



## Full wwPDB EM Validation Report ⓘ

Jul 2, 2026 – 06:08 PM JST

PDB ID : 9L9V / pdb\_0000919v  
EMDB ID : EMD-62914  
Title : State A of archaeal pre-50S ribosome  
Authors : Li, Z.Q.; Yang, X.Y.  
Deposited on : 2024-12-31  
Resolution : 2.77 Å (reported)

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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

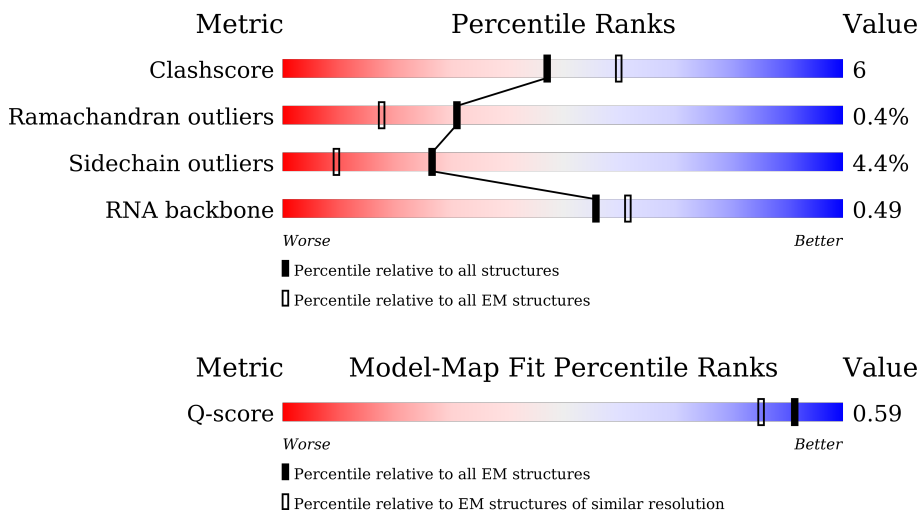
EMDB validation analysis : 0.0.1.dev133  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.50

# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:  
*ELECTRON MICROSCOPY*

The reported resolution of this entry is 2.77 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	10695 ( 2.27 - 3.27 )

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  $\geq 3$ , 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	0	2916	 8% 66% 24% 5% 5%
2	9	122	 8% 70% 20% 9% 5%
3	B	221	 8% 63% 33% 5% 5%

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Mol	Chain	Length	Quality of chain
4	E	120	71% 27% ..
5	F	176	79% 19% ..
6	G	196	80% 16% ...
7	H	116	76% 22% ..
8	I	184	81% 18% .
9	J	151	83% 16% .
10	K	96	85% 14% .
11	L	153	84% 15% .
12	M	67	72% 15% 13%
13	N	118	71% 25% ..
14	O	154	78% 21% .
15	P	92	82% 15% .
16	Q	234	50% 11% 39%
17	R	89	71% 18% • 10%
18	S	58	83% 16% .
19	T	93	88% 12%
20	U	241	76% 20% ..
21	V	338	87% 12% .
22	W	248	79% 19% .
23	X	172	15% 60% 37% ..
24	Y	178	75% 21% ..
25	b	145	84% 12% ..
26	f	132	78% 22%
27	i	406	40% 23% 6% 31%

## 2 Entry composition

There are 29 unique types of molecules in this entry. The entry contains 92125 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 RNA chain called 23S RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	0	2758	59124	26388	10885	19093	2758	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	9	120	2551	1138	453	840	120	0	0

- Molecule 3 is a protein called Translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	B	220	1612	993	273	342	4	0	0

- Molecule 4 is a protein called Large ribosomal subunit protein eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	E	119	880	546	141	192	1	0	0

- Molecule 5 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	F	174	1372	852	251	261	8	0	0

- Molecule 6 is a protein called Large ribosomal subunit protein eL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	G	193	1575	961	337	275	2	0	0

- Molecule 7 is a protein called Large ribosomal subunit protein eL18.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
7	H	115	887	544	167	176	0	0

- Molecule 8 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	I	183	1417	880	258	278	1	0	0

- Molecule 9 is a protein called Large ribosomal subunit protein eL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	J	150	1205	728	247	229	1	0	0

- Molecule 10 is a protein called Large ribosomal subunit protein eL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	K	95	736	451	150	133	2	0	0

- Molecule 11 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	L	151	1174	730	214	226	4	0	0

- Molecule 12 is a protein called Large ribosomal subunit protein eL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	M	58	466	287	83	94	2	0	0

- Molecule 13 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
13	N	114	903	545	171	187	0	0

- Molecule 14 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	O	154	Total	C	N	O	S	0	0
			1200	731	220	245	4		

- Molecule 15 is a protein called Large ribosomal subunit protein eL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	P	89	Total	C	N	O	S	0	0
			726	448	138	139	1		

- Molecule 16 is a protein called Large ribosomal subunit protein eL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Q	142	Total	C	N	O	S	0	0
			1146	698	231	216	1		

- Molecule 17 is a protein called Large ribosomal subunit protein eL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	R	80	Total	C	N	O	S	0	0
			617	374	125	117	1		

- Molecule 18 is a protein called Large ribosomal subunit protein eL37.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	S	57	Total	C	N	O	S	0	0
			439	265	90	80	4		

- Molecule 19 is a protein called Large ribosomal subunit protein eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	T	93	Total	C	N	O	S	0	0
			746	457	152	129	8		

- Molecule 20 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	U	235	Total	C	N	O	S	0	0
			1766	1089	349	323	5		

- Molecule 21 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	V	337	2619	1623	484	502	10	0	0

- Molecule 22 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	W	248	1898	1164	354	377	3	0	0

- Molecule 23 is a protein called Large ribosomal subunit protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	X	169	1308	808	229	268	3	0	0

- Molecule 24 is a protein called Large ribosomal subunit protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	Y	174	1346	832	228	283	3	0	0

- Molecule 25 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	b	144	1127	701	201	220	5	0	0

- Molecule 26 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	f	132	996	612	188	191	5	0	0

- Molecule 27 is a protein called CBS domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	i	281	2131	1331	364	432	4	1	0

- Molecule 28 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
28	0	140	Total 140	Mg 140	0
28	9	7	Total 7	Mg 7	0
28	G	3	Total 3	Mg 3	0
28	U	1	Total 1	Mg 1	0
28	V	3	Total 3	Mg 3	0
28	W	1	Total 1	Mg 1	0
28	f	1	Total 1	Mg 1	0

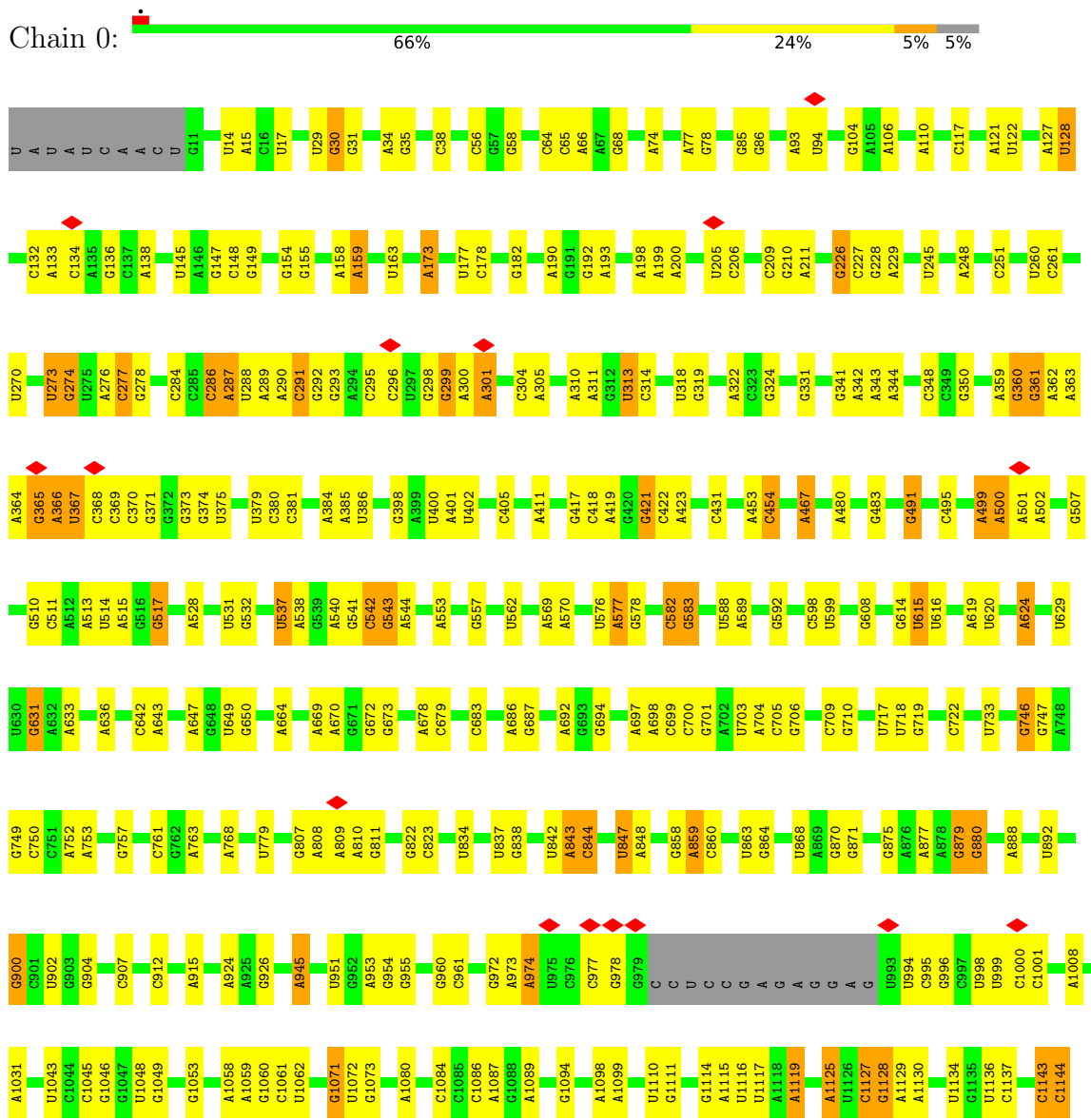
- Molecule 29 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

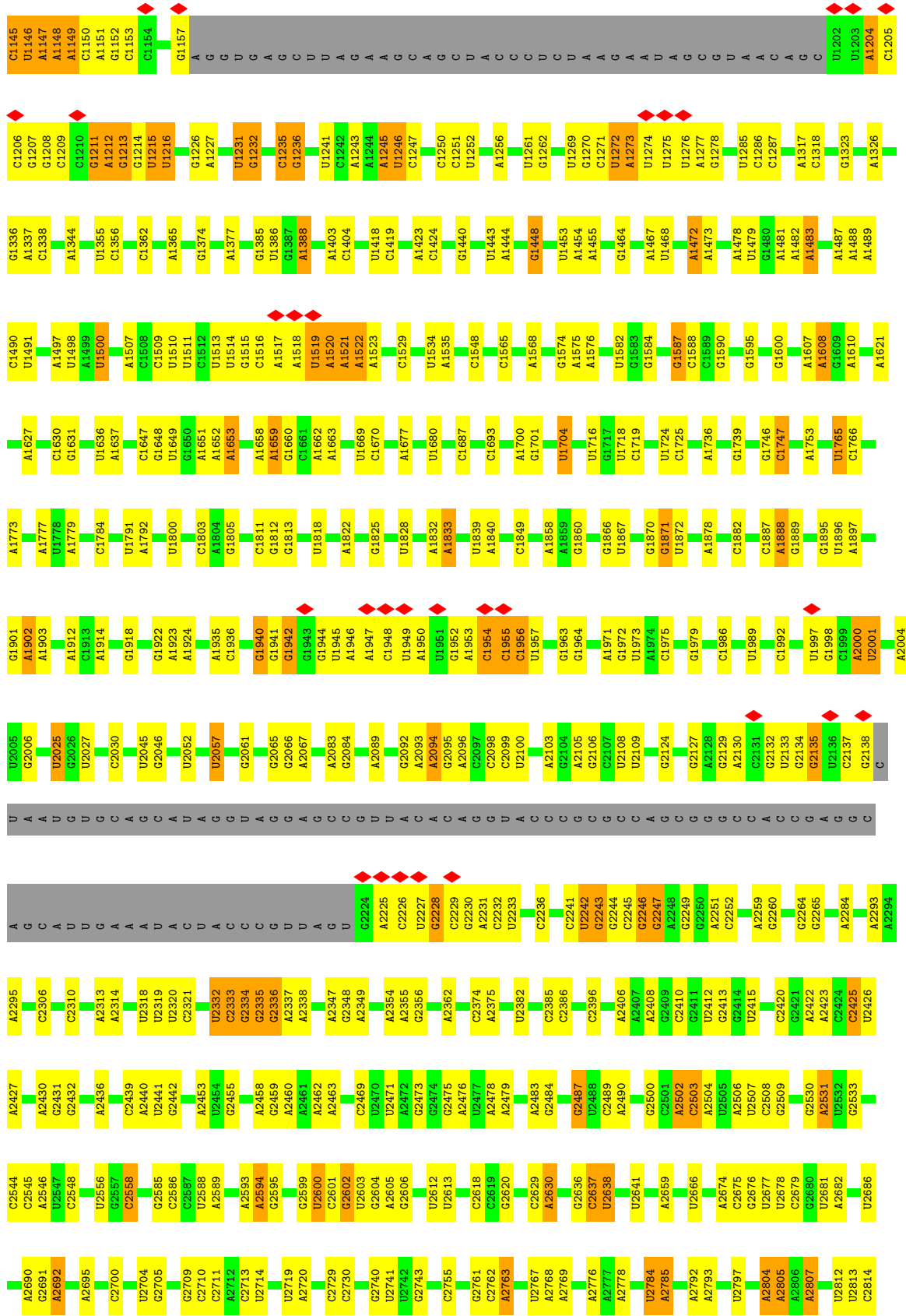
Mol	Chain	Residues	Atoms		AltConf
29	S	1	Total 1	Zn 1	0
29	T	1	Total 1	Zn 1	0

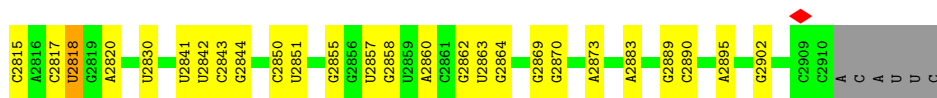
### 3 Residue-property plots

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: 23S RNA







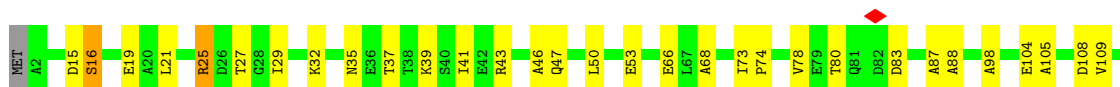
• Molecule 2: 5S RNA



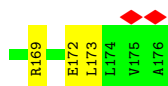
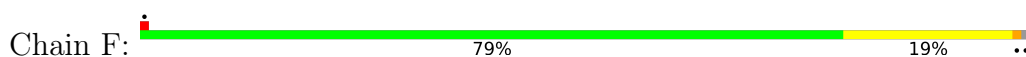
• Molecule 3: Translation initiation factor 6



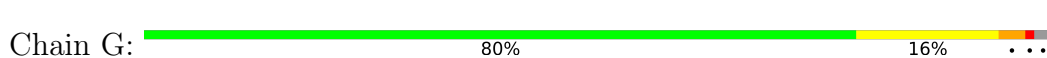
• Molecule 4: Large ribosomal subunit protein eL8



• Molecule 5: Large ribosomal subunit protein uL16

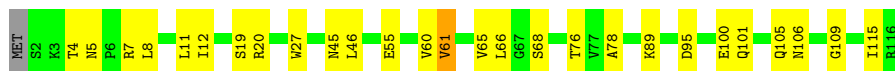


• Molecule 6: Large ribosomal subunit protein eL15

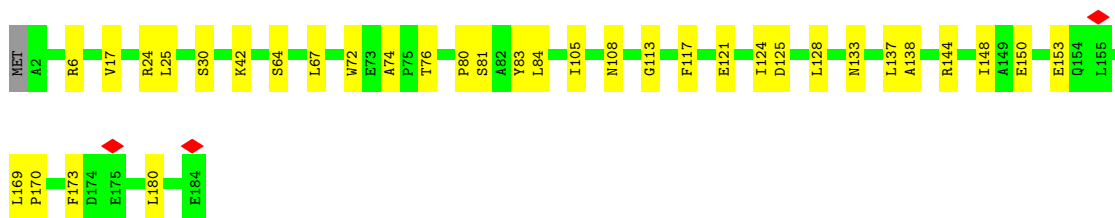
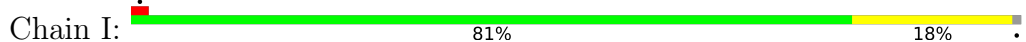




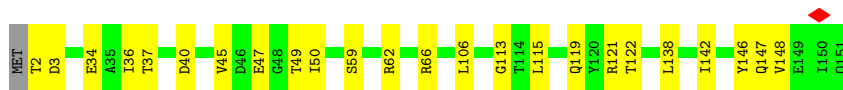
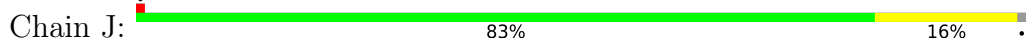
• Molecule 7: Large ribosomal subunit protein eL18



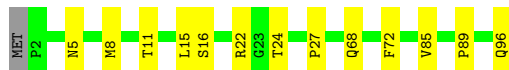
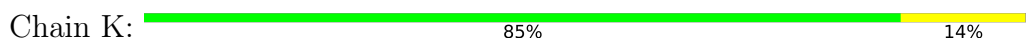
• Molecule 8: Large ribosomal subunit protein uL18



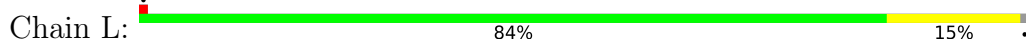
• Molecule 9: Large ribosomal subunit protein eL19



• Molecule 10: Large ribosomal subunit protein eL21



• Molecule 11: Large ribosomal subunit protein uL22



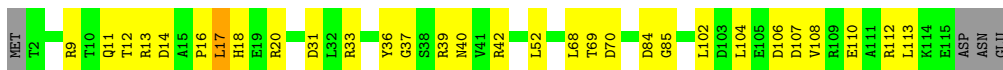
• Molecule 12: Large ribosomal subunit protein eL24





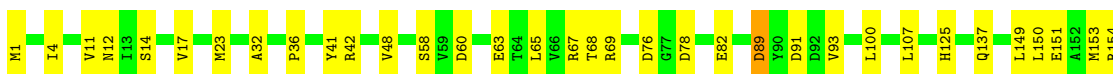
- Molecule 13: Large ribosomal subunit protein uL24

Chain N: 71% 25%



- Molecule 14: Large ribosomal subunit protein uL30

Chain O: 78% 21%



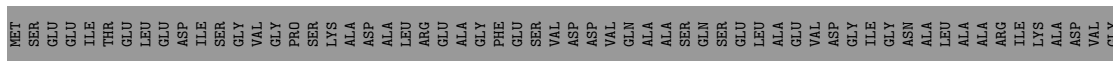
- Molecule 15: Large ribosomal subunit protein eL31

Chain P: 82% 15%



- Molecule 16: Large ribosomal subunit protein eL32

Chain Q: 50% 11% 39%



- Molecule 17: Large ribosomal subunit protein eL43

Chain R: 71% 18% 10%

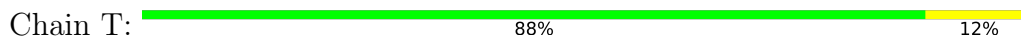


- Molecule 18: Large ribosomal subunit protein eL37

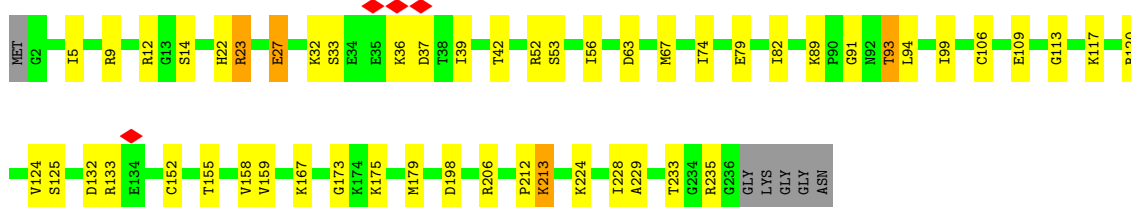
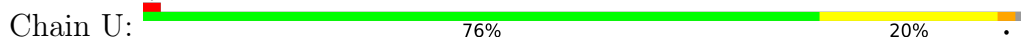
Chain S: 83% 16%



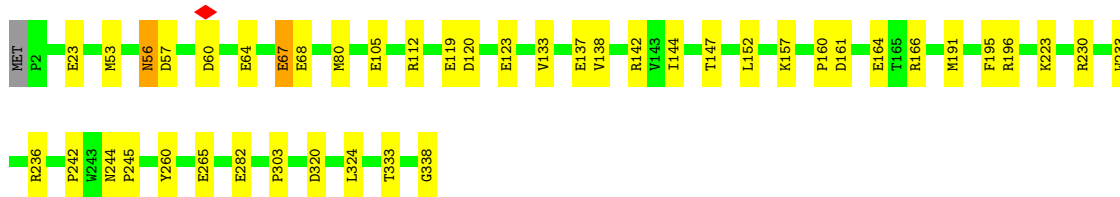
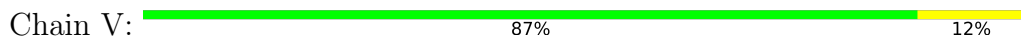
- Molecule 19: Large ribosomal subunit protein eL42



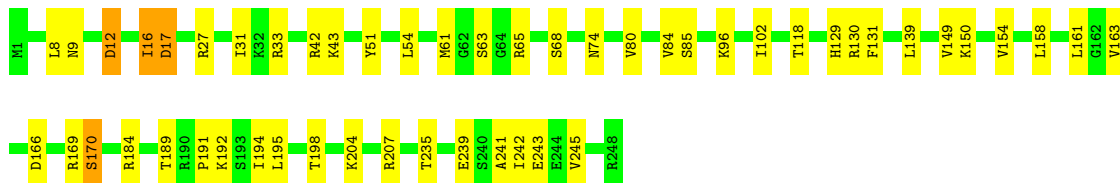
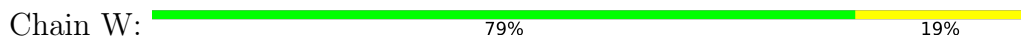
- Molecule 20: Large ribosomal subunit protein uL2



- Molecule 21: Large ribosomal subunit protein uL3



- Molecule 22: Large ribosomal subunit protein uL4

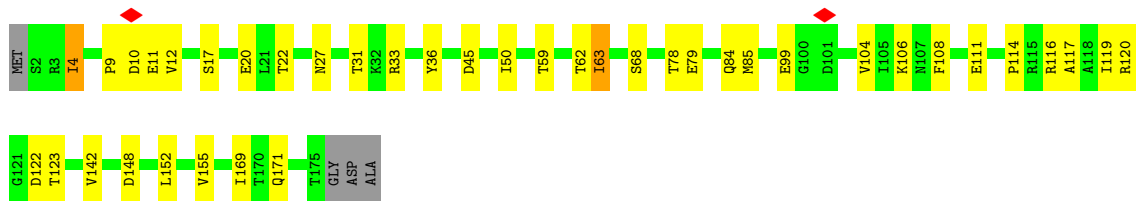
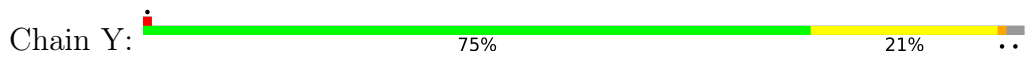


- Molecule 23: Large ribosomal subunit protein uL5

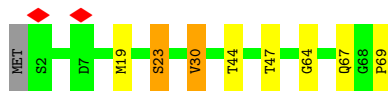
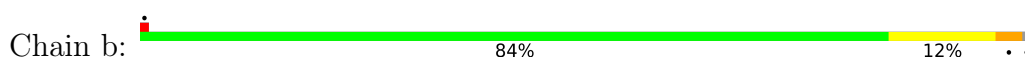




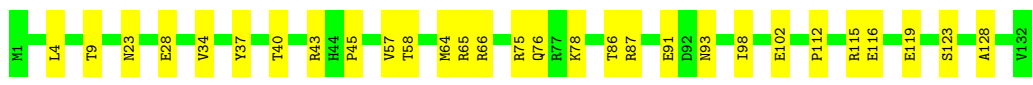
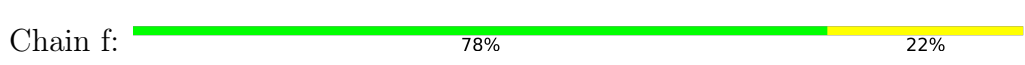
• Molecule 24: Large ribosomal subunit protein uL6



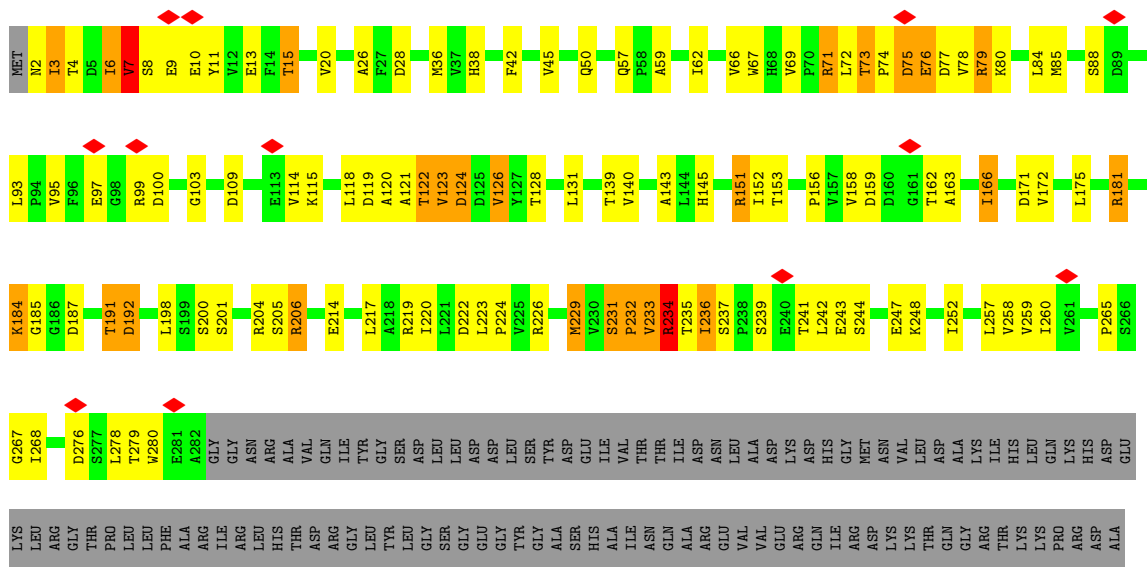
• Molecule 25: Large ribosomal subunit protein uL13



• Molecule 26: Large ribosomal subunit protein uL14



• Molecule 27: CBS domain-containing protein



GLU  
TYR  
TRP  
GLU  
LYS  
ARG  
PHE  
GLY  
TRP  
MET  
LEU  
GLU  
GLY  
GLU

## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	918876	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TECNAI F30	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	50	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	1.697	Depositor
Minimum map value	-0.986	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.059	Depositor
Recommended contour level	0.16	Depositor
Map size ( $\text{\AA}$ )	427.52, 427.52, 427.52	wwPDB
Map dimensions	640, 640, 640	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	0.668, 0.668, 0.668	Depositor

## 5 Model quality i

### 5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, MG

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	0	0.33	0/66202	0.37	0/103250
2	9	0.28	0/2848	0.33	0/4436
3	B	0.20	0/1631	0.40	0/2225
4	E	0.25	0/889	0.41	0/1209
5	F	0.29	0/1395	0.44	0/1875
6	G	0.31	0/1602	0.37	0/2140
7	H	0.27	0/895	0.43	0/1210
8	I	0.22	0/1447	0.38	0/1969
9	J	0.28	0/1217	0.41	0/1622
10	K	0.31	0/750	0.39	0/1001
11	L	0.29	0/1199	0.42	0/1619
12	M	0.27	0/474	0.35	0/634
13	N	0.27	0/911	0.36	0/1232
14	O	0.29	0/1218	0.41	0/1651
15	P	0.27	0/741	0.40	0/998
16	Q	0.29	0/1165	0.37	0/1561
17	R	0.30	0/624	0.45	0/835
18	S	0.30	0/446	0.47	0/586
19	T	0.25	0/764	0.36	0/1015
20	U	0.32	0/1800	0.47	0/2420
21	V	0.30	0/2677	0.39	0/3617
22	W	0.28	0/1925	0.39	0/2598
23	X	0.25	0/1329	0.55	0/1793
24	Y	0.24	0/1368	0.40	0/1859
25	b	0.30	0/1144	0.42	0/1541
26	f	0.27	0/1004	0.40	0/1347
27	i	0.60	2/2169 (0.1%)	0.83	4/2951 (0.1%)
All	All	0.33	2/99834 (0.0%)	0.39	4/149194 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected

by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
19	T	0	1
20	U	0	2
27	i	0	8
All	All	0	11

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
27	i	181[A]	ARG	C-O	6.35	1.31	1.23
27	i	181[B]	ARG	C-O	6.35	1.31	1.23

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
27	i	181[A]	ARG	CA-C-O	8.62	130.68	121.45
27	i	181[B]	ARG	CA-C-O	8.62	130.68	121.45
27	i	126	VAL	N-CA-C	-5.31	106.69	112.80
27	i	185	GLY	N-CA-C	-5.00	105.88	111.63

There are no chirality outliers.

All (11) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
19	T	42	ARG	Sidechain
20	U	23	ARG	Sidechain
20	U	235	ARG	Sidechain
27	i	151	ARG	Sidechain
27	i	181[A]	ARG	Sidechain
27	i	181[B]	ARG	Sidechain
27	i	204	ARG	Sidechain
27	i	206	ARG	Sidechain
27	i	234	ARG	Sidechain
27	i	71	ARG	Sidechain
27	i	79	ARG	Sidechain

## 5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen

atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	59124	0	29819	374	0
2	9	2551	0	1298	17	0
3	B	1612	0	1567	51	0
4	E	880	0	852	24	0
5	F	1372	0	1371	30	0
6	G	1575	0	1603	27	0
7	H	887	0	907	19	0
8	I	1417	0	1365	27	0
9	J	1205	0	1208	18	0
10	K	736	0	745	8	0
11	L	1174	0	1146	13	0
12	M	466	0	443	7	0
13	N	903	0	886	17	0
14	O	1200	0	1159	24	0
15	P	726	0	703	11	0
16	Q	1146	0	1146	16	0
17	R	617	0	618	10	0
18	S	439	0	445	7	0
19	T	746	0	736	5	0
20	U	1766	0	1799	31	0
21	V	2619	0	2572	33	0
22	W	1898	0	1895	33	0
23	X	1308	0	1251	44	0
24	Y	1346	0	1292	21	0
25	b	1127	0	1118	13	0
26	f	996	0	1046	25	0
27	i	2131	0	2117	93	0
28	0	140	0	0	0	0
28	9	7	0	0	0	0
28	G	3	0	0	0	0
28	U	1	0	0	0	0
28	V	3	0	0	0	0
28	W	1	0	0	0	0
28	f	1	0	0	0	0
29	S	1	0	0	0	0
29	T	1	0	0	0	0
All	All	92125	0	61107	906	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 6.

All (906) 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:i:234:ARG:NH2	27:i:252:ILE:HG21	1.42	1.33
5:F:27:PRO:HA	27:i:234:ARG:NH1	1.47	1.26
5:F:27:PRO:CA	27:i:234:ARG:HH12	1.48	1.25
27:i:11:TYR:CE1	27:i:13:GLU:OE2	1.94	1.20
27:i:115:LYS:HG3	27:i:243:GLU:HG3	1.30	1.11
5:F:27:PRO:HB3	27:i:234:ARG:HH11	1.10	1.10
5:F:27:PRO:CA	27:i:234:ARG:NH1	2.09	1.10
5:F:27:PRO:CB	27:i:234:ARG:NH1	2.27	0.98
5:F:27:PRO:CB	27:i:234:ARG:HH11	1.76	0.97
27:i:236:ILE:HG23	27:i:259:VAL:HG12	1.45	0.96
27:i:234:ARG:NH2	27:i:252:ILE:CG2	2.29	0.95
1:0:1519:U:H3'	1:0:1520:A:H5''	1.50	0.94
27:i:11:TYR:HE1	27:i:13:GLU:OE2	1.40	0.92
1:0:1116:U:H3	1:0:1245:A:H61	1.07	0.89
5:F:27:PRO:HB3	27:i:234:ARG:NH1	1.85	0.88
27:i:234:ARG:HH21	27:i:252:ILE:HG21	1.07	0.88
5:F:27:PRO:HA	27:i:234:ARG:HH12	0.70	0.86
1:0:1115:A:N1	1:0:1246:U:C5	2.45	0.84
1:0:1736:A:H61	1:0:2030:C:H42	1.24	0.83
1:0:1116:U:H3	1:0:1245:A:N6	1.76	0.83
1:0:1146:U:H4'	1:0:1147:A:H5''	1.60	0.83
1:0:1519:U:H3'	1:0:1520:A:C5'	2.11	0.80
5:F:104:THR:HG21	27:i:226:ARG:HD3	1.63	0.80
3:B:87:LEU:HD22	3:B:88:PRO:HD2	1.60	0.80
6:G:191:SER:C	6:G:193:ARG:H	1.90	0.79
27:i:115:LYS:HG3	27:i:243:GLU:CG	2.10	0.78
1:0:1115:A:C2	1:0:1246:U:H5	2.01	0.78
14:O:58:SER:OG	14:O:60:ASP:OD1	2.02	0.77
3:B:161:ARG:HG2	3:B:163:PRO:HD2	1.68	0.76
1:0:159:A:H5'	18:S:58:ASN:HB3	1.66	0.76
1:0:421:G:OP2	1:0:2436:A:O2'	2.01	0.76
9:J:37:THR:OG1	9:J:40:ASP:OD1	2.03	0.76
7:H:101:GLN:OE1	7:H:105:GLN:NE2	2.19	0.76
1:0:359:A:H3'	1:0:360:G:H5''	1.66	0.76
3:B:195:ASN:O	3:B:219:TYR:OH	2.05	0.75
23:X:30:LEU:HD21	23:X:47:ARG:HD2	1.67	0.75
1:0:2245:C:C2	1:0:2246:G:H1'	2.22	0.74
1:0:499:A:N1	1:0:1386:U:C4	2.55	0.74
21:V:137:GLU:N	21:V:137:GLU:OE1	2.21	0.74
1:0:295:C:N3	1:0:367:U:O4	2.21	0.73
27:i:234:ARG:HH22	27:i:252:ILE:HG21	1.50	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1115:A:N1	1:0:1246:U:C4	2.56	0.73
11:L:114:HIS:HB3	11:L:147:ILE:HG12	1.68	0.73
23:X:71:LEU:HD13	23:X:76:ALA:HA	1.70	0.73
14:O:125:HIS:HB2	14:O:137:GLN:HE21	1.54	0.73
5:F:172:GLU:OE2	5:F:172:GLU:N	2.22	0.73
21:V:133:VAL:HG22	21:V:138:VAL:HG21	1.71	0.72
11:L:114:HIS:NE2	11:L:145:GLU:OE2	2.20	0.72
27:i:231:SER:O	27:i:232:PRO:C	2.32	0.72
1:0:1115:A:N1	1:0:1246:U:H5	1.86	0.72
1:0:2700:C:O2'	21:V:60:ASP:OD2	2.08	0.71
1:0:1144:C:H3'	1:0:1145:C:H6	1.55	0.71
10:K:11:THR:HB	10:K:15:LEU:HD12	1.72	0.70
1:0:1385:G:N2	1:0:1388:A:OP2	2.23	0.70
3:B:154:VAL:HG13	3:B:174:VAL:HG21	1.73	0.70
1:0:348:C:OP1	13:N:40:ASN:ND2	2.24	0.70
2:9:7:G:OP1	8:I:24:ARG:NH1	2.25	0.70
13:N:42:ARG:HH21	13:N:68:LEU:HD21	1.56	0.70
15:P:47:GLU:N	15:P:47:GLU:OE1	2.21	0.70
16:Q:90:GLU:N	16:Q:230:VAL:O	2.25	0.70
3:B:107:ASP:OD1	3:B:151:ASN:ND2	2.25	0.70
1:0:38:C:H5'	13:N:13:ARG:HH12	1.58	0.69
23:X:132:ARG:HH21	23:X:159:VAL:HG11	1.57	0.69
23:X:84:LEU:HG	23:X:168:VAL:HG21	1.75	0.68
1:0:1636:U:H2'	1:0:1637:A:H8	1.59	0.68
5:F:70:LEU:O	5:F:74:ARG:HG3	1.94	0.68
1:0:582:C:O2'	1:0:583:G:OP1	2.12	0.68
1:0:2094:A:H5'	22:W:63:SER:HB3	1.76	0.68
1:0:2336:G:OP2	1:0:2336:G:N2	2.26	0.67
1:0:2713:C:O2	26:f:87:ARG:NH2	2.28	0.67
1:0:299:G:O6	1:0:301:A:N6	2.23	0.67
3:B:152:ARG:NH2	3:B:218:ASP:O	2.26	0.67
21:V:23:GLU:OE2	21:V:260:TYR:OH	2.08	0.67
1:0:360:G:O2'	1:0:361:G:N3	2.26	0.67
23:X:74:GLU:N	23:X:74:GLU:OE2	2.27	0.67
3:B:19:THR:HG22	3:B:22:VAL:HG12	1.76	0.67
3:B:21:ASP:OD1	3:B:21:ASP:N	2.26	0.67
3:B:61:THR:HG23	3:B:100:GLY:HA2	1.76	0.67
1:0:624:A:O2'	16:Q:126:ASP:OD2	2.12	0.66
24:Y:123:THR:HG23	24:Y:142:VAL:HG22	1.78	0.66
27:i:260:ILE:HG22	27:i:265:PRO:HA	1.77	0.66
1:0:1887:C:H4'	1:0:1888:A:H5''	1.77	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:X:137:VAL:HA	23:X:140:ARG:HE	1.61	0.66
1:O:1736:A:H61	1:O:2030:C:N4	1.93	0.66
7:H:7:ARG:HH12	7:H:11:LEU:HD22	1.61	0.66
4:E:41:ILE:HD11	4:E:68:ALA:HA	1.77	0.66
16:Q:113:GLN:NE2	16:Q:117:GLU:OE2	2.29	0.66
25:b:131:SER:OG	25:b:134:GLU:OE2	2.14	0.66
6:G:191:SER:C	6:G:193:ARG:N	2.52	0.66
6:G:157:ASP:O	6:G:162:ARG:NH1	2.29	0.65
9:J:146:TYR:O	9:J:147:GLN:NE2	2.29	0.65
3:B:13:GLY:H	3:B:191:GLY:HA2	1.60	0.65
14:O:100:LEU:HD11	14:O:107:LEU:HD21	1.77	0.65
27:i:123:VAL:HG12	27:i:241:THR:H	1.60	0.65
3:B:102:VAL:HB	3:B:113:HIS:HB2	1.78	0.65
1:O:2804:A:H4'	1:O:2805:A:H5'	1.77	0.65
14:O:89:ASP:OD1	14:O:89:ASP:N	2.24	0.65
1:O:1701:G:N1	1:O:1704:U:OP2	2.30	0.65
1:O:2083:A:H2'	1:O:2084:G:C8	2.32	0.65
23:X:130:ILE:HG22	23:X:153:MET:HE3	1.79	0.65
1:O:1700:A:OP1	9:J:66:ARG:NH1	2.30	0.65
1:O:56:C:O2	18:S:46:ARG:NH1	2.30	0.64
1:O:1489:A:O2'	1:O:1500:U:O2	2.15	0.64
2:9:18:U:O2	2:9:61:G:O6	2.15	0.64
23:X:12:PRO:HG3	23:X:159:VAL:HB	1.80	0.64
20:U:212:PRO:O	20:U:213:LYS:HB2	1.97	0.64
1:O:14:U:H2'	1:O:15:A:C8	2.33	0.64
1:O:537:U:OP2	1:O:2807:A:N6	2.29	0.64
1:O:1902:A:H2'	1:O:1903:A:C8	2.32	0.64
17:R:49:THR:HG23	17:R:65:THR:HG23	1.80	0.64
11:L:112:ILE:HA	11:L:148:ILE:HG22	1.80	0.64
25:b:121:LEU:HD11	25:b:126:ASN:HD22	1.62	0.63
9:J:34:GLU:N	9:J:34:GLU:OE2	2.30	0.63
23:X:165:THR:HB	23:X:170:VAL:HG13	1.81	0.63
1:O:1649:U:N3	17:R:48:GLU:OE1	2.31	0.63
1:O:1736:A:N6	1:O:2030:C:H42	1.95	0.63
5:F:110:ARG:HD3	27:i:220:ILE:HD11	1.81	0.63
3:B:165:LEU:O	3:B:169:GLU:HG2	1.98	0.63
21:V:56:ASN:HB3	21:V:64:GLU:HA	1.79	0.63
24:Y:108:PHE:O	24:Y:111:GLU:HG3	1.99	0.63
20:U:56:ILE:HD12	20:U:67:MET:HG2	1.80	0.62
1:O:2487:G:N2	5:F:103:ALA:O	2.32	0.62
3:B:121:VAL:HG13	3:B:132:VAL:HG11	1.80	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:163:U:OP2	6:G:189:SER:OG	2.18	0.62
1:0:2763:A:H61	1:0:2797:U:H3	1.47	0.62
1:0:694:G:N3	1:0:733:U:O2'	2.32	0.62
8:I:72:TRP:NE1	8:I:74:ALA:O	2.33	0.62
26:f:115:ARG:O	26:f:119:GLU:HG2	1.99	0.62
1:0:1129:A:H2'	1:0:1130:A:C8	2.34	0.62
3:B:81:LEU:O	3:B:85:VAL:HG22	1.99	0.62
1:0:2319:U:H2'	1:0:2320:U:C6	2.34	0.62
8:I:6:ARG:O	10:K:22:ARG:NH2	2.33	0.62
13:N:20:ARG:NH2	13:N:69:THR:O	2.31	0.62
4:E:37:THR:HG23	4:E:98:ALA:HB2	1.81	0.61
7:H:55:GLU:N	7:H:55:GLU:OE1	2.33	0.61
1:0:2243:G:H3'	1:0:2244:G:H8	1.64	0.61
16:Q:210:ARG:HG3	16:Q:210:ARG:HH11	1.65	0.61
1:0:2556:U:H2'	1:0:2558:C:H5''	1.82	0.61
23:X:102:PHE:HB2	23:X:126:VAL:HG12	1.83	0.61
1:0:1144:C:H3'	1:0:1145:C:C6	2.35	0.61
1:0:1940:G:H2'	1:0:1941:G:C8	2.36	0.61
1:0:2730:C:OP2	9:J:62:ARG:NH2	2.33	0.61
2:9:38:U:O2'	2:9:43:A:N6	2.34	0.61
9:J:119:GLN:HB3	9:J:146:TYR:CE2	2.36	0.61
5:F:84:GLN:N	5:F:84:GLN:OE1	2.33	0.60
20:U:224:LYS:HD2	20:U:228:ILE:HG23	1.82	0.60
3:B:114:THR:HA	3:B:134:ARG:HB3	1.83	0.60
25:b:19:MET:O	25:b:23:SER:OG	2.18	0.60
27:i:235:THR:O	27:i:248:LYS:NZ	2.33	0.60
1:0:499:A:O2'	1:0:500:A:OP1	2.17	0.60
1:0:1636:U:H2'	1:0:1637:A:C8	2.35	0.60
1:0:1765:U:O2'	17:R:24:ARG:NH2	2.32	0.60
22:W:27:ARG:O	22:W:31:ILE:HG13	2.02	0.60
1:0:2134:G:N2	1:0:2228:G:O2'	2.34	0.60
1:0:2000:A:N3	1:0:2620:G:O2'	2.33	0.60
1:0:2057:U:O2	25:b:67:GLN:NE2	2.35	0.60
1:0:1953:A:H2'	1:0:1954:C:C5	2.36	0.60
13:N:106:ASP:OD1	13:N:106:ASP:N	2.35	0.60
27:i:231:SER:O	27:i:233:VAL:N	2.35	0.60
3:B:74:THR:HG22	3:B:76:ARG:H	1.67	0.59
12:M:46:GLU:HG3	12:M:48:ARG:HG2	1.83	0.59
21:V:56:ASN:ND2	21:V:68:GLU:OE1	2.35	0.59
1:0:1548:C:HO2'	1:0:1627:A:HO2'	1.51	0.59
23:X:95:ASP:OD1	23:X:96:GLU:N	2.34	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1115:A:C2	1:0:1246:U:C5	2.88	0.59
27:i:57:GLN:O	27:i:59:ALA:N	2.32	0.59
27:i:234:ARG:HH22	27:i:252:ILE:CG2	2.08	0.59
1:0:1818:U:O2'	1:0:1992:C:OP1	2.17	0.59
1:0:1953:A:H2'	1:0:1954:C:H5	1.68	0.59
8:I:150:GLU:OE2	8:I:150:GLU:N	2.36	0.59
19:T:11:CYS:HB2	19:T:20:HIS:CE1	2.38	0.59
24:Y:117:ALA:HB2	24:Y:152:LEU:HD22	1.84	0.58
27:i:6:ILE:HG21	27:i:109:ASP:HB3	1.84	0.58
1:0:2318:U:H2'	1:0:2319:U:C6	2.38	0.58
21:V:142:ARG:HG2	21:V:166:ARG:HA	1.84	0.58
1:0:945:A:C6	14:O:23:MET:HE3	2.38	0.58
1:0:1998:G:O2'	1:0:2001:U:OP1	2.17	0.58
1:0:2129:G:N2	1:0:2130:A:H62	2.01	0.58
3:B:136:ASP:OD1	3:B:136:ASP:N	2.37	0.58
1:0:86:G:H22	1:0:104:G:H1'	1.67	0.58
23:X:105:GLU:HA	23:X:123:GLY:HA2	1.84	0.58
1:0:1116:U:N3	1:0:1245:A:N6	2.39	0.58
1:0:2855:G:H4'	21:V:338:GLY:HA2	1.86	0.58
8:I:64:SER:OG	8:I:76:THR:HB	2.04	0.58
1:0:2841:U:OP2	21:V:112:ARG:NH2	2.35	0.58
23:X:162:ILE:HD12	23:X:163:GLU:N	2.18	0.58
3:B:63:ASN:ND2	3:B:128:LEU:O	2.34	0.58
4:E:39:LYS:O	4:E:43:ARG:HG3	2.04	0.58
23:X:86:ILE:HG23	23:X:109:GLU:HG2	1.84	0.58
24:Y:120:ARG:NH2	24:Y:148:ASP:OD2	2.37	0.58
11:L:9:ALA:HB2	11:L:147:ILE:HD12	1.86	0.57
22:W:170:SER:OG	22:W:191:PRO:O	2.22	0.57
24:Y:27:ASN:ND2	24:Y:27:ASN:O	2.36	0.57
1:0:847:U:OP1	18:S:6:THR:OG1	2.15	0.57
1:0:2439:C:H2'	1:0:2440:A:H8	1.69	0.57
24:Y:84:GLN:HB2	24:Y:171:GLN:HB3	1.87	0.57
1:0:454:C:OP1	22:W:184:ARG:NH1	2.36	0.57
1:0:1658:A:H5''	1:0:1659:A:H2'	1.85	0.57
23:X:164:SER:O	23:X:168:VAL:HG22	2.05	0.57
27:i:236:ILE:HG13	27:i:237:SER:H	1.69	0.57
1:0:304:C:H2'	1:0:305:A:C8	2.39	0.57
1:0:1472:A:H8	1:0:1860:G:O2'	1.87	0.57
1:0:1902:A:H2'	1:0:1903:A:H8	1.70	0.57
1:0:2105:A:H2'	1:0:2106:G:C8	2.39	0.57
1:0:2629:C:O2'	1:0:2630:A:OP1	2.23	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:Q:90:GLU:HG3	16:Q:92:ARG:HH11	1.69	0.57
1:0:1261:U:H2'	1:0:1262:G:H8	1.70	0.57
1:0:1152:G:H2'	1:0:1153:C:C6	2.40	0.57
22:W:169:ARG:NH2	22:W:192:LYS:O	2.37	0.57
27:i:38:HIS:HA	27:i:42:PHE:HA	1.85	0.57
1:0:417:G:H2'	1:0:418:C:C6	2.39	0.57
1:0:1662:A:H2'	1:0:1663:A:C8	2.40	0.57
4:E:37:THR:O	4:E:41:ILE:HG22	2.05	0.56
3:B:101:ASN:ND2	26:f:128:ALA:O	2.36	0.56
1:0:642:C:H2'	1:0:643:A:C8	2.41	0.56
3:B:98:ALA:HB1	3:B:101:ASN:HB2	1.86	0.56
17:R:43:ASN:HB2	17:R:55:GLU:HG3	1.87	0.56
27:i:3:ILE:HG13	27:i:77:ASP:HA	1.87	0.56
27:i:6:ILE:O	27:i:7:VAL:C	2.49	0.56
1:0:1520:A:H1'	1:0:1521:A:C5	2.40	0.56
1:0:2245:C:C4	1:0:2246:G:H1'	2.41	0.56
3:B:137:LEU:HD11	3:B:168:LEU:HD11	1.87	0.56
1:0:300:A:H1'	1:0:301:A:C8	2.40	0.56
4:E:21:LEU:HD13	4:E:50:LEU:HD13	1.88	0.55
1:0:1241:U:OP2	25:b:47:THR:OG1	2.25	0.55
27:i:114:VAL:HG11	27:i:278:LEU:HD12	1.89	0.55
1:0:277:C:H5'	1:0:278:G:H5'	1.88	0.55
1:0:1116:U:C2	1:0:1245:A:N6	2.75	0.55
1:0:2243:G:H3'	1:0:2244:G:C8	2.42	0.55
26:f:75:ARG:NH1	26:f:112:PRO:O	2.38	0.55
20:U:36:LYS:HD3	20:U:39:ILE:HD11	1.88	0.55
21:V:144:ILE:HG12	21:V:164:GLU:HG3	1.88	0.55
22:W:129:HIS:ND1	22:W:166:ASP:OD2	2.36	0.55
23:X:19:VAL:HG22	23:X:126:VAL:HG23	1.89	0.55
1:0:200:A:O2'	1:0:431:C:O2	2.20	0.55
1:0:2245:C:N3	1:0:2246:G:H1'	2.22	0.55
2:9:76:A:H4'	2:9:77:G:OP1	2.07	0.55
1:0:863:U:O2'	1:0:1483:A:N6	2.40	0.55
2:9:22:G:O2'	2:9:23:U:O5'	2.18	0.55
27:i:131:LEU:HB3	27:i:267:GLY:HA2	1.89	0.55
13:N:108:VAL:HG12	13:N:112:ARG:HH21	1.72	0.55
22:W:149:VAL:HG23	22:W:150:LYS:HG3	1.89	0.55
24:Y:85:MET:HE3	24:Y:169:ILE:HG13	1.88	0.55
21:V:157:LYS:NZ	21:V:161:ASP:OD2	2.32	0.54
27:i:45:VAL:HG23	27:i:69:VAL:HG21	1.89	0.54
1:0:1510:U:H2'	1:0:1511:U:C6	2.43	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:2319:U:H2'	1:0:2320:U:H6	1.71	0.54
22:W:8:LEU:HD12	22:W:8:LEU:H	1.71	0.54
20:U:32:LYS:HE3	20:U:113:GLY:HA2	1.90	0.54
1:0:1520:A:H1'	1:0:1521:A:C6	2.43	0.54
1:0:1534:U:H2'	1:0:1535:A:C8	2.42	0.54
1:0:1647:C:N4	20:U:167:LYS:O	2.40	0.54
4:E:108:ASP:O	4:E:112:ILE:HD12	2.07	0.54
5:F:82:GLU:HG2	5:F:83:LYS:HG2	1.88	0.54
27:i:156:PRO:HD3	27:i:268:ILE:HD12	1.88	0.54
27:i:224:PRO:HB2	27:i:226:ARG:HG2	1.88	0.54
1:0:499:A:N1	1:0:1386:U:N3	2.55	0.54
1:0:1509:C:H2'	1:0:1510:U:C6	2.42	0.54
3:B:51:GLY:O	26:f:115:ARG:NH1	2.41	0.54
5:F:30:LYS:HG3	5:F:62:HIS:CE1	2.43	0.54
20:U:52:ARG:NH1	20:U:120:ARG:O	2.40	0.54
25:b:115:MET:HE3	25:b:120:SER:HB3	1.90	0.54
1:0:398:G:N1	6:G:182:GLU:OE1	2.29	0.54
1:0:1115:A:N1	1:0:1246:U:O4	2.41	0.54
14:O:4:ILE:O	14:O:32:ALA:HA	2.08	0.54
9:J:47:GLU:OE2	9:J:49:THR:OG1	2.25	0.54
16:Q:94:ARG:NH1	16:Q:212:GLU:OE1	2.41	0.54
1:0:417:G:H2'	1:0:418:C:H6	1.73	0.54
7:H:106:ASN:OD1	7:H:109:GLY:N	2.40	0.54
18:S:26:LYS:O	18:S:26:LYS:HD3	2.08	0.54
20:U:36:LYS:NZ	20:U:37:ASP:H	2.06	0.54
22:W:241:ALA:O	22:W:245:VAL:HG13	2.07	0.54
26:f:4:LEU:HD22	26:f:116:GLU:HB3	1.89	0.54
12:M:45:ARG:HD2	12:M:50:LEU:HD21	1.90	0.54
24:Y:22:THR:OG1	24:Y:31:THR:HG22	2.08	0.54
24:Y:78:THR:HG22	24:Y:79:GLU:HG3	1.90	0.54
1:0:1157:G:H21	1:0:1204:A:H62	1.55	0.53
8:I:84:LEU:HD12	8:I:180:LEU:HD12	1.90	0.53
14:O:68:THR:HG22	14:O:69:ARG:HG2	1.90	0.53
25:b:64:GLY:HA2	25:b:69:PRO:HD2	1.90	0.53
27:i:236:ILE:HG13	27:i:237:SER:N	2.23	0.53
7:H:61:VAL:HG21	7:H:65:VAL:HG23	1.90	0.53
23:X:78:GLU:O	23:X:82:THR:HG23	2.08	0.53
1:0:1323:G:N2	1:0:1326:A:OP2	2.34	0.53
1:0:1534:U:H2'	1:0:1535:A:H8	1.72	0.53
1:0:38:C:OP2	13:N:9:ARG:NH1	2.41	0.53
1:0:1896:U:O2'	1:0:1897:A:H8	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:9:48:G:H5'	8:I:148:ILE:HD11	1.91	0.53
3:B:178:ILE:O	3:B:212:ARG:NH1	2.39	0.53
10:K:8:MET:O	10:K:11:THR:OG1	2.24	0.53
10:K:72:PHE:HE2	10:K:89:PRO:HG3	1.71	0.53
19:T:5:ARG:NH2	19:T:93:GLU:OE2	2.40	0.53
1:0:2483:A:H2'	1:0:2484:G:H8	1.74	0.53
5:F:43:PRO:HB3	5:F:139:TYR:CE2	2.44	0.53
12:M:25:THR:OG1	26:f:91:GLU:OE1	2.23	0.53
1:0:29:U:C2'	1:0:30:G:H5'	2.38	0.53
1:0:1098:A:H2'	1:0:1099:A:C8	2.44	0.53
1:0:2092:G:O2'	27:i:192:ASP:HA	2.09	0.53
23:X:90:SER:O	23:X:93:SER:OG	2.24	0.53
25:b:30:VAL:HG21	25:b:101:VAL:HB	1.90	0.53
1:0:1212:A:H1'	1:0:1213:G:O4'	2.09	0.53
27:i:26:ALA:C	27:i:28:ASP:H	2.17	0.53
1:0:2092:G:N2	27:i:192:ASP:OD2	2.41	0.53
26:f:34:VAL:HB	26:f:37:TYR:HB2	1.90	0.53
27:i:11:TYR:HE1	27:i:13:GLU:CD	2.15	0.53
27:i:123:VAL:O	27:i:124:ASP:C	2.51	0.53
27:i:191:THR:O	27:i:198:LEU:HG	2.09	0.53
1:0:2242:U:H1'	1:0:2246:G:N2	2.24	0.53
1:0:2426:U:H2'	1:0:2427:A:C8	2.44	0.53
26:f:28:GLU:OE2	26:f:58:THR:OG1	2.26	0.53
27:i:143:ALA:C	27:i:145:HIS:H	2.17	0.53
5:F:109:ASP:OD1	5:F:109:ASP:N	2.38	0.52
1:0:299:G:H3'	1:0:299:G:N3	2.24	0.52
2:9:3:C:O2	2:9:21:G:N2	2.36	0.52
11:L:100:ALA:HB1	11:L:110:MET:HE3	1.90	0.52
1:0:2099:C:H2'	1:0:2100:U:C6	2.45	0.52
5:F:146:GLU:N	5:F:146:GLU:OE2	2.42	0.52
14:O:42:ARG:HG3	14:O:42:ARG:HH11	1.73	0.52
1:0:1828:U:H5	1:0:1833:A:N7	2.08	0.52
1:0:2099:C:H2'	1:0:2100:U:H6	1.74	0.52
3:B:16:ALA:HB3	3:B:193:VAL:HG21	1.92	0.52
27:i:236:ILE:CG2	27:i:259:VAL:HG12	2.30	0.52
1:0:1215:U:H2'	1:0:1216:U:C5	2.45	0.52
15:P:47:GLU:H	15:P:47:GLU:CD	2.13	0.52
21:V:196:ARG:HG2	21:V:324:LEU:HD22	1.91	0.52
27:i:234:ARG:HB3	27:i:257:LEU:HD23	1.92	0.52
1:0:453:A:C8	22:W:43:LYS:HD2	2.45	0.52
13:N:84:ASP:OD1	13:N:85:GLY:N	2.42	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:528:A:H5''	11:L:30:LYS:HD2	1.92	0.52
1:0:2690:A:H8	1:0:2690:A:OP1	1.93	0.52
1:0:2135:G:N1	1:0:2228:G:N7	2.58	0.52
1:0:879:G:H5'	1:0:880:G:OP1	2.09	0.52
4:E:27:THR:OG1	4:E:104:GLU:OE2	2.27	0.52
6:G:166:ASN:OD1	6:G:167:ALA:N	2.43	0.52
1:0:273:U:O2'	1:0:274:G:OP1	2.28	0.51
23:X:54:SER:HB3	23:X:59:VAL:HG23	1.92	0.51
23:X:74:GLU:HA	23:X:77:VAL:HG12	1.90	0.51
24:Y:104:VAL:HG12	24:Y:116:ARG:HB3	1.93	0.51
26:f:116:GLU:N	26:f:116:GLU:OE2	2.42	0.51
1:0:1448:G:O2'	1:0:1482:A:N3	2.43	0.51
1:0:2129:G:H21	1:0:2130:A:H62	1.57	0.51
1:0:2242:U:H1'	1:0:2246:G:C2	2.46	0.51
1:0:2784:U:H1'	1:0:2785:A:H5''	1.90	0.51
27:i:13:GLU:OE1	27:i:38:HIS:HB3	2.11	0.51
18:S:43:SER:OG	18:S:45:LYS:O	2.28	0.51
23:X:29:GLU:O	23:X:32:LYS:HG3	2.10	0.51
1:0:1986:C:O2	1:0:2588:U:O2'	2.24	0.51
1:0:2441:U:H2'	1:0:2442:G:H8	1.76	0.51
3:B:150:ASN:OD1	3:B:153:GLY:N	2.44	0.51
24:Y:4:ILE:HG22	24:Y:50:ILE:HB	1.93	0.51
27:i:121:ALA:O	27:i:122:THR:C	2.53	0.51
1:0:1271:C:H2'	1:0:1272:U:C6	2.45	0.51
24:Y:106:LYS:HG2	24:Y:114:PRO:HB3	1.91	0.51
1:0:2678:U:H2'	1:0:2679:C:H6	1.75	0.51
14:O:17:VAL:HG13	14:O:48:VAL:HG12	1.92	0.51
25:b:76:ASP:OD1	25:b:76:ASP:N	2.43	0.51
1:0:251:C:OP1	6:G:2:ALA:N	2.44	0.51
1:0:304:C:H2'	1:0:305:A:H8	1.75	0.51
1:0:1522:A:H1'	1:0:1523:A:C8	2.46	0.51
7:H:7:ARG:NH1	7:H:11:LEU:HD22	2.26	0.51
20:U:22:HIS:CD2	20:U:23:ARG:HG3	2.45	0.51
1:0:2720:A:H4'	15:P:19:LYS:HE3	1.92	0.51
23:X:36:ILE:O	23:X:40:ILE:HG22	2.11	0.51
27:i:244:SER:HA	27:i:247:GLU:HG3	1.93	0.51
1:0:614:G:H2'	1:0:615:U:C6	2.46	0.51
1:0:2244:G:C2	1:0:2245:C:C2	2.99	0.51
4:E:80:THR:OG1	4:E:83:ASP:OD1	2.24	0.51
8:I:121:GLU:O	8:I:124:ILE:HD12	2.11	0.51
9:J:119:GLN:HA	9:J:122:THR:HG22	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:954:G:N3	1:0:2295:A:H2'	2.26	0.50
3:B:49:THR:C	3:B:50:ILE:HD13	2.36	0.50
26:f:98:ILE:HD12	26:f:102:GLU:HA	1.92	0.50
1:0:311:A:OP2	13:N:39:ARG:NE	2.45	0.50
1:0:1251:C:H2'	1:0:1252:U:C6	2.46	0.50
1:0:2600:U:H5''	1:0:2602:G:H4'	1.92	0.50
27:i:85:MET:HG2	27:i:93:LEU:HG	1.93	0.50
22:W:17:ASP:OD1	22:W:17:ASP:N	2.26	0.50
1:0:951:U:H4'	10:K:96:GLN:HB2	1.93	0.50
7:H:61:VAL:HG12	7:H:115:ILE:HB	1.92	0.50
11:L:37:LYS:HD3	11:L:115:ILE:HG22	1.93	0.50
1:0:2704:U:H2'	1:0:2705:G:H8	1.76	0.50
1:0:1464:G:O2'	1:0:1858:A:N3	2.40	0.50
15:P:7:GLU:OE2	15:P:77:ARG:NH2	2.45	0.50
27:i:231:SER:HB3	27:i:232:PRO:HD3	1.93	0.50
1:0:226:G:H5'	1:0:227:C:H5''	1.94	0.50
1:0:499:A:C2	1:0:1386:U:C4	3.00	0.50
1:0:875:G:OP2	20:U:9:ARG:NH2	2.45	0.50
1:0:2678:U:H2'	1:0:2679:C:C6	2.47	0.50
5:F:30:LYS:HG3	5:F:62:HIS:ND1	2.26	0.50
6:G:191:SER:O	6:G:193:ARG:N	2.45	0.50
1:0:960:G:H2'	1:0:961:C:C6	2.47	0.49
1:0:1739:G:O2'	1:0:2025:U:O4	2.27	0.49
1:0:2691:G:H2'	1:0:2692:A:C8	2.47	0.49
4:E:66:GLU:OE2	6:G:20:LYS:NZ	2.33	0.49
19:T:6:ARG:HB3	19:T:19:GLU:OE1	2.13	0.49
1:0:768:A:N3	1:0:2471:U:O2'	2.41	0.49
1:0:2105:A:H2'	1:0:2106:G:H8	1.75	0.49
16:Q:96:HIS:CD2	16:Q:219:GLU:HA	2.47	0.49
1:0:1467:A:H2'	1:0:1468:U:C6	2.47	0.49
1:0:2705:G:H4'	26:f:40:THR:HG23	1.93	0.49
3:B:128:LEU:HB3	3:B:130:VAL:HG22	1.94	0.49
21:V:53:MET:HG3	21:V:67:GLU:OE2	2.12	0.49
21:V:57:ASP:N	21:V:57:ASP:OD1	2.46	0.49
1:0:1157:G:N2	1:0:1204:A:H62	2.10	0.49
7:H:8:LEU:O	7:H:12:ILE:HD12	2.11	0.49
1:0:491:G:O2'	1:0:517:G:O6	2.18	0.49
1:0:1212:A:N3	1:0:1213:G:H1'	2.27	0.49
1:0:1986:C:H5''	26:f:66:ARG:HE	1.77	0.49
20:U:132:ASP:CG	20:U:133:ARG:H	2.21	0.49
27:i:140:VAL:HG11	27:i:175:LEU:HD11	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:2508:C:H2'	1:0:2509:G:O4'	2.12	0.49
7:H:11:LEU:HD13	7:H:100:GLU:HG3	1.94	0.49
20:U:125:SER:HB3	20:U:158:VAL:HG12	1.93	0.49
22:W:12:ASP:N	22:W:12:ASP:OD1	2.46	0.49
1:0:1261:U:H2'	1:0:1262:G:C8	2.48	0.49
1:0:1454:A:H2'	1:0:1455:A:C8	2.48	0.49
8:I:64:SER:HG	8:I:76:THR:HB	1.78	0.49
20:U:179:MET:HE2	20:U:179:MET:HA	1.95	0.49
27:i:73:THR:O	27:i:75:ASP:N	2.45	0.49
1:0:360:G:O2'	1:0:361:G:H2'	2.13	0.49
2:9:55:A:C6	23:X:9:MET:HE2	2.48	0.49
23:X:38:GLU:OE1	23:X:44:GLU:HA	2.13	0.49
23:X:91:ALA:HA	23:X:161:PHE:HZ	1.78	0.49
1:0:588:U:O4	1:0:589:A:N6	2.46	0.49
1:0:647:A:N1	1:0:904:G:O2'	2.40	0.49
6:G:16:PRO:HA	6:G:21:LEU:HD23	1.95	0.49
9:J:119:GLN:HB3	9:J:146:TYR:HE2	1.76	0.49
3:B:161:ARG:O	3:B:165:LEU:HD12	2.13	0.48
7:H:60:VAL:HG12	7:H:78:ALA:HB3	1.95	0.48
1:0:319:G:N1	1:0:322:A:OP2	2.42	0.48
23:X:34:GLU:O	23:X:38:GLU:HG2	2.14	0.48
1:0:2093:A:H2'	1:0:2531:A:N1	2.27	0.48
1:0:2245:C:N4	1:0:2246:G:N3	2.61	0.48
13:N:16:PRO:O	13:N:20:ARG:HG2	2.14	0.48
23:X:52:ARG:O	23:X:52:ARG:NE	2.41	0.48
27:i:114:VAL:HG13	27:i:118:LEU:HB2	1.96	0.48
5:F:62:HIS:H	5:F:62:HIS:CD2	2.32	0.48
21:V:282:GLU:HG3	21:V:333:THR:O	2.12	0.48
21:V:320:ASP:OD1	21:V:320:ASP:N	2.47	0.48
1:0:1127:C:H4'	1:0:1128:G:O5'	2.14	0.48
14:O:65:LEU:HD11	14:O:150:LEU:HB3	1.95	0.48
1:0:324:G:OP1	1:0:343:A:O2'	2.32	0.48
1:0:709:C:H2'	1:0:710:G:O4'	2.14	0.48
1:0:1058:A:H2'	1:0:1059:A:C8	2.49	0.48
1:0:2137:C:H2'	1:0:2138:G:C8	2.49	0.48
1:0:2332:U:O2'	1:0:2333:C:OP2	2.32	0.48
13:N:14:ASP:N	13:N:14:ASP:OD1	2.46	0.48
15:P:83:GLU:OE1	15:P:83:GLU:N	2.42	0.48
23:X:139:LYS:HE3	23:X:139:LYS:HB3	1.49	0.48
24:Y:20:GLU:HG3	24:Y:33:ARG:HB2	1.94	0.48
1:0:1226:G:OP2	1:0:1227:A:O2'	2.27	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1235:C:H5'	1:0:1236:G:OP2	2.14	0.48
1:0:2620:G:N7	20:U:206:ARG:NH2	2.61	0.48
18:S:5:GLY:O	18:S:9:GLN:HG2	2.14	0.48
27:i:235:THR:OG1	27:i:236:ILE:N	2.47	0.48
1:0:1607:A:H2'	1:0:1608:A:C8	2.49	0.48
1:0:2335:G:O6	1:0:2338:A:N6	2.47	0.48
25:b:110:ASP:OD1	25:b:110:ASP:N	2.46	0.48
25:b:111:GLU:OE1	25:b:111:GLU:N	2.38	0.48
27:i:158:VAL:HG22	27:i:163:ALA:HA	1.94	0.48
1:0:2232:C:H2'	1:0:2233:U:C6	2.49	0.48
1:0:2334:G:H3'	1:0:2335:G:C2	2.48	0.48
4:E:25:ARG:NH1	4:E:87:ALA:O	2.47	0.48
9:J:36:ILE:HG13	9:J:37:THR:HG23	1.96	0.48
16:Q:90:GLU:HG3	16:Q:92:ARG:NH1	2.28	0.48
23:X:151:HIS:O	23:X:151:HIS:ND1	2.47	0.48
1:0:1129:A:H2'	1:0:1130:A:H8	1.75	0.47
1:0:2244:G:H2'	1:0:2245:C:C6	2.49	0.47
22:W:74:ASN:OD1	22:W:74:ASN:O	2.32	0.47
1:0:531:U:H2'	1:0:532:G:H8	1.79	0.47
1:0:1587:G:O2'	1:0:1588:C:O5'	2.32	0.47
1:0:2094:A:OP2	1:0:2531:A:N6	2.44	0.47
23:X:155:VAL:O	23:X:159:VAL:HG22	2.13	0.47
1:0:295:C:N3	1:0:367:U:C4	2.83	0.47
1:0:373:G:H2'	1:0:374:G:H8	1.79	0.47
1:0:1080:A:N1	1:0:2061:G:O2'	2.39	0.47
1:0:1270:G:H2'	1:0:1271:C:C6	2.49	0.47
1:0:1587:G:O2'	1:0:1588:C:O4'	2.28	0.47
3:B:206:THR:HG22	3:B:207:GLY:H	1.79	0.47
1:0:1510:U:H2'	1:0:1511:U:H6	1.79	0.47
16:Q:172:HIS:CD2	16:Q:223:LEU:HD13	2.49	0.47
1:0:499:A:C6	1:0:1386:U:N3	2.83	0.47
1:0:2441:U:H2'	1:0:2442:G:C8	2.50	0.47
27:i:26:ALA:C	27:i:28:ASP:N	2.72	0.47
1:0:290:A:C2	1:0:291:C:H1'	2.49	0.47
1:0:642:C:H2'	1:0:643:A:H8	1.78	0.47
1:0:1652:A:H2'	1:0:1653:A:C8	2.49	0.47
3:B:181:ILE:HG13	3:B:182:ASN:N	2.29	0.47
5:F:55:GLU:CD	5:F:164:ARG:HG2	2.40	0.47
1:0:705:C:O4'	1:0:746:G:N2	2.48	0.47
1:0:1031:A:N3	1:0:1269:U:O2'	2.45	0.47
1:0:1213:G:C4	1:0:1214:G:C8	3.02	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:9:41:C:O2	23:X:72:ARG:NE	2.45	0.47
6:G:48:ASP:O	6:G:52:GLU:HG2	2.15	0.47
17:R:33:GLU:OE1	17:R:33:GLU:C	2.58	0.47
22:W:239:GLU:O	22:W:242:ILE:HG22	2.15	0.47
1:0:2863:U:H2'	1:0:2864:G:H8	1.80	0.47
3:B:17:ARG:NH2	3:B:57:GLY:O	2.48	0.47
1:0:697:A:H2'	1:0:698:A:C8	2.50	0.47
1:0:868:U:O2'	20:U:12:ARG:NH2	2.48	0.47
5:F:72:ALA:HB3	5:F:87:MET:HE1	1.97	0.46
21:V:80:MET:HE3	21:V:147:THR:HG23	1.96	0.46
22:W:16:ILE:HD11	22:W:239:GLU:HG2	1.97	0.46
1:0:614:G:H2'	1:0:615:U:H6	1.80	0.46
13:N:33:ARG:O	13:N:37:GLY:HA2	2.15	0.46
1:0:1839:U:H2'	1:0:1840:A:C8	2.50	0.46
1:0:2259:A:H2'	1:0:2260:G:C8	2.51	0.46
6:G:145:ASP:O	6:G:149:ASN:N	2.49	0.46
14:O:42:ARG:HG3	14:O:42:ARG:NH1	2.29	0.46
7:H:45:ASN:OD1	7:H:68:SER:HB3	2.14	0.46
20:U:79:GLU:O	20:U:89:LYS:NZ	2.34	0.46
3:B:83:ASP:C	3:B:83:ASP:OD1	2.58	0.46
4:E:116:VAL:O	4:E:120:ARG:HG3	2.15	0.46
1:0:629:U:O2'	1:0:631:G:N7	2.34	0.46
1:0:1149:A:H1'	1:0:1213:G:N2	2.30	0.46
1:0:1867:U:O2'	20:U:117:LYS:O	2.27	0.46
1:0:1895:G:H2'	1:0:1896:U:C6	2.51	0.46
3:B:6:PHE:HE1	3:B:37:MET:HE1	1.80	0.46
3:B:154:VAL:HG23	3:B:176:ALA:HA	1.98	0.46
16:Q:104:ASP:OD2	16:Q:106:GLU:HG2	2.14	0.46
1:0:1509:C:H2'	1:0:1510:U:H6	1.79	0.46
4:E:105:ALA:O	4:E:109:VAL:HG23	2.16	0.46
16:Q:166:LYS:HE3	16:Q:166:LYS:HB2	1.71	0.46
1:0:1574:G:O2'	1:0:1575:A:H2	1.98	0.46
1:0:2320:U:H2'	1:0:2321:C:C6	2.51	0.46
1:0:2385:C:H2'	1:0:2386:C:O4'	2.16	0.46
1:0:2850:C:H2'	1:0:2851:U:C6	2.50	0.46
6:G:41:ILE:HD11	6:G:131:GLU:OE1	2.16	0.46
6:G:114:ARG:NH1	6:G:151:ILE:O	2.43	0.46
14:O:63:GLU:OE2	14:O:67:ARG:NH1	2.48	0.46
27:i:166:ILE:HD11	27:i:258:VAL:HG23	1.98	0.46
1:0:310:A:N3	1:0:331:G:O2'	2.49	0.46
1:0:679:C:H1'	22:W:42:ARG:HD3	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:112:ILE:O	4:E:116:VAL:HG13	2.16	0.46
15:P:74:ARG:NH2	15:P:92:GLU:OE1	2.48	0.46
1:0:1753:A:N3	1:0:1811:C:H2'	2.31	0.45
1:0:2714:U:H4'	26:f:87:ARG:HG3	1.97	0.45
3:B:180:THR:HB	3:B:184:GLY:HA2	1.98	0.45
8:I:25:LEU:HB2	10:K:27:PRO:HB3	1.98	0.45
1:0:1212:A:N3	1:0:1213:G:C1'	2.79	0.45
1:0:1955:C:O2'	1:0:1956:C:H5''	2.16	0.45
6:G:178:GLY:O	6:G:181:THR:OG1	2.33	0.45
22:W:61:MET:H	22:W:61:MET:HG2	1.65	0.45
1:0:1116:U:O2	1:0:1245:A:N6	2.50	0.45
1:0:1513:U:H2'	1:0:1514:U:C6	2.52	0.45
1:0:2124:G:N2	6:G:125:GLY:O	2.48	0.45
1:0:2814:C:H2'	1:0:2815:C:C6	2.51	0.45
6:G:70:LYS:HB3	6:G:70:LYS:HE2	1.74	0.45
25:b:19:MET:HE3	25:b:82:ALA:CB	2.47	0.45
1:0:843:A:O2'	1:0:844:C:H3'	2.17	0.45
1:0:2406:A:H4'	8:I:133:ASN:HD21	1.82	0.45
1:0:2408:A:O2'	8:I:30:SER:HB3	2.17	0.45
2:9:50:A:N6	8:I:42:LYS:HD3	2.32	0.45
3:B:137:LEU:O	3:B:140:VAL:HG12	2.17	0.45
3:B:172:LEU:O	3:B:174:VAL:HG13	2.16	0.45
14:O:76:ASP:N	14:O:76:ASP:OD1	2.49	0.45
20:U:82:ILE:HG22	20:U:93:THR:CG2	2.47	0.45
1:0:85:G:H2'	1:0:86:G:O4'	2.17	0.45
1:0:1272:U:O2'	1:0:1273:A:OP1	2.31	0.45
1:0:1662:A:H2'	1:0:1663:A:H8	1.78	0.45
8:I:72:TRP:CZ2	8:I:74:ALA:HB3	2.51	0.45
8:I:113:GLY:HA2	8:I:138:ALA:HB2	1.97	0.45
20:U:132:ASP:CG	20:U:133:ARG:N	2.75	0.45
22:W:242:ILE:HD12	22:W:242:ILE:HA	1.86	0.45
23:X:136:ARG:O	23:X:140:ARG:HG2	2.16	0.45
27:i:9:GLU:O	27:i:10:GLU:C	2.60	0.45
1:0:182:G:H2'	6:G:192:ARG:HD2	1.98	0.45
1:0:822:G:O2'	1:0:858:G:H4'	2.16	0.45
1:0:1129:A:N6	1:0:1226:G:H2'	2.31	0.45
1:0:1150:C:H41	1:0:1211:G:H21	1.64	0.45
7:H:46:LEU:HD12	7:H:89:LYS:HD2	1.98	0.45
15:P:22:PRO:HD2	15:P:25:GLU:OE2	2.16	0.45
1:0:1208:G:H2'	1:0:1209:C:C6	2.52	0.45
1:0:1747:C:H6	21:V:230:ARG:HH22	1.65	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:2768:A:H2'	1:0:2769:A:C8	2.52	0.45
13:N:104:LEU:HD13	13:N:110:GLU:OE1	2.16	0.45
16:Q:207:LYS:HE3	16:Q:207:LYS:HB2	1.76	0.45
20:U:5:ILE:HG22	20:U:198:ASP:O	2.17	0.45
20:U:109:GLU:HB2	20:U:152:CYS:HB2	1.99	0.45
1:0:569:A:H2'	1:0:570:A:C8	2.52	0.45
1:0:1669:U:H2'	1:0:1670:C:C6	2.52	0.45
1:0:2533:G:C8	27:i:206:ARG:HD2	2.52	0.45
1:0:2599:G:N2	21:V:242:PRO:HG3	2.32	0.45
11:L:39:MET:O	11:L:112:ILE:HG13	2.16	0.45
19:T:71:ILE:HD12	19:T:71:ILE:N	2.32	0.45
1:0:418:C:H2'	1:0:419:A:H8	1.82	0.45
1:0:423:A:H1'	1:0:1914:A:C2	2.52	0.45
14:O:82:GLU:CD	14:O:82:GLU:H	2.25	0.45
27:i:118:LEU:C	27:i:120:ALA:H	2.24	0.45
1:0:85:G:H21	1:0:106:A:H62	1.65	0.44
1:0:1145:C:H4'	1:0:1148:A:H4'	1.98	0.44
2:9:120:C:H5''	2:9:121:U:OP2	2.17	0.44
6:G:53:LEU:HD13	6:G:117:ASN:HB3	2.00	0.44
1:0:510:G:N1	1:0:513:A:OP2	2.50	0.44
1:0:619:A:H2'	1:0:620:U:C6	2.52	0.44
8:I:83:TYR:OH	8:I:125:ASP:OD2	2.26	0.44
14:O:1:MET:HE2	14:O:1:MET:HB3	1.82	0.44
14:O:63:GLU:HG2	14:O:93:VAL:HG12	1.99	0.44
20:U:94:LEU:HB2	20:U:99:ILE:HD11	2.00	0.44
26:f:75:ARG:O	26:f:93:ASN:HA	2.17	0.44
1:0:1791:U:H2'	1:0:1792:A:O4'	2.17	0.44
4:E:27:THR:HG21	4:E:104:GLU:H	1.82	0.44
20:U:132:ASP:OD1	20:U:133:ARG:N	2.40	0.44
21:V:233:TRP:CD1	21:V:236:ARG:HD2	2.53	0.44
27:i:226:ARG:HA	27:i:229:MET:HE3	1.99	0.44
1:0:173:A:O2'	1:0:900:G:O6	2.28	0.44
1:0:2354:A:H2'	1:0:2355:A:C8	2.51	0.44
3:B:155:LEU:HA	3:B:155:LEU:HD23	1.66	0.44
27:i:7:VAL:HG12	27:i:103:GLY:HA3	1.99	0.44
1:0:543:G:H2'	1:0:544:A:C8	2.53	0.44
1:0:1143:C:C4	1:0:1144:C:C5	3.05	0.44
1:0:1213:G:H2'	1:0:1214:G:O4'	2.18	0.44
3:B:49:THR:OG1	3:B:53:SER:O	2.30	0.44
3:B:110:ALA:HB3	3:B:132:VAL:HG23	2.00	0.44
8:I:108:ASN:OD1	23:X:142:LYS:NZ	2.43	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:J:113:GLY:C	9:J:115:LEU:H	2.26	0.44
14:O:149:LEU:O	14:O:153:MET:HG3	2.18	0.44
20:U:36:LYS:HZ3	20:U:37:ASP:H	1.65	0.44
20:U:106:CYS:N	20:U:155:THR:O	2.45	0.44
21:V:105:GLU:HA	21:V:105:GLU:OE2	2.17	0.44
1:O:1936:C:O4'	20:U:212:PRO:HA	2.17	0.44
24:Y:59:THR:O	24:Y:63:ILE:HD13	2.18	0.44
26:f:23:ASN:O	26:f:23:ASN:ND2	2.50	0.44
1:O:248:A:H1'	6:G:52:GLU:OE1	2.17	0.44
1:O:1440:G:O2'	1:O:1497:A:N1	2.44	0.44
1:O:2355:A:H2'	1:O:2356:G:C8	2.52	0.44
1:O:2681:U:H2'	1:O:2682:A:H8	1.81	0.44
4:E:35:ASN:O	4:E:39:LYS:HG2	2.17	0.44
11:L:10:ASP:O	11:L:14:THR:OG1	2.25	0.44
16:Q:210:ARG:HG3	16:Q:210:ARG:NH1	2.30	0.44
20:U:82:ILE:HG22	20:U:93:THR:HG23	1.99	0.44
1:O:228:G:H2'	1:O:229:A:C8	2.53	0.44
1:O:1150:C:H41	1:O:1211:G:N2	2.15	0.44
1:O:2098:C:H2'	1:O:2099:C:C6	2.52	0.44
1:O:2710:C:O2'	1:O:2711:C:H5'	2.18	0.44
3:B:88:PRO:HB2	3:B:90:TYR:CE1	2.53	0.44
4:E:53:GLU:HG3	4:E:78:VAL:O	2.17	0.44
6:G:103:GLU:HG2	6:G:115:VAL:HG11	1.99	0.44
22:W:33:ARG:HG2	22:W:102:ILE:HD12	1.99	0.44
27:i:184:LYS:HE2	27:i:184:LYS:HB3	1.56	0.44
1:O:373:G:H2'	1:O:374:G:C8	2.53	0.44
1:O:2244:G:C5	1:O:2245:C:C4	3.06	0.44
1:O:2479:A:O2'	27:i:214:GLU:OE1	2.35	0.44
12:M:5:ARG:HE	12:M:5:ARG:HB2	1.68	0.44
19:T:1:MET:HE3	19:T:1:MET:HB2	1.77	0.44
21:V:223:LYS:HE3	21:V:223:LYS:HB2	1.73	0.44
22:W:139:LEU:HD23	22:W:161:LEU:HD23	2.00	0.44
27:i:36:MET:SD	27:i:45:VAL:HG22	2.57	0.44
3:B:33:LEU:HA	3:B:36:GLN:OE1	2.18	0.43
24:Y:120:ARG:O	24:Y:123:THR:OG1	2.34	0.43
27:i:115:LYS:HE2	27:i:115:LYS:HB3	1.62	0.43
1:O:154:G:OP2	1:O:154:G:N2	2.43	0.43
1:O:1355:U:C5	22:W:68:SER:HA	2.53	0.43
1:O:2241:C:C2	1:O:2247:G:C2	3.06	0.43
7:H:76:THR:HG23	7:H:95:ASP:OD2	2.17	0.43
10:K:72:PHE:CE2	10:K:89:PRO:HG3	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:R:65:THR:HG22	17:R:66:TYR:CE1	2.53	0.43
20:U:74:ILE:HD11	20:U:91:GLY:HA3	2.00	0.43
20:U:124:VAL:O	20:U:159:VAL:HG23	2.18	0.43
23:X:159:VAL:HG23	23:X:160:ALA:N	2.33	0.43
1:0:117:C:O2'	1:0:128:U:O2'	2.27	0.43
1:0:209:C:H2'	1:0:210:G:O4'	2.18	0.43
1:0:650:G:H5''	22:W:96:LYS:HD2	2.00	0.43
1:0:1923:A:H2'	1:0:1924:A:C8	2.53	0.43
1:0:2137:C:H2'	1:0:2138:G:H8	1.82	0.43
4:E:46:ALA:O	4:E:73:ILE:HD13	2.18	0.43
6:G:99:PRO:HB3	6:G:130:GLN:NE2	2.34	0.43
11:L:18:MET:HE3	11:L:20:ARG:CZ	2.48	0.43
15:P:50:ARG:HD3	15:P:87:GLU:OE2	2.18	0.43
22:W:194:ILE:H	22:W:194:ILE:HG13	1.63	0.43
1:0:577:A:H2'	1:0:578:G:C8	2.53	0.43
1:0:1478:A:H2'	1:0:1479:U:O4'	2.18	0.43
1:0:2705:G:OP1	26:f:43:ARG:NH1	2.51	0.43
22:W:130:ARG:HD3	22:W:169:ARG:HD3	2.00	0.43
27:i:276:ASP:O	27:i:279:THR:HG22	2.18	0.43
1:0:286:C:O2'	1:0:287:A:O5'	2.37	0.43
1:0:2422:A:H2'	1:0:2423:A:H8	1.83	0.43
5:F:52:LEU:HD13	5:F:152:PHE:HB3	1.99	0.43
27:i:11:TYR:CD1	27:i:13:GLU:OE2	2.62	0.43
27:i:217:LEU:HD12	27:i:217:LEU:HA	1.81	0.43
1:0:2500:G:O6	1:0:2503:C:O2'	2.18	0.43
8:I:121:GLU:HA	8:I:124:ILE:HD11	2.00	0.43
9:J:146:TYR:O	9:J:148:VAL:HG13	2.19	0.43
27:i:72:LEU:HD22	27:i:76:GLU:HG3	2.00	0.43
1:0:34:A:H2'	1:0:35:G:C8	2.53	0.43
1:0:2045:U:H2'	1:0:2046:G:O4'	2.18	0.43
1:0:2108:U:H2'	1:0:2109:U:C6	2.53	0.43
2:9:46:A:H2'	2:9:47:C:C6	2.53	0.43
3:B:33:LEU:O	3:B:37:MET:HG3	2.19	0.43
6:G:100:ARG:HD3	6:G:168:GLY:HA2	2.00	0.43
7:H:19:SER:HB2	7:H:27:TRP:HB2	1.99	0.43
8:I:17:VAL:HB	23:X:143:ARG:HA	2.01	0.43
22:W:51:TYR:HA	22:W:54:LEU:HD12	2.00	0.43
27:i:242:LEU:HD23	27:i:242:LEU:HA	1.84	0.43
1:0:1071:G:OP2	1:0:1072:U:O2'	2.34	0.43
1:0:2241:C:H6	1:0:2241:C:O5'	2.02	0.43
1:0:2713:C:H4'	12:M:18:THR:HG22	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:2813:U:H2'	1:0:2814:C:C6	2.53	0.43
26:f:9:THR:O	26:f:76:GLN:NE2	2.42	0.43
1:0:1273:A:P	7:H:20:ARG:HD3	2.59	0.43
1:0:2318:U:OP1	1:0:2410:C:O2'	2.35	0.43
1:0:2585:G:H2'	1:0:2586:C:H6	1.84	0.43
4:E:15:ASP:OD1	4:E:16:SER:N	2.51	0.43
4:E:32:LYS:HE2	4:E:32:LYS:HB2	1.91	0.43
27:i:131:LEU:HD13	27:i:156:PRO:HG2	2.00	0.43
27:i:229:MET:HE3	27:i:229:MET:HB3	1.70	0.43
1:0:542:C:H5''	1:0:543:G:C8	2.54	0.43
1:0:2243:G:C5	1:0:2244:G:C5	3.07	0.43
1:0:2863:U:H2'	1:0:2864:G:C8	2.53	0.43
15:P:78:PHE:HB2	15:P:85:ILE:HG13	2.01	0.43
21:V:233:TRP:HD1	21:V:236:ARG:HD2	1.84	0.43
27:i:158:VAL:HG12	27:i:159:ASP:O	2.19	0.43
1:0:1084:C:O2'	1:0:1125:A:N1	2.42	0.42
8:I:80:PRO:HB3	8:I:173:PHE:HD2	1.84	0.42
8:I:150:GLU:O	8:I:153:GLU:HG3	2.19	0.42
1:0:892:U:O2'	18:S:51:TRP:O	2.34	0.42
1:0:1487:A:H2'	1:0:1488:A:C8	2.54	0.42
15:P:92:GLU:H	15:P:92:GLU:CD	2.27	0.42
17:R:54:ASN:HD22	17:R:54:ASN:HA	1.68	0.42
27:i:50:GLN:N	27:i:50:GLN:OE1	2.53	0.42
1:0:313:U:H2'	13:N:52:LEU:HD13	2.02	0.42
1:0:1048:U:H2'	1:0:1049:G:H8	1.84	0.42
1:0:2588:U:H2'	1:0:2589:A:C8	2.54	0.42
1:0:2857:U:H2'	1:0:2858:G:O4'	2.19	0.42
4:E:32:LYS:HG2	4:E:88:ALA:HB1	2.00	0.42
5:F:153:ARG:HA	5:F:156:TYR:CE2	2.54	0.42
21:V:152:LEU:HD23	21:V:152:LEU:HA	1.84	0.42
23:X:29:GLU:O	23:X:32:LYS:HE3	2.19	0.42
23:X:170:VAL:O	23:X:171:GLU:HG3	2.19	0.42
25:b:134:GLU:H	25:b:134:GLU:HG3	1.72	0.42
1:0:859:A:H5''	20:U:173:GLY:HA2	2.00	0.42
1:0:1146:U:H5''	1:0:1148:A:C4	2.55	0.42
1:0:2332:U:H5''	23:X:103:GLY:O	2.19	0.42
5:F:147:ILE:HD13	5:F:147:ILE:HA	1.89	0.42
27:i:123:VAL:HA	27:i:241:THR:HA	2.01	0.42
1:0:2320:U:H2'	1:0:2321:C:H6	1.84	0.42
1:0:2814:C:H2'	1:0:2815:C:H6	1.83	0.42
11:L:122:GLU:HG2	11:L:140:PRO:HA	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:O:36:PRO:HD2	14:O:41:TYR:CE2	2.55	0.42
27:i:84:LEU:O	27:i:88:SER:OG	2.20	0.42
1:0:418:C:H2'	1:0:419:A:C8	2.55	0.42
1:0:686:A:H5'	1:0:687:G:OP2	2.20	0.42
1:0:1117:U:O2'	1:0:1119:A:N7	2.40	0.42
1:0:1901:G:N1	1:0:1923:A:OP2	2.29	0.42
1:0:2502:A:H2'	1:0:2502:A:N3	2.33	0.42
1:0:2677:U:H2'	1:0:2678:U:C6	2.55	0.42
11:L:61:LYS:HD3	11:L:76:TRP:CD2	2.54	0.42
1:0:669:A:H2'	1:0:670:A:C8	2.55	0.42
1:0:973:A:H2'	1:0:974:A:C8	2.55	0.42
1:0:1270:G:H2'	1:0:1271:C:H6	1.85	0.42
1:0:2244:G:C6	1:0:2245:C:C4	3.07	0.42
2:9:40:C:H1'	23:X:44:GLU:O	2.20	0.42
3:B:17:ARG:HD3	3:B:17:ARG:HA	1.73	0.42
4:E:66:GLU:OE1	4:E:66:GLU:N	2.45	0.42
9:J:45:VAL:HG22	9:J:50:ILE:HB	2.01	0.42
9:J:119:GLN:H	9:J:119:GLN:HG3	1.68	0.42
21:V:196:ARG:CZ	21:V:196:ARG:HB2	2.49	0.42
22:W:131:PHE:HB3	22:W:163:VAL:HG12	2.01	0.42
27:i:99:ARG:O	27:i:99:ARG:HG2	2.19	0.42
27:i:118:LEU:C	27:i:120:ALA:N	2.77	0.42
1:0:366:A:H4'	1:0:367:U:OP1	2.20	0.42
1:0:1214:G:H3'	1:0:1215:U:O2	2.20	0.42
1:0:2489:C:H2'	1:0:2490:A:C8	2.54	0.42
1:0:2544:C:O2'	1:0:2545:C:H5'	2.20	0.42
2:9:71:U:H2'	2:9:72:G:C8	2.54	0.42
4:E:29:ILE:N	4:E:29:ILE:HD12	2.35	0.42
5:F:107:GLY:O	5:F:110:ARG:HG3	2.20	0.42
13:N:31:ASP:OD1	13:N:31:ASP:N	2.53	0.42
21:V:123:GLU:OE1	21:V:123:GLU:N	2.52	0.42
1:0:1942:G:OP2	1:0:1942:G:H8	2.02	0.42
1:0:2637:C:O2'	1:0:2638:U:O5'	2.32	0.42
1:0:2817:C:H5''	1:0:2818:U:O5'	2.20	0.42
3:B:158:PRO:HA	3:B:178:ILE:HD12	2.00	0.42
13:N:102:LEU:HD23	13:N:102:LEU:HA	1.85	0.42
24:Y:45:ASP:OD1	24:Y:45:ASP:C	2.62	0.42
26:f:57:VAL:HG21	26:f:64:MET:HE2	2.01	0.42
1:0:700:C:H2'	1:0:701:G:O4'	2.20	0.42
1:0:1832:A:H5'	1:0:2636:G:H4'	2.02	0.42
1:0:2870:G:N2	1:0:2873:A:OP2	2.31	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:G:188:LEU:O	6:G:192:ARG:HG3	2.20	0.42
23:X:36:ILE:O	23:X:39:GLU:HG3	2.19	0.42
26:f:76:GLN:HE21	26:f:78:LYS:HB3	1.85	0.42
27:i:198:LEU:HD23	27:i:198:LEU:HA	1.83	0.42
27:i:247:GLU:C	27:i:247:GLU:OE1	2.63	0.42
1:O:1136:U:H2'	1:O:1137:C:C6	2.55	0.41
14:O:60:ASP:OD1	14:O:60:ASP:N	2.53	0.41
23:X:6:PHE:HB2	23:X:11:ASP:OD1	2.20	0.41
23:X:159:VAL:HG23	23:X:160:ALA:H	1.84	0.41
27:i:6:ILE:H	27:i:6:ILE:HG12	1.62	0.41
27:i:93:LEU:HD23	27:i:93:LEU:HA	1.88	0.41
1:O:953:A:C2'	1:O:954:G:H5'	2.50	0.41
1:O:2704:U:H2'	1:O:2705:G:C8	2.53	0.41
7:H:46:LEU:HD23	7:H:46:LEU:HA	1.83	0.41
8:I:67:LEU:HB3	8:I:72:TRP:HB3	2.03	0.41
14:O:91:ASP:OD1	14:O:91:ASP:N	2.53	0.41
16:Q:183:ASN:HA	16:Q:211:ILE:HD11	2.02	0.41
21:V:265:GLU:CD	21:V:303:PRO:HD3	2.46	0.41
1:O:577:A:H2'	1:O:578:G:H8	1.85	0.41
1:O:1086:C:H2'	1:O:1087:A:O4'	2.21	0.41
1:O:1423:A:N3	1:O:1423:A:H2'	2.35	0.41
21:V:123:GLU:H	21:V:123:GLU:CD	2.24	0.41
22:W:84:VAL:O	22:W:85:SER:OG	2.32	0.41
22:W:195:LEU:HB3	22:W:235:THR:HG22	2.02	0.41
23:X:153:MET:SD	23:X:159:VAL:HG21	2.60	0.41
26:f:65:ARG:C	26:f:65:ARG:HD2	2.45	0.41
27:i:20:VAL:HG12	27:i:62:ILE:HG22	2.02	0.41
1:O:2422:A:H2'	1:O:2423:A:C8	2.55	0.41
1:O:2629:C:HO2'	1:O:2630:A:P	2.43	0.41
3:B:148:VAL:HG23	3:B:188:VAL:HG12	2.03	0.41
7:H:5:ASN:HB3	7:H:8:LEU:HB2	2.03	0.41
8:I:105:ILE:O	8:I:108:ASN:ND2	2.54	0.41
12:M:22:TYR:OH	26:f:91:GLU:HG3	2.19	0.41
13:N:17:LEU:HD12	13:N:17:LEU:HA	1.79	0.41
14:O:11:VAL:O	14:O:12:ASN:HB2	2.20	0.41
22:W:158:LEU:CD1	22:W:163:VAL:HG23	2.50	0.41
1:O:365:G:O2'	1:O:366:A:O5'	2.36	0.41
1:O:752:A:H2'	1:O:753:A:C8	2.55	0.41
1:O:1270:G:C6	1:O:1271:C:N4	2.88	0.41
1:O:1418:U:H2'	1:O:1419:C:C6	2.56	0.41
1:O:2396:C:O2	10:K:68:GLN:NE2	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:2593:A:H2'	1:0:2594:A:O4'	2.19	0.41
2:9:69:U:H2'	2:9:70:C:C6	2.56	0.41
27:i:139:THR:HB	27:i:222:ASP:HA	2.02	0.41
1:0:1779:A:H61	1:0:1800:U:H3	1.68	0.41
1:0:2232:C:H2'	1:0:2233:U:H6	1.83	0.41
21:V:147:THR:O	21:V:160:PRO:HB3	2.20	0.41
24:Y:9:PRO:O	24:Y:11:GLU:N	2.52	0.41
1:0:190:A:H4'	6:G:157:ASP:HB3	2.03	0.41
1:0:467:A:N1	1:0:480:A:H5''	2.35	0.41
1:0:1213:G:O2'	1:0:1214:G:H5'	2.21	0.41
1:0:1975:C:O2	27:i:145:HIS:HB2	2.21	0.41
2:9:46:A:H2'	2:9:47:C:H6	1.85	0.41
11:L:18:MET:HG3	11:L:144:VAL:O	2.21	0.41
16:Q:181:VAL:HG12	16:Q:186:ASP:HB3	2.02	0.41
22:W:204:LYS:HA	22:W:207:ARG:HG3	2.02	0.41
24:Y:27:ASN:HD22	24:Y:27:ASN:C	2.25	0.41
1:0:1251:C:H2'	1:0:1252:U:H6	1.85	0.41
5:F:74:ARG:NH1	5:F:74:ARG:HG2	2.36	0.41
8:I:169:LEU:HD12	8:I:169:LEU:O	2.20	0.41
15:P:6:PHE:HE1	15:P:78:PHE:CE1	2.38	0.41
22:W:65:ARG:HA	27:i:191:THR:OG1	2.21	0.41
26:f:37:TYR:CZ	26:f:45:PRO:HA	2.55	0.41
27:i:97:GLU:HB3	27:i:100:ASP:OD2	2.21	0.41
27:i:140:VAL:HG23	27:i:223:LEU:O	2.21	0.41
1:0:405:C:H5''	6:G:97:SER:HB3	2.03	0.41
1:0:582:C:O2'	1:0:583:G:H5'	2.21	0.41
1:0:1231:U:O2'	1:0:1232:G:H5'	2.21	0.41
1:0:1590:G:N7	9:J:121:ARG:NH2	2.69	0.41
1:0:2374:C:H2'	1:0:2375:A:H8	1.85	0.41
2:9:77:G:HO2'	2:9:78:U:P	2.43	0.41
7:H:45:ASN:HA	7:H:66:LEU:O	2.20	0.41
9:J:138:LEU:O	9:J:142:ILE:HG13	2.20	0.41
21:V:265:GLU:OE1	21:V:303:PRO:HD3	2.20	0.41
22:W:158:LEU:HD11	22:W:194:ILE:HD13	2.03	0.41
24:Y:99:GLU:O	24:Y:99:GLU:HG3	2.21	0.41
27:i:76:GLU:O	27:i:77:ASP:C	2.64	0.41
27:i:172:VAL:O	27:i:175:LEU:HG	2.21	0.41
1:0:1317:A:H2'	1:0:1318:C:C6	2.56	0.41
1:0:1490:C:H2'	1:0:1491:U:C6	2.56	0.41
3:B:11:TYR:CZ	26:f:123:SER:HB2	2.56	0.41
4:E:47:GLN:O	4:E:74:PRO:HD2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:I:124:ILE:HG22	8:I:128:LEU:O	2.21	0.41
17:R:8:SER:O	17:R:28:LYS:NZ	2.38	0.41
24:Y:99:GLU:OE2	24:Y:116:ARG:NH2	2.47	0.41
1:O:915:A:C2	1:O:1043:U:H4'	2.56	0.40
1:O:2812:U:H2'	1:O:2813:U:C6	2.56	0.40
3:B:111:TYR:OH	3:B:135:GLY:HA3	2.21	0.40
5:F:49:GLU:HB3	5:F:169:ARG:HB3	2.03	0.40
14:O:78:ASP:OD1	14:O:78:ASP:N	2.54	0.40
16:Q:229:GLU:H	16:Q:229:GLU:CD	2.29	0.40
21:V:191:MET:HE3	21:V:195:PHE:CD2	2.56	0.40
21:V:244:ASN:HA	21:V:245:PRO:C	2.47	0.40
27:i:237:SER:C	27:i:239:SER:H	2.27	0.40
1:O:318:U:H2'	1:O:319:G:O4'	2.21	0.40
1:O:1061:C:H2'	1:O:1062:U:C6	2.56	0.40
1:O:2681:U:H2'	1:O:2682:A:C8	2.56	0.40
3:B:41:LEU:O	3:B:43:VAL:HG13	2.21	0.40
4:E:16:SER:O	4:E:19:GLU:HG2	2.21	0.40
5:F:140:CYS:HB2	5:F:144:ASP:HB2	2.03	0.40
8:I:144:ARG:CG	8:I:170:PRO:HB3	2.51	0.40
9:J:106:LEU:HD23	9:J:106:LEU:HA	1.95	0.40
12:M:10:SER:HA	12:M:53:THR:HB	2.03	0.40
1:O:64:C:H2'	1:O:65:C:C6	2.56	0.40
1:O:2612:U:H2'	1:O:2613:U:C6	2.56	0.40
1:O:2686:U:H5	1:O:2695:A:N7	2.20	0.40
21:V:119:GLU:HG3	21:V:120:ASP:H	1.86	0.40
24:Y:36:TYR:CG	24:Y:62:THR:HG21	2.57	0.40
1:O:749:G:H2'	1:O:750:C:C6	2.56	0.40
1:O:1870:G:O2'	1:O:1871:G:H5'	2.20	0.40
1:O:2098:C:H2'	1:O:2099:C:H6	1.87	0.40
1:O:2729:C:OP2	9:J:62:ARG:NH1	2.55	0.40
6:G:24:LEU:HA	6:G:24:LEU:HD23	1.83	0.40
7:H:45:ASN:HB3	7:H:68:SER:O	2.21	0.40
14:O:151:GLU:O	14:O:154:ARG:NH1	2.52	0.40
17:R:36:ASN:OD1	17:R:36:ASN:C	2.64	0.40
20:U:27:GLU:H	20:U:27:GLU:HG2	1.67	0.40
23:X:52:ARG:HE	23:X:52:ARG:C	2.27	0.40
1:O:1870:G:C2'	1:O:1871:G:H5'	2.51	0.40
1:O:2425:C:H2'	1:O:2426:U:C6	2.57	0.40
3:B:161:ARG:HB3	3:B:164:GLU:CD	2.47	0.40
3:B:165:LEU:HD23	3:B:176:ALA:HB1	2.04	0.40
8:I:117:PHE:HB3	8:I:137:LEU:HD23	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:O:153:MET:HE2	14:O:153:MET:HB3	1.89	0.40
17:R:84:LEU:HD12	17:R:84:LEU:HA	1.90	0.40
22:W:154:VAL:O	22:W:158:LEU:HD23	2.21	0.40
26:f:65:ARG:HD2	26:f:66:ARG:HB2	2.03	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	
3	B	218/221 (99%)	204 (94%)	14 (6%)	0	100	100
4	E	117/120 (98%)	115 (98%)	2 (2%)	0	100	100
5	F	172/176 (98%)	161 (94%)	11 (6%)	0	100	100
6	G	191/196 (97%)	185 (97%)	4 (2%)	2 (1%)	12	35
7	H	113/116 (97%)	111 (98%)	2 (2%)	0	100	100
8	I	181/184 (98%)	175 (97%)	6 (3%)	0	100	100
9	J	148/151 (98%)	144 (97%)	4 (3%)	0	100	100
10	K	93/96 (97%)	89 (96%)	4 (4%)	0	100	100
11	L	149/153 (97%)	146 (98%)	3 (2%)	0	100	100
12	M	56/67 (84%)	55 (98%)	1 (2%)	0	100	100
13	N	112/118 (95%)	106 (95%)	6 (5%)	0	100	100
14	O	152/154 (99%)	146 (96%)	6 (4%)	0	100	100
15	P	87/92 (95%)	85 (98%)	2 (2%)	0	100	100
16	Q	140/234 (60%)	137 (98%)	3 (2%)	0	100	100
17	R	78/89 (88%)	74 (95%)	4 (5%)	0	100	100
18	S	55/58 (95%)	53 (96%)	2 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	T	91/93 (98%)	88 (97%)	3 (3%)	0	100	100
20	U	233/241 (97%)	213 (91%)	18 (8%)	2 (1%)	14	37
21	V	335/338 (99%)	325 (97%)	10 (3%)	0	100	100
22	W	246/248 (99%)	235 (96%)	11 (4%)	0	100	100
23	X	167/172 (97%)	150 (90%)	17 (10%)	0	100	100
24	Y	172/178 (97%)	163 (95%)	8 (5%)	1 (1%)	21	47
25	b	142/145 (98%)	135 (95%)	7 (5%)	0	100	100
26	f	130/132 (98%)	126 (97%)	4 (3%)	0	100	100
27	i	280/406 (69%)	227 (81%)	44 (16%)	9 (3%)	3	10
All	All	3858/4178 (92%)	3648 (95%)	196 (5%)	14 (0%)	31	57

All (14) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
27	i	75	ASP
27	i	191	THR
27	i	192	ASP
20	U	213	LYS
6	G	192	ARG
24	Y	10	ASP
20	U	229	ALA
27	i	4	THR
27	i	15	THR
27	i	124	ASP
27	i	232	PRO
6	G	193	ARG
27	i	7	VAL
27	i	74	PRO

### 5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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	
3	B	170/171 (99%)	161 (95%)	9 (5%)	20	49
4	E	93/94 (99%)	91 (98%)	2 (2%)	45	75
5	F	145/147 (99%)	139 (96%)	6 (4%)	27	59
6	G	161/163 (99%)	155 (96%)	6 (4%)	30	62
7	H	98/99 (99%)	96 (98%)	2 (2%)	48	77
8	I	144/145 (99%)	143 (99%)	1 (1%)	76	90
9	J	120/121 (99%)	117 (98%)	3 (2%)	42	73
10	K	77/78 (99%)	73 (95%)	4 (5%)	21	50
11	L	122/124 (98%)	120 (98%)	2 (2%)	55	81
12	M	48/55 (87%)	48 (100%)	0	100	100
13	N	98/102 (96%)	90 (92%)	8 (8%)	10	30
14	O	132/132 (100%)	130 (98%)	2 (2%)	57	81
15	P	78/80 (98%)	78 (100%)	0	100	100
16	Q	120/191 (63%)	117 (98%)	3 (2%)	42	73
17	R	61/68 (90%)	56 (92%)	5 (8%)	10	30
18	S	48/49 (98%)	48 (100%)	0	100	100
19	T	77/77 (100%)	75 (97%)	2 (3%)	40	72
20	U	183/186 (98%)	174 (95%)	9 (5%)	22	52
21	V	277/278 (100%)	275 (99%)	2 (1%)	76	90
22	W	198/198 (100%)	188 (95%)	10 (5%)	21	50
23	X	141/147 (96%)	131 (93%)	10 (7%)	13	36
24	Y	149/151 (99%)	141 (95%)	8 (5%)	20	48
25	b	122/123 (99%)	113 (93%)	9 (7%)	13	34
26	f	106/106 (100%)	105 (99%)	1 (1%)	70	87
27	i	241/344 (70%)	203 (84%)	38 (16%)	2	7
All	All	3209/3429 (94%)	3067 (96%)	142 (4%)	27	56

All (142) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	B	10	SER
3	B	21	ASP
3	B	114	THR
3	B	132	VAL

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
3	B	142	THR
3	B	172	LEU
3	B	188	VAL
3	B	192	LEU
3	B	206	THR
4	E	16	SER
4	E	25	ARG
5	F	24	THR
5	F	33	GLN
5	F	62	HIS
5	F	125	THR
5	F	160	SER
5	F	173	LEU
6	G	24	LEU
6	G	103	GLU
6	G	188	LEU
6	G	189	SER
6	G	193	ARG
6	G	194	ARG
7	H	4	THR
7	H	61	VAL
8	I	81	SER
9	J	2	THR
9	J	3	ASP
9	J	59	SER
10	K	5	ASN
10	K	16	SER
10	K	24	THR
10	K	85	VAL
11	L	83	GLU
11	L	103	GLN
13	N	11	GLN
13	N	12	THR
13	N	17	LEU
13	N	18	HIS
13	N	36	TYR
13	N	70	ASP
13	N	107	ASP
13	N	113	LEU
14	O	14	SER
14	O	89	ASP
16	Q	179	VAL

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
16	Q	199	ILE
16	Q	202	SER
17	R	8	SER
17	R	11	SER
17	R	35	ARG
17	R	57	THR
17	R	81	ARG
19	T	22	VAL
19	T	55	LYS
20	U	14	SER
20	U	27	GLU
20	U	33	SER
20	U	42	THR
20	U	53	SER
20	U	63	ASP
20	U	93	THR
20	U	175	LYS
20	U	233	THR
21	V	56	ASN
21	V	67	GLU
22	W	9	ASN
22	W	12	ASP
22	W	16	ILE
22	W	17	ASP
22	W	80	VAL
22	W	118	THR
22	W	170	SER
22	W	189	THR
22	W	198	THR
22	W	243	GLU
23	X	9	MET
23	X	37	LEU
23	X	46	VAL
23	X	99	ASN
23	X	108	THR
23	X	127	THR
23	X	137	VAL
23	X	138	LYS
23	X	139	LYS
23	X	147	ILE
24	Y	4	ILE
24	Y	12	VAL

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
24	Y	17	SER
24	Y	63	ILE
24	Y	68	SER
24	Y	119	ILE
24	Y	122	ASP
24	Y	155	VAL
25	b	23	SER
25	b	30	VAL
25	b	44	THR
25	b	105	VAL
25	b	112	ASP
25	b	115	MET
25	b	131	SER
25	b	134	GLU
25	b	136	SER
26	f	86	THR
27	i	2	ASN
27	i	3	ILE
27	i	6	ILE
27	i	7	VAL
27	i	8	SER
27	i	15	THR
27	i	66	VAL
27	i	67	TRP
27	i	71	ARG
27	i	73	THR
27	i	76	GLU
27	i	78	VAL
27	i	79	ARG
27	i	80	LYS
27	i	95	VAL
27	i	119	ASP
27	i	122	THR
27	i	123	VAL
27	i	126	VAL
27	i	128	THR
27	i	151	ARG
27	i	152	ILE
27	i	153	THR
27	i	162	THR
27	i	166	ILE
27	i	171	ASP

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Mol	Chain	Res	Type
27	i	184	LYS
27	i	187	ASP
27	i	200	SER
27	i	201	SER
27	i	205	SER
27	i	219	ARG
27	i	229	MET
27	i	231	SER
27	i	233	VAL
27	i	234	ARG
27	i	236	ILE
27	i	280	TRP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (23) such sidechains are listed below:

Mol	Chain	Res	Type
3	B	65	ASN
6	G	35	GLN
7	H	105	GLN
9	J	58	ASN
10	K	38	GLN
11	L	95	ASN
13	N	4	GLN
14	O	49	ASN
14	O	98	GLN
14	O	137	GLN
14	O	141	HIS
16	Q	195	GLN
20	U	6	GLN
20	U	65	GLN
21	V	231	GLN
21	V	287	ASN
21	V	306	ASN
22	W	44	GLN
23	X	107	HIS
24	Y	107	ASN
25	b	40	ASN
25	b	126	ASN
27	i	56	HIS

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	0	2754/2916 (94%)	485 (17%)	10 (0%)
2	9	119/122 (97%)	20 (16%)	2 (1%)
All	All	2873/3038 (94%)	505 (17%)	12 (0%)

All (505) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	0	17	U
1	0	30	G
1	0	31	G
1	0	58	G
1	0	66	A
1	0	68	G
1	0	74	A
1	0	77	A
1	0	78	G
1	0	93	A
1	0	94	U
1	0	110	A
1	0	121	A
1	0	122	U
1	0	127	A
1	0	128	U
1	0	132	C
1	0	133	A
1	0	134	C
1	0	136	G
1	0	138	A
1	0	145	U
1	0	147	G
1	0	148	C
1	0	149	G
1	0	155	G
1	0	158	A
1	0	159	A
1	0	173	A
1	0	177	U
1	0	178	C
1	0	192	G
1	0	193	A
1	0	198	A
1	0	199	A
1	0	205	U

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	0	206	C
1	0	211	A
1	0	226	G
1	0	245	U
1	0	260	U
1	0	261	C
1	0	270	U
1	0	274	G
1	0	276	A
1	0	277	C
1	0	284	C
1	0	286	C
1	0	287	A
1	0	288	U
1	0	289	A
1	0	291	C
1	0	292	G
1	0	293	G
1	0	296	C
1	0	298	G
1	0	299	G
1	0	301	A
1	0	313	U
1	0	314	C
1	0	341	G
1	0	342	A
1	0	344	A
1	0	350	G
1	0	360	G
1	0	361	G
1	0	362	A
1	0	363	A
1	0	364	A
1	0	365	G
1	0	366	A
1	0	367	U
1	0	368	C
1	0	369	C
1	0	370	C
1	0	371	G
1	0	375	U
1	0	379	U

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	0	380	C
1	0	381	C
1	0	384	A
1	0	385	A
1	0	386	U
1	0	400	U
1	0	401	A
1	0	402	U
1	0	411	A
1	0	421	G
1	0	422	C
1	0	454	C
1	0	467	A
1	0	483	G
1	0	491	G
1	0	495	C
1	0	500	A
1	0	501	A
1	0	502	A
1	0	507	G
1	0	511	C
1	0	514	U
1	0	515	A
1	0	517	G
1	0	537	U
1	0	538	A
1	0	540	A
1	0	541	G
1	0	542	C
1	0	543	G
1	0	553	A
1	0	557	G
1	0	562	U
1	0	576	U
1	0	577	A
1	0	583	G
1	0	592	G
1	0	598	C
1	0	599	U
1	0	608	G
1	0	615	U
1	0	616	U

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	0	624	A
1	0	631	G
1	0	633	A
1	0	636	A
1	0	649	U
1	0	664	A
1	0	672	G
1	0	673	G
1	0	678	A
1	0	683	C
1	0	692	A
1	0	699	C
1	0	703	U
1	0	704	A
1	0	706	G
1	0	717	U
1	0	718	U
1	0	719	G
1	0	722	C
1	0	746	G
1	0	747	G
1	0	757	G
1	0	761	C
1	0	763	A
1	0	779	U
1	0	807	G
1	0	808	A
1	0	809	A
1	0	810	A
1	0	811	G
1	0	823	C
1	0	834	U
1	0	837	U
1	0	838	G
1	0	842	U
1	0	843	A
1	0	844	C
1	0	847	U
1	0	848	A
1	0	859	A
1	0	860	C
1	0	864	G

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	0	870	G
1	0	871	G
1	0	877	A
1	0	879	G
1	0	880	G
1	0	888	A
1	0	900	G
1	0	902	U
1	0	907	C
1	0	912	C
1	0	924	A
1	0	926	G
1	0	945	A
1	0	955	G
1	0	972	G
1	0	974	A
1	0	977	C
1	0	978	G
1	0	994	U
1	0	995	C
1	0	996	G
1	0	998	U
1	0	1000	C
1	0	1001	C
1	0	1008	A
1	0	1045	C
1	0	1046	G
1	0	1053	G
1	0	1060	G
1	0	1071	G
1	0	1073	G
1	0	1089	A
1	0	1094	G
1	0	1110	U
1	0	1111	G
1	0	1114	G
1	0	1119	A
1	0	1125	A
1	0	1127	C
1	0	1128	G
1	0	1134	U
1	0	1143	C

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	0	1144	C
1	0	1145	C
1	0	1146	U
1	0	1147	A
1	0	1148	A
1	0	1149	A
1	0	1151	A
1	0	1204	A
1	0	1205	C
1	0	1206	C
1	0	1207	G
1	0	1211	G
1	0	1212	A
1	0	1213	G
1	0	1215	U
1	0	1216	U
1	0	1231	U
1	0	1232	G
1	0	1235	C
1	0	1236	G
1	0	1243	A
1	0	1245	A
1	0	1246	U
1	0	1247	C
1	0	1250	C
1	0	1256	A
1	0	1273	A
1	0	1274	U
1	0	1275	U
1	0	1276	U
1	0	1277	A
1	0	1278	G
1	0	1285	U
1	0	1286	C
1	0	1287	C
1	0	1336	G
1	0	1337	A
1	0	1338	C
1	0	1344	A
1	0	1356	C
1	0	1362	C
1	0	1365	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	0	1374	G
1	0	1377	A
1	0	1388	A
1	0	1403	A
1	0	1404	C
1	0	1424	C
1	0	1443	U
1	0	1444	A
1	0	1448	G
1	0	1453	U
1	0	1472	A
1	0	1473	A
1	0	1481	A
1	0	1483	A
1	0	1498	U
1	0	1500	U
1	0	1507	A
1	0	1515	G
1	0	1516	C
1	0	1517	A
1	0	1518	A
1	0	1519	U
1	0	1520	A
1	0	1521	A
1	0	1522	A
1	0	1529	C
1	0	1565	C
1	0	1568	A
1	0	1576	A
1	0	1582	U
1	0	1584	G
1	0	1587	G
1	0	1595	G
1	0	1600	G
1	0	1608	A
1	0	1610	A
1	0	1621	A
1	0	1630	C
1	0	1631	G
1	0	1648	G
1	0	1651	A
1	0	1653	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	0	1659	A
1	0	1660	G
1	0	1677	A
1	0	1680	U
1	0	1687	C
1	0	1693	C
1	0	1704	U
1	0	1716	U
1	0	1718	U
1	0	1719	C
1	0	1724	U
1	0	1725	C
1	0	1746	G
1	0	1747	C
1	0	1765	U
1	0	1766	C
1	0	1773	A
1	0	1777	A
1	0	1784	C
1	0	1803	C
1	0	1805	G
1	0	1812	G
1	0	1813	G
1	0	1822	A
1	0	1825	G
1	0	1833	A
1	0	1849	C
1	0	1866	G
1	0	1871	G
1	0	1872	U
1	0	1878	A
1	0	1882	C
1	0	1888	A
1	0	1889	G
1	0	1902	A
1	0	1912	A
1	0	1918	G
1	0	1922	G
1	0	1935	A
1	0	1940	G
1	0	1942	G
1	0	1944	G

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	0	1945	U
1	0	1946	A
1	0	1947	A
1	0	1948	C
1	0	1949	U
1	0	1950	A
1	0	1952	G
1	0	1954	C
1	0	1955	C
1	0	1956	C
1	0	1957	U
1	0	1963	G
1	0	1964	G
1	0	1971	A
1	0	1972	G
1	0	1973	U
1	0	1979	G
1	0	1989	U
1	0	1997	U
1	0	2000	A
1	0	2001	U
1	0	2004	A
1	0	2006	G
1	0	2025	U
1	0	2027	U
1	0	2052	U
1	0	2057	U
1	0	2065	G
1	0	2066	G
1	0	2067	A
1	0	2089	A
1	0	2094	A
1	0	2095	G
1	0	2096	A
1	0	2103	A
1	0	2127	G
1	0	2132	G
1	0	2133	U
1	0	2135	G
1	0	2225	A
1	0	2226	C
1	0	2227	U

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	0	2228	G
1	0	2229	C
1	0	2230	G
1	0	2231	A
1	0	2236	C
1	0	2242	U
1	0	2243	G
1	0	2246	G
1	0	2247	G
1	0	2249	G
1	0	2251	A
1	0	2252	C
1	0	2264	G
1	0	2265	G
1	0	2284	A
1	0	2293	A
1	0	2306	C
1	0	2310	C
1	0	2313	A
1	0	2314	A
1	0	2332	U
1	0	2333	C
1	0	2334	G
1	0	2335	G
1	0	2336	G
1	0	2337	A
1	0	2347	A
1	0	2348	G
1	0	2349	A
1	0	2362	A
1	0	2382	U
1	0	2412	U
1	0	2413	G
1	0	2415	U
1	0	2420	C
1	0	2425	C
1	0	2430	A
1	0	2431	G
1	0	2432	G
1	0	2453	A
1	0	2455	G
1	0	2458	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	0	2459	G
1	0	2460	A
1	0	2462	A
1	0	2463	A
1	0	2469	C
1	0	2473	G
1	0	2475	G
1	0	2476	A
1	0	2478	A
1	0	2487	G
1	0	2502	A
1	0	2503	C
1	0	2504	A
1	0	2506	A
1	0	2507	U
1	0	2530	G
1	0	2531	A
1	0	2546	A
1	0	2548	C
1	0	2558	C
1	0	2594	A
1	0	2595	G
1	0	2600	U
1	0	2601	C
1	0	2602	G
1	0	2603	U
1	0	2604	G
1	0	2605	A
1	0	2606	G
1	0	2618	C
1	0	2630	A
1	0	2637	C
1	0	2638	U
1	0	2641	U
1	0	2659	A
1	0	2666	U
1	0	2674	A
1	0	2675	C
1	0	2676	G
1	0	2692	A
1	0	2709	G
1	0	2719	U

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	0	2740	G
1	0	2741	U
1	0	2743	G
1	0	2755	C
1	0	2761	G
1	0	2762	C
1	0	2763	A
1	0	2767	U
1	0	2776	A
1	0	2778	A
1	0	2785	A
1	0	2792	A
1	0	2793	A
1	0	2804	A
1	0	2805	A
1	0	2807	A
1	0	2818	U
1	0	2820	A
1	0	2830	U
1	0	2843	C
1	0	2844	G
1	0	2860	A
1	0	2862	G
1	0	2869	G
1	0	2883	A
1	0	2889	G
1	0	2890	C
1	0	2895	A
1	0	2902	G
2	9	3	C
2	9	11	A
2	9	23	U
2	9	33	A
2	9	38	U
2	9	39	C
2	9	40	C
2	9	43	A
2	9	54	U
2	9	55	A
2	9	56	A
2	9	61	G
2	9	65	G

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
2	9	77	G
2	9	84	A
2	9	100	G
2	9	113	G
2	9	119	C
2	9	120	C
2	9	121	U

All (12) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	0	273	U
1	0	366	A
1	0	499	A
1	0	582	C
1	0	879	G
1	0	999	U
1	0	1127	C
1	0	1272	U
1	0	2784	U
1	0	2842	U
2	9	22	G
2	9	120	C

## 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](#)

Of 158 ligands modelled in this entry, 158 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

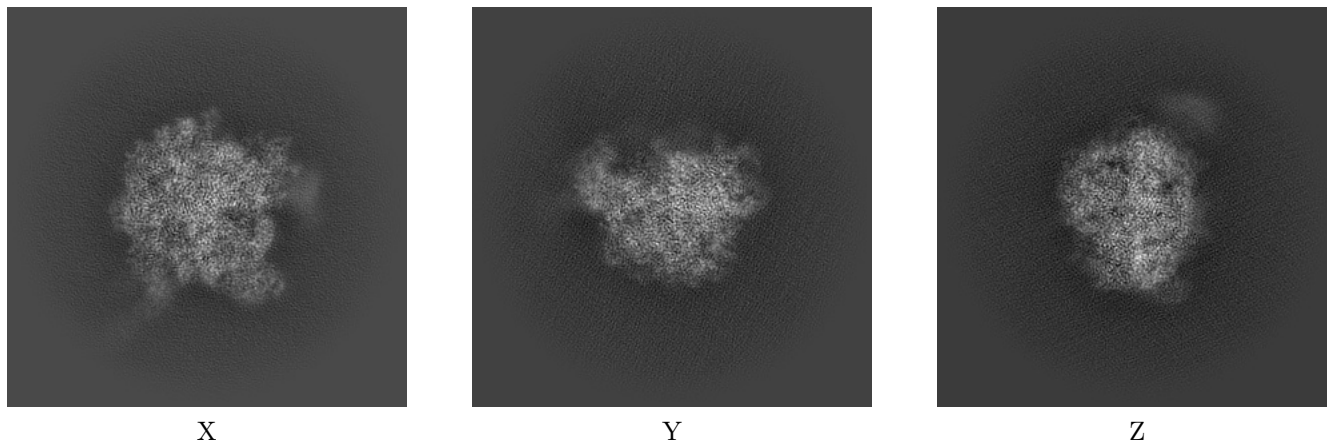
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-62914. These allow visual inspection of the internal detail of the map and identification of artifacts.

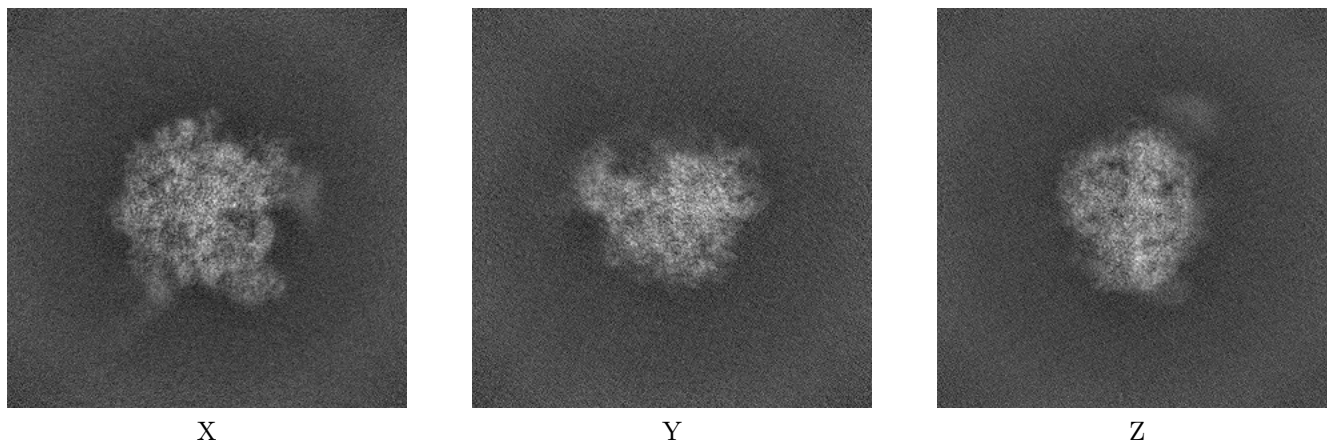
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

#### 6.1.1 Primary map



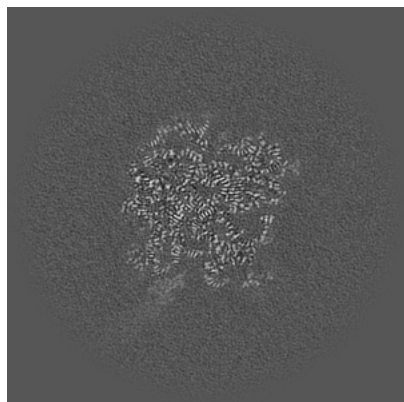
#### 6.1.2 Raw map



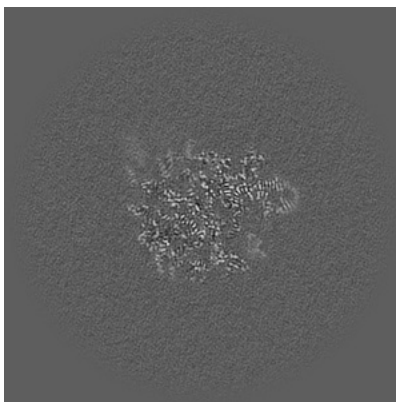
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

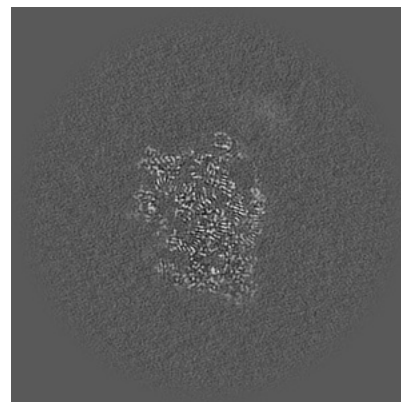
### 6.2.1 Primary map



X Index: 320

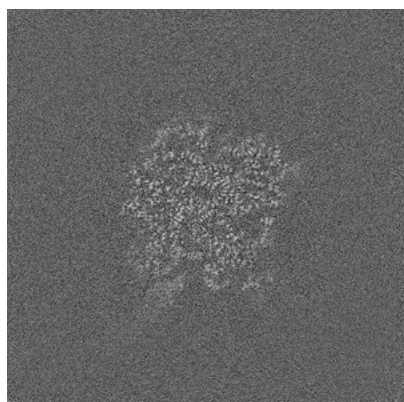


Y Index: 320

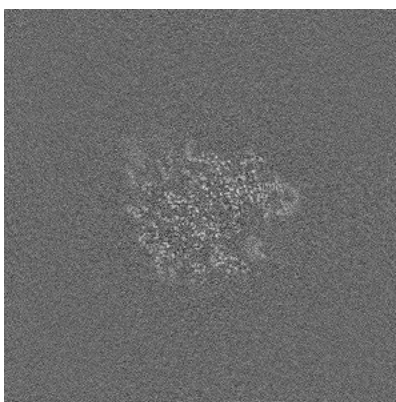


Z Index: 320

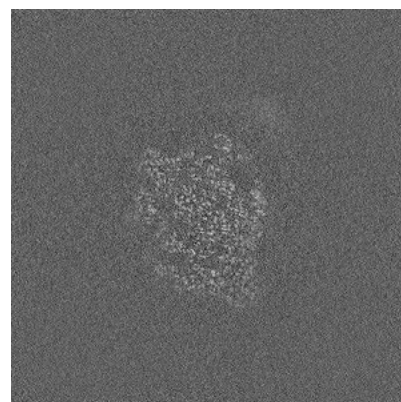
### 6.2.2 Raw map



X Index: 320



Y Index: 320

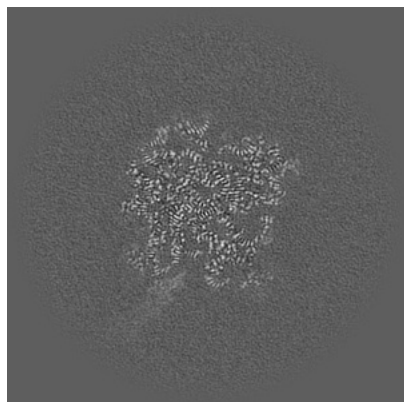


Z Index: 320

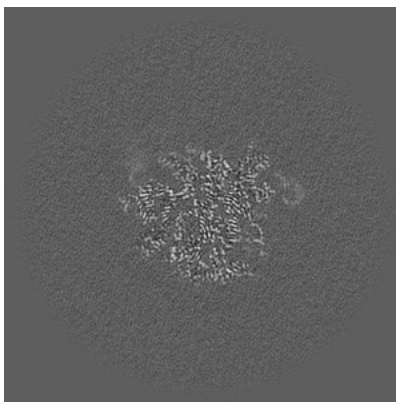
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

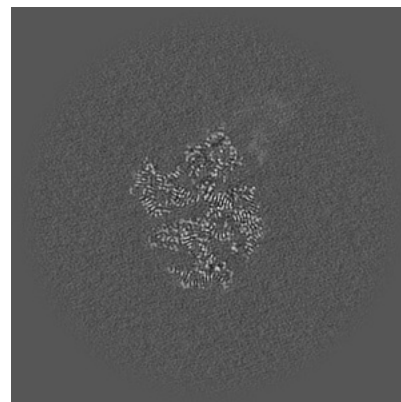
### 6.3.1 Primary map



X Index: 321

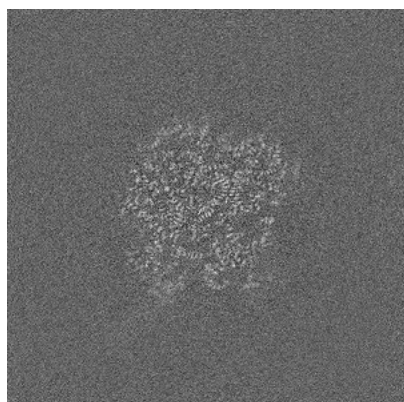


Y Index: 331

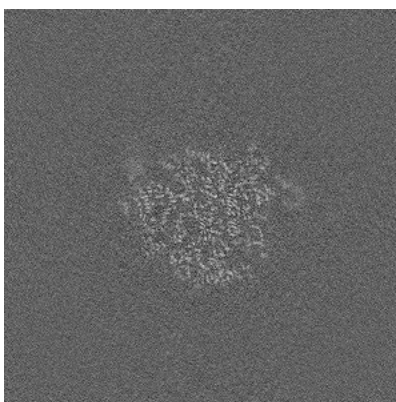


Z Index: 361

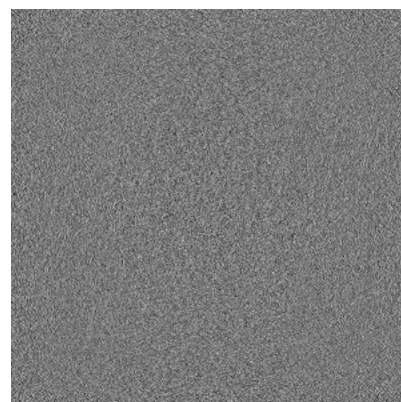
### 6.3.2 Raw map



X Index: 319



Y Index: 332

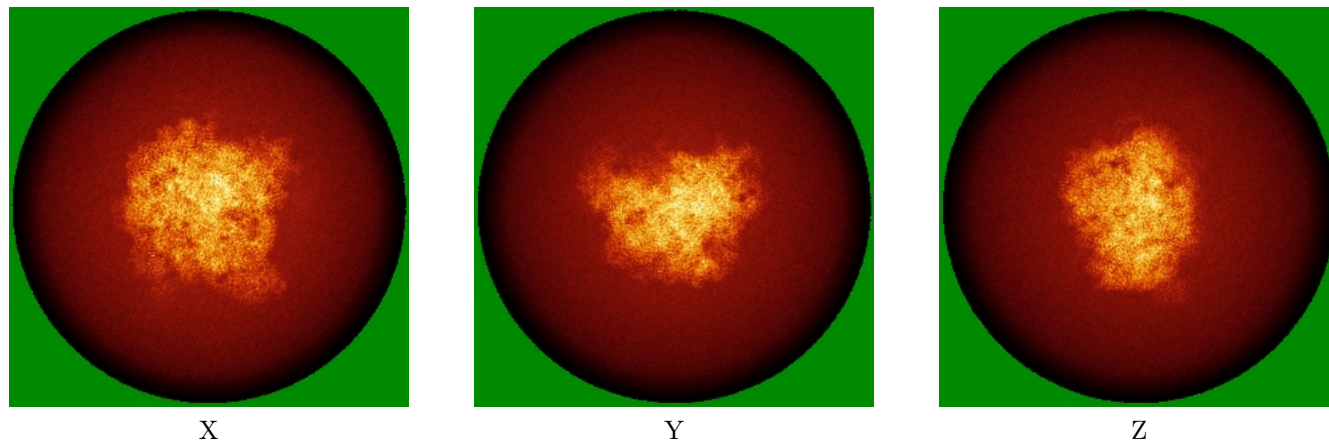


Z Index: 0

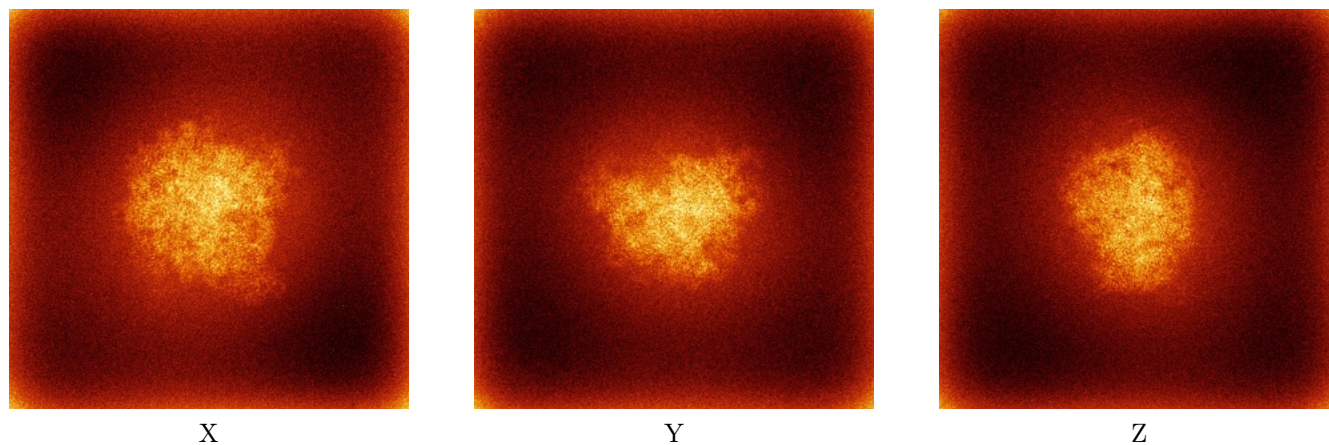
The images above show the largest variance slices of the map in three orthogonal directions.

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

### 6.4.1 Primary map



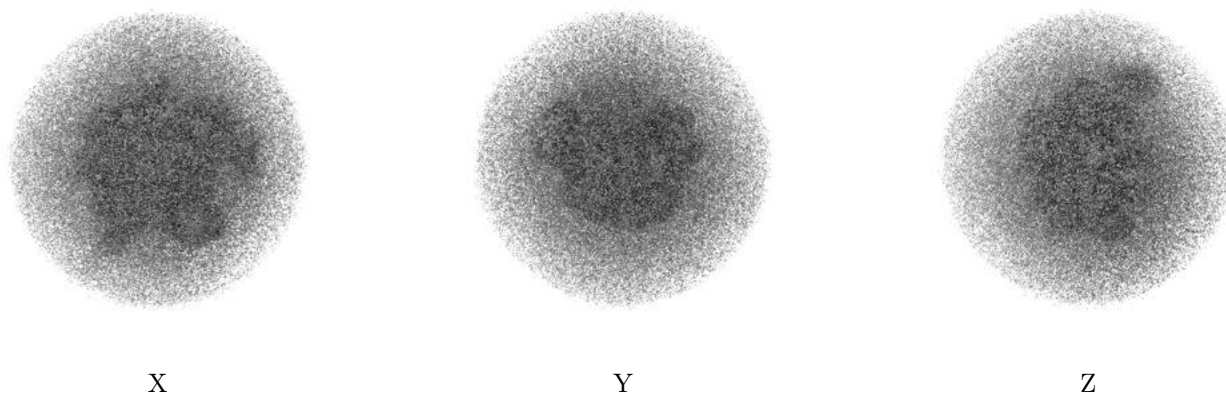
### 6.4.2 Raw map



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.

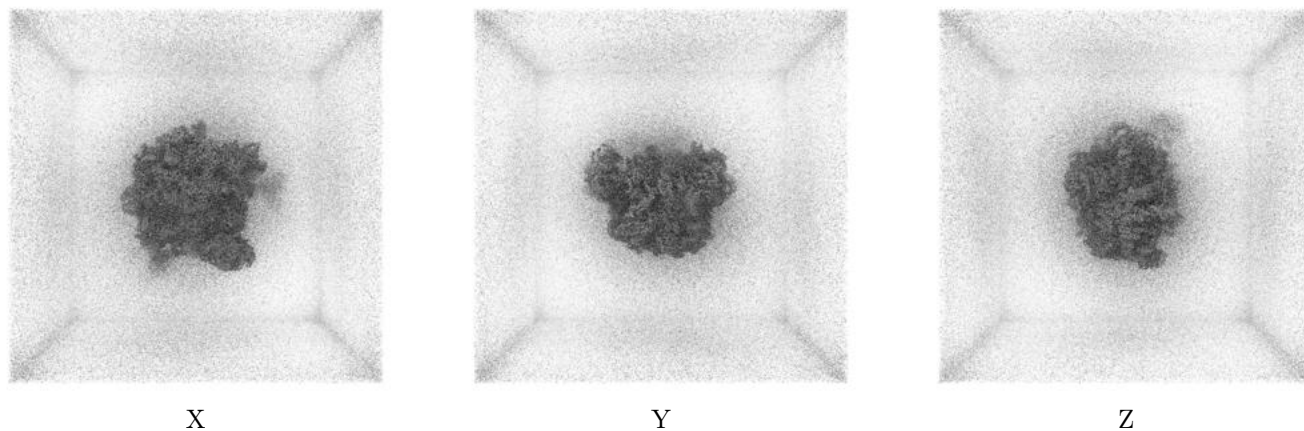
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.16. 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.

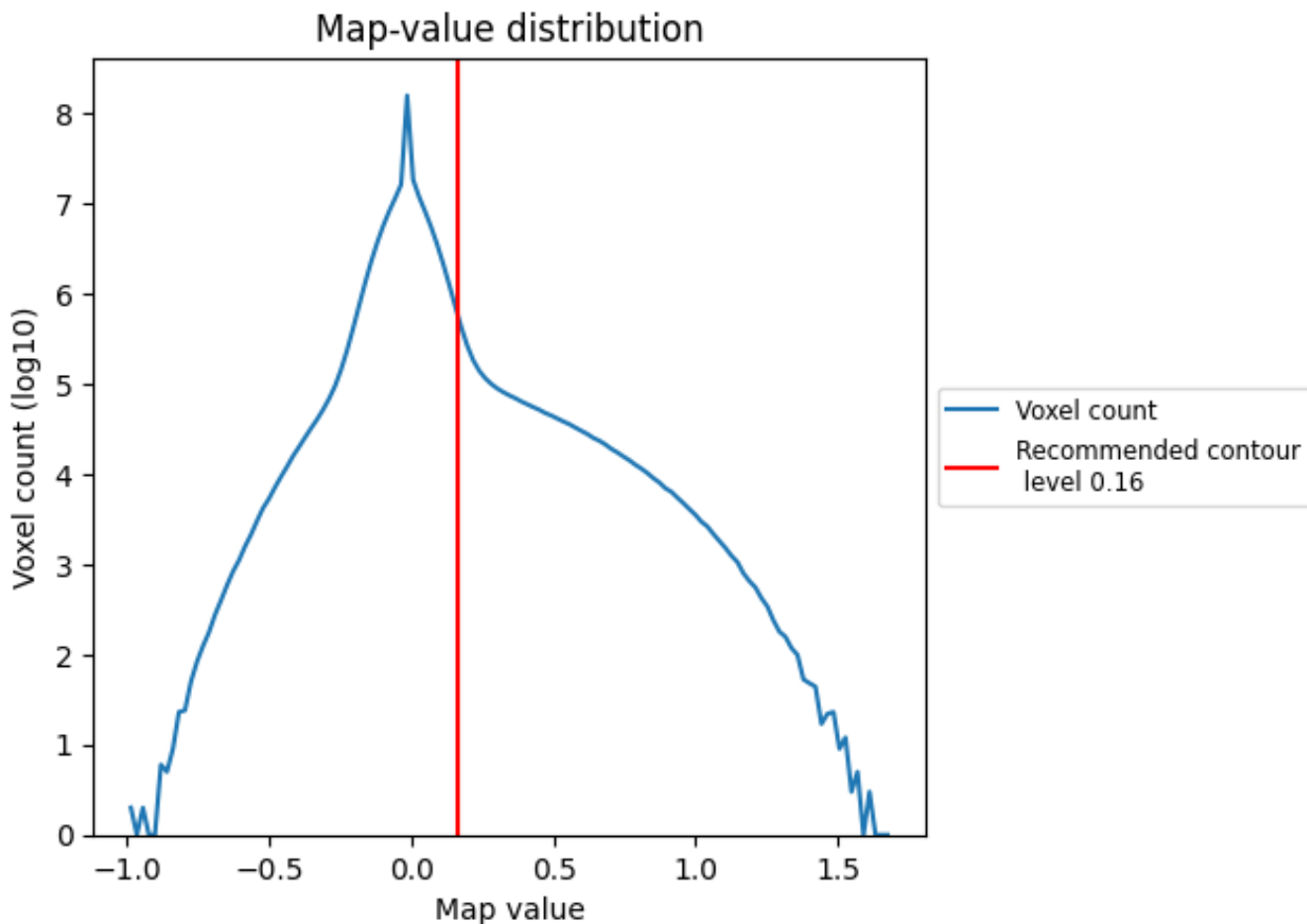
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

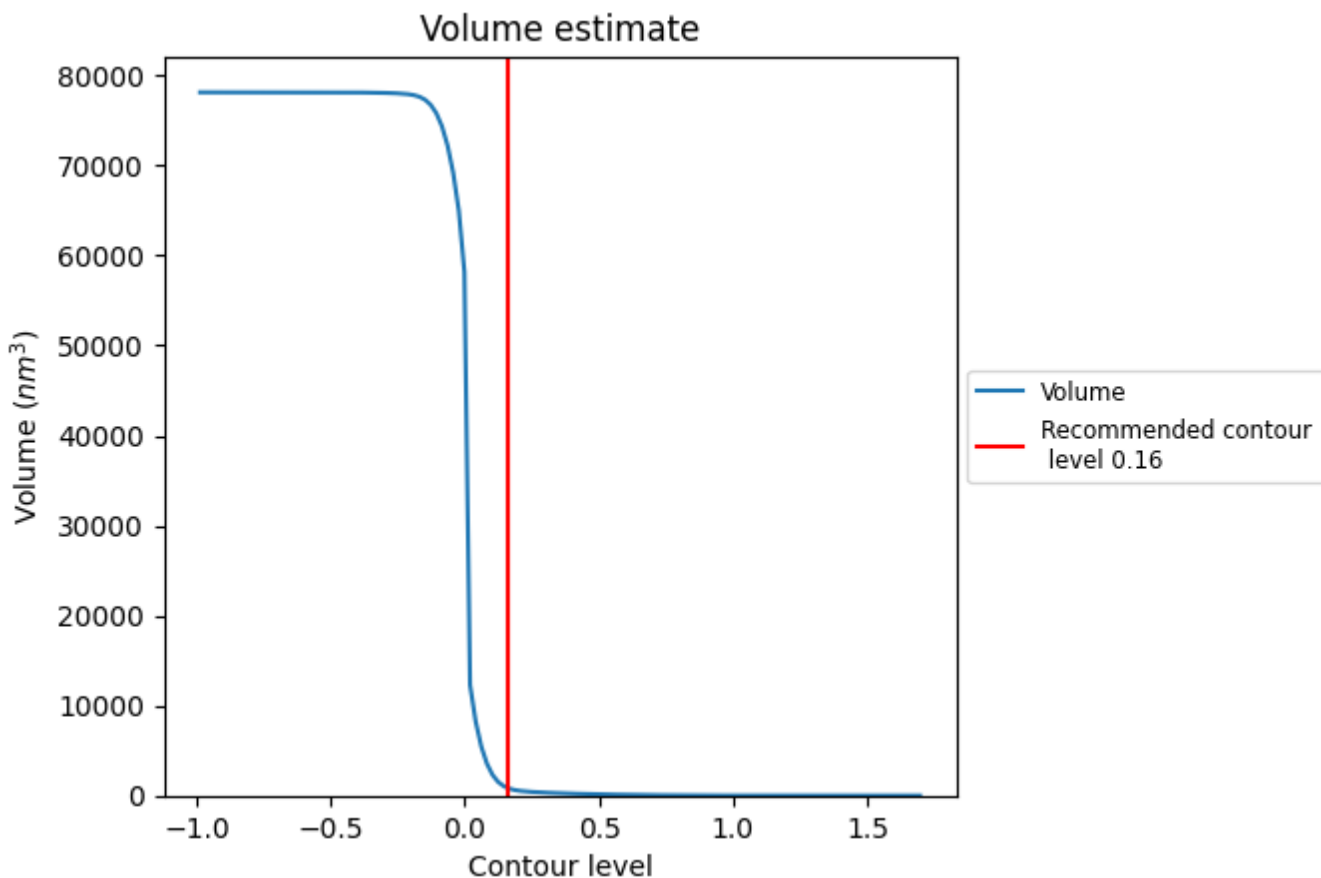
This section contains the results of statistical analysis of the map.

### 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.

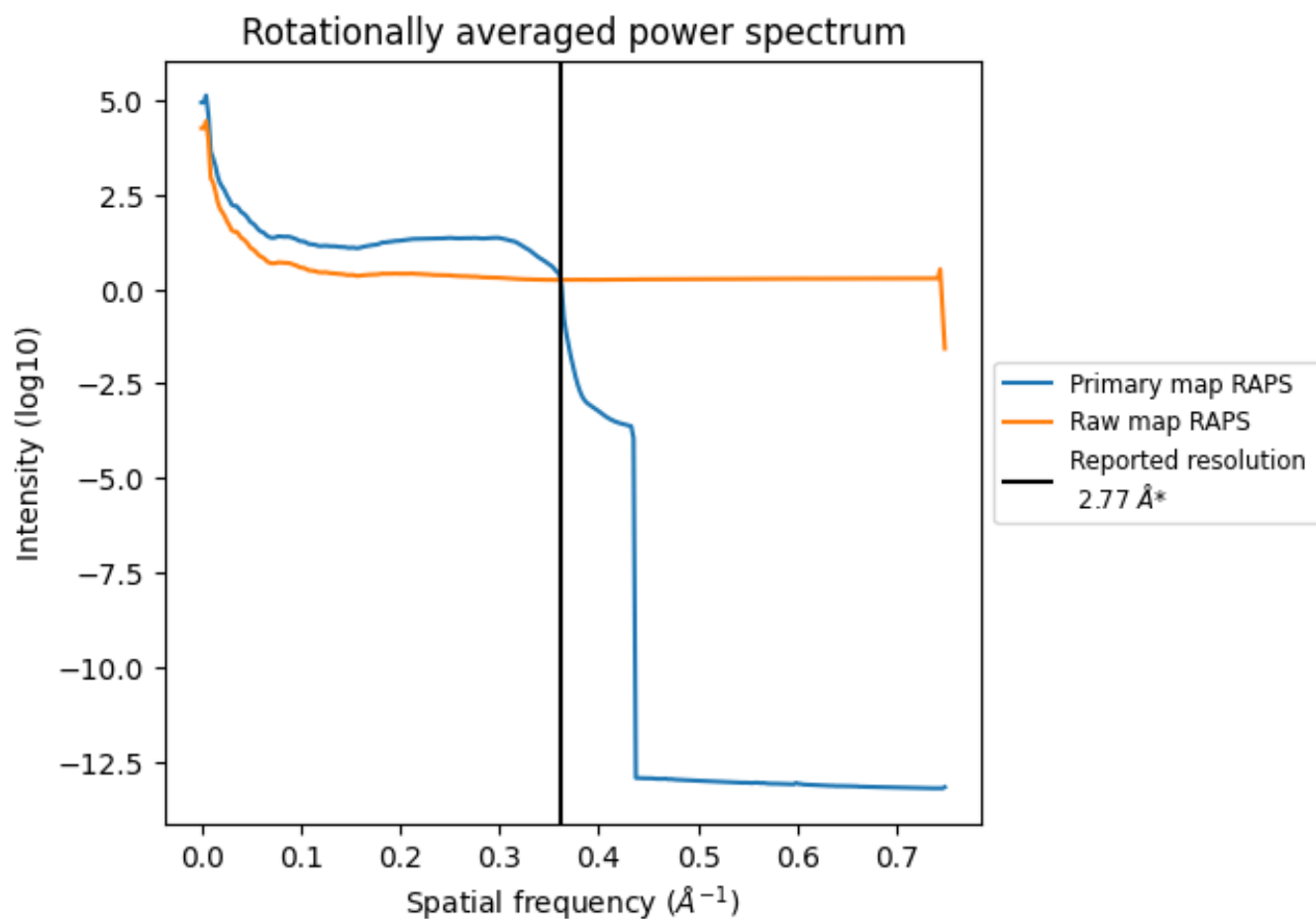
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 854 nm<sup>3</sup>; this corresponds to an approximate mass of 772 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 [i](#)

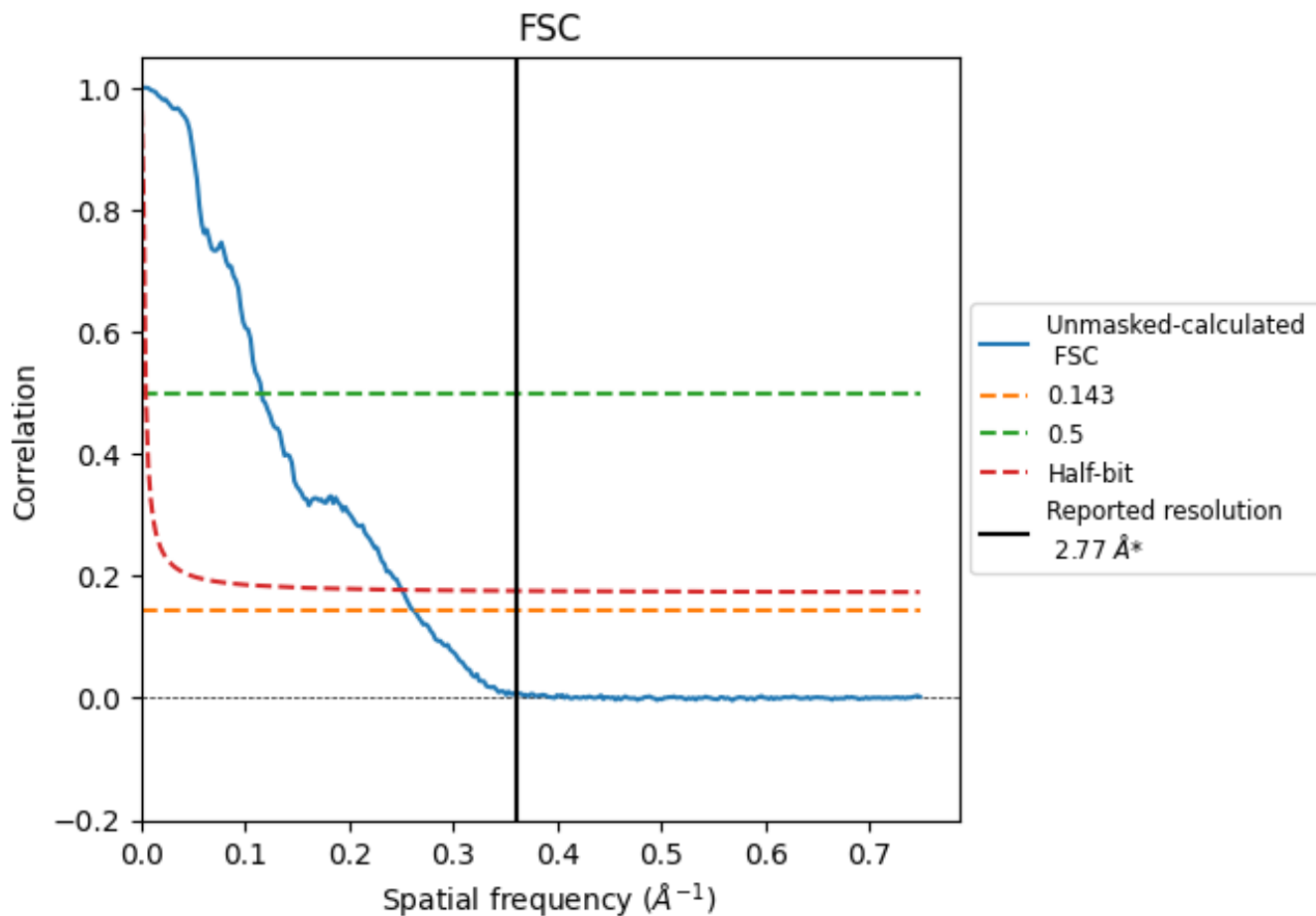


\*Reported resolution corresponds to spatial frequency of 0.361 Å<sup>-1</sup>

## 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 0.361 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

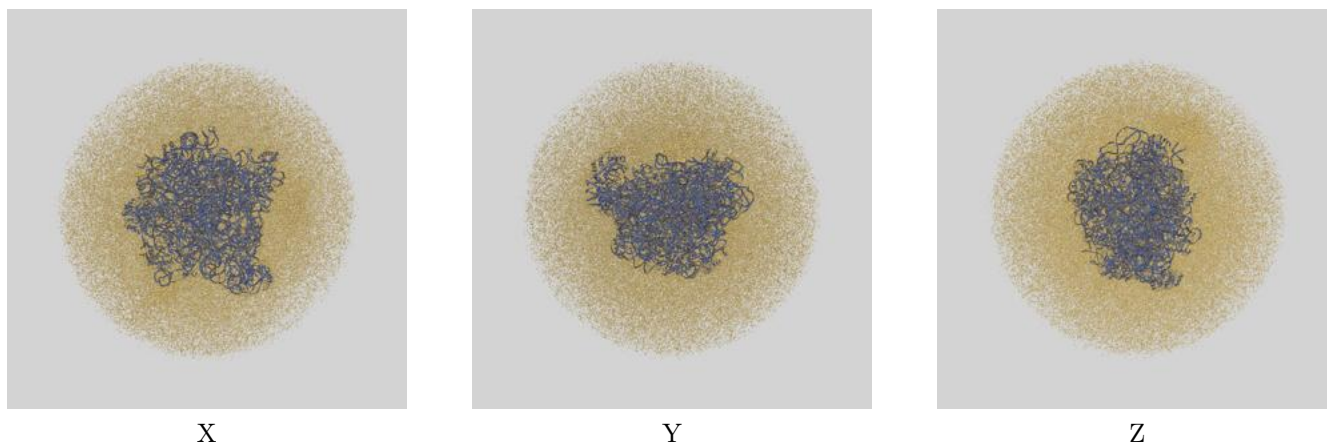
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.77	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.82	8.63	3.99

\*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 3.82 differs from the reported value 2.77 by more than 10 %

## 9 Map-model fit [i](#)

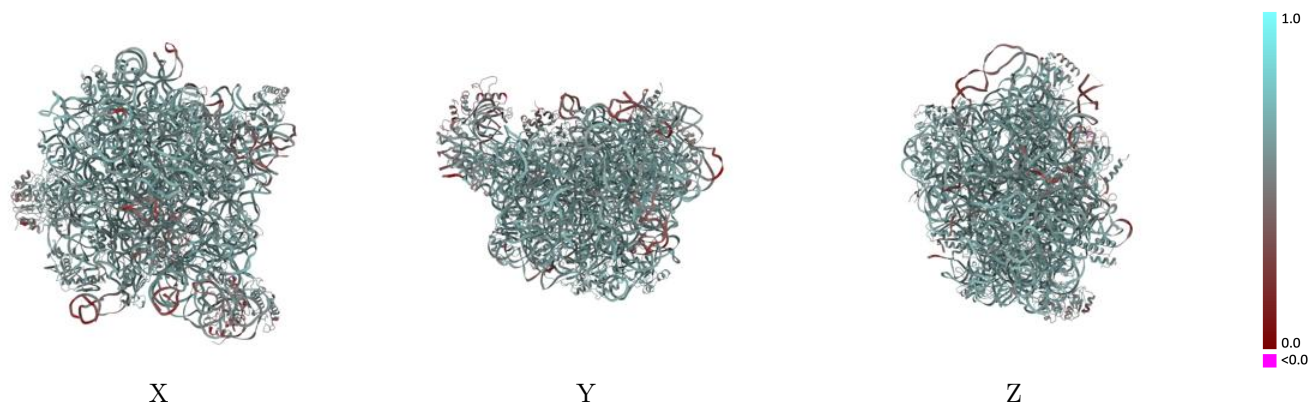
This section contains information regarding the fit between EMDB map EMD-62914 and PDB model 9L9V. Per-residue inclusion information can be found in section [3](#) on page [9](#).

### 9.1 Map-model overlay [i](#)



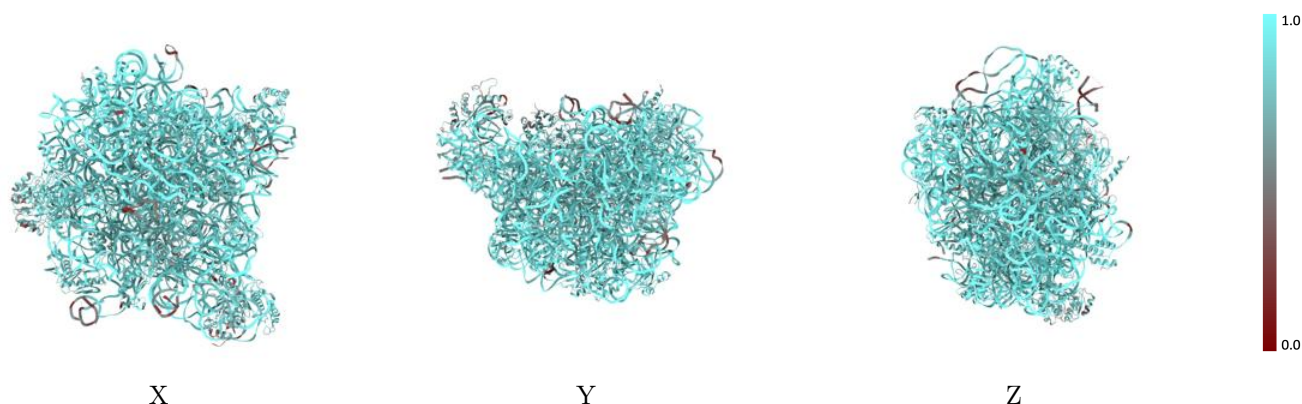
The images above show the 3D surface view of the map at the recommended contour level 0.16 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



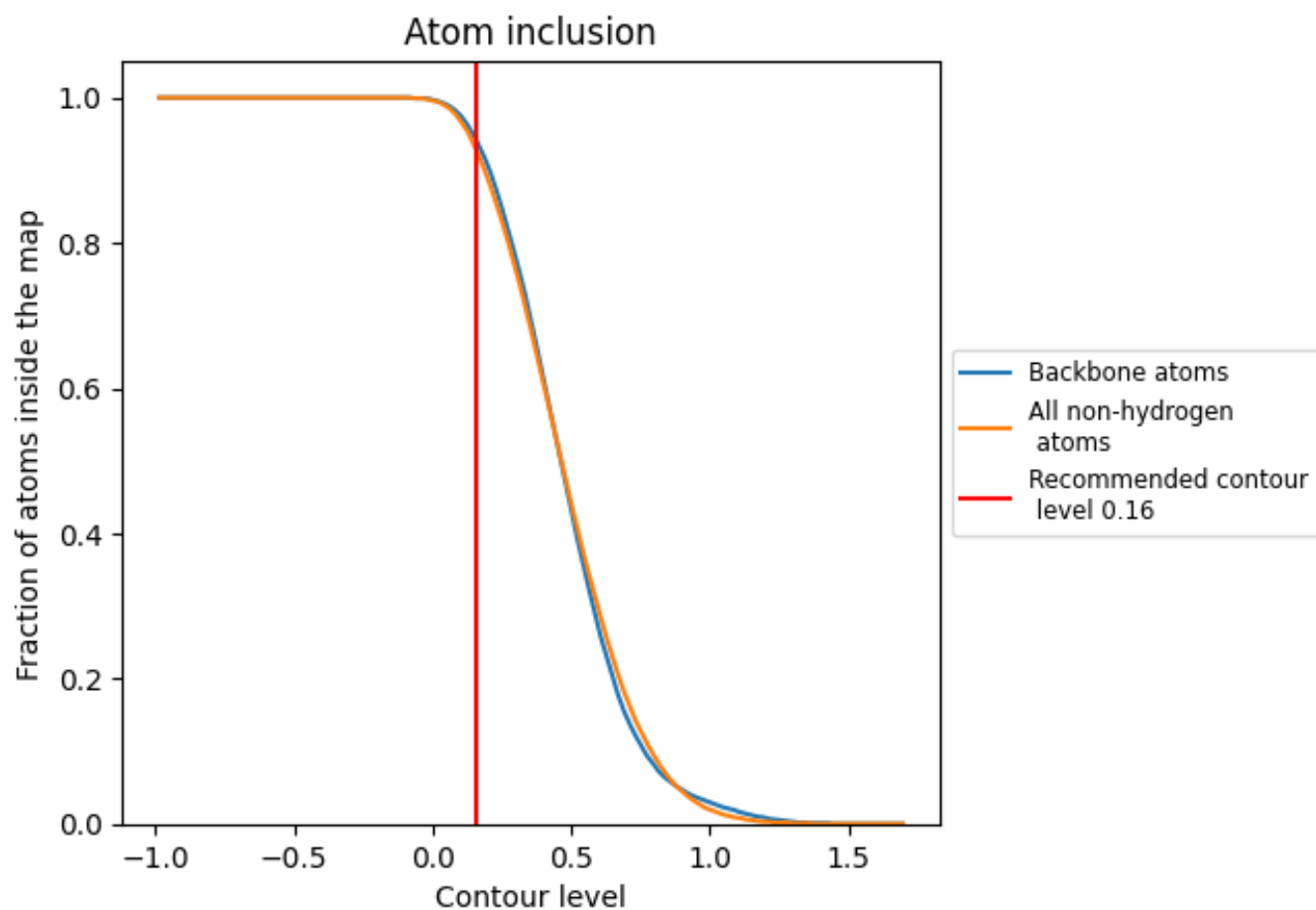
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.16).

























































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 93% 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 (0.16) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9260	 0.5900
0	 0.9490	 0.5950
9	 0.9390	 0.5690
B	 0.7210	 0.5060
E	 0.8440	 0.5530
F	 0.9180	 0.6040
G	 0.9620	 0.6300
H	 0.8890	 0.5870
I	 0.8770	 0.5600
J	 0.9100	 0.5930
K	 0.9440	 0.6180
L	 0.9310	 0.6190
M	 0.9110	 0.6040
N	 0.9070	 0.5950
O	 0.9230	 0.6040
P	 0.8740	 0.5840
Q	 0.9160	 0.6000
R	 0.8760	 0.5780
S	 0.9580	 0.6320
T	 0.9060	 0.6130
U	 0.9300	 0.6020
V	 0.9410	 0.6170
W	 0.9190	 0.6080
X	 0.6440	 0.4270
Y	 0.8300	 0.5570
b	 0.9190	 0.6060
f	 0.9200	 0.6040
i	 0.7790	 0.5090

