Full wwPDB EM Validation Report

Mar 29, 2026 – 10:00 AM UTC

PDB ID	:	7WTN / pdb_00007wtn
EMDB ID	:	EMD-32792
Title	:	Cryo-EM structure of a yeast pre-40S ribosomal subunit - State Tsr1-1 (with Rps2)
Authors	:	Cheng, J.; Lau, B.; Thoms, M.; Ameismeier, M.; Berninghausen, O.; Hurt, E.; Beckmann, R.
Deposited on	:	2022-02-05
Resolution	:	3.40 Å(reported)

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the (i) 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 (i)) were used in the production of this report:

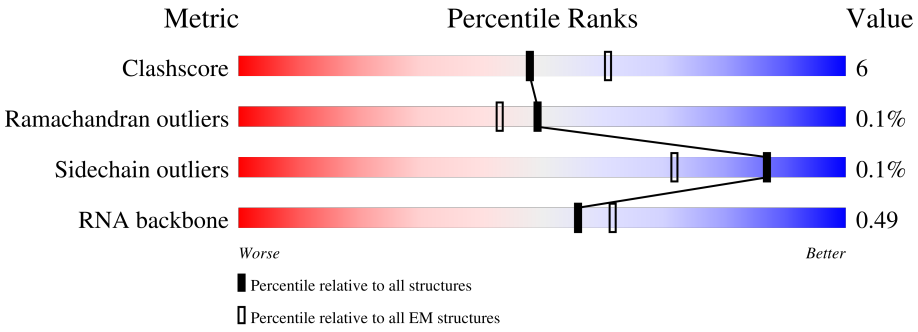
EMDB validation analysis	:	0.0.1.dev132
MolProbity	:	4-5-2 with Phenix2.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh &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

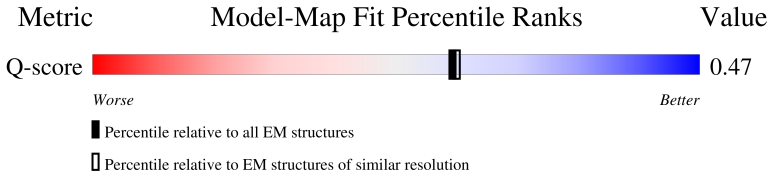
1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.40 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	14717 (2.90 - 3.90)

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 <=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	C2	1800	41% 22% • 33%
2	SB	255	66% 18% 15%
3	SC	254	• 68% 17% 15%

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Mol	Chain	Length	Quality of chain
4	SE	261	86% 13%
5	SG	236	75% 17% 8%
6	SH	190	79% 17%
7	SI	200	76% 18% 6%
8	SJ	197	77% 17% 6%
9	SL	156	82% 12% 6%
10	SN	151	85% 14%
11	SO	137	73% 20% 7%
12	SW	130	89% 10%
13	SX	145	77% 23%
14	SY	135	76% 23%
15	Sb	82	83% 16%
16	Se	63	8% 46% 14% 40%
17	CA	274	54% 12% 34%
18	CB	275	9% 87%

2 Entry composition

There are 19 unique types of molecules in this entry. The entry contains 46427 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 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	C2	1200	25592	11448	4555	8389	1200	0	0

- Molecule 2 is a protein called 40S ribosomal protein S1-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	SB	216	1722	1091	312	315	4	0	0

- Molecule 3 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	SC	217	1635	1047	289	297	2	0	0

- Molecule 4 is a protein called 40S ribosomal protein S4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	SE	260	2068	1316	389	360	3	0	0

- Molecule 5 is a protein called 40S ribosomal protein S6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	SG	218	1755	1102	337	313	3	0	0

- Molecule 6 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
6	SH	185	1486	954	266	266	0	0

- Molecule 7 is a protein called 40S ribosomal protein S8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	SI	188	Total	C	N	O	S	0	0
			1489	925	298	264	2		

- Molecule 8 is a protein called 40S ribosomal protein S9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	SJ	185	Total	C	N	O	S	0	0
			1494	943	289	261	1		

- Molecule 9 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	SL	146	Total	C	N	O	S	0	0
			1168	747	221	197	3		

- Molecule 10 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	SN	150	Total	C	N	O	S	0	0
			1192	759	224	207	2		

- Molecule 11 is a protein called 40S ribosomal protein S14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	SO	128	Total	C	N	O	S	0	0
			949	582	188	176	3		

- Molecule 12 is a protein called 40S ribosomal protein S22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	SW	129	Total	C	N	O	S	0	0
			1021	650	188	180	3		

- Molecule 13 is a protein called 40S ribosomal protein S23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	SX	144	Total	C	N	O	S	0	0
			1121	708	220	191	2		

- Molecule 14 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	SY	134	Total	C	N	O	0	0
			1073	676	208	189		

- Molecule 15 is a protein called 40S ribosomal protein S27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	Sb	81	Total	C	N	O	S	0	0
			610	382	110	113	5		

- Molecule 16 is a protein called 40S ribosomal protein S30-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Se	38	Total	C	N	O	S	0	0
			313	198	65	49	1		

- Molecule 17 is a protein called Pre-rRNA-processing protein PNO1.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	CA	181	Total	C	N	O	S	0	0
			1436	917	261	254	4		

- Molecule 18 is a protein called 18S rRNA (guanine(1575)-N(7))-methyltransferase.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	CB	35	Total	C	N	O	S	0	0
			302	189	69	43	1		

- Molecule 19 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
19	Sb	1	Total	Zn	0
			1	1	

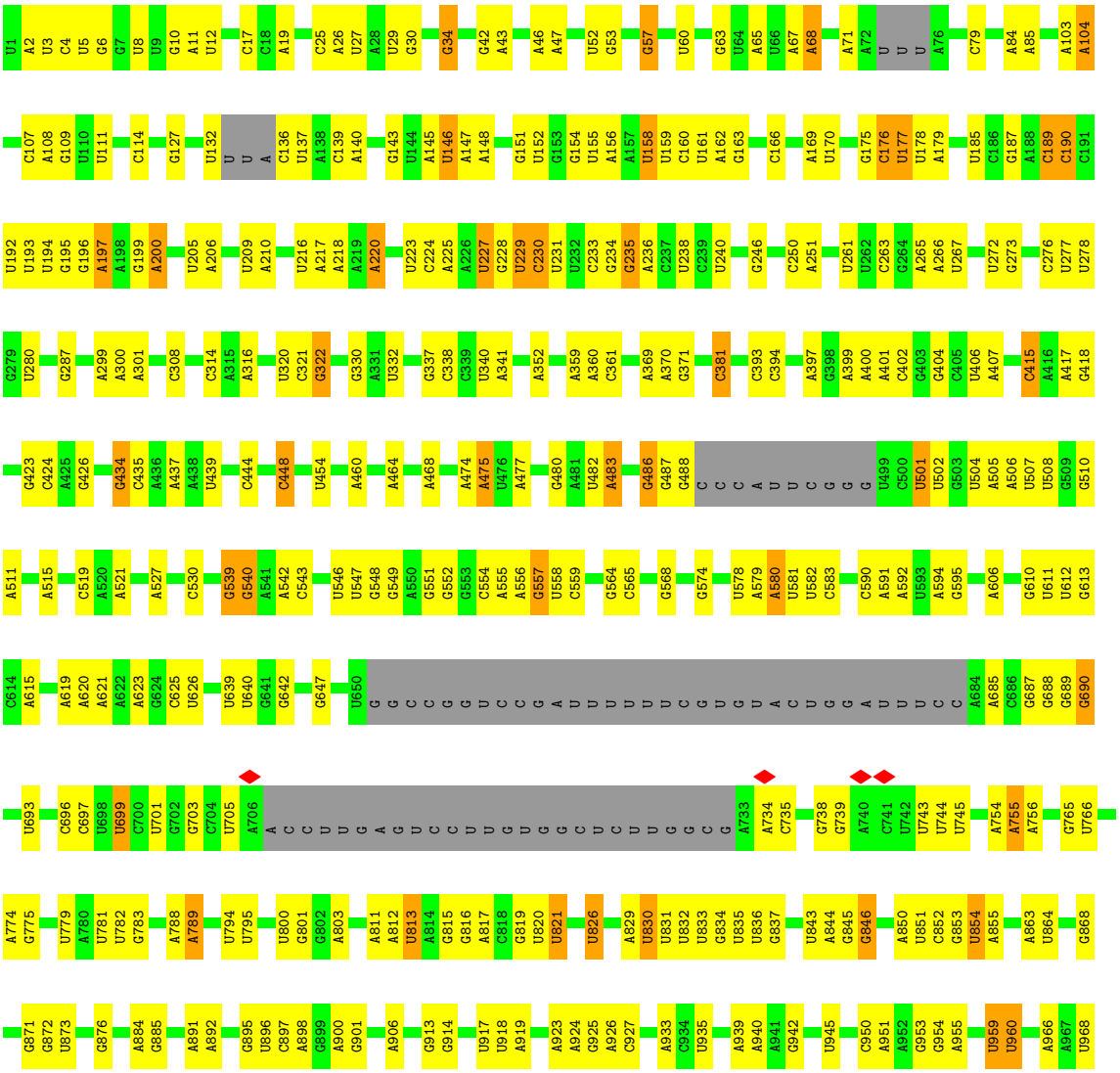
3 Residue-property plots (i)

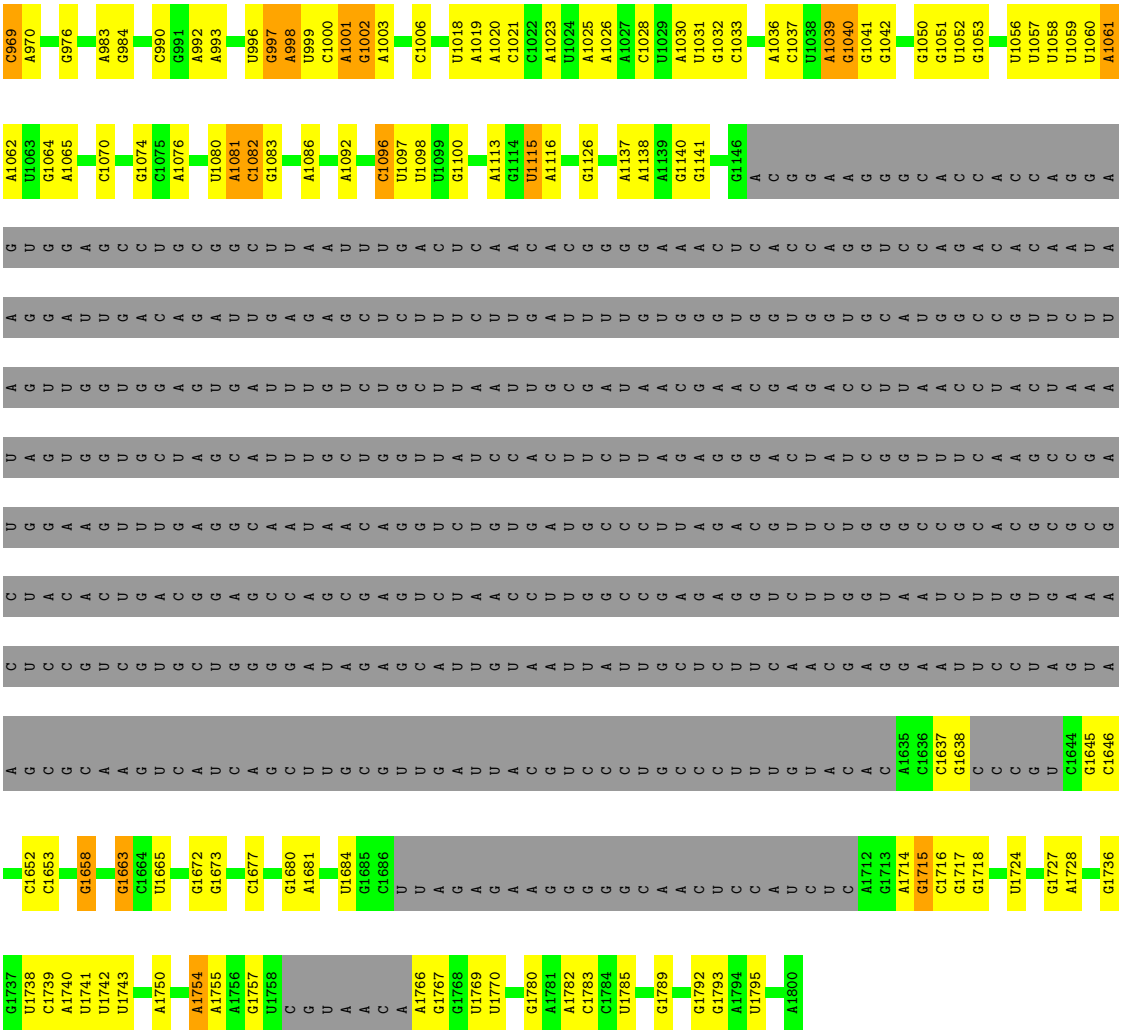
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: 18S rRNA

Chain C2:



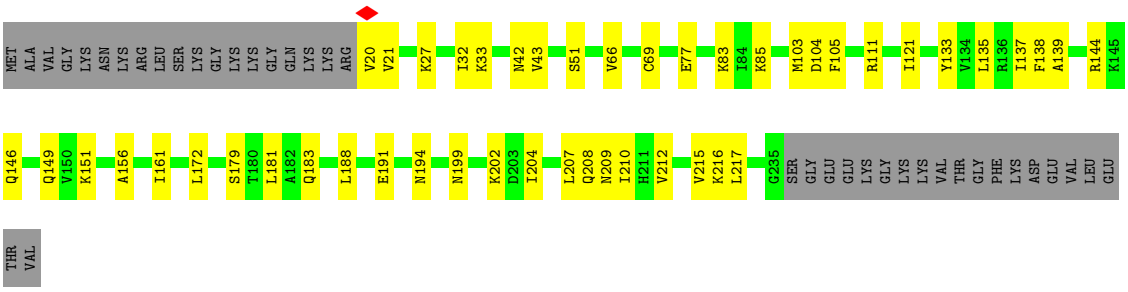




• Molecule 2: 40S ribosomal protein S1-A

Chain SB:



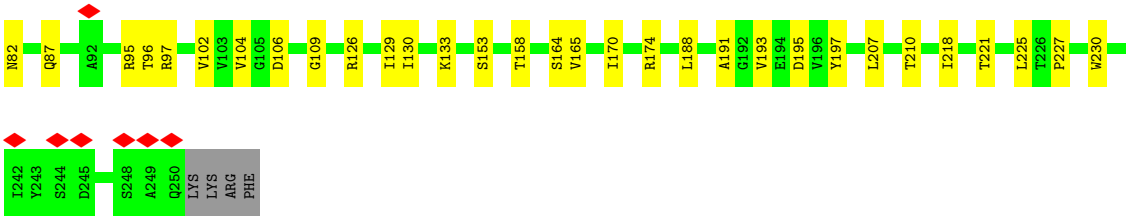


• Molecule 3: 40S ribosomal protein S2

Chain SC:







• Molecule 4: 40S ribosomal protein S4-A

Chain SE:

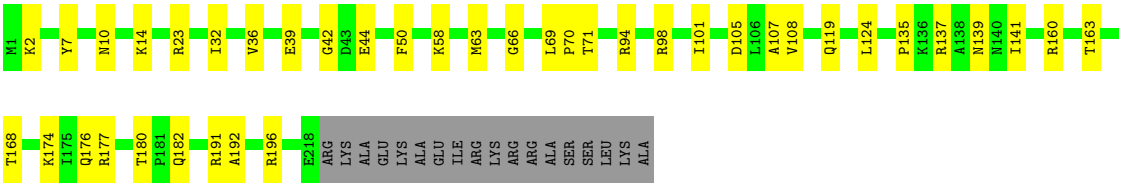




• Molecule 5: 40S ribosomal protein S6-A

Chain SG:

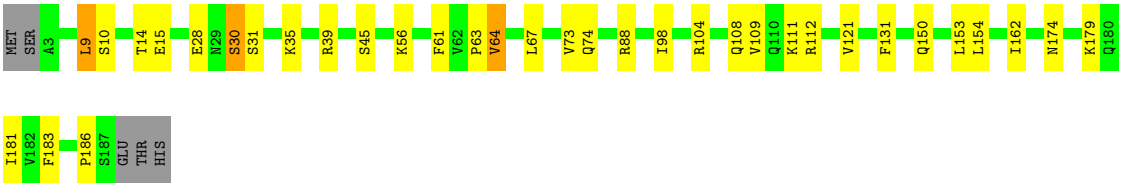




• Molecule 6: 40S ribosomal protein S7-A

Chain SH:





• Molecule 7: 40S ribosomal protein S8-A

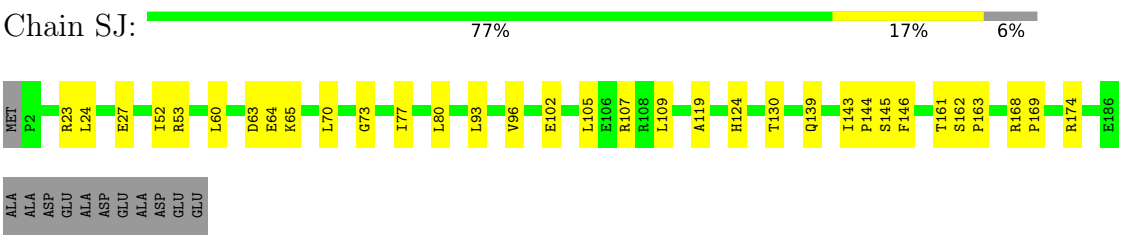
Chain SI:





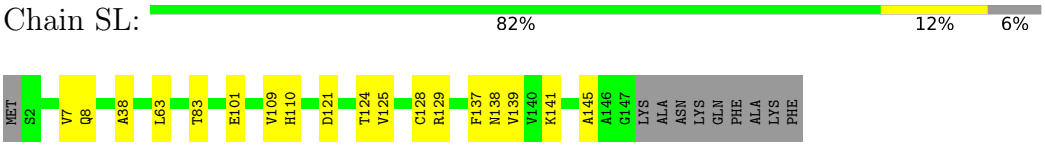
• Molecule 8: 40S ribosomal protein S9-A

Chain SJ:



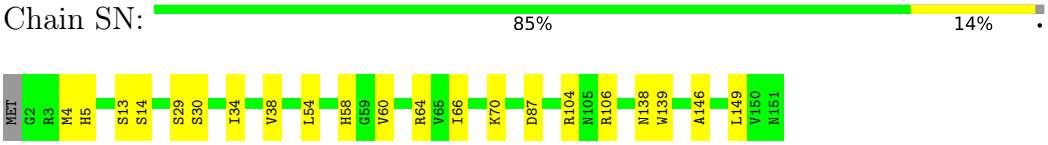
• Molecule 9: 40S ribosomal protein S11-A

Chain SL:



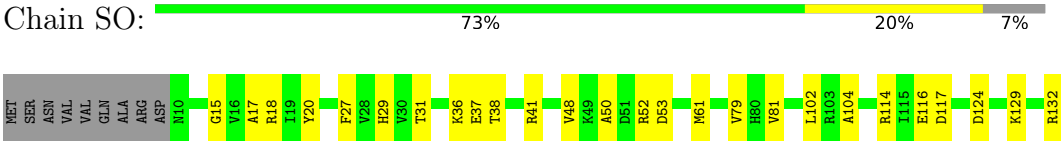
• Molecule 10: 40S ribosomal protein S13

Chain SN:



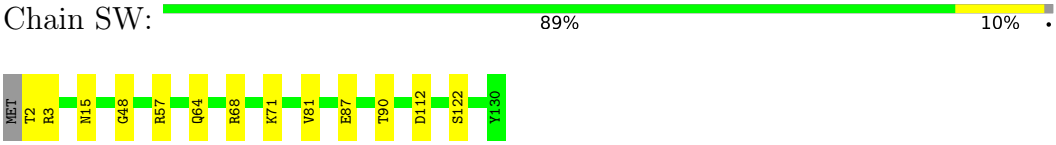
• Molecule 11: 40S ribosomal protein S14-A

Chain SO:



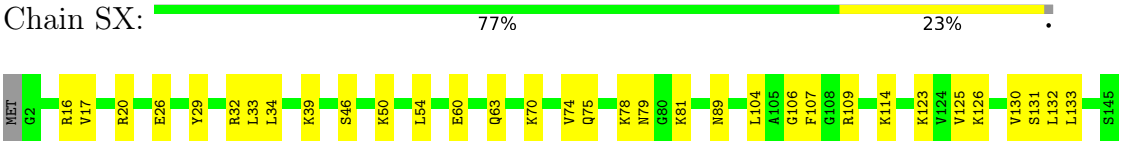
• Molecule 12: 40S ribosomal protein S22-A

Chain SW:



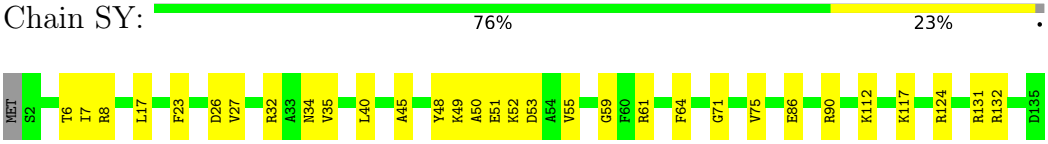
• Molecule 13: 40S ribosomal protein S23-A

Chain SX:



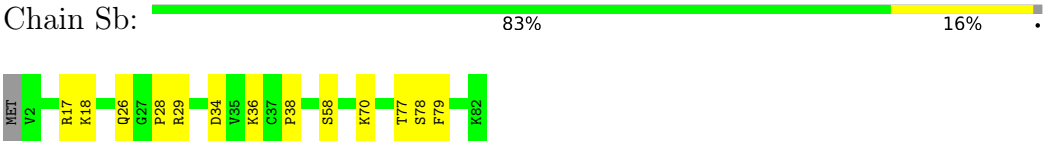
• Molecule 14: 40S ribosomal protein S24-A

Chain SY:



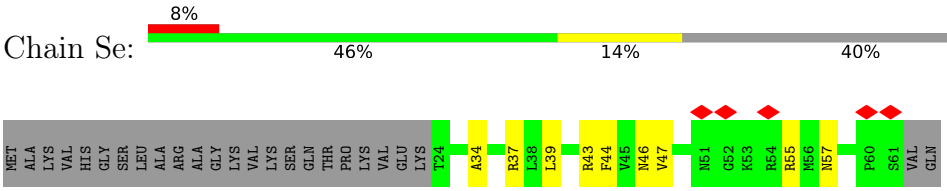
• Molecule 15: 40S ribosomal protein S27-A

Chain Sb:



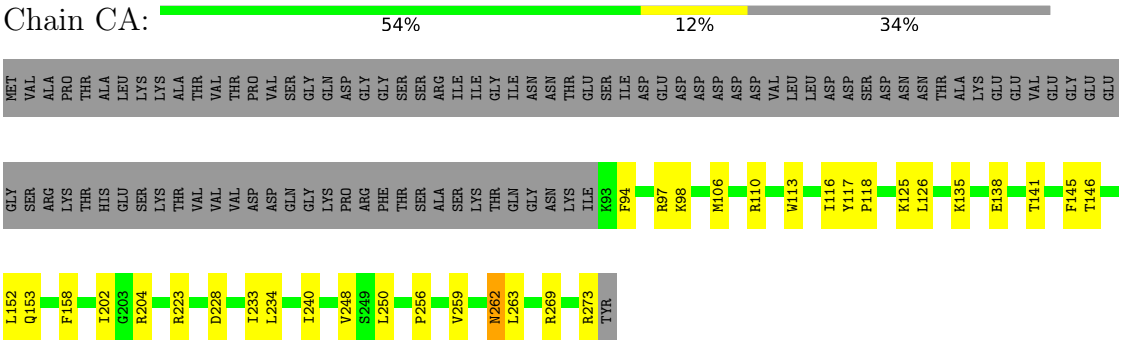
• Molecule 16: 40S ribosomal protein S30-A

Chain Se:



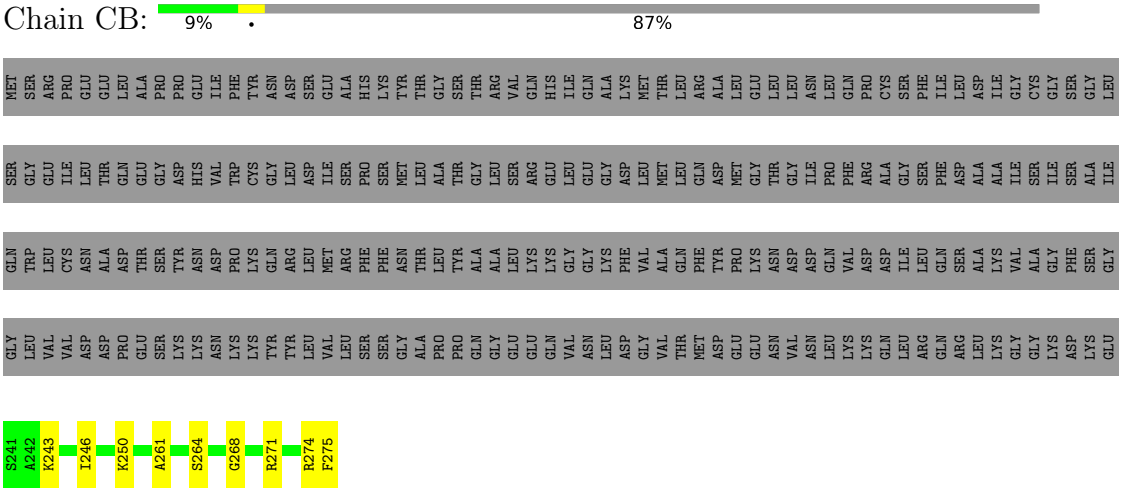
• Molecule 17: Pre-rRNA-processing protein PNO1

Chain CA:



• Molecule 18: 18S rRNA (guanine(1575)-N(7))-methyltransferase

Chain CB:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	57203	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION; Relion	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	44	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.369	Depositor
Minimum map value	-0.184	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.01	Depositor
Map size (Å)	381.24, 381.24, 381.24	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.059, 1.059, 1.059	Depositor

5 Model quality

5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|$ >5	RMSZ	#$\|Z\|$ >5
1	C2	0.22	0/28630	0.35	0/44592
2	SB	0.23	0/1748	0.56	0/2352
3	SC	0.18	0/1665	0.47	0/2263
4	SE	0.24	0/2109	0.55	0/2839
5	SG	0.19	0/1779	0.42	0/2379
6	SH	0.27	0/1511	0.76	5/2036 (0.2%)
7	SI	0.26	0/1514	0.55	2/2021 (0.1%)
8	SJ	0.23	0/1519	0.55	0/2035
9	SL	0.27	0/1194	0.54	0/1610
10	SN	0.22	0/1215	0.53	0/1638
11	SO	0.21	0/960	0.49	0/1290
12	SW	0.26	0/1038	0.49	0/1395
13	SX	0.27	0/1139	0.60	0/1518
14	SY	0.23	0/1087	0.60	0/1449
15	Sb	0.25	0/620	0.69	2/838 (0.2%)
16	Se	0.25	0/319	0.67	0/425
17	CA	0.22	0/1462	0.53	0/1969
18	CB	0.18	0/305	0.54	0/394
All	All	0.23	0/49814	0.44	9/73043 (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
6	SH	0	2
13	SX	0	1
All	All	0	3

There are no bond length outliers.

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
6	SH	162	ILE	N-CA-C	-6.05	106.86	112.43
6	SH	30	SER	CA-C-N	6.05	132.59	121.70
6	SH	30	SER	C-N-CA	6.05	132.59	121.70
6	SH	63	PRO	CA-C-N	5.53	132.35	122.13
6	SH	63	PRO	C-N-CA	5.53	132.35	122.13
7	SI	31	ARG	CA-C-N	5.06	128.34	120.60
7	SI	31	ARG	C-N-CA	5.06	128.34	120.60
15	Sb	58	SER	CA-C-N	5.05	131.19	121.54
15	Sb	58	SER	C-N-CA	5.05	131.19	121.54

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	SH	64	VAL	Peptide
6	SH	9	LEU	Peptide
13	SX	63	GLN	Peptide

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C2	25592	0	12869	225	0
2	SB	1722	0	1793	30	0
3	SC	1635	0	1723	28	0
4	SE	2068	0	2154	23	0
5	SG	1755	0	1846	25	0
6	SH	1486	0	1576	18	0
7	SI	1489	0	1525	26	0
8	SJ	1494	0	1573	22	0
9	SL	1168	0	1233	10	0
10	SN	1192	0	1255	13	0
11	SO	949	0	985	22	0
12	SW	1021	0	1060	9	0
13	SX	1121	0	1196	19	0
14	SY	1073	0	1132	22	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
15	Sb	610	0	633	9	0
16	Se	313	0	343	6	0
17	CA	1436	0	1515	22	0
18	CB	302	0	340	8	0
19	Sb	1	0	0	0	0
All	All	46427	0	34751	466	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 (466) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C2:868:G:H1	1:C2:960:U:H3	1.15	0.95
1:C2:486:G:H1	1:C2:501:U:H3	1.13	0.92
1:C2:1665:U:H3	1:C2:1736:G:H1	0.94	0.92
1:C2:826:U:H3	1:C2:846:G:H1	0.96	0.89
1:C2:34:G:H1	1:C2:474:A:H2	1.20	0.86
1:C2:1677:C:H42	1:C2:1724:U:H3	1.20	0.85
18:CB:246:ILE:O	18:CB:250:LYS:HB2	1.78	0.83
2:SB:149:GLN:HE21	2:SB:151:LYS:HB3	1.44	0.81
1:C2:1057:U:C2	1:C2:1062:A:N6	2.53	0.76
7:SI:62:THR:HA	7:SI:76:THR:O	1.84	0.76
6:SH:9:LEU:HD12	6:SH:10:SER:H	1.52	0.74
1:C2:1057:U:N3	1:C2:1062:A:C6	2.55	0.74
1:C2:231:U:O2	1:C2:234:G:C6	2.41	0.73
1:C2:1663:G:H1	1:C2:1738:U:H3	1.33	0.73
17:CA:269:ARG:HH21	17:CA:273:ARG:HH22	1.36	0.73
1:C2:152:U:O2	1:C2:163:G:N2	2.22	0.73
1:C2:895:G:H1	1:C2:917:U:H3	1.37	0.72
1:C2:1645:G:C8	1:C2:1757:G:N2	2.58	0.72
1:C2:1057:U:N3	1:C2:1061:A:C6	2.59	0.71
1:C2:231:U:C2	1:C2:234:G:O6	2.44	0.70
1:C2:1646:C:N4	1:C2:1754:A:N6	2.40	0.69
9:SL:7:VAL:HG13	9:SL:8:GLN:HG2	1.74	0.69
17:CA:223:ARG:HB2	17:CA:234:LEU:HB3	1.75	0.69
8:SJ:163:PRO:HB3	8:SJ:169:PRO:HA	1.75	0.69
1:C2:229:U:O4	1:C2:235:G:O6	2.11	0.69
1:C2:557:G:N7	18:CB:271:ARG:NH2	2.41	0.68
1:C2:65:A:H2	1:C2:84:A:H62	1.42	0.68
4:SE:31:PRO:HG3	4:SE:43:PRO:HG3	1.75	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:SH:150:GLN:HB3	6:SH:181:ILE:HG22	1.77	0.67
1:C2:190:C:H41	7:SI:137:LYS:HD3	1.58	0.67
11:SO:48:VAL:HG11	11:SO:53:ASP:HB2	1.77	0.66
7:SI:99:ALA:N	7:SI:169:ILE:O	2.28	0.66
1:C2:873:U:O4	1:C2:954:G:O6	2.15	0.65
1:C2:1645:G:N7	1:C2:1757:G:C2	2.65	0.65
1:C2:1646:C:N3	1:C2:1754:A:N1	2.45	0.65
17:CA:110:ARG:HA	17:CA:113:TRP:HB2	1.80	0.64
17:CA:262:ASN:HD22	17:CA:262:ASN:C	2.04	0.64
1:C2:1646:C:N4	1:C2:1754:A:H61	1.95	0.64
1:C2:895:G:H21	11:SO:38:THR:HG21	1.63	0.64
11:SO:20:TYR:HB3	11:SO:27:PHE:HB2	1.80	0.63
1:C2:1645:G:C5	1:C2:1757:G:C2	2.86	0.63
1:C2:521:A:N3	14:SY:34:ASN:ND2	2.46	0.63
1:C2:1684:U:O2	1:C2:1717:G:N2	2.31	0.63
1:C2:539:G:N3	1:C2:540:G:N2	2.47	0.63
1:C2:803:A:N3	6:SH:104:ARG:NH1	2.45	0.63
1:C2:187:G:H5"	7:SI:138:ASN:HD21	1.64	0.62
1:C2:647:G:H22	1:C2:687:G:H1	1.46	0.62
1:C2:1081:A:O2'	1:C2:1083:G:N7	2.31	0.62
17:CA:94:PHE:HA	17:CA:141:THR:O	2.00	0.61
14:SY:59:GLY:O	14:SY:71:GLY:HA2	2.00	0.61
17:CA:250:LEU:HD21	17:CA:259:VAL:HG11	1.80	0.61
7:SI:137:LYS:HG3	7:SI:141:ARG:HH12	1.65	0.61
17:CA:125:LYS:HG2	17:CA:145:PHE:HD1	1.64	0.61
14:SY:45:ALA:HA	14:SY:50:ALA:HB3	1.83	0.61
14:SY:35:VAL:HB	14:SY:40:LEU:HD11	1.82	0.61
2:SB:111:ARG:NH1	11:SO:117:ASP:OD2	2.34	0.60
18:CB:250:LYS:NZ	18:CB:261:ALA:O	2.33	0.60
1:C2:175:G:N3	1:C2:176:C:N4	2.49	0.60
1:C2:564:G:N2	1:C2:578:U:O2	2.34	0.60
3:SC:87:GLN:HG2	3:SC:96:THR:HG22	1.84	0.60
15:Sb:38:PRO:HD3	15:Sb:77:THR:HG22	1.83	0.60
5:SG:180:THR:HG22	5:SG:182:GLN:H	1.67	0.60
10:SN:138:ASN:OD1	10:SN:139:TRP:N	2.31	0.60
1:C2:788:A:OP2	4:SE:108:ARG:NH2	2.35	0.60
1:C2:530:C:O2	14:SY:61:ARG:NH1	2.35	0.60
1:C2:551:G:OP2	18:CB:271:ARG:NH1	2.35	0.60
1:C2:953:G:H2'	1:C2:954:G:C8	2.36	0.60
1:C2:10:G:N2	1:C2:12:U:OP2	2.35	0.60
6:SH:64:VAL:HG23	6:SH:67:LEU:HB2	1.82	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C2:1646:C:H42	1:C2:1754:A:N6	1.98	0.59
11:SO:61:MET:HG2	11:SO:104:ALA:HB2	1.84	0.59
1:C2:330:G:OP2	7:SI:172:ARG:NH1	2.36	0.59
1:C2:1658:G:O6	1:C2:1743:U:O4	2.21	0.59
2:SB:208:GLN:HG3	2:SB:209:ASN:HB2	1.85	0.58
10:SN:64:ARG:HD3	10:SN:70:LYS:HG2	1.85	0.58
1:C2:565:C:N3	1:C2:578:U:O2	2.36	0.58
1:C2:1681:A:H1'	5:SG:66:GLY:HA2	1.84	0.58
11:SO:50:ALA:O	11:SO:52:ARG:NH1	2.37	0.58
3:SC:63:VAL:HG13	3:SC:68:ILE:HD11	1.85	0.58
1:C2:502:U:O2'	16:Se:46:ASN:ND2	2.38	0.57
1:C2:1065:A:N3	2:SB:146:GLN:NE2	2.50	0.57
13:SX:34:LEU:O	13:SX:39:LYS:NZ	2.37	0.57
13:SX:60:GLU:OE2	13:SX:70:LYS:NZ	2.38	0.57
2:SB:77:GLU:OE1	17:CA:98:LYS:NZ	2.37	0.57
1:C2:231:U:O2	1:C2:234:G:O6	2.20	0.57
1:C2:1096:C:OP2	12:SW:71:LYS:NZ	2.36	0.57
1:C2:833:U:H5'	1:C2:834:G:H5"	1.88	0.56
1:C2:897:C:O2	11:SO:41:ARG:NH2	2.38	0.56
1:C2:927:C:O2'	11:SO:124:ASP:OD2	2.23	0.56
2:SB:103:MET:HB3	2:SB:215:VAL:HG22	1.86	0.56
3:SC:109:GLY:N	3:SC:191:ALA:O	2.37	0.56
5:SG:44:GLU:O	5:SG:119:GLN:NE2	2.38	0.56
1:C2:487:G:C2	1:C2:501:U:O2	2.59	0.56
1:C2:1081:A:H2	1:C2:1082:C:H41	1.53	0.56
1:C2:177:U:O2'	5:SG:191:ARG:NH1	2.39	0.56
1:C2:218:A:H61	1:C2:844:A:H1'	1.71	0.56
4:SE:19:LEU:HD11	4:SE:108:ARG:HD2	1.86	0.55
1:C2:34:G:N1	1:C2:474:A:C2	2.70	0.55
1:C2:1020:A:OP1	10:SN:106:ARG:NH2	2.36	0.55
5:SG:163:THR:HG22	5:SG:168:THR:HG22	1.86	0.55
1:C2:564:G:C6	1:C2:580:A:C6	2.95	0.55
5:SG:137:ARG:HD3	5:SG:177:ARG:HD2	1.88	0.55
1:C2:159:U:H5'	14:SY:117:LYS:HB3	1.88	0.55
1:C2:789:A:OP1	4:SE:108:ARG:NH1	2.39	0.55
6:SH:111:LYS:HG3	6:SH:112:ARG:H	1.72	0.55
1:C2:34:G:O6	1:C2:474:A:N1	2.39	0.55
1:C2:235:G:H2'	1:C2:236:A:C8	2.42	0.55
13:SX:54:LEU:HD11	13:SX:75:GLN:HB2	1.89	0.55
2:SB:83:LYS:NZ	11:SO:116:GLU:OE2	2.40	0.55
8:SJ:119:ALA:O	8:SJ:124:HIS:ND1	2.37	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:SE:100:ARG:NH2	4:SE:118:GLU:O	2.40	0.55
4:SE:170:THR:HG22	4:SE:171:ASP:H	1.71	0.54
1:C2:919:A:H1'	11:SO:36:LYS:HG3	1.89	0.54
2:SB:121:ILE:HG12	2:SB:161:ILE:HG23	1.89	0.54
1:C2:227:U:O2	1:C2:834:G:O6	2.25	0.54
1:C2:984:G:C6	1:C2:1018:U:N3	2.76	0.54
4:SE:11:ARG:NH1	4:SE:21:ASP:O	2.40	0.54
6:SH:108:GLN:NE2	6:SH:109:VAL:O	2.39	0.54
9:SL:109:VAL:HG12	9:SL:137:PHE:HB2	1.90	0.54
17:CA:98:LYS:HG2	17:CA:138:GLU:HG3	1.88	0.54
1:C2:800:U:H2'	1:C2:801:G:H8	1.72	0.54
1:C2:900:A:H3'	1:C2:901:G:H21	1.73	0.54
8:SJ:109:LEU:HB2	8:SJ:146:PHE:HB3	1.89	0.54
1:C2:220:A:C8	1:C2:832:U:C2	2.96	0.53
1:C2:1658:G:O6	1:C2:1743:U:C4	2.61	0.53
1:C2:564:G:N1	1:C2:580:A:C6	2.76	0.53
1:C2:954:G:H2'	1:C2:955:A:H8	1.72	0.53
1:C2:1645:G:N7	1:C2:1757:G:N2	2.57	0.53
1:C2:5:U:H2'	1:C2:6:G:H8	1.74	0.53
1:C2:924:A:H2'	1:C2:925:G:C8	2.44	0.52
5:SG:58:LYS:HD2	5:SG:107:ALA:HB2	1.91	0.52
6:SH:73:VAL:HG13	6:SH:74:GLN:H	1.74	0.52
1:C2:642:G:C2	1:C2:693:U:O2	2.62	0.52
8:SJ:161:THR:HG22	8:SJ:162:SER:H	1.74	0.52
9:SL:101:GLU:OE1	13:SX:16:ARG:NH1	2.42	0.52
17:CA:116:ILE:HG23	17:CA:158:PHE:HE2	1.74	0.52
1:C2:322:G:O2'	7:SI:10:LYS:NZ	2.42	0.52
1:C2:984:G:N1	1:C2:1018:U:C2	2.77	0.52
4:SE:85:GLY:N	4:SE:88:ASP:OD2	2.42	0.52
10:SN:13:SER:OG	10:SN:14:SER:N	2.43	0.52
1:C2:475:A:OP1	8:SJ:130:THR:OG1	2.20	0.52
1:C2:699:U:O2	1:C2:739:G:O6	2.28	0.52
1:C2:1789:G:N7	11:SO:132:ARG:NH2	2.58	0.52
1:C2:205:U:O2	1:C2:263:C:N3	2.43	0.52
14:SY:59:GLY:O	14:SY:71:GLY:CA	2.58	0.52
17:CA:259:VAL:O	17:CA:263:LEU:HB2	2.10	0.52
1:C2:1057:U:N3	1:C2:1061:A:N6	2.57	0.52
11:SO:81:VAL:HG11	11:SO:102:LEU:HD13	1.92	0.52
16:Se:55:ARG:NH2	16:Se:57:ASN:O	2.41	0.52
1:C2:1057:U:C2	1:C2:1061:A:N6	2.78	0.52
9:SL:63:LEU:O	9:SL:129:ARG:NH2	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:SW:57:ARG:HE	15:Sb:26:GLN:NE2	2.08	0.52
1:C2:896:U:O2	11:SO:41:ARG:NH1	2.42	0.51
1:C2:1140:G:H2'	1:C2:1141:G:C8	2.46	0.51
7:SI:3:ILE:O	7:SI:30:GLY:N	2.38	0.51
13:SX:131:SER:OG	13:SX:132:LEU:N	2.41	0.51
2:SB:137:ILE:HD12	2:SB:172:LEU:HD22	1.92	0.51
2:SB:199:ASN:HA	2:SB:202:LYS:HE3	1.92	0.51
4:SE:103:TYR:O	4:SE:182:TYR:OH	2.28	0.51
1:C2:474:A:H5"	8:SJ:144:PRO:HD2	1.91	0.51
13:SX:32:ARG:HG2	13:SX:33:LEU:HD12	1.93	0.51
5:SG:98:ARG:NH2	5:SG:105:ASP:OD1	2.44	0.51
1:C2:151:G:O6	14:SY:124:ARG:NH1	2.34	0.51
1:C2:371:G:N2	1:C2:612:U:O2	2.44	0.51
1:C2:1677:C:N4	1:C2:1724:U:H3	1.99	0.51
1:C2:688:G:H2'	1:C2:689:G:C8	2.45	0.51
1:C2:689:G:H2'	1:C2:690:G:C8	2.46	0.51
2:SB:137:ILE:HG22	2:SB:215:VAL:HG12	1.93	0.51
7:SI:34:ALA:HB2	7:SI:56:ARG:HD2	1.93	0.51
1:C2:52:U:H2'	1:C2:53:G:H8	1.75	0.51
1:C2:434:G:N1	1:C2:437:A:OP2	2.40	0.51
1:C2:1064:G:O2'	2:SB:204:ILE:O	2.29	0.51
3:SC:227:PRO:O	3:SC:230:TRP:HB2	2.11	0.51
1:C2:6:G:O2'	1:C2:552:G:N2	2.44	0.51
1:C2:154:G:OP2	14:SY:131:ARG:NH2	2.43	0.51
1:C2:155:U:OP2	14:SY:132:ARG:NH1	2.44	0.51
1:C2:34:G:N1	1:C2:474:A:H2	2.00	0.50
13:SX:106:GLY:O	13:SX:123:LYS:NZ	2.42	0.50
14:SY:7:ILE:HG12	14:SY:27:VAL:HG12	1.93	0.50
3:SC:174:ARG:O	8:SJ:53:ARG:NH1	2.43	0.50
7:SI:159:GLN:HE21	7:SI:166:TYR:HD2	1.60	0.50
1:C2:486:G:N2	1:C2:501:U:O2	2.39	0.50
1:C2:813:U:O2'	1:C2:815:G:OP1	2.30	0.50
1:C2:984:G:C2	1:C2:1018:U:O2	2.65	0.50
1:C2:1057:U:C2	1:C2:1062:A:C6	2.99	0.50
8:SJ:168:ARG:HG2	8:SJ:174:ARG:HH22	1.77	0.50
17:CA:228:ASP:N	17:CA:228:ASP:OD1	2.42	0.50
1:C2:143:G:OP2	5:SG:139:ASN:ND2	2.43	0.50
1:C2:486:G:O6	1:C2:501:U:O4	2.29	0.50
3:SC:45:VAL:HG11	3:SC:68:ILE:HG22	1.94	0.50
13:SX:89:ASN:HB2	18:CB:274:ARG:HB2	1.93	0.50
1:C2:826:U:O4	1:C2:846:G:O6	2.30	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C2:1665:U:O4	1:C2:1736:G:O6	2.30	0.50
1:C2:156:A:C2	1:C2:415:C:O2	2.65	0.50
2:SB:139:ALA:HA	2:SB:212:VAL:HA	1.93	0.50
5:SG:2:LYS:HB3	5:SG:108:VAL:HG22	1.93	0.50
8:SJ:169:PRO:O	8:SJ:174:ARG:NH2	2.45	0.50
10:SN:54:LEU:HD23	10:SN:58:HIS:HD2	1.76	0.50
11:SO:117:ASP:OD1	11:SO:117:ASP:N	2.45	0.50
6:SH:154:LEU:HD11	6:SH:183:PHE:HD1	1.77	0.49
2:SB:191:GLU:HB2	2:SB:194:ASN:HD22	1.77	0.49
1:C2:1041:G:H2'	1:C2:1042:G:C8	2.47	0.49
1:C2:954:G:H2'	1:C2:955:A:C8	2.48	0.49
1:C2:1739:C:H2'	1:C2:1740:A:H8	1.78	0.49
1:C2:816:G:H2'	1:C2:817:A:H8	1.78	0.49
2:SB:27:LYS:NZ	11:SO:37:GLU:OE2	2.41	0.49
1:C2:843:U:H2'	1:C2:844:A:H8	1.77	0.49
5:SG:192:ALA:O	5:SG:196:ARG:HG2	2.13	0.49
1:C2:448:C:OP2	4:SE:49:ARG:NH2	2.45	0.49
3:SC:80:VAL:HA	3:SC:102:VAL:HG23	1.94	0.49
7:SI:172:ARG:HE	7:SI:175:GLN:HG3	1.77	0.49
2:SB:188:LEU:HD11	2:SB:212:VAL:HG21	1.94	0.49
13:SX:46:SER:OG	13:SX:78:LYS:NZ	2.46	0.49
1:C2:1672:G:H2'	1:C2:1673:G:C8	2.47	0.48
3:SC:218:ILE:HA	3:SC:221:THR:HG22	1.95	0.48
5:SG:32:ILE:HD11	5:SG:63:MET:HE2	1.95	0.48
12:SW:87:GLU:O	12:SW:90:THR:OG1	2.27	0.48
1:C2:406:U:H2'	1:C2:407:A:H8	1.78	0.48
1:C2:143:G:O6	5:SG:177:ARG:NH2	2.43	0.48
1:C2:640:U:O2	6:SH:179:LYS:NZ	2.45	0.48
6:SH:28:GLU:OE2	6:SH:39:ARG:NH2	2.45	0.48
8:SJ:23:ARG:NH1	8:SJ:27:GLU:OE2	2.42	0.48
2:SB:20:VAL:HG13	2:SB:21:VAL:HG13	1.94	0.48
1:C2:871:G:H2'	1:C2:872:G:C8	2.48	0.48
1:C2:1001:A:H3'	1:C2:1002:G:C8	2.47	0.48
9:SL:121:ASP:H	9:SL:145:ALA:HB2	1.78	0.48
13:SX:17:VAL:HG12	13:SX:20:ARG:HH21	1.79	0.48
1:C2:57:G:OP1	14:SY:112:LYS:NZ	2.44	0.48
8:SJ:143:ILE:HG22	8:SJ:145:SER:H	1.79	0.48
1:C2:156:A:N1	1:C2:415:C:O2	2.47	0.48
1:C2:1039:A:O2'	1:C2:1040:G:O5'	2.30	0.48
5:SG:14:LYS:HB2	5:SG:124:LEU:HD13	1.96	0.48
2:SB:133:TYR:HE1	2:SB:181:LEU:HD22	1.77	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C2:1727:G:H2'	1:C2:1728:A:C8	2.48	0.48
6:SH:14:THR:OG1	6:SH:15:GLU:N	2.46	0.48
17:CA:233:ILE:HG22	17:CA:240:ILE:HG22	1.96	0.48
1:C2:52:U:H2'	1:C2:53:G:C8	2.50	0.47
2:SB:33:LYS:HG2	2:SB:42:ASN:HA	1.96	0.47
17:CA:126:LEU:HD11	17:CA:152:LEU:HA	1.96	0.47
1:C2:170:U:OP1	1:C2:267:U:O2'	2.33	0.47
1:C2:399:A:H4'	4:SE:3:ARG:HG3	1.96	0.47
1:C2:1050:G:OP1	15:Sb:70:LYS:NZ	2.35	0.47
12:SW:2:THR:OG1	12:SW:3:ARG:N	2.46	0.47
13:SX:107:PHE:HD2	13:SX:114:LYS:HB3	1.79	0.47
17:CA:256:PRO:HA	17:CA:259:VAL:HG12	1.96	0.47
2:SB:144:ARG:HD3	2:SB:208:GLN:HB3	1.96	0.47
14:SY:8:ARG:NH2	14:SY:26:ASP:OD2	2.48	0.47
1:C2:104:A:OP2	1:C2:308:C:N4	2.33	0.47
1:C2:1070:C:H4'	15:Sb:17:ARG:HD2	1.97	0.47
15:Sb:18:LYS:O	15:Sb:29:ARG:NH2	2.43	0.47
9:SL:128:CYS:SG	9:SL:138:ASN:HB2	2.55	0.47
1:C2:1115:U:H2'	1:C2:1116:A:H8	1.80	0.47
4:SE:121:TYR:HA	4:SE:163:ASP:HA	1.96	0.47
10:SN:60:VAL:HG13	10:SN:66:ILE:HD12	1.97	0.47
4:SE:147:ILE:HG21	4:SE:169:ILE:HG13	1.95	0.47
13:SX:74:VAL:HG11	13:SX:104:LEU:HD11	1.96	0.47
14:SY:51:GLU:O	14:SY:53:ASP:N	2.48	0.47
1:C2:891:A:H2'	1:C2:892:A:H8	1.80	0.47
11:SO:137:LEU:HB2	17:CA:248:VAL:HG11	1.96	0.47
1:C2:250:C:H2'	1:C2:251:A:H8	1.79	0.46
1:C2:381:C:O2'	1:C2:755:A:N1	2.44	0.46
8:SJ:52:ILE:HD13	8:SJ:80:LEU:HD11	1.97	0.46
17:CA:125:LYS:HD3	17:CA:146:THR:HG23	1.97	0.46
1:C2:218:A:N7	1:C2:830:U:C4	2.83	0.46
1:C2:558:U:OP1	16:Se:55:ARG:NH2	2.43	0.46
1:C2:688:G:H2'	1:C2:689:G:H8	1.80	0.46
3:SC:95:ARG:HH12	3:SC:97:ARG:HH21	1.62	0.46
4:SE:92:LEU:HD12	14:SY:17:LEU:HD11	1.98	0.46
7:SI:67:TRP:CG	7:SI:183:ILE:HD11	2.50	0.46
12:SW:112:ASP:OD1	12:SW:112:ASP:N	2.47	0.46
14:SY:23:PHE:HZ	14:SY:75:VAL:HG23	1.80	0.46
1:C2:1057:U:C4	1:C2:1061:A:C6	3.04	0.46
5:SG:39:GLU:OE2	5:SG:39:GLU:N	2.48	0.46
10:SN:87:ASP:OD1	10:SN:87:ASP:N	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C2:158:U:O2'	1:C2:160:C:OP2	2.29	0.46
1:C2:340:U:H2'	1:C2:341:A:C8	2.51	0.46
1:C2:5:U:H2'	1:C2:6:G:C8	2.50	0.46
1:C2:17:C:O2'	1:C2:1137:A:N1	2.42	0.46
1:C2:246:G:N2	9:SL:38:ALA:O	2.48	0.46
1:C2:1663:G:O6	1:C2:1738:U:O4	2.34	0.46
3:SC:126:ARG:O	3:SC:130:ILE:HG12	2.16	0.46
1:C2:68:A:OP1	5:SG:160:ARG:NH2	2.41	0.46
3:SC:53:ILE:HD12	3:SC:57:PHE:HE2	1.79	0.46
13:SX:125:VAL:HG12	13:SX:126:LYS:HG3	1.98	0.46
1:C2:397:A:OP2	7:SI:47:ARG:NH2	2.45	0.46
1:C2:959:U:H5'	15:Sb:28:PRO:HB3	1.97	0.46
2:SB:51:SER:O	2:SB:51:SER:OG	2.31	0.46
1:C2:19:A:H4'	13:SX:109:ARG:HH11	1.81	0.46
7:SI:84:HIS:NE2	7:SI:97:THR:OG1	2.35	0.46
1:C2:79:C:H1'	5:SG:174:LYS:HG3	1.97	0.45
3:SC:53:ILE:HD13	3:SC:73:LEU:HD11	1.98	0.45
4:SE:126:VAL:HA	4:SE:141:THR:HA	1.97	0.45
6:SH:45:SER:HB3	6:SH:61:PHE:HB2	1.98	0.45
1:C2:146:U:H2'	1:C2:147:A:H8	1.81	0.45
1:C2:435:C:H5"	13:SX:50:LYS:HE2	1.97	0.45
6:SH:74:GLN:HG2	6:SH:131:PHE:CD2	2.51	0.45
8:SJ:93:LEU:HA	8:SJ:96:VAL:HG12	1.98	0.45
1:C2:162:A:H2'	1:C2:163:G:C8	2.51	0.45
1:C2:230:C:H2'	1:C2:231:U:H6	1.81	0.45
1:C2:984:G:N1	1:C2:1018:U:N3	2.65	0.45
1:C2:406:U:H2'	1:C2:407:A:C8	2.52	0.45
1:C2:642:G:N1	1:C2:693:U:C2	2.84	0.45
11:SO:15:GLY:O	11:SO:79:VAL:HA	2.16	0.45
4:SE:176:ASP:OD1	4:SE:176:ASP:N	2.49	0.45
8:SJ:107:ARG:HA	8:SJ:107:ARG:HD2	1.80	0.45
1:C2:590:C:H2'	1:C2:591:A:H8	1.82	0.45
3:SC:66:PHE:HB2	3:SC:133:LYS:HD2	1.98	0.45
1:C2:108:A:H2'	1:C2:109:G:C8	2.51	0.45
1:C2:238:U:OP2	1:C2:834:G:O2'	2.29	0.45
1:C2:984:G:C2	1:C2:1018:U:C2	3.04	0.45
15:Sb:34:ASP:O	15:Sb:79:PHE:HA	2.17	0.45
7:SI:99:ALA:CA	7:SI:169:ILE:O	2.65	0.44
3:SC:129:ILE:HG22	3:SC:133:LYS:HZ1	1.82	0.44
17:CA:97:ARG:NH1	17:CA:153:GLN:OE1	2.50	0.44
1:C2:1115:U:H2'	1:C2:1116:A:C8	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:CA:204:ARG:NH1	17:CA:250:LEU:O	2.40	0.44
1:C2:209:U:H2'	1:C2:210:A:H8	1.82	0.44
2:SB:156:ALA:HB3	2:SB:161:ILE:HD11	1.98	0.44
1:C2:997:G:H2'	1:C2:998:A:C8	2.52	0.44
1:C2:189:C:N4	1:C2:197:A:N6	2.65	0.44
1:C2:564:G:C6	1:C2:580:A:N6	2.85	0.44
3:SC:95:ARG:NH1	3:SC:97:ARG:HH21	2.16	0.44
5:SG:69:LEU:O	5:SG:71:THR:N	2.46	0.44
5:SG:135:PRO:HB2	5:SG:141:ILE:HD13	1.99	0.44
1:C2:1766:A:H2'	1:C2:1767:G:C8	2.53	0.44
3:SC:76:LEU:HD12	3:SC:104:VAL:HG22	1.99	0.44
1:C2:1036:A:H2'	1:C2:1037:C:C6	2.53	0.44
3:SC:44:LEU:HA	3:SC:49:LYS:HZ3	1.82	0.43
1:C2:1742:U:H2'	1:C2:1743:U:C6	2.53	0.43
4:SE:231:GLN:OE1	4:SE:232:GLY:N	2.50	0.43
9:SL:83:THR:HG22	9:SL:110:HIS:HA	1.99	0.43
14:SY:55:VAL:HG22	14:SY:75:VAL:HG22	2.00	0.43
1:C2:209:U:H2'	1:C2:210:A:C8	2.52	0.43
1:C2:482:U:H2'	1:C2:483:A:C8	2.53	0.43
1:C2:836:U:H2'	1:C2:837:G:C8	2.53	0.43
1:C2:844:A:H2'	1:C2:845:G:H8	1.82	0.43
1:C2:85:A:N3	1:C2:148:A:O2'	2.47	0.43
1:C2:480:G:H1	1:C2:508:U:H3	1.67	0.43
1:C2:819:G:O2'	1:C2:821:U:OP2	2.32	0.43
8:SJ:73:GLY:O	8:SJ:77:ILE:HG12	2.19	0.43
1:C2:923:A:H2'	1:C2:924:A:C8	2.53	0.43
7:SI:89:GLU:OE1	7:SI:92:ARG:NH2	2.44	0.43
11:SO:18:ARG:NH1	11:SO:31:THR:OG1	2.52	0.43
1:C2:1673:G:OP1	5:SG:94:ARG:NH2	2.47	0.43
1:C2:1714:A:H2'	1:C2:1715:G:C8	2.54	0.43
6:SH:30:SER:N	6:SH:31:SER:HA	2.33	0.43
16:Se:39:LEU:O	16:Se:43:ARG:N	2.51	0.43
1:C2:504:U:O4	1:C2:505:A:N6	2.52	0.43
3:SC:158:THR:HG21	3:SC:221:THR:HB	2.00	0.43
8:SJ:63:ASP:OD1	8:SJ:64:GLU:N	2.52	0.43
1:C2:29:U:H2'	1:C2:30:G:H8	1.82	0.43
1:C2:591:A:H2'	1:C2:592:A:C8	2.53	0.43
1:C2:1652:C:H2'	1:C2:1653:C:C6	2.53	0.43
3:SC:188:LEU:HD22	3:SC:193:VAL:HG11	2.00	0.43
6:SH:153:LEU:HB3	6:SH:186:PRO:HG3	2.00	0.43
1:C2:107:C:H2'	1:C2:108:A:C8	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C2:950:C:O2'	10:SN:104:ARG:NH2	2.49	0.43
11:SO:17:ALA:HA	11:SO:29:HIS:O	2.19	0.43
14:SY:6:THR:O	14:SY:27:VAL:HA	2.19	0.43
1:C2:169:A:H5"	5:SG:176:GLN:HG2	2.01	0.42
1:C2:205:U:H2'	1:C2:206:A:H8	1.83	0.42
1:C2:647:G:N2	1:C2:687:G:H22	2.16	0.42
1:C2:843:U:H2'	1:C2:844:A:C8	2.54	0.42
1:C2:968:U:OP1	1:C2:1033:C:O2'	2.37	0.42
3:SC:76:LEU:HD22	3:SC:106:ASP:HB3	2.01	0.42
1:C2:558:U:H4'	18:CB:264:SER:HB2	2.00	0.42
7:SI:76:THR:HG22	7:SI:108:PRO:HG2	2.01	0.42
1:C2:152:U:O2	1:C2:163:G:C2	2.72	0.42
1:C2:332:U:O2'	7:SI:5:ARG:NH2	2.51	0.42
1:C2:1000:C:N3	1:C2:1003:A:N6	2.67	0.42
1:C2:1086:A:H5'	3:SC:164:SER:HB2	2.00	0.42
2:SB:135:LEU:HD21	2:SB:217:LEU:HD22	2.02	0.42
2:SB:207:LEU:HB3	2:SB:210:ILE:HD11	2.01	0.42
6:SH:56:LYS:HB2	6:SH:88:ARG:HG2	2.00	0.42
1:C2:884:A:H2'	1:C2:885:G:C8	2.54	0.42
1:C2:891:A:H2'	1:C2:892:A:C8	2.54	0.42
3:SC:170:ILE:HB	3:SC:197:TYR:HB2	2.01	0.42
4:SE:238:LEU:HD12	4:SE:242:LYS:HG3	2.01	0.42
1:C2:189:C:H41	7:SI:141:ARG:HH22	1.67	0.42
4:SE:132:GLY:N	4:SE:136:VAL:O	2.45	0.42
8:SJ:24:LEU:HD23	8:SJ:24:LEU:HA	1.94	0.42
9:SL:124:THR:HB	9:SL:141:LYS:HB3	2.01	0.42
17:CA:117:TYR:CD1	17:CA:118:PRO:HD3	2.55	0.42
1:C2:487:G:C2	1:C2:501:U:C2	3.08	0.42
7:SI:171:SER:HB3	7:SI:180:ASP:H	1.84	0.42
10:SN:4:MET:HE3	10:SN:5:HIS:CE1	2.55	0.42
1:C2:615:A:O2'	1:C2:621:A:N1	2.48	0.42
1:C2:1785:U:P	11:SO:133:ARG:HH22	2.42	0.42
3:SC:164:SER:O	3:SC:164:SER:OG	2.31	0.42
4:SE:64:ILE:HG23	14:SY:17:LEU:HD12	2.01	0.42
17:CA:106:MET:HE1	17:CA:135:LYS:HA	2.01	0.42
1:C2:228:G:H2'	1:C2:229:U:C6	2.55	0.42
1:C2:844:A:H2'	1:C2:845:G:C8	2.54	0.42
1:C2:854:U:O4	1:C2:855:A:N6	2.53	0.42
5:SG:7:TYR:HD2	5:SG:10:ASN:HB2	1.85	0.42
7:SI:178:ARG:H	7:SI:178:ARG:HG2	1.64	0.42
1:C2:968:U:H2'	1:C2:969:C:O4'	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:SJ:102:GLU:HA	8:SJ:105:LEU:HB2	2.01	0.42
1:C2:836:U:H2'	1:C2:837:G:H8	1.85	0.42
5:SG:70:PRO:HB3	5:SG:101:ILE:HB	2.01	0.42
13:SX:26:GLU:HB2	13:SX:29:TYR:HB3	2.01	0.42
1:C2:224:C:H2'	1:C2:225:A:H8	1.85	0.41
2:SB:32:ILE:HG23	2:SB:43:VAL:HG13	2.01	0.41
2:SB:69:CYS:SG	11:SO:114:ARG:NH1	2.93	0.41
2:SB:138:PHE:HE1	2:SB:216:LYS:HE2	1.85	0.41
4:SE:18:TRP:HH2	4:SE:31:PRO:HD3	1.84	0.41
6:SH:35:LYS:HD2	6:SH:35:LYS:HA	1.81	0.41
9:SL:125:VAL:HG12	9:SL:139:VAL:HA	2.01	0.41
2:SB:104:ASP:OD1	2:SB:105:PHE:N	2.53	0.41
4:SE:163:ASP:O	4:SE:164:LEU:HD22	2.20	0.41
13:SX:79:ASN:HB3	13:SX:81:LYS:HG3	2.01	0.41
1:C2:250:C:H2'	1:C2:251:A:C8	2.56	0.41
1:C2:393:C:H2'	1:C2:394:C:C6	2.55	0.41
1:C2:546:U:H2'	1:C2:547:U:C6	2.55	0.41
2:SB:179:SER:HB2	2:SB:183:GLN:HB2	2.03	0.41
5:SG:23:ARG:HD2	5:SG:42:GLY:HA2	2.02	0.41
15:Sb:36:LYS:HB3	15:Sb:78:SER:HB2	2.02	0.41
3:SC:39:THR:HG23	3:SC:42:GLY:H	1.85	0.41
8:SJ:70:LEU:HD23	8:SJ:70:LEU:HA	1.90	0.41
10:SN:146:ALA:HA	10:SN:149:LEU:HB3	2.02	0.41
14:SY:86:GLU:OE2	14:SY:90:ARG:NH1	2.53	0.41
17:CA:202:ILE:HD13	17:CA:202:ILE:HA	1.91	0.41
3:SC:82:ASN:HD22	3:SC:207:LEU:HD23	1.86	0.41
7:SI:86:SER:OG	7:SI:87:ASN:N	2.53	0.41
8:SJ:139:GLN:NE2	14:SY:64:PHE:O	2.39	0.41
1:C2:925:G:H2'	1:C2:926:A:H8	1.86	0.41
6:SH:98:ILE:HG22	6:SH:121:VAL:HG21	2.02	0.41
12:SW:15:ASN:HD21	12:SW:71:LYS:HG3	1.84	0.41
16:Se:34:ALA:O	16:Se:37:ARG:HB3	2.21	0.41
5:SG:36:VAL:HG23	5:SG:50:PHE:HB2	2.03	0.41
7:SI:84:HIS:HE2	7:SI:97:THR:HG1	1.64	0.41
13:SX:133:LEU:HD13	18:CB:275:PHE:HD1	1.86	0.41
7:SI:6:ASP:OD1	7:SI:6:ASP:N	2.52	0.41
1:C2:625:C:H2'	1:C2:626:U:C6	2.56	0.41
1:C2:1018:U:H2'	1:C2:1019:A:H8	1.86	0.41
1:C2:1080:U:H2'	1:C2:1081:A:C8	2.56	0.41
7:SI:69:SER:OG	7:SI:70:GLU:OE1	2.33	0.41
10:SN:34:ILE:O	10:SN:38:VAL:HG23	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:CB:243:LYS:HE3	18:CB:268:GLY:H	1.86	0.41
1:C2:1741:U:H2'	1:C2:1742:U:C6	2.56	0.41
12:SW:81:VAL:O	12:SW:122:SER:OG	2.31	0.41
14:SY:48:TYR:HB2	14:SY:49:LYS:H	1.66	0.41
1:C2:487:G:N1	1:C2:501:U:C2	2.90	0.40
1:C2:864:U:OP2	15:Sb:26:GLN:NE2	2.55	0.40
1:C2:976:G:N1	1:C2:1023:A:O2'	2.37	0.40
3:SC:165:VAL:HG11	3:SC:210:THR:HG22	2.03	0.40
1:C2:107:C:H2'	1:C2:108:A:H8	1.85	0.40
3:SC:153:SER:OG	3:SC:195:ASP:O	2.36	0.40
8:SJ:60:LEU:HD23	8:SJ:60:LEU:HA	1.92	0.40
1:C2:175:G:H22	1:C2:266:A:P	2.44	0.40
1:C2:224:C:H2'	1:C2:225:A:C8	2.57	0.40
1:C2:918:U:H2'	1:C2:919:A:H8	1.86	0.40
2:SB:66:VAL:O	2:SB:85:LYS:HA	2.22	0.40
3:SC:225:LEU:HD23	12:SW:68:ARG:HA	2.02	0.40
4:SE:48:LEU:HD11	4:SE:70:VAL:HG21	2.02	0.40
8:SJ:64:GLU:OE2	8:SJ:65:LYS:HD3	2.21	0.40
1:C2:199:G:O2'	1:C2:200:A:H8	2.05	0.40
1:C2:990:C:H5"	11:SO:129:LYS:HG2	2.04	0.40
7:SI:83:TYR:HB3	7:SI:101:ILE:HB	2.04	0.40
12:SW:48:GLY:HA3	12:SW:64:GLN:O	2.22	0.40
1:C2:300:A:H2'	1:C2:301:A:C8	2.57	0.40
1:C2:939:A:H2'	1:C2:940:A:C8	2.57	0.40
10:SN:29:SER:OG	10:SN:30:SER:N	2.54	0.40
10:SN:54:LEU:HB3	10:SN:60:VAL:HB	2.04	0.40
13:SX:130:VAL:HG13	13:SX:131:SER:H	1.85	0.40
16:Se:44:PHE:HA	16:Se:47:VAL:HG22	2.02	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	
2	SB	214/255 (84%)	197 (92%)	17 (8%)	0	100	100
3	SC	215/254 (85%)	202 (94%)	13 (6%)	0	100	100
4	SE	258/261 (99%)	235 (91%)	23 (9%)	0	100	100
5	SG	216/236 (92%)	204 (94%)	12 (6%)	0	100	100
6	SH	183/190 (96%)	165 (90%)	18 (10%)	0	100	100
7	SI	184/200 (92%)	176 (96%)	8 (4%)	0	100	100
8	SJ	183/197 (93%)	169 (92%)	14 (8%)	0	100	100
9	SL	144/156 (92%)	129 (90%)	15 (10%)	0	100	100
10	SN	148/151 (98%)	137 (93%)	11 (7%)	0	100	100
11	SO	126/137 (92%)	109 (86%)	17 (14%)	0	100	100
12	SW	127/130 (98%)	120 (94%)	7 (6%)	0	100	100
13	SX	142/145 (98%)	124 (87%)	18 (13%)	0	100	100
14	SY	132/135 (98%)	115 (87%)	15 (11%)	2 (2%)	8	30
15	Sb	79/82 (96%)	68 (86%)	11 (14%)	0	100	100
16	Se	36/63 (57%)	30 (83%)	6 (17%)	0	100	100
17	CA	179/274 (65%)	173 (97%)	6 (3%)	0	100	100
18	CB	33/275 (12%)	29 (88%)	4 (12%)	0	100	100
All	All	2599/3141 (83%)	2382 (92%)	215 (8%)	2 (0%)	49	78

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
14	SY	52	LYS
14	SY	32	ARG

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	
2	SB	192/224 (86%)	192 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
3	SC	176/205 (86%)	176 (100%)	0	100 100
4	SE	221/222 (100%)	221 (100%)	0	100 100
5	SG	187/201 (93%)	187 (100%)	0	100 100
6	SH	165/170 (97%)	164 (99%)	1 (1%)	78 80
7	SI	150/161 (93%)	150 (100%)	0	100 100
8	SJ	158/166 (95%)	158 (100%)	0	100 100
9	SL	129/137 (94%)	129 (100%)	0	100 100
10	SN	127/128 (99%)	127 (100%)	0	100 100
11	SO	97/105 (92%)	97 (100%)	0	100 100
12	SW	110/111 (99%)	110 (100%)	0	100 100
13	SX	119/120 (99%)	119 (100%)	0	100 100
14	SY	112/113 (99%)	112 (100%)	0	100 100
15	Sb	70/71 (99%)	70 (100%)	0	100 100
16	Se	34/54 (63%)	34 (100%)	0	100 100
17	CA	158/238 (66%)	157 (99%)	1 (1%)	78 80
18	CB	31/233 (13%)	31 (100%)	0	100 100
All	All	2236/2659 (84%)	2234 (100%)	2 (0%)	87 89

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	SH	174	ASN
17	CA	262	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (21) such sidechains are listed below:

Mol	Chain	Res	Type
2	SB	101	HIS
2	SB	149	GLN
2	SB	177	GLN
2	SB	194	ASN
2	SB	199	ASN
3	SC	89	GLN
4	SE	112	HIS
4	SE	142	HIS

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Mol	Chain	Res	Type
4	SE	153	ASN
6	SH	160	GLN
9	SL	92	HIS
9	SL	127	GLN
10	SN	105	ASN
12	SW	64	GLN
12	SW	70	ASN
12	SW	92	ASN
12	SW	113	HIS
13	SX	18	HIS
14	SY	63	GLN
15	Sb	26	GLN
16	Se	46	ASN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	C2	1191/1800 (66%)	253 (21%)	11 (0%)

All (253) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	C2	2	A
1	C2	3	U
1	C2	4	C
1	C2	8	U
1	C2	11	A
1	C2	25	C
1	C2	26	A
1	C2	27	U
1	C2	34	G
1	C2	42	G
1	C2	43	A
1	C2	46	A
1	C2	47	A
1	C2	57	G
1	C2	60	U
1	C2	63	G
1	C2	67	A
1	C2	68	A
1	C2	71	A

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Mol	Chain	Res	Type
1	C2	104	A
1	C2	111	U
1	C2	114	C
1	C2	127	G
1	C2	132	U
1	C2	137	U
1	C2	140	A
1	C2	145	A
1	C2	146	U
1	C2	158	U
1	C2	161	U
1	C2	166	C
1	C2	176	C
1	C2	177	U
1	C2	178	U
1	C2	179	A
1	C2	185	U
1	C2	189	C
1	C2	190	C
1	C2	192	U
1	C2	193	U
1	C2	194	U
1	C2	195	G
1	C2	196	G
1	C2	197	A
1	C2	200	A
1	C2	216	U
1	C2	217	A
1	C2	220	A
1	C2	223	U
1	C2	227	U
1	C2	229	U
1	C2	230	C
1	C2	233	C
1	C2	235	G
1	C2	240	U
1	C2	261	U
1	C2	265	A
1	C2	273	G
1	C2	276	C
1	C2	277	U
1	C2	278	U

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Mol	Chain	Res	Type
1	C2	280	U
1	C2	287	G
1	C2	299	A
1	C2	314	C
1	C2	316	A
1	C2	320	U
1	C2	321	C
1	C2	322	G
1	C2	337	G
1	C2	338	C
1	C2	352	A
1	C2	359	A
1	C2	360	A
1	C2	361	C
1	C2	369	A
1	C2	370	A
1	C2	381	C
1	C2	400	A
1	C2	401	A
1	C2	402	C
1	C2	404	G
1	C2	415	C
1	C2	418	G
1	C2	423	G
1	C2	424	C
1	C2	426	G
1	C2	434	G
1	C2	439	U
1	C2	444	C
1	C2	448	C
1	C2	454	U
1	C2	460	A
1	C2	464	A
1	C2	468	A
1	C2	475	A
1	C2	477	A
1	C2	483	A
1	C2	486	G
1	C2	488	G
1	C2	501	U
1	C2	506	A
1	C2	507	U

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Mol	Chain	Res	Type
1	C2	510	G
1	C2	511	A
1	C2	515	A
1	C2	519	C
1	C2	527	A
1	C2	539	G
1	C2	540	G
1	C2	542	A
1	C2	543	C
1	C2	548	G
1	C2	549	G
1	C2	554	C
1	C2	555	A
1	C2	556	A
1	C2	557	G
1	C2	559	C
1	C2	568	G
1	C2	574	G
1	C2	579	A
1	C2	580	A
1	C2	581	U
1	C2	582	U
1	C2	583	C
1	C2	594	A
1	C2	595	G
1	C2	606	A
1	C2	610	G
1	C2	611	U
1	C2	613	G
1	C2	619	A
1	C2	620	A
1	C2	623	A
1	C2	639	U
1	C2	685	A
1	C2	690	G
1	C2	696	C
1	C2	697	C
1	C2	699	U
1	C2	701	U
1	C2	703	G
1	C2	705	U
1	C2	734	A

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Mol	Chain	Res	Type
1	C2	735	C
1	C2	738	G
1	C2	743	U
1	C2	744	U
1	C2	745	U
1	C2	754	A
1	C2	755	A
1	C2	756	A
1	C2	765	G
1	C2	766	U
1	C2	774	A
1	C2	775	G
1	C2	779	U
1	C2	781	U
1	C2	782	U
1	C2	783	G
1	C2	789	A
1	C2	794	U
1	C2	795	U
1	C2	811	A
1	C2	812	A
1	C2	813	U
1	C2	820	U
1	C2	821	U
1	C2	826	U
1	C2	829	A
1	C2	830	U
1	C2	831	U
1	C2	835	U
1	C2	846	G
1	C2	850	A
1	C2	851	U
1	C2	852	C
1	C2	853	G
1	C2	854	U
1	C2	863	A
1	C2	876	G
1	C2	898	A
1	C2	906	A
1	C2	913	G
1	C2	914	G
1	C2	933	A

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Mol	Chain	Res	Type
1	C2	935	U
1	C2	942	G
1	C2	945	U
1	C2	951	A
1	C2	959	U
1	C2	960	U
1	C2	966	A
1	C2	969	C
1	C2	970	A
1	C2	983	A
1	C2	992	A
1	C2	993	A
1	C2	996	U
1	C2	998	A
1	C2	999	U
1	C2	1001	A
1	C2	1002	G
1	C2	1006	C
1	C2	1021	C
1	C2	1025	A
1	C2	1026	A
1	C2	1028	C
1	C2	1030	A
1	C2	1031	U
1	C2	1032	G
1	C2	1039	A
1	C2	1040	G
1	C2	1052	U
1	C2	1053	G
1	C2	1056	U
1	C2	1058	U
1	C2	1059	U
1	C2	1060	U
1	C2	1061	A
1	C2	1074	G
1	C2	1076	A
1	C2	1081	A
1	C2	1082	C
1	C2	1092	A
1	C2	1096	C
1	C2	1097	U
1	C2	1098	U

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Mol	Chain	Res	Type
1	C2	1100	G
1	C2	1113	A
1	C2	1115	U
1	C2	1126	G
1	C2	1138	A
1	C2	1637	C
1	C2	1638	G
1	C2	1658	G
1	C2	1663	G
1	C2	1680	G
1	C2	1715	G
1	C2	1716	C
1	C2	1718	G
1	C2	1750	A
1	C2	1754	A
1	C2	1755	A
1	C2	1769	U
1	C2	1770	U
1	C2	1780	G
1	C2	1782	A
1	C2	1783	C
1	C2	1792	G
1	C2	1793	G
1	C2	1795	U

All (11) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	C2	25	C
1	C2	103	A
1	C2	136	C
1	C2	139	C
1	C2	272	U
1	C2	417	A
1	C2	555	A
1	C2	755	A
1	C2	997	G
1	C2	1051	G
1	C2	1097	U

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 1 ligands modelled in this entry, 1 is 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.

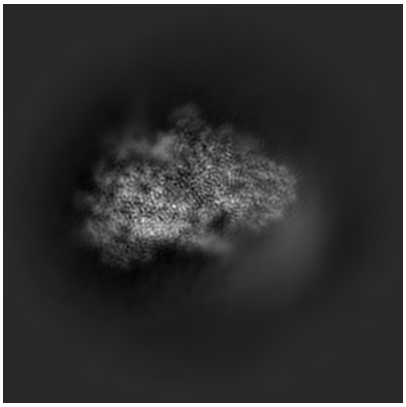
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-32792. These allow visual inspection of the internal detail of the map and identification of artifacts.

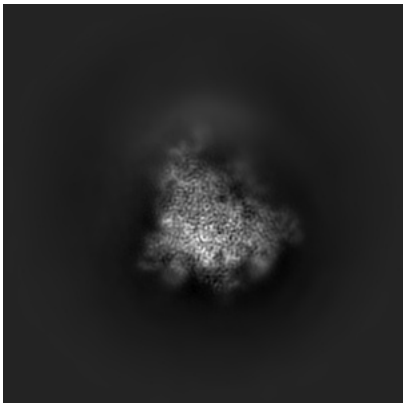
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

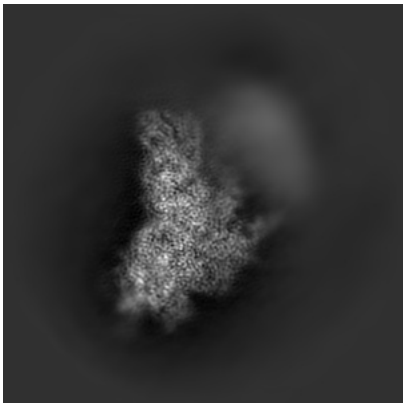
6.1.1 Primary map



X



Y

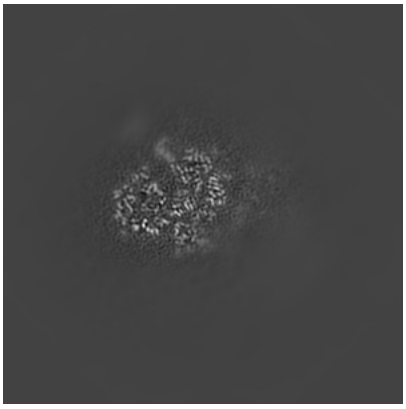


Z

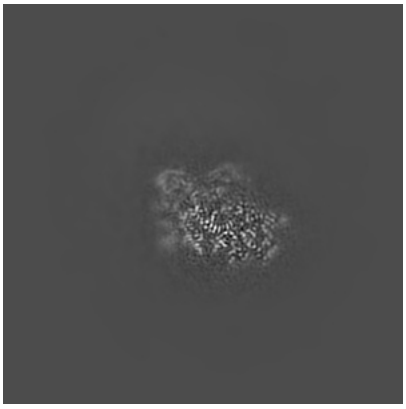
The images above show the map projected in three orthogonal directions.

6.2 Central slices

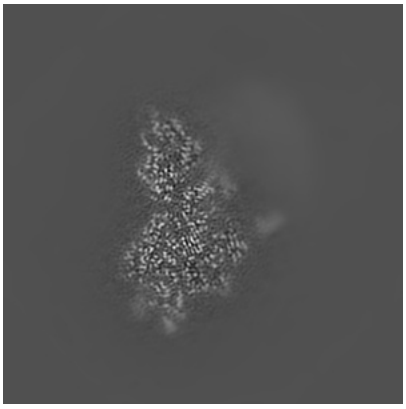
6.2.1 Primary map



X Index: 180



Y Index: 180

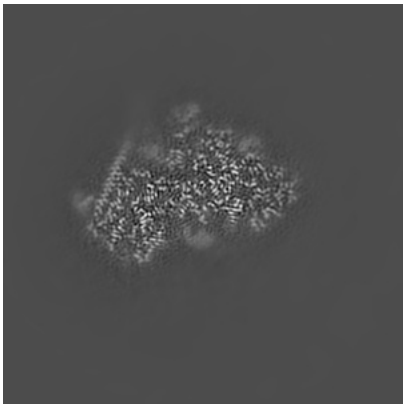


Z Index: 180

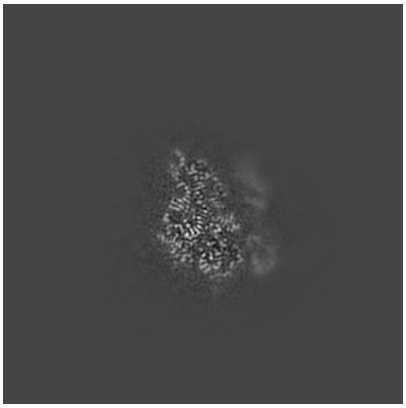
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

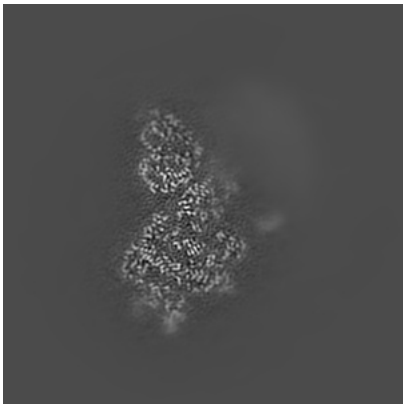
6.3.1 Primary map



X Index: 147



Y Index: 139

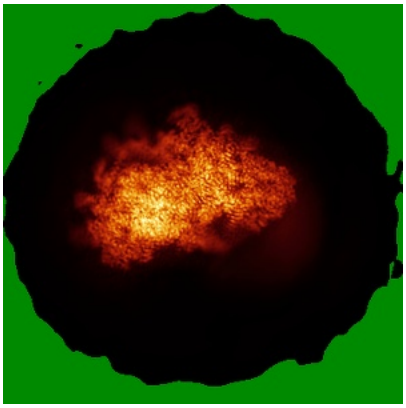


Z Index: 182

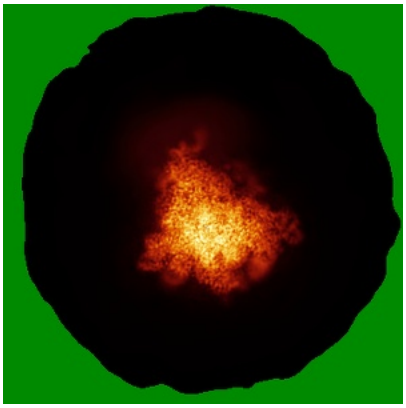
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

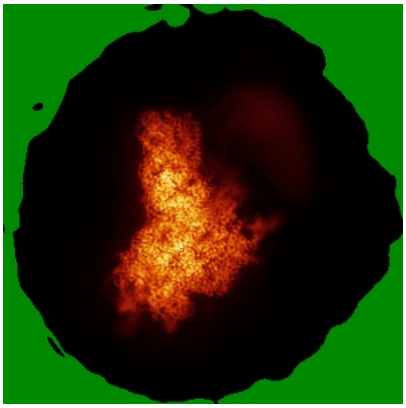
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views (i)

6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.01. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

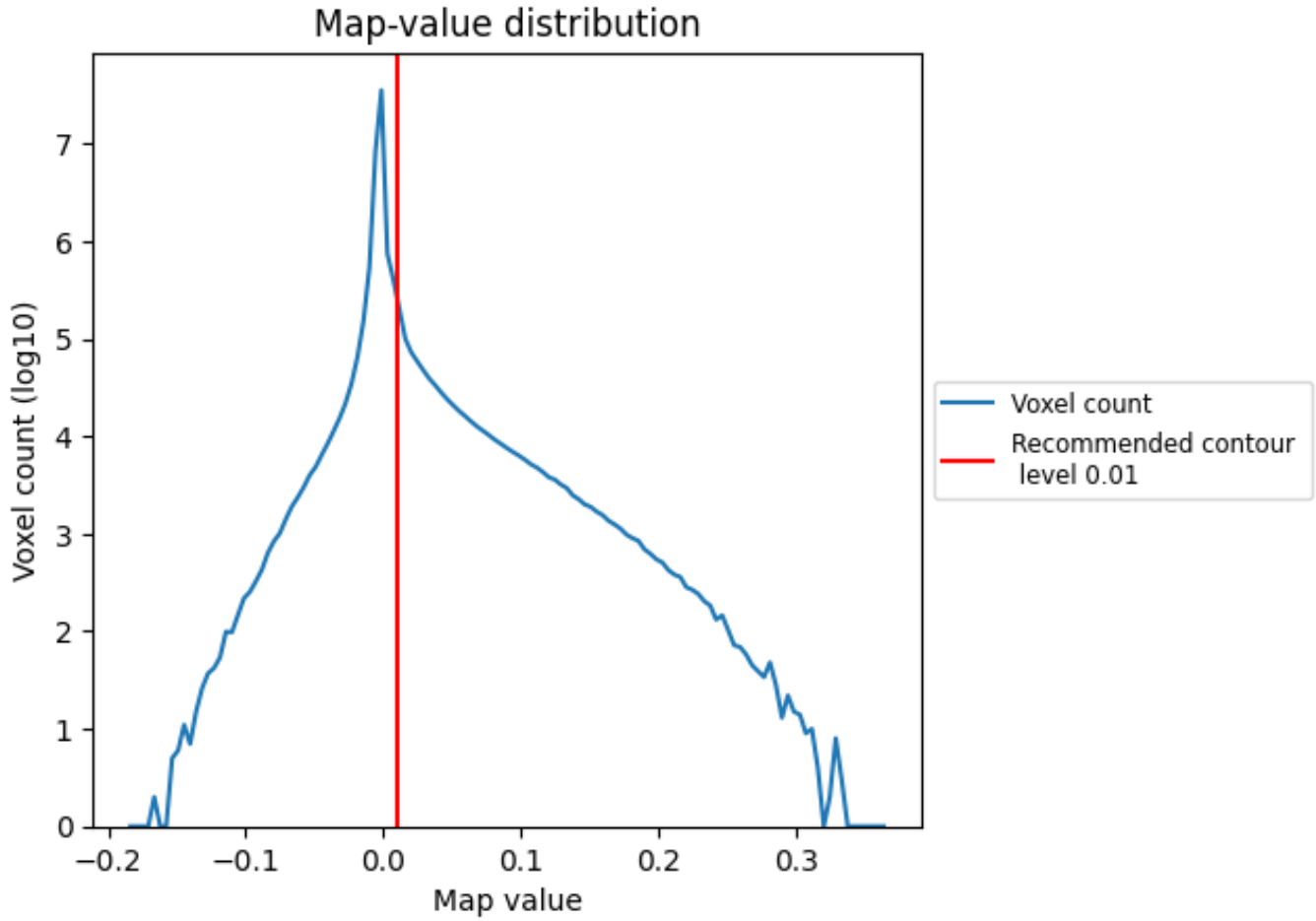
6.6 Mask visualisation (i)

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

7 Map analysis

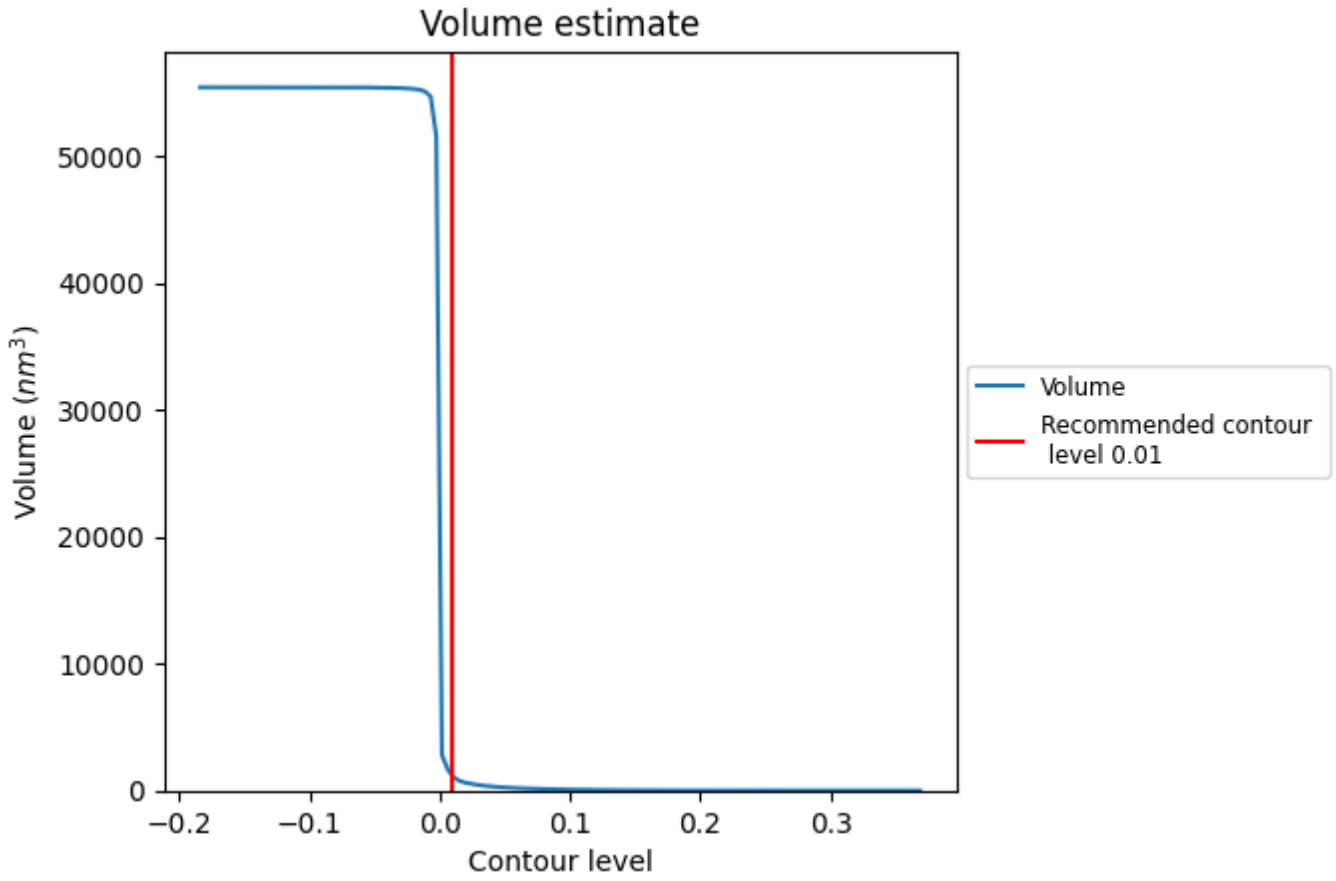
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

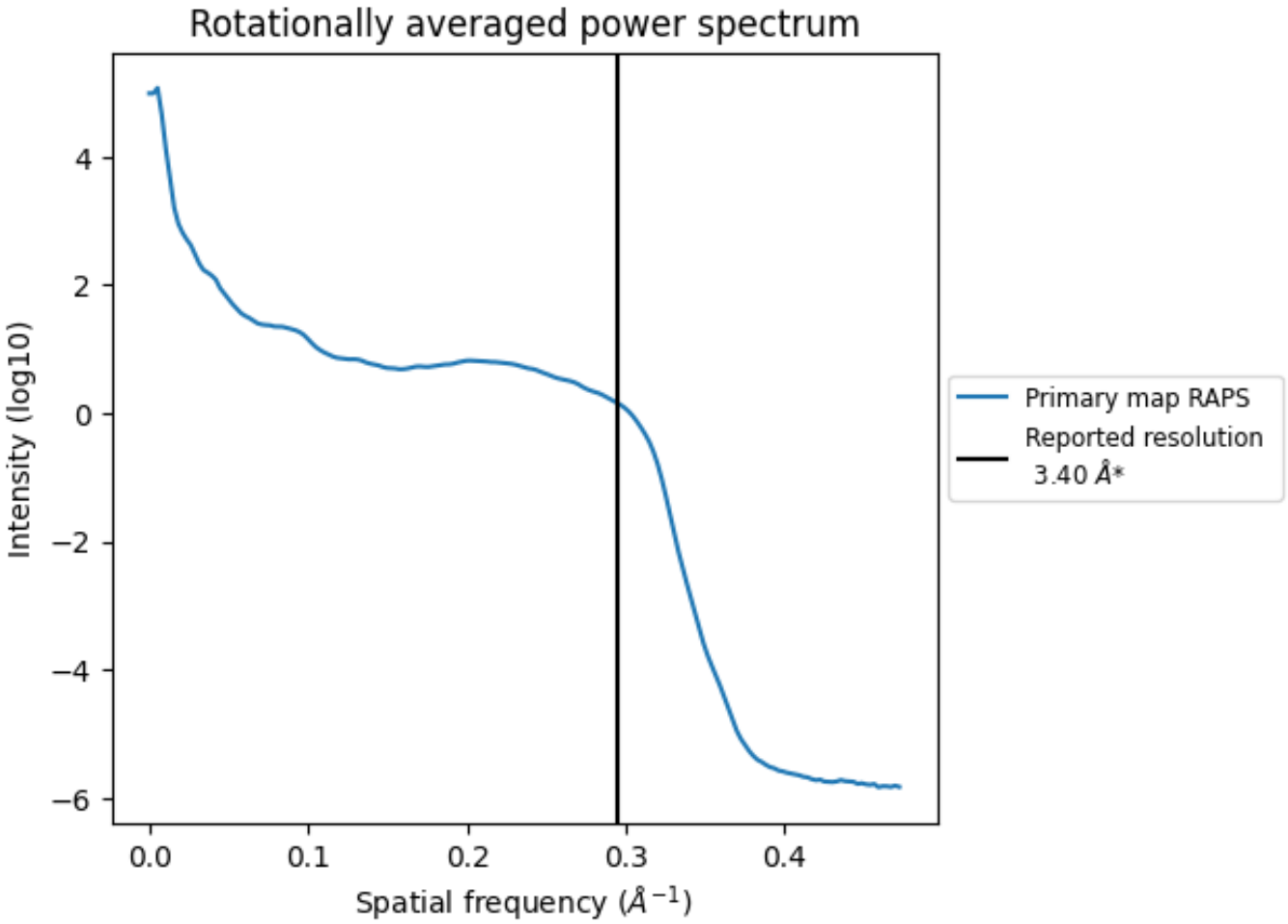
7.2 Volume estimate



The volume at the recommended contour level is 1138 nm^3; this corresponds to an approximate mass of 1028 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)

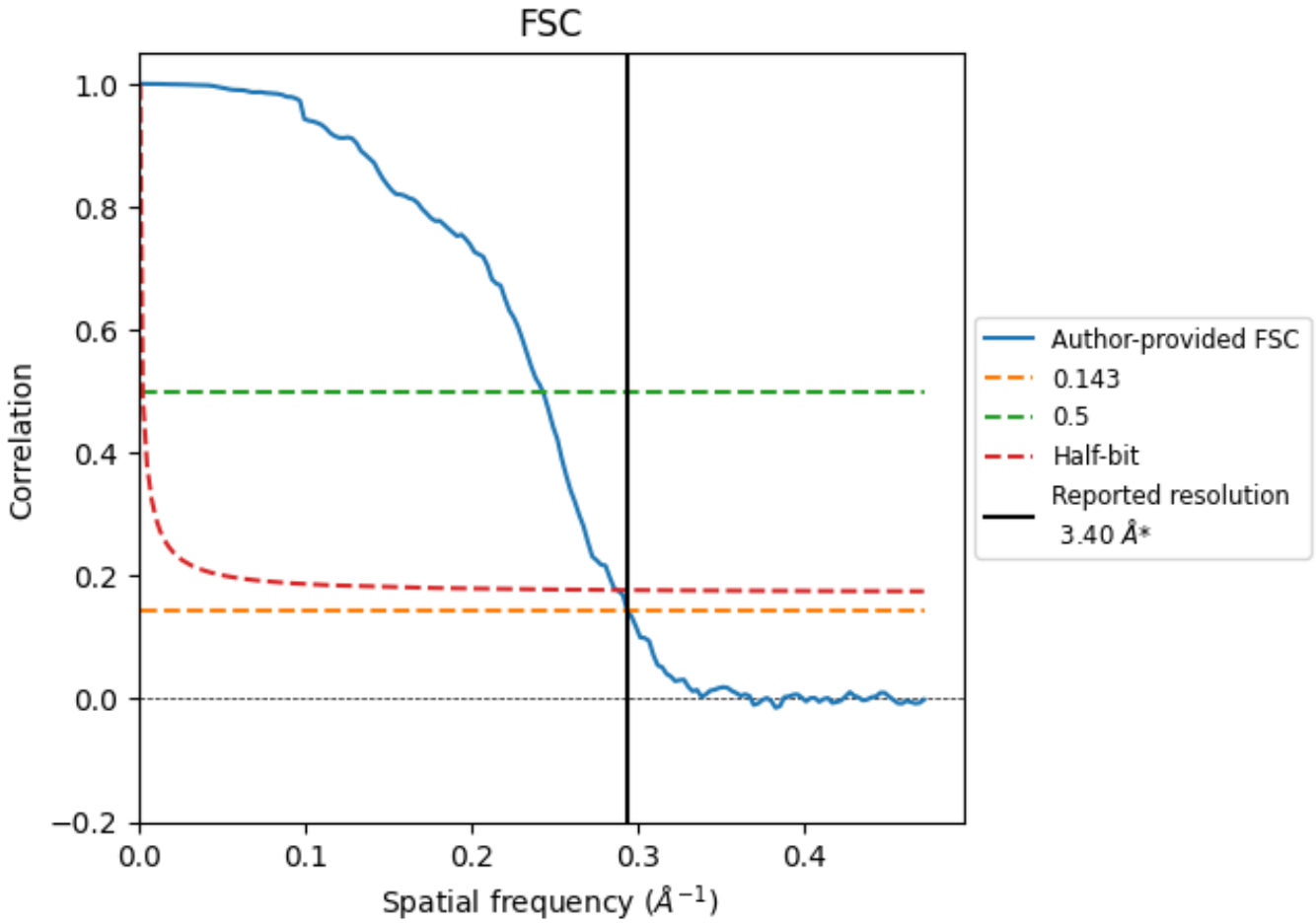


*Reported resolution corresponds to spatial frequency of 0.294 Å^{-1}

8 Fourier-Shell correlation

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



*Reported resolution corresponds to spatial frequency of 0.294 Å^{-1}

8.2 Resolution estimates (i)

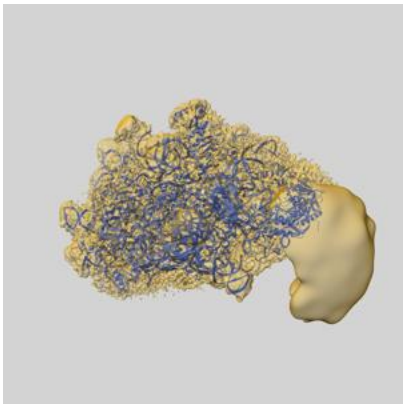
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	3.40	4.12	3.47
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

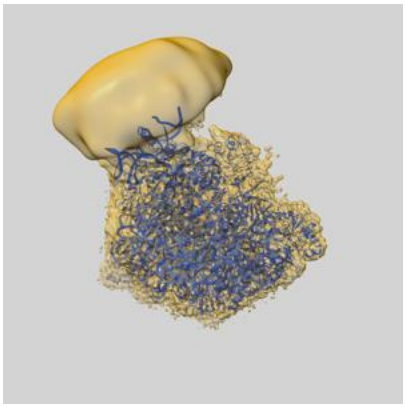
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-32792 and PDB model 7WTN. Per-residue inclusion information can be found in section 3 on page 7.

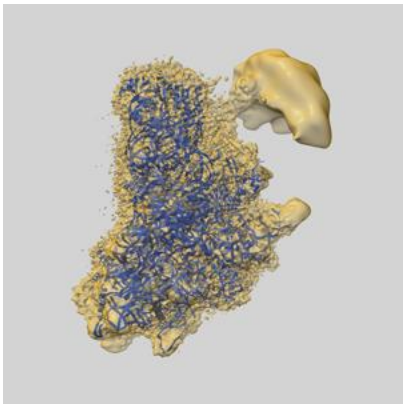
9.1 Map-model overlay



X



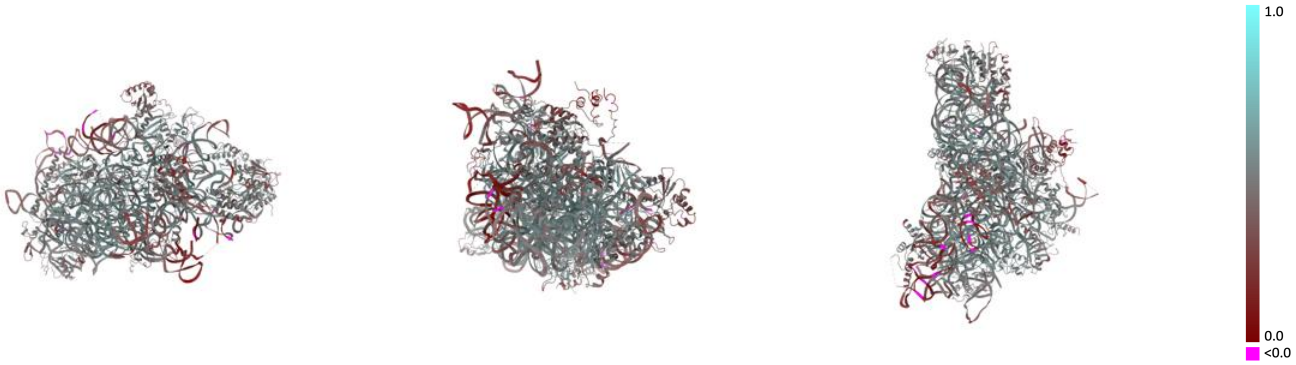
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.01 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.

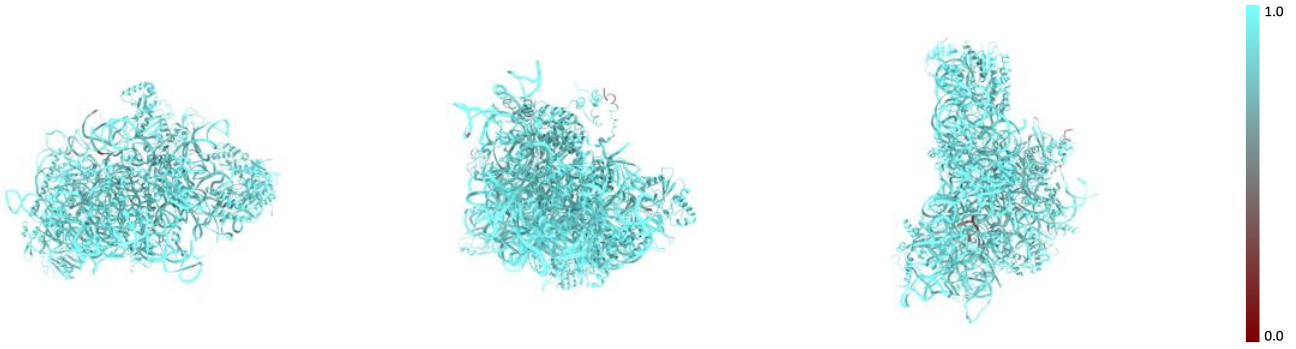
9.2 Q-score mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according 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.

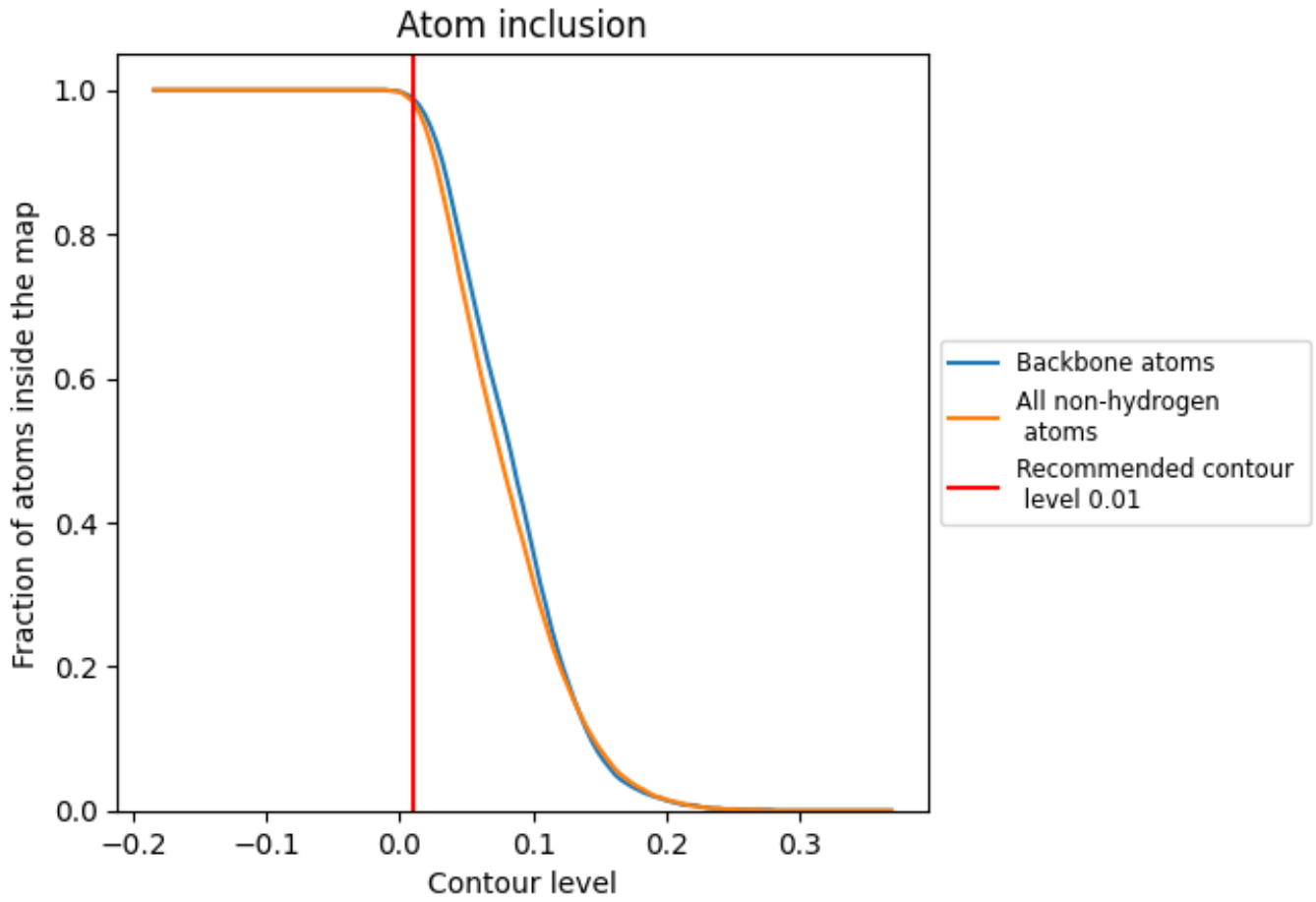
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (0.01).

9.4 Atom inclusion (i)



At the recommended contour level, 99% of all backbone atoms, 98% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9840	0.4700
C2	0.9880	0.4610
CA	0.9780	0.4410
CB	0.9480	0.4420
SB	0.9820	0.4890
SC	0.9320	0.3630
SE	0.9890	0.5360
SG	0.9960	0.4690
SH	0.9840	0.4070
SI	0.9910	0.5100
SJ	0.9900	0.5080
SL	0.9850	0.5380
SN	0.9890	0.5150
SO	0.9730	0.4860
SW	0.9910	0.5530
SX	0.9690	0.4760
SY	0.9900	0.5040
Sb	0.9870	0.4880
Se	0.8030	0.3900

