



Full wwPDB EM Validation Report ⓘ

Mar 20, 2026 – 11:57 AM UTC

PDB ID : 8WI8 / pdb_00008wi8
EMDB ID : EMD-37560
Title : Cryo- EM structure of Mycobacterium smegmatis 50S ribosomal subunit (body 1) of 70S ribosome, bS1 and RafH.
Authors : Kumar, N.; Sharma, S.; Kaushal, P.S.
Deposited on : 2023-09-24
Resolution : 2.70 Å(reported)
Based on initial model : 8WHX

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
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

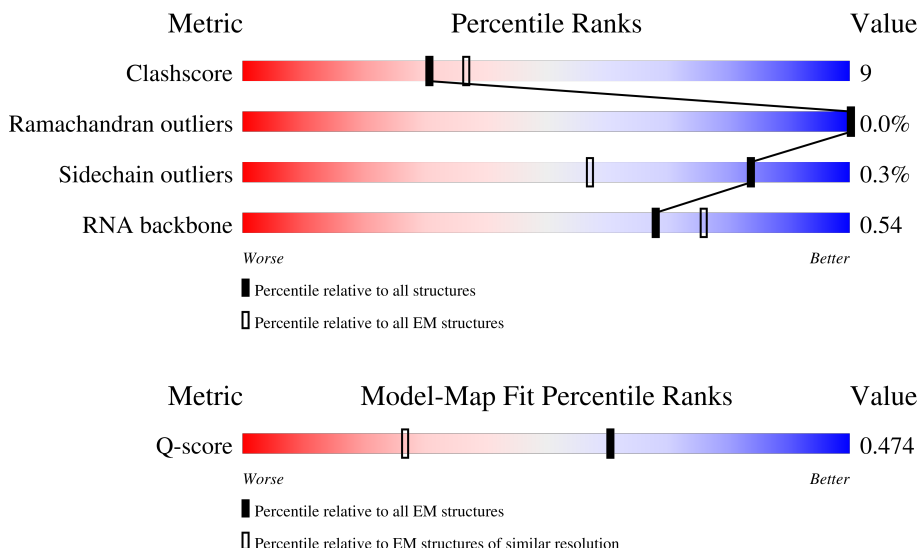
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.70 Å.

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



Metric	Whole archive (#Entries)	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	10327 (2.20 - 3.20)

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	E	278	 83% 16% .
2	F	217	 85% 13% .
3	G	215	 85% 12% .

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Mol	Chain	Length	Quality of chain
4	H	187	
5	I	179	
6	J	151	
7	M	147	
8	N	122	
9	O	147	
10	Q	199	
11	R	127	
12	S	113	
13	T	129	
14	U	103	
15	V	153	
16	W	100	
17	X	105	
18	Z	88	
19	1	64	
20	2	77	
21	3	61	
22	5	57	
23	6	55	
24	7	47	
25	8	64	
26	4	75	
27	A	3119	
28	B	118	

2 Entry composition [i](#)

There are 28 unique types of molecules in this entry. The entry contains 89877 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 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	E	275	Total	C	N	O	S	0	0
			2110	1298	438	370	4		

- Molecule 2 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	F	214	Total	C	N	O	S	0	0
			1587	982	310	290	5		

- Molecule 3 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	G	209	Total	C	N	O	S	0	0
			1569	969	295	303	2		

- Molecule 4 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	H	182	Total	C	N	O	S	0	0
			1445	907	271	261	6		

- Molecule 5 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	I	165	Total	C	N	O	S	0	0
			1260	792	229	238	1		

- Molecule 6 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	J	41	Total	C	N	O	S	0	0
			308	195	55	57	1		

- Molecule 7 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	M	146	Total	C	N	O	S	0	0
			1130	722	207	200	1		

- Molecule 8 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	N	122	Total	C	N	O	S	0	0
			938	586	179	170	3		

- Molecule 9 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	O	145	Total	C	N	O	S	0	0
			1078	676	205	194	3		

- Molecule 10 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	Q	118	Total	C	N	O	S	0	0
			928	583	180	163	2		

- Molecule 11 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	R	126	Total	C	N	O	0	0
			956	586	199	171		

- Molecule 12 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	S	113	Total	C	N	O	S	0	0
			907	570	171	165	1		

- Molecule 13 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	T	124	Total	C	N	O	0	0
			988	613	203	172		

- Molecule 14 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	U	100	Total	C	N	O	0	0
			754	478	137	139		

- Molecule 15 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	V	114	Total	C	N	O	0	0
			873	543	171	159		

- Molecule 16 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	W	95	Total	C	N	O	0	0
			747	474	136	137		

- Molecule 17 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	X	93	Total	C	N	O	S	0	0
			710	443	133	132	2		

- Molecule 18 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	Z	76	Total	C	N	O	0	0
			568	352	120	96		

- Molecule 19 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	1	63	Total	C	N	O	S	0	0
			470	283	103	80	4		

- Molecule 20 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	2	64	Total	C	N	O	S	0	0
			531	324	103	103	1		

- Molecule 21 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	3	59	Total	C	N	O	0	0
			474	292	95	87		

- Molecule 22 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	5	54	Total	C	N	O	S	0	0
			423	260	93	69	1		

- Molecule 23 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	6	48	Total	C	N	O	S	0	0
			397	244	81	68	4		

- Molecule 24 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	7	46	Total	C	N	O	S	0	0
			377	225	97	54	1		

- Molecule 25 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	8	62	Total	C	N	O	0	0
			498	300	114	84		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
26	4	48	Total	C	N	O	S	0	0
			364	225	63	71	5		

- Molecule 27 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	A	3025	Total	C	N	O	P	0	0
			64965	28956	11946	21038	3025		

- Molecule 28 is a RNA chain called 5S rRNA.

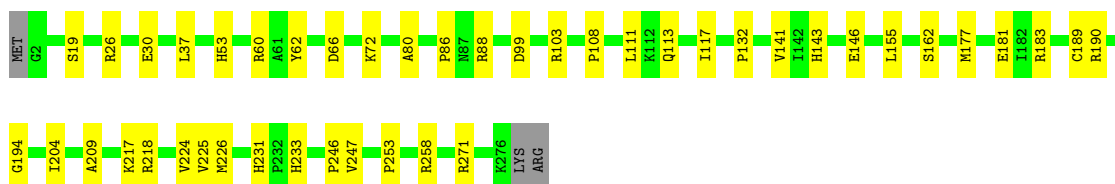
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
28	B	118	2522	1126	468	810	118	0	0

3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: 50S ribosomal protein L2

Chain E: 



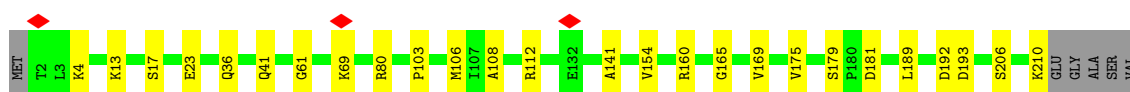
- Molecule 2: 50S ribosomal protein L3

Chain F: 



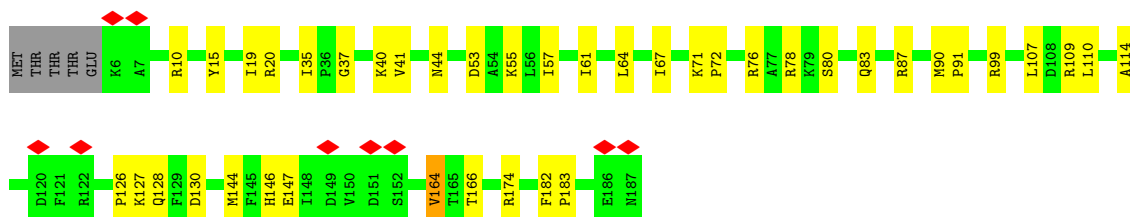
- Molecule 3: 50S ribosomal protein L4

Chain G: 



- Molecule 4: 50S ribosomal protein L5

Chain H: 



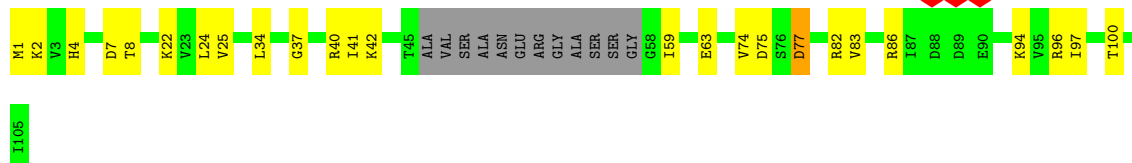
- Molecule 5: 50S ribosomal protein L6

Chain W:  87% 8% 5%



- Molecule 17: 50S ribosomal protein L24

Chain X:  65% 23% 11%



- Molecule 18: 50S ribosomal protein L27

Chain Z:  73% 14% 14%



- Molecule 19: 50S ribosomal protein L28

Chain 1:  6% 81% 17%



- Molecule 20: 50S ribosomal protein L29

Chain 2:  60% 23% 17%



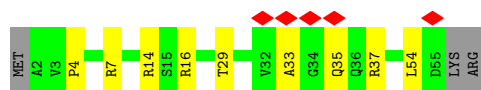
- Molecule 21: 50S ribosomal protein L30

Chain 3:  72% 25%

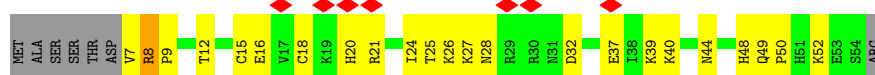
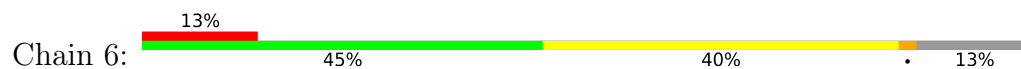


- Molecule 22: 50S ribosomal protein L32

Chain 5:  9% 79% 16% 5%



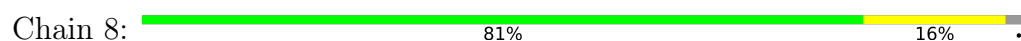
- Molecule 23: 50S ribosomal protein L33



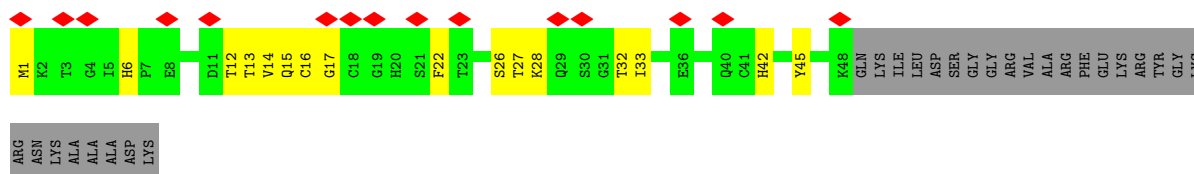
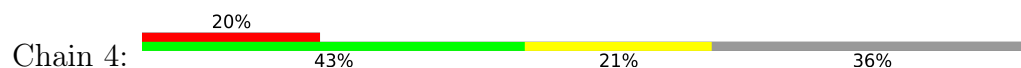
- Molecule 24: 50S ribosomal protein L34



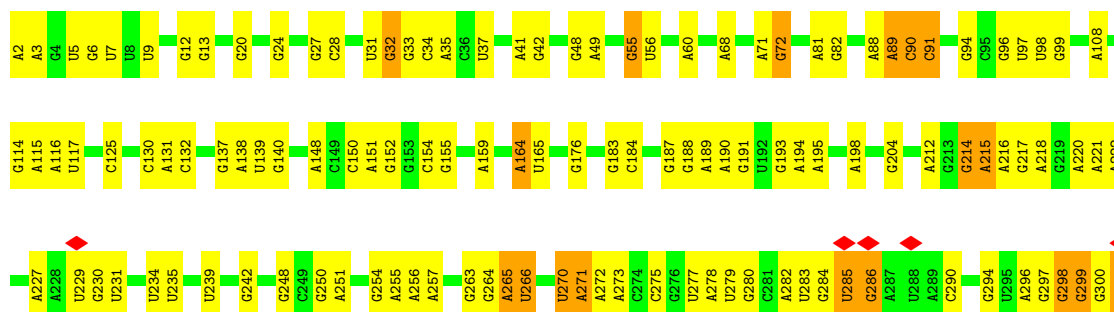
- Molecule 25: 50S ribosomal protein L35



- Molecule 26: 50S ribosomal protein L31

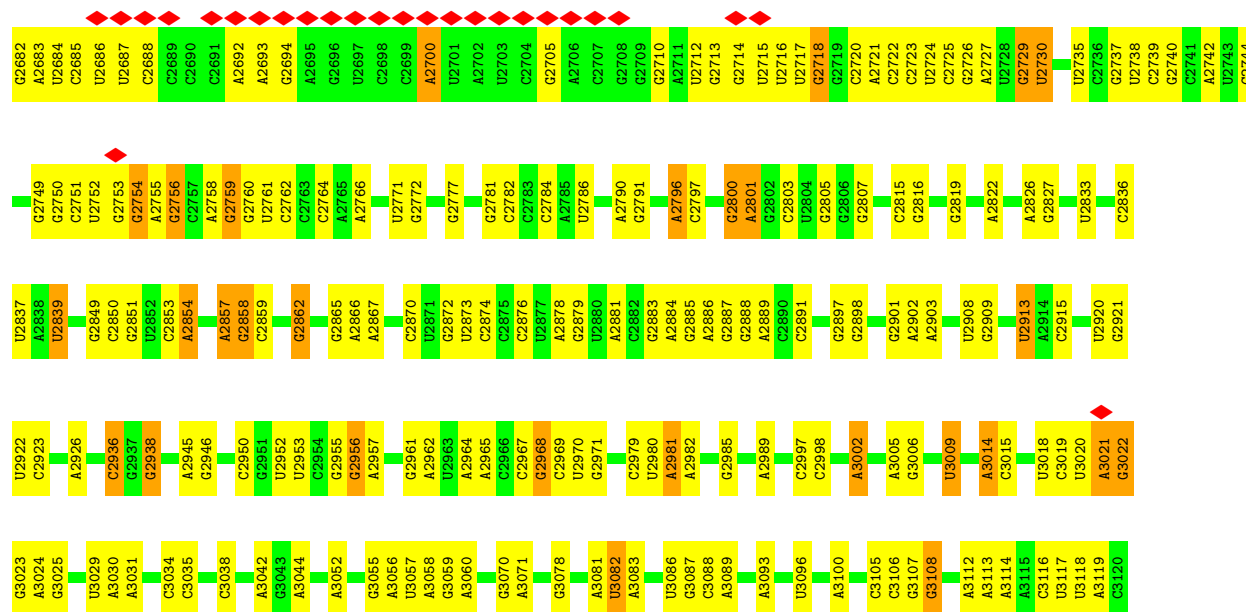


- Molecule 27: 23S rRNA

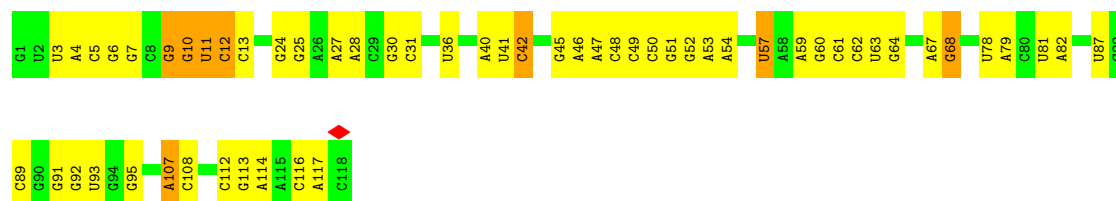








• Molecule 28: 5S rRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	110934	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE; CTF correction in Relion3.1.4	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.34	Depositor
Minimum defocus (nm)	1800	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.213	Depositor
Minimum map value	-0.038	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.011	Depositor
Recommended contour level	0.045	Depositor
Map size ($\text{\AA}$)	406.6, 406.6, 406.6	wwPDB
Map dimensions	380, 380, 380	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.07, 1.07, 1.07	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	E	0.12	0/2153	0.27	0/2895
2	F	0.17	0/1609	0.41	0/2165
3	G	0.12	0/1592	0.27	0/2153
4	H	0.13	0/1467	0.35	0/1973
5	I	0.13	0/1281	0.35	0/1733
6	J	0.21	0/311	0.46	0/419
7	M	0.14	0/1157	0.32	0/1567
8	N	0.12	0/946	0.29	0/1268
9	O	0.13	0/1091	0.37	0/1457
10	Q	0.13	0/945	0.30	0/1267
11	R	0.15	0/966	0.43	0/1298
12	S	0.14	0/921	0.34	0/1236
13	T	0.14	0/1000	0.29	0/1341
14	U	0.15	0/764	0.30	0/1030
15	V	0.13	0/887	0.30	0/1204
16	W	0.15	0/757	0.33	0/1018
17	X	0.14	0/716	0.35	0/957
18	Z	0.14	0/577	0.31	0/774
19	1	0.11	0/478	0.30	0/641
20	2	0.13	0/534	0.32	0/713
21	3	0.15	0/477	0.32	0/640
22	5	0.13	0/427	0.28	0/572
23	6	0.19	0/405	0.47	0/542
24	7	0.11	0/380	0.29	0/500
25	8	0.10	0/503	0.27	0/667
26	4	0.14	0/372	0.37	0/503
27	A	0.12	0/72743	0.26	0/113499
28	B	0.11	0/2821	0.24	0/4396
All	All	0.12	0/98280	0.28	0/148428

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	2110	0	2165	30	0
2	F	1587	0	1630	24	0
3	G	1569	0	1607	20	0
4	H	1445	0	1476	33	0
5	I	1260	0	1300	48	0
6	J	308	0	323	11	0
7	M	1130	0	1167	19	0
8	N	938	0	1000	15	0
9	O	1078	0	1151	22	0
10	Q	928	0	972	14	0
11	R	956	0	991	19	0
12	S	907	0	938	14	0
13	T	988	0	1038	14	0
14	U	754	0	802	11	0
15	V	873	0	909	12	0
16	W	747	0	794	7	0
17	X	710	0	760	20	0
18	Z	568	0	586	12	0
19	1	470	0	484	9	0
20	2	531	0	541	11	0
21	3	474	0	500	10	0
22	5	423	0	463	9	0
23	6	397	0	407	22	0
24	7	377	0	411	7	0
25	8	498	0	538	8	0
26	4	364	0	352	14	0
27	A	64965	0	32687	939	0
28	B	2522	0	1285	38	0
All	All	89877	0	57277	1281	0

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

All (1281) 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)
27:A:2971:G:H21	27:A:2981:A:N6	1.45	1.14
27:A:2971:G:N2	27:A:2981:A:H62	1.52	1.05
27:A:1610:C:H2'	27:A:1611:A:C8	1.96	0.99
27:A:1547:G:H1	27:A:1623:U:H3	1.01	0.96
27:A:1550:G:H1	27:A:1620:U:H3	1.13	0.96
27:A:1562:C:H42	27:A:1608:U:H3	0.97	0.92
27:A:334:G:H1	27:A:347:U:H3	1.09	0.91
27:A:2971:G:H21	27:A:2981:A:H62	0.95	0.91
27:A:1559:A:H2'	27:A:1560:U:H6	1.34	0.90
27:A:1540:U:H3	27:A:1632:G:H1	1.22	0.85
27:A:2086:U:H3	27:A:2096:G:H1	0.85	0.85
27:A:1559:A:H2'	27:A:1560:U:C6	2.13	0.83
27:A:337:U:H3	27:A:344:G:H1	0.83	0.82
27:A:1609:G:H2'	27:A:1610:C:C6	2.14	0.82
6:J:10:GLU:OE2	6:J:11:HIS:ND1	2.13	0.82
18:Z:64:PRO:HB3	27:A:759:G:H1	1.48	0.79
27:A:1754:G:N2	27:A:1759:A:N1	2.33	0.77
2:F:156:THR:HB	2:F:157:PRO:CD	2.15	0.77
27:A:1996:U:OP2	27:A:2001:A:N6	2.19	0.76
27:A:1533:U:OP2	27:A:1535:C:N4	2.18	0.75
10:Q:103:ARG:HD3	10:Q:110:MET:HE2	1.67	0.75
27:A:747:A:N6	27:A:768:G:O2'	2.19	0.75
2:F:156:THR:HB	2:F:157:PRO:HD2	1.68	0.75
27:A:2333:G:O2'	27:A:2343:G:OP2	2.04	0.75
27:A:279:U:H3	27:A:307:G:H1	1.35	0.74
27:A:217:G:H22	27:A:235:U:H4'	1.53	0.73
27:A:2386:U:OP1	27:A:2393:A:O2'	2.05	0.73
27:A:329:U:O2	27:A:446:G:O6	2.07	0.72
27:A:2883:G:N2	27:A:2886:A:OP2	2.19	0.71
27:A:337:U:O2	27:A:344:G:N2	2.18	0.71
8:N:93:PRO:HG3	8:N:114:ILE:HG12	1.72	0.70
9:O:55:MET:HE2	27:A:2616:A:H2	1.56	0.70
16:W:18:GLU:OE2	16:W:18:GLU:N	2.22	0.70
22:5:16:ARG:NH2	27:A:1379:G:OP1	2.22	0.70
27:A:499:G:OP2	27:A:2630:A:O2'	2.09	0.70
27:A:1426:G:OP2	27:A:1426:G:N2	2.21	0.70
11:R:71:ARG:NH2	28:B:28:A:OP1	2.25	0.70
3:G:41:GLN:HG2	27:A:709:U:H1'	1.72	0.69
4:H:53:ASP:OD2	4:H:55:LYS:NZ	2.24	0.69
27:A:1863:G:H5''	27:A:1864:U:H5'	1.72	0.69
17:X:4:HIS:NE2	27:A:81:A:OP1	2.25	0.69
27:A:2422:A:N1	27:A:2450:C:N4	2.40	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:H:44:ASN:ND2	27:A:2537:C:O4'	2.26	0.69
27:A:2674:A:N6	27:A:2725:C:C2	2.61	0.68
23:6:12:THR:HG23	23:6:24:ILE:HG22	1.75	0.68
27:A:334:G:N2	27:A:347:U:O2	2.20	0.68
22:5:37:ARG:HD3	22:5:54:LEU:HD22	1.74	0.68
27:A:1541:G:H2'	27:A:1542:A:H8	1.59	0.68
27:A:2106:A:H3'	27:A:2107:G:H5''	1.75	0.68
13:T:73:ASP:O	13:T:114:ARG:NH2	2.27	0.67
25:8:47:ARG:NH2	27:A:724:G:OP1	2.28	0.67
27:A:1562:C:N4	27:A:1608:U:H3	1.82	0.67
27:A:989:G:O6	27:A:990:G:N2	2.27	0.67
27:A:176:G:OP2	27:A:176:G:N2	2.23	0.67
27:A:2342:A:N6	27:A:2390:U:O2'	2.28	0.67
27:A:1147:A:N6	27:A:1243:G:O2'	2.28	0.66
27:A:159:A:N3	27:A:2431:C:O2'	2.27	0.66
27:A:1542:A:H61	27:A:1628:A:H1'	1.61	0.66
27:A:1609:G:H2'	27:A:1610:C:H6	1.60	0.66
6:J:3:LEU:HD13	6:J:36:ALA:HB1	1.77	0.66
4:H:15:TYR:HA	4:H:19:ILE:HB	1.76	0.66
20:2:28:GLU:OE1	20:2:46:ARG:NH2	2.27	0.66
27:A:2482:U:O2'	27:A:2651:C:OP2	2.13	0.66
27:A:539:C:N4	27:A:542:A:OP2	2.26	0.66
10:Q:42:ARG:NH2	27:A:3038:C:OP1	2.29	0.65
19:1:57:LYS:NZ	27:A:488:G:N7	2.43	0.65
27:A:567:A:H4'	27:A:568:A:H5'	1.78	0.65
27:A:1165:G:H4'	27:A:1166:A:H5'	1.79	0.65
16:W:68:ARG:NH2	27:A:1449:C:OP1	2.28	0.65
17:X:37:GLY:HA2	17:X:40:ARG:HH21	1.61	0.65
27:A:2674:A:OP1	27:A:2721:A:O2'	2.12	0.65
9:O:74:GLU:N	9:O:74:GLU:OE1	2.29	0.65
27:A:2552:A:H2'	27:A:2553:G:C8	2.32	0.65
28:B:67:A:H4'	28:B:68:G:H5'	1.79	0.65
3:G:179:SER:OG	3:G:181:ASP:OD1	2.14	0.65
27:A:365:U:H3	27:A:437:G:H1	1.45	0.65
15:V:69:GLU:OE2	15:V:69:GLU:N	2.31	0.64
1:E:108:PRO:HD2	1:E:111:LEU:HD22	1.79	0.64
17:X:63:GLU:OE2	17:X:63:GLU:N	2.30	0.64
10:Q:70:ILE:HG22	10:Q:72:ASP:H	1.62	0.64
7:M:108:MET:HE2	27:A:1256:G:N2	2.12	0.64
27:A:2332:U:N3	27:A:2333:G:O6	2.30	0.64
27:A:3034:C:H2'	27:A:3035:C:H6	1.62	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:1500:A:O2'	27:A:1511:U:O2	2.15	0.64
5:I:150:ARG:HD2	5:I:163:VAL:HG23	1.79	0.64
4:H:76:ARG:HH21	28:B:42:C:H42	1.45	0.64
6:J:9:VAL:HG13	6:J:12:LEU:HB2	1.78	0.63
23:6:39:LYS:HA	23:6:50:PRO:HA	1.80	0.63
27:A:1476:G:H2'	27:A:1477:C:C6	2.33	0.63
3:G:192:ASP:OD1	9:O:5:LYS:NZ	2.28	0.63
27:A:1033:A:N3	28:B:81:U:O2'	2.31	0.63
27:A:1610:C:H2'	27:A:1611:A:H8	1.60	0.63
27:A:1710:A:H61	27:A:1716:A:H5''	1.63	0.63
21:3:58:GLU:OE1	21:3:58:GLU:N	2.30	0.63
27:A:1886:A:N3	27:A:1888:C:N4	2.46	0.63
27:A:2351:A:N3	27:A:2396:A:O2'	2.31	0.63
4:H:80:SER:HB2	4:H:87:ARG:HE	1.64	0.63
27:A:990:G:O6	27:A:1018:U:O4	2.17	0.63
21:3:57:GLU:N	21:3:57:GLU:OE1	2.32	0.63
27:A:271:A:OP2	27:A:314:G:N2	2.29	0.63
27:A:1547:G:N2	27:A:1623:U:O2	2.28	0.63
27:A:2756:G:O2'	27:A:2881:A:N1	2.30	0.63
9:O:65:LYS:HB2	27:A:2640:G:H5''	1.80	0.63
27:A:273:A:H62	27:A:313:G:H21	1.46	0.62
27:A:384:G:H2'	27:A:385:G:H8	1.64	0.62
21:3:15:ALA:O	21:3:20:ARG:NH1	2.32	0.62
27:A:2372:U:H2'	27:A:2373:G:C8	2.34	0.62
9:O:89:GLN:OE1	9:O:89:GLN:N	2.25	0.62
11:R:11:SER:HB2	28:B:31:C:H5'	1.80	0.62
27:A:2371:G:H2'	27:A:2372:U:C6	2.35	0.62
27:A:2682:G:H21	27:A:2683:A:H61	1.47	0.62
27:A:1562:C:H2'	27:A:1563:A:H4'	1.81	0.62
27:A:551:G:N2	27:A:554:A:OP2	2.29	0.62
27:A:2470:A:H2'	27:A:2471:A:H8	1.63	0.62
13:T:25:ARG:NH1	27:A:2245:C:OP1	2.33	0.62
27:A:2248:C:H2'	27:A:2249:G:H8	1.64	0.62
27:A:2819:G:N2	27:A:2822:A:OP2	2.25	0.62
27:A:1755:A:O2'	27:A:1758:G:N2	2.28	0.61
27:A:2176:A:N3	27:A:2784:C:O2'	2.33	0.61
27:A:2224:C:O2'	27:A:2913:U:OP2	2.17	0.61
27:A:2674:A:N6	27:A:2725:C:O2	2.33	0.61
27:A:2752:U:O2'	27:A:2754:G:OP1	2.16	0.61
2:F:19:GLU:N	2:F:19:GLU:OE1	2.32	0.61
5:I:58:ASP:O	5:I:63:ARG:NH1	2.33	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:1556:A:N1	27:A:1615:G:O6	2.33	0.61
27:A:1754:G:N1	27:A:1759:A:N6	2.47	0.61
27:A:3078:G:N2	27:A:3081:A:OP2	2.29	0.61
5:I:108:LEU:HD21	5:I:153:ARG:HD2	1.82	0.61
27:A:389:G:N1	27:A:392:A:OP2	2.27	0.61
27:A:2064:A:H8	27:A:2065:A:H62	1.47	0.61
4:H:61:ILE:HD12	4:H:72:PRO:HG2	1.81	0.61
11:R:127:PHE:O	27:A:2601:A:O2'	2.15	0.61
5:I:87:LYS:HD2	5:I:88:MET:N	2.15	0.61
20:2:13:LEU:HB3	20:2:17:GLU:HG3	1.83	0.61
27:A:308:U:H2'	27:A:309:G:H8	1.65	0.61
21:3:37:ARG:HH22	27:A:1043:G:H4'	1.66	0.61
24:7:37:ARG:NH1	24:7:44:ALA:O	2.34	0.61
27:A:813:C:O2'	27:A:849:A:N6	2.31	0.61
27:A:1921:G:H2'	27:A:1922:G:H8	1.66	0.61
27:A:2344:G:H4'	27:A:2391:G:H22	1.66	0.61
27:A:3014:A:N6	27:A:3113:A:OP2	2.34	0.61
15:V:90:LYS:HB3	15:V:102:ARG:HD2	1.82	0.61
27:A:2394:A:O2'	27:A:2396:A:OP1	2.13	0.61
2:F:151:ILE:HG12	27:A:2275:A:H4'	1.83	0.60
27:A:929:C:H1'	27:A:1339:G:H21	1.66	0.60
27:A:2407:C:N4	27:A:2408:G:O6	2.34	0.60
27:A:2805:G:N2	27:A:2805:G:OP2	2.33	0.60
27:A:2902:A:H2'	27:A:2903:A:C8	2.37	0.60
6:J:12:LEU:HD22	6:J:19:VAL:HG11	1.82	0.60
26:4:15:GLN:N	26:4:33:ILE:O	2.33	0.60
5:I:104:LEU:HD21	5:I:132:PHE:HE2	1.66	0.60
27:A:2211:C:H2'	27:A:2212:A:H8	1.66	0.60
8:N:80:ASP:OD2	12:S:103:ARG:NH2	2.35	0.60
12:S:1:MET:HE1	12:S:3:THR:HA	1.84	0.60
27:A:1530:G:H21	27:A:1805:G:H22	1.49	0.60
8:N:104:ARG:HH22	12:S:38:ARG:HH21	1.49	0.60
1:E:60:ARG:HA	27:A:1788:G:H5'	1.84	0.59
7:M:108:MET:HE2	27:A:1256:G:H21	1.67	0.59
27:A:220:A:H2	27:A:266:U:H5''	1.67	0.59
27:A:1018:U:O2	27:A:1019:C:N4	2.35	0.59
3:G:160:ARG:NH2	27:A:706:G:O2'	2.34	0.59
7:M:141:GLU:O	7:M:143:LYS:NZ	2.33	0.59
27:A:681:C:H2'	27:A:682:A:H8	1.67	0.59
27:A:1640:A:H2'	27:A:1642:G:N7	2.18	0.59
27:A:857:U:H2'	27:A:858:A:C8	2.37	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:1165:G:O2'	27:A:1228:A:N6	2.26	0.59
27:A:1543:A:N1	27:A:1628:A:O2'	2.34	0.59
8:N:17:LYS:HE3	8:N:47:ILE:HG13	1.83	0.59
14:U:26:LYS:HA	14:U:95:THR:HG23	1.83	0.59
27:A:1554:U:H2'	27:A:1555:A:C8	2.38	0.59
27:A:2074:G:H21	27:A:2109:A:H62	1.50	0.59
18:Z:14:ARG:NH2	27:A:2503:G:N7	2.51	0.59
24:7:14:ARG:NH2	27:A:885:G:OP2	2.36	0.59
27:A:2425:U:O2'	27:A:2427:G:OP1	2.21	0.59
27:A:2677:A:O2'	27:A:2796:A:N3	2.35	0.59
27:A:2879:G:O2'	27:A:2888:G:O6	2.17	0.59
27:A:1530:G:N2	27:A:1805:G:H1	2.00	0.59
27:A:1696:G:O2'	27:A:1736:G:O6	2.20	0.59
1:E:132:PRO:HA	1:E:190:ARG:HA	1.85	0.59
14:U:12:LYS:NZ	27:A:1112:C:O2	2.35	0.59
23:6:40:LYS:NZ	27:A:2571:C:OP1	2.35	0.59
27:A:114:G:OP2	27:A:116:A:O2'	2.20	0.59
5:I:87:LYS:HD2	5:I:88:MET:H	1.68	0.59
5:I:111:SER:OG	27:A:2891:C:N3	2.36	0.59
21:3:5:LYS:HE2	21:3:34:SER:HB3	1.84	0.59
27:A:255:A:O2'	27:A:472:C:OP2	2.21	0.59
27:A:974:G:H4'	27:A:975:U:O5'	2.03	0.59
27:A:911:U:H2'	27:A:912:C:C6	2.38	0.58
4:H:144:MET:SD	4:H:144:MET:N	2.75	0.58
1:E:143:HIS:ND1	1:E:194:GLY:O	2.29	0.58
8:N:2:ILE:HG21	8:N:8:LEU:HD11	1.85	0.58
16:W:62:ARG:NH2	27:A:1455:U:OP2	2.36	0.58
20:2:9:GLU:HA	20:2:12:GLU:HG2	1.85	0.58
27:A:2902:A:H2'	27:A:2903:A:H8	1.68	0.58
11:R:90:GLU:HA	11:R:93:LYS:HB2	1.84	0.58
27:A:1035:G:H21	27:A:2493:A:H8	1.51	0.58
4:H:128:GLN:O	27:A:2527:G:O2'	2.20	0.58
27:A:1468:A:H2'	27:A:1469:A:H8	1.69	0.58
26:4:14:VAL:HB	26:4:22:PHE:HB3	1.86	0.58
27:A:1637:G:HO2'	27:A:1805:G:HO2'	1.50	0.58
27:A:2043:C:O2'	27:A:2195:U:OP2	2.21	0.58
9:O:97:GLU:N	9:O:97:GLU:OE2	2.35	0.58
27:A:473:C:O2'	27:A:476:G:N2	2.37	0.58
10:Q:10:LEU:HB2	10:Q:17:GLN:HG3	1.85	0.58
27:A:285:U:H3'	27:A:286:G:H4'	1.86	0.58
27:A:337:U:O4	27:A:344:G:O6	2.22	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:990:G:H1	27:A:1018:U:H3	0.79	0.58
27:A:1562:C:H2'	27:A:1563:A:C4'	2.34	0.58
15:V:53:PRO:O	15:V:57:VAL:HG23	2.04	0.58
3:G:36:GLN:OE1	27:A:774:G:N2	2.32	0.57
27:A:191:G:N2	27:A:191:G:OP2	2.36	0.57
27:A:357:U:H4'	27:A:358:G:O5'	2.05	0.57
27:A:1540:U:O4	27:A:1632:G:O6	2.23	0.57
27:A:2870:C:OP2	27:A:2956:G:O2'	2.21	0.57
9:O:15:GLU:OE1	9:O:16:LYS:HG2	2.04	0.57
12:S:73:PHE:HB3	12:S:80:ILE:HD11	1.85	0.57
27:A:692:C:H2'	27:A:693:G:H8	1.70	0.57
27:A:2922:U:H2'	27:A:2923:C:C6	2.40	0.57
22:5:33:ALA:HB3	22:5:35:GLN:HE22	1.68	0.57
27:A:284:G:H1'	27:A:303:G:C2	2.39	0.57
27:A:1677:G:H2'	27:A:1678:U:O4'	2.05	0.57
10:Q:118:GLU:OE1	10:Q:118:GLU:N	2.38	0.57
27:A:28:C:O2'	27:A:1353:G:OP1	2.21	0.57
27:A:993:G:N1	27:A:1015:A:OP2	2.26	0.57
27:A:1651:C:H2'	27:A:1652:A:H8	1.69	0.57
27:A:1673:A:H5''	27:A:1674:G:H5''	1.87	0.57
27:A:2420:U:H1'	27:A:2421:A:C8	2.39	0.57
27:A:2552:A:H2'	27:A:2553:G:H8	1.66	0.57
27:A:1229:A:H8	27:A:1230:G:H1'	1.69	0.57
27:A:3022:G:H2'	27:A:3023:G:O4'	2.05	0.57
27:A:3057:U:H2'	27:A:3058:A:H8	1.69	0.57
5:I:139:LYS:HG2	27:A:2970:U:H5''	1.86	0.57
27:A:412:A:HO2'	27:A:413:G:H21	1.51	0.57
27:A:752:C:H2'	27:A:753:A:H8	1.70	0.57
2:F:5:GLY:HA3	2:F:84:LEU:HD21	1.87	0.57
27:A:2287:C:H42	27:A:2725:C:H1'	1.68	0.57
19:1:24:ARG:NH1	27:A:469:G:OP1	2.38	0.56
27:A:1532:G:O2'	27:A:1803:A:N1	2.34	0.56
5:I:96:ARG:HH22	5:I:98:GLN:HG2	1.70	0.56
12:S:61:ARG:NH1	12:S:70:GLU:OE1	2.37	0.56
19:1:47:GLN:OE1	19:1:47:GLN:N	2.38	0.56
26:4:16:CYS:SG	26:4:17:GLY:N	2.78	0.56
27:A:808:A:O2'	27:A:1468:A:N3	2.36	0.56
27:A:2047:C:H2'	27:A:2048:G:H8	1.70	0.56
27:A:2682:G:H21	27:A:2683:A:N6	2.02	0.56
27:A:2758:A:H2'	27:A:2759:G:O4'	2.05	0.56
11:R:68:ALA:HA	11:R:71:ARG:HB2	1.85	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:1791:A:H2'	27:A:1792:A:H8	1.71	0.56
27:A:1825:C:N4	27:A:1840:G:OP2	2.31	0.56
7:M:22:ASP:OD1	27:A:1260:C:N4	2.38	0.56
13:T:12:LYS:O	13:T:16:THR:HG23	2.05	0.56
27:A:1552:A:N6	27:A:1616:A:OP2	2.39	0.56
27:A:1705:C:H2'	27:A:1706:A:H8	1.69	0.56
27:A:1754:G:H1	27:A:1759:A:N6	2.03	0.56
27:A:2470:A:H2'	27:A:2471:A:C8	2.40	0.56
8:N:30:ARG:HG3	27:A:2898:G:H4'	1.86	0.56
27:A:1710:A:N6	27:A:1716:A:OP2	2.39	0.56
13:T:33:ARG:NH2	27:A:672:C:OP1	2.38	0.56
27:A:1009:U:H2'	27:A:1010:U:C6	2.41	0.56
27:A:2716:U:H2'	27:A:2717:U:C6	2.41	0.56
5:I:102:GLN:CD	5:I:102:GLN:H	2.14	0.56
27:A:1637:G:O2'	27:A:1805:G:O2'	2.24	0.56
4:H:110:LEU:HD12	4:H:114:ALA:HB3	1.87	0.56
11:R:73:ILE:HG12	11:R:75:GLY:H	1.70	0.56
27:A:279:U:H2'	27:A:280:G:H8	1.69	0.56
27:A:1468:A:H2'	27:A:1469:A:C8	2.40	0.56
27:A:3071:A:N7	27:A:3089:A:O2'	2.36	0.56
11:R:37:ARG:NH2	11:R:54:ASP:OD1	2.38	0.56
27:A:353:G:O6	27:A:442:U:O2	2.25	0.55
27:A:2682:G:O2'	27:A:2684:U:O4	2.24	0.55
23:6:15:CYS:SG	23:6:16:GLU:N	2.78	0.55
27:A:34:C:H2'	27:A:35:A:C8	2.41	0.55
27:A:664:A:H3'	27:A:665:G:H8	1.72	0.55
27:A:935:A:H4'	27:A:951:G:N2	2.20	0.55
27:A:2356:G:H2'	27:A:2380:G:H1	1.71	0.55
5:I:144:GLN:OE1	27:A:2968:G:N2	2.39	0.55
15:V:23:LYS:NZ	27:A:2236:G:N7	2.55	0.55
27:A:429:A:H2'	27:A:430:A:H8	1.71	0.55
27:A:2271:C:H2'	27:A:2272:G:H8	1.72	0.55
6:J:10:GLU:OE2	6:J:11:HIS:N	2.40	0.55
21:3:8:GLN:HB2	21:3:28:LEU:HD13	1.88	0.55
27:A:1560:U:H3'	27:A:1561:C:C6	2.42	0.55
27:A:2764:C:O2'	27:A:2964:A:N3	2.33	0.55
27:A:2238:A:H2'	27:A:2239:A:C8	2.42	0.55
27:A:2367:G:N2	27:A:2369:C:O2	2.40	0.55
22:5:14:ARG:HB3	27:A:13:G:H5''	1.87	0.55
27:A:470:G:N2	27:A:481:C:N3	2.55	0.55
3:G:106:MET:HE2	27:A:773:G:H21	1.72	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:1476:G:H2'	27:A:1477:C:H6	1.70	0.55
27:A:380:A:N1	27:A:404:A:O2'	2.35	0.55
27:A:1396:G:H2'	27:A:1397:U:C6	2.42	0.55
5:I:153:ARG:HE	5:I:154:ARG:H	1.55	0.55
27:A:429:A:H2'	27:A:430:A:C8	2.42	0.54
28:B:10:G:O2'	28:B:11:U:OP1	2.20	0.54
27:A:857:U:H2'	27:A:858:A:H8	1.71	0.54
4:H:147:GLU:OE2	26:4:26:SER:OG	2.23	0.54
18:Z:49:VAL:HG22	18:Z:79:ASN:HB3	1.89	0.54
27:A:380:A:N3	27:A:401:C:O2'	2.36	0.54
27:A:2088:C:H2'	27:A:2089:C:C5	2.42	0.54
3:G:103:PRO:HD2	3:G:106:MET:HE3	1.88	0.54
27:A:667:A:H4'	27:A:2724:U:H5'	1.88	0.54
27:A:2261:U:H2'	27:A:2262:C:C6	2.42	0.54
27:A:2901:G:H2'	27:A:2902:A:H8	1.72	0.54
27:A:800:A:N1	27:A:902:C:H1'	2.22	0.54
27:A:844:G:O2'	27:A:878:G:H4'	2.08	0.54
27:A:2672:A:H5'	27:A:2673:U:H2'	1.89	0.54
27:A:2378:U:H2'	27:A:2379:G:H8	1.73	0.54
4:H:146:HIS:O	26:4:28:LYS:NZ	2.36	0.54
17:X:24:LEU:HD12	17:X:25:VAL:HG23	1.90	0.54
27:A:218:A:N3	27:A:234:U:O2'	2.32	0.54
27:A:933:G:N1	27:A:1303:U:OP2	2.33	0.54
27:A:339:U:H2'	27:A:340:A:C8	2.43	0.54
27:A:668:U:H2'	27:A:669:G:C8	2.42	0.54
27:A:1076:A:H2'	27:A:1077:A:C8	2.43	0.54
27:A:3005:A:H5'	27:A:3006:G:H5'	1.88	0.54
1:E:88:ARG:NH2	27:A:2034:G:OP1	2.40	0.54
23:6:25:THR:HG21	27:A:2510:A:N6	2.23	0.54
27:A:138:A:H2'	27:A:139:U:O2	2.07	0.54
27:A:190:A:H2'	27:A:191:G:N3	2.23	0.54
27:A:1710:A:H62	27:A:1716:A:H8	1.56	0.54
28:B:116:C:H2'	28:B:117:A:C8	2.43	0.54
27:A:657:C:H2'	27:A:658:U:C6	2.43	0.54
27:A:2070:A:H2'	27:A:2071:A:C8	2.43	0.54
28:B:50:C:H2'	28:B:51:G:H8	1.73	0.54
1:E:26:ARG:HH22	1:E:30:GLU:HG2	1.73	0.53
3:G:4:LYS:HD2	3:G:17:SER:HB3	1.90	0.53
27:A:2364:C:H2'	27:A:2365:A:C8	2.43	0.53
4:H:20:ARG:HG2	4:H:35:ILE:HG21	1.89	0.53
27:A:1099:A:OP2	27:A:1100:C:N4	2.42	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:19:SER:HB2	1:E:204:ILE:HD11	1.89	0.53
27:A:997:G:H2'	27:A:998:G:C8	2.42	0.53
27:A:1656:A:H2'	27:A:1657:G:H8	1.73	0.53
27:A:2086:U:H2'	27:A:2087:C:C6	2.44	0.53
27:A:2457:U:H2'	27:A:2458:G:H8	1.72	0.53
27:A:3020:U:O2'	27:A:3021:A:O5'	2.26	0.53
11:R:77:LYS:HB3	11:R:112:ARG:HD3	1.90	0.53
21:3:23:LEU:HD22	21:3:28:LEU:HD11	1.89	0.53
27:A:310:C:H2'	27:A:311:G:H8	1.73	0.53
27:A:1002:C:H2'	27:A:1003:A:H5''	1.91	0.53
27:A:1544:U:O4	27:A:1626:G:O6	2.27	0.53
5:I:151:ARG:NH2	27:A:2967:C:O2	2.36	0.53
27:A:298:G:O2'	27:A:299:G:O4'	2.24	0.53
27:A:987:A:H2	27:A:1021:G:H22	1.55	0.53
27:A:2854:A:N3	27:A:3112:A:O2'	2.39	0.53
4:H:57:ILE:HG13	4:H:91:PRO:HB2	1.90	0.53
10:Q:95:THR:HG22	10:Q:115:LEU:HD23	1.89	0.53
20:2:9:GLU:OE2	20:2:9:GLU:N	2.31	0.53
27:A:34:C:H2'	27:A:35:A:H8	1.72	0.53
27:A:928:U:H2'	27:A:929:C:C6	2.44	0.53
27:A:1501:C:H2'	27:A:1502:G:C8	2.43	0.53
27:A:1621:C:H2'	27:A:1622:G:H8	1.73	0.53
27:A:1690:A:H2'	27:A:1691:A:C8	2.43	0.53
27:A:1791:A:H2'	27:A:1792:A:C8	2.44	0.53
5:I:140:GLN:NE2	27:A:2969:C:O2	2.37	0.53
7:M:56:VAL:HB	7:M:124:VAL:HG12	1.91	0.53
9:O:131:GLY:O	9:O:135:GLU:HG2	2.09	0.53
11:R:41:ASN:ND2	28:B:7:G:O3'	2.41	0.53
17:X:7:ASP:OD2	17:X:96:ARG:NH2	2.41	0.53
23:6:8:ARG:HA	23:6:27:LYS:O	2.08	0.53
27:A:908:A:OP2	27:A:2294:A:O2'	2.26	0.53
27:A:1970:G:N2	27:A:1973:C:OP2	2.37	0.53
27:A:2961:G:H2'	27:A:2962:A:C8	2.43	0.53
27:A:1529:U:H3'	27:A:1530:G:H8	1.73	0.53
27:A:1651:C:H2'	27:A:1652:A:C8	2.43	0.53
27:A:2387:U:H3'	27:A:2388:G:C8	2.44	0.53
27:A:1148:G:O6	27:A:1243:G:N2	2.42	0.53
28:B:5:C:OP1	28:B:62:C:O2'	2.26	0.53
4:H:71:LYS:H	26:4:6:HIS:CE1	2.25	0.52
27:A:296:A:N1	27:A:340:A:N6	2.57	0.52
27:A:929:C:H1'	27:A:1339:G:N2	2.24	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:2739:C:H2'	27:A:2740:G:H8	1.74	0.52
5:I:108:LEU:HD11	5:I:153:ARG:HB2	1.91	0.52
27:A:89:A:O2'	27:A:90:C:OP1	2.25	0.52
2:F:83:GLU:OE2	27:A:2859:C:O2'	2.27	0.52
27:A:2088:C:H2'	27:A:2089:C:C6	2.45	0.52
27:A:2299:C:OP2	27:A:2462:G:N2	2.41	0.52
27:A:2872:G:H2'	27:A:2873:U:C6	2.45	0.52
4:H:147:GLU:HA	26:4:28:LYS:HD3	1.91	0.52
27:A:1020:A:H2'	27:A:1021:G:C8	2.45	0.52
27:A:2216:G:N2	27:A:2220:C:O2'	2.42	0.52
20:2:62:ARG:NH1	20:2:65:GLU:OE1	2.43	0.52
25:8:33:LEU:HD23	25:8:36:LYS:HD2	1.92	0.52
4:H:147:GLU:OE1	26:4:27:THR:OG1	2.23	0.52
27:A:564:G:N1	27:A:567:A:OP2	2.38	0.52
27:A:639:C:O2'	27:A:640:G:H8	1.92	0.52
27:A:2131:G:O6	27:A:2148:C:N4	2.42	0.52
19:1:36:VAL:HG13	19:1:63:ARG:HE	1.75	0.52
27:A:2342:A:H61	27:A:2390:U:H1'	1.75	0.52
2:F:96:GLU:N	2:F:96:GLU:OE1	2.42	0.52
13:T:36:LYS:NZ	27:A:1367:G:N7	2.56	0.52
27:A:1790:A:H2'	27:A:1791:A:C8	2.44	0.52
27:A:2465:A:H2'	27:A:2466:G:C8	2.45	0.52
27:A:2901:G:H2'	27:A:2902:A:C8	2.44	0.52
18:Z:12:ASN:HD21	27:A:2501:G:H3'	1.75	0.52
27:A:1285:G:H2'	27:A:1286:C:C6	2.45	0.52
5:I:84:TYR:CZ	5:I:139:LYS:HB2	2.45	0.52
27:A:639:C:HO2'	27:A:640:G:H8	1.56	0.52
27:A:994:A:H5''	27:A:1014:G:N2	2.25	0.52
28:B:81:U:H2'	28:B:82:A:C8	2.44	0.52
2:F:148:PRO:O	27:A:2735:U:O2'	2.21	0.51
9:O:15:GLU:O	27:A:690:G:N2	2.42	0.51
12:S:93:ARG:NH1	27:A:1971:C:OP1	2.39	0.51
23:6:27:LYS:NZ	23:6:32:ASP:O	2.43	0.51
27:A:154:C:H2'	27:A:155:G:H8	1.73	0.51
27:A:1001:C:C5	27:A:1002:C:H1'	2.45	0.51
27:A:1804:G:H2'	27:A:1805:G:C8	2.45	0.51
27:A:2356:G:H2'	27:A:2380:G:H22	1.75	0.51
27:A:3057:U:H2'	27:A:3058:A:C8	2.45	0.51
13:T:83:LEU:HD22	13:T:88:VAL:HG11	1.92	0.51
17:X:75:ASP:OD2	17:X:100:THR:OG1	2.28	0.51
23:6:25:THR:HG21	27:A:2510:A:H62	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:137:G:H21	27:A:1524:G:H1'	1.75	0.51
27:A:1656:A:H2'	27:A:1657:G:C8	2.46	0.51
1:E:99:ASP:O	27:A:1720:G:N2	2.42	0.51
3:G:23:GLU:OE2	3:G:23:GLU:N	2.27	0.51
18:Z:11:ARG:NH2	18:Z:12:ASN:OD1	2.44	0.51
27:A:736:G:N2	27:A:738:A:H3'	2.25	0.51
27:A:2363:A:H2'	27:A:2364:C:C6	2.46	0.51
27:A:242:G:O2'	27:A:254:G:O6	2.24	0.51
27:A:1523:U:H2'	27:A:1524:G:C8	2.46	0.51
4:H:40:LYS:HE2	4:H:164:VAL:HG11	1.93	0.51
7:M:27:ARG:HH22	27:A:1260:C:HO2'	1.56	0.51
27:A:277:U:H2'	27:A:278:A:C8	2.46	0.51
27:A:310:C:H2'	27:A:311:G:C8	2.46	0.51
27:A:728:G:H2'	27:A:729:C:C6	2.46	0.51
27:A:1501:C:H2'	27:A:1502:G:H8	1.75	0.51
27:A:2329:G:O6	27:A:2406:U:O4	2.28	0.51
27:A:666:A:N6	27:A:2258:U:OP1	2.43	0.51
27:A:691:U:H2'	27:A:692:C:C6	2.46	0.51
27:A:1087:G:H2'	27:A:1088:U:C6	2.45	0.51
27:A:1621:C:H2'	27:A:1622:G:C8	2.46	0.51
27:A:1922:G:H2'	27:A:1923:G:H8	1.75	0.51
27:A:2720:C:H2'	27:A:2721:A:O4'	2.10	0.51
27:A:2752:U:H3'	27:A:2754:G:C8	2.45	0.51
5:I:61:ARG:O	5:I:65:LEU:HD22	2.10	0.51
7:M:36:LEU:HD11	7:M:122:LEU:HB2	1.93	0.51
27:A:2042:A:H2'	27:A:2043:C:C6	2.46	0.51
27:A:608:C:H2'	27:A:609:G:H8	1.76	0.51
27:A:1393:C:H2'	27:A:1394:A:H8	1.76	0.51
27:A:1479:G:H4'	27:A:2025:C:H5	1.75	0.51
27:A:1547:G:O6	27:A:1623:U:O4	2.28	0.51
27:A:3014:A:O2'	27:A:3015:C:H5''	2.11	0.51
8:N:122:LEU:HD13	12:S:69:VAL:HG11	1.92	0.51
17:X:82:ARG:NH2	27:A:382:A:OP2	2.41	0.51
21:3:5:LYS:HB2	21:3:59:VAL:HG22	1.93	0.51
23:6:9:PRO:HD2	23:6:27:LYS:O	2.11	0.51
27:A:273:A:H62	27:A:313:G:N2	2.08	0.51
27:A:673:C:H2'	27:A:674:U:C6	2.46	0.51
27:A:2366:C:H2'	27:A:2367:G:O4'	2.11	0.50
9:O:55:MET:HE2	27:A:2616:A:C2	2.43	0.50
14:U:47:ASN:OD1	14:U:47:ASN:N	2.41	0.50
27:A:640:G:O2'	27:A:642:G:OP2	2.25	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:880:G:H2'	27:A:881:C:C6	2.46	0.50
27:A:2386:U:OP1	27:A:2394:A:H5''	2.12	0.50
5:I:89:GLU:HA	5:I:131:LYS:HA	1.94	0.50
27:A:1073:G:O2'	27:A:1076:A:N6	2.44	0.50
27:A:1704:U:H2'	27:A:1705:C:C6	2.46	0.50
27:A:2074:G:O6	27:A:2075:G:N1	2.45	0.50
27:A:2686:U:H2'	27:A:2687:U:C6	2.47	0.50
24:7:11:ASN:ND2	27:A:885:G:OP1	2.41	0.50
27:A:1025:A:N3	27:A:2488:C:O2'	2.41	0.50
27:A:1287:C:H2'	27:A:1288:A:H8	1.77	0.50
27:A:1373:A:H2'	27:A:1374:G:C8	2.47	0.50
27:A:2563:G:H2'	27:A:2564:A:H8	1.75	0.50
27:A:2850:C:H2'	27:A:2851:G:H8	1.76	0.50
27:A:2873:U:H2'	27:A:2874:C:C6	2.47	0.50
3:G:61:GLY:HA3	3:G:80:ARG:HG2	1.93	0.50
27:A:971:G:H2'	27:A:972:A:C8	2.47	0.50
27:A:1478:C:O2'	27:A:2026:A:N3	2.43	0.50
27:A:1907:A:H2'	27:A:1908:A:C8	2.46	0.50
27:A:2467:U:H2'	27:A:2468:U:C6	2.46	0.50
27:A:678:A:N1	27:A:924:G:O2'	2.40	0.50
27:A:724:G:N2	27:A:727:A:OP2	2.32	0.50
27:A:1233:A:H2'	27:A:1234:U:O4'	2.11	0.50
27:A:2752:U:H3'	27:A:2754:G:H8	1.76	0.50
27:A:752:C:H2'	27:A:753:A:C8	2.47	0.50
23:6:7:VAL:HG13	23:6:9:PRO:HD3	1.94	0.50
23:6:49:GLN:OE1	23:6:49:GLN:N	2.45	0.50
27:A:151:A:H2'	27:A:152:G:C8	2.47	0.50
27:A:2029:A:H2'	27:A:2030:C:C6	2.47	0.50
2:F:27:THR:OG1	2:F:196:GLY:O	2.28	0.50
2:F:157:PRO:HB2	2:F:159:ARG:HG3	1.94	0.50
27:A:2:A:H2'	27:A:3:A:C8	2.47	0.50
27:A:680:U:H2'	27:A:681:C:C6	2.46	0.50
27:A:681:C:H2'	27:A:682:A:C8	2.47	0.50
27:A:815:G:O2'	27:A:1850:A:N3	2.38	0.50
27:A:1381:G:O2'	27:A:2236:G:O6	2.28	0.50
5:I:46:ALA:N	5:I:50:ALA:O	2.44	0.49
23:6:44:ASN:OD1	23:6:44:ASN:N	2.40	0.49
27:A:2190:A:N3	27:A:2816:G:O2'	2.40	0.49
27:A:2515:U:H2'	27:A:2516:U:C6	2.47	0.49
27:A:3034:C:H2'	27:A:3035:C:C6	2.46	0.49
1:E:225:VAL:HG11	27:A:2005:C:H5''	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:R:9:ASN:ND2	28:B:59:A:N3	2.60	0.49
27:A:294:G:O6	27:A:342:C:N4	2.43	0.49
27:A:1738:G:C2	27:A:1739:A:C8	3.00	0.49
27:A:130:C:H2'	27:A:131:A:H8	1.76	0.49
27:A:2622:C:H2'	27:A:2623:A:H8	1.78	0.49
1:E:72:LYS:NZ	1:E:99:ASP:OD2	2.45	0.49
27:A:1091:A:H5'	27:A:1303:U:H1'	1.95	0.49
27:A:1052:U:H2'	27:A:1053:G:H8	1.77	0.49
1:E:37:LEU:HD13	1:E:62:TYR:HB2	1.93	0.49
7:M:104:ALA:O	7:M:108:MET:HG3	2.13	0.49
11:R:118:ASP:O	11:R:122:GLU:HG3	2.13	0.49
27:A:222:A:O2'	27:A:508:G:N3	2.36	0.49
27:A:502:C:H2'	27:A:503:A:H8	1.77	0.49
27:A:2385:G:H5''	27:A:2394:A:H2'	1.93	0.49
1:E:86:PRO:HG3	27:A:1787:A:H2'	1.93	0.49
2:F:186:ASP:OD2	2:F:189:ASN:ND2	2.37	0.49
23:6:37:GLU:OE1	23:6:52:LYS:NZ	2.44	0.49
27:A:665:G:O2'	27:A:666:A:O5'	2.27	0.49
27:A:1296:G:H2'	27:A:1297:G:C8	2.48	0.49
27:A:2074:G:N2	27:A:2109:A:H62	2.10	0.49
19:1:14:PHE:CG	27:A:187:G:H5''	2.46	0.49
27:A:2387:U:H3'	27:A:2388:G:H8	1.78	0.49
27:A:2465:A:H2'	27:A:2466:G:H8	1.78	0.49
15:V:25:ARG:NH2	27:A:604:C:O2'	2.45	0.49
17:X:94:LYS:NZ	27:A:377:C:O3'	2.40	0.49
27:A:1015:A:H2'	27:A:1016:C:O4'	2.12	0.49
27:A:2862:G:O2'	27:A:3002:A:N6	2.44	0.49
27:A:2297:U:H2'	27:A:2298:U:C6	2.48	0.49
27:A:2865:G:H2'	27:A:2866:A:H8	1.77	0.49
2:F:60:ARG:NH2	27:A:3052:A:OP1	2.27	0.48
4:H:83:GLN:N	4:H:83:GLN:OE1	2.46	0.48
5:I:126:VAL:HG22	5:I:132:PHE:HB2	1.95	0.48
27:A:586:U:H2'	27:A:587:G:O4'	2.13	0.48
27:A:635:G:O2'	27:A:636:U:O4'	2.29	0.48
27:A:735:U:H2'	27:A:736:G:O4'	2.13	0.48
27:A:1537:U:H2'	27:A:1538:G:H8	1.78	0.48
27:A:2351:A:H2'	27:A:2352:C:C6	2.48	0.48
4:H:126:PRO:O	4:H:174:ARG:NH1	2.36	0.48
6:J:1:MET:N	6:J:21:VAL:O	2.46	0.48
27:A:90:C:H2'	27:A:91:C:O4'	2.13	0.48
27:A:2673:U:H4'	27:A:2674:A:H5'	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:M:98:THR:HB	7:M:124:VAL:HG23	1.95	0.48
13:T:68:ALA:O	13:T:72:ASN:ND2	2.45	0.48
27:A:32:G:H1'	27:A:542:A:C4	2.48	0.48
27:A:726:A:H2'	27:A:727:A:C8	2.48	0.48
27:A:1314:C:H2'	27:A:1315:C:H6	1.78	0.48
27:A:1451:A:H2'	27:A:1452:G:C8	2.48	0.48
27:A:1560:U:H3	27:A:1611:A:H61	1.60	0.48
27:A:1705:C:H2'	27:A:1706:A:C8	2.47	0.48
27:A:2096:G:H2'	27:A:2097:G:H8	1.78	0.48
27:A:2443:U:H2'	27:A:2444:C:H6	1.78	0.48
27:A:1537:U:H2'	27:A:1538:G:C8	2.48	0.48
27:A:1554:U:H2'	27:A:1555:A:H8	1.78	0.48
27:A:1950:G:H2'	27:A:1951:G:H8	1.79	0.48
27:A:2249:G:H2'	27:A:2250:A:C8	2.48	0.48
27:A:2364:C:H2'	27:A:2365:A:H8	1.78	0.48
13:T:31:LEU:HD13	27:A:672:C:H4'	1.95	0.48
23:6:24:ILE:HD11	25:8:34:GLU:HB2	1.94	0.48
27:A:264:G:H4'	27:A:516:G:H22	1.78	0.48
27:A:270:U:H1'	27:A:512:G:N2	2.28	0.48
27:A:1137:U:O2'	27:A:1139:A:N7	2.34	0.48
27:A:1560:U:H2'	27:A:1561:C:O4'	2.13	0.48
27:A:1620:U:H2'	27:A:1621:C:C6	2.48	0.48
27:A:1627:U:H2'	27:A:1628:A:H8	1.79	0.48
27:A:2288:C:H2'	27:A:2289:C:H6	1.78	0.48
27:A:2385:G:OP2	27:A:2387:U:N3	2.38	0.48
27:A:2729:G:O2'	27:A:2730:U:O5'	2.30	0.48
20:2:49:THR:O	20:2:53:GLU:HG3	2.14	0.48
23:6:12:THR:HG21	23:6:21:ARG:HB3	1.95	0.48
5:I:142:VAL:O	5:I:146:SER:OG	2.30	0.48
13:T:119:GLU:H	13:T:119:GLU:CD	2.20	0.48
27:A:2800:G:O2'	27:A:2803:C:OP2	2.21	0.48
1:E:258:ARG:NH1	27:A:2016:G:OP1	2.41	0.48
25:8:7:HIS:HB3	25:8:10:ALA:HB3	1.94	0.48
27:A:250:G:H2'	27:A:251:A:C8	2.49	0.48
27:A:317:G:H2'	27:A:509:U:OP2	2.14	0.48
27:A:587:G:N1	27:A:590:A:OP2	2.41	0.48
27:A:987:A:H2'	27:A:988:U:H5'	1.95	0.48
27:A:2275:A:H8	27:A:2275:A:OP2	1.96	0.48
27:A:2439:C:H2'	27:A:2440:G:H8	1.78	0.48
17:X:42:LYS:HB3	17:X:59:ILE:HD11	1.96	0.48
27:A:27:G:H2'	27:A:28:C:C6	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:329:U:O2	27:A:446:G:C6	2.66	0.48
27:A:672:C:H2'	27:A:673:C:C6	2.49	0.48
27:A:943:U:H4'	27:A:946:G:N1	2.29	0.48
27:A:979:G:H2'	27:A:980:C:C6	2.49	0.48
27:A:1544:U:C4	27:A:1626:G:O6	2.67	0.48
27:A:1719:C:C2	27:A:1720:G:C8	3.02	0.48
27:A:2530:C:H5''	27:A:2531:G:H2'	1.96	0.48
27:A:2883:G:N2	27:A:2885:G:H3'	2.29	0.48
17:X:24:LEU:HD11	17:X:34:LEU:HD23	1.95	0.48
18:Z:18:ALA:HB1	27:A:2495:G:OP1	2.14	0.48
27:A:81:A:N1	27:A:96:G:O2'	2.40	0.48
27:A:139:U:H2'	27:A:140:G:O4'	2.13	0.48
27:A:159:A:OP2	27:A:164:A:N6	2.46	0.48
27:A:995:U:H2'	27:A:996:G:C8	2.48	0.48
9:O:32:THR:HG22	9:O:35:ARG:H	1.79	0.47
27:A:2781:G:H2'	27:A:2782:C:C6	2.49	0.47
5:I:39:GLU:CD	5:I:40:PRO:HD3	2.39	0.47
12:S:48:ARG:NH1	27:A:2909:G:OP1	2.39	0.47
27:A:750:C:H2'	27:A:751:A:C8	2.49	0.47
27:A:1122:C:H2'	27:A:1129:G:H2'	1.95	0.47
27:A:1297:G:H2'	27:A:1298:C:C6	2.49	0.47
27:A:2086:U:O2	27:A:2096:G:N2	2.27	0.47
2:F:44:ARG:NH1	27:A:3009:U:OP1	2.47	0.47
11:R:62:ALA:O	11:R:91:ARG:NH1	2.46	0.47
14:U:61:THR:O	14:U:100:THR:OG1	2.30	0.47
27:A:947:U:H2'	27:A:948:G:C8	2.49	0.47
27:A:1690:A:H2'	27:A:1691:A:H8	1.78	0.47
27:A:2678:G:N1	27:A:2723:C:N3	2.62	0.47
27:A:2729:G:H2'	27:A:2800:G:N1	2.29	0.47
27:A:2750:G:H2'	27:A:2751:C:C6	2.50	0.47
27:A:2997:C:H2'	27:A:2998:C:H6	1.79	0.47
28:B:10:G:O2'	28:B:11:U:H5'	2.14	0.47
27:A:641:U:H5''	27:A:642:G:OP2	2.15	0.47
27:A:1003:A:H2'	27:A:1003:A:OP1	2.15	0.47
27:A:1758:G:H2'	27:A:1759:A:H8	1.80	0.47
27:A:2294:A:H2'	27:A:2295:C:C6	2.50	0.47
27:A:2510:A:H4'	27:A:2511:A:O4'	2.14	0.47
27:A:2642:G:H2'	27:A:2643:U:O4'	2.14	0.47
27:A:2849:G:H2'	27:A:2850:C:C6	2.49	0.47
27:A:2971:G:N2	27:A:2981:A:N6	2.23	0.47
1:E:247:VAL:HG12	1:E:253:PRO:HA	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:T:69:ALA:HB1	13:T:74:ILE:HG23	1.97	0.47
27:A:839:U:H2'	27:A:840:G:C8	2.49	0.47
27:A:1665:U:H2'	27:A:1666:A:H8	1.79	0.47
27:A:2635:A:H2'	27:A:2636:A:C8	2.49	0.47
2:F:69:GLN:NE2	27:A:3009:U:O2	2.48	0.47
5:I:77:VAL:HA	5:I:80:VAL:HG22	1.96	0.47
25:8:19:THR:HG23	27:A:745:G:H5''	1.96	0.47
27:A:2:A:H2'	27:A:3:A:H8	1.78	0.47
27:A:1373:A:H2'	27:A:1374:G:H8	1.78	0.47
27:A:1487:U:O2'	27:A:2436:A:N3	2.42	0.47
27:A:2147:U:H2'	27:A:2148:C:C6	2.48	0.47
27:A:2304:C:H2'	27:A:2305:A:H8	1.79	0.47
27:A:3086:U:OP2	27:A:3087:G:O2'	2.24	0.47
4:H:127:LYS:HD2	4:H:127:LYS:N	2.30	0.47
17:X:2:LYS:HB3	17:X:83:VAL:HG21	1.97	0.47
24:7:27:THR:HG23	24:7:30:GLY:H	1.79	0.47
26:4:13:THR:HB	26:4:32:THR:HG23	1.97	0.47
26:4:42:HIS:HB3	26:4:45:TYR:HD1	1.79	0.47
27:A:188:G:O6	27:A:204:G:O2'	2.29	0.47
27:A:665:G:N2	27:A:2255:A:OP1	2.47	0.47
27:A:1906:U:O2'	27:A:1918:A:N7	2.45	0.47
27:A:2361:U:H3	27:A:2376:G:H22	1.62	0.47
27:A:2363:A:N6	27:A:2375:G:O6	2.48	0.47
27:A:2376:G:H2'	27:A:2377:G:H8	1.79	0.47
1:E:271:ARG:NH2	27:A:2016:G:OP2	2.47	0.47
4:H:64:LEU:HB2	4:H:72:PRO:HG3	1.97	0.47
4:H:87:ARG:HB2	4:H:90:MET:HE1	1.97	0.47
8:N:68:GLU:OE2	27:A:2908:U:O2'	2.33	0.47
27:A:729:C:O2'	27:A:733:U:OP1	2.33	0.47
27:A:1313:U:H2'	27:A:1314:C:C6	2.50	0.47
27:A:2603:G:H2'	27:A:2604:U:C6	2.50	0.47
17:X:37:GLY:HA2	17:X:40:ARG:NH2	2.27	0.47
27:A:256:A:H2'	27:A:257:A:H8	1.80	0.47
27:A:362:A:H2'	27:A:363:A:C8	2.50	0.47
27:A:782:U:H2'	27:A:783:G:O4'	2.15	0.47
5:I:82:GLU:OE1	5:I:82:GLU:N	2.48	0.47
7:M:45:THR:HG22	7:M:47:ASN:H	1.78	0.47
7:M:60:ASP:OD1	7:M:60:ASP:N	2.48	0.47
9:O:22:VAL:HG12	9:O:29:LYS:HD2	1.97	0.47
27:A:1633:U:H2'	27:A:1634:C:C6	2.50	0.47
27:A:2474:G:O2'	27:A:2720:C:OP1	2.23	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:N:34:GLY:N	8:N:37:ASP:OD2	2.46	0.46
11:R:73:ILE:HG23	11:R:80:HIS:HD2	1.79	0.46
27:A:1223:U:H2'	27:A:1224:G:H8	1.80	0.46
27:A:2400:C:H2'	27:A:2401:U:O4'	2.15	0.46
27:A:282:A:C6	27:A:305:G:C6	3.03	0.46
27:A:388:U:H2'	27:A:389:G:O4'	2.14	0.46
27:A:502:C:H2'	27:A:503:A:C8	2.49	0.46
27:A:875:G:H2'	27:A:876:A:O4'	2.16	0.46
27:A:1523:U:H2'	27:A:1524:G:H8	1.81	0.46
1:E:181:GLU:HG3	1:E:271:ARG:HA	1.97	0.46
3:G:13:LYS:HB3	3:G:13:LYS:HE2	1.59	0.46
18:Z:12:ASN:ND2	27:A:2501:G:H3'	2.31	0.46
27:A:1311:C:C2	27:A:1312:G:C8	3.04	0.46
27:A:1434:G:H2'	27:A:1435:C:C6	2.50	0.46
27:A:1608:U:H2'	27:A:1609:G:C8	2.50	0.46
27:A:265:A:N1	27:A:515:U:O2'	2.42	0.46
27:A:654:U:H1'	27:A:664:A:H1'	1.97	0.46
27:A:932:C:O2'	27:A:954:U:H5''	2.16	0.46
27:A:1614:G:H2'	27:A:1615:G:H8	1.81	0.46
27:A:2613:G:H5''	27:A:2614:U:O4'	2.16	0.46
27:A:2761:U:H2'	27:A:2762:C:C6	2.50	0.46
2:F:104:GLU:H	2:F:104:GLU:CD	2.23	0.46
3:G:69:LYS:HZ1	27:A:2284:A:H3'	1.81	0.46
5:I:90:ILE:HG12	5:I:130:THR:HA	1.96	0.46
19:1:49:ILE:HD11	19:1:61:VAL:HG23	1.98	0.46
22:5:7:ARG:NH1	27:A:671:G:O2'	2.48	0.46
27:A:1314:C:H2'	27:A:1315:C:C6	2.50	0.46
27:A:1900:C:H2'	27:A:1901:C:C6	2.51	0.46
27:A:2857:A:H2'	27:A:2858:G:H8	1.80	0.46
5:I:98:GLN:HE22	5:I:100:LYS:HB2	1.81	0.46
6:J:10:GLU:CD	6:J:11:HIS:N	2.73	0.46
27:A:988:U:O2'	27:A:990:G:O4'	2.33	0.46
27:A:1437:A:N1	27:A:1448:C:O2'	2.41	0.46
27:A:1717:U:H5''	27:A:1718:C:H5	1.81	0.46
27:A:1937:U:H2'	27:A:1938:G:O4'	2.15	0.46
27:A:2471:A:H2'	27:A:2472:C:C6	2.50	0.46
2:F:127:MET:HE2	2:F:146:ARG:HG2	1.98	0.46
9:O:77:VAL:HG11	27:A:730:G:N1	2.31	0.46
10:Q:8:PRO:HG2	27:A:1870:U:C4	2.51	0.46
21:3:40:ASN:O	21:3:44:ARG:HG2	2.16	0.46
23:6:8:ARG:HG2	23:6:28:ASN:OD1	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:6:18:CYS:HB2	23:6:20:HIS:CE1	2.50	0.46
27:A:402:G:H4'	27:A:404:A:N7	2.31	0.46
27:A:722:G:H2'	27:A:723:C:C6	2.51	0.46
27:A:1088:U:H2'	27:A:1089:C:C6	2.51	0.46
27:A:1127:A:N3	27:A:1272:C:O2'	2.39	0.46
27:A:2288:C:H2'	27:A:2289:C:C6	2.50	0.46
27:A:2329:G:N1	27:A:2406:U:N3	2.63	0.46
2:F:153:GLY:H	27:A:2276:G:H4'	1.80	0.46
8:N:24:VAL:HG13	8:N:33:ALA:HB2	1.96	0.46
23:6:37:GLU:OE2	23:6:37:GLU:HA	2.15	0.46
27:A:154:C:H2'	27:A:155:G:C8	2.51	0.46
27:A:1332:G:C6	27:A:1347:G:C6	3.04	0.46
27:A:1541:G:OP2	27:A:1629:G:N2	2.49	0.46
27:A:1611:A:C6	27:A:1612:U:C4	3.03	0.46
27:A:1659:U:H2'	27:A:1660:A:H8	1.79	0.46
27:A:2005:C:C2	27:A:2006:A:C8	3.03	0.46
27:A:2401:U:H2'	27:A:2402:C:C6	2.51	0.46
27:A:263:G:O2'	27:A:517:A:N3	2.43	0.46
27:A:610:C:O2	27:A:646:U:O2'	2.31	0.46
27:A:1529:U:H3'	27:A:1530:G:C8	2.50	0.46
27:A:2094:G:O2'	27:A:2095:G:H8	1.99	0.46
5:I:119:PRO:HD2	5:I:122:ILE:HD11	1.97	0.46
17:X:41:ILE:HD12	27:A:568:A:H5''	1.99	0.46
20:2:14:THR:HG22	20:2:17:GLU:OE2	2.16	0.46
27:A:479:A:H1'	27:A:499:G:O4'	2.16	0.46
27:A:1430:C:H2'	27:A:1431:U:C6	2.51	0.46
27:A:1524:G:H2'	27:A:1525:U:C6	2.51	0.46
27:A:1562:C:C4	27:A:1563:A:C8	3.04	0.46
27:A:1620:U:H2'	27:A:1621:C:H6	1.79	0.46
27:A:2581:G:H2'	27:A:2583:C:OP2	2.16	0.46
27:A:3055:G:H2'	27:A:3100:A:H61	1.81	0.46
27:A:639:C:O2'	27:A:640:G:O5'	2.34	0.45
27:A:845:C:OP1	27:A:1992:U:O2'	2.23	0.45
27:A:1259:U:H1'	27:A:1261:A:C6	2.51	0.45
27:A:1652:A:H2'	27:A:1653:G:H8	1.82	0.45
27:A:2381:A:H4'	27:A:2382:G:O5'	2.16	0.45
27:A:2421:A:O2'	27:A:2422:A:H8	2.00	0.45
27:A:2671:G:C8	27:A:2724:U:H3'	2.51	0.45
28:B:11:U:O2'	28:B:12:C:H5'	2.16	0.45
3:G:154:VAL:HG23	3:G:193:ASP:HB2	1.98	0.45
14:U:28:ASP:OD1	14:U:28:ASP:N	2.42	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:X:34:LEU:HD12	17:X:34:LEU:HA	1.85	0.45
17:X:86:ARG:HB3	17:X:97:ILE:HD13	1.97	0.45
27:A:358:G:O5'	27:A:358:G:H8	1.99	0.45
27:A:502:C:H1'	27:A:2081:U:H1'	1.97	0.45
27:A:1288:A:H2'	27:A:1289:A:C8	2.51	0.45
27:A:1313:U:H2'	27:A:1314:C:H6	1.81	0.45
27:A:2443:U:H2'	27:A:2444:C:C6	2.51	0.45
28:B:40:A:C2	28:B:45:G:C2	3.04	0.45
28:B:50:C:H2'	28:B:51:G:C8	2.51	0.45
2:F:94:GLU:N	2:F:94:GLU:OE1	2.50	0.45
5:I:104:LEU:HG	5:I:106:PHE:HE1	1.82	0.45
27:A:1762:C:H2'	27:A:1763:G:O4'	2.16	0.45
27:A:2096:G:H2'	27:A:2097:G:C8	2.51	0.45
27:A:2098:U:H2'	27:A:2099:G:O4'	2.15	0.45
27:A:2673:U:O3'	27:A:2674:A:H8	1.99	0.45
2:F:52:LEU:HD11	2:F:84:LEU:HD22	1.99	0.45
2:F:153:GLY:N	27:A:2276:G:H4'	2.31	0.45
27:A:1154:G:C6	27:A:1238:G:C6	3.05	0.45
27:A:1437:A:C2	27:A:1438:G:C8	3.04	0.45
27:A:2685:C:H2'	27:A:2686:U:C6	2.52	0.45
27:A:2815:C:H2'	27:A:2816:G:H8	1.82	0.45
9:O:80:VAL:HB	9:O:118:LEU:HD12	1.98	0.45
27:A:265:A:N6	27:A:359:A:N7	2.64	0.45
27:A:506:C:H2'	27:A:507:G:H8	1.81	0.45
27:A:543:U:H3'	27:A:544:U:H5''	1.99	0.45
27:A:736:G:H1'	27:A:740:A:N6	2.32	0.45
27:A:1236:G:H2'	27:A:1237:U:O4'	2.16	0.45
2:F:174:ARG:NE	27:A:2997:C:OP1	2.48	0.45
18:Z:35:GLU:HG3	27:A:2578:A:H4'	1.98	0.45
27:A:183:G:H2'	27:A:184:C:C6	2.51	0.45
27:A:664:A:H3'	27:A:665:G:C8	2.52	0.45
27:A:795:G:H2'	27:A:796:A:C8	2.51	0.45
27:A:1509:U:H2'	27:A:1510:A:O4'	2.17	0.45
27:A:1563:A:C6	27:A:1608:U:C4	3.05	0.45
27:A:2609:A:H2'	27:A:2610:C:C6	2.52	0.45
27:A:2729:G:HO2'	27:A:2730:U:P	2.39	0.45
27:A:1287:C:H2'	27:A:1288:A:C8	2.52	0.45
27:A:2079:C:H2'	27:A:2080:G:H8	1.82	0.45
27:A:2439:C:H2'	27:A:2440:G:C8	2.51	0.45
27:A:2563:G:H2'	27:A:2564:A:C8	2.51	0.45
27:A:2771:U:H2'	27:A:2772:G:H8	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:H:10:ARG:NE	26:4:22:PHE:HZ	2.15	0.45
11:R:12:GLU:OE1	28:B:60:G:O2'	2.24	0.45
13:T:10:ALA:HA	13:T:13:LYS:HZ3	1.82	0.45
22:5:29:THR:HG22	27:A:3108:G:OP1	2.17	0.45
25:8:43:ARG:HH22	27:A:2586:G:H3'	1.82	0.45
27:A:49:A:OP2	27:A:114:G:N1	2.48	0.45
27:A:1875:U:H2'	27:A:1876:A:H8	1.82	0.45
27:A:2759:G:H2'	27:A:2760:G:H8	1.82	0.45
27:A:2920:U:H2'	27:A:2921:G:H8	1.81	0.45
9:O:37:THR:HG22	27:A:1060:U:OP1	2.17	0.45
10:Q:106:ASP:OD2	27:A:1867:G:O2'	2.27	0.45
19:1:32:ASN:HB2	27:A:485:U:H5''	1.99	0.45
27:A:193:G:H2'	27:A:194:A:O4'	2.16	0.45
27:A:392:A:C4	27:A:394:G:C8	3.05	0.45
27:A:660:U:N3	27:A:663:A:OP2	2.32	0.45
27:A:1703:G:H2'	27:A:1704:U:C6	2.52	0.45
27:A:2635:A:H2'	27:A:2636:A:H8	1.81	0.45
27:A:2751:C:H2'	27:A:2752:U:O4'	2.17	0.45
1:E:217:LYS:HE3	1:E:217:LYS:HB3	1.72	0.45
8:N:17:LYS:HB2	8:N:45:ASP:HB3	1.99	0.45
21:3:43:THR:O	21:3:47:ILE:HG23	2.17	0.45
26:4:1:MET:HE2	26:4:6:HIS:CD2	2.51	0.45
27:A:1001:C:N4	27:A:1007:G:O6	2.50	0.45
27:A:1295:U:H2'	27:A:1296:G:H8	1.82	0.45
27:A:1896:A:C4	27:A:1897:A:C8	3.05	0.45
27:A:2712:U:H2'	27:A:2713:G:C8	2.52	0.45
28:B:49:C:H2'	28:B:50:C:H6	1.82	0.45
5:I:132:PHE:HZ	5:I:149:ILE:HG21	1.81	0.44
9:O:31:LYS:HE3	27:A:658:U:H5''	1.98	0.44
24:7:21:PHE:HB2	24:7:46:THR:HG21	2.00	0.44
27:A:882:U:H2'	27:A:883:G:H8	1.82	0.44
27:A:947:U:H2'	27:A:948:G:H8	1.80	0.44
27:A:1086:C:H2'	27:A:1087:G:H8	1.82	0.44
27:A:1284:A:H2'	27:A:1285:G:H8	1.82	0.44
27:A:2248:C:H2'	27:A:2249:G:C8	2.47	0.44
1:E:224:VAL:HG13	27:A:2043:C:OP1	2.17	0.44
5:I:104:LEU:HD21	5:I:132:PHE:CE2	2.50	0.44
7:M:65:SER:OG	27:A:1259:U:OP2	2.26	0.44
18:Z:32:LYS:HB3	27:A:759:G:C6	2.52	0.44
20:2:15:ASP:O	20:2:19:LYS:HG2	2.16	0.44
25:8:34:GLU:OE1	25:8:35:HIS:N	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:72:G:N3	27:A:72:G:H2'	2.32	0.44
27:A:1052:U:H2'	27:A:1053:G:C8	2.52	0.44
27:A:2639:G:H2'	27:A:2640:G:H8	1.81	0.44
26:4:12:THR:HG21	26:4:26:SER:HB3	1.99	0.44
27:A:722:G:H2'	27:A:723:C:H6	1.83	0.44
27:A:1407:G:H2'	27:A:1408:C:C6	2.52	0.44
27:A:1675:U:O2'	27:A:1676:G:N7	2.50	0.44
27:A:2343:G:H2'	27:A:2344:G:C8	2.52	0.44
5:I:90:ILE:HG22	5:I:163:VAL:HG12	2.00	0.44
8:N:110:LYS:HA	8:N:110:LYS:HD2	1.77	0.44
12:S:48:ARG:HB2	12:S:95:LYS:HG2	1.99	0.44
27:A:1815:G:H5''	27:A:1816:C:H5'	2.00	0.44
27:A:2604:U:H2'	27:A:2605:C:C6	2.53	0.44
27:A:2729:G:H2'	27:A:2800:G:C6	2.52	0.44
27:A:2754:G:OP2	27:A:2759:G:N2	2.50	0.44
22:5:4:PRO:HG2	27:A:2240:U:O2	2.18	0.44
27:A:55:G:H2'	27:A:56:U:C6	2.53	0.44
27:A:151:A:H2'	27:A:152:G:H8	1.80	0.44
27:A:1634:C:H2'	27:A:1635:A:C8	2.52	0.44
27:A:2029:A:H2'	27:A:2030:C:H6	1.83	0.44
27:A:2070:A:H2'	27:A:2071:A:H8	1.81	0.44
27:A:2450:C:C2	27:A:2451:A:C8	3.05	0.44
27:A:2569:G:N3	27:A:2605:C:H2'	2.33	0.44
27:A:2897:G:H2'	27:A:2898:G:H8	1.81	0.44
18:Z:15:ASP:OD1	18:Z:16:SER:N	2.51	0.44
27:A:412:A:O2'	27:A:413:G:N2	2.29	0.44
27:A:1609:G:C2	27:A:1610:C:C2	3.05	0.44
3:G:108:ALA:HB1	3:G:112:ARG:NH1	2.32	0.44
19:1:45:ASN:OD1	19:1:45:ASN:N	2.49	0.44
27:A:190:A:H3'	27:A:191:G:H21	1.82	0.44
27:A:546:G:O2'	27:A:557:G:O6	2.32	0.44
27:A:1223:U:H2'	27:A:1224:G:C8	2.52	0.44
27:A:2084:A:H2'	27:A:2085:C:O4'	2.18	0.44
27:A:2375:G:H2'	27:A:2376:G:C8	2.53	0.44
27:A:2678:G:N3	27:A:2678:G:H2'	2.33	0.44
27:A:3018:U:H2'	27:A:3019:C:C6	2.53	0.44
14:U:39:VAL:HG12	14:U:55:LEU:HD22	2.00	0.44
20:2:56:ARG:O	20:2:60:VAL:HG23	2.18	0.44
27:A:990:G:O2'	27:A:991:C:OP2	2.31	0.44
27:A:1400:G:N2	27:A:1443:G:H5''	2.32	0.44
27:A:1849:G:N2	27:A:1852:A:OP2	2.40	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:1854:U:H2'	27:A:1855:A:C8	2.52	0.44
27:A:1922:G:H2'	27:A:1923:G:C8	2.51	0.44
27:A:2061:U:H2'	27:A:2062:G:H8	1.83	0.44
27:A:2279:C:N4	27:A:2724:U:H1'	2.33	0.44
27:A:2343:G:H1	27:A:2401:U:H3	1.64	0.44
27:A:621:U:H2'	27:A:622:C:C6	2.53	0.44
27:A:1611:A:H2'	27:A:1612:U:O4'	2.18	0.44
27:A:1678:U:H5'	27:A:1679:A:OP2	2.17	0.44
27:A:2081:U:OP1	27:A:2634:G:O2'	2.36	0.44
28:B:6:G:OP1	28:B:61:C:O2'	2.35	0.44
4:H:67:ILE:O	4:H:109:ARG:NH2	2.51	0.43
27:A:316:U:O2'	27:A:317:G:OP1	2.29	0.43
27:A:671:G:C2	27:A:1377:A:C5	3.06	0.43
27:A:1064:A:H2'	27:A:1065:C:C6	2.53	0.43
27:A:1118:A:H2'	27:A:1119:A:C8	2.53	0.43
27:A:1645:G:H2'	27:A:1646:U:C6	2.53	0.43
27:A:1714:A:H2'	27:A:1715:A:C8	2.53	0.43
27:A:1853:A:H2'	27:A:1854:U:O4'	2.18	0.43
27:A:2297:U:H2'	27:A:2298:U:H6	1.83	0.43
1:E:155:LEU:HD13	1:E:177:MET:HE1	1.99	0.43
2:F:88:ASP:C	2:F:88:ASP:OD1	2.60	0.43
23:6:8:ARG:O	23:6:26:LYS:HD3	2.18	0.43
27:A:131:A:H2'	27:A:132:C:C6	2.53	0.43
27:A:277:U:H2'	27:A:278:A:H8	1.81	0.43
27:A:632:G:H2'	27:A:633:A:C8	2.53	0.43
27:A:1296:G:H2'	27:A:1297:G:H8	1.81	0.43
27:A:1559:A:C4	27:A:1560:U:C5	3.05	0.43
27:A:1706:A:H2'	27:A:1707:G:H8	1.83	0.43
27:A:1716:A:H2'	27:A:1718:C:C5	2.53	0.43
27:A:1770:G:H2'	27:A:1771:U:C6	2.53	0.43
27:A:1963:G:H2'	27:A:1964:U:C6	2.53	0.43
27:A:2329:G:O6	27:A:2406:U:C4	2.71	0.43
2:F:87:ASP:OD1	2:F:88:ASP:N	2.51	0.43
27:A:278:A:H2'	27:A:279:U:C6	2.52	0.43
27:A:303:G:H2'	27:A:304:U:O4'	2.19	0.43
27:A:1412:C:H2'	27:A:1413:C:H6	1.82	0.43
27:A:1640:A:O2'	27:A:1641:U:OP1	2.34	0.43
27:A:1758:G:H2'	27:A:1759:A:C8	2.53	0.43
27:A:2323:G:H2'	27:A:2324:A:C8	2.54	0.43
27:A:2490:A:H4'	27:A:2491:A:N3	2.33	0.43
27:A:2692:A:P	27:A:2700:A:H61	2.41	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:X:8:THR:HG23	17:X:74:VAL:HG12	2.00	0.43
27:A:89:A:HO2'	27:A:90:C:P	2.40	0.43
27:A:214:G:H4'	27:A:215:A:H4'	2.00	0.43
27:A:363:A:H2'	27:A:364:A:O4'	2.18	0.43
27:A:543:U:H3'	27:A:544:U:C5'	2.49	0.43
27:A:3014:A:N6	27:A:3112:A:H3'	2.33	0.43
5:I:12:PRO:HB2	5:I:15:VAL:HG12	2.00	0.43
14:U:27:LEU:H	14:U:95:THR:HG21	1.83	0.43
23:6:48:HIS:ND1	27:A:2595:G:O2'	2.42	0.43
27:A:9:U:O2	27:A:2850:C:H4'	2.18	0.43
27:A:563:U:H4'	27:A:597:C:H5'	2.01	0.43
27:A:978:A:H2'	27:A:979:G:C8	2.53	0.43
27:A:994:A:H5''	27:A:1014:G:H21	1.84	0.43
27:A:1650:G:H2'	27:A:1651:C:C6	2.53	0.43
27:A:2170:U:H2'	27:A:2171:C:C6	2.53	0.43
27:A:2441:G:H2'	27:A:2442:U:C6	2.54	0.43
27:A:3082:U:H2'	27:A:3083:A:H8	1.84	0.43
11:R:42:ARG:HG3	11:R:47:ILE:HD12	2.01	0.43
14:U:53:ASP:OD1	14:U:54:ASP:N	2.51	0.43
15:V:52:GLU:HB2	15:V:53:PRO:HD3	1.99	0.43
20:2:35:GLN:HB3	20:2:41:LEU:HD22	2.01	0.43
23:6:18:CYS:HB2	23:6:20:HIS:NE2	2.33	0.43
24:7:8:PHE:O	27:A:1830:C:O2'	2.34	0.43
27:A:27:G:H2'	27:A:28:C:H6	1.83	0.43
27:A:301:U:C2	27:A:338:C:H5'	2.53	0.43
27:A:858:A:O2'	27:A:1877:U:OP1	2.34	0.43
27:A:965:U:H2'	27:A:966:U:C6	2.54	0.43
27:A:1393:C:H2'	27:A:1394:A:C8	2.52	0.43
27:A:2326:A:H2'	27:A:2327:C:C6	2.54	0.43
28:B:45:G:N2	28:B:49:C:C2	2.87	0.43
28:B:113:G:C2	28:B:114:A:C8	3.06	0.43
12:S:33:GLU:O	12:S:36:LYS:HG3	2.19	0.43
27:A:88:A:H1'	27:A:89:A:C8	2.53	0.43
27:A:750:C:H2'	27:A:751:A:H8	1.84	0.43
27:A:1288:A:H2'	27:A:1289:A:H8	1.84	0.43
27:A:1515:C:N4	27:A:1516:G:O6	2.52	0.43
27:A:1652:A:H2'	27:A:1653:G:C8	2.53	0.43
27:A:1939:U:H2'	27:A:1940:A:H8	1.82	0.43
27:A:2384:C:H5''	27:A:2387:U:O4	2.19	0.43
1:E:226:MET:SD	1:E:231:HIS:HB2	2.59	0.43
5:I:35:LEU:HB2	5:I:76:LEU:HD13	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:I:158:TYR:CE2	27:A:2755:A:H4'	2.53	0.43
27:A:1530:G:H21	27:A:1805:G:N2	2.17	0.43
27:A:1535:C:H2'	27:A:1536:A:O4'	2.18	0.43
27:A:1630:U:H2'	27:A:1631:A:C8	2.53	0.43
27:A:2338:G:O2'	27:A:2340:A:N7	2.37	0.43
27:A:3059:G:C4	27:A:3060:A:C8	3.07	0.43
9:O:65:LYS:HG2	25:8:25:GLN:HE22	1.82	0.43
10:Q:24:LEU:HB3	10:Q:44:LEU:HD22	1.99	0.43
17:X:42:LYS:HD2	27:A:586:U:H5''	2.01	0.43
18:Z:29:GLN:OE1	27:A:1037:C:O2'	2.31	0.43
27:A:663:A:N3	27:A:663:A:H2'	2.34	0.43
27:A:804:A:H2'	27:A:805:C:C6	2.54	0.43
27:A:1146:A:OP2	27:A:1244:A:N6	2.30	0.43
27:A:1396:G:H2'	27:A:1397:U:H6	1.83	0.43
27:A:1611:A:C5	27:A:1612:U:C4	3.07	0.43
27:A:1630:U:H2'	27:A:1631:A:H8	1.84	0.43
27:A:1733:C:H2'	27:A:1734:C:C6	2.53	0.43
27:A:2303:A:H2'	27:A:2304:C:C6	2.54	0.43
12:S:1:MET:N	27:A:3096:U:O2	2.52	0.43
27:A:24:G:N2	27:A:599:G:H1'	2.34	0.43
27:A:366:G:H2'	27:A:367:U:C6	2.54	0.43
27:A:460:G:O2'	27:A:488:G:O6	2.30	0.43
27:A:738:A:O2'	27:A:740:A:OP1	2.37	0.43
27:A:781:C:H2'	27:A:782:U:C6	2.54	0.43
27:A:1560:U:H3'	27:A:1561:C:H6	1.82	0.43
27:A:1562:C:C2	27:A:1609:G:C2	3.06	0.43
27:A:1907:A:H2'	27:A:1908:A:H8	1.83	0.43
27:A:2265:U:H2'	27:A:2266:A:C8	2.54	0.43
27:A:2394:A:H3'	27:A:2396:A:N7	2.34	0.43
27:A:2716:U:H2'	27:A:2717:U:H6	1.84	0.43
27:A:2777:G:C2	27:A:2807:G:H1'	2.54	0.43
4:H:57:ILE:O	4:H:61:ILE:HG12	2.18	0.42
4:H:78:ARG:NH2	27:A:2537:C:OP2	2.52	0.42
5:I:147:ALA:O	5:I:151:ARG:HG3	2.19	0.42
27:A:239:U:O2'	27:A:716:G:O2'	2.18	0.42
27:A:619:C:H4'	27:A:620:G:C8	2.54	0.42
27:A:646:U:H2'	27:A:647:G:O4'	2.19	0.42
27:A:1733:C:H2'	27:A:1734:C:H6	1.83	0.42
27:A:1900:C:H2'	27:A:1901:C:H6	1.83	0.42
27:A:2007:C:H2'	27:A:2008:A:C8	2.54	0.42
28:B:40:A:H2'	28:B:41:U:C6	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:N:5:GLU:HG3	27:A:1887:A:O4'	2.19	0.42
27:A:284:G:H1'	27:A:303:G:N1	2.34	0.42
27:A:430:A:H2'	27:A:431:C:C6	2.54	0.42
27:A:618:C:OP1	27:A:653:G:N2	2.48	0.42
27:A:844:G:H5'	27:A:845:C:H5''	2.02	0.42
27:A:1822:C:O2'	27:A:1828:A:N1	2.43	0.42
27:A:2074:G:H21	27:A:2109:A:N6	2.15	0.42
27:A:2090:U:O2	27:A:2093:G:N2	2.52	0.42
27:A:2412:U:H2'	27:A:2413:G:C8	2.54	0.42
27:A:2457:U:H2'	27:A:2458:G:C8	2.52	0.42
27:A:2599:G:N2	27:A:2602:A:OP2	2.46	0.42
27:A:3118:U:H2'	27:A:3119:A:C8	2.55	0.42
1:E:80:ALA:O	1:E:113:GLN:NE2	2.49	0.42
2:F:16:VAL:HG23	2:F:24:VAL:HB	2.01	0.42
8:N:63:VAL:HG23	8:N:64:ARG:HG3	2.00	0.42
10:Q:7:GLY:O	10:Q:9:ARG:NH1	2.52	0.42
12:S:51:GLY:HA2	12:S:56:GLU:OE2	2.19	0.42
15:V:41:ASP:OD1	15:V:41:ASP:N	2.52	0.42
15:V:48:GLN:O	15:V:51:SER:OG	2.36	0.42
27:A:130:C:H2'	27:A:131:A:C8	2.54	0.42
27:A:977:G:H2'	27:A:978:A:O4'	2.18	0.42
27:A:1435:C:C5	27:A:1444:U:H5''	2.55	0.42
27:A:2249:G:H2'	27:A:2250:A:H8	1.84	0.42
27:A:2686:U:H2'	27:A:2687:U:H6	1.84	0.42
27:A:2873:U:H2'	27:A:2874:C:H6	1.83	0.42
4:H:44:ASN:HD21	27:A:2536:U:H2'	1.83	0.42
27:A:978:A:H2'	27:A:979:G:H8	1.84	0.42
27:A:1150:A:H2	27:A:1240:G:H1	1.67	0.42
27:A:1900:C:OP2	27:A:1917:G:N2	2.46	0.42
27:A:2361:U:H3	27:A:2376:G:H1	1.66	0.42
27:A:3020:U:H1'	27:A:3022:G:O6	2.19	0.42
27:A:3070:G:H4'	27:A:3071:A:H5'	2.00	0.42
5:I:118:ALA:HB2	5:I:124:PHE:CE2	2.54	0.42
14:U:30:GLU:OE1	14:U:30:GLU:HA	2.19	0.42
17:X:77:ASP:OD1	17:X:77:ASP:N	2.34	0.42
20:2:66:LEU:HD23	20:2:66:LEU:HA	1.80	0.42
27:A:609:G:H2'	27:A:610:C:C6	2.54	0.42
27:A:733:U:H2'	27:A:734:C:C6	2.54	0.42
27:A:824:G:H2'	27:A:825:C:C6	2.54	0.42
27:A:1076:A:HO2'	27:A:2681:U:HO2'	1.64	0.42
27:A:1271:C:H2'	27:A:1272:C:H6	1.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:1555:A:C2	27:A:1556:A:H1'	2.54	0.42
27:A:1560:U:H3	27:A:1611:A:N6	2.17	0.42
27:A:1679:A:H4'	27:A:1679:A:OP1	2.20	0.42
27:A:1939:U:H3	27:A:1955:A:H62	1.66	0.42
27:A:2074:G:H5'	27:A:2075:G:OP2	2.20	0.42
27:A:2336:U:O4	27:A:2337:A:N6	2.53	0.42
27:A:2363:A:H2'	27:A:2364:C:H6	1.84	0.42
27:A:2866:A:H2'	27:A:2867:A:H8	1.85	0.42
28:B:81:U:H2'	28:B:82:A:H8	1.84	0.42
5:I:96:ARG:HH22	5:I:98:GLN:CG	2.31	0.42
5:I:104:LEU:HB3	5:I:116:ILE:HB	2.00	0.42
27:A:216:A:C4	27:A:217:G:C8	3.08	0.42
27:A:483:G:H2'	27:A:484:C:C6	2.54	0.42
27:A:747:A:H2'	27:A:748:U:O4'	2.19	0.42
27:A:869:U:H2'	27:A:870:G:H8	1.83	0.42
27:A:1089:C:O2'	27:A:1101:A:N3	2.47	0.42
27:A:1412:C:H2'	27:A:1413:C:C6	2.54	0.42
27:A:1732:U:H2'	27:A:1733:C:H6	1.85	0.42
27:A:2357:A:N7	27:A:2379:G:N2	2.67	0.42
27:A:2887:G:H2'	27:A:2888:G:O4'	2.19	0.42
27:A:3116:C:H2'	27:A:3117:U:C6	2.55	0.42
28:B:63:U:H2'	28:B:64:G:H8	1.84	0.42
1:E:53:HIS:HA	1:E:218:ARG:HB2	2.02	0.42
12:S:26:ASN:OD1	12:S:26:ASN:N	2.53	0.42
18:Z:11:ARG:O	18:Z:14:ARG:NH1	2.53	0.42
27:A:215:A:C8	27:A:520:A:N6	2.87	0.42
27:A:270:U:C2'	27:A:271:A:H5'	2.49	0.42
27:A:1076:A:O2'	27:A:2681:U:O2'	2.34	0.42
27:A:1534:C:H3'	27:A:1535:C:O2	2.19	0.42
27:A:2460:U:H2'	27:A:2461:G:O4'	2.20	0.42
27:A:2480:G:H2'	27:A:2481:U:C6	2.54	0.42
27:A:2717:U:C4	27:A:2718:G:C8	3.07	0.42
28:B:63:U:H2'	28:B:64:G:C8	2.55	0.42
9:O:5:LYS:HD2	9:O:5:LYS:HA	1.82	0.42
9:O:122:VAL:HG12	9:O:124:VAL:HG23	2.00	0.42
10:Q:65:GLU:O	10:Q:68:LYS:HG2	2.20	0.42
24:7:45:LEU:HD12	24:7:45:LEU:HA	1.87	0.42
27:A:72:G:H22	27:A:108:A:H2	1.66	0.42
27:A:979:G:H2'	27:A:980:C:H6	1.85	0.42
27:A:1456:G:H8	27:A:1456:G:OP2	2.03	0.42
27:A:3024:A:H2'	27:A:3025:G:H8	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:307:G:H2'	27:A:308:U:C6	2.55	0.42
27:A:465:A:C6	27:A:486:G:C6	3.08	0.42
27:A:1155:C:H2'	27:A:1156:A:C8	2.55	0.42
27:A:1732:U:H2'	27:A:1733:C:C6	2.55	0.42
27:A:2374:U:H2'	27:A:2375:G:H8	1.84	0.42
28:B:46:A:C4	28:B:47:A:C8	3.07	0.42
1:E:141:VAL:HG13	1:E:162:SER:HB2	2.02	0.42
4:H:130:ASP:HB3	27:A:2527:G:O4'	2.20	0.42
10:Q:20:LEU:HD11	27:A:1392:G:H4'	2.01	0.42
11:R:113:ILE:O	11:R:116:LEU:HD23	2.19	0.42
27:A:189:A:N3	27:A:794:G:O2'	2.49	0.42
27:A:377:C:H2'	27:A:378:G:H8	1.84	0.42
27:A:661:U:H2'	27:A:662:G:C8	2.54	0.42
27:A:1859:A:H2'	27:A:1860:G:O4'	2.20	0.42
27:A:2170:U:H2'	27:A:2171:C:H6	1.85	0.42
27:A:2262:C:H2'	27:A:2263:G:O4'	2.19	0.42
27:A:2340:A:H62	27:A:2388:G:H1	1.68	0.42
28:B:92:G:H2'	28:B:93:U:C6	2.55	0.42
9:O:133:ALA:O	9:O:137:ILE:HG13	2.20	0.41
10:Q:33:ARG:NH2	10:Q:114:GLU:OE2	2.48	0.41
27:A:751:A:H2'	27:A:752:C:C6	2.55	0.41
27:A:1001:C:C6	27:A:1002:C:H1'	2.55	0.41
27:A:1475:G:C6	27:A:1487:U:C2	3.07	0.41
27:A:1756:G:H1'	27:A:1758:G:C6	2.54	0.41
27:A:2011:U:H2'	27:A:2012:C:C6	2.55	0.41
28:B:112:C:C2	28:B:113:G:C8	3.08	0.41
1:E:209:ALA:HB2	27:A:2007:C:O2'	2.20	0.41
7:M:19:ASP:OD1	7:M:19:ASP:C	2.63	0.41
7:M:71:LYS:NZ	27:A:1140:G:OP1	2.53	0.41
19:1:18:VAL:HG22	19:1:24:ARG:HG3	2.01	0.41
23:6:25:THR:HG22	23:6:26:LYS:N	2.35	0.41
27:A:41:A:H2'	27:A:42:G:O4'	2.21	0.41
27:A:183:G:H2'	27:A:184:C:H6	1.84	0.41
27:A:384:G:H2'	27:A:385:G:C8	2.50	0.41
27:A:503:A:H2'	27:A:504:C:C6	2.54	0.41
27:A:690:G:C6	27:A:776:G:C6	3.08	0.41
27:A:729:C:H2'	27:A:730:G:O4'	2.19	0.41
27:A:737:A:N1	27:A:2593:A:O2'	2.50	0.41
27:A:1886:A:O2'	27:A:1892:G:N7	2.42	0.41
27:A:2011:U:H2'	27:A:2012:C:H6	1.85	0.41
27:A:2323:G:N2	27:A:2412:U:O2	2.41	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:2738:U:H2'	27:A:2739:C:C6	2.56	0.41
3:G:141:ALA:HB1	3:G:169:VAL:HG12	2.01	0.41
3:G:169:VAL:HB	3:G:175:VAL:HG11	2.02	0.41
7:M:70:THR:O	7:M:70:THR:OG1	2.34	0.41
16:W:10:ILE:HD13	16:W:10:ILE:HA	1.90	0.41
16:W:52:VAL:HG21	16:W:86:LEU:HD13	2.02	0.41
16:W:55:ASP:OD1	16:W:55:ASP:C	2.62	0.41
22:5:4:PRO:HA	27:A:2839:U:C2	2.55	0.41
27:A:37:U:C2	27:A:528:G:N2	2.88	0.41
27:A:369:G:C6	27:A:434:G:C6	3.09	0.41
27:A:443:C:H2'	27:A:444:U:O4'	2.20	0.41
27:A:818:U:H2'	27:A:819:G:O4'	2.20	0.41
27:A:935:A:H4'	27:A:951:G:H22	1.83	0.41
27:A:966:U:H2'	27:A:967:G:H8	1.84	0.41
27:A:1048:A:C6	27:A:1050:A:C8	3.08	0.41
27:A:1149:G:H2'	27:A:1150:A:C8	2.55	0.41
27:A:1378:U:C4	27:A:1379:G:C6	3.08	0.41
27:A:1485:C:H2'	27:A:1486:G:O4'	2.20	0.41
27:A:2376:G:H2'	27:A:2377:G:C8	2.55	0.41
27:A:2952:U:H2'	27:A:2953:U:C6	2.56	0.41
5:I:19:ILE:HG12	5:I:24:LEU:HG	2.01	0.41
7:M:47:ASN:HD21	27:A:623:A:H2	1.68	0.41
12:S:16:ILE:HD13	12:S:16:ILE:HA	1.94	0.41
27:A:327:U:O2	27:A:449:G:N2	2.53	0.41
27:A:740:A:O2'	27:A:741:G:H8	2.03	0.41
27:A:991:C:H2'	27:A:992:C:C6	2.55	0.41
27:A:1244:A:H4'	27:A:1245:U:O4'	2.20	0.41
27:A:1323:G:O2'	27:A:1352:A:N1	2.44	0.41
27:A:1639:G:H5'	27:A:1640:A:OP1	2.20	0.41
27:A:1789:A:H2'	27:A:1790:A:C8	2.55	0.41
27:A:1982:G:O6	27:A:2212:A:N6	2.53	0.41
27:A:2313:A:H2'	27:A:2314:U:C6	2.54	0.41
27:A:2588:C:H2'	27:A:2589:G:O4'	2.19	0.41
27:A:2623:A:H2'	27:A:2624:C:C6	2.55	0.41
27:A:2681:U:H2'	27:A:2682:G:C8	2.55	0.41
27:A:2801:A:O4'	27:A:2836:C:N4	2.53	0.41
28:B:107:A:H2'	28:B:108:C:C6	2.56	0.41
11:R:37:ARG:HA	11:R:101:VAL:HG23	2.02	0.41
13:T:108:ALA:O	13:T:112:VAL:HG13	2.20	0.41
22:5:35:GLN:H	22:5:35:GLN:CD	2.27	0.41
27:A:1149:G:H2'	27:A:1150:A:H8	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:1153:U:H2'	27:A:1154:G:H8	1.85	0.41
27:A:1888:C:H2'	27:A:1889:U:O4'	2.20	0.41
27:A:1988:C:H2'	27:A:1989:G:C8	2.56	0.41
27:A:2330:U:H3'	27:A:2331:U:C6	2.55	0.41
27:A:2415:G:H2'	27:A:2416:C:C6	2.55	0.41
27:A:2884:A:H3'	27:A:2885:G:C8	2.56	0.41
5:I:46:ALA:H	5:I:51:ILE:HA	1.84	0.41
6:J:2:LYS:HA	6:J:2:LYS:HD3	1.77	0.41
15:V:104:ARG:HH11	27:A:2237:A:H5'	1.85	0.41
27:A:1378:U:H2'	27:A:1379:G:C8	2.56	0.41
27:A:2945:A:C4	27:A:2946:G:C8	3.08	0.41
1:E:66:ASP:OD2	1:E:103:ARG:NH1	2.53	0.41
1:E:117:ILE:HD13	1:E:117:ILE:HA	1.89	0.41
4:H:37:GLY:H	4:H:166:THR:HB	1.85	0.41
6:J:10:GLU:CD	6:J:11:HIS:H	2.28	0.41
14:U:43:VAL:HG22	14:U:48:VAL:HG22	2.02	0.41
27:A:838:G:C4	27:A:839:U:C5	3.08	0.41
27:A:1284:A:H2'	27:A:1285:G:C8	2.55	0.41
27:A:1451:A:H2'	27:A:1452:G:H8	1.86	0.41
27:A:1556:A:N1	27:A:1615:G:C6	2.89	0.41
27:A:2556:C:O2'	27:A:2559:A:O2'	2.37	0.41
27:A:2936:C:OP1	27:A:2938:G:H4'	2.21	0.41
27:A:2964:A:H2'	27:A:2965:A:C8	2.55	0.41
3:G:165:GLY:O	3:G:169:VAL:HG22	2.21	0.41
11:R:113:ILE:HA	11:R:116:LEU:CD2	2.51	0.41
13:T:37:GLU:OE2	27:A:1367:G:N1	2.44	0.41
17:X:22:LYS:HE3	17:X:22:LYS:HB2	1.89	0.41
27:A:150:C:H2'	27:A:151:A:H8	1.85	0.41
27:A:263:G:H2'	27:A:264:G:O4'	2.21	0.41
27:A:672:C:H2'	27:A:673:C:H6	1.85	0.41
27:A:919:A:H5'	27:A:920:G:P	2.61	0.41
27:A:1294:U:H2'	27:A:1295:U:C6	2.55	0.41
27:A:1532:G:H2'	27:A:1533:U:C6	2.55	0.41
27:A:1739:A:C4	27:A:1740:G:C8	3.09	0.41
27:A:1897:A:H2	27:A:1981:U:O4'	2.04	0.41
27:A:2334:U:H4'	27:A:2341:U:H1'	2.03	0.41
28:B:52:G:H2'	28:B:53:A:C8	2.56	0.41
3:G:108:ALA:HB1	3:G:112:ARG:HH11	1.86	0.41
4:H:40:LYS:HD2	4:H:99:ARG:NH2	2.36	0.41
9:O:80:VAL:HG22	9:O:114:GLY:HA2	2.02	0.41
13:T:66:ASN:ND2	27:A:1129:G:OP2	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:V:104:ARG:NH1	27:A:2237:A:H5'	2.35	0.41
17:X:1:MET:O	17:X:2:LYS:HB2	2.21	0.41
27:A:164:A:H2'	27:A:165:U:C6	2.56	0.41
27:A:187:G:H2'	27:A:188:G:O4'	2.20	0.41
27:A:445:U:H1'	27:A:446:G:OP2	2.20	0.41
27:A:736:G:H1'	27:A:740:A:H61	1.86	0.41
27:A:826:G:H2'	27:A:827:G:H8	1.85	0.41
27:A:1000:C:H3'	27:A:1001:C:H5''	2.02	0.41
27:A:1938:G:N1	27:A:1955:A:OP2	2.38	0.41
27:A:2151:A:H2'	27:A:2152:A:C8	2.56	0.41
27:A:2339:G:N1	27:A:2385:G:OP2	2.43	0.41
27:A:2342:A:C2	27:A:2392:A:H2'	2.56	0.41
27:A:2486:U:H2'	27:A:2487:C:H6	1.86	0.41
27:A:2878:A:N1	27:A:2889:A:H5''	2.35	0.41
27:A:2955:G:H2'	27:A:2956:G:C8	2.56	0.41
27:A:2968:G:N7	27:A:2979:C:H1'	2.36	0.41
28:B:24:G:H2'	28:B:25:G:C8	2.56	0.41
28:B:47:A:C5	28:B:48:C:C5	3.09	0.41
3:G:189:LEU:HD13	9:O:9:LEU:HD11	2.02	0.41
5:I:30:LYS:HD2	5:I:30:LYS:HA	1.66	0.41
27:A:742:G:C2	27:A:743:G:N7	2.89	0.41
27:A:1040:U:H2'	27:A:1041:A:C8	2.56	0.41
27:A:1043:G:C4	27:A:1044:U:C5	3.09	0.41
27:A:1407:G:H2'	27:A:1408:C:H6	1.85	0.41
27:A:1471:G:H2'	27:A:1472:C:C6	2.56	0.41
27:A:1532:G:N2	27:A:1804:G:C4	2.89	0.41
27:A:2235:C:H2'	27:A:2236:G:O4'	2.21	0.41
1:E:108:PRO:HB3	1:E:143:HIS:CE1	2.57	0.40
1:E:146:GLU:HB2	1:E:189:CYS:HB3	2.04	0.40
1:E:233:HIS:NE2	1:E:246:PRO:HA	2.37	0.40
4:H:41:VAL:HG21	4:H:107:LEU:HD13	2.03	0.40
4:H:76:ARG:HH21	28:B:42:C:N4	2.13	0.40
4:H:182:PHE:HA	4:H:183:PRO:HD3	1.89	0.40
5:I:104:LEU:HD12	5:I:104:LEU:HA	1.90	0.40
7:M:92:LEU:HD12	7:M:92:LEU:HA	1.91	0.40
26:4:13:THR:HA	26:4:22:PHE:O	2.21	0.40
27:A:298:G:H2'	27:A:299:G:C4	2.55	0.40
27:A:993:G:N2	27:A:1015:A:O5'	2.50	0.40
27:A:1296:G:C2	27:A:1297:G:C5	3.10	0.40
27:A:1608:U:C6	27:A:1608:U:H5''	2.56	0.40
6:J:33:ARG:HG3	6:J:35:LEU:HG	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:M:69:LEU:HD12	7:M:69:LEU:HA	1.97	0.40
10:Q:78:THR:O	10:Q:82:GLU:HG2	2.21	0.40
15:V:17:VAL:HG12	15:V:19:VAL:HG22	2.03	0.40
27:A:600:A:H2'	27:A:601:A:H8	1.86	0.40
27:A:883:G:H22	27:A:1494:U:H1'	1.86	0.40
27:A:1146:A:N3	27:A:2710:G:O2'	2.43	0.40
27:A:2398:C:H2'	27:A:2399:A:H8	1.85	0.40
27:A:2857:A:H2'	27:A:2858:G:C8	2.57	0.40
27:A:2961:G:H2'	27:A:2962:A:H8	1.86	0.40
28:B:91:G:H2'	28:B:92:G:H8	1.86	0.40
5:I:149:ILE:O	5:I:152:LEU:HD23	2.21	0.40
7:M:143:LYS:HB3	7:M:143:LYS:HE3	1.83	0.40
11:R:37:ARG:HH12	28:B:9:G:P	2.44	0.40
15:V:100:ALA:HB2	27:A:1832:A:C2	2.56	0.40
27:A:5:U:C2	27:A:6:G:C8	3.09	0.40
27:A:216:A:H2'	27:A:217:G:H8	1.86	0.40
27:A:1121:G:H2'	27:A:1122:C:C6	2.57	0.40
27:A:1321:C:O2'	27:A:1344:A:N1	2.50	0.40
27:A:2363:A:C6	27:A:2375:G:C6	3.08	0.40
27:A:2506:G:H4'	27:A:2613:G:O2'	2.21	0.40
27:A:2540:G:H2'	27:A:2541:U:C6	2.56	0.40
1:E:177:MET:HE2	1:E:183:ARG:HB3	2.03	0.40
3:G:206:SER:O	3:G:210:LYS:HB3	2.20	0.40
5:I:22:GLN:NE2	5:I:38:ALA:O	2.54	0.40
5:I:22:GLN:HE21	5:I:39:GLU:HA	1.86	0.40
5:I:103:ASN:ND2	5:I:117:GLU:OE2	2.55	0.40
8:N:115:VAL:HG13	8:N:121:VAL:HG21	2.03	0.40
16:W:48:LYS:HB2	16:W:48:LYS:HE2	1.68	0.40
27:A:308:U:H2'	27:A:309:G:C8	2.52	0.40
27:A:400:C:H2'	27:A:401:C:H6	1.87	0.40
27:A:1472:C:H2'	27:A:1473:G:O4'	2.22	0.40
27:A:1560:U:C5	27:A:1561:C:C4	3.10	0.40
27:A:1629:G:H4'	27:A:1630:U:H5	1.86	0.40
27:A:2305:A:C4	27:A:2463:G:N2	2.89	0.40
27:A:2771:U:H2'	27:A:2772:G:C8	2.55	0.40
27:A:2815:C:H2'	27:A:2816:G:C8	2.57	0.40
27:A:2879:G:H22	27:A:2888:G:H3'	1.87	0.40
27:A:3030:A:H2'	27:A:3031:A:C8	2.57	0.40
5:I:44:SER:O	5:I:52:VAL:N	2.45	0.40
5:I:87:LYS:HD3	5:I:133:SER:OG	2.21	0.40
6:J:31:LEU:N	6:J:32:PRO:HD2	2.36	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:U:77:LYS:NZ	27:A:1110:C:OP1	2.41	0.40
27:A:1033:A:H5''	28:B:95:G:O2'	2.22	0.40
27:A:1167:C:C2	27:A:1168:A:C8	3.09	0.40
27:A:1501:C:H1'	27:A:1691:A:H1'	2.04	0.40
27:A:2532:G:H2'	27:A:2532:G:N3	2.36	0.40
27:A:2538:A:H2'	27:A:2539:G:H8	1.87	0.40
27:A:2548:U:H5''	27:A:2549:G:H5''	2.03	0.40
28:B:25:G:N7	28:B:57:U:H2'	2.36	0.40
28:B:78:U:H2'	28:B:79:A:H8	1.87	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	E	273/278 (98%)	265 (97%)	8 (3%)	0	100	100
2	F	212/217 (98%)	204 (96%)	7 (3%)	1 (0%)	24	48
3	G	207/215 (96%)	205 (99%)	2 (1%)	0	100	100
4	H	180/187 (96%)	173 (96%)	7 (4%)	0	100	100
5	I	163/179 (91%)	162 (99%)	1 (1%)	0	100	100
6	J	39/151 (26%)	39 (100%)	0	0	100	100
7	M	144/147 (98%)	141 (98%)	3 (2%)	0	100	100
8	N	120/122 (98%)	117 (98%)	3 (2%)	0	100	100
9	O	143/147 (97%)	131 (92%)	12 (8%)	0	100	100
10	Q	116/199 (58%)	114 (98%)	2 (2%)	0	100	100
11	R	124/127 (98%)	124 (100%)	0	0	100	100
12	S	111/113 (98%)	104 (94%)	7 (6%)	0	100	100
13	T	122/129 (95%)	120 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
14	U	98/103 (95%)	95 (97%)	3 (3%)	0	100	100
15	V	112/153 (73%)	111 (99%)	1 (1%)	0	100	100
16	W	93/100 (93%)	92 (99%)	1 (1%)	0	100	100
17	X	89/105 (85%)	88 (99%)	1 (1%)	0	100	100
18	Z	74/88 (84%)	71 (96%)	3 (4%)	0	100	100
19	1	61/64 (95%)	60 (98%)	1 (2%)	0	100	100
20	2	62/77 (80%)	60 (97%)	2 (3%)	0	100	100
21	3	57/61 (93%)	55 (96%)	2 (4%)	0	100	100
22	5	52/57 (91%)	51 (98%)	1 (2%)	0	100	100
23	6	46/55 (84%)	42 (91%)	4 (9%)	0	100	100
24	7	44/47 (94%)	44 (100%)	0	0	100	100
25	8	60/64 (94%)	58 (97%)	2 (3%)	0	100	100
26	4	46/75 (61%)	45 (98%)	1 (2%)	0	100	100
All	All	2848/3260 (87%)	2771 (97%)	76 (3%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	F	156	THR

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	E	215/218 (99%)	215 (100%)	0	100	100
2	F	160/163 (98%)	158 (99%)	2 (1%)	61	83
3	G	169/173 (98%)	169 (100%)	0	100	100
4	H	151/156 (97%)	150 (99%)	1 (1%)	76	90
5	I	139/150 (93%)	138 (99%)	1 (1%)	76	90

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	J	31/116 (27%)	31 (100%)	0	100	100
7	M	119/120 (99%)	119 (100%)	0	100	100
8	N	100/100 (100%)	100 (100%)	0	100	100
9	O	112/114 (98%)	112 (100%)	0	100	100
10	Q	97/158 (61%)	97 (100%)	0	100	100
11	R	93/94 (99%)	93 (100%)	0	100	100
12	S	100/100 (100%)	100 (100%)	0	100	100
13	T	97/99 (98%)	97 (100%)	0	100	100
14	U	81/83 (98%)	81 (100%)	0	100	100
15	V	90/117 (77%)	90 (100%)	0	100	100
16	W	83/85 (98%)	83 (100%)	0	100	100
17	X	79/86 (92%)	78 (99%)	1 (1%)	61	83
18	Z	55/63 (87%)	55 (100%)	0	100	100
19	1	50/51 (98%)	50 (100%)	0	100	100
20	2	58/66 (88%)	58 (100%)	0	100	100
21	3	52/54 (96%)	52 (100%)	0	100	100
22	5	43/46 (94%)	43 (100%)	0	100	100
23	6	46/52 (88%)	45 (98%)	1 (2%)	45	74
24	7	35/36 (97%)	35 (100%)	0	100	100
25	8	53/54 (98%)	53 (100%)	0	100	100
26	4	43/63 (68%)	43 (100%)	0	100	100
All	All	2351/2617 (90%)	2345 (100%)	6 (0%)	84	94

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	F	154	CYS
2	F	156	THR
4	H	164	VAL
5	I	76	LEU
17	X	77	ASP
23	6	8	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	E	109	GLN
2	F	20	ASN
3	G	91	HIS
5	I	22	GLN
5	I	98	GLN
7	M	58	ASN
9	O	69	ASN
10	Q	61	HIS
12	S	28	HIS
12	S	82	HIS
13	T	27	GLN
14	U	93	GLN
20	2	40	GLN
22	5	12	ASN
23	6	20	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
27	A	3022/3119 (96%)	539 (17%)	16 (0%)
28	B	117/118 (99%)	16 (13%)	1 (0%)
All	All	3139/3237 (96%)	555 (17%)	17 (0%)

All (555) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
27	A	7	U
27	A	12	G
27	A	20	G
27	A	31	U
27	A	32	G
27	A	33	G
27	A	48	G
27	A	55	G
27	A	60	A
27	A	68	A
27	A	71	A
27	A	72	G
27	A	82	G
27	A	90	C
27	A	91	C
27	A	94	G

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Mol	Chain	Res	Type
27	A	98	U
27	A	99	G
27	A	115	A
27	A	117	U
27	A	125	C
27	A	148	A
27	A	164	A
27	A	195	A
27	A	198	A
27	A	212	A
27	A	214	G
27	A	215	A
27	A	221	A
27	A	227	A
27	A	229	U
27	A	230	G
27	A	231	U
27	A	248	G
27	A	265	A
27	A	266	U
27	A	270	U
27	A	271	A
27	A	272	A
27	A	275	C
27	A	283	U
27	A	285	U
27	A	286	G
27	A	290	C
27	A	297	G
27	A	298	G
27	A	299	G
27	A	300	G
27	A	301	U
27	A	302	U
27	A	303	G
27	A	305	G
27	A	315	U
27	A	317	G
27	A	318	U
27	A	319	G
27	A	324	C
27	A	330	U

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Mol	Chain	Res	Type
27	A	331	U
27	A	336	C
27	A	337	U
27	A	338	C
27	A	344	G
27	A	346	C
27	A	350	A
27	A	351	G
27	A	353	G
27	A	357	U
27	A	358	G
27	A	361	A
27	A	364	A
27	A	370	U
27	A	371	G
27	A	384	G
27	A	393	U
27	A	399	G
27	A	406	A
27	A	412	A
27	A	413	G
27	A	424	G
27	A	426	G
27	A	434	G
27	A	437	G
27	A	438	U
27	A	445	U
27	A	446	G
27	A	450	G
27	A	452	G
27	A	454	U
27	A	460	G
27	A	474	G
27	A	489	A
27	A	493	U
27	A	494	G
27	A	505	C
27	A	512	G
27	A	543	U
27	A	544	U
27	A	555	G
27	A	566	A

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Mol	Chain	Res	Type
27	A	568	A
27	A	569	G
27	A	589	A
27	A	591	G
27	A	592	A
27	A	594	U
27	A	595	A
27	A	596	C
27	A	605	G
27	A	617	U
27	A	618	C
27	A	619	C
27	A	620	G
27	A	635	G
27	A	636	U
27	A	637	G
27	A	638	U
27	A	639	C
27	A	640	G
27	A	642	G
27	A	644	G
27	A	655	G
27	A	664	A
27	A	667	A
27	A	679	G
27	A	684	G
27	A	685	G
27	A	696	A
27	A	706	G
27	A	707	G
27	A	708	G
27	A	709	U
27	A	721	A
27	A	731	A
27	A	738	A
27	A	740	A
27	A	754	C
27	A	756	A
27	A	758	A
27	A	760	U
27	A	764	U
27	A	765	G

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Mol	Chain	Res	Type
27	A	766	G
27	A	768	G
27	A	784	G
27	A	785	A
27	A	801	U
27	A	832	G
27	A	839	U
27	A	841	G
27	A	845	C
27	A	862	U
27	A	863	G
27	A	868	C
27	A	872	G
27	A	878	G
27	A	879	A
27	A	880	G
27	A	890	G
27	A	891	G
27	A	897	A
27	A	899	G
27	A	907	A
27	A	920	G
27	A	927	C
27	A	942	U
27	A	945	G
27	A	960	G
27	A	961	U
27	A	972	A
27	A	975	U
27	A	981	U
27	A	982	A
27	A	988	U
27	A	989	G
27	A	990	G
27	A	991	C
27	A	994	A
27	A	995	U
27	A	1001	C
27	A	1002	C
27	A	1003	A
27	A	1004	C
27	A	1005	A

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Mol	Chain	Res	Type
27	A	1008	G
27	A	1009	U
27	A	1010	U
27	A	1012	C
27	A	1013	U
27	A	1014	G
27	A	1015	A
27	A	1018	U
27	A	1019	C
27	A	1022	C
27	A	1025	A
27	A	1030	C
27	A	1047	A
27	A	1049	G
27	A	1058	A
27	A	1063	G
27	A	1076	A
27	A	1078	G
27	A	1085	G
27	A	1092	G
27	A	1101	A
27	A	1114	G
27	A	1130	C
27	A	1131	G
27	A	1138	A
27	A	1144	A
27	A	1151	U
27	A	1158	U
27	A	1164	A
27	A	1230	G
27	A	1232	G
27	A	1235	U
27	A	1238	G
27	A	1240	G
27	A	1242	C
27	A	1244	A
27	A	1245	U
27	A	1248	U
27	A	1250	U
27	A	1251	A
27	A	1252	G
27	A	1253	C

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Mol	Chain	Res	Type
27	A	1260	C
27	A	1261	A
27	A	1292	U
27	A	1293	G
27	A	1298	C
27	A	1335	G
27	A	1344	A
27	A	1351	G
27	A	1353	G
27	A	1359	G
27	A	1362	A
27	A	1371	G
27	A	1386	G
27	A	1387	A
27	A	1389	U
27	A	1415	A
27	A	1416	A
27	A	1436	C
27	A	1440	C
27	A	1456	G
27	A	1465	C
27	A	1467	U
27	A	1480	A
27	A	1493	A
27	A	1494	U
27	A	1499	A
27	A	1507	G
27	A	1508	A
27	A	1510	A
27	A	1511	U
27	A	1522	G
27	A	1531	C
27	A	1533	U
27	A	1534	C
27	A	1539	A
27	A	1540	U
27	A	1543	A
27	A	1550	G
27	A	1551	U
27	A	1552	A
27	A	1553	C
27	A	1554	U

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Mol	Chain	Res	Type
27	A	1562	C
27	A	1563	A
27	A	1609	G
27	A	1611	A
27	A	1625	G
27	A	1627	U
27	A	1628	A
27	A	1629	G
27	A	1630	U
27	A	1633	U
27	A	1639	G
27	A	1640	A
27	A	1641	U
27	A	1648	A
27	A	1649	C
27	A	1670	G
27	A	1676	G
27	A	1679	A
27	A	1680	A
27	A	1681	U
27	A	1703	G
27	A	1710	A
27	A	1711	G
27	A	1714	A
27	A	1717	U
27	A	1724	G
27	A	1728	U
27	A	1731	A
27	A	1737	A
27	A	1754	G
27	A	1755	A
27	A	1756	G
27	A	1757	U
27	A	1767	U
27	A	1786	G
27	A	1789	A
27	A	1798	U
27	A	1826	A
27	A	1864	U
27	A	1866	C
27	A	1871	G
27	A	1872	A

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Mol	Chain	Res	Type
27	A	1892	G
27	A	1933	G
27	A	1946	U
27	A	1947	U
27	A	1949	C
27	A	1950	G
27	A	1973	C
27	A	1975	A
27	A	1981	U
27	A	1990	A
27	A	2003	A
27	A	2017	C
27	A	2018	G
27	A	2026	A
27	A	2033	U
27	A	2046	A
27	A	2064	A
27	A	2065	A
27	A	2074	G
27	A	2075	G
27	A	2085	C
27	A	2086	U
27	A	2087	C
27	A	2088	C
27	A	2089	C
27	A	2091	U
27	A	2092	U
27	A	2093	G
27	A	2094	G
27	A	2095	G
27	A	2096	G
27	A	2107	G
27	A	2130	G
27	A	2137	A
27	A	2141	U
27	A	2153	G
27	A	2154	G
27	A	2160	A
27	A	2161	A
27	A	2162	A
27	A	2163	U
27	A	2179	U

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Mol	Chain	Res	Type
27	A	2191	C
27	A	2194	A
27	A	2195	U
27	A	2196	G
27	A	2215	U
27	A	2217	U
27	A	2221	A
27	A	2244	A
27	A	2247	A
27	A	2251	G
27	A	2254	A
27	A	2255	A
27	A	2256	G
27	A	2257	A
27	A	2263	G
27	A	2267	C
27	A	2276	G
27	A	2279	C
27	A	2280	G
27	A	2283	A
27	A	2284	A
27	A	2285	G
27	A	2286	A
27	A	2287	C
27	A	2316	G
27	A	2320	C
27	A	2322	C
27	A	2324	A
27	A	2325	U
27	A	2328	G
27	A	2330	U
27	A	2331	U
27	A	2334	U
27	A	2335	G
27	A	2338	G
27	A	2339	G
27	A	2340	A
27	A	2341	U
27	A	2342	A
27	A	2343	G
27	A	2345	U
27	A	2346	G

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Mol	Chain	Res	Type
27	A	2351	A
27	A	2353	U
27	A	2354	G
27	A	2355	U
27	A	2356	G
27	A	2357	A
27	A	2368	C
27	A	2370	A
27	A	2371	G
27	A	2372	U
27	A	2382	G
27	A	2384	C
27	A	2386	U
27	A	2387	U
27	A	2388	G
27	A	2390	U
27	A	2393	A
27	A	2394	A
27	A	2395	U
27	A	2396	A
27	A	2399	A
27	A	2401	U
27	A	2402	C
27	A	2403	U
27	A	2404	G
27	A	2405	A
27	A	2407	C
27	A	2408	G
27	A	2410	A
27	A	2413	G
27	A	2421	A
27	A	2422	A
27	A	2427	G
27	A	2434	A
27	A	2436	A
27	A	2447	G
27	A	2449	A
27	A	2462	G
27	A	2463	G
27	A	2467	U
27	A	2503	G
27	A	2507	C

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Mol	Chain	Res	Type
27	A	2511	A
27	A	2512	A
27	A	2529	A
27	A	2532	G
27	A	2544	U
27	A	2545	G
27	A	2548	U
27	A	2549	G
27	A	2558	C
27	A	2559	A
27	A	2560	A
27	A	2569	G
27	A	2571	C
27	A	2574	C
27	A	2585	U
27	A	2607	G
27	A	2609	A
27	A	2626	U
27	A	2627	C
27	A	2647	U
27	A	2649	A
27	A	2653	G
27	A	2654	A
27	A	2655	U
27	A	2659	A
27	A	2665	C
27	A	2671	G
27	A	2672	A
27	A	2673	U
27	A	2677	A
27	A	2678	G
27	A	2679	G
27	A	2688	C
27	A	2693	A
27	A	2694	G
27	A	2700	A
27	A	2705	G
27	A	2714	G
27	A	2715	U
27	A	2718	G
27	A	2722	C
27	A	2726	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
27	A	2727	A
27	A	2729	G
27	A	2730	U
27	A	2737	G
27	A	2742	A
27	A	2744	C
27	A	2749	G
27	A	2753	G
27	A	2754	G
27	A	2756	G
27	A	2759	G
27	A	2766	A
27	A	2786	U
27	A	2790	A
27	A	2791	G
27	A	2796	A
27	A	2797	C
27	A	2800	G
27	A	2801	A
27	A	2826	A
27	A	2827	G
27	A	2833	U
27	A	2837	U
27	A	2839	U
27	A	2853	C
27	A	2854	A
27	A	2857	A
27	A	2858	G
27	A	2862	G
27	A	2876	C
27	A	2913	U
27	A	2915	C
27	A	2926	A
27	A	2936	C
27	A	2938	G
27	A	2950	C
27	A	2956	G
27	A	2957	A
27	A	2968	G
27	A	2980	U
27	A	2981	A
27	A	2982	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
27	A	2985	G
27	A	2989	A
27	A	3002	A
27	A	3009	U
27	A	3014	A
27	A	3021	A
27	A	3022	G
27	A	3029	U
27	A	3042	A
27	A	3044	A
27	A	3056	A
27	A	3082	U
27	A	3088	C
27	A	3093	A
27	A	3105	C
27	A	3106	C
27	A	3107	G
27	A	3108	G
27	A	3114	A
28	B	3	U
28	B	4	A
28	B	9	G
28	B	11	U
28	B	12	C
28	B	13	C
28	B	27	A
28	B	30	G
28	B	36	U
28	B	42	C
28	B	54	A
28	B	57	U
28	B	68	G
28	B	87	U
28	B	89	C
28	B	107	A

All (17) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
27	A	89	A
27	A	97	U
27	A	316	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
27	A	357	U
27	A	445	U
27	A	641	U
27	A	643	G
27	A	974	G
27	A	1002	C
27	A	1004	C
27	A	1084	U
27	A	1561	C
27	A	2094	G
27	A	2350	G
27	A	2381	A
27	A	2729	G
28	B	10	G

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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.

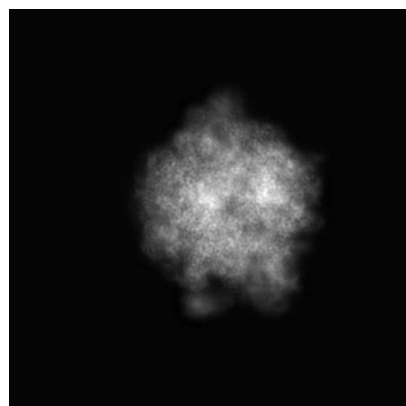
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-37560. These allow visual inspection of the internal detail of the map and identification of artifacts.

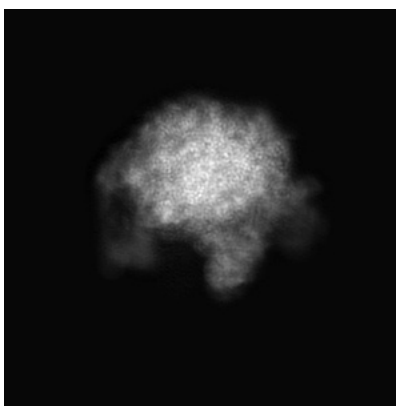
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

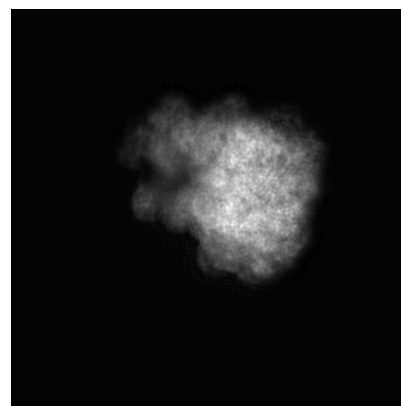
6.1.1 Primary map



X

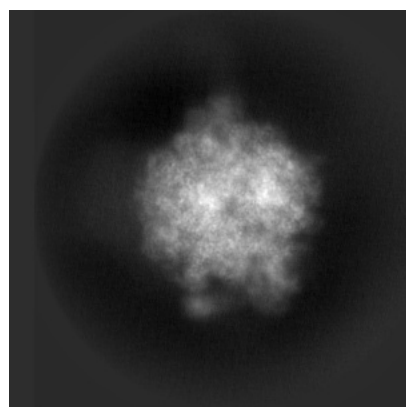


Y

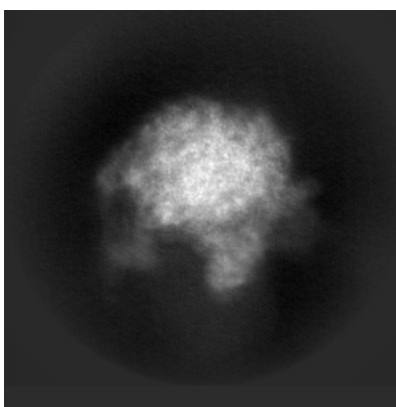


Z

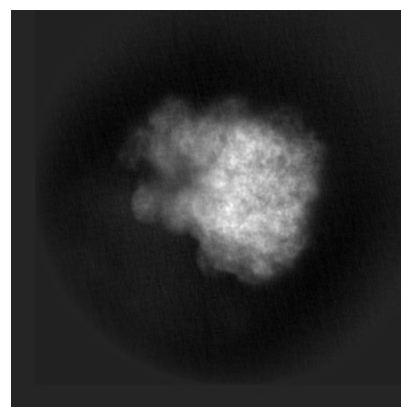
6.1.2 Raw map



X



Y

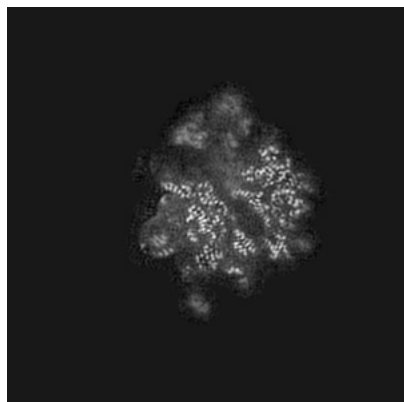


Z

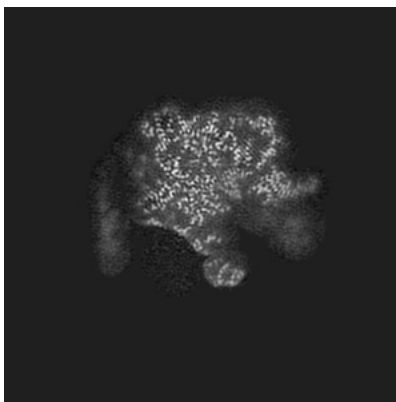
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

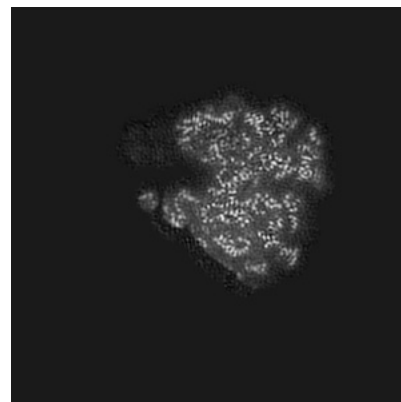
6.2.1 Primary map



X Index: 190

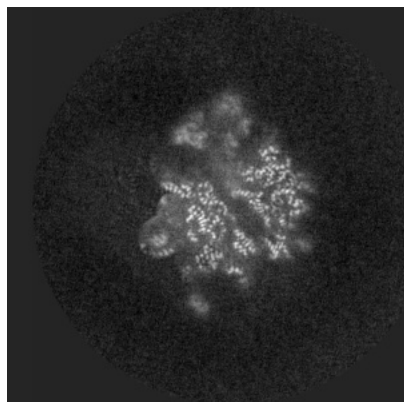


Y Index: 190

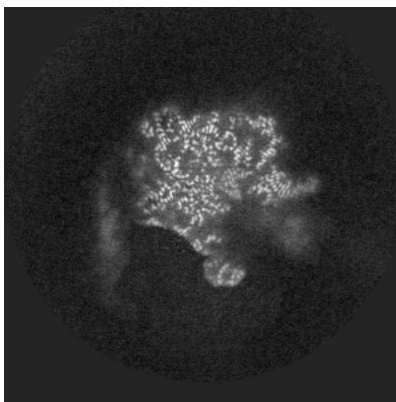


Z Index: 190

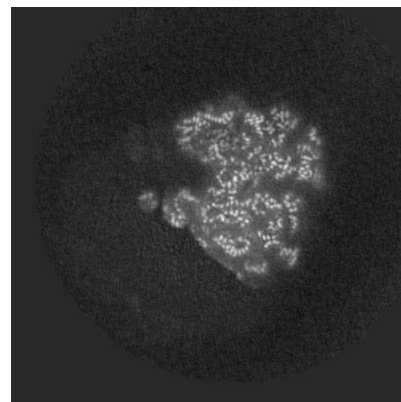
6.2.2 Raw map



X Index: 190



Y Index: 190

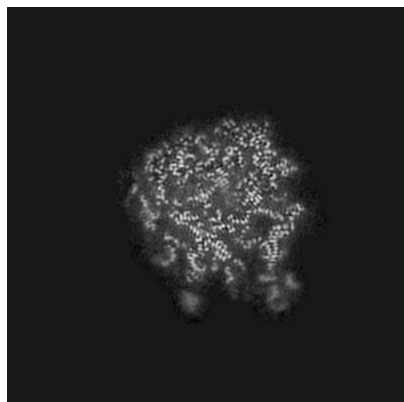


Z Index: 190

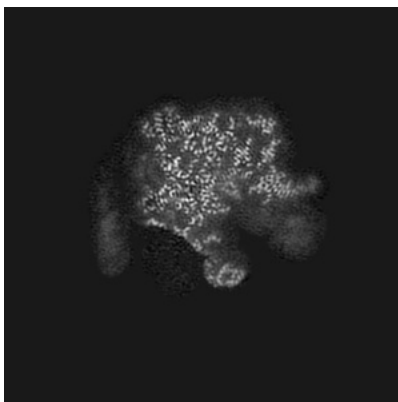
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

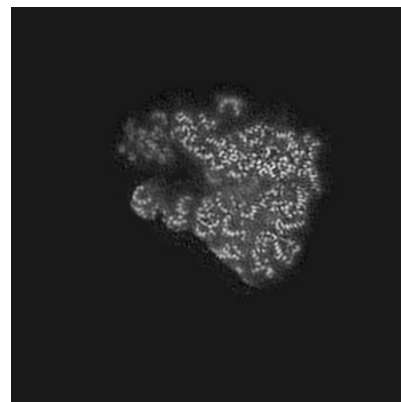
6.3.1 Primary map



X Index: 230

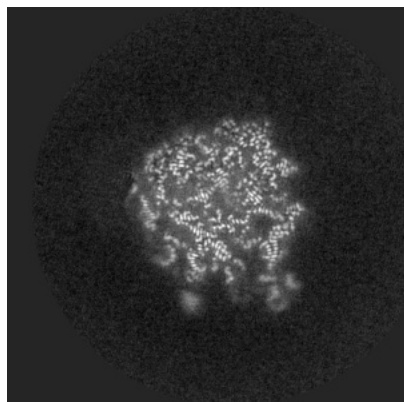


Y Index: 191

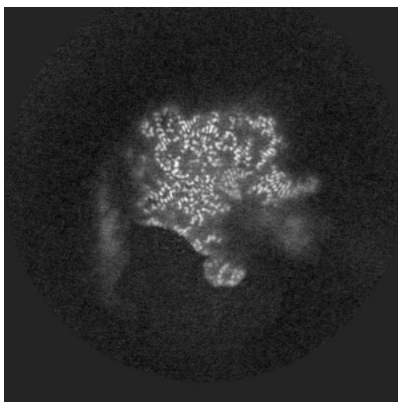


Z Index: 200

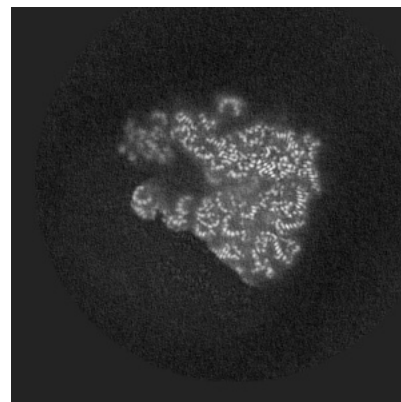
6.3.2 Raw map



X Index: 230



Y Index: 190

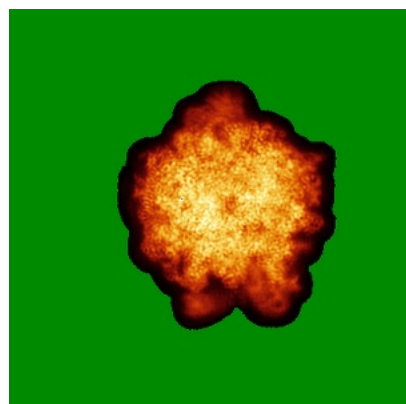


Z Index: 200

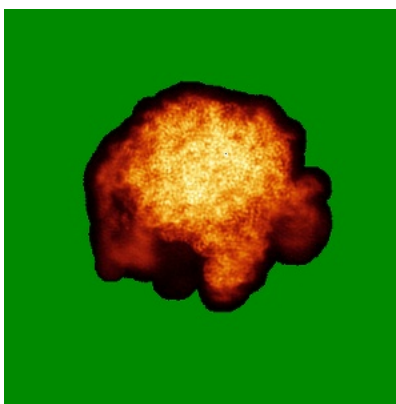
The images above show the largest variance slices of the map in three orthogonal directions.

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

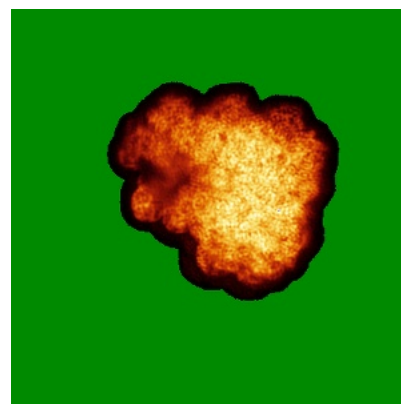
6.4.1 Primary map



X

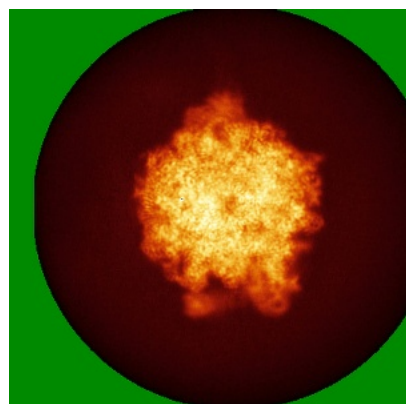


Y

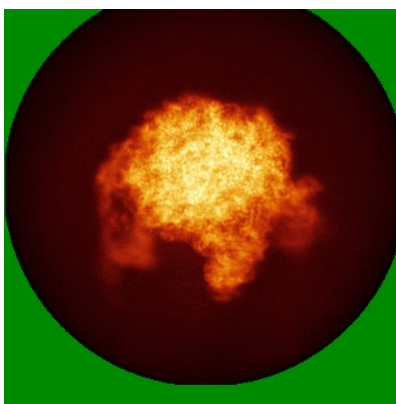


Z

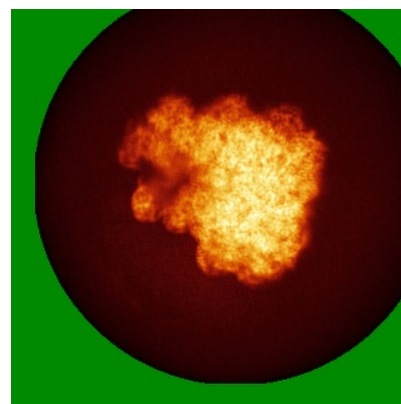
6.4.2 Raw map



X



Y

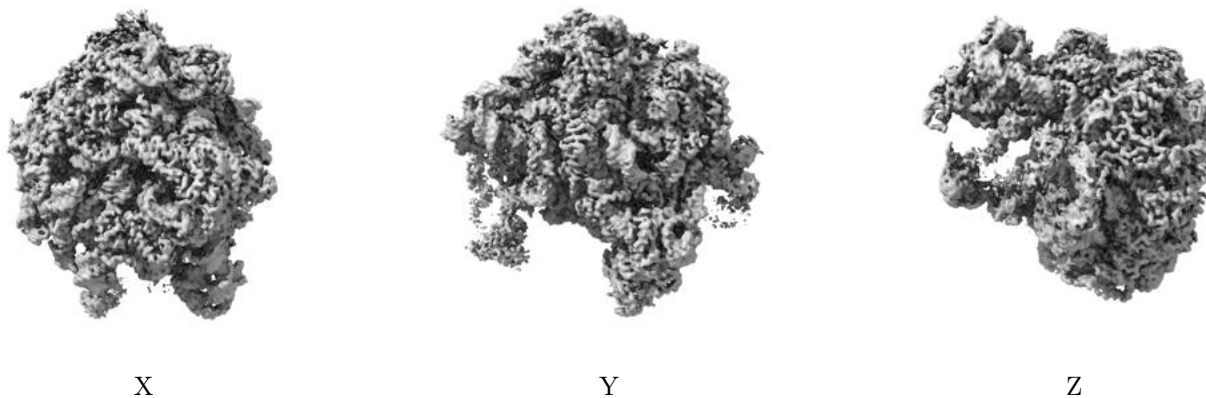


Z

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.

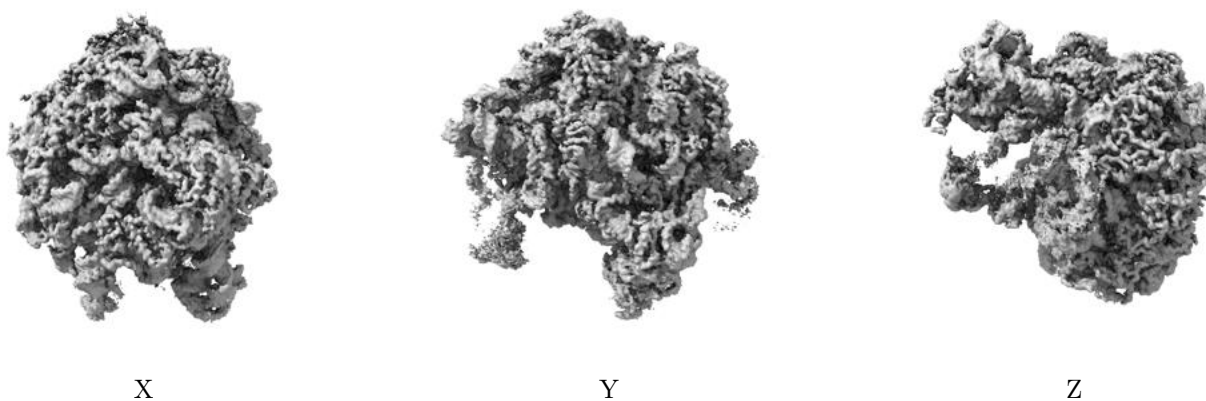
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.045. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

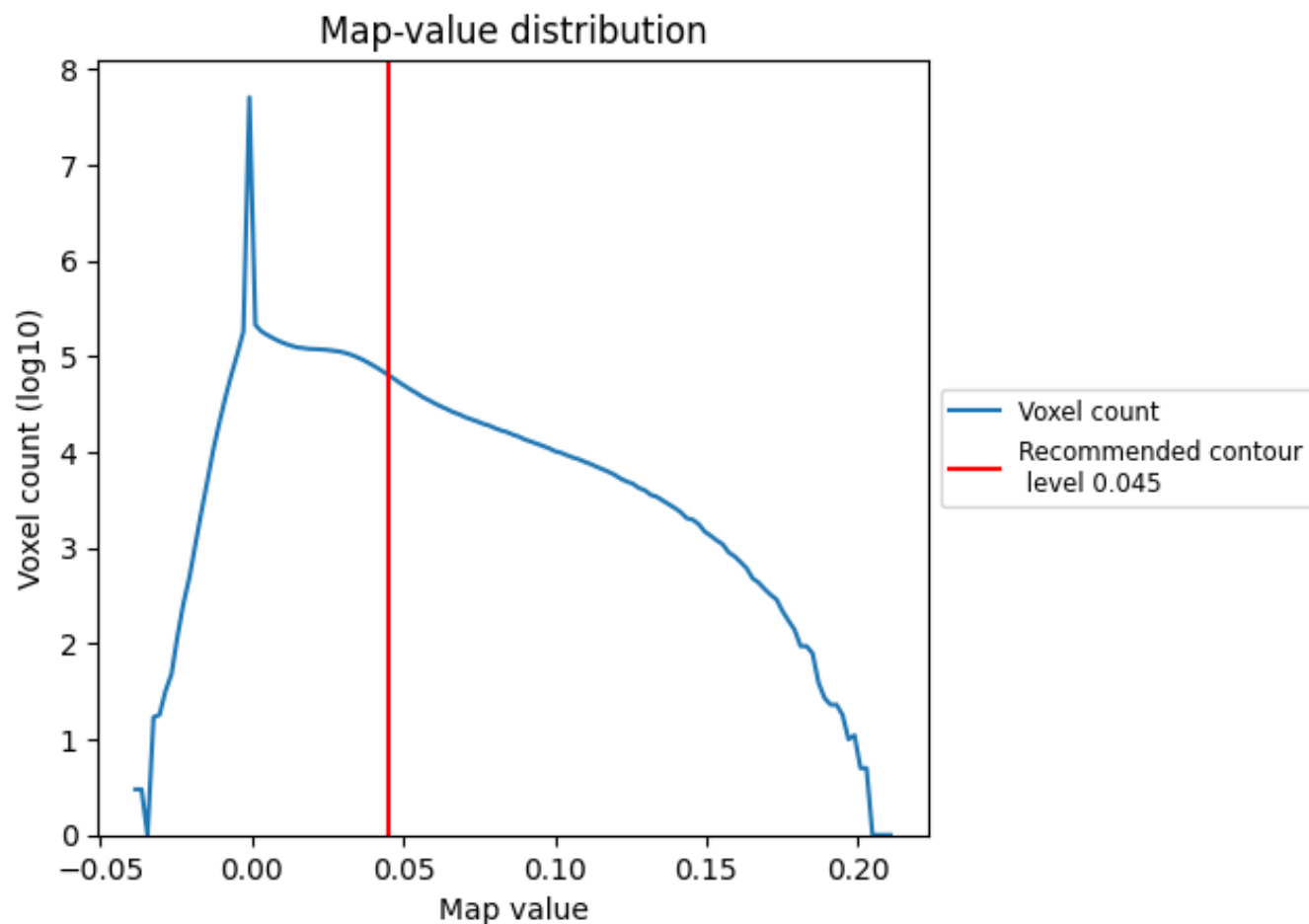
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

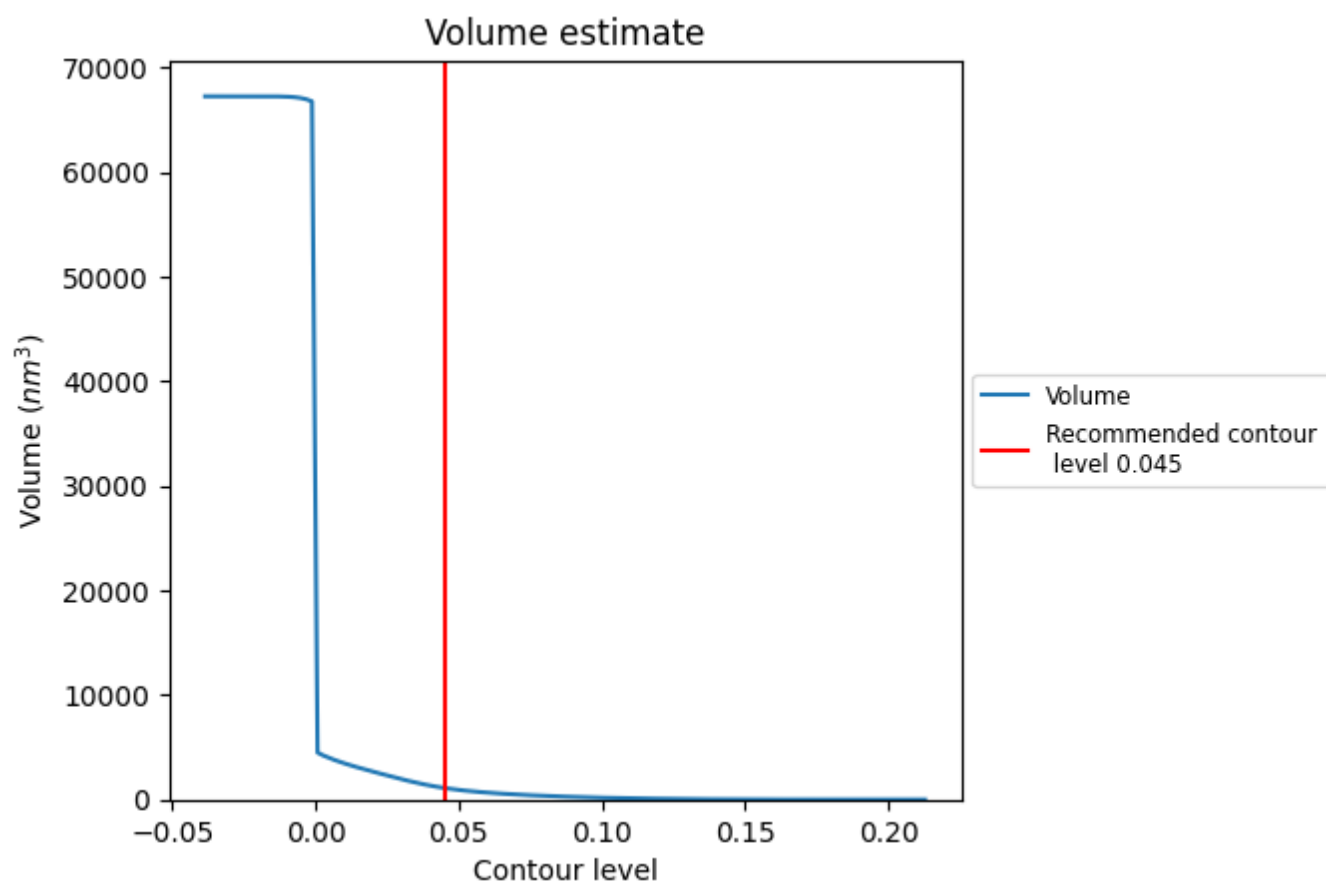
This section contains the results of statistical analysis of the map.

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.

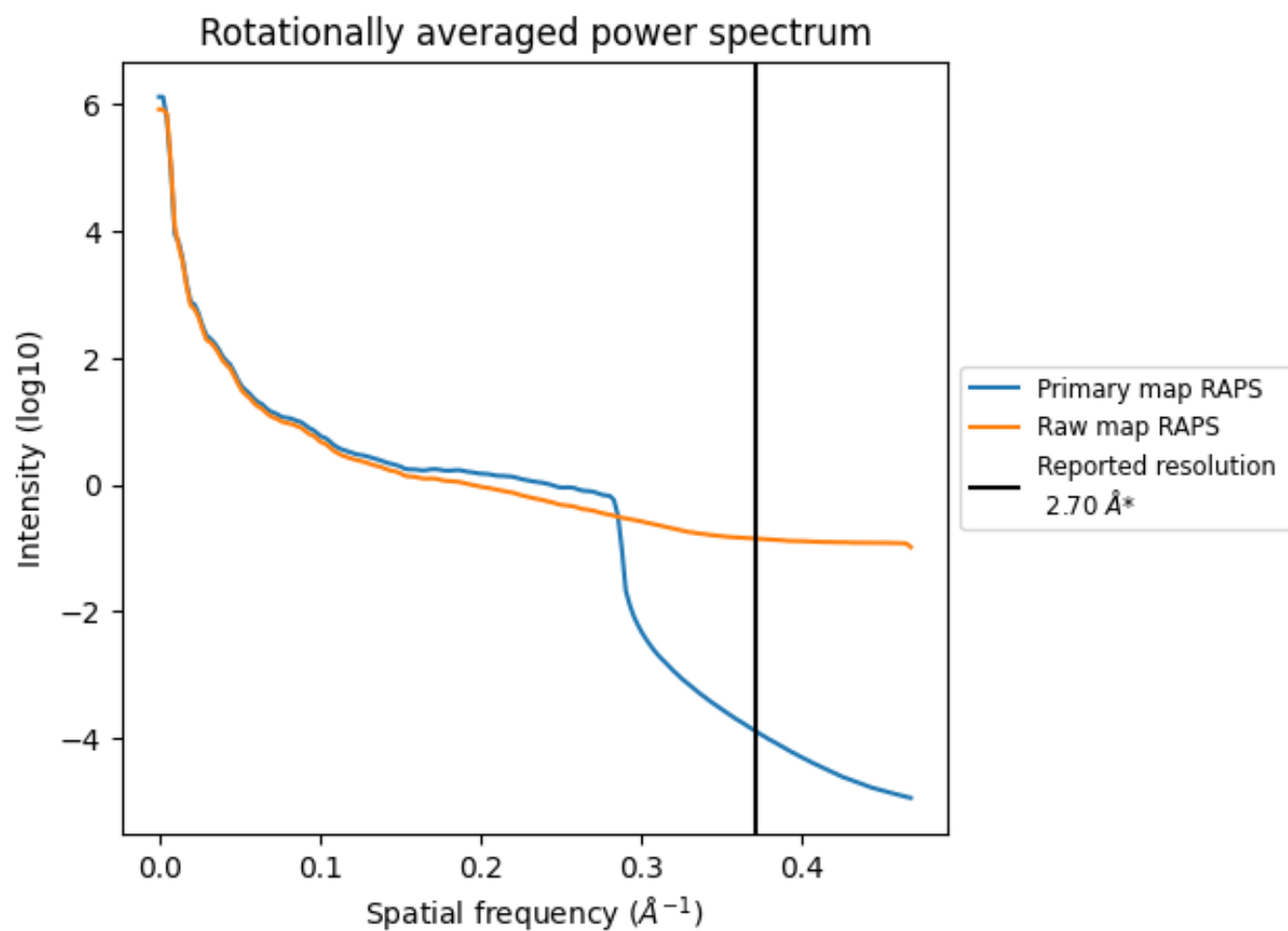
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1110 nm³; this corresponds to an approximate mass of 1002 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 ⓘ

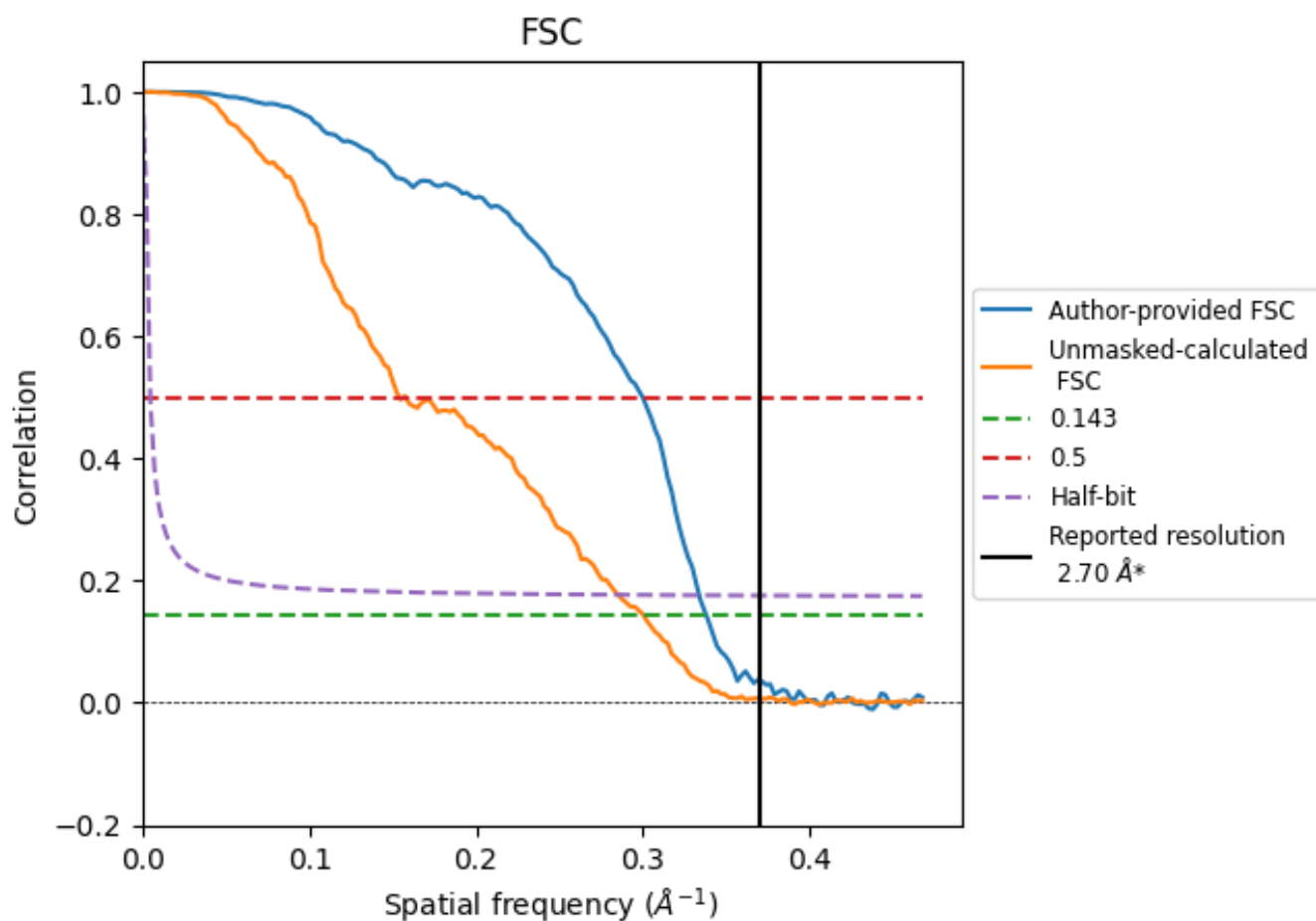


*Reported resolution corresponds to spatial frequency of 0.370 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.370 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

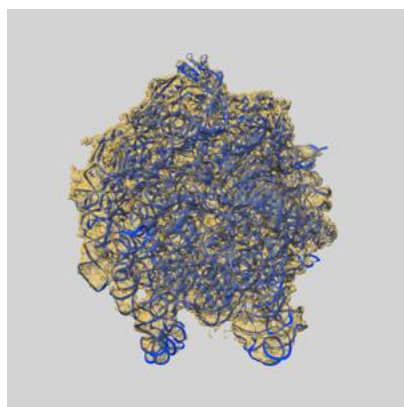
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.70	-	-
Author-provided FSC curve	2.96	3.33	3.00
Unmasked-calculated*	3.33	6.49	3.51

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.33 differs from the reported value 2.7 by more than 10 %

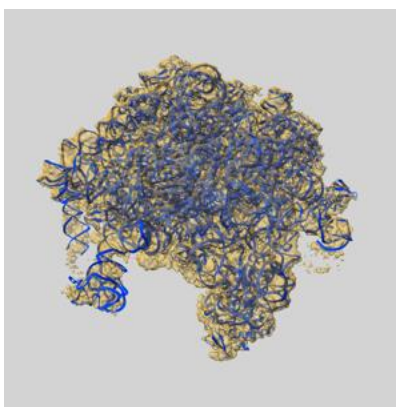
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-37560 and PDB model 8WI8. Per-residue inclusion information can be found in section [3](#) on page [9](#).

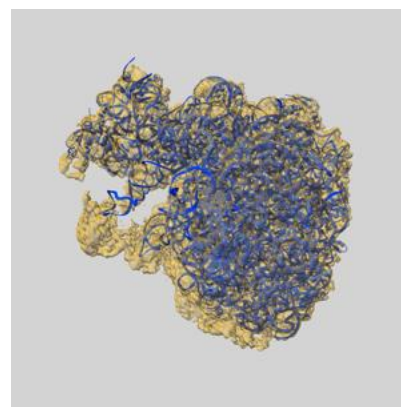
9.1 Map-model overlay [i](#)



X



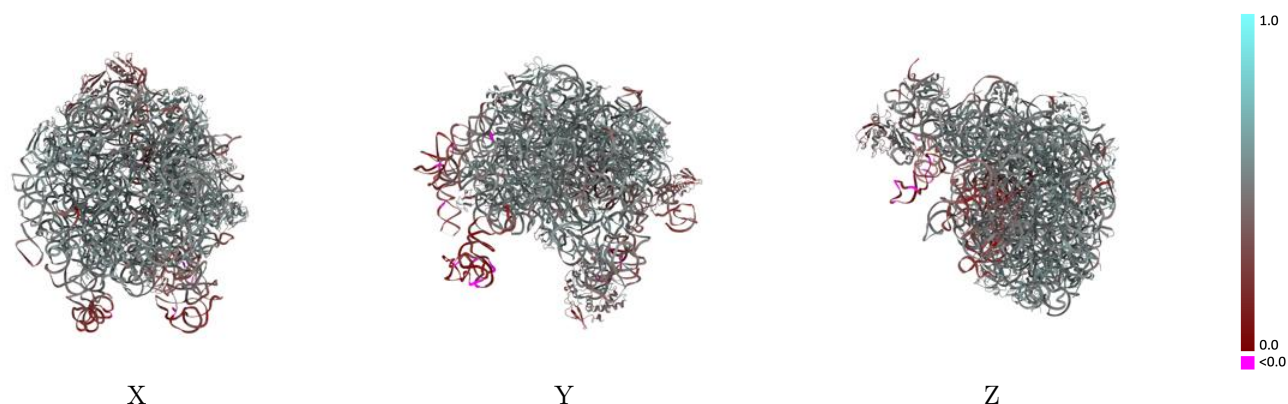
Y



Z

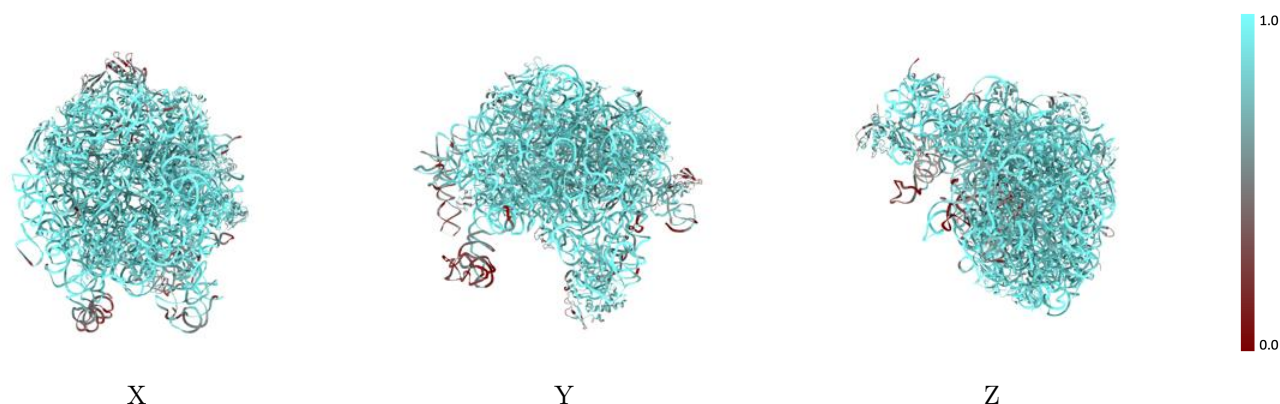
The images above show the 3D surface view of the map at the recommended contour level 0.045 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



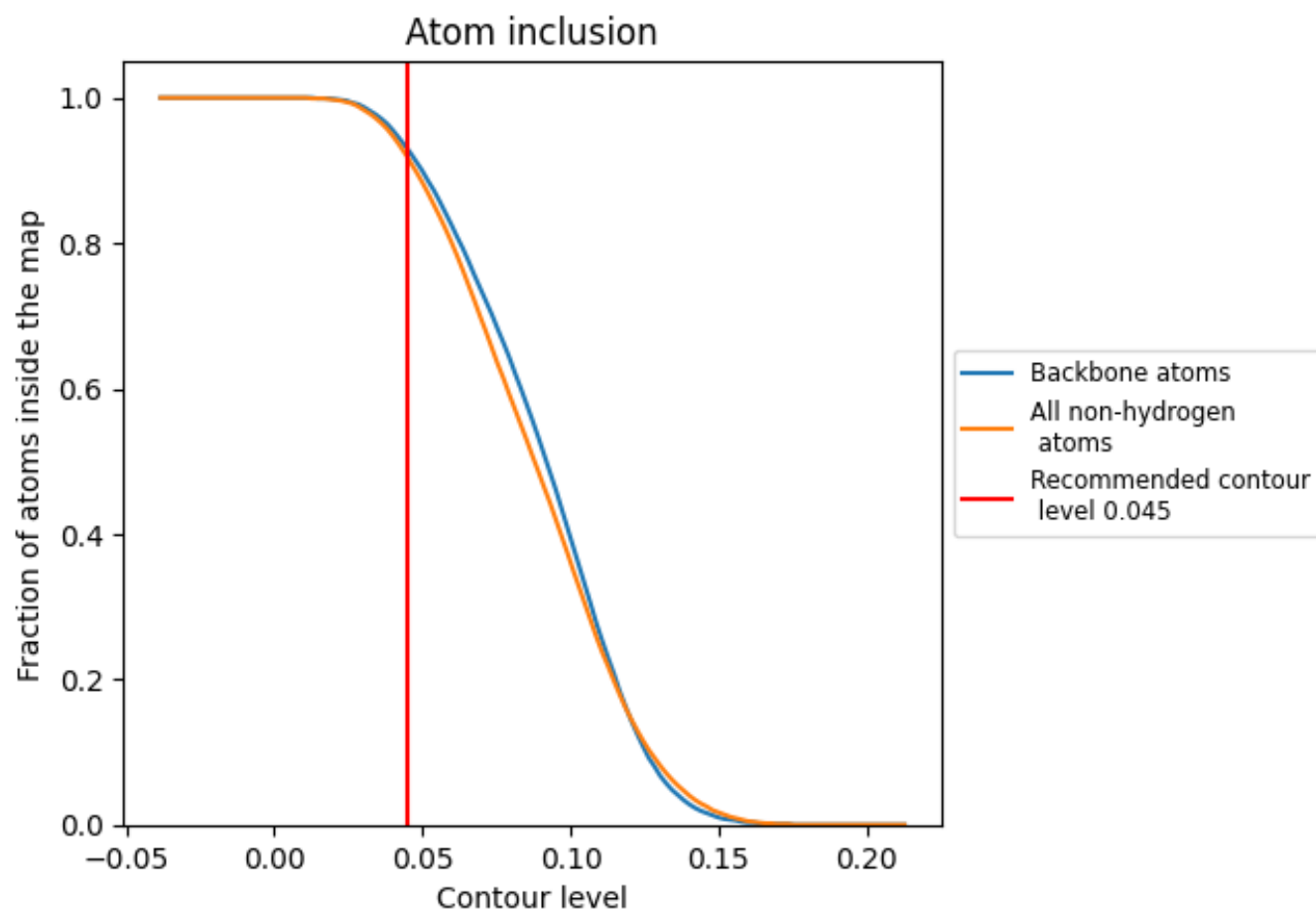
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.045).

9.4 Atom inclusion ⓘ



At the recommended contour level, 93% of all backbone atoms, 92% 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 (0.045) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9180	 0.4740
1	 0.8980	 0.4910
2	 0.8470	 0.4960
3	 0.9060	 0.5350
4	 0.5580	 0.2870
5	 0.8480	 0.5190
6	 0.7050	 0.4680
7	 0.9970	 0.5480
8	 0.9080	 0.5400
A	 0.9290	 0.4650
B	 0.9560	 0.4540
E	 0.9730	 0.5470
F	 0.9340	 0.5390
G	 0.8950	 0.5170
H	 0.8070	 0.4310
I	 0.5430	 0.3030
J	 0.6970	 0.4270
M	 0.9410	 0.5370
N	 0.9500	 0.5350
O	 0.8930	 0.5270
Q	 0.9700	 0.5470
R	 0.8190	 0.4670
S	 0.9330	 0.5260
T	 0.9540	 0.5340
U	 0.8940	 0.5500
V	 0.9690	 0.5430
W	 0.9060	 0.5270
X	 0.8350	 0.4990
Z	 0.9530	 0.5360

