS
38	h	127	GLN
40	j	69	ASN
40	j	79	ASN
40	j	116	ASN
41	k	43	ASN
41	k	52	GLN
41	k	63	ASN
41	k	107	ASN
41	k	117	GLN
42	l	4	HIS
42	l	6	GLN
42	l	23	GLN
42	l	100	ASN
43	m	132	ASN
43	m	187	HIS
43	m	194	ASN

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Mol	Chain	Res	Type
44	n	80	ASN
45	o	190	HIS
46	p	39	GLN
47	r	195	HIS
47	r	202	GLN
47	r	225	GLN
47	r	244	HIS
47	r	267	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	2	3455/5070 (68%)	899 (26%)	18 (0%)
4	5	119/120 (99%)	20 (16%)	0
7	8	155/156 (99%)	32 (20%)	0
All	All	3729/5346 (69%)	951 (25%)	18 (0%)

All (951) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	2	2	G
2	2	15	A
2	2	17	A
2	2	21	G
2	2	25	A
2	2	28	C
2	2	39	A
2	2	42	A
2	2	48	G
2	2	56	A
2	2	59	A
2	2	64	A
2	2	65	A
2	2	66	A
2	2	69	A
2	2	73	A
2	2	84	A
2	2	91	G
2	2	96	U
2	2	98	A
2	2	104	G

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Mol	Chain	Res	Type
2	2	108	A
2	2	109	G
2	2	110	C
2	2	116	G
2	2	119	G
2	2	120	A
2	2	122	U
2	2	127	G
2	2	128	C
2	2	130	C
2	2	131	C
2	2	133	C
2	2	134	G
2	2	135	G
2	2	136	C
2	2	137	G
2	2	141	C
2	2	143	C
2	2	144	G
2	2	151	G
2	2	152	U
2	2	159	C
2	2	172	C
2	2	176	G
2	2	177	G
2	2	178	C
2	2	182	G
2	2	183	C
2	2	184	U
2	2	185	C
2	2	187	U
2	2	188	G
2	2	197	A
2	2	200	U
2	2	207	G
2	2	209	U
2	2	213	G
2	2	218	A
2	2	219	G
2	2	220	C
2	2	226	G
2	2	233	U

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Mol	Chain	Res	Type
2	2	234	G
2	2	237	B9B
2	2	254	G
2	2	255	C
2	2	256	G
2	2	257	C
2	2	259	C
2	2	260	C
2	2	262	G
2	2	264	C
2	2	265	C
2	2	266	C
2	2	267	G
2	2	278	G
2	2	279	A
2	2	280	G
2	2	297	U
2	2	306	A
2	2	315	G
2	2	316	U
2	2	326	C
2	2	340	C
2	2	341	G
2	2	349	A
2	2	379	G
2	2	387	G
2	2	398	A2M
2	2	399	G
2	2	406	C
2	2	407	A
2	2	408	A
2	2	409	G
2	2	410	A
2	2	411	G
2	2	412	G
2	2	433	A
2	2	440	U
2	2	449	C
2	2	450	G
2	2	452	A
2	2	453	G
2	2	454	U

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Mol	Chain	Res	Type
2	2	456	C
2	2	457	G
2	2	465	G
2	2	466	A
2	2	467	U
2	2	479	G
2	2	483	G
2	2	484	U
2	2	485	C
2	2	486	C
2	2	489	C
2	2	491	G
2	2	493	G
2	2	494	U
2	2	496	G
2	2	497	G
2	2	498	C
2	2	499	G
2	2	500	G
2	2	501	C
2	2	502	C
2	2	503	C
2	2	504	G
2	2	505	G
2	2	507	G
2	2	509	A
2	2	510	U
2	2	511	C
2	2	512	U
2	2	513	U
2	2	514	U
2	2	516	C
2	2	517	C
2	2	518	G
2	2	519	C
2	2	647	G
2	2	648	G
2	2	656	C
2	2	657	C
2	2	658	C
2	2	667	A
2	2	668	C

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Mol	Chain	Res	Type
2	2	673	C
2	2	686	A
2	2	687	U
2	2	692	A
2	2	694	C
2	2	696	C
2	2	703	G
2	2	704	C
2	2	730	G
2	2	731	G
2	2	738	C
2	2	739	G
2	2	740	G
2	2	742	G
2	2	752	G
2	2	753	C
2	2	756	G
2	2	758	G
2	2	759	G
2	2	904	C
2	2	905	C
2	2	910	G
2	2	913	U
2	2	914	U
2	2	915	A
2	2	916	C
2	2	917	A
2	2	923	C
2	2	924	C
2	2	925	C
2	2	926	G
2	2	929	A
2	2	932	A
2	2	933	G
2	2	935	A
2	2	936	C
2	2	941	C
2	2	943	A
2	2	944	A
2	2	945	U
2	2	956	A
2	2	959	G

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Mol	Chain	Res	Type
2	2	960	A
2	2	961	G
2	2	962	C
2	2	965	G
2	2	966	A
2	2	967	C
2	2	969	C
2	2	970	G
2	2	972	C
2	2	982	U
2	2	983	C
2	2	985	C
2	2	988	C
2	2	992	C
2	2	993	G
2	2	994	G
2	2	995	C
2	2	1048	G
2	2	1049	C
2	2	1051	G
2	2	1065	G
2	2	1070	G
2	2	1072	C
2	2	1082	C
2	2	1083	U
2	2	1095	A
2	2	1100	U
2	2	1168	G
2	2	1171	G
2	2	1173	G
2	2	1176	C
2	2	1178	G
2	2	1179	U
2	2	1180	C
2	2	1181	C
2	2	1182	C
2	2	1183	C
2	2	1187	G
2	2	1193	C
2	2	1194	G
2	2	1196	G
2	2	1197	C

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Mol	Chain	Res	Type
2	2	1198	G
2	2	1199	G
2	2	1200	G
2	2	1201	U
2	2	1202	C
2	2	1203	G
2	2	1210	C
2	2	1211	G
2	2	1215	C
2	2	1216	C
2	2	1219	G
2	2	1220	G
2	2	1221	G
2	2	1222	A
2	2	1240	G
2	2	1241	C
2	2	1245	C
2	2	1253	G
2	2	1254	A
2	2	1255	A
2	2	1260	G
2	2	1265	G
2	2	1266	G
2	2	1269	G
2	2	1270	A
2	2	1271	G
2	2	1272	C
2	2	1274	A
2	2	1275	G
2	2	1280	C
2	2	1283	G
2	2	1284	G
2	2	1285	U
2	2	1287	G
2	2	1294	A
2	2	1296	G
2	2	1301	C
2	2	1302	U
2	2	1303	A
2	2	1314	C
2	2	1324	A
2	2	1326	A2M

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Mol	Chain	Res	Type
2	2	1354	A
2	2	1358	G
2	2	1359	G
2	2	1365	C
2	2	1366	G
2	2	1367	C
2	2	1377	G
2	2	1378	C
2	2	1379	C
2	2	1387	A
2	2	1394	G
2	2	1397	A
2	2	1398	A
2	2	1402	C
2	2	1403	G
2	2	1404	G
2	2	1405	C
2	2	1407	C
2	2	1409	C
2	2	1410	U
2	2	1411	C
2	2	1412	G
2	2	1414	C
2	2	1419	G
2	2	1420	A
2	2	1433	A
2	2	1435	G
2	2	1438	U
2	2	1439	C
2	2	1442	C
2	2	1443	A
2	2	1444	G
2	2	1446	C
2	2	1453	G
2	2	1482	G
2	2	1483	C
2	2	1497	A
2	2	1498	G
2	2	1502	G
2	2	1503	A
2	2	1518	A
2	2	1519	C

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Mol	Chain	Res	Type
2	2	1534	A2M
2	2	1547	A
2	2	1559	G
2	2	1564	A
2	2	1576	G
2	2	1578	U
2	2	1582	PSU
2	2	1596	U
2	2	1597	G
2	2	1613	A
2	2	1624	G
2	2	1625	OMG
2	2	1626	G
2	2	1631	A
2	2	1632	A
2	2	1633	G
2	2	1638	A
2	2	1641	G
2	2	1642	A
2	2	1649	U
2	2	1654	G
2	2	1661	C
2	2	1671	U
2	2	1676	C
2	2	1677	PSU
2	2	1691	G
2	2	1694	C
2	2	1697	G
2	2	1699	A
2	2	1700	G
2	2	1701	A
2	2	1703	C
2	2	1704	C
2	2	1705	G
2	2	1707	C
2	2	1715	C
2	2	1718	C
2	2	1719	A
2	2	1734	G
2	2	1789	C
2	2	1790	U
2	2	1797	E7G

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Mol	Chain	Res	Type
2	2	1801	A
2	2	1803	G
2	2	1804	A
2	2	1806	G
2	2	1810	G
2	2	1815	G
2	2	1821	G
2	2	1822	U
2	2	1832	C
2	2	1834	U
2	2	1836	G
2	2	1837	A
2	2	1842	G
2	2	1843	A
2	2	1854	G
2	2	1855	G
2	2	1856	C
2	2	1859	C
2	2	1860	B8H
2	2	1866	UR3
2	2	1867	A
2	2	1868	A
2	2	1871	A2M
2	2	1881	C
2	2	1882	U
2	2	1883	OMG
2	2	1886	G
2	2	1893	C
2	2	1897	A
2	2	1910	G
2	2	1918	U
2	2	1919	G
2	2	1920	C
2	2	1921	C
2	2	1922	G
2	2	1925	G
2	2	1931	C
2	2	1932	A
2	2	1935	C
2	2	1938	C
2	2	1940	G
2	2	1945	G

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Mol	Chain	Res	Type
2	2	1948	G
2	2	1949	U
2	2	1960	A
2	2	1961	G
2	2	1965	G
2	2	1967	A
2	2	1968	G
2	2	1970	A
2	2	2018	C
2	2	2022	C
2	2	2024	G
2	2	2025	A
2	2	2026	A
2	2	2033	A
2	2	2034	G
2	2	2039	G
2	2	2040	A
2	2	2044	U
2	2	2046	G
2	2	2048	U
2	2	2055	G
2	2	2056	G
2	2	2062	C
2	2	2064	G
2	2	2069	A
2	2	2070	U
2	2	2071	A
2	2	2084	C
2	2	2091	C
2	2	2092	G
2	2	2093	A
2	2	2095	A
2	2	2096	G
2	2	2098	G
2	2	2100	A
2	2	2101	C
2	2	2102	G
2	2	2104	G
2	2	2105	A
2	2	2106	G
2	2	2107	C
2	2	2110	C

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Mol	Chain	Res	Type
2	2	2111	G
2	2	2112	G
2	2	2113	C
2	2	2250	C
2	2	2253	A
2	2	2255	C
2	2	2256	C
2	2	2257	C
2	2	2258	C
2	2	2259	G
2	2	2260	C
2	2	2261	G
2	2	2266	C
2	2	2289	C
2	2	2300	A
2	2	2301	G
2	2	2306	G
2	2	2310	C
2	2	2313	A
2	2	2314	G
2	2	2316	G
2	2	2332	A
2	2	2333	G
2	2	2348	G
2	2	2351	C
2	2	2357	G
2	2	2381	A
2	2	2395	A
2	2	2409	U
2	2	2416	G
2	2	2417	A
2	2	2418	A
2	2	2419	C
2	2	2422	OMC
2	2	2424	OMG
2	2	2425	U
2	2	2432	U
2	2	2437	C
2	2	2441	C
2	2	2447	U
2	2	2450	G
2	2	2453	A

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Mol	Chain	Res	Type
2	2	2460	A
2	2	2464	C
2	2	2465	C
2	2	2471	G
2	2	2475	G
2	2	2480	G
2	2	2483	G
2	2	2485	U
2	2	2488	C
2	2	2489	C
2	2	2490	U
2	2	2491	C
2	2	2493	G
2	2	2496	G
2	2	2503	G
2	2	2504	C
2	2	2505	C
2	2	2512	A
2	2	2513	A
2	2	2519	U
2	2	2520	C
2	2	2529	A
2	2	2543	A
2	2	2544	G
2	2	2545	U
2	2	2546	G
2	2	2547	G
2	2	2553	A
2	2	2554	U
2	2	2555	G
2	2	2558	C
2	2	2559	G
2	2	2560	C
2	2	2561	C
2	2	2563	C
2	2	2564	G
2	2	2565	A
2	2	2566	G
2	2	2573	A
2	2	2583	C
2	2	2586	G
2	2	2587	A

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Mol	Chain	Res	Type
2	2	2589	C
2	2	2601	A
2	2	2618	G
2	2	2627	C
2	2	2651	C
2	2	2653	C
2	2	2659	A
2	2	2661	U
2	2	2662	G
2	2	2663	G
2	2	2669	C
2	2	2670	C
2	2	2675	G
2	2	2687	U
2	2	2688	G
2	2	2689	C
2	2	2694	G
2	2	2695	A
2	2	2696	A
2	2	2707	U
2	2	2708	U
2	2	2709	C
2	2	2710	C
2	2	2711	G
2	2	2719	C
2	2	2721	G
2	2	2724	G
2	2	2726	G
2	2	2732	G
2	2	2739	C
2	2	2742	G
2	2	2743	A
2	2	2752	G
2	2	2756	G
2	2	2761	U
2	2	2763	U
2	2	2769	U
2	2	2770	C
2	2	2787	A
2	2	2788	U
2	2	2789	A
2	2	2790	U

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Mol	Chain	Res	Type
2	2	2814	C
2	2	2815	A
2	2	2826	U
2	2	2827	G
2	2	2829	U
2	2	2842	G
2	2	2853	C
2	2	2855	G
2	2	2856	C
2	2	2862	G
2	2	2877	G
2	2	2892	C
2	2	2897	G
2	2	2901	G
2	2	2903	G
2	2	2904	U
2	2	2905	C
2	2	2906	G
2	2	2907	G
2	2	2908	U
2	2	2909	C
2	2	3585	G
2	2	3587	C
2	2	3588	C
2	2	3590	G
2	2	3591	C
2	2	3593	C
2	2	3594	C
2	2	3595	U
2	2	3596	A
2	2	3597	G
2	2	3598	C
2	2	3599	A
2	2	3603	G
2	2	3604	A
2	2	3605	C
2	2	3606	U
2	2	3615	G
2	2	3619	G
2	2	3626	G
2	2	3635	A
2	2	3644	U

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Mol	Chain	Res	Type
2	2	3646	A
2	2	3662	A
2	2	3663	A
2	2	3664	G
2	2	3670	C
2	2	3673	C
2	2	3674	G
2	2	3680	U
2	2	3691	G
2	2	3696	C
2	2	3710	G
2	2	3711	A
2	2	3713	U
2	2	3714	G
2	2	3728	A
2	2	3734	U
2	2	3735	G
2	2	3736	A
2	2	3748	A
2	2	3750	G
2	2	3775	A
2	2	3776	G
2	2	3823	G
2	2	3838	U
2	2	3839	G
2	2	3840	U
2	2	3843	C
2	2	3865	A
2	2	3867	A2M
2	2	3877	A
2	2	3878	C
2	2	3879	G
2	2	3881	G
2	2	3897	B8K
2	2	3903	A
2	2	3904	G
2	2	3905	A
2	2	3906	A
2	2	3915	U
2	2	3916	G
2	2	3923	A
2	2	3938	G

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Mol	Chain	Res	Type
2	2	3939	G
2	2	4076	G
2	2	4084	G
2	2	4095	G
2	2	4097	G
2	2	4099	G
2	2	4100	C
2	2	4101	C
2	2	4102	C
2	2	4103	C
2	2	4104	G
2	2	4111	U
2	2	4112	C
2	2	4114	C
2	2	4115	G
2	2	4116	C
2	2	4117	U
2	2	4119	C
2	2	4120	U
2	2	4121	G
2	2	4122	G
2	2	4131	G
2	2	4137	C
2	2	4139	G
2	2	4140	C
2	2	4141	G
2	2	4142	C
2	2	4143	G
2	2	4144	C
2	2	4162	C
2	2	4163	U
2	2	4170	A
2	2	4177	C
2	2	4183	G
2	2	4184	G
2	2	4191	G
2	2	4194	I4U
2	2	4196	OMG
2	2	4201	G
2	2	4202	U
2	2	4203	A
2	2	4212	A

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Mol	Chain	Res	Type
2	2	4220	6MZ
2	2	4222	G
2	2	4225	G
2	2	4229	U
2	2	4230	C
2	2	4233	A
2	2	4243	C
2	2	4249	G
2	2	4250	G
2	2	4251	A
2	2	4254	G
2	2	4256	A
2	2	4265	U
2	2	4267	G
2	2	4268	A
2	2	4271	A
2	2	4273	A
2	2	4280	A
2	2	4281	A
2	2	4282	A
2	2	4291	G
2	2	4293	PSU
2	2	4297	G
2	2	4303	C
2	2	4305	G
2	2	4313	A
2	2	4314	C
2	2	4316	G
2	2	4319	C
2	2	4329	G
2	2	4330	G
2	2	4332	C
2	2	4336	A
2	2	4349	C
2	2	4350	C
2	2	4354	U
2	2	4364	G
2	2	4371	MHG
2	2	4373	G
2	2	4377	G
2	2	4378	A
2	2	4379	A

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Mol	Chain	Res	Type
2	2	4380	A
2	2	4381	A
2	2	4387	C
2	2	4395	U
2	2	4396	A
2	2	4405	G
2	2	4413	C
2	2	4414	A
2	2	4415	1MA
2	2	4418	G
2	2	4422	A
2	2	4428	A
2	2	4429	C
2	2	4449	A
2	2	4451	G
2	2	4452	U
2	2	4453	C
2	2	4464	A
2	2	4466	C
2	2	4475	G
2	2	4476	C
2	2	4477	A
2	2	4484	A
2	2	4491	G
2	2	4498	U
2	2	4499	G
2	2	4510	A
2	2	4512	U
2	2	4513	A
2	2	4518	A
2	2	4519	C
2	2	4523	A2M
2	2	4524	G
2	2	4529	B8W
2	2	4531	U
2	2	4545	G
2	2	4548	A
2	2	4549	G
2	2	4555	U
2	2	4556	U
2	2	4557	U
2	2	4558	U

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Mol	Chain	Res	Type
2	2	4560	C
2	2	4567	G
2	2	4574	U
2	2	4575	G
2	2	4589	A
2	2	4590	A
2	2	4594	U
2	2	4600	G
2	2	4601	U
2	2	4606	G
2	2	4607	A
2	2	4608	G
2	2	4629	U
2	2	4636	PSU
2	2	4637	OMG
2	2	4652	G
2	2	4656	A
2	2	4670	C
2	2	4671	B8T
2	2	4672	A
2	2	4678	G
2	2	4679	G
2	2	4682	U
2	2	4684	A
2	2	4687	A
2	2	4691	A
2	2	4694	G
2	2	4695	C
2	2	4702	G
2	2	4703	U
2	2	4708	A
2	2	4709	U
2	2	4719	G
2	2	4720	C
2	2	4721	G
2	2	4722	G
2	2	4728	U
2	2	4729	A
2	2	4730	C
2	2	4733	C
2	2	4734	A
2	2	4735	G

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Mol	Chain	Res	Type
2	2	4740	G
2	2	4741	C
2	2	4742	G
2	2	4745	G
2	2	4750	G
2	2	4754	G
2	2	4757	C
2	2	4759	C
2	2	4761	G
2	2	4765	G
2	2	4770	U
2	2	4771	C
2	2	4775	C
2	2	4776	G
2	2	4859	C
2	2	4864	U
2	2	4870	OMG
2	2	4871	C
2	2	4872	2MG
2	2	4875	G
2	2	4877	G
2	2	4882	U
2	2	4883	C
2	2	4889	G
2	2	4895	C
2	2	4896	G
2	2	4899	G
2	2	4900	C
2	2	4901	G
2	2	4909	A
2	2	4910	G
2	2	4911	A
2	2	4912	G
2	2	4914	C
2	2	4915	G
2	2	4916	G
2	2	4923	C
2	2	4924	C
2	2	4927	G
2	2	4928	C
2	2	4931	G
2	2	4934	A

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Mol	Chain	Res	Type
2	2	4937	C
2	2	4938	A
2	2	4941	G
2	2	4943	A
2	2	4944	C
2	2	4949	G
2	2	4950	U
2	2	4955	A
2	2	4958	C
2	2	4960	G
2	2	4966	A
2	2	4975	G
2	2	4976	U
2	2	4979	A
2	2	4989	U
2	2	4990	C
2	2	4991	U
2	2	5014	A
2	2	5021	C
2	2	5022	U
2	2	5025	C
2	2	5026	U
2	2	5027	C
2	2	5028	G
2	2	5030	U
2	2	5031	G
2	2	5034	A
2	2	5040	U
2	2	5041	G
2	2	5048	A
2	2	5050	C
2	2	5053	U
2	2	5054	C
2	2	5058	A
2	2	5060	A
2	2	5061	A
2	2	5062	G
2	2	5069	U
4	5	4	U
4	5	7	G
4	5	11	A
4	5	22	A

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Mol	Chain	Res	Type
4	5	23	A
4	5	37	G
4	5	38	U
4	5	40	U
4	5	48	G
4	5	50	A
4	5	53	U
4	5	54	A
4	5	63	C
4	5	64	G
4	5	70	G
4	5	71	G
4	5	78	C
4	5	100	A
4	5	110	G
4	5	111	C
7	8	2	G
7	8	25	G
7	8	34	U
7	8	35	C
7	8	39	G
7	8	48	A
7	8	49	G
7	8	59	A
7	8	60	G
7	8	62	A
7	8	63	U
7	8	68	G
7	8	75	G
7	8	80	A
7	8	82	A
7	8	84	A
7	8	85	U
7	8	87	G
7	8	103	A
7	8	105	C
7	8	110	U
7	8	111	U
7	8	114	G
7	8	123	U
7	8	124	U
7	8	125	C

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Mol	Chain	Res	Type
7	8	126	C
7	8	127	U
7	8	129	C
7	8	150	C
7	8	153	C
7	8	156	U

All (18) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	2	406	C
2	2	914	U
2	2	955	G
2	2	1071	C
2	2	1613	A
2	2	1625	OMG
2	2	2033	A
2	2	2760	G
2	2	3596	A
2	2	3673	C
2	2	3905	A
2	2	4378	A
2	2	4395	U
2	2	4498	U
2	2	4529	B8W
2	2	4555	U
2	2	4694	G
2	2	4913	G

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

92 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
2	PSU	2	1683	2	18,21,22	1.13	2 (11%)	22,30,33	1.80	4 (18%)
2	OMC	2	2804	2	19,22,23	2.74	7 (36%)	26,31,34	0.99	1 (3%)
2	B9B	2	1574	2	25,28,29	3.49	12 (48%)	35,40,43	2.22	15 (42%)
2	B8W	2	2380	2	23,26,27	3.72	11 (47%)	33,38,41	2.46	15 (45%)
2	PSU	2	1677	2	18,21,22	1.13	2 (11%)	22,30,33	1.95	5 (22%)
2	OMG	2	2773	2	23,26,27	2.27	9 (39%)	33,38,41	1.88	9 (27%)
2	B9H	2	2786	2,49	20,25,26	2.73	5 (25%)	22,35,38	2.13	6 (27%)
2	OMG	2	2050	2	23,26,27	2.28	7 (30%)	33,38,41	1.89	7 (21%)
2	1MA	2	1322	2,49	21,25,26	2.79	5 (23%)	31,37,40	1.76	7 (22%)
7	OMU	8	14	2,7	19,22,23	2.73	7 (36%)	26,31,34	1.75	6 (23%)
2	UR3	2	4530	2	19,22,23	2.77	5 (26%)	26,32,35	1.31	2 (7%)
2	P7G	2	3880	2	24,28,29	4.73	11 (45%)	27,41,44	1.80	4 (14%)
2	E7G	2	1797	2	24,27,28	3.78	11 (45%)	30,40,43	2.18	9 (30%)
2	B8H	2	4296	2	19,22,23	6.78	7 (36%)	22,32,35	2.29	5 (22%)
2	OMG	2	4637	2	23,26,27	2.30	8 (34%)	33,38,41	1.94	9 (27%)
2	OMG	2	4623	2	23,26,27	2.27	7 (30%)	33,38,41	1.75	8 (24%)
2	OMC	2	2861	2	19,22,23	2.84	7 (36%)	26,31,34	0.95	1 (3%)
2	OMG	2	1522	2	23,26,27	2.28	9 (39%)	33,38,41	1.79	7 (21%)
2	2MG	2	978	2	23,26,27	2.74	8 (34%)	32,38,41	2.25	10 (31%)
2	OMU	2	4306	2	19,22,23	2.78	8 (42%)	26,31,34	1.89	5 (19%)
2	B8T	2	4483	2	19,22,23	3.52	8 (42%)	26,31,34	1.26	4 (15%)
2	PSU	2	4628	2	18,21,22	1.04	1 (5%)	22,30,33	1.75	4 (18%)
2	7MG	2	4550	2	22,26,27	3.57	10 (45%)	29,39,42	1.97	9 (31%)
2	A2M	2	3867	2	22,25,26	3.52	9 (40%)	31,36,39	2.68	12 (38%)
2	PSU	2	4636	2	18,21,22	1.14	3 (16%)	22,30,33	1.88	4 (18%)
2	OMG	2	4370	2	23,26,27	2.30	9 (39%)	33,38,41	1.80	9 (27%)
2	MHG	2	4371	2	29,32,33	3.92	12 (41%)	34,46,49	2.25	11 (32%)
2	B8W	2	4472	2	23,26,27	3.67	9 (39%)	33,38,41	2.53	10 (30%)
2	7MG	2	2522	2	22,26,27	3.38	10 (45%)	29,39,42	1.98	9 (31%)
2	1MA	2	4415	2	21,25,26	2.86	5 (23%)	31,37,40	1.81	6 (19%)
2	PSU	2	4403	2	18,21,22	1.02	1 (5%)	22,30,33	1.84	5 (22%)
2	B8W	2	4529	2	23,26,27	3.79	8 (34%)	33,38,41	2.70	13 (39%)
2	OMG	2	373	2	23,26,27	2.26	8 (34%)	33,38,41	1.98	9 (27%)
2	P7G	2	1909	2	24,28,29	4.57	11 (45%)	27,41,44	1.68	4 (14%)
2	B9B	2	237	2	25,28,29	3.49	12 (48%)	35,40,43	2.46	11 (31%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	I4U	2	1659	2,49	21,24,25	4.70	14 (66%)	27,34,37	1.56	6 (22%)
2	A2M	2	1871	2	22,25,26	3.41	10 (45%)	31,36,39	2.58	10 (32%)
2	OMG	2	2364	2	23,26,27	2.29	7 (30%)	33,38,41	1.91	9 (27%)
2	BGH	2	3899	2	25,29,30	4.40	17 (68%)	31,43,46	2.56	12 (38%)
2	A2M	2	398	2	22,25,26	3.44	9 (40%)	31,36,39	2.43	8 (25%)
2	5MU	2	4083	2	19,22,23	4.69	7 (36%)	28,32,35	3.63	10 (35%)
2	B8K	2	4690	2	24,28,29	4.45	16 (66%)	30,42,45	2.65	11 (36%)
2	A2M	2	2363	2,49	22,25,26	3.56	10 (45%)	31,36,39	2.64	9 (29%)
2	5MC	2	4335	2	18,22,23	3.40	7 (38%)	26,32,35	1.24	2 (7%)
2	2MG	2	729	2	23,26,27	2.66	7 (30%)	32,38,41	2.24	8 (25%)
2	OMG	2	4494	2	23,26,27	2.31	9 (39%)	33,38,41	1.86	7 (21%)
2	UR3	2	4597	2	19,22,23	2.69	7 (36%)	26,32,35	1.87	3 (11%)
2	B8Q	2	1456	2	17,22,23	2.91	4 (23%)	22,32,35	2.23	6 (27%)
2	B9B	2	2754	2	25,28,29	3.44	11 (44%)	35,40,43	2.23	12 (34%)
2	OMG	2	4870	2	23,26,27	2.34	9 (39%)	33,38,41	1.83	9 (27%)
2	A2M	2	1524	2	22,25,26	3.44	9 (40%)	31,36,39	2.71	12 (38%)
2	B8K	2	3897	2	24,28,29	4.36	15 (62%)	30,42,45	2.49	13 (43%)
2	PSU	2	1582	2	18,21,22	1.04	1 (5%)	22,30,33	1.65	3 (13%)
2	B8W	2	4129	2	23,26,27	3.77	7 (30%)	33,38,41	2.67	14 (42%)
2	M7A	2	4564	2	20,25,26	1.96	3 (15%)	28,37,40	3.82	7 (25%)
2	PSU	2	4293	2	18,21,22	1.01	1 (5%)	22,30,33	1.96	4 (18%)
2	A2M	2	4523	2	22,25,26	3.47	10 (45%)	31,36,39	2.58	12 (38%)
2	A2M	2	1534	2,49	22,25,26	3.42	9 (40%)	31,36,39	2.74	12 (38%)
2	6MZ	2	4220	2	22,25,26	2.62	4 (18%)	30,36,39	3.34	10 (33%)
2	OMC	2	3887	2	19,22,23	2.91	8 (42%)	26,31,34	0.96	0
2	OMC	2	2365	2,49	19,22,23	2.75	8 (42%)	26,31,34	0.77	0
2	A2M	2	3723	2	22,25,26	3.49	9 (40%)	31,36,39	2.52	9 (29%)
2	OMC	2	3701	2,49	19,22,23	2.82	8 (42%)	26,31,34	0.64	0
2	B8H	2	1860	2	19,22,23	6.76	6 (31%)	22,32,35	2.29	5 (22%)
2	B8W	2	4185	2	23,26,27	3.71	9 (39%)	33,38,41	2.51	14 (42%)
2	PSU	2	2508	2	18,21,22	1.00	1 (5%)	22,30,33	1.69	3 (13%)
2	OMC	2	2422	2,49	19,22,23	2.89	8 (42%)	26,31,34	1.06	2 (7%)
2	7MG	2	1605	2	22,26,27	3.38	10 (45%)	29,39,42	1.94	9 (31%)
2	OMG	2	1883	2	23,26,27	2.28	7 (30%)	33,38,41	1.93	7 (21%)
2	UR3	2	1866	2	19,22,23	2.88	6 (31%)	26,32,35	1.30	2 (7%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	2MG	2	4872	2	23,26,27	2.75	7 (30%)	32,38,41	2.25	8 (25%)
2	E7G	2	2297	2	24,27,28	3.65	11 (45%)	30,40,43	2.19	10 (33%)
2	A2M	2	1326	2,49	22,25,26	3.52	9 (40%)	31,36,39	2.57	10 (32%)
2	OMG	2	4196	2	23,26,27	2.37	8 (34%)	33,38,41	1.90	9 (27%)
2	P4U	2	1348	2	21,24,25	3.74	8 (38%)	27,33,36	1.17	2 (7%)
2	B8T	2	4671	2	19,22,23	3.43	8 (42%)	26,31,34	0.90	1 (3%)
2	OMG	2	2424	2	23,26,27	2.36	9 (39%)	33,38,41	1.86	8 (24%)
2	OMC	2	3869	2	19,22,23	2.84	8 (42%)	26,31,34	1.39	3 (11%)
2	OMG	2	1316	2,49	23,26,27	2.37	9 (39%)	33,38,41	2.06	10 (30%)
2	PSU	2	3715	2	18,21,22	1.08	1 (5%)	22,30,33	1.67	4 (18%)
2	A2M	2	2401	2	22,25,26	3.52	10 (45%)	31,36,39	2.66	9 (29%)
2	A2M	2	3718	2	22,25,26	3.51	9 (40%)	31,36,39	2.43	10 (32%)
2	OMC	2	4536	2	19,22,23	2.75	7 (36%)	26,31,34	0.92	1 (3%)
2	PSU	2	3729	2	18,21,22	1.07	1 (5%)	22,30,33	1.69	4 (18%)
2	A2M	2	3825	2	22,25,26	3.51	10 (45%)	31,36,39	2.47	10 (32%)
2	A2M	2	4571	2	22,25,26	3.54	10 (45%)	31,36,39	2.49	8 (25%)
2	OMG	2	1625	2	23,26,27	2.27	8 (34%)	33,38,41	1.99	10 (30%)
2	2MG	2	1517	2	23,26,27	2.65	8 (34%)	32,38,41	2.46	8 (25%)
2	OMC	2	3909	2	19,22,23	2.91	8 (42%)	26,31,34	1.10	2 (7%)
2	OMU	2	4620	2	19,22,23	2.72	7 (36%)	26,31,34	1.72	5 (19%)
2	E6G	2	4355	2	24,27,28	3.56	12 (50%)	34,39,42	2.52	13 (38%)
2	I4U	2	4194	2,49	21,24,25	4.89	15 (71%)	27,34,37	1.07	1 (3%)

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
2	PSU	2	1683	2	-	0/7/25/26	0/2/2/2
2	OMC	2	2804	2	-	0/9/27/28	0/2/2/2
2	B9B	2	1574	2	-	3/11/29/30	0/3/3/3
2	B8W	2	2380	2	-	0/9/27/28	0/3/3/3
2	PSU	2	1677	2	-	1/7/25/26	0/2/2/2
2	OMG	2	2773	2	-	2/9/27/28	0/3/3/3
2	B9H	2	2786	2,49	-	1/12/47/48	0/2/2/2
2	OMG	2	2050	2	-	0/9/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	1MA	2	1322	2,49	-	2/7/25/26	0/3/3/3
7	OMU	8	14	2,7	-	1/9/27/28	0/2/2/2
2	UR3	2	4530	2	-	0/7/25/26	0/2/2/2
2	P7G	2	3880	2	-	4/10/40/41	0/3/3/3
2	E7G	2	1797	2	-	4/9/39/40	0/3/3/3
2	B8H	2	4296	2	-	0/7/25/26	0/2/2/2
2	OMG	2	4637	2	-	0/9/27/28	0/3/3/3
2	OMG	2	4623	2	-	0/9/27/28	0/3/3/3
2	OMC	2	2861	2	-	2/9/27/28	0/2/2/2
2	OMG	2	1522	2	-	0/9/27/28	0/3/3/3
2	2MG	2	978	2	-	0/9/27/28	0/3/3/3
2	OMU	2	4306	2	-	0/9/27/28	0/2/2/2
2	B8T	2	4483	2	-	0/7/27/28	0/2/2/2
2	PSU	2	4628	2	-	0/7/25/26	0/2/2/2
2	7MG	2	4550	2	-	2/7/37/38	0/3/3/3
2	A2M	2	3867	2	-	4/9/27/28	0/3/3/3
2	PSU	2	4636	2	-	4/7/25/26	0/2/2/2
2	OMG	2	4370	2	-	0/9/27/28	0/3/3/3
2	MHG	2	4371	2	-	9/16/46/47	0/3/3/3
2	B8W	2	4472	2	-	2/9/27/28	0/3/3/3
2	7MG	2	2522	2	-	0/7/37/38	0/3/3/3
2	1MA	2	4415	2	-	3/7/25/26	0/3/3/3
2	PSU	2	4403	2	-	2/7/25/26	0/2/2/2
2	B8W	2	4529	2	-	3/9/27/28	0/3/3/3
2	OMG	2	373	2	-	1/9/27/28	0/3/3/3
2	P7G	2	1909	2	-	2/10/40/41	0/3/3/3
2	B9B	2	237	2	-	5/11/29/30	0/3/3/3
2	I4U	2	1659	2,49	-	2/9/29/30	0/2/2/2
2	A2M	2	1871	2	-	2/9/27/28	0/3/3/3
2	OMG	2	2364	2	-	2/9/27/28	0/3/3/3
2	BGH	2	3899	2	-	1/13/43/44	0/3/3/3
2	A2M	2	398	2	-	2/9/27/28	0/3/3/3
2	5MU	2	4083	2	-	0/7/25/26	0/2/2/2
2	B8K	2	4690	2	-	0/11/41/42	0/3/3/3
2	A2M	2	2363	2,49	-	0/9/27/28	0/3/3/3
2	5MC	2	4335	2	-	0/7/25/26	0/2/2/2
2	2MG	2	729	2	-	1/9/27/28	0/3/3/3
2	OMG	2	4494	2	-	0/9/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	UR3	2	4597	2	-	0/7/25/26	0/2/2/2
2	B8Q	2	1456	2	-	1/7/42/43	0/2/2/2
2	B9B	2	2754	2	-	2/11/29/30	0/3/3/3
2	OMG	2	4870	2	-	3/9/27/28	0/3/3/3
2	A2M	2	1524	2	-	1/9/27/28	0/3/3/3
2	B8K	2	3897	2	-	3/11/41/42	0/3/3/3
2	PSU	2	1582	2	-	2/7/25/26	0/2/2/2
2	B8W	2	4129	2	-	2/9/27/28	0/3/3/3
2	M7A	2	4564	2	-	0/7/37/38	0/3/3/3
2	PSU	2	4293	2	-	2/7/25/26	0/2/2/2
2	A2M	2	4523	2	-	2/9/27/28	0/3/3/3
2	A2M	2	1534	2,49	-	3/9/27/28	0/3/3/3
2	6MZ	2	4220	2	-	2/9/27/28	0/3/3/3
2	OMC	2	3887	2	-	1/9/27/28	0/2/2/2
2	OMC	2	2365	2,49	-	0/9/27/28	0/2/2/2
2	A2M	2	3723	2	-	0/9/27/28	0/3/3/3
2	OMC	2	3701	2,49	-	4/9/27/28	0/2/2/2
2	B8H	2	1860	2	-	2/7/25/26	0/2/2/2
2	B8W	2	4185	2	-	2/9/27/28	0/3/3/3
2	PSU	2	2508	2	-	1/7/25/26	0/2/2/2
2	OMC	2	2422	2,49	-	1/9/27/28	0/2/2/2
2	7MG	2	1605	2	-	0/7/37/38	0/3/3/3
2	OMG	2	1883	2	-	2/9/27/28	0/3/3/3
2	UR3	2	1866	2	-	1/7/25/26	0/2/2/2
2	2MG	2	4872	2	-	2/9/27/28	0/3/3/3
2	E7G	2	2297	2	-	2/9/39/40	0/3/3/3
2	A2M	2	1326	2,49	-	1/9/27/28	0/3/3/3
2	OMG	2	4196	2	-	0/9/27/28	0/3/3/3
2	P4U	2	1348	2	-	1/10/29/30	0/2/2/2
2	B8T	2	4671	2	-	2/7/27/28	0/2/2/2
2	OMG	2	2424	2	-	2/9/27/28	0/3/3/3
2	OMC	2	3869	2	-	4/9/27/28	0/2/2/2
2	OMG	2	1316	2,49	-	0/9/27/28	0/3/3/3
2	PSU	2	3715	2	-	0/7/25/26	0/2/2/2
2	A2M	2	2401	2	-	0/9/27/28	0/3/3/3
2	A2M	2	3718	2	-	0/9/27/28	0/3/3/3
2	OMC	2	4536	2	-	0/9/27/28	0/2/2/2
2	PSU	2	3729	2	-	2/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	A2M	2	3825	2	-	0/9/27/28	0/3/3/3
2	A2M	2	4571	2	-	0/9/27/28	0/3/3/3
2	OMG	2	1625	2	-	2/9/27/28	0/3/3/3
2	2MG	2	1517	2	-	0/9/27/28	0/3/3/3
2	OMC	2	3909	2	-	2/9/27/28	0/2/2/2
2	OMU	2	4620	2	-	0/9/27/28	0/2/2/2
2	E6G	2	4355	2	-	2/10/28/29	0/3/3/3
2	I4U	2	4194	2,49	-	5/9/29/30	0/2/2/2

All (730) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	2	4296	B8H	C6-C5	-16.73	1.11	1.34
2	2	1860	B8H	C6-C5	-16.52	1.11	1.34
2	2	4296	B8H	C4-N3	-16.04	1.09	1.38
2	2	1860	B8H	C4-N3	-15.68	1.09	1.38
2	2	3880	P7G	C8-N9	14.43	1.54	1.46
2	2	1909	P7G	C8-N9	14.12	1.53	1.46
2	2	1860	B8H	C4-C5	13.13	1.81	1.44
2	2	4296	B8H	C4-C5	12.71	1.80	1.44
2	2	1860	B8H	C6-N1	12.16	1.66	1.36
2	2	4296	B8H	C6-N1	11.87	1.65	1.36
2	2	4194	I4U	C3'-C2'	-10.86	1.23	1.53
2	2	4083	5MU	C6-N1	10.67	1.56	1.38
2	2	1348	P4U	C4-N3	10.66	1.45	1.31
2	2	1659	I4U	C3'-C2'	-10.58	1.24	1.53
2	2	4220	6MZ	C6-N6	10.58	1.45	1.34
2	2	4083	5MU	C2-N1	10.52	1.55	1.38
2	2	3897	B8K	O4'-C4'	10.38	1.68	1.45
2	2	4194	I4U	C4-N3	10.30	1.44	1.31
2	2	4690	B8K	C3'-C4'	-10.21	1.26	1.53
2	2	4529	B8W	O4'-C1'	10.21	1.66	1.42
2	2	4690	B8K	O4'-C4'	10.10	1.67	1.45
2	2	4472	B8W	O4'-C1'	10.10	1.65	1.42
2	2	4129	B8W	O4'-C1'	10.01	1.65	1.42
2	2	1797	E7G	C8-N9	9.95	1.51	1.46
2	2	3899	BGH	C3'-C4'	-9.95	1.27	1.53
2	2	3880	P7G	C5-N7	9.94	1.46	1.35
2	2	3897	B8K	C3'-C4'	-9.89	1.27	1.53
2	2	2380	B8W	O4'-C1'	9.88	1.65	1.42
2	2	4185	B8W	O4'-C1'	9.75	1.65	1.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	2	1659	I4U	C4-N3	9.64	1.43	1.31
2	2	1909	P7G	C5-N7	9.60	1.46	1.35
2	2	3899	BGH	O4'-C4'	9.52	1.66	1.45
2	2	4371	MHG	C8-N9	9.35	1.51	1.46
2	2	2363	A2M	C2'-C1'	-9.19	1.29	1.53
2	2	1326	A2M	C2'-C1'	-9.06	1.29	1.53
2	2	4571	A2M	C2'-C1'	-9.03	1.29	1.53
2	2	3867	A2M	C2'-C1'	-8.99	1.29	1.53
2	2	2401	A2M	C2'-C1'	-8.97	1.30	1.53
2	2	3825	A2M	C2'-C1'	-8.97	1.30	1.53
2	2	2297	E7G	C5-N7	8.85	1.45	1.35
2	2	3718	A2M	C2'-C1'	-8.82	1.30	1.53
2	2	4083	5MU	C4-C5	8.82	1.59	1.44
2	2	1534	A2M	C2'-C1'	-8.78	1.30	1.53
2	2	2297	E7G	C8-N9	8.77	1.50	1.46
2	2	4371	MHG	C5-N7	8.76	1.45	1.35
2	2	4355	E6G	O4'-C1'	8.72	1.62	1.42
2	2	398	A2M	C2'-C1'	-8.70	1.30	1.53
2	2	3723	A2M	O4'-C1'	8.69	1.62	1.42
2	2	3723	A2M	C2'-C1'	-8.68	1.30	1.53
2	2	4335	5MC	C6-C5	8.68	1.48	1.34
2	2	1871	A2M	O4'-C1'	8.64	1.62	1.42
2	2	4550	7MG	C8-N9	8.63	1.50	1.46
2	2	1524	A2M	C2'-C1'	-8.61	1.30	1.53
2	2	237	B9B	O4'-C1'	8.55	1.62	1.42
2	2	4523	A2M	C2'-C1'	-8.53	1.31	1.53
2	2	1871	A2M	C2'-C1'	-8.53	1.31	1.53
2	2	3718	A2M	O4'-C1'	8.53	1.62	1.42
2	2	1326	A2M	O4'-C1'	8.50	1.62	1.42
2	2	1574	B9B	O4'-C1'	8.50	1.62	1.42
2	2	4415	1MA	C2-N3	8.49	1.46	1.30
2	2	2754	B9B	O4'-C1'	8.47	1.62	1.42
2	2	1797	E7G	C5-N7	8.46	1.45	1.35
2	2	4523	A2M	O4'-C1'	8.45	1.62	1.42
2	2	4129	B8W	C2-N2	8.43	1.50	1.33
2	2	1456	B8Q	C6-C5	8.38	1.52	1.33
2	2	4571	A2M	O4'-C1'	8.36	1.61	1.42
2	2	1322	1MA	C2-N3	8.34	1.46	1.30
2	2	398	A2M	O4'-C1'	8.32	1.61	1.42
2	2	4529	B8W	C2-N2	8.26	1.50	1.33
2	2	3825	A2M	O4'-C1'	8.26	1.61	1.42
2	2	3867	A2M	O4'-C1'	8.24	1.61	1.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	2	2401	A2M	O4'-C1'	8.22	1.61	1.42
2	2	2786	B9H	C2-N3	8.20	1.47	1.37
2	2	1524	A2M	O4'-C1'	8.18	1.61	1.42
2	2	2363	A2M	O4'-C1'	8.18	1.61	1.42
2	2	4472	B8W	C2-N2	8.17	1.50	1.33
2	2	237	B9B	O4'-C4'	-8.16	1.26	1.45
2	2	1534	A2M	O4'-C1'	8.07	1.61	1.42
2	2	4185	B8W	C2-N2	8.04	1.50	1.33
2	2	2522	7MG	C5-N7	8.02	1.44	1.35
2	2	4355	E6G	O4'-C4'	-8.01	1.27	1.45
2	2	4083	5MU	C4-N3	-7.93	1.24	1.38
2	2	1605	7MG	C5-N7	7.78	1.44	1.35
2	2	1574	B9B	O4'-C4'	-7.77	1.27	1.45
2	2	2754	B9B	O4'-C4'	-7.73	1.27	1.45
2	2	237	B9B	C2'-C1'	-7.72	1.28	1.53
2	2	4355	E6G	C2'-C1'	-7.70	1.28	1.53
2	2	4371	MHG	C2-N3	7.68	1.46	1.31
2	2	4872	2MG	C2-N3	7.66	1.46	1.31
2	2	3899	BGH	C8-N9	7.66	1.50	1.46
2	2	2380	B8W	C2-N2	7.62	1.49	1.33
2	2	1574	B9B	C2'-C1'	-7.61	1.29	1.53
2	2	4550	7MG	C5-N7	7.54	1.44	1.35
2	2	2754	B9B	C2'-C1'	-7.54	1.29	1.53
2	2	1659	I4U	O4'-C4'	-7.50	1.28	1.45
2	2	1605	7MG	C8-N9	7.48	1.50	1.46
2	2	4194	I4U	O4'-C4'	-7.28	1.28	1.45
2	2	729	2MG	C2-N3	7.27	1.45	1.31
2	2	1866	UR3	C2-N1	7.19	1.48	1.38
2	2	2380	B8W	C2'-C1'	-7.15	1.30	1.53
2	2	978	2MG	C2-N3	7.14	1.45	1.31
2	2	4129	B8W	C2'-C1'	-7.12	1.30	1.53
2	2	4483	B8T	C2-N3	7.11	1.50	1.36
2	2	4529	B8W	C2'-C1'	-7.11	1.30	1.53
2	2	2522	7MG	C8-N9	7.08	1.49	1.46
2	2	4185	B8W	C2'-C1'	-7.07	1.30	1.53
2	2	2363	A2M	O4'-C4'	-7.04	1.29	1.45
2	2	1348	P4U	C2-N3	6.97	1.50	1.36
2	2	3867	A2M	O4'-C4'	-6.95	1.29	1.45
2	2	1456	B8Q	C2-N3	6.94	1.47	1.35
2	2	4571	A2M	O4'-C4'	-6.91	1.29	1.45
2	2	4671	B8T	C2-N3	6.90	1.50	1.36
2	2	4472	B8W	C2'-C1'	-6.74	1.31	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	2	4415	1MA	C4-N3	6.73	1.49	1.35
2	2	1524	A2M	O4'-C4'	-6.73	1.30	1.45
2	2	1517	2MG	C2-N3	6.69	1.44	1.31
2	2	3825	A2M	O4'-C4'	-6.68	1.30	1.45
2	2	4371	MHG	C8-N7	6.67	1.52	1.45
2	2	1866	UR3	C6-C5	6.67	1.50	1.35
2	2	4671	B8T	C4-N3	6.67	1.44	1.32
2	2	4483	B8T	C4-N3	6.66	1.44	1.32
2	2	4530	UR3	C2-N1	6.65	1.48	1.38
2	2	2401	A2M	O4'-C4'	-6.61	1.30	1.45
2	2	4483	B8T	C6-C5	6.61	1.50	1.35
2	2	3880	P7G	C4-N3	6.59	1.49	1.37
2	2	4597	UR3	C6-C5	6.56	1.50	1.35
2	2	398	A2M	O4'-C4'	-6.53	1.30	1.45
2	2	4690	B8K	C8-N9	6.50	1.49	1.46
2	2	1909	P7G	C4-N3	6.50	1.49	1.37
2	2	1322	1MA	C4-N3	6.48	1.49	1.35
2	2	4671	B8T	C6-C5	6.48	1.50	1.35
2	2	3723	A2M	O4'-C4'	-6.43	1.30	1.45
2	2	4530	UR3	C6-C5	6.42	1.50	1.35
2	2	4523	A2M	O4'-C4'	-6.42	1.30	1.45
2	2	4194	I4U	C6-C5	6.42	1.50	1.35
2	2	1326	A2M	O4'-C4'	-6.41	1.30	1.45
2	2	3718	A2M	O4'-C4'	-6.37	1.30	1.45
2	2	1534	A2M	O4'-C4'	-6.35	1.30	1.45
2	2	3887	OMC	C2-N3	6.35	1.49	1.36
2	2	3909	OMC	C6-C5	6.33	1.49	1.35
2	2	4371	MHG	C2-N2	6.32	1.47	1.33
2	2	4306	OMU	C2-N3	6.30	1.49	1.38
2	2	1659	I4U	C6-C5	6.29	1.49	1.35
2	2	1871	A2M	O4'-C4'	-6.27	1.31	1.45
2	2	4483	B8T	C4-N4	6.26	1.48	1.35
2	2	978	2MG	C4-N3	6.24	1.49	1.34
2	2	4671	B8T	C4-N4	6.23	1.48	1.35
2	2	4196	OMG	C4-N3	6.21	1.49	1.34
2	2	2786	B9H	C6-C5	6.19	1.47	1.33
2	2	1348	P4U	C6-C5	6.18	1.49	1.35
2	2	1659	I4U	C2-N3	6.18	1.48	1.36
2	2	4335	5MC	C4-N3	6.17	1.44	1.34
2	2	4620	OMU	C2-N3	6.16	1.48	1.38
7	8	14	OMU	C2-N1	6.16	1.48	1.38
2	2	3701	OMC	C2-N3	6.10	1.48	1.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	2	1517	2MG	C4-N3	6.09	1.48	1.34
2	2	4870	OMG	C4-N3	6.05	1.48	1.34
2	2	2422	OMC	C2-N3	6.04	1.48	1.36
2	2	2861	OMC	C6-C5	6.03	1.49	1.35
2	2	4371	MHG	C2-N1	6.01	1.46	1.36
2	2	1522	OMG	C4-N3	6.01	1.48	1.34
2	2	4194	I4U	C2-N3	6.01	1.48	1.36
2	2	3897	B8K	O4'-C1'	-6.01	1.27	1.42
2	2	4872	2MG	C4-N3	5.99	1.48	1.34
2	2	1883	OMG	C4-N3	5.98	1.48	1.34
2	2	4494	OMG	C4-N3	5.98	1.48	1.34
2	2	4637	OMG	C4-N3	5.98	1.48	1.34
2	2	2364	OMG	C4-N3	5.97	1.48	1.34
2	2	729	2MG	C4-N3	5.96	1.48	1.34
2	2	4370	OMG	C4-N3	5.96	1.48	1.34
2	2	2804	OMC	C2-N3	5.95	1.48	1.36
2	2	2424	OMG	C4-N3	5.94	1.48	1.34
2	2	2861	OMC	C2-N3	5.93	1.48	1.36
2	2	4690	B8K	C2-N3	5.93	1.47	1.33
2	2	2773	OMG	C4-N3	5.93	1.48	1.34
7	8	14	OMU	C2-N3	5.88	1.48	1.38
2	2	1625	OMG	C4-N3	5.88	1.48	1.34
2	2	2050	OMG	C4-N3	5.88	1.48	1.34
2	2	3701	OMC	C6-C5	5.87	1.48	1.35
2	2	4597	UR3	C2-N3	5.87	1.50	1.39
2	2	4536	OMC	C2-N3	5.86	1.48	1.36
2	2	1316	OMG	C4-N3	5.85	1.48	1.34
2	2	373	OMG	C4-N3	5.85	1.48	1.34
2	2	2422	OMC	C6-C5	5.84	1.48	1.35
2	2	4335	5MC	C2-N3	5.83	1.48	1.36
2	2	3897	B8K	C2-N3	5.82	1.47	1.33
2	2	3880	P7G	C2-N2	5.79	1.48	1.34
2	2	4623	OMG	C4-N3	5.78	1.48	1.34
2	2	2365	OMC	C2-N3	5.74	1.48	1.36
2	2	3869	OMC	C2-N3	5.71	1.47	1.36
2	2	1909	P7G	C2-N2	5.69	1.47	1.34
2	2	4536	OMC	C6-C5	5.68	1.48	1.35
2	2	4185	B8W	O4'-C4'	-5.67	1.32	1.45
2	2	4550	7MG	C2-N3	5.66	1.46	1.33
2	2	4196	OMG	C2-N3	5.65	1.46	1.33
2	2	4083	5MU	C6-C5	5.64	1.43	1.34
2	2	2365	OMC	C6-C5	5.64	1.48	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	2	4620	OMU	C2-N1	5.63	1.47	1.38
2	2	3869	OMC	C6-C5	5.61	1.48	1.35
2	2	1866	UR3	C2-N3	5.60	1.49	1.39
2	2	4371	MHG	C4-N3	5.58	1.47	1.34
2	2	3909	OMC	C4-N4	5.58	1.47	1.33
2	2	4597	UR3	C2-N1	5.57	1.46	1.38
2	2	4306	OMU	C2-N1	5.55	1.47	1.38
2	2	4530	UR3	C2-N3	5.55	1.49	1.39
2	2	4529	B8W	O4'-C4'	-5.54	1.32	1.45
2	2	3887	OMC	C6-C5	5.54	1.47	1.35
2	2	2380	B8W	O4'-C4'	-5.52	1.32	1.45
2	2	4620	OMU	C6-C5	5.50	1.47	1.35
2	2	4129	B8W	O4'-C4'	-5.50	1.32	1.45
2	2	237	B9B	C2-N2	5.49	1.44	1.33
2	2	4306	OMU	C6-C5	5.49	1.47	1.35
2	2	2804	OMC	C6-C5	5.47	1.47	1.35
2	2	4550	7MG	C4-N3	5.46	1.47	1.34
2	2	2754	B9B	C2-N2	5.46	1.44	1.33
2	2	4371	MHG	C4-N9	5.44	1.44	1.37
2	2	2424	OMG	C2-N3	5.43	1.46	1.33
2	2	1574	B9B	C2-N2	5.43	1.44	1.33
2	2	4355	E6G	C2-N2	5.42	1.44	1.33
2	2	3880	P7G	C2-N1	5.41	1.46	1.33
2	2	4690	B8K	O4'-C1'	-5.39	1.29	1.42
2	2	2297	E7G	C2-N3	5.38	1.46	1.33
2	2	4494	OMG	C2-N3	5.37	1.46	1.33
2	2	2297	E7G	C4-N3	5.36	1.47	1.34
2	2	3880	P7G	C4-N9	5.36	1.43	1.35
2	2	4870	OMG	C2-N3	5.35	1.46	1.33
2	2	1797	E7G	C2-N3	5.34	1.46	1.33
2	2	3899	BGH	C2-N3	5.32	1.46	1.33
2	2	2050	OMG	C2-N3	5.32	1.46	1.33
2	2	978	2MG	C2-N2	5.32	1.45	1.33
2	2	1316	OMG	C2-N3	5.31	1.46	1.33
2	2	3899	BGH	C4-N3	5.31	1.46	1.34
2	2	1797	E7G	C4-N3	5.31	1.46	1.34
2	2	2522	7MG	C2-N3	5.30	1.46	1.33
2	2	4637	OMG	C2-N3	5.29	1.45	1.33
2	2	2522	7MG	C4-N3	5.28	1.46	1.34
2	2	4129	B8W	O6-C6	5.27	1.43	1.35
2	2	3909	OMC	C2-N3	5.27	1.47	1.36
2	2	1625	OMG	C2-N3	5.26	1.45	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	2	1348	P4U	C5-C4	5.25	1.50	1.43
2	2	4472	B8W	O4'-C4'	-5.24	1.33	1.45
2	2	1517	2MG	C2-N2	5.21	1.45	1.33
2	2	4550	7MG	C4-N9	5.19	1.43	1.37
2	2	1605	7MG	C2-N3	5.17	1.45	1.33
2	2	2364	OMG	C2-N3	5.13	1.45	1.33
2	2	1797	E7G	C8-N7	5.12	1.50	1.45
2	2	1605	7MG	C4-N3	5.12	1.46	1.34
2	2	1909	P7G	C2-N1	5.11	1.45	1.33
2	2	3887	OMC	C4-N3	5.09	1.44	1.34
2	2	3897	B8K	C8-N9	5.07	1.48	1.46
2	2	4370	OMG	C2-N3	5.06	1.45	1.33
2	2	3880	P7G	C8-N7	5.02	1.50	1.45
2	2	1348	P4U	O4-C4	5.02	1.40	1.35
2	2	1883	OMG	C2-N3	5.02	1.45	1.33
2	2	3897	B8K	C4-N9	5.01	1.43	1.37
2	2	4564	M7A	C6-N6	5.00	1.46	1.34
2	2	2786	B9H	C2-N1	5.00	1.45	1.38
2	2	4194	I4U	C1'-N1	-4.99	1.33	1.47
2	2	2773	OMG	C2-N3	4.96	1.45	1.33
2	2	4690	B8K	C4-N3	4.95	1.46	1.34
2	2	3897	B8K	C4-N3	4.93	1.46	1.34
2	2	4623	OMG	C2-N3	4.93	1.45	1.33
2	2	1522	OMG	C2-N3	4.89	1.45	1.33
2	2	4564	M7A	C4-N9	4.89	1.47	1.38
7	8	14	OMU	C6-C5	4.88	1.46	1.35
2	2	3899	BGH	O4'-C1'	-4.87	1.30	1.42
2	2	1909	P7G	C4-N9	4.87	1.42	1.35
2	2	4194	I4U	C3'-C4'	4.85	1.65	1.53
2	2	4185	B8W	O3'-C3'	-4.85	1.31	1.43
2	2	3869	OMC	C4-N4	4.85	1.45	1.33
2	2	3887	OMC	C4-N4	4.82	1.45	1.33
2	2	4872	2MG	C2-N2	4.81	1.44	1.33
2	2	1797	E7G	C2-N2	4.81	1.45	1.34
2	2	3899	BGH	C71-N7	4.80	1.50	1.39
2	2	1909	P7G	C8-N7	4.77	1.50	1.45
2	2	4415	1MA	C2-N1	4.75	1.44	1.35
2	2	4529	B8W	O6-C6	4.75	1.42	1.35
2	2	3909	OMC	C4-N3	4.74	1.44	1.34
2	2	2297	E7G	C8-N7	4.73	1.50	1.45
2	2	4483	B8T	C2-N1	4.71	1.50	1.40
2	2	729	2MG	C2-N2	4.70	1.43	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	2	2422	OMC	C4-N4	4.67	1.44	1.33
2	2	2297	E7G	C2-N2	4.67	1.45	1.34
2	2	3869	OMC	C2-N1	4.65	1.50	1.40
2	2	373	OMG	C2-N3	4.65	1.44	1.33
2	2	4690	B8K	O2'-C2'	-4.64	1.32	1.43
2	2	2422	OMC	C2-N1	4.63	1.50	1.40
2	2	1605	7MG	C2-N2	4.62	1.45	1.34
2	2	3701	OMC	C4-N4	4.60	1.44	1.33
2	2	3880	P7G	C6-N1	4.60	1.46	1.38
2	2	2804	OMC	C4-N4	4.60	1.44	1.33
2	2	2422	OMC	C4-N3	4.60	1.43	1.34
2	2	2380	B8W	O3'-C3'	-4.59	1.32	1.43
2	2	1326	A2M	C6-N6	4.58	1.45	1.34
2	2	4550	7MG	C2-N2	4.58	1.45	1.34
2	2	4472	B8W	O3'-C3'	-4.58	1.32	1.43
2	2	4529	B8W	O3'-C3'	-4.58	1.32	1.43
2	2	4536	OMC	C4-N4	4.58	1.44	1.33
2	2	2804	OMC	C4-N3	4.57	1.43	1.34
2	2	3701	OMC	C4-N3	4.56	1.43	1.34
2	2	2365	OMC	C4-N4	4.56	1.44	1.33
2	2	2522	7MG	C2-N2	4.53	1.45	1.34
2	2	2861	OMC	C4-N4	4.51	1.44	1.33
2	2	3825	A2M	C6-N6	4.51	1.45	1.34
2	2	1322	1MA	C2-N1	4.50	1.44	1.35
2	2	3899	BGH	C2-N2	4.50	1.44	1.34
2	2	2365	OMC	C4-N3	4.49	1.43	1.34
2	2	2522	7MG	C4-N9	4.49	1.42	1.37
2	2	1797	E7G	C4-N9	4.48	1.42	1.37
2	2	4690	B8K	C4-N9	4.47	1.42	1.37
2	2	1659	I4U	C1'-N1	-4.45	1.34	1.47
2	2	3897	B8K	O2'-C2'	-4.40	1.32	1.43
2	2	2861	OMC	C4-N3	4.40	1.43	1.34
2	2	2861	OMC	C2-N1	4.39	1.49	1.40
2	2	4129	B8W	O3'-C3'	-4.39	1.32	1.43
2	2	4523	A2M	C6-N6	4.38	1.45	1.34
2	2	2380	B8W	O6-C6	4.37	1.42	1.35
2	2	1524	A2M	C6-N6	4.36	1.45	1.34
2	2	1909	P7G	C6-N1	4.35	1.45	1.38
2	2	3723	A2M	C6-N6	4.35	1.45	1.34
2	2	4671	B8T	C2-N1	4.33	1.49	1.40
2	2	4185	B8W	O6-C6	4.33	1.41	1.35
2	2	4536	OMC	C4-N3	4.33	1.43	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	2	3869	OMC	C4-N3	4.32	1.43	1.34
2	2	1871	A2M	C6-N6	4.31	1.45	1.34
2	2	3899	BGH	O2'-C2'	-4.30	1.31	1.42
2	2	3867	A2M	C6-N6	4.27	1.44	1.34
2	2	1605	7MG	C4-N9	4.27	1.42	1.37
2	2	1534	A2M	C6-N6	4.26	1.44	1.34
2	2	978	2MG	C2-N1	4.25	1.43	1.36
2	2	4335	5MC	C4-N4	4.25	1.45	1.34
2	2	398	A2M	C6-N6	4.24	1.44	1.34
2	2	4536	OMC	C2-N1	4.23	1.49	1.40
2	2	4571	A2M	C6-N6	4.23	1.44	1.34
2	2	3887	OMC	C2-N1	4.23	1.49	1.40
2	2	2804	OMC	C2-N1	4.22	1.49	1.40
2	2	2401	A2M	C6-N6	4.20	1.44	1.34
2	2	4872	2MG	C2-N1	4.19	1.43	1.36
2	2	1659	I4U	O4'-C1'	4.18	1.51	1.42
2	2	1659	I4U	C2-N1	4.16	1.49	1.40
2	2	1860	B8H	C2-N3	4.15	1.45	1.38
2	2	3718	A2M	C6-N6	4.15	1.44	1.34
2	2	2363	A2M	C6-N6	4.14	1.44	1.34
2	2	1348	P4U	C2-N1	4.12	1.48	1.40
2	2	4196	OMG	C2-N2	4.10	1.43	1.34
2	2	4194	I4U	C5-C4	4.10	1.48	1.43
2	2	2297	E7G	C4-N9	4.06	1.42	1.37
2	2	4194	I4U	C2-N1	4.03	1.48	1.40
2	2	3899	BGH	C5-N7	4.01	1.46	1.39
2	2	3701	OMC	C2-N1	4.00	1.48	1.40
2	2	1348	P4U	C6-N1	3.99	1.47	1.38
2	2	4194	I4U	O4'-C1'	3.99	1.51	1.42
2	2	2424	OMG	C2-N2	3.99	1.43	1.34
2	2	4690	B8K	C5-N7	3.98	1.46	1.39
2	2	4472	B8W	O6-C6	3.94	1.41	1.35
2	2	3880	P7G	C2-N3	3.94	1.47	1.37
7	8	14	OMU	C4-N3	3.94	1.45	1.38
2	2	4296	B8H	C2-N3	3.93	1.45	1.38
2	2	1517	2MG	C2-N1	3.93	1.43	1.36
2	2	729	2MG	C2-N1	3.90	1.43	1.36
2	2	2773	OMG	C2-N2	3.90	1.43	1.34
2	2	4335	5MC	C6-N1	3.89	1.44	1.38
2	2	4494	OMG	C2-N2	3.87	1.43	1.34
2	2	4370	OMG	C2-N2	3.87	1.43	1.34
2	2	3899	BGH	C4-N9	3.86	1.42	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	2	3897	B8K	C2-N2	3.85	1.43	1.34
2	2	4335	5MC	C2-N1	3.85	1.48	1.40
2	2	3880	P7G	C5-C4	3.83	1.45	1.37
2	2	1316	OMG	C2-N2	3.83	1.43	1.34
2	2	4872	2MG	C5-N7	-3.80	1.31	1.39
2	2	4637	OMG	C2-N2	3.79	1.43	1.34
2	2	373	OMG	C2-N2	3.79	1.43	1.34
2	2	1797	E7G	C2-N1	3.78	1.47	1.37
2	2	4564	M7A	C5-N7	3.77	1.48	1.39
2	2	3880	P7G	O6-C6	-3.74	1.17	1.23
2	2	1625	OMG	C2-N2	3.74	1.43	1.34
2	2	1322	1MA	C5-C6	3.74	1.53	1.43
2	2	2050	OMG	C2-N2	3.73	1.43	1.34
2	2	4623	OMG	C2-N2	3.73	1.43	1.34
2	2	1883	OMG	C2-N2	3.73	1.43	1.34
2	2	1659	I4U	C3'-C4'	3.72	1.62	1.53
2	2	2365	OMC	C2-N1	3.72	1.48	1.40
2	2	1909	P7G	O6-C6	-3.72	1.17	1.23
2	2	4870	OMG	C2-N2	3.71	1.43	1.34
2	2	4306	OMU	C4-N3	3.68	1.45	1.38
2	2	2297	E7G	C2-N1	3.68	1.46	1.37
2	2	1909	P7G	C5-C4	3.67	1.44	1.37
2	2	4690	B8K	C2-N2	3.67	1.42	1.34
2	2	4671	B8T	C5-C4	3.66	1.48	1.40
2	2	1522	OMG	C2-N2	3.64	1.42	1.34
2	2	4415	1MA	C5-C6	3.63	1.53	1.43
2	2	4690	B8K	C5-C6	3.63	1.52	1.43
2	2	729	2MG	C5-N7	-3.61	1.32	1.39
2	2	1574	B9B	O6-C6	3.60	1.40	1.35
2	2	2364	OMG	C2-N2	3.60	1.42	1.34
2	2	3897	B8K	C5-N7	3.58	1.45	1.39
2	2	2401	A2M	C5-C4	-3.56	1.32	1.39
2	2	3897	B8K	C5-C6	3.55	1.52	1.43
2	2	2754	B9B	O2'-C2'	3.53	1.51	1.43
2	2	4355	E6G	O6-C6	3.53	1.40	1.35
2	2	3718	A2M	C5-N7	-3.52	1.32	1.39
2	2	1456	B8Q	C2-N1	3.51	1.43	1.38
2	2	1534	A2M	C5-N7	-3.47	1.32	1.39
2	2	4483	B8T	C5-C4	3.46	1.48	1.40
2	2	4690	B8K	O6-C6	-3.44	1.17	1.23
2	2	3909	OMC	C2-N1	3.44	1.47	1.40
2	2	4483	B8T	C6-N1	3.44	1.46	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	2	3909	OMC	C6-N1	3.43	1.46	1.38
2	2	4571	A2M	O3'-C3'	-3.43	1.34	1.43
2	2	3715	PSU	C6-C5	3.43	1.39	1.35
2	2	2363	A2M	C5-C4	-3.42	1.32	1.39
2	2	4371	MHG	C5-C6	3.42	1.52	1.43
2	2	1522	OMG	C5-N7	-3.39	1.32	1.39
2	2	4620	OMU	C4-N3	3.39	1.44	1.38
2	2	1517	2MG	C5-N7	-3.39	1.32	1.39
2	2	237	B9B	O3'-C3'	-3.39	1.35	1.43
2	2	1909	P7G	C2-N3	3.39	1.46	1.37
2	2	3899	BGH	C5-C6	3.38	1.52	1.43
2	2	1866	UR3	C6-N1	3.38	1.46	1.38
2	2	1605	7MG	C2-N1	3.38	1.46	1.37
2	2	1316	OMG	C5-N7	-3.38	1.32	1.39
2	2	1574	B9B	O2'-C2'	3.37	1.50	1.43
2	2	4355	E6G	O2'-C2'	3.37	1.50	1.43
2	2	3897	B8K	O6-C6	-3.37	1.17	1.23
2	2	237	B9B	O6-C6	3.36	1.40	1.35
2	2	1574	B9B	C5-C4	-3.36	1.32	1.39
2	2	2754	B9B	O6-C6	3.36	1.40	1.35
2	2	4870	OMG	C5-N7	-3.33	1.32	1.39
2	2	1625	OMG	C5-N7	-3.33	1.32	1.39
2	2	2522	7MG	C2-N1	3.32	1.45	1.37
2	2	2050	OMG	O6-C6	-3.32	1.17	1.23
2	2	3899	BGH	C2-N1	3.32	1.45	1.37
2	2	2401	A2M	C5-N7	-3.32	1.32	1.39
2	2	4194	I4U	O2-C2	-3.31	1.17	1.23
2	2	1316	OMG	O6-C6	-3.31	1.17	1.23
2	2	3899	BGH	O6-C6	-3.30	1.17	1.23
2	2	4623	OMG	C5-N7	-3.29	1.32	1.39
2	2	1883	OMG	O6-C6	-3.29	1.17	1.23
2	2	3869	OMC	O2-C2	-3.28	1.17	1.23
2	2	2364	OMG	O6-C6	-3.28	1.17	1.23
2	2	3729	PSU	C6-C5	3.28	1.39	1.35
2	2	1659	I4U	C5-C4	3.27	1.47	1.43
2	2	1605	7MG	C5-C6	3.27	1.52	1.43
2	2	2424	OMG	C5-N7	-3.26	1.32	1.39
2	2	4530	UR3	C6-N1	3.26	1.45	1.38
2	2	4620	OMU	O4-C4	-3.26	1.18	1.24
2	2	3718	A2M	O3'-C3'	-3.26	1.35	1.43
2	2	4523	A2M	C5-C4	-3.25	1.32	1.39
2	2	3723	A2M	O3'-C3'	-3.25	1.35	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	2	3899	BGH	C6-N1	3.25	1.44	1.38
2	2	1534	A2M	C5-C4	-3.25	1.32	1.39
2	2	2364	OMG	C5-N7	-3.23	1.32	1.39
2	2	4637	OMG	O6-C6	-3.23	1.17	1.23
2	2	1659	I4U	O2-C2	-3.22	1.17	1.23
2	2	4494	OMG	C5-N7	-3.22	1.32	1.39
2	2	4403	PSU	C6-C5	3.21	1.39	1.35
2	2	4355	E6G	O3'-C3'	-3.21	1.35	1.43
2	2	237	B9B	O2'-C2'	3.21	1.50	1.43
2	2	4083	5MU	O4-C4	-3.20	1.17	1.23
2	2	4550	7MG	C5-C6	3.20	1.51	1.43
2	2	1326	A2M	C5-C4	-3.20	1.33	1.39
2	2	1522	OMG	O6-C6	-3.20	1.17	1.23
2	2	3825	A2M	O3'-C3'	-3.19	1.35	1.43
2	2	373	OMG	C5-N7	-3.19	1.32	1.39
2	2	3867	A2M	O3'-C3'	-3.19	1.35	1.43
2	2	3718	A2M	C5-C4	-3.18	1.33	1.39
2	2	4637	OMG	C5-N7	-3.18	1.32	1.39
2	2	4194	I4U	O2'-C2'	3.17	1.50	1.43
2	2	398	A2M	O3'-C3'	-3.17	1.35	1.43
2	2	3723	A2M	O2'-C2'	3.17	1.50	1.42
2	2	1574	B9B	C5-N7	-3.17	1.33	1.39
2	2	4571	A2M	C5-C4	-3.16	1.33	1.39
2	2	4335	5MC	O2-C2	-3.16	1.17	1.23
2	2	1524	A2M	O3'-C3'	-3.16	1.35	1.43
2	2	3897	B8K	C2-N1	3.15	1.45	1.37
2	2	4550	7MG	C2-N1	3.15	1.45	1.37
2	2	4636	PSU	C6-C5	3.14	1.39	1.35
2	2	3825	A2M	C5-C4	-3.14	1.33	1.39
2	2	2050	OMG	C5-N7	-3.14	1.33	1.39
2	2	4220	6MZ	C5-C4	-3.14	1.33	1.39
2	2	978	2MG	C5-N7	-3.13	1.33	1.39
2	2	1797	E7G	C5-C6	3.12	1.51	1.43
2	2	237	B9B	C5-C4	-3.12	1.33	1.39
2	2	4371	MHG	C6-N1	3.12	1.44	1.38
2	2	1524	A2M	C5-C4	-3.11	1.33	1.39
2	2	2401	A2M	O3'-C3'	-3.11	1.35	1.43
2	2	4415	1MA	C5-N7	-3.11	1.33	1.39
2	2	4355	E6G	C5-N7	-3.11	1.33	1.39
2	2	2754	B9B	C5-C4	-3.11	1.33	1.39
2	2	4623	OMG	O6-C6	-3.11	1.17	1.23
2	2	3825	A2M	C5-N7	-3.10	1.33	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	2	4220	6MZ	C5-N7	-3.10	1.33	1.39
2	2	4370	OMG	O6-C6	-3.10	1.17	1.23
7	8	14	OMU	O4-C4	-3.10	1.18	1.24
2	2	4690	B8K	C2-N1	3.08	1.45	1.37
2	2	1574	B9B	O3'-C3'	-3.08	1.35	1.43
2	2	4306	OMU	O4-C4	-3.08	1.18	1.24
2	2	2861	OMC	C6-N1	3.08	1.45	1.38
2	2	2297	E7G	C6-N1	3.08	1.44	1.38
2	2	2363	A2M	O3'-C3'	-3.06	1.35	1.43
2	2	1883	OMG	C5-N7	-3.06	1.33	1.39
2	2	4355	E6G	C5-C4	-3.05	1.33	1.39
2	2	4370	OMG	C5-N7	-3.04	1.33	1.39
2	2	4523	A2M	O3'-C3'	-3.04	1.35	1.43
2	2	2754	B9B	C5-N7	-3.04	1.33	1.39
2	2	2754	B9B	O3'-C3'	-3.03	1.35	1.43
2	2	1659	I4U	O4-C4	3.02	1.41	1.35
2	2	3867	A2M	C5-N7	-3.01	1.33	1.39
2	2	2522	7MG	C5-C6	3.01	1.51	1.43
2	2	4523	A2M	C5-N7	-3.01	1.33	1.39
2	2	2363	A2M	C5-N7	-3.00	1.33	1.39
2	2	398	A2M	C5-C4	-3.00	1.33	1.39
2	2	3867	A2M	C5-C4	-3.00	1.33	1.39
2	2	3701	OMC	C6-N1	2.99	1.45	1.38
2	2	4494	OMG	O6-C6	-2.99	1.17	1.23
2	2	1517	2MG	O6-C6	-2.99	1.17	1.23
2	2	1582	PSU	C6-C5	2.99	1.38	1.35
2	2	1871	A2M	O3'-C3'	-2.98	1.36	1.43
2	2	1871	A2M	C5-C4	-2.97	1.33	1.39
2	2	4196	OMG	C5-N7	-2.97	1.33	1.39
2	2	2380	B8W	C5-C4	-2.97	1.33	1.39
2	2	4597	UR3	C6-N1	2.97	1.45	1.38
2	2	2297	E7G	C5-C6	2.97	1.51	1.43
2	2	1683	PSU	C6-C5	2.96	1.38	1.35
2	2	373	OMG	O6-C6	-2.95	1.18	1.23
2	2	2365	OMC	O2-C2	-2.94	1.18	1.23
2	2	1677	PSU	C6-C5	2.94	1.38	1.35
2	2	1797	E7G	C6-N1	2.93	1.44	1.38
2	2	2424	OMG	O6-C6	-2.93	1.18	1.23
2	2	1326	A2M	O3'-C3'	-2.92	1.36	1.43
2	2	3723	A2M	C5-C4	-2.92	1.33	1.39
2	2	1322	1MA	C5-N7	-2.92	1.33	1.39
2	2	3887	OMC	C6-N1	2.92	1.45	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	2	2773	OMG	O6-C6	-2.91	1.18	1.23
2	2	4483	B8T	O2-C2	-2.91	1.18	1.23
2	2	398	A2M	C5-N7	-2.91	1.33	1.39
2	2	2365	OMC	C6-N1	2.91	1.45	1.38
2	2	3909	OMC	O2-C2	-2.91	1.18	1.23
2	2	4571	A2M	C5-N7	-2.90	1.33	1.39
2	2	4306	OMU	O2-C2	-2.90	1.17	1.23
2	2	4194	I4U	C6-N1	2.89	1.45	1.38
2	2	4671	B8T	O2-C2	-2.89	1.18	1.23
2	2	1326	A2M	O2'-C2'	2.89	1.50	1.42
2	2	4690	B8K	C6-N1	2.87	1.44	1.38
2	2	3718	A2M	C8-N9	-2.87	1.32	1.37
2	2	1524	A2M	C5-N7	-2.87	1.33	1.39
2	2	1605	7MG	C6-N1	2.87	1.44	1.38
2	2	1625	OMG	O6-C6	-2.86	1.18	1.23
2	2	4671	B8T	C6-N1	2.86	1.44	1.38
2	2	2422	OMC	O2-C2	-2.86	1.18	1.23
2	2	2773	OMG	C5-N7	-2.85	1.33	1.39
2	2	2297	E7G	O6-C6	-2.85	1.18	1.23
2	2	2422	OMC	C6-N1	2.85	1.44	1.38
2	2	4550	7MG	O6-C6	-2.85	1.18	1.23
2	2	4523	A2M	O2'-C2'	2.85	1.49	1.42
2	2	4870	OMG	O6-C6	-2.85	1.18	1.23
2	2	2522	7MG	O6-C6	-2.83	1.18	1.23
2	2	2522	7MG	C6-N1	2.82	1.44	1.38
2	2	3867	A2M	O2'-C2'	2.81	1.49	1.42
2	2	4083	5MU	O2-C2	-2.81	1.17	1.23
2	2	1534	A2M	O3'-C3'	-2.79	1.36	1.43
2	2	2508	PSU	C6-C5	2.79	1.38	1.35
2	2	3723	A2M	C5-N7	-2.78	1.33	1.39
2	2	4571	A2M	O2'-C2'	2.78	1.49	1.42
2	2	4196	OMG	O6-C6	-2.77	1.18	1.23
7	8	14	OMU	O2-C2	-2.77	1.18	1.23
2	2	2363	A2M	C8-N9	-2.76	1.32	1.37
2	2	1534	A2M	C8-N9	-2.76	1.32	1.37
2	2	4129	B8W	O2'-C2'	2.74	1.49	1.43
2	2	4690	B8K	O3'-C3'	2.74	1.49	1.43
2	2	4628	PSU	C6-C5	2.73	1.38	1.35
2	2	1326	A2M	C5-N7	-2.73	1.33	1.39
2	2	3869	OMC	C6-N1	2.73	1.44	1.38
2	2	1659	I4U	C6-N1	2.72	1.44	1.38
2	2	4620	OMU	O2-C2	-2.72	1.18	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	2	2861	OMC	O2-C2	-2.71	1.18	1.23
2	2	978	2MG	O6-C6	-2.71	1.18	1.23
2	2	1797	E7G	O6-C6	-2.71	1.18	1.23
2	2	1605	7MG	O6-C6	-2.70	1.18	1.23
2	2	4185	B8W	O2'-C2'	2.68	1.49	1.43
2	2	4185	B8W	C5-C4	-2.68	1.34	1.39
2	2	4536	OMC	O2-C2	-2.68	1.18	1.23
2	2	4194	I4U	O4-C4	2.68	1.40	1.35
2	2	398	A2M	O2'-C2'	2.67	1.49	1.42
2	2	2380	B8W	C4-N9	-2.67	1.31	1.37
2	2	4293	PSU	C6-C5	2.66	1.38	1.35
2	2	2401	A2M	C8-N9	-2.66	1.32	1.37
2	2	3825	A2M	C8-N9	-2.65	1.32	1.37
2	2	3897	B8K	O3'-C3'	2.65	1.49	1.43
2	2	3887	OMC	O2-C2	-2.65	1.18	1.23
2	2	1871	A2M	C5-N7	-2.63	1.34	1.39
2	2	4872	2MG	O6-C6	-2.63	1.18	1.23
2	2	1456	B8Q	C6-N1	2.63	1.44	1.38
2	2	2804	OMC	O2-C2	-2.63	1.18	1.23
2	2	1524	A2M	O2'-C2'	2.62	1.49	1.42
2	2	729	2MG	O6-C6	-2.62	1.18	1.23
2	2	3897	B8K	C6-N1	2.62	1.43	1.38
2	2	2363	A2M	O2'-C2'	2.62	1.49	1.42
2	2	2804	OMC	C6-N1	2.62	1.44	1.38
2	2	4371	MHG	C72-C71	2.62	1.58	1.52
2	2	4529	B8W	O2'-C2'	2.60	1.49	1.43
2	2	1574	B9B	C8-N9	-2.60	1.32	1.37
2	2	4623	OMG	C4-N9	-2.60	1.31	1.38
2	2	4371	MHG	O6-C6	-2.60	1.18	1.23
2	2	4536	OMC	C6-N1	2.59	1.44	1.38
2	2	237	B9B	C5-N7	-2.58	1.34	1.39
2	2	3825	A2M	O2'-C2'	2.57	1.49	1.42
2	2	2380	B8W	O2'-C2'	2.57	1.49	1.43
2	2	1659	I4U	O2'-C2'	2.57	1.49	1.43
2	2	1871	A2M	O2'-C2'	2.56	1.49	1.42
2	2	4196	OMG	C2-N1	2.56	1.44	1.37
2	2	3701	OMC	O2-C2	-2.56	1.19	1.23
2	2	4690	B8K	C71-N7	2.55	1.45	1.39
2	2	4220	6MZ	C8-N9	-2.55	1.32	1.37
2	2	3867	A2M	C8-N9	-2.54	1.33	1.37
2	2	1524	A2M	C8-N9	-2.53	1.33	1.37
2	2	4550	7MG	C6-N1	2.53	1.43	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	2	3718	A2M	O2'-C2'	2.52	1.49	1.42
2	2	4523	A2M	C8-N9	-2.51	1.33	1.37
2	2	4472	B8W	O2'-C2'	2.50	1.48	1.43
2	2	1326	A2M	C8-N9	-2.50	1.33	1.37
2	2	1316	OMG	C4-N9	-2.48	1.31	1.38
2	2	4196	OMG	C6-N1	2.47	1.43	1.38
2	2	4306	OMU	C6-N1	2.45	1.43	1.38
2	2	2401	A2M	O2'-C2'	2.44	1.48	1.42
2	2	4370	OMG	C2-N1	2.44	1.43	1.37
2	2	2786	B9H	C6-N1	2.43	1.43	1.38
2	2	373	OMG	C4-N9	-2.43	1.31	1.38
2	2	2424	OMG	C6-N1	2.42	1.43	1.38
2	2	4296	B8H	O4-C4	-2.41	1.19	1.23
2	2	1574	B9B	C4-N9	-2.41	1.32	1.37
2	2	2754	B9B	C8-N9	-2.40	1.33	1.37
2	2	2364	OMG	C4-N9	-2.39	1.31	1.38
2	2	4571	A2M	C8-N9	-2.39	1.33	1.37
2	2	2424	OMG	C4-N9	-2.39	1.31	1.38
2	2	4870	OMG	C5-C6	2.39	1.53	1.44
2	2	4472	B8W	C5-C4	-2.39	1.34	1.39
2	2	2424	OMG	C2-N1	2.37	1.43	1.37
2	2	3723	A2M	C8-N9	-2.37	1.33	1.37
2	2	3899	BGH	O5'-C5'	-2.37	1.39	1.44
7	8	14	OMU	C6-N1	2.36	1.43	1.38
2	2	2773	OMG	C6-N1	2.35	1.43	1.38
2	2	4196	OMG	C5-C6	2.35	1.53	1.44
2	2	1316	OMG	C5-C6	2.35	1.53	1.44
2	2	1316	OMG	C2-N1	2.34	1.43	1.37
2	2	4870	OMG	C2-N1	2.34	1.43	1.37
2	2	4597	UR3	O2-C2	-2.34	1.18	1.22
2	2	4370	OMG	C4-N9	-2.34	1.32	1.38
2	2	2773	OMG	C5-C6	2.34	1.53	1.44
2	2	4870	OMG	C6-N1	2.33	1.43	1.38
2	2	978	2MG	C5-C6	2.31	1.53	1.44
2	2	2380	B8W	C5-N7	-2.31	1.34	1.39
2	2	3909	OMC	C5-C4	2.31	1.48	1.42
2	2	1574	B9B	C5-C6	-2.30	1.37	1.41
2	2	1534	A2M	O2'-C2'	2.30	1.48	1.42
2	2	1316	OMG	C6-N1	2.29	1.43	1.38
2	2	1677	PSU	O4'-C1'	-2.29	1.40	1.43
2	2	2786	B9H	O2-C2	-2.27	1.18	1.22
2	2	237	B9B	C8-N9	-2.27	1.33	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	2	237	B9B	O5'-C5'	-2.26	1.39	1.44
2	2	1522	OMG	C4-N9	-2.25	1.32	1.38
2	2	4306	OMU	C5-C4	2.25	1.48	1.43
2	2	4870	OMG	C4-N9	-2.25	1.32	1.38
2	2	2773	OMG	C2-N1	2.25	1.43	1.37
2	2	2050	OMG	C4-N9	-2.24	1.32	1.38
2	2	4529	B8W	C5-C4	-2.24	1.34	1.39
2	2	2401	A2M	O5'-C5'	-2.24	1.39	1.44
2	2	2754	B9B	C5-C6	-2.23	1.37	1.41
2	2	4571	A2M	O5'-C5'	-2.22	1.39	1.44
2	2	1683	PSU	C4-C5	-2.22	1.37	1.44
2	2	1625	OMG	C2-N1	2.21	1.43	1.37
2	2	4494	OMG	C6-N1	2.21	1.42	1.38
2	2	4523	A2M	O5'-C5'	-2.21	1.39	1.44
2	2	4296	B8H	C2-N1	-2.21	1.34	1.38
2	2	4623	OMG	C2-N1	2.20	1.43	1.37
2	2	373	OMG	C5-C6	2.20	1.52	1.44
2	2	1866	UR3	C5-C4	2.20	1.49	1.43
2	2	4494	OMG	C4-N9	-2.19	1.32	1.38
2	2	1883	OMG	C5-C6	2.19	1.52	1.44
2	2	4370	OMG	C5-C6	2.18	1.52	1.44
2	2	1625	OMG	C6-N1	2.17	1.42	1.38
2	2	4370	OMG	C6-N1	2.17	1.42	1.38
2	2	4637	OMG	C4-N9	-2.17	1.32	1.38
2	2	729	2MG	C5-C6	2.17	1.52	1.44
2	2	2422	OMC	C5-C4	2.17	1.47	1.42
2	2	4597	UR3	C5-C4	2.16	1.49	1.43
2	2	4620	OMU	C6-N1	2.16	1.43	1.38
2	2	398	A2M	C8-N9	-2.16	1.33	1.37
2	2	4636	PSU	C4-C5	-2.16	1.38	1.44
2	2	1883	OMG	C4-N9	-2.16	1.32	1.38
2	2	4355	E6G	C5-C6	-2.16	1.37	1.41
2	2	1871	A2M	O5'-C5'	-2.15	1.39	1.44
2	2	2363	A2M	O5'-C5'	-2.15	1.39	1.44
2	2	4636	PSU	O4'-C1'	-2.14	1.40	1.43
2	2	4355	E6G	C8-N9	-2.14	1.33	1.37
2	2	1866	UR3	C4-N3	2.14	1.45	1.40
2	2	1522	OMG	C5-C6	2.13	1.52	1.44
2	2	2364	OMG	C5-C6	2.13	1.52	1.44
2	2	237	B9B	C5-C6	-2.13	1.37	1.41
2	2	978	2MG	C6-N1	2.12	1.42	1.38
2	2	1625	OMG	C5-C6	2.12	1.52	1.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	2	1871	A2M	C8-N9	-2.12	1.33	1.37
2	2	4355	E6G	O5'-C5'	-2.12	1.39	1.44
2	2	4872	2MG	C5-C6	2.11	1.52	1.44
2	2	3701	OMC	C5-C4	2.10	1.47	1.42
2	2	3869	OMC	C5-C4	2.10	1.47	1.42
2	2	1860	B8H	O4-C4	-2.09	1.19	1.23
2	2	4494	OMG	C2-N1	2.09	1.42	1.37
2	2	1517	2MG	C5-C6	2.08	1.52	1.44
2	2	2380	B8W	C5-C6	-2.07	1.37	1.41
2	2	1522	OMG	C2-N1	2.07	1.42	1.37
2	2	4597	UR3	C4-N3	2.07	1.45	1.40
2	2	4530	UR3	O2-C2	-2.06	1.18	1.22
2	2	373	OMG	C6-N1	2.06	1.42	1.38
2	2	2424	OMG	C5-C6	2.06	1.52	1.44
2	2	1348	P4U	O2-C2	-2.06	1.19	1.23
2	2	3825	A2M	O5'-C5'	-2.05	1.39	1.44
2	2	2050	OMG	C5-C6	2.05	1.52	1.44
2	2	3899	BGH	O3'-C3'	2.05	1.47	1.43
2	2	4185	B8W	C4-N9	-2.04	1.33	1.37
2	2	4637	OMG	C2-N1	2.04	1.42	1.37
2	2	4494	OMG	C5-C6	2.04	1.52	1.44
2	2	1522	OMG	C6-N1	2.04	1.42	1.38
2	2	4194	I4U	O5'-C5'	-2.03	1.39	1.44
2	2	2773	OMG	C4-N9	-2.03	1.32	1.38
2	2	4472	B8W	C5-N7	-2.02	1.35	1.39
2	2	3887	OMC	C5-C4	2.02	1.47	1.42
2	2	2365	OMC	C5-C4	2.01	1.47	1.42
2	2	4637	OMG	C5-C6	2.00	1.51	1.44
2	2	1517	2MG	C4-N9	-2.00	1.32	1.38

All (661) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	2	4564	M7A	C5-C6-N6	13.64	147.03	123.74
2	2	4083	5MU	C5-C4-N3	11.90	125.47	115.31
2	2	4564	M7A	N6-C6-N1	-11.41	93.35	118.35
2	2	4220	6MZ	C4-N9-C1'	-9.41	104.18	126.59
2	2	4083	5MU	C5-C6-N1	-9.34	113.73	123.34
2	2	4220	6MZ	C1'-N9-C8	9.30	148.14	127.14
2	2	4597	UR3	C4-N3-C2	-7.78	117.24	124.56
2	2	1517	2MG	C2-N3-C4	7.72	121.61	112.04
2	2	4472	B8W	C5-C4-N3	-7.61	118.63	127.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	2	3880	P7G	C4-C5-N7	7.60	110.68	106.67
2	2	4185	B8W	C5-C4-N3	-7.17	119.12	127.19
2	2	237	B9B	C5-C4-N3	-7.14	119.16	127.19
2	2	4529	B8W	C5-C4-N3	-7.12	119.18	127.19
2	2	978	2MG	C2-N3-C4	6.86	120.54	112.04
2	2	4355	E6G	N2-C2-N3	6.75	127.75	117.25
2	2	4129	B8W	C5-C4-N3	-6.68	119.67	127.19
2	2	2363	A2M	N6-C6-N1	-6.68	103.72	118.35
2	2	4355	E6G	C5-C4-N3	-6.67	119.69	127.19
2	2	2786	B9H	C31-N3-C2	6.64	125.51	117.21
2	2	1860	B8H	C4-N3-C2	-6.59	118.81	127.35
2	2	4296	B8H	C4-N3-C2	-6.49	118.95	127.35
2	2	2380	B8W	C5-C4-N3	-6.49	119.89	127.19
2	2	2401	A2M	N3-C2-N1	-6.41	118.58	128.60
2	2	1909	P7G	C4-C5-N7	6.32	110.00	106.67
2	2	1517	2MG	C5-C4-N3	-6.29	118.25	128.46
2	2	4129	B8W	C61-O6-C6	6.29	123.45	117.21
2	2	4371	MHG	C2-N3-C4	6.28	119.83	112.04
2	2	1524	A2M	N6-C6-N1	-6.24	104.68	118.35
2	2	3867	A2M	N6-C6-N1	-6.23	104.71	118.35
2	2	729	2MG	C2-N3-C4	6.22	119.75	112.04
2	2	4690	B8K	C72-C71-N7	6.21	128.21	118.86
2	2	1574	B9B	C5-C4-N3	-6.21	120.21	127.19
2	2	1534	A2M	C5-C4-N3	-6.19	118.67	126.75
2	2	2401	A2M	N6-C6-N1	-6.18	104.82	118.35
2	2	1534	A2M	N6-C6-N1	-6.09	105.02	118.35
2	2	4220	6MZ	C5-C4-N3	-6.08	118.82	126.75
2	2	1326	A2M	N6-C6-N1	-6.07	105.07	118.35
2	2	2754	B9B	C5-C4-N3	-6.05	120.39	127.19
2	2	3867	A2M	C5-C4-N3	-6.05	118.86	126.75
2	2	4690	B8K	C5-C6-N1	6.05	121.64	110.99
2	2	4564	M7A	N3-C2-N1	-6.04	119.16	128.60
2	2	3723	A2M	N6-C6-N1	-6.00	105.22	118.35
2	2	4523	A2M	N6-C6-N1	-5.97	105.28	118.35
2	2	3718	A2M	C5-C4-N3	-5.94	119.00	126.75
2	2	3899	BGH	C72-C71-N7	5.94	127.80	118.86
2	2	3825	A2M	N6-C6-N1	-5.93	105.36	118.35
2	2	1456	B8Q	C31-N3-C4	5.93	123.18	114.25
2	2	3723	A2M	N3-C2-N1	-5.92	119.34	128.60
2	2	237	B9B	O6-C6-C5	5.92	124.06	116.57
2	2	4690	B8K	C4-C5-N7	5.92	110.17	104.91
2	2	729	2MG	C5-C4-N3	-5.89	118.91	128.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	2	1326	A2M	N3-C2-N1	-5.88	119.41	128.60
2	2	4571	A2M	N6-C6-N1	-5.86	105.51	118.35
2	2	4872	2MG	C5-C4-N3	-5.85	118.97	128.46
2	2	1871	A2M	N3-C2-N1	-5.84	119.47	128.60
2	2	4523	A2M	N3-C2-N1	-5.82	119.49	128.60
2	2	398	A2M	N6-C6-N1	-5.82	105.61	118.35
2	2	3899	BGH	C5-C6-N1	5.79	121.19	110.99
2	2	1871	A2M	N6-C6-N1	-5.76	105.74	118.35
2	2	1871	A2M	C5-C4-N3	-5.76	119.24	126.75
2	2	1524	A2M	N3-C2-N1	-5.72	119.65	128.60
2	2	2363	A2M	N3-C2-N1	-5.72	119.65	128.60
2	2	3718	A2M	N6-C6-N1	-5.71	105.84	118.35
2	2	1524	A2M	C5-C4-N3	-5.71	119.30	126.75
2	2	4571	A2M	N3-C2-N1	-5.69	119.70	128.60
2	2	3897	B8K	C72-C71-N7	5.69	127.42	118.86
2	2	3897	B8K	C5-C6-N1	5.68	121.00	110.99
2	2	2297	E7G	C4-C5-N7	5.67	109.95	104.91
2	2	4872	2MG	C2-N3-C4	5.67	119.07	112.04
2	2	2363	A2M	C5-C6-N6	5.66	135.76	123.43
2	2	4306	OMU	C4-N3-C2	-5.64	119.14	126.58
2	2	398	A2M	N3-C2-N1	-5.60	119.84	128.60
2	2	1534	A2M	N3-C2-N1	-5.60	119.85	128.60
2	2	2363	A2M	C5-C4-N3	-5.51	119.57	126.75
2	2	4872	2MG	C2-N1-C6	-5.49	118.17	124.48
2	2	4296	B8H	N3-C2-N1	5.49	121.07	115.14
2	2	1456	B8Q	N3-C2-N1	5.47	123.56	117.13
2	2	1797	E7G	C4-C5-N7	5.45	109.76	104.91
2	2	2401	A2M	C5-C4-N3	-5.45	119.64	126.75
2	2	2297	E7G	C5-C6-N1	5.45	120.59	110.99
2	2	1625	OMG	C5-C4-N3	-5.44	119.63	128.46
2	2	1326	A2M	C5-C6-N6	5.43	135.25	123.43
2	2	4371	MHG	C4-C5-N7	5.41	109.73	104.91
2	2	4571	A2M	C5-C4-N3	-5.41	119.69	126.75
2	2	3867	A2M	N3-C2-N1	-5.40	120.15	128.60
2	2	3825	A2M	N3-C2-N1	-5.37	120.21	128.60
2	2	4529	B8W	N2-C2-N3	5.37	125.60	117.25
2	2	3825	A2M	C5-C4-N3	-5.36	119.75	126.75
2	2	4083	5MU	O4-C4-C5	-5.35	118.70	124.90
2	2	4293	PSU	N1-C2-N3	5.32	121.16	115.13
2	2	1517	2MG	C2-N1-C6	-5.31	118.37	124.48
2	2	1316	OMG	C5-C4-N3	-5.30	119.86	128.46
2	2	4196	OMG	C5-C4-N3	-5.29	119.87	128.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	2	4220	6MZ	N1-C2-N3	-5.29	120.33	128.60
2	2	3723	A2M	C5-C4-N3	-5.26	119.89	126.75
2	2	2364	OMG	C5-C4-N3	-5.25	119.94	128.46
2	2	4129	B8W	N2-C2-N3	5.25	125.42	117.25
2	2	1860	B8H	N3-C2-N1	5.24	120.80	115.14
2	2	978	2MG	C5-C4-N3	-5.23	119.98	128.46
2	2	4523	A2M	C5-C4-N3	-5.23	119.93	126.75
2	2	3899	BGH	C4-C5-N7	5.21	109.54	104.91
2	2	3718	A2M	N3-C2-N1	-5.18	120.50	128.60
2	2	1677	PSU	C4-N3-C2	-5.18	118.88	126.34
2	2	2401	A2M	C5-C6-N6	5.16	134.66	123.43
2	2	1797	E7G	C5-C6-N1	5.15	120.07	110.99
2	2	1883	OMG	C5-C4-N3	-5.14	120.12	128.46
2	2	1524	A2M	C5-C6-N6	5.14	134.62	123.43
2	2	4529	B8W	O6-C6-N1	5.14	126.10	119.01
2	2	2380	B8W	O6-C6-N1	5.13	126.08	119.01
2	2	2050	OMG	C5-C4-N3	-5.12	120.15	128.46
2	2	2522	7MG	C5-C6-N1	5.10	119.97	110.99
2	2	4637	OMG	C5-C4-N3	-5.10	120.19	128.46
2	2	3723	A2M	C5-C6-N6	5.08	134.48	123.43
2	2	3825	A2M	C5-C6-N6	5.06	134.44	123.43
2	2	4870	OMG	C5-C4-N3	-5.06	120.26	128.46
2	2	4415	1MA	N1-C2-N3	-5.05	119.99	126.00
2	2	729	2MG	C2-N1-C6	-5.05	118.67	124.48
2	2	398	A2M	C5-C4-N3	-5.03	120.19	126.75
2	2	4371	MHG	C5-C6-N1	5.00	119.81	110.99
2	2	2754	B9B	O6-C6-C5	5.00	122.90	116.57
2	2	4494	OMG	C5-C4-N3	-4.98	120.38	128.46
2	2	3867	A2M	C5-C6-N6	4.97	134.25	123.43
2	2	1322	1MA	C5-C4-N3	-4.97	119.85	127.26
2	2	1534	A2M	C5-C6-N6	4.95	134.21	123.43
2	2	1677	PSU	N1-C2-N3	4.95	120.74	115.13
2	2	4550	7MG	C5-C6-N1	4.95	119.71	110.99
2	2	4636	PSU	C4-N3-C2	-4.95	119.21	126.34
7	8	14	OMU	C4-N3-C2	-4.93	120.08	126.58
2	2	4523	A2M	C5-C6-N6	4.92	134.15	123.43
2	2	4620	OMU	C4-N3-C2	-4.91	120.10	126.58
2	2	4472	B8W	N2-C2-N3	4.91	124.88	117.25
2	2	398	A2M	C5-C6-N6	4.88	134.05	123.43
2	2	1522	OMG	C5-C4-N3	-4.87	120.56	128.46
2	2	4403	PSU	N1-C2-N3	4.87	120.64	115.13
2	2	4220	6MZ	C4-C5-C6	4.86	120.58	116.81

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	2	1605	7MG	C5-C6-N1	4.86	119.55	110.99
2	2	2773	OMG	C5-C4-N3	-4.84	120.61	128.46
2	2	1574	B9B	O6-C6-C5	4.84	122.69	116.57
2	2	373	OMG	C2-N3-C4	4.83	120.91	112.30
2	2	4083	5MU	N3-C2-N1	4.83	121.30	114.89
2	2	1316	OMG	C2-N3-C4	4.82	120.89	112.30
2	2	1326	A2M	C5-C4-N3	-4.81	120.47	126.75
2	2	373	OMG	C5-C4-N3	-4.81	120.66	128.46
2	2	4293	PSU	C4-N3-C2	-4.77	119.46	126.34
2	2	4083	5MU	C4-N3-C2	-4.77	121.18	127.35
2	2	1866	UR3	C4-N3-C2	-4.75	120.09	124.56
2	2	1883	OMG	C2-N3-C4	4.74	120.74	112.30
2	2	3718	A2M	C5-C6-N6	4.73	133.71	123.43
2	2	2424	OMG	C5-C4-N3	-4.69	120.86	128.46
2	2	4628	PSU	N1-C2-N3	4.67	120.43	115.13
2	2	1322	1MA	N1-C2-N3	-4.64	120.48	126.00
2	2	4571	A2M	C5-C6-N6	4.64	133.53	123.43
2	2	3899	BGH	C2-N3-C4	4.64	120.57	112.30
2	2	4636	PSU	N1-C2-N3	4.63	120.38	115.13
2	2	4306	OMU	N3-C2-N1	4.62	121.03	114.89
2	2	1871	A2M	C5-C6-N6	4.62	133.48	123.43
2	2	4472	B8W	N3-C4-N9	4.60	133.38	126.99
2	2	1326	A2M	N9-C8-N7	-4.57	107.66	113.91
2	2	4403	PSU	C4-N3-C2	-4.56	119.77	126.34
2	2	4185	B8W	N2-C2-N3	4.55	124.32	117.25
2	2	2508	PSU	C4-N3-C2	-4.53	119.81	126.34
2	2	4530	UR3	C4-N3-C2	-4.51	120.32	124.56
2	2	2773	OMG	C2-N3-C4	4.51	120.33	112.30
2	2	1683	PSU	C4-N3-C2	-4.49	119.87	126.34
2	2	1683	PSU	N1-C2-N3	4.48	120.20	115.13
2	2	4185	B8W	N9-C8-N7	-4.45	107.82	113.91
2	2	2380	B8W	N9-C8-N7	-4.45	107.83	113.91
2	2	2424	OMG	C2-N3-C4	4.44	120.20	112.30
2	2	237	B9B	N9-C8-N7	-4.43	107.85	113.91
2	2	3715	PSU	N1-C2-N3	4.43	120.15	115.13
2	2	4690	B8K	C2-N3-C4	4.43	120.19	112.30
2	2	4370	OMG	C5-C4-N3	-4.43	121.28	128.46
2	2	4564	M7A	N3-C4-N9	4.43	132.46	126.87
2	2	4494	OMG	C2-N3-C4	4.42	120.17	112.30
2	2	3897	B8K	C4-C5-N7	4.40	108.83	104.91
2	2	4529	B8W	N3-C4-N9	4.39	133.08	126.99
2	2	2050	OMG	C2-N3-C4	4.39	120.11	112.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	2	4196	OMG	C2-N3-C4	4.36	120.07	112.30
2	2	4083	5MU	C5M-C5-C6	-4.36	117.02	122.85
2	2	1456	B8Q	O2-C2-N3	-4.35	116.56	122.95
2	2	2297	E7G	C2-N3-C4	4.35	120.05	112.30
2	2	1625	OMG	C2-N3-C4	4.34	120.03	112.30
2	2	2401	A2M	N9-C8-N7	-4.33	108.00	113.91
2	2	4129	B8W	N9-C8-N7	-4.33	108.00	113.91
2	2	1659	I4U	C5-C4-N3	-4.32	118.33	124.91
2	2	4637	OMG	C2-N3-C4	4.32	120.00	112.30
2	2	1522	OMG	C2-N3-C4	4.32	119.99	112.30
2	2	4623	OMG	C5-C4-N3	-4.32	121.46	128.46
2	2	3715	PSU	C4-N3-C2	-4.31	120.13	126.34
2	2	4523	A2M	N9-C8-N7	-4.30	108.03	113.91
2	2	4415	1MA	C5-C4-N3	-4.29	120.86	127.26
2	2	1797	E7G	C2-N3-C4	4.29	119.94	112.30
2	2	1517	2MG	N9-C4-N3	4.27	134.51	125.94
2	2	237	B9B	N3-C4-N9	4.26	132.89	126.99
2	2	1534	A2M	O4'-C1'-C2'	-4.25	99.12	106.57
2	2	978	2MG	C2-N1-C6	-4.25	119.59	124.48
2	2	2364	OMG	C2-N3-C4	4.24	119.86	112.30
2	2	1582	PSU	C4-N3-C2	-4.23	120.25	126.34
2	2	2508	PSU	N1-C2-N3	4.23	119.92	115.13
2	2	2380	B8W	N2-C2-N3	4.23	123.83	117.25
2	2	1605	7MG	C2-N3-C4	4.22	119.81	112.30
2	2	4370	OMG	C2-N3-C4	4.21	119.79	112.30
2	2	4083	5MU	C5M-C5-C4	4.20	123.39	118.77
2	2	4335	5MC	C5-C6-N1	-4.20	119.02	123.34
2	2	4472	B8W	O6-C6-N1	4.19	124.79	119.01
2	2	3729	PSU	N1-C2-N3	4.19	119.88	115.13
2	2	3897	B8K	C2-N3-C4	4.19	119.76	112.30
2	2	4220	6MZ	N3-C4-N9	4.18	133.97	127.08
2	2	4690	B8K	N9-C8-N7	4.17	108.92	103.33
2	2	2522	7MG	C2-N3-C4	4.17	119.72	112.30
2	2	4870	OMG	C2-N3-C4	4.14	119.68	112.30
2	2	398	A2M	N9-C8-N7	-4.10	108.31	113.91
2	2	4620	OMU	N3-C2-N1	4.08	120.31	114.89
2	2	1871	A2M	N9-C8-N7	-4.07	108.35	113.91
2	2	2363	A2M	N9-C8-N7	-4.07	108.35	113.91
2	2	4623	OMG	C2-N3-C4	4.05	119.51	112.30
2	2	237	B9B	O6-C6-N1	-4.03	114.39	120.00
2	2	3867	A2M	N9-C8-N7	-4.02	108.42	113.91
2	2	1574	B9B	N9-C8-N7	-4.01	108.42	113.91

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	2	3723	A2M	N9-C8-N7	-4.00	108.44	113.91
2	2	4550	7MG	C2-N3-C4	4.00	119.43	112.30
2	2	4185	B8W	N3-C4-N9	3.99	132.52	126.99
2	2	729	2MG	N9-C4-N3	3.98	133.94	125.94
2	2	4628	PSU	C4-N3-C2	-3.97	120.62	126.34
2	2	1524	A2M	N9-C8-N7	-3.96	108.50	113.91
2	2	4872	2MG	N9-C4-N3	3.96	133.88	125.94
2	2	4129	B8W	C5-N7-C8	3.94	109.11	103.51
2	2	4872	2MG	CM2-N2-C2	-3.94	115.16	123.86
2	2	4472	B8W	N9-C8-N7	-3.94	108.53	113.91
2	2	3867	A2M	N3-C4-N9	3.94	133.57	127.08
2	2	1582	PSU	N1-C2-N3	3.93	119.59	115.13
2	2	1322	1MA	C2-N3-C4	3.92	120.12	112.41
2	2	2754	B9B	N9-C8-N7	-3.92	108.55	113.91
2	2	1534	A2M	C2-N3-C4	3.92	121.02	111.75
2	2	3825	A2M	N9-C8-N7	-3.92	108.56	113.91
2	2	1871	A2M	C2-N3-C4	3.91	120.98	111.75
2	2	1524	A2M	C2-N3-C4	3.91	120.98	111.75
2	2	4529	B8W	O4'-C4'-C3'	-3.89	97.41	105.11
2	2	3869	OMC	O2-C2-N3	-3.87	116.04	122.33
2	2	2401	A2M	C2-N3-C4	3.86	120.87	111.75
2	2	4571	A2M	N9-C8-N7	-3.85	108.65	113.91
2	2	4550	7MG	C5-C4-N3	-3.84	120.81	128.13
2	2	1534	A2M	N3-C4-N9	3.83	133.40	127.08
7	8	14	OMU	C5-C4-N3	3.82	120.55	114.84
2	2	3867	A2M	C2-N3-C4	3.80	120.72	111.75
2	2	4185	B8W	O6-C6-N1	3.80	124.25	119.01
2	2	1348	P4U	C5-C4-N3	-3.77	119.17	124.91
2	2	2363	A2M	C2-N3-C4	3.76	120.63	111.75
2	2	2786	B9H	C6-N1-C2	-3.75	118.43	121.79
2	2	4220	6MZ	C2-N3-C4	3.74	120.59	111.75
2	2	4185	B8W	N1-C2-N3	-3.72	119.58	125.42
2	2	4355	E6G	O6-C6-N1	3.72	125.17	120.00
2	2	1871	A2M	N3-C4-N9	3.72	133.21	127.08
2	2	4571	A2M	C2-N3-C4	3.71	120.52	111.75
2	2	3723	A2M	C2-N3-C4	3.71	120.50	111.75
2	2	3899	BGH	N9-C8-N7	3.70	108.30	103.33
2	2	4529	B8W	N9-C8-N7	-3.68	108.88	113.91
2	2	4415	1MA	C2-N3-C4	3.68	119.64	112.41
2	2	4523	A2M	C2-N3-C4	3.68	120.44	111.75
2	2	4129	B8W	N3-C4-N9	3.68	132.09	126.99
2	2	373	OMG	N9-C8-N7	-3.66	106.50	113.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	2	1860	B8H	C5-C4-N3	3.65	124.83	116.58
2	2	4472	B8W	N1-C2-N3	-3.64	119.70	125.42
2	2	4355	E6G	N9-C8-N7	-3.64	108.93	113.91
2	2	3729	PSU	C4-N3-C2	-3.63	121.11	126.34
2	2	4220	6MZ	N9-C8-N7	-3.63	108.95	113.91
2	2	1797	E7G	C5-C4-N3	-3.61	121.25	128.13
2	2	3899	BGH	C5-C4-N9	3.60	111.02	106.35
2	2	4306	OMU	O2-C2-N1	-3.60	118.00	122.79
2	2	3825	A2M	C2-N3-C4	3.60	120.25	111.75
2	2	4296	B8H	C5-C4-N3	3.59	124.69	116.58
2	2	3718	A2M	C2-N3-C4	3.57	120.17	111.75
2	2	1316	OMG	C2-N1-C6	-3.56	118.61	125.10
2	2	4355	E6G	N3-C4-N9	3.54	131.91	126.99
2	2	4185	B8W	C5-N7-C8	3.50	108.49	103.51
2	2	237	B9B	N3-C2-N1	-3.49	119.95	125.42
2	2	1797	E7G	C5-C4-N9	3.48	110.87	106.35
2	2	2786	B9H	O3'-C3'-C2'	3.47	121.03	111.17
2	2	2297	E7G	C5-C4-N3	-3.47	121.51	128.13
2	2	1524	A2M	N3-C4-N9	3.47	132.80	127.08
2	2	2754	B9B	N3-C4-N9	3.47	131.81	126.99
2	2	4371	MHG	C5-C4-N3	-3.47	121.52	128.13
2	2	2522	7MG	C5-C4-N3	-3.47	121.53	128.13
2	2	4355	E6G	N3-C2-N1	-3.46	119.98	125.42
2	2	398	A2M	C2-N3-C4	3.45	119.91	111.75
2	2	2380	B8W	N3-C4-N9	3.45	131.78	126.99
2	2	4129	B8W	N1-C2-N3	-3.45	120.00	125.42
2	2	1326	A2M	C2-N3-C4	3.45	119.89	111.75
2	2	2401	A2M	N3-C4-N9	3.43	132.74	127.08
2	2	1625	OMG	N9-C4-N3	3.40	132.78	125.94
2	2	3718	A2M	N3-C4-N9	3.40	132.68	127.08
2	2	3729	PSU	C6-N1-C2	-3.40	119.21	122.68
2	2	4415	1MA	C1'-N9-C4	-3.40	116.42	126.50
2	2	2380	B8W	C5-N7-C8	3.39	108.33	103.51
2	2	1605	7MG	C5-C4-N3	-3.39	121.68	128.13
2	2	2364	OMG	C2-N1-C6	-3.38	118.94	125.10
2	2	4637	OMG	N9-C4-N3	3.38	132.72	125.94
2	2	4196	OMG	N9-C4-N3	3.37	132.71	125.94
2	2	1605	7MG	C5-C4-N9	3.36	110.71	106.35
2	2	4623	OMG	N9-C8-N7	-3.36	107.06	113.39
2	2	2050	OMG	C2-N1-C6	-3.35	118.99	125.10
2	2	4637	OMG	N9-C8-N7	-3.34	107.11	113.39
2	2	4529	B8W	N1-C2-N3	-3.33	120.19	125.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	8	14	OMU	O4-C4-C5	-3.33	119.30	125.16
2	2	3723	A2M	N3-C4-N9	3.33	132.57	127.08
2	2	4370	OMG	N9-C8-N7	-3.33	107.13	113.39
2	2	2773	OMG	N9-C8-N7	-3.33	107.13	113.39
2	2	1316	OMG	N9-C8-N7	-3.32	107.14	113.39
2	2	237	B9B	C5-N7-C8	3.31	108.21	103.51
2	2	4564	M7A	C2-N3-C4	3.30	119.56	111.75
2	2	4637	OMG	C2-N1-C6	-3.29	119.11	125.10
2	2	3897	B8K	C5-C4-N9	3.27	110.60	106.35
2	2	1326	A2M	C5-N7-C8	3.26	108.14	103.51
2	2	4690	B8K	C5-C4-N9	3.25	110.57	106.35
2	2	2424	OMG	N9-C8-N7	-3.25	107.28	113.39
2	2	4371	MHG	C2-N1-C6	-3.25	120.75	124.48
2	2	2754	B9B	N3-C2-N1	-3.24	120.33	125.42
2	2	4129	B8W	C4-C5-N7	-3.24	106.68	110.62
2	2	4129	B8W	C5-C6-N1	-3.23	118.96	123.46
2	2	4355	E6G	O4'-C4'-C3'	-3.23	98.73	105.11
2	2	1883	OMG	C2-N1-C6	-3.21	119.24	125.10
2	2	4355	E6G	N2-C2-N1	-3.21	112.26	117.25
2	2	1860	B8H	O2-C2-N1	-3.20	119.26	122.87
2	2	4494	OMG	N9-C4-N3	3.20	132.36	125.94
2	2	2363	A2M	N3-C4-N9	3.19	132.34	127.08
2	2	4571	A2M	N3-C4-N9	3.18	132.33	127.08
2	2	978	2MG	N9-C4-N3	3.18	132.33	125.94
2	2	1534	A2M	N9-C8-N7	-3.18	109.57	113.91
2	2	4550	7MG	C5-C4-N9	3.17	110.46	106.35
2	2	4494	OMG	N9-C8-N7	-3.17	107.42	113.39
2	2	2050	OMG	N9-C4-N3	3.16	132.29	125.94
2	2	4415	1MA	C1'-N9-C8	3.16	135.70	126.70
2	2	4628	PSU	C6-N1-C2	-3.14	119.47	122.68
2	2	4690	B8K	C6-C5-C4	-3.14	116.15	122.62
2	2	3729	PSU	O2-C2-N1	-3.14	119.33	122.79
2	2	1883	OMG	N9-C4-N3	3.13	132.23	125.94
2	2	2424	OMG	C2-N1-C6	-3.13	119.39	125.10
2	2	4494	OMG	C2-N1-C6	-3.12	119.40	125.10
2	2	1517	2MG	C5-C6-N1	3.12	121.11	113.19
2	2	4523	A2M	C5-N7-C8	3.12	107.94	103.51
2	2	2364	OMG	N9-C4-N3	3.11	132.19	125.94
2	2	1909	P7G	N9-C8-N7	3.11	107.83	103.38
7	8	14	OMU	C1'-N1-C2	3.11	123.20	117.57
2	2	2522	7MG	C5-C4-N9	3.11	110.38	106.35
2	2	4129	B8W	C2-N1-C6	3.11	120.86	115.93

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	2	4194	I4U	C5-C4-N3	-3.10	120.19	124.91
2	2	1883	OMG	C5-C6-N1	3.09	121.04	113.19
2	2	1574	B9B	N3-C2-N1	-3.09	120.57	125.42
2	2	1625	OMG	C2-N1-C6	-3.09	119.46	125.10
2	2	1574	B9B	N3-C4-N9	3.09	131.27	126.99
2	2	4523	A2M	N3-C4-N9	3.08	132.16	127.08
2	2	2754	B9B	O6-C6-N1	-3.08	115.71	120.00
2	2	2363	A2M	C5-N7-C8	3.07	107.87	103.51
2	2	4529	B8W	C4'-O4'-C1'	-3.07	102.70	109.47
2	2	2050	OMG	N9-C8-N7	-3.07	107.62	113.39
2	2	3825	A2M	N3-C4-N9	3.06	132.12	127.08
2	2	3899	BGH	C6-C5-C4	-3.06	116.31	122.62
2	2	3899	BGH	C5-C4-N3	-3.06	122.31	128.13
2	2	4306	OMU	C5-C4-N3	3.06	119.41	114.84
2	2	2050	OMG	C5-C6-N1	3.05	120.94	113.19
2	2	1883	OMG	N9-C8-N7	-3.05	107.65	113.39
2	2	4870	OMG	N9-C4-N3	3.05	132.06	125.94
2	2	3869	OMC	C1'-N1-C2	3.05	125.22	118.42
2	2	4472	B8W	C5-N7-C8	3.04	107.83	103.51
2	2	1683	PSU	O2-C2-N1	-3.04	119.44	122.79
2	2	1316	OMG	C5-C6-N1	3.03	120.89	113.19
2	2	2364	OMG	N9-C8-N7	-3.02	107.69	113.39
2	2	978	2MG	N9-C8-N7	-3.01	107.72	113.39
2	2	3897	B8K	N9-C8-N7	3.01	107.37	103.33
2	2	3718	A2M	N9-C8-N7	-3.01	109.80	113.91
2	2	2424	OMG	O6-C6-C5	-3.01	118.62	126.60
2	2	2401	A2M	C5-N7-C8	3.01	107.78	103.51
2	2	4550	7MG	C4-C5-N7	3.00	109.70	105.53
2	2	1625	OMG	N9-C8-N7	-3.00	107.73	113.39
2	2	4371	MHG	C5-C4-N9	3.00	110.25	106.35
2	2	4870	OMG	C2-N1-C6	-3.00	119.62	125.10
2	2	4690	B8K	C5-C4-N3	-3.00	122.42	128.13
2	2	4335	5MC	CM5-C5-C6	-2.99	118.85	122.85
2	2	4637	OMG	C5-C6-N1	2.99	120.78	113.19
2	2	2424	OMG	N9-C4-N3	2.99	131.94	125.94
2	2	4296	B8H	O2-C2-N1	-2.99	119.51	122.87
2	2	1517	2MG	O6-C6-C5	-2.99	118.68	126.60
2	2	4628	PSU	O2-C2-N1	-2.99	119.50	122.79
2	2	373	OMG	N9-C4-N3	2.97	131.91	125.94
2	2	3867	A2M	C5-N7-C8	2.97	107.73	103.51
2	2	1522	OMG	C2-N1-C6	-2.97	119.68	125.10
2	2	4620	OMU	C5-C4-N3	2.97	119.29	114.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	2	3825	A2M	C5-N7-C8	2.96	107.72	103.51
2	2	1625	OMG	C1'-N9-C8	-2.96	118.28	126.70
2	2	2424	OMG	C5-C6-N1	2.95	120.68	113.19
2	2	3897	B8K	C5-C4-N3	-2.95	122.52	128.13
2	2	1871	A2M	C5-N7-C8	2.94	107.69	103.51
2	2	1456	B8Q	C6-N1-C2	-2.93	119.16	121.79
2	2	4355	E6G	C5-C6-N1	-2.93	119.39	123.46
2	2	4355	E6G	C2-N1-C6	2.92	120.58	115.93
2	2	4196	OMG	C2-N1-C6	-2.92	119.77	125.10
2	2	398	A2M	N3-C4-N9	2.92	131.89	127.08
2	2	373	OMG	C2-N1-C6	-2.91	119.79	125.10
2	2	4494	OMG	C5-C6-N1	2.91	120.58	113.19
2	2	3897	B8K	C6-C5-C4	-2.91	116.62	122.62
2	2	4870	OMG	N9-C8-N7	-2.91	107.92	113.39
2	2	2522	7MG	C4-C5-N7	2.90	109.56	105.53
2	2	398	A2M	C5-N7-C8	2.90	107.64	103.51
2	2	2422	OMC	O2-C2-N3	-2.89	117.64	122.33
2	2	4620	OMU	O2-C2-N1	-2.88	118.95	122.79
2	2	4355	E6G	C5-N7-C8	2.88	107.60	103.51
2	2	2773	OMG	C2-N1-C6	-2.86	119.88	125.10
2	2	373	OMG	C5-C6-N1	2.86	120.45	113.19
2	2	1605	7MG	C4-C5-N7	2.86	109.49	105.53
2	2	4872	2MG	O6-C6-C5	-2.85	119.04	126.60
2	2	2297	E7G	O6-C6-C5	-2.85	120.55	127.54
2	2	4564	M7A	C4-N9-C1'	-2.85	119.84	126.60
2	2	1524	A2M	C5-N7-C8	2.84	107.54	103.51
2	2	2364	OMG	C5-C6-N1	2.83	120.39	113.19
2	2	4637	OMG	O6-C6-C5	-2.83	119.08	126.60
2	2	4293	PSU	C6-N1-C2	-2.83	119.79	122.68
2	2	4597	UR3	C3U-N3-C2	2.83	122.27	117.31
2	2	4550	7MG	N9-C8-N7	2.83	107.42	103.38
2	2	4370	OMG	C2-N1-C6	-2.82	119.95	125.10
2	2	4403	PSU	O2-C2-N1	-2.82	119.68	122.79
2	2	1522	OMG	N9-C8-N7	-2.82	108.08	113.39
2	2	2786	B9H	O2-C2-N1	-2.81	116.13	122.72
2	2	1574	B9B	O6-C6-N1	-2.80	116.09	120.00
2	2	978	2MG	C5-C6-N1	2.80	120.30	113.19
2	2	4371	MHG	N1-C2-N3	-2.78	119.65	123.95
2	2	4571	A2M	C5-N7-C8	2.77	107.45	103.51
2	2	4623	OMG	C2-N1-C6	-2.77	120.04	125.10
2	2	4083	5MU	O2-C2-N1	-2.77	119.10	122.79
2	2	1316	OMG	O6-C6-C5	-2.77	119.25	126.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	2	4185	B8W	C2-N1-C6	2.77	120.33	115.93
2	2	4196	OMG	C1'-N9-C8	-2.77	118.83	126.70
2	2	2297	E7G	C2-N1-C6	-2.76	120.06	125.10
2	2	1574	B9B	C5-N7-C8	2.76	107.43	103.51
2	2	1316	OMG	N9-C4-N3	2.76	131.48	125.94
2	2	2754	B9B	C5-N7-C8	2.76	107.43	103.51
2	2	1522	OMG	C5-C6-N1	2.75	120.17	113.19
2	2	1326	A2M	N3-C4-N9	2.75	131.61	127.08
2	2	1797	E7G	N9-C8-N7	2.74	107.30	103.38
2	2	4494	OMG	O6-C6-C5	-2.74	119.33	126.60
2	2	2297	E7G	C5-C4-N9	2.74	109.90	106.35
7	8	14	OMU	N3-C2-N1	2.74	118.53	114.89
2	2	4636	PSU	O2-C2-N1	-2.73	119.78	122.79
2	2	978	2MG	N1-C2-N3	-2.71	119.75	123.95
2	2	4530	UR3	C6-N1-C2	-2.71	119.36	121.79
2	2	2050	OMG	O6-C6-C5	-2.71	119.42	126.60
2	2	4370	OMG	C5-C6-N1	2.71	120.06	113.19
2	2	1683	PSU	C6-N1-C2	-2.70	119.92	122.68
2	2	4623	OMG	C5-C6-N1	2.70	120.06	113.19
2	2	4529	B8W	C5-N7-C8	2.70	107.34	103.51
2	2	1797	E7G	C2-N1-C6	-2.70	120.18	125.10
2	2	1677	PSU	O2-C2-N1	-2.70	119.82	122.79
2	2	3723	A2M	C5-N7-C8	2.70	107.34	103.51
2	2	2773	OMG	N9-C4-N3	2.69	131.33	125.94
2	2	4690	B8K	C2-N1-C6	-2.68	120.21	125.10
2	2	4472	B8W	C2-N3-C4	2.68	121.29	113.89
2	2	1522	OMG	N9-C4-N3	2.67	131.30	125.94
2	2	4415	1MA	N9-C8-N7	-2.66	108.38	113.39
2	2	1883	OMG	O6-C6-C5	-2.66	119.53	126.60
2	2	4293	PSU	O2-C2-N1	-2.66	119.86	122.79
2	2	4185	B8W	C5-C6-N1	-2.66	119.77	123.46
2	2	4196	OMG	N9-C8-N7	-2.65	108.39	113.39
2	2	4872	2MG	C5-C6-N1	2.65	119.92	113.19
2	2	237	B9B	C2-N3-C4	2.64	121.20	113.89
2	2	237	B9B	C3'-C2'-C1'	2.64	106.44	101.43
2	2	4185	B8W	C4-C5-N7	-2.64	107.41	110.62
2	2	729	2MG	N9-C8-N7	-2.63	108.43	113.39
2	2	2773	OMG	C5-C6-N1	2.63	119.87	113.19
2	2	729	2MG	C5-C6-N1	2.62	119.85	113.19
2	2	3897	B8K	O3'-C3'-C2'	-2.62	103.34	111.82
2	2	4623	OMG	O6-C6-C5	-2.61	119.69	126.60
2	2	4220	6MZ	C5-N7-C8	2.60	107.21	103.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	2	4371	MHG	C71-C72-C73	-2.60	106.91	114.20
2	2	4185	B8W	C2-N3-C4	2.60	121.07	113.89
2	2	4196	OMG	C5-C6-N1	2.58	119.74	113.19
2	2	4483	B8T	O3'-C3'-C2'	2.58	120.16	111.82
2	2	2861	OMC	O2-C2-N3	-2.57	118.14	122.33
2	2	1524	A2M	C4'-O4'-C1'	-2.57	103.80	109.47
2	2	1534	A2M	C5-N7-C8	2.57	107.16	103.51
2	2	1322	1MA	N9-C8-N7	-2.57	108.55	113.39
2	2	4529	B8W	O6-C6-C5	-2.57	113.75	116.97
2	2	4623	OMG	N9-C4-N3	2.57	131.09	125.94
2	2	3718	A2M	C6-C5-C4	2.56	120.63	117.18
2	2	1517	2MG	N9-C8-N7	-2.56	108.58	113.39
2	2	4690	B8K	O6-C6-C5	-2.55	121.29	127.54
2	2	2754	B9B	C2'-C1'-N9	-2.55	106.85	113.30
2	2	1860	B8H	O4-C4-N3	-2.54	115.24	120.12
2	2	2380	B8W	C61-O6-C6	-2.54	114.69	117.21
2	2	2380	B8W	C5-C6-N1	-2.54	119.93	123.46
2	2	2380	B8W	N1-C2-N3	-2.53	121.44	125.42
2	2	4083	5MU	C6-N1-C2	-2.53	118.74	121.30
2	2	2364	OMG	O6-C6-C5	-2.52	119.92	126.60
2	2	1326	A2M	C4-N9-C8	2.52	108.46	105.73
2	2	1605	7MG	N9-C8-N7	2.51	106.97	103.38
2	2	1625	OMG	C5-C6-N1	2.51	119.56	113.19
2	2	1582	PSU	O2-C2-N1	-2.51	120.03	122.79
2	2	373	OMG	O6-C6-C5	-2.50	119.95	126.60
2	2	4671	B8T	C6-C5-C4	2.50	120.02	116.96
2	2	729	2MG	O6-C6-C5	-2.50	119.97	126.60
2	2	3869	OMC	C6-C5-C4	2.50	121.54	117.50
2	2	4196	OMG	O6-C6-C5	-2.50	119.97	126.60
2	2	1316	OMG	N2-C2-N1	2.50	122.03	116.71
2	2	4296	B8H	O4-C4-N3	-2.50	115.33	120.12
2	2	1534	A2M	C2'-C1'-N9	2.49	117.73	113.53
2	2	2380	B8W	C4-C5-N7	-2.49	107.58	110.62
2	2	1625	OMG	O6-C6-C5	-2.49	119.99	126.60
2	2	1797	E7G	O6-C6-C5	-2.49	121.44	127.54
2	2	1456	B8Q	C31-N3-C2	2.49	121.40	117.79
2	2	3897	B8K	O4'-C1'-C2'	-2.48	101.23	106.64
2	2	2522	7MG	C2-N1-C6	-2.48	120.58	125.10
2	2	978	2MG	O6-C6-C5	-2.48	120.02	126.60
2	2	4370	OMG	O6-C6-C5	-2.48	120.03	126.60
2	2	1517	2MG	N1-C2-N3	-2.48	120.12	123.95
2	2	2522	7MG	O6-C6-C5	-2.48	121.47	127.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	2	4870	OMG	C5-C6-N1	2.47	119.47	113.19
2	2	4483	B8T	O3'-C3'-C4'	2.47	118.20	111.05
2	2	3897	B8K	C2-N1-C6	-2.46	120.61	125.10
2	2	1316	OMG	C8-N7-C5	2.46	108.69	104.24
2	2	1522	OMG	O6-C6-C5	-2.45	120.10	126.60
2	2	4220	6MZ	C5-C6-N1	2.44	120.81	118.20
2	2	4306	OMU	O4-C4-C5	-2.44	120.87	125.16
2	2	1871	A2M	C2'-C1'-N9	-2.43	109.43	113.53
2	2	3899	BGH	C2-N1-C6	-2.43	120.67	125.10
2	2	4550	7MG	C2-N1-C6	-2.42	120.68	125.10
2	2	3718	A2M	C5-N7-C8	2.42	106.95	103.51
2	2	1574	B9B	C4-N9-C1'	-2.41	120.84	126.59
2	2	1659	I4U	O4'-C1'-C2'	-2.41	101.38	106.64
2	2	3909	OMC	C5-C4-N4	2.41	124.36	120.57
2	2	2522	7MG	N9-C8-N7	2.41	106.82	103.38
2	2	4536	OMC	O2-C2-N3	-2.40	118.42	122.33
2	2	4370	OMG	N9-C4-N3	2.40	130.76	125.94
2	2	1524	A2M	O4'-C1'-N9	2.40	112.79	108.06
2	2	1605	7MG	O6-C6-C5	-2.40	121.65	127.54
2	2	1574	B9B	C2'-C1'-N9	-2.40	107.23	113.30
2	2	4529	B8W	C5-C6-N1	-2.39	120.14	123.46
2	2	2786	B9H	O3'-C3'-C4'	2.38	117.94	111.05
2	2	2380	B8W	O6-C6-C5	-2.38	113.98	116.97
2	2	729	2MG	CM2-N2-C2	-2.38	118.62	123.86
2	2	1534	A2M	C6-C5-C4	2.37	120.37	117.18
2	2	3715	PSU	O2-C2-N1	-2.36	120.19	122.79
2	2	3880	P7G	N9-C8-N7	2.36	106.76	103.38
2	2	4620	OMU	O4-C4-C5	-2.36	121.00	125.16
2	2	2508	PSU	O2-C2-N1	-2.36	120.19	122.79
2	2	1605	7MG	C2-N1-C6	-2.36	120.80	125.10
2	2	1909	P7G	C71-N7-C5	2.36	130.10	124.52
2	2	2754	B9B	C3'-C2'-C1'	2.36	105.91	101.43
2	2	3715	PSU	C6-N1-C2	-2.36	120.27	122.68
2	2	4355	E6G	C2-N3-C4	2.35	120.39	113.89
2	2	1574	B9B	C5-C4-N9	2.35	108.52	105.78
2	2	4483	B8T	C6-C5-C4	2.35	119.84	116.96
2	2	4403	PSU	C6-N1-C2	-2.35	120.28	122.68
2	2	3899	BGH	N1-C2-N3	-2.35	118.94	123.32
2	2	4529	B8W	C2-N3-C4	2.35	120.38	113.89
2	2	4523	A2M	C2'-C1'-N9	-2.34	109.59	113.53
2	2	4870	OMG	O6-C6-C5	-2.33	120.41	126.60
2	2	2773	OMG	C8-N7-C5	2.33	108.46	104.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	2	4529	B8W	C2-N1-C6	2.33	119.63	115.93
2	2	1322	1MA	N9-C4-N3	2.33	132.36	126.94
2	2	4483	B8T	O2-C2-N3	-2.32	118.56	122.33
2	2	1574	B9B	C2-N3-C4	2.32	120.30	113.89
2	2	1322	1MA	C1'-N9-C4	-2.31	119.63	126.50
2	2	1316	OMG	C4-C5-N7	-2.31	107.06	110.72
2	2	1625	OMG	C1'-N9-C4	2.31	133.37	126.50
2	2	373	OMG	C8-N7-C5	2.31	108.42	104.24
2	2	1524	A2M	O4'-C4'-C3'	-2.30	100.55	105.11
2	2	978	2MG	C1'-N9-C4	-2.30	119.66	126.50
2	2	1326	A2M	C4-C5-N7	-2.30	107.82	110.62
2	2	2773	OMG	O6-C6-C5	-2.29	120.52	126.60
2	2	4371	MHG	O6-C6-C5	-2.29	121.93	127.54
2	2	2364	OMG	C1'-N9-C8	-2.29	120.19	126.70
2	2	1524	A2M	C2'-C1'-N9	-2.28	109.69	113.53
2	2	3867	A2M	O4'-C4'-C3'	-2.28	100.60	105.11
2	2	1909	P7G	N3-C2-N1	-2.28	119.07	123.32
2	2	1534	A2M	O4'-C1'-N9	-2.27	103.58	108.06
7	8	14	OMU	C1'-N1-C6	-2.27	115.90	120.84
2	2	1348	P4U	O2-C2-N3	-2.27	118.65	122.33
2	2	4129	B8W	C2-N3-C4	2.26	120.13	113.89
2	2	4355	E6G	C5-C4-N9	2.25	108.40	105.78
2	2	4083	5MU	O4-C4-N3	-2.24	115.82	120.12
2	2	4637	OMG	C1'-N9-C8	-2.24	120.32	126.70
2	2	237	B9B	C4-C5-N7	-2.24	107.89	110.62
2	2	2786	B9H	C32-C31-N3	2.23	117.14	112.47
2	2	2422	OMC	C1'-N1-C2	2.23	123.40	118.42
2	2	4472	B8W	O6-C6-C5	-2.23	114.17	116.97
2	2	1574	B9B	O4'-C1'-N9	2.23	112.45	108.06
2	2	3880	P7G	N2-C2-N3	2.22	121.44	116.71
2	2	2754	B9B	C2-N3-C4	2.22	120.02	113.89
2	2	4597	UR3	O2-C2-N1	-2.22	117.53	122.72
2	2	4564	M7A	C5-C4-N3	-2.22	121.42	126.62
2	2	2754	B9B	N2-C2-N3	2.21	120.70	117.25
2	2	373	OMG	N1-C2-N3	-2.21	119.19	123.32
2	2	4636	PSU	C6-N1-C2	-2.21	120.42	122.68
2	2	2773	OMG	N2-C2-N1	2.21	121.42	116.71
2	2	4185	B8W	C5-C4-N9	2.21	108.35	105.78
2	2	2363	A2M	C4-C5-N7	-2.21	107.93	110.62
2	2	1659	I4U	O4'-C4'-C3'	-2.20	100.76	105.11
2	2	2804	OMC	O2-C2-N3	-2.20	118.75	122.33
2	2	1625	OMG	C8-N7-C5	2.19	108.21	104.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	2	4472	B8W	C2-N1-C6	2.19	119.41	115.93
2	2	3723	A2M	C4-N9-C8	2.19	108.11	105.73
2	2	237	B9B	C4-N9-C8	2.19	108.10	105.73
2	2	2380	B8W	C5-C4-N9	2.19	108.33	105.78
2	2	3718	A2M	C5-C4-N9	2.18	108.32	105.78
2	2	4550	7MG	N9-C4-N3	2.18	128.73	125.47
2	2	2297	E7G	N9-C8-N7	2.18	106.50	103.38
2	2	4129	B8W	O6-C6-N1	2.17	122.00	119.01
2	2	4370	OMG	C8-N7-C5	2.17	108.17	104.24
2	2	978	2MG	C8-N7-C5	2.17	108.16	104.24
2	2	1659	I4U	O2-C2-N3	-2.16	118.81	122.33
2	2	2297	E7G	C6-C5-C4	-2.16	118.16	122.62
2	2	4550	7MG	O6-C6-C5	-2.16	122.24	127.54
2	2	2380	B8W	C4-N9-C1'	-2.16	121.45	126.59
2	2	4403	PSU	O4'-C1'-C2'	2.16	108.19	105.14
2	2	3909	OMC	C4-N3-C2	2.15	123.73	120.25
2	2	3867	A2M	C4'-O4'-C1'	-2.15	104.73	109.47
2	2	3867	A2M	C6-C5-C4	2.14	120.06	117.18
2	2	4637	OMG	C8-N7-C5	2.14	108.12	104.24
2	2	1574	B9B	C4-C5-N7	-2.14	108.02	110.62
2	2	3825	A2M	C4-C5-N7	-2.14	108.02	110.62
2	2	4870	OMG	C1'-N9-C8	-2.13	120.64	126.70
2	2	4523	A2M	C4-N9-C8	2.12	108.02	105.73
2	2	2754	B9B	C4-N9-C1'	-2.11	121.56	126.59
2	2	4371	MHG	C72-C71-N7	2.11	114.49	112.41
2	2	2401	A2M	C4-N9-C8	2.11	108.01	105.73
2	2	4129	B8W	C5-C4-N9	2.11	108.24	105.78
2	2	4690	B8K	N1-C2-N3	-2.11	119.39	123.32
2	2	1677	PSU	C6-N1-C2	-2.10	120.53	122.68
2	2	4872	2MG	N9-C8-N7	-2.10	109.44	113.39
2	2	4370	OMG	N2-C2-N1	2.10	121.18	116.71
2	2	4870	OMG	C8-N7-C5	2.10	108.03	104.24
2	2	3880	P7G	N3-C2-N1	-2.09	119.42	123.32
2	2	2364	OMG	C8-N7-C5	2.09	108.02	104.24
2	2	3899	BGH	O6-C6-N1	-2.09	116.12	120.12
2	2	1456	B8Q	C1'-N1-C2	2.08	120.51	116.99
2	2	2380	B8W	C3'-C2'-C1'	2.08	105.38	101.43
2	2	4196	OMG	C1'-N9-C4	2.08	132.68	126.50
2	2	1866	UR3	C1'-N1-C2	2.08	120.50	116.99
2	2	1574	B9B	C3'-C2'-C1'	2.08	105.37	101.43
2	2	2297	E7G	N9-C4-N3	2.08	128.57	125.47
2	2	3899	BGH	C2'-C1'-N9	-2.08	109.92	114.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	2	1797	E7G	C8-N7-C71	2.07	125.43	120.50
2	2	4129	B8W	C4-N9-C8	2.07	107.97	105.73
2	2	4523	A2M	C4-C5-N7	-2.07	108.10	110.62
2	2	2424	OMG	N1-C2-N3	-2.07	119.47	123.32
2	2	1605	7MG	C6-C5-C4	-2.06	118.36	122.62
2	2	1659	I4U	C6-N1-C2	-2.06	116.92	120.49
2	2	1677	PSU	O4'-C1'-C2'	2.06	108.04	105.14
2	2	2522	7MG	C6-C5-C4	-2.05	118.39	122.62
2	2	3897	B8K	N1-C2-N3	-2.05	119.49	123.32
2	2	4185	B8W	O4'-C4'-C3'	-2.05	101.06	105.11
2	2	1574	B9B	N2-C2-N1	2.04	120.43	117.25
2	2	1871	A2M	C4-N9-C8	2.04	107.94	105.73
2	2	2380	B8W	C4-N9-C8	2.03	107.93	105.73
2	2	4185	B8W	C4-N9-C8	2.03	107.93	105.73
2	2	4623	OMG	C8-N7-C5	2.02	107.90	104.24
2	2	4371	MHG	C6-C5-C4	-2.02	118.45	122.62
2	2	1322	1MA	C1'-N9-C8	2.02	132.45	126.70
2	2	3867	A2M	C4-N9-C8	2.02	107.91	105.73
2	2	3825	A2M	C5-C4-N9	2.01	108.12	105.78
2	2	3897	B8K	O6-C6-N1	-2.01	116.26	120.12
2	2	1659	I4U	O4-C41-C42	2.01	112.47	107.14
2	2	4523	A2M	C3'-C2'-C1'	2.00	106.66	102.89

There are no chirality outliers.

All (131) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	8	14	OMU	C1'-C2'-O2'-CM2
2	2	237	B9B	C5-C6-O6-C61
2	2	237	B9B	N1-C6-O6-C61
2	2	237	B9B	C3'-C4'-C5'-O5'
2	2	237	B9B	O4'-C4'-C5'-O5'
2	2	398	A2M	O4'-C4'-C5'-O5'
2	2	1348	P4U	N3-C4-O4-C41
2	2	1574	B9B	C5-C6-O6-C61
2	2	1574	B9B	N1-C6-O6-C61
2	2	1582	PSU	C3'-C4'-C5'-O5'
2	2	1582	PSU	O4'-C4'-C5'-O5'
2	2	1625	OMG	C3'-C4'-C5'-O5'
2	2	1797	E7G	C72-C71-N7-C5
2	2	1871	A2M	O4'-C4'-C5'-O5'
2	2	1871	A2M	C3'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
2	2	1883	OMG	O4'-C4'-C5'-O5'
2	2	1883	OMG	C3'-C4'-C5'-O5'
2	2	2297	E7G	C72-C71-N7-C5
2	2	2424	OMG	O4'-C4'-C5'-O5'
2	2	2424	OMG	C3'-C4'-C5'-O5'
2	2	2754	B9B	C5-C6-O6-C61
2	2	2754	B9B	N1-C6-O6-C61
2	2	2861	OMC	C1'-C2'-O2'-CM2
2	2	3701	OMC	C2'-C1'-N1-C2
2	2	3701	OMC	C2'-C1'-N1-C6
2	2	3867	A2M	C3'-C4'-C5'-O5'
2	2	3867	A2M	C1'-C2'-O2'-CM'
2	2	3869	OMC	O4'-C1'-N1-C2
2	2	4129	B8W	C5-C6-O6-C61
2	2	4129	B8W	N1-C6-O6-C61
2	2	4185	B8W	C5-C6-O6-C61
2	2	4185	B8W	N1-C6-O6-C61
2	2	4194	I4U	C3'-C4'-C5'-O5'
2	2	4194	I4U	O4'-C4'-C5'-O5'
2	2	4355	E6G	C5-C6-O6-C61
2	2	4355	E6G	N1-C6-O6-C61
2	2	4403	PSU	O4'-C1'-C5-C4
2	2	4403	PSU	O4'-C1'-C5-C6
2	2	4415	1MA	O4'-C4'-C5'-O5'
2	2	4472	B8W	C5-C6-O6-C61
2	2	4472	B8W	N1-C6-O6-C61
2	2	4523	A2M	O4'-C4'-C5'-O5'
2	2	4529	B8W	C5-C6-O6-C61
2	2	4529	B8W	N1-C6-O6-C61
2	2	4636	PSU	C2'-C1'-C5-C6
2	2	4636	PSU	C3'-C4'-C5'-O5'
2	2	4636	PSU	O4'-C4'-C5'-O5'
2	2	4870	OMG	O4'-C4'-C5'-O5'
2	2	4870	OMG	C3'-C4'-C5'-O5'
2	2	1659	I4U	O4'-C4'-C5'-O5'
2	2	1797	E7G	O4'-C4'-C5'-O5'
2	2	2364	OMG	O4'-C4'-C5'-O5'
2	2	3897	B8K	C3'-C4'-C5'-O5'
2	2	3897	B8K	O4'-C4'-C5'-O5'
2	2	4220	6MZ	C3'-C4'-C5'-O5'
2	2	4293	PSU	O4'-C4'-C5'-O5'
2	2	4371	MHG	O4'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
2	2	4415	1MA	C3'-C4'-C5'-O5'
2	2	4872	2MG	O4'-C4'-C5'-O5'
2	2	1574	B9B	O6-C61-C62-C63
2	2	398	A2M	C3'-C4'-C5'-O5'
2	2	1797	E7G	C3'-C4'-C5'-O5'
2	2	3867	A2M	O4'-C4'-C5'-O5'
2	2	3880	P7G	O4'-C4'-C5'-O5'
2	2	4220	6MZ	O4'-C4'-C5'-O5'
2	2	4293	PSU	C3'-C4'-C5'-O5'
2	2	4523	A2M	C3'-C4'-C5'-O5'
2	2	4529	B8W	O4'-C4'-C5'-O5'
2	2	4872	2MG	C3'-C4'-C5'-O5'
2	2	3909	OMC	O4'-C4'-C5'-O5'
2	2	237	B9B	O6-C61-C62-C63
2	2	3869	OMC	O4'-C1'-N1-C6
2	2	1625	OMG	O4'-C4'-C5'-O5'
2	2	2364	OMG	C3'-C4'-C5'-O5'
2	2	3880	P7G	N7-C71-C72-C73
2	2	1797	E7G	C72-C71-N7-C8
2	2	2773	OMG	O4'-C4'-C5'-O5'
2	2	3729	PSU	O4'-C4'-C5'-O5'
2	2	3899	BGH	O4'-C4'-C5'-O5'
2	2	4371	MHG	C3'-C4'-C5'-O5'
2	2	4371	MHG	C2'-C1'-N9-C8
2	2	4371	MHG	C75-C73-C74-C76
2	2	1534	A2M	C3'-C2'-O2'-CM'
2	2	4371	MHG	C72-C73-C74-C76
2	2	1326	A2M	C4'-C5'-O5'-P
2	2	3867	A2M	C4'-C5'-O5'-P
2	2	4870	OMG	C4'-C5'-O5'-P
2	2	3880	P7G	C3'-C4'-C5'-O5'
2	2	4371	MHG	C72-C71-N7-C5
2	2	2861	OMC	O4'-C4'-C5'-O5'
2	2	1909	P7G	C72-C71-N7-C8
2	2	3887	OMC	C4'-C5'-O5'-P
2	2	3897	B8K	C4'-C5'-O5'-P
2	2	4194	I4U	C4'-C5'-O5'-P
2	2	4550	7MG	O4'-C4'-C5'-O5'
2	2	3869	OMC	C3'-C2'-O2'-CM2
2	2	2786	B9H	C32-C31-N3-C2
2	2	1866	UR3	C4'-C5'-O5'-P
2	2	3701	OMC	O4'-C1'-N1-C6

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Mol	Chain	Res	Type	Atoms
2	2	2297	E7G	C72-C71-N7-C8
2	2	1534	A2M	C4'-C5'-O5'-P
2	2	4550	7MG	C3'-C4'-C5'-O5'
2	2	4371	MHG	C72-C71-N7-C8
2	2	4194	I4U	C42-C41-O4-C4
2	2	1860	B8H	O4'-C1'-C5-C4
2	2	3869	OMC	C4'-C5'-O5'-P
2	2	4671	B8T	C2'-C1'-N1-C6
2	2	1322	1MA	C2'-C1'-N9-C8
2	2	1860	B8H	C4'-C5'-O5'-P
2	2	1909	P7G	O4'-C4'-C5'-O5'
2	2	2422	OMC	O4'-C4'-C5'-O5'
2	2	2508	PSU	O4'-C4'-C5'-O5'
2	2	4371	MHG	O4'-C1'-N9-C8
2	2	373	OMG	C4'-C5'-O5'-P
2	2	4415	1MA	C4'-C5'-O5'-P
2	2	1659	I4U	C3'-C4'-C5'-O5'
2	2	2773	OMG	C3'-C4'-C5'-O5'
2	2	3729	PSU	C3'-C4'-C5'-O5'
2	2	3909	OMC	C3'-C4'-C5'-O5'
2	2	4671	B8T	O4'-C1'-N1-C6
2	2	1524	A2M	O4'-C1'-N9-C8
2	2	3701	OMC	O4'-C1'-N1-C2
2	2	729	2MG	O4'-C4'-C5'-O5'
2	2	1456	B8Q	C3'-C4'-C5'-O5'
2	2	1677	PSU	O4'-C1'-C5-C6
2	2	4636	PSU	O4'-C1'-C5-C6
2	2	1534	A2M	O4'-C4'-C5'-O5'
2	2	3880	P7G	C72-C71-N7-C8
2	2	4194	I4U	C43-C41-O4-C4
2	2	1322	1MA	C2'-C1'-N9-C4
2	2	4371	MHG	C4'-C5'-O5'-P

There are no ring outliers.

26 monomers are involved in 31 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	2	1574	B9B	1	0
2	2	2380	B8W	2	0
7	8	14	OMU	1	0
2	2	1797	E7G	1	0
2	2	4296	B8H	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	2	4637	OMG	1	0
2	2	4623	OMG	1	0
2	2	3867	A2M	1	0
2	2	4636	PSU	1	0
2	2	4472	B8W	1	0
2	2	2522	7MG	1	0
2	2	4529	B8W	2	0
2	2	373	OMG	1	0
2	2	2364	OMG	1	0
2	2	3899	BGH	2	0
2	2	4690	B8K	1	0
2	2	729	2MG	2	0
2	2	3897	B8K	1	0
2	2	4129	B8W	1	0
2	2	4220	6MZ	1	0
2	2	3887	OMC	1	0
2	2	1860	B8H	1	0
2	2	4185	B8W	1	0
2	2	1883	OMG	1	0
2	2	3718	A2M	2	0
2	2	1517	2MG	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 250 ligands modelled in this entry, 250 are monoatomic - leaving 0 for Mogul analysis.

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.

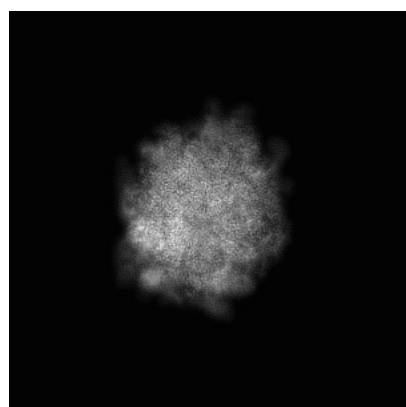
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0964. These allow visual inspection of the internal detail of the map and identification of artifacts.

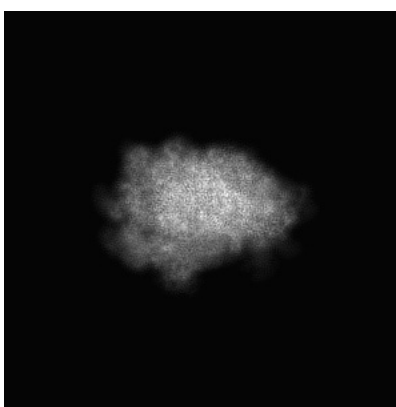
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

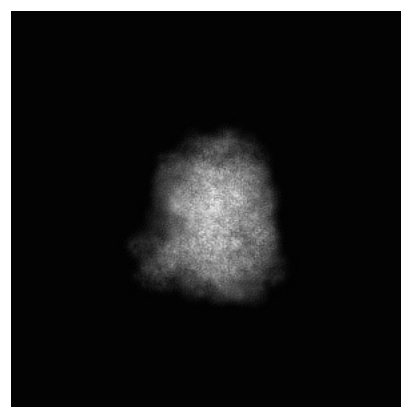
6.1.1 Primary map



X



Y

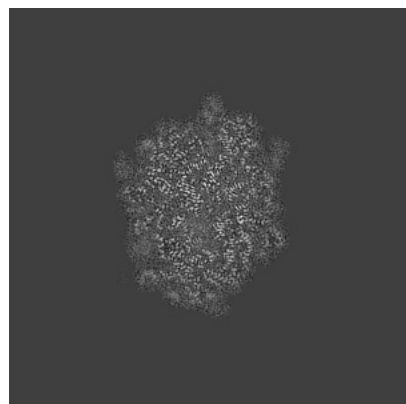


Z

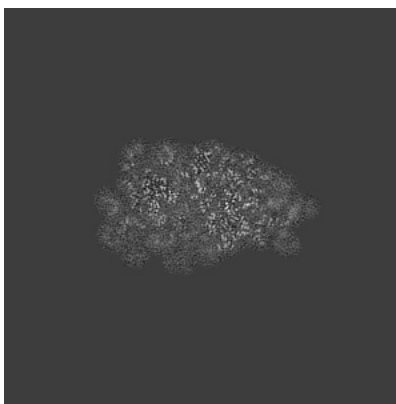
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

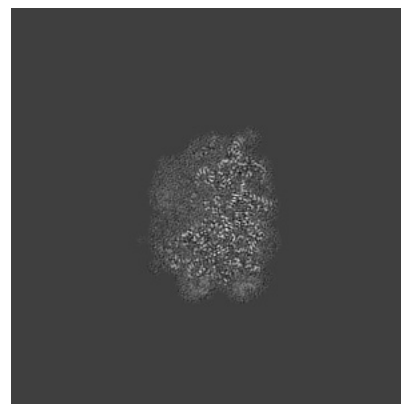
6.2.1 Primary map



X Index: 240



Y Index: 240

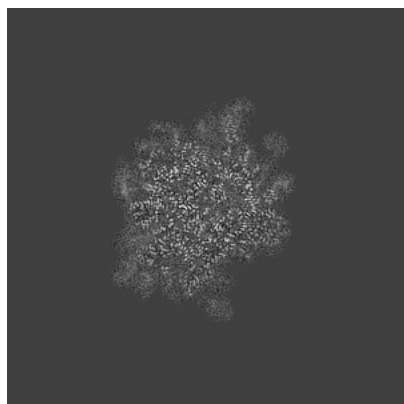


Z Index: 240

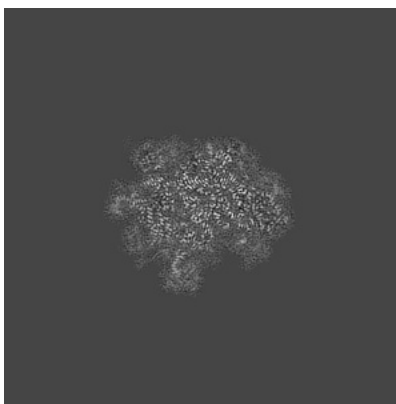
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

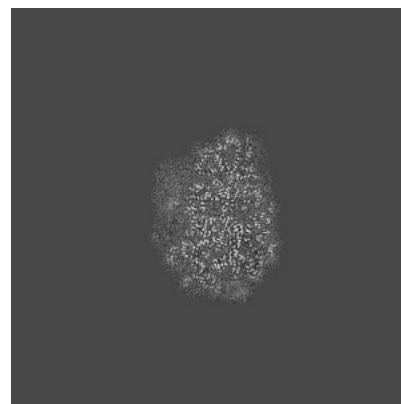
6.3.1 Primary map



X Index: 258



Y Index: 201

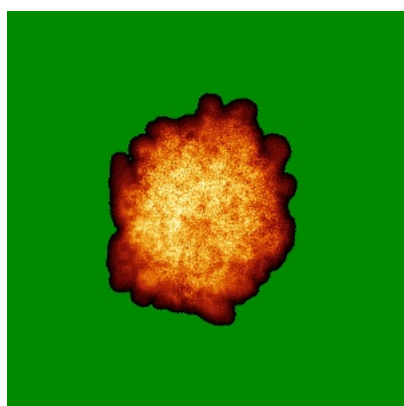


Z Index: 252

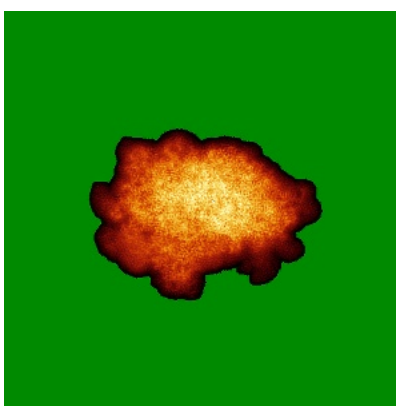
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

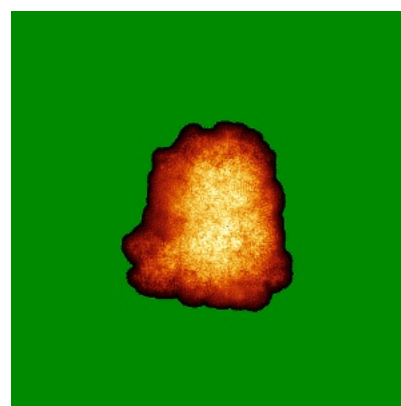
6.4.1 Primary map



X



Y

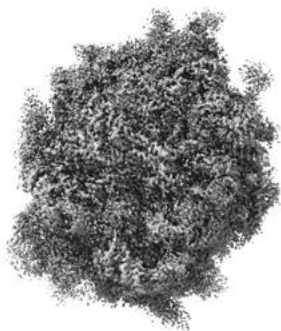


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

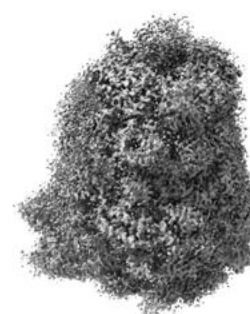
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.065. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

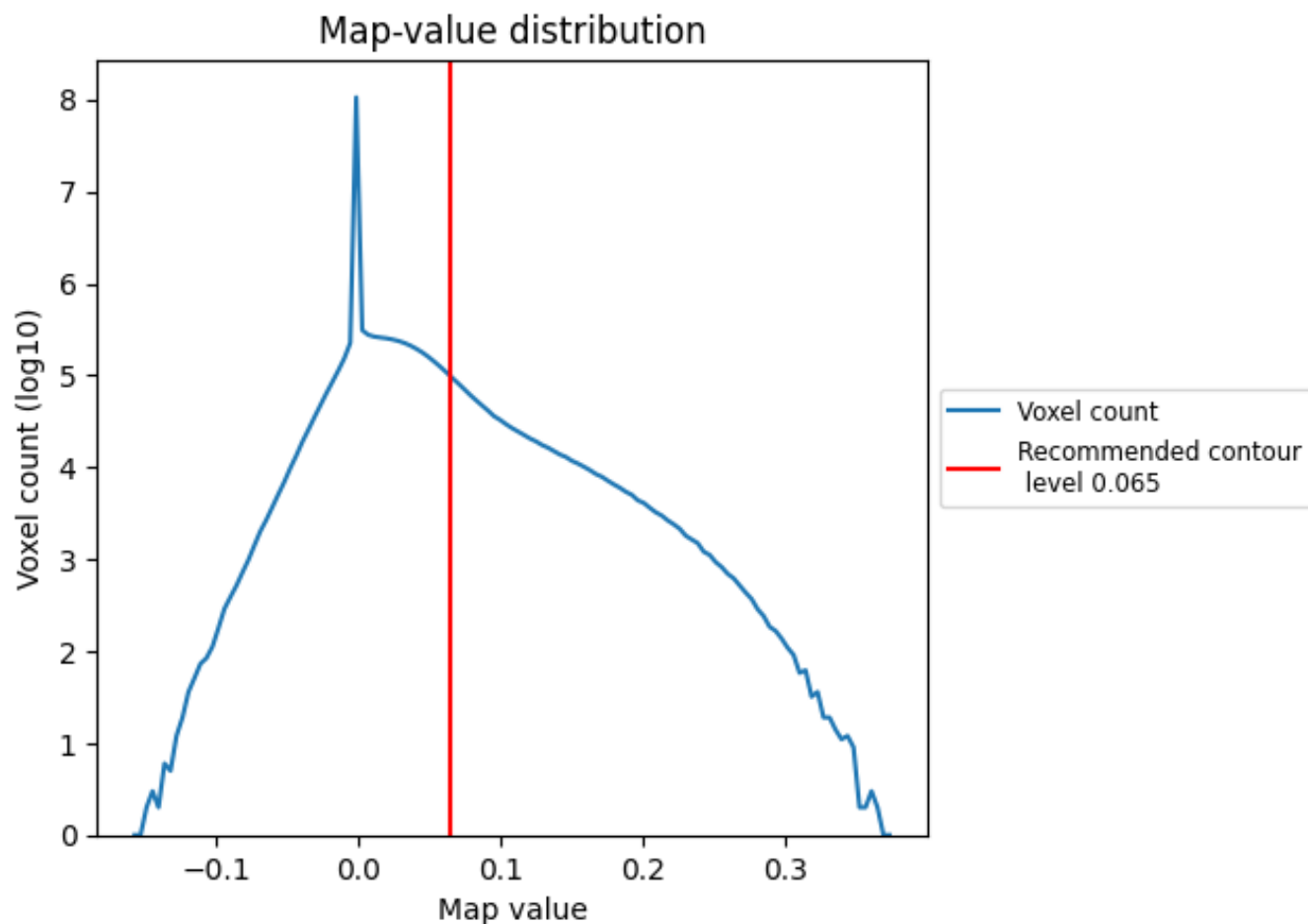
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

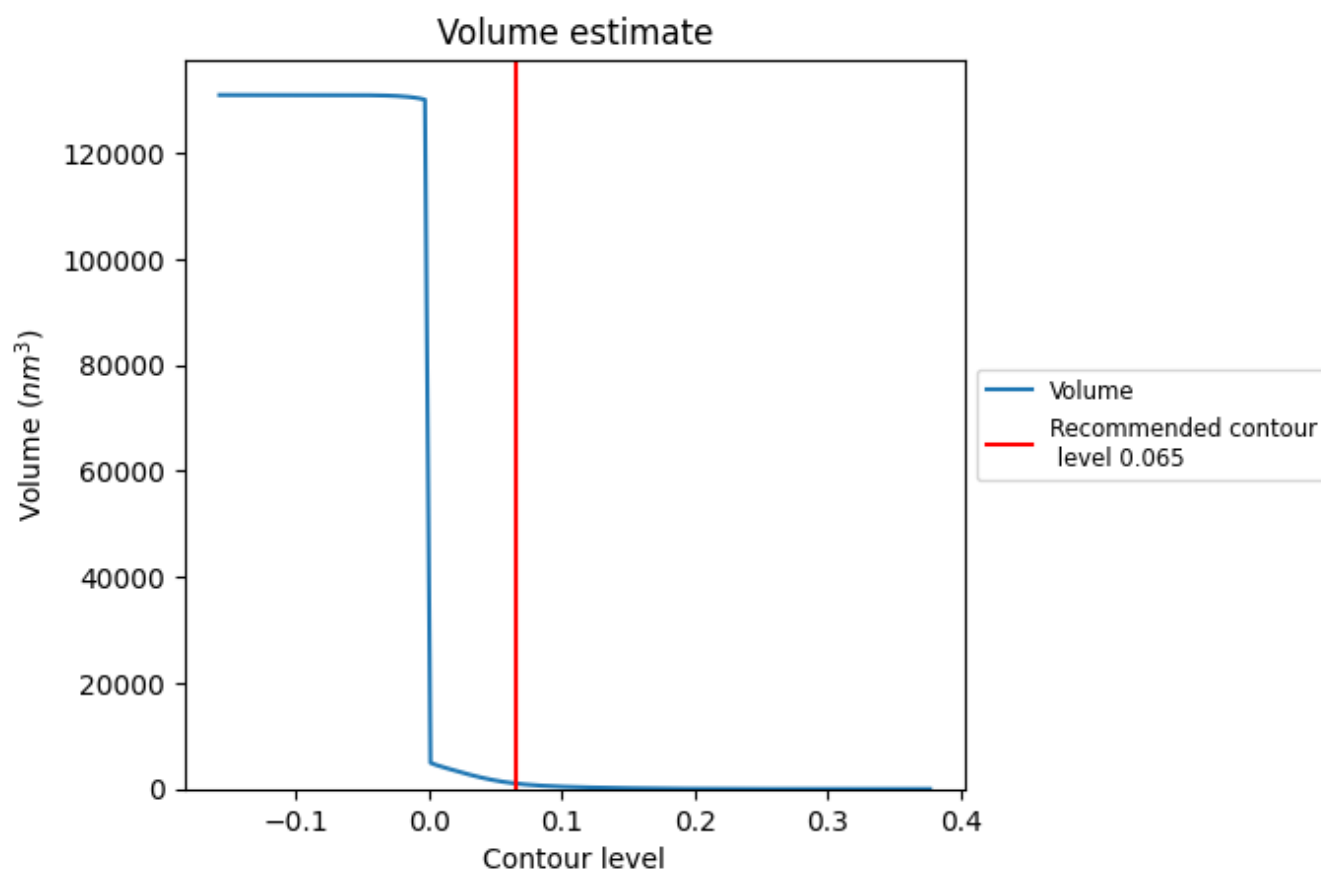
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

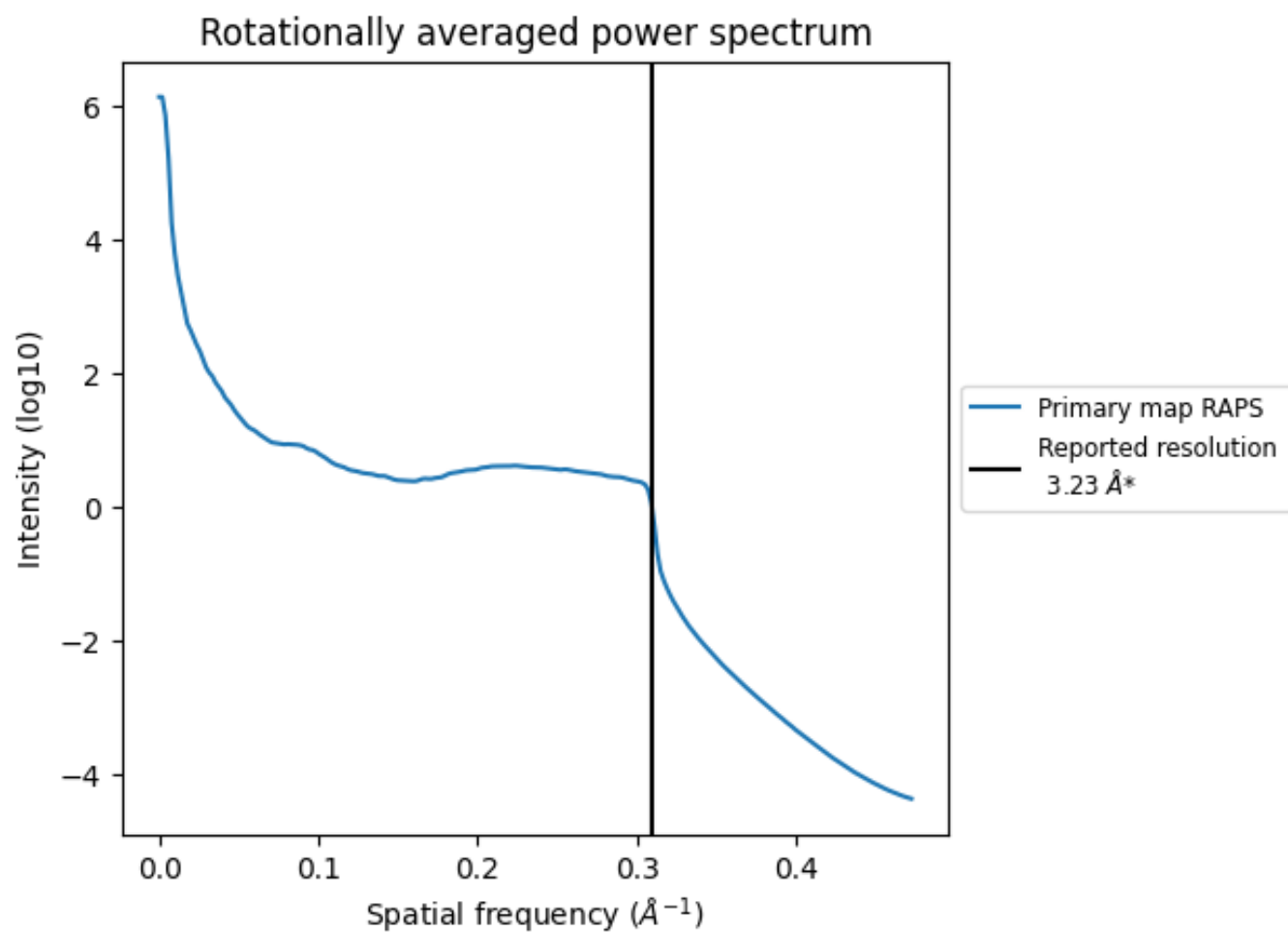
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1045 nm^3 ; this corresponds to an approximate mass of 944 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.310 Å⁻¹

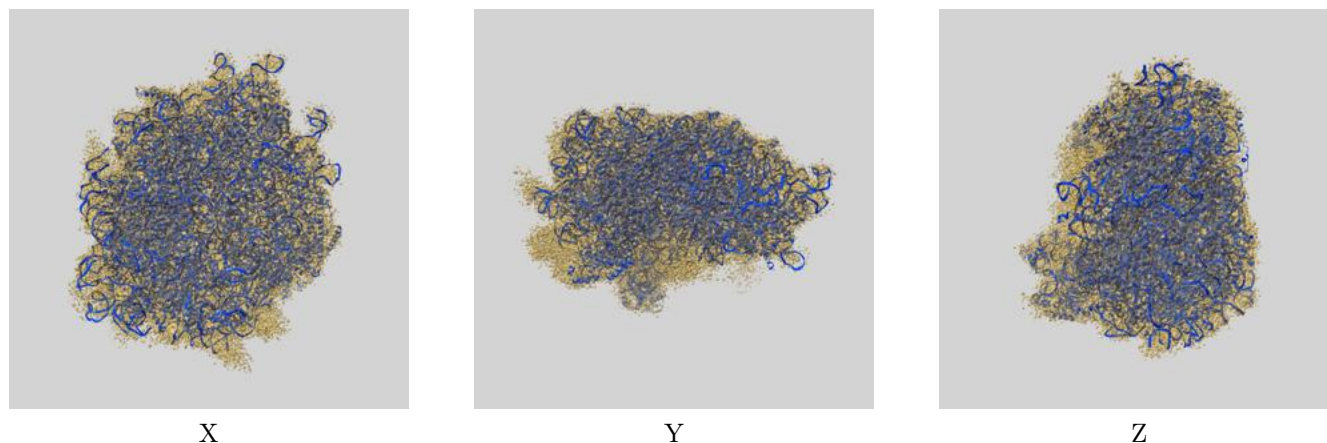
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

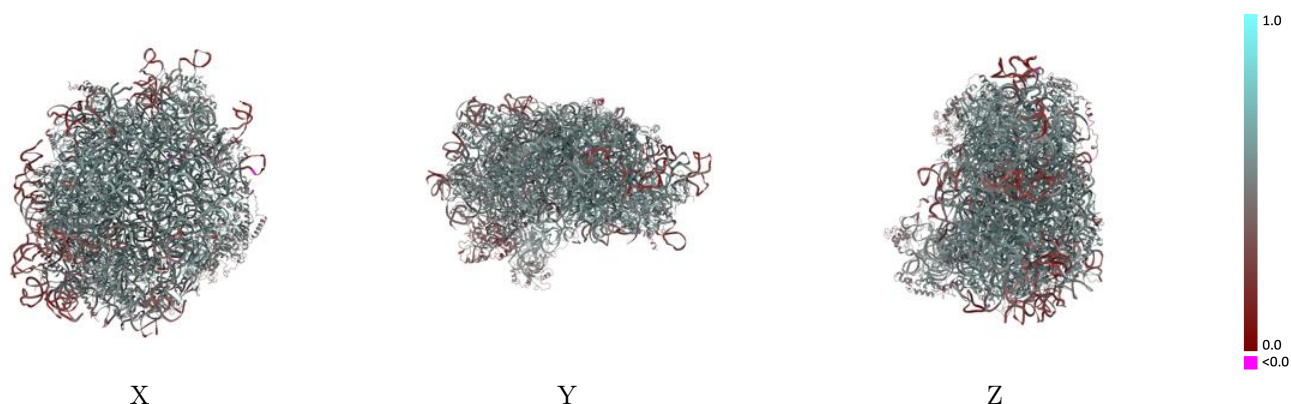
This section contains information regarding the fit between EMDB map EMD-0964 and PDB model 6LSS. Per-residue inclusion information can be found in section [3](#) on page [13](#).

9.1 Map-model overlay [i](#)



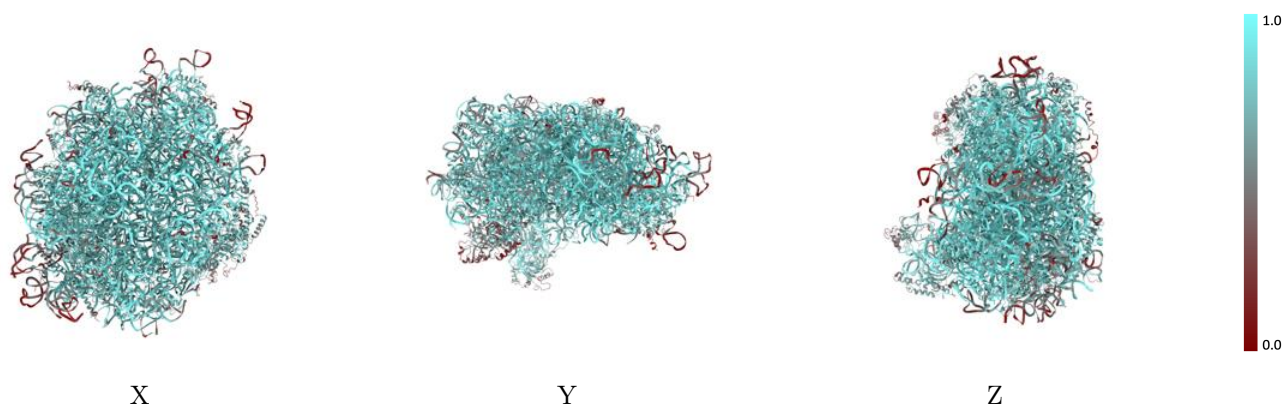
The images above show the 3D surface view of the map at the recommended contour level 0.065 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



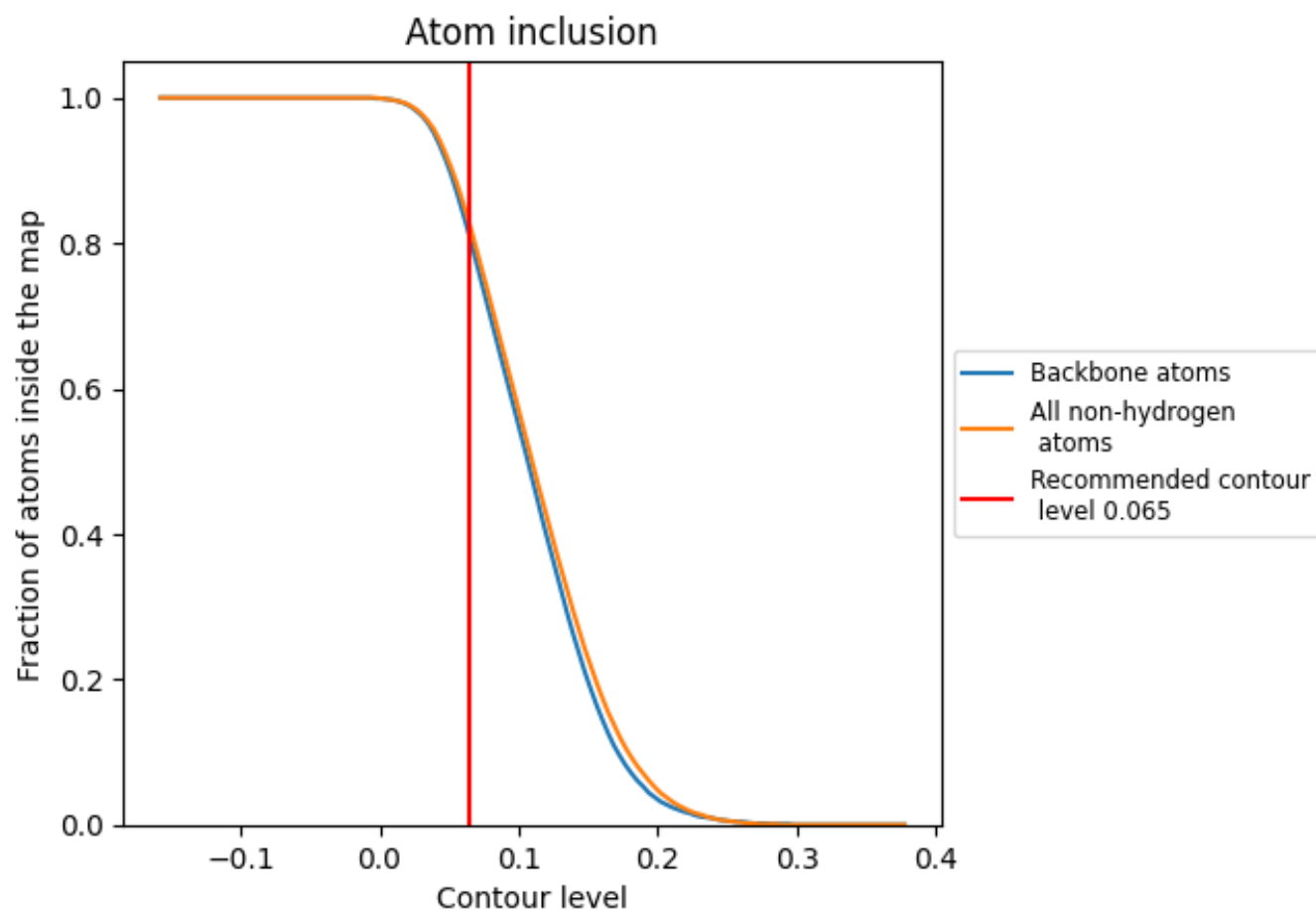
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.065).

9.4 Atom inclusion [i](#)



At the recommended contour level, 81% of all backbone atoms, 82% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.065) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8240	 0.5150
1	 0.2250	 0.3490
2	 0.8480	 0.5010
4	 0.6350	 0.4600
5	 0.9100	 0.5160
6	 0.7040	 0.5070
7	 0.7970	 0.5370
8	 0.9110	 0.5400
9	 0.7750	 0.5180
B	 0.8620	 0.5620
C	 0.7330	 0.4790
D	 0.8830	 0.5660
E	 0.7150	 0.5260
F	 0.8560	 0.5530
G	 0.7140	 0.5090
H	 0.8140	 0.5490
I	 0.7600	 0.5200
K	 0.7830	 0.5200
L	 0.8970	 0.5790
M	 0.9440	 0.5800
N	 0.5780	 0.4230
O	 0.6800	 0.5060
P	 0.9170	 0.5750
Q	 0.7950	 0.5280
R	 0.4480	 0.3980
S	 0.8330	 0.5430
U	 0.9310	 0.5890
V	 0.8710	 0.5640
W	 0.8190	 0.5370
X	 0.8240	 0.5460
Y	 0.8960	 0.5710
Z	 0.8960	 0.5800
a	 0.8370	 0.5550
b	 0.8760	 0.5710
c	 0.8610	 0.5510



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Chain	Atom inclusion	Q-score
d	 0.7340	 0.5120
e	 0.8380	 0.5350
g	 0.8310	 0.5480
h	 0.8250	 0.5530
i	 0.7730	 0.5370
j	 0.8160	 0.5480
k	 0.8930	 0.5780
l	 0.8540	 0.5610
m	 0.8810	 0.5670
n	 0.9040	 0.5820
o	 0.7010	 0.4950
p	 0.8580	 0.5540
r	 0.6740	 0.4820
z	 0.7400	 0.5190