Full wwPDB EM Validation Report

Jun 10, 2025 – 01:36 pm BST

PDB ID	:	9G25 / pdb_00009g25
EMDB ID	:	EMD-50964
Title	:	snR30 snoRNP - State 1 - Utp23-Krr1-deltaC3
Authors	:	Thoms, M.; Berninghausen, O.; Beckmann, R.
Deposited on	:	2024-07-10
Resolution	:	2.89 Å(reported)

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

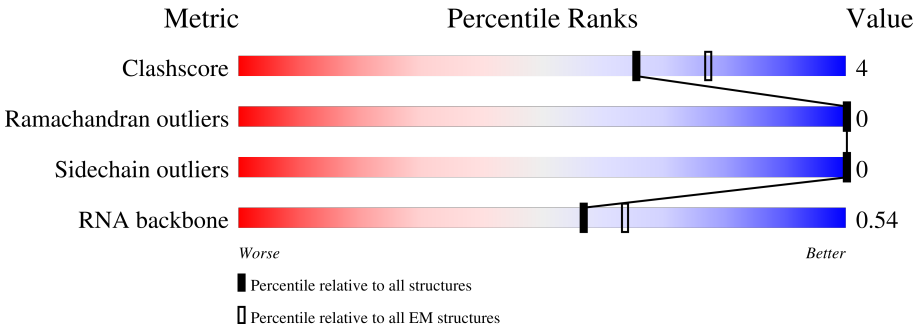
EMDB validation analysis	:	0.0.1.dev118
MolProbity	:	4-5-2 with Phenix2.0rc1
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.43.1

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 2.89 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)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	3	1800	6% · 91%
2	4	609	22% 9% · 68%
3	A	483	64% 7% 29%
3	E	483	67% 9% 24%
4	B	58	93% 7%
4	F	58	90% 10%
5	C	205	41% · 54%

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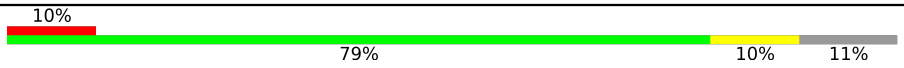
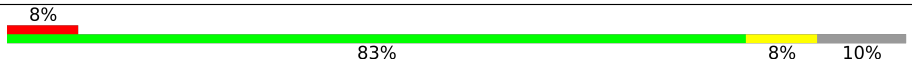
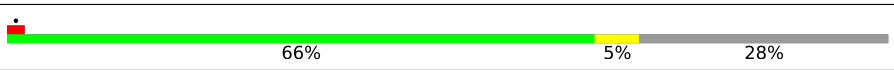
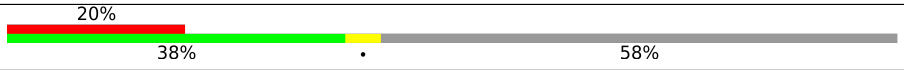
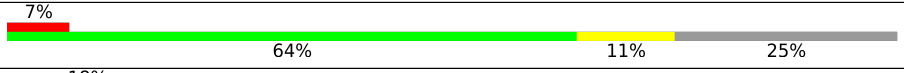
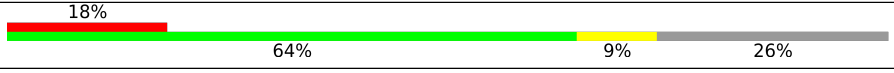
Mol	Chain	Length	Quality of chain
6	D	156	
6	G	156	
7	H	316	
8	I	591	
9	J	151	
10	K	254	
11	L	137	

2 Entry composition

There are 12 unique types of molecules in this entry. The entry contains 24015 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 RDN18-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	3	170	Total	C	N	O	P	0	0
			3629	1623	643	1193	170		

- Molecule 2 is a RNA chain called snR30.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	4	197	Total	C	N	O	P	0	0
			4199	1878	753	1371	197		

- Molecule 3 is a protein called H/ACA ribonucleoprotein complex subunit CBF5.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A	344	Total	C	N	O	S	0	0
			2686	1697	482	490	17		
3	E	368	Total	C	N	O	S	0	0
			2876	1813	505	540	18		

- Molecule 4 is a protein called H/ACA ribonucleoprotein complex subunit NOP10.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	B	58	Total	C	N	O	S	0	0
			467	296	86	83	2		
4	F	58	Total	C	N	O	S	0	0
			467	296	86	83	2		

- Molecule 5 is a protein called H/ACA ribonucleoprotein complex subunit GAR1.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	C	94	Total	C	N	O	S	0	0
			733	478	115	136	4		

- Molecule 6 is a protein called H/ACA ribonucleoprotein complex subunit NHP2.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	D	139	Total	C	N	O	S	0	0
			1046	670	182	192	2		
6	G	141	Total	C	N	O	S	0	0
			1064	682	185	195	2		

- Molecule 7 is a protein called KRR1 small subunit processome component.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	H	226	Total	C	N	O	S	0	0
			1839	1174	322	333	10		

- Molecule 8 is a protein called Protein KRI1.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	I	251	Total	C	N	O	0	0
			1753	1099	324	330		

- Molecule 9 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	J	114	Total	C	N	O	S	0	0
			928	593	174	160	1		

- Molecule 10 is a protein called rRNA-processing protein UTP23.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	K	187	Total	C	N	O	S	0	0
			1485	932	274	270	9		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
11	L	116	Total	C	N	O	S	0	0
			842	522	158	159	3		

- Molecule 12 is ZINC ION (CCD ID: ZN) (formula: Zn).

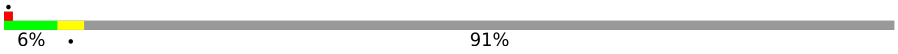
Mol	Chain	Residues	Atoms		AltConf
12	K	1	Total	Zn	0
			1	1	

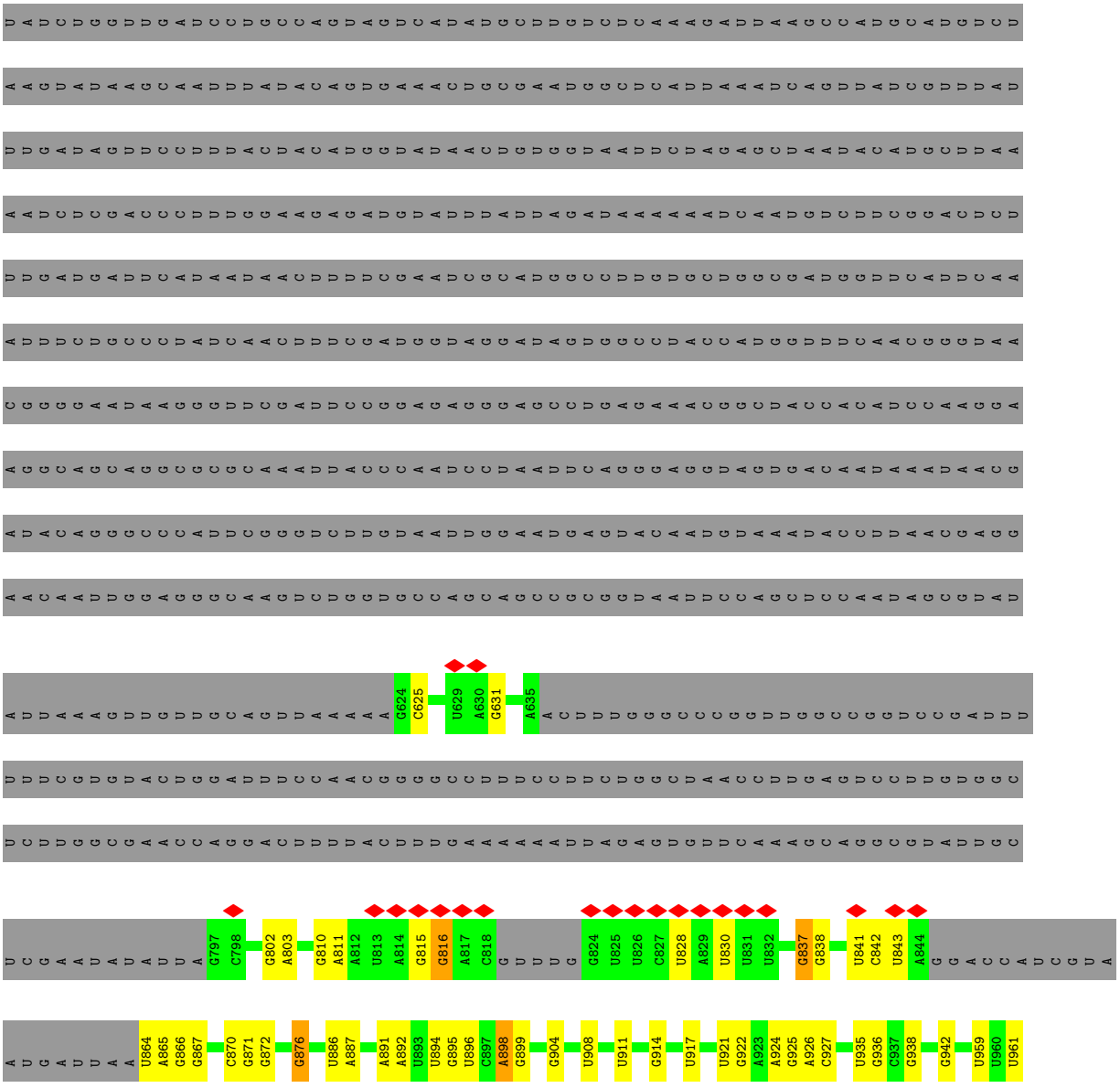
3 Residue-property plots (i)

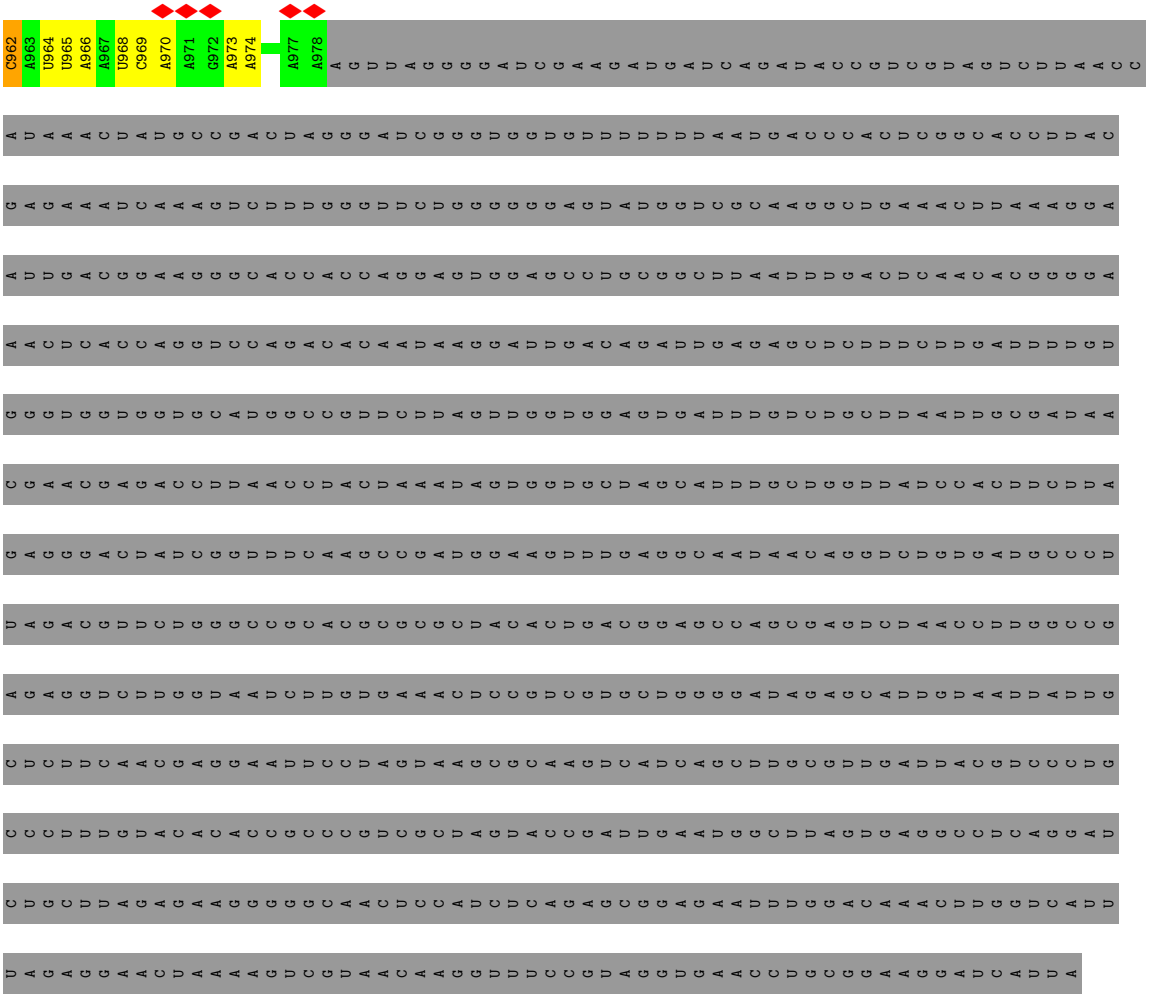
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: RDN18-1

Chain 3:

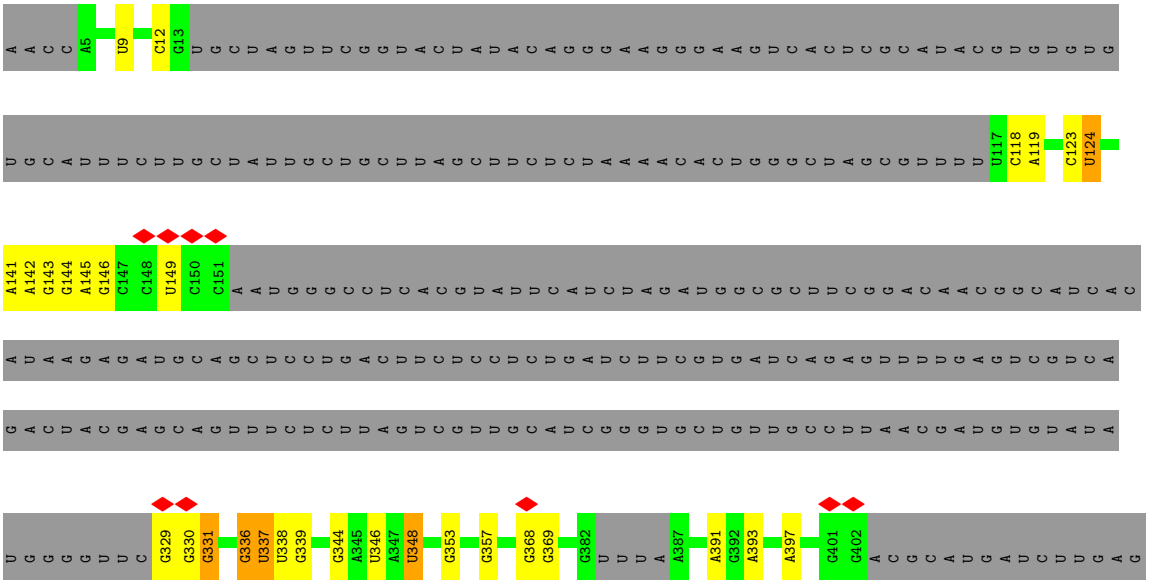


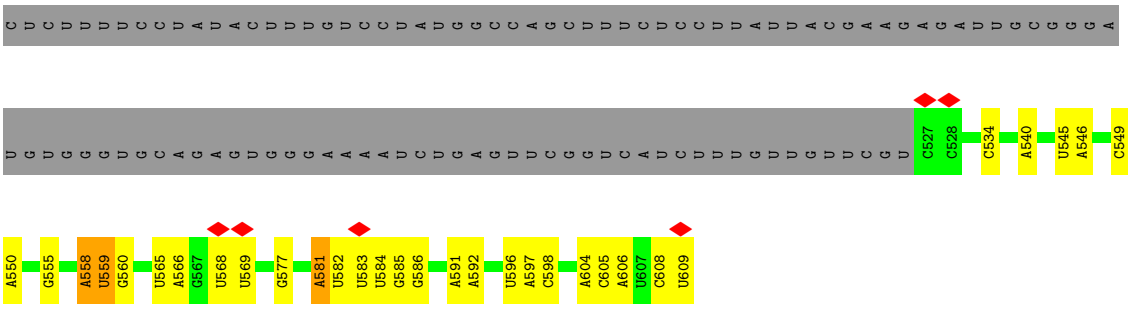




• Molecule 2: snR30

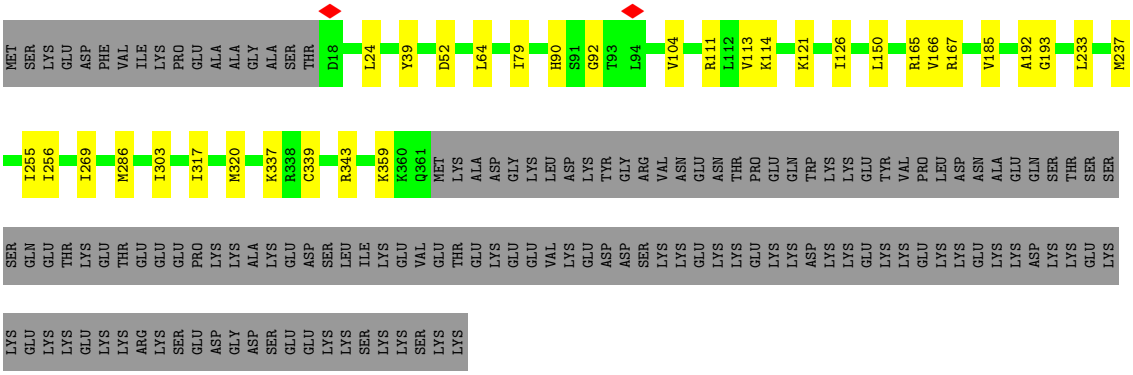
Chain 4:





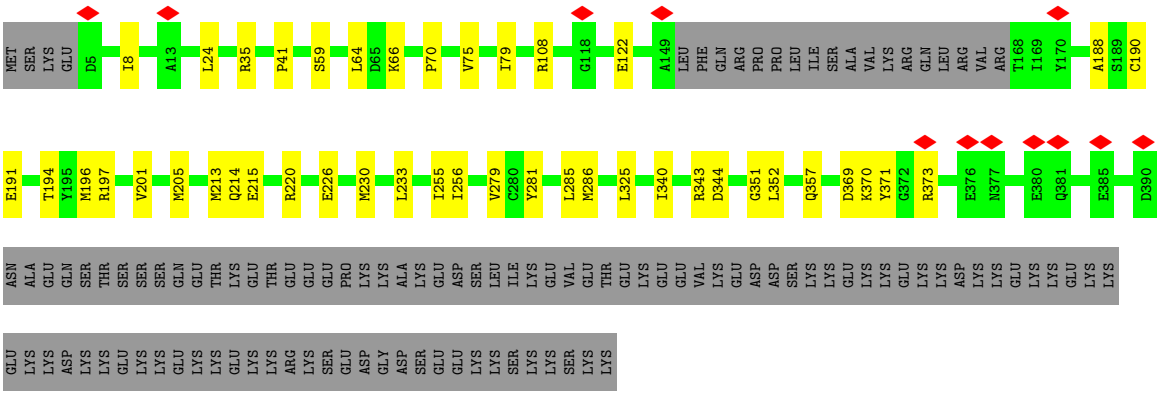
• Molecule 3: H/ACA ribonucleoprotein complex subunit CBF5

Chain A:



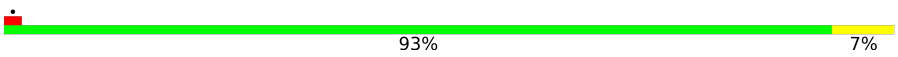
• Molecule 3: H/ACA ribonucleoprotein complex subunit CBF5

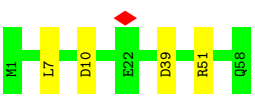
Chain E:



• Molecule 4: H/ACA ribonucleoprotein complex subunit NOP10

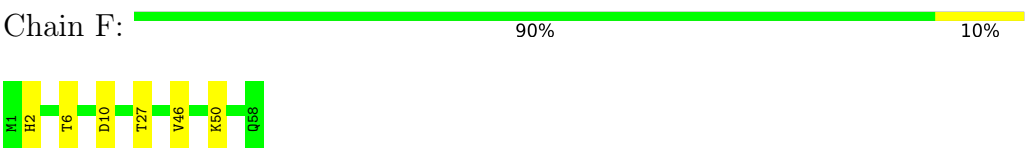
Chain B:





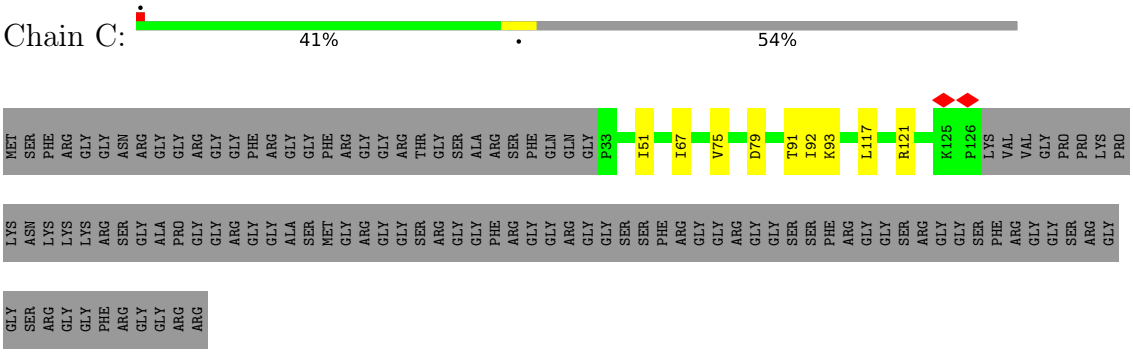
• Molecule 4: H/ACA ribonucleoprotein complex subunit NOP10

Chain F:



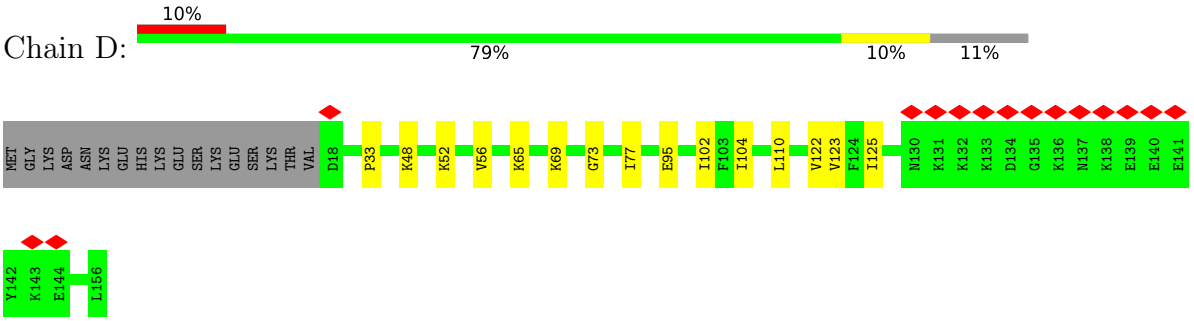
• Molecule 5: H/ACA ribonucleoprotein complex subunit GAR1

Chain C:



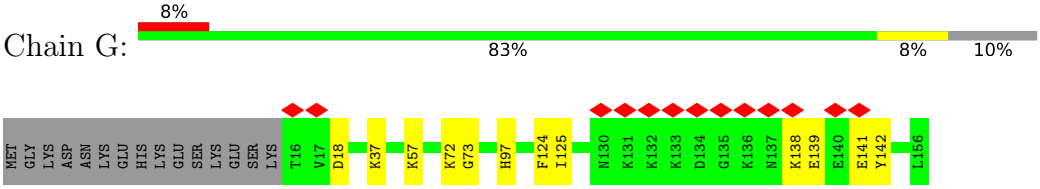
• Molecule 6: H/ACA ribonucleoprotein complex subunit NHP2

Chain D:



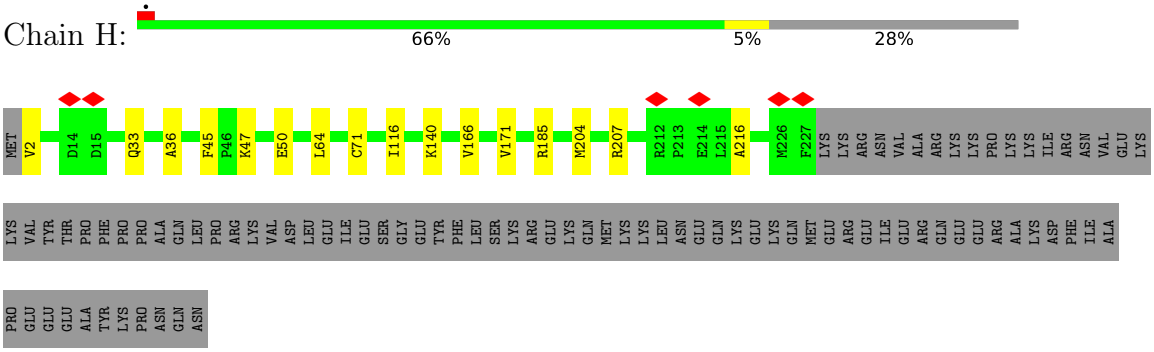
• Molecule 6: H/ACA ribonucleoprotein complex subunit NHP2

Chain G:



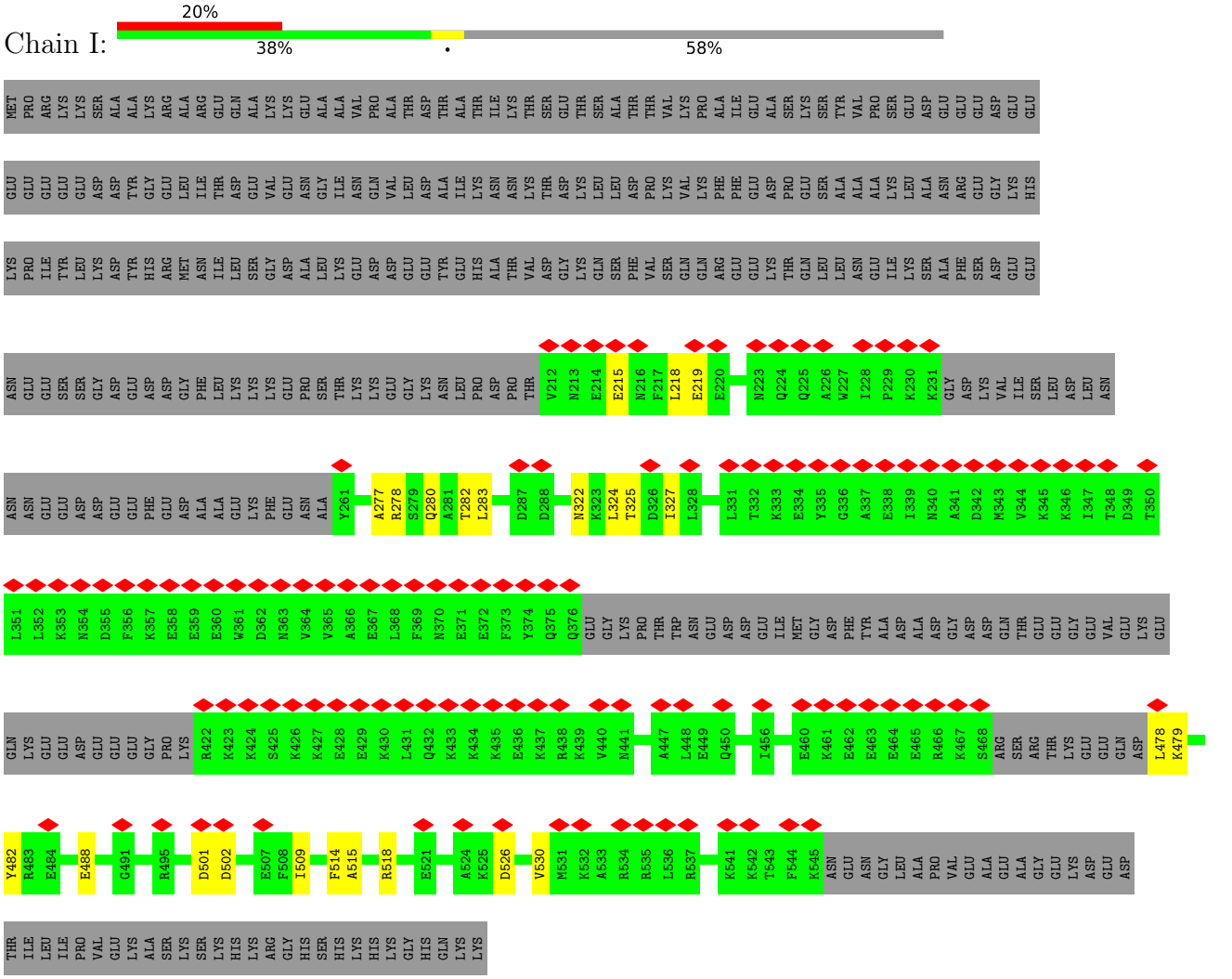
• Molecule 7: KRR1 small subunit processome component

Chain H:



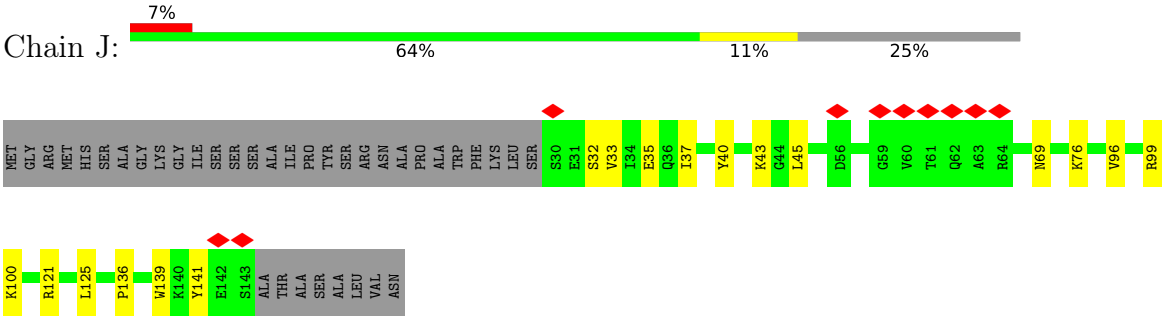
• Molecule 8: Protein KRI1

Chain I:



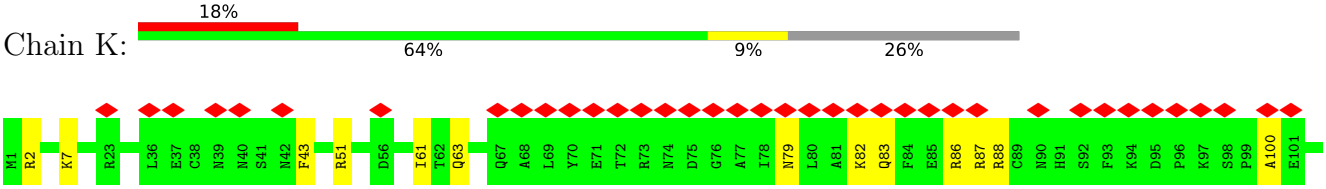
• Molecule 9: 40S ribosomal protein S13

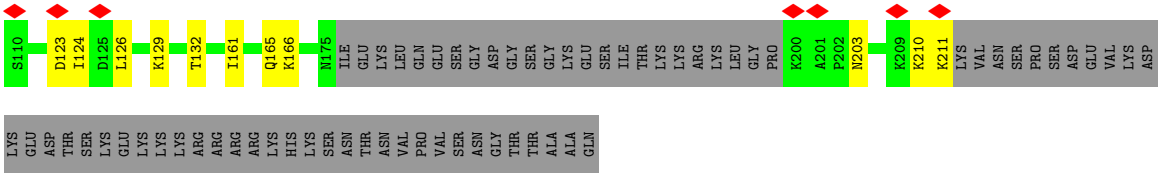
Chain J:



• Molecule 10: rRNA-processing protein UTP23

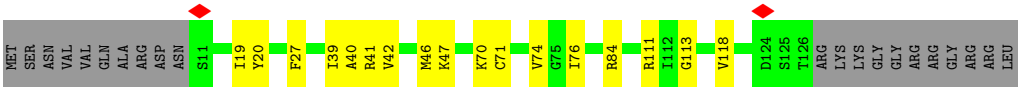
Chain K:





• Molecule 11: 40S ribosomal protein S14-A

Chain L:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	171224	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	46.4	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	5.929	Depositor
Minimum map value	-0.397	Depositor
Average map value	0.008	Depositor
Map value standard deviation	0.093	Depositor
Recommended contour level	0.6	Depositor
Map size (Å)	334.4, 334.4, 334.4	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.045, 1.045, 1.045	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	3	0.14	0/4058	0.30	0/6315
2	4	0.15	0/4693	0.29	0/7301
3	A	0.19	0/2732	0.50	3/3694 (0.1%)
3	E	0.19	0/2926	0.50	3/3955 (0.1%)
4	B	0.15	0/477	0.37	0/637
4	F	0.14	0/477	0.38	0/637
5	C	0.19	0/752	0.48	0/1021
6	D	0.21	0/1063	0.52	0/1432
6	G	0.19	0/1081	0.48	0/1456
7	H	0.17	0/1876	0.44	0/2531
8	I	0.19	0/1774	0.47	1/2406 (0.0%)
9	J	0.20	0/944	0.51	0/1272
10	K	0.21	0/1508	0.53	0/2029
11	L	0.19	0/853	0.46	0/1153
All	All	0.18	0/25214	0.42	7/35839 (0.0%)

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	E	286	MET	CA-C-N	7.05	124.68	120.24
3	E	286	MET	C-N-CA	7.05	124.68	120.24
3	A	286	MET	CA-C-N	6.60	124.40	120.24
3	A	286	MET	C-N-CA	6.60	124.40	120.24
8	I	219	GLU	N-CA-CB	5.56	118.87	110.30
3	E	24	LEU	CB-CA-C	-5.21	110.14	117.23
3	A	24	LEU	CB-CA-C	-5.21	110.15	117.23

There are no chirality outliers.

There are no planarity outliers.

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	3	3629	0	1821	29	0
2	4	4199	0	2124	23	0
3	A	2686	0	2762	20	0
3	E	2876	0	2921	25	0
4	B	467	0	487	4	0
4	F	467	0	487	4	0
5	C	733	0	730	6	0
6	D	1046	0	1096	9	0
6	G	1064	0	1123	6	0
7	H	1839	0	1880	14	0
8	I	1753	0	1448	16	0
9	J	928	0	983	12	0
10	K	1485	0	1538	17	0
11	L	842	0	858	13	0
12	K	1	0	0	0	0
All	All	24015	0	20258	166	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

All (166) 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)
1:3:837:G:H5”	10:K:203:ASN:HB2	1.70	0.73
6:D:73:GLY:HA3	6:D:125:ILE:O	1.89	0.71
10:K:61:ILE:O	10:K:86:ARG:NH1	2.29	0.66
11:L:20:TYR:HB3	11:L:27:PHE:HB2	1.78	0.64
8:I:514:PHE:HB2	9:J:76:LYS:HE3	1.81	0.62
3:E:59:SER:OG	3:E:108:ARG:NH1	2.32	0.62
2:4:336:G:H4’	2:4:337:U:H5’	1.83	0.61
3:E:351:GLY:O	3:E:357:GLN:NE2	2.35	0.59
10:K:79:ASN:OD1	10:K:83:GLN:NE2	2.35	0.59
2:4:558:A:H4’	2:4:559:U:H5’	1.83	0.59
3:A:126:ILE:HG12	3:A:185:VAL:HG22	1.82	0.59
2:4:9:U:O2	3:E:343:ARG:NH2	2.35	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:I:515:ALA:HB3	8:I:518:ARG:HB2	1.84	0.58
3:E:201:VAL:HG12	3:E:205:MET:HE2	1.85	0.58
11:L:42:VAL:HG13	11:L:46:MET:HE2	1.86	0.58
8:I:277:ALA:O	8:I:280:GLN:NE2	2.37	0.57
6:D:65:LYS:HG2	6:D:69:LYS:HE2	1.87	0.57
5:C:75:VAL:HG12	8:I:283:LEU:HD11	1.84	0.57
2:4:534:C:O2	3:A:343:ARG:NH2	2.38	0.57
1:3:904:G:N2	7:H:216:ALA:O	2.38	0.56
3:A:90:HIS:HD1	3:A:92:GLY:H	1.54	0.56
3:A:64:LEU:HD21	3:A:233:LEU:HG	1.88	0.56
6:D:56:VAL:HG13	6:D:123:VAL:HG13	1.88	0.56
3:E:190:CYS:SG	3:E:191:GLU:N	2.79	0.55
11:L:84:ARG:HB2	11:L:118:VAL:HG23	1.89	0.55
3:A:255:ILE:HG13	3:A:256:ILE:HG13	1.89	0.55
3:E:255:ILE:HG13	3:E:256:ILE:HG13	1.88	0.55
3:E:279:VAL:HG21	3:E:285:LEU:HD12	1.89	0.54
2:4:397:A:OP1	3:A:359:LYS:NZ	2.39	0.54
7:H:47:LYS:HD3	8:I:282:THR:HG21	1.89	0.54
1:3:904:G:OP1	7:H:185:ARG:NH1	2.41	0.54
3:A:111:ARG:NH1	3:A:339:CYS:O	2.41	0.53
3:A:113:VAL:HG13	3:A:114:LYS:HG3	1.91	0.53
3:A:150:LEU:O	3:A:166:VAL:HA	2.08	0.53
3:E:66:LYS:NZ	3:E:70:PRO:O	2.41	0.53
3:A:64:LEU:HD22	3:A:79:ILE:HD11	1.90	0.53
3:A:269:ILE:HD12	3:A:303:ILE:HD12	1.91	0.53
1:3:876:G:N7	8:I:278:ARG:NH2	2.54	0.53
6:D:104:ILE:HD11	6:D:110:LEU:HB2	1.90	0.52
10:K:63:GLN:OE1	10:K:86:ARG:NH2	2.31	0.52
1:3:908:U:OP2	7:H:2:VAL:N	2.42	0.52
1:3:864:U:H2'	1:3:865:A:H8	1.74	0.52
3:A:165:ARG:NH2	3:A:193:GLY:O	2.43	0.52
6:G:72:LYS:NZ	6:G:97:HIS:O	2.42	0.52
7:H:33:GLN:OE1	11:L:111:ARG:NH1	2.43	0.51
7:H:207:ARG:NH1	8:I:215:GLU:OE1	2.41	0.51
2:4:545:U:H2'	2:4:546:A:H8	1.76	0.51
3:E:194:THR:HA	3:E:197:ARG:HD3	1.91	0.51
3:A:166:VAL:O	3:A:167:ARG:NH1	2.43	0.51
4:B:51:ARG:NH2	6:D:95:GLU:OE2	2.43	0.51
2:4:344:G:N2	2:4:348:U:OP2	2.44	0.51
1:3:973:A:H2'	1:3:974:A:H8	1.75	0.50
7:H:45:PHE:HE1	7:H:50:GLU:HG2	1.75	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:4:149:U:H3	2:4:331:G:H1	1.60	0.50
3:E:352:LEU:HA	3:E:357:GLN:HE21	1.76	0.50
1:3:962:C:OP1	9:J:69:ASN:ND2	2.45	0.50
8:I:324:LEU:HD13	8:I:327:ILE:HD11	1.93	0.49
3:E:64:LEU:HD21	3:E:233:LEU:HG	1.94	0.49
3:E:197:ARG:NH1	3:E:213:MET:SD	2.85	0.49
11:L:39:ILE:HG21	11:L:74:VAL:HG11	1.93	0.49
1:3:631:G:H1	1:3:968:U:H3	1.60	0.48
3:E:214:GLN:HG3	3:E:215:GLU:HG3	1.95	0.48
3:E:281:TYR:OH	3:E:344:ASP:OD1	2.29	0.48
10:K:79:ASN:HA	10:K:82:LYS:HG2	1.96	0.48
3:E:64:LEU:HD22	3:E:79:ILE:HD11	1.95	0.48
1:3:864:U:H2'	1:3:865:A:C8	2.48	0.48
3:A:121:LYS:HE2	3:A:192:ALA:HA	1.96	0.48
3:E:188:ALA:HB3	3:E:196:MET:HE1	1.96	0.48
10:K:87:ARG:NH1	10:K:88:ARG:O	2.46	0.48
6:D:77:ILE:HG23	6:D:122:VAL:HG12	1.95	0.48
3:E:226:GLU:HA	3:E:230:MET:HE3	1.95	0.48
10:K:86:ARG:NH1	10:K:87:ARG:O	2.47	0.48
1:3:867:G:H4'	9:J:121:ARG:HD3	1.96	0.48
8:I:482:TYR:OH	9:J:45:LEU:O	2.29	0.48
10:K:123:ASP:OD1	10:K:124:ILE:N	2.47	0.48
3:E:369:ASP:OD1	3:E:373:ARG:N	2.47	0.47
6:G:57:LYS:HB2	6:G:124:PHE:HB3	1.96	0.47
1:3:896:U:O2	11:L:41:ARG:NH2	2.38	0.47
3:E:108:ARG:HH21	3:E:340:ILE:HG22	1.78	0.47
8:I:501:ASP:OD1	8:I:502:ASP:N	2.48	0.47
9:J:40:TYR:HA	9:J:43:LYS:HG2	1.97	0.47
1:3:866:G:H5"	10:K:2:ARG:HG3	1.97	0.47
1:3:842:C:H5	5:C:121:ARG:HE	1.63	0.47
3:E:122:GLU:HB2	3:E:220:ARG:HB3	1.97	0.47
7:H:64:LEU:HD12	7:H:71:CYS:HB3	1.96	0.47
2:4:118:C:H2'	2:4:119:A:H8	1.80	0.47
5:C:51:ILE:O	5:C:91:THR:HA	2.14	0.47
9:J:32:SER:O	9:J:35:GLU:HG3	2.15	0.47
1:3:891:A:H2'	1:3:892:A:H8	1.81	0.46
3:A:320:MET:HE2	3:E:41:PRO:HG2	1.96	0.46
6:G:73:GLY:HA3	6:G:125:ILE:O	2.15	0.46
8:I:509:ILE:HD12	8:I:530:VAL:HG21	1.98	0.46
2:4:591:A:H2'	2:4:592:A:C8	2.51	0.46
7:H:166:VAL:HG22	7:H:171:VAL:HG22	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:K:43:PHE:HZ	10:K:51:ARG:HH22	1.62	0.46
11:L:40:ALA:HB2	11:L:70:LYS:HG2	1.98	0.46
1:3:924:A:H2'	1:3:925:G:C8	2.51	0.46
6:D:33:PRO:HG2	6:D:102:ILE:HD12	1.97	0.45
3:E:35:ARG:NH1	3:E:325:LEU:O	2.49	0.45
7:H:36:ALA:HB3	11:L:113:GLY:HA2	1.98	0.45
11:L:47:LYS:HD3	11:L:47:LYS:HA	1.85	0.45
11:L:71:CYS:HB3	11:L:76:ILE:HB	1.97	0.45
1:3:625:C:H42	1:3:974:A:H61	1.63	0.45
2:4:145:A:H2'	2:4:146:G:H8	1.82	0.45
4:F:46:VAL:O	4:F:50:LYS:HB2	2.17	0.45
8:I:478:LEU:HB3	8:I:479:LYS:H	1.55	0.45
3:A:317:ILE:HD11	3:A:337:LYS:HD2	1.98	0.45
11:L:20:TYR:HD1	11:L:84:ARG:HD3	1.82	0.45
5:C:79:ASP:HB2	5:C:93:LYS:HB2	1.98	0.45
1:3:938:G:H3'	10:K:7:LYS:HZ2	1.82	0.45
11:L:19:ILE:HA	11:L:27:PHE:O	2.17	0.45
9:J:99:ARG:NH1	9:J:141:TYR:OH	2.39	0.44
1:3:935:U:O4	10:K:166:LYS:NZ	2.50	0.44
2:4:585:G:H2'	2:4:586:G:C8	2.53	0.44
3:A:52:ASP:OD2	3:A:52:ASP:N	2.49	0.44
4:B:7:LEU:HD23	4:B:7:LEU:HA	1.89	0.44
6:D:48:LYS:HB2	6:D:48:LYS:HE3	1.86	0.44
3:A:39:TYR:OH	3:E:8:ILE:O	2.32	0.44
9:J:33:VAL:O	9:J:37:ILE:HG12	2.18	0.44
2:4:353:G:OP1	4:F:2:HIS:NE2	2.45	0.44
1:3:895:G:H1	1:3:917:U:H3	1.66	0.44
2:4:598:C:H5"	10:K:211:LYS:HE2	2.00	0.44
2:4:123:C:O2'	2:4:124:U:O2	2.28	0.43
2:4:550:A:H2	2:4:586:G:H22	1.66	0.43
7:H:36:ALA:HA	11:L:111:ARG:HH21	1.82	0.43
3:A:79:ILE:HD12	3:A:104:VAL:HG21	1.99	0.43
3:A:237:MET:HE1	4:B:39:ASP:HB3	2.00	0.43
8:I:518:ARG:NH1	8:I:526:ASP:OD2	2.46	0.43
1:3:871:G:H2'	1:3:872:G:C8	2.54	0.43
4:B:10:ASP:OD1	4:B:10:ASP:N	2.51	0.43
7:H:140:LYS:HE3	7:H:140:LYS:HB2	1.77	0.43
8:I:322:ASN:HA	8:I:325:THR:HG22	2.00	0.43
10:K:100:ALA:HB1	10:K:126:LEU:HD13	2.01	0.43
8:I:488:GLU:OE1	9:J:76:LYS:NZ	2.52	0.42
2:4:118:C:H2'	2:4:119:A:C8	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:K:129:LYS:HA	10:K:132:THR:HG23	2.01	0.42
1:3:810:G:H2'	1:3:811:A:H8	1.85	0.42
1:3:815:G:H2'	1:3:816:G:H8	1.85	0.42
6:G:18:ASP:OD1	6:G:37:LYS:NZ	2.53	0.42
5:C:67:ILE:HG21	5:C:92:ILE:HD13	2.02	0.42
4:F:10:ASP:OD1	4:F:10:ASP:N	2.53	0.42
7:H:204:MET:HE2	8:I:218:LEU:HD12	2.02	0.42
2:4:142:A:N6	2:4:339:G:H1'	2.34	0.42
1:3:870:C:H2'	1:3:871:G:H8	1.85	0.42
1:3:921:U:H2'	1:3:922:G:H8	1.84	0.42
1:3:886:U:H2'	1:3:887:A:C8	2.54	0.42
6:D:48:LYS:HG2	6:D:52:LYS:HE3	2.01	0.42
2:4:145:A:H2'	2:4:146:G:C8	2.54	0.42
9:J:136:PRO:HG2	9:J:139:TRP:HB2	2.02	0.42
1:3:898:A:N1	1:3:911:U:O2'	2.48	0.41
2:4:596:U:H2'	2:4:597:A:C8	2.55	0.41
2:4:555:G:O6	2:4:581:A:N6	2.53	0.41
6:G:139:GLU:HA	6:G:142:TYR:CE1	2.55	0.41
9:J:96:VAL:HG12	9:J:100:LYS:HE2	2.02	0.41
1:3:802:G:H2'	1:3:803:A:H8	1.86	0.41
3:E:370:LYS:HE2	3:E:371:TYR:CZ	2.54	0.41
3:E:66:LYS:HG3	3:E:75:VAL:HG21	2.01	0.41
4:F:6:THR:HG23	4:F:27:THR:HG22	2.02	0.41
2:4:549:C:H2'	2:4:550:A:C8	2.56	0.41
10:K:161:ILE:O	10:K:165:GLN:HG2	2.21	0.41
1:3:891:A:H2'	1:3:892:A:C8	2.56	0.40
5:C:117:LEU:HD12	5:C:121:ARG:HD3	2.03	0.40
6:G:138:LYS:HA	6:G:141:GLU:HG3	2.02	0.40
9:J:125:LEU:HD23	9:J:125:LEU:HA	1.91	0.40
2:4:597:A:H5"	10:K:210:LYS:HG2	2.03	0.40
7:H:116:ILE:HD12	7:H:116:ILE:HA	1.99	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	A	342/483 (71%)	337 (98%)	5 (2%)	0	100	100
3	E	364/483 (75%)	355 (98%)	9 (2%)	0	100	100
4	B	56/58 (97%)	56 (100%)	0	0	100	100
4	F	56/58 (97%)	56 (100%)	0	0	100	100
5	C	92/205 (45%)	91 (99%)	1 (1%)	0	100	100
6	D	137/156 (88%)	137 (100%)	0	0	100	100
6	G	139/156 (89%)	138 (99%)	1 (1%)	0	100	100
7	H	224/316 (71%)	222 (99%)	2 (1%)	0	100	100
8	I	243/591 (41%)	242 (100%)	1 (0%)	0	100	100
9	J	112/151 (74%)	111 (99%)	1 (1%)	0	100	100
10	K	183/254 (72%)	183 (100%)	0	0	100	100
11	L	114/137 (83%)	111 (97%)	3 (3%)	0	100	100
All	All	2062/3048 (68%)	2039 (99%)	23 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	A	295/427 (69%)	295 (100%)	0	100	100
3	E	316/427 (74%)	316 (100%)	0	100	100
4	B	51/51 (100%)	51 (100%)	0	100	100
4	F	51/51 (100%)	51 (100%)	0	100	100
5	C	81/147 (55%)	81 (100%)	0	100	100
6	D	112/134 (84%)	112 (100%)	0	100	100
6	G	115/134 (86%)	115 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	H	204/289 (71%)	204 (100%)	0	100	100
8	I	128/524 (24%)	128 (100%)	0	100	100
9	J	100/128 (78%)	100 (100%)	0	100	100
10	K	168/230 (73%)	168 (100%)	0	100	100
11	L	85/105 (81%)	85 (100%)	0	100	100
All	All	1706/2647 (64%)	1706 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (22) such sidechains are listed below:

Mol	Chain	Res	Type
3	A	116	GLN
3	A	182	ASN
3	A	234	HIS
3	A	257	GLN
3	A	357	GLN
6	D	40	ASN
6	D	130	ASN
3	E	73	HIS
3	E	117	GLN
3	E	227	ASN
3	E	234	HIS
3	E	245	ASN
3	E	277	ASN
3	E	357	GLN
7	H	68	ASN
7	H	130	ASN
7	H	143	GLN
8	I	269	ASN
8	I	506	ASN
10	K	54	GLN
10	K	108	ASN
10	K	165	GLN

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	3	166/1800 (9%)	24 (14%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	4	193/609 (31%)	35 (18%)	2 (1%)
All	All	359/2409 (14%)	59 (16%)	2 (0%)

All (59) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	3	816	G
1	3	828	U
1	3	830	U
1	3	837	G
1	3	838	G
1	3	841	U
1	3	843	U
1	3	876	G
1	3	894	U
1	3	898	A
1	3	899	G
1	3	914	G
1	3	926	A
1	3	927	C
1	3	936	G
1	3	942	G
1	3	959	U
1	3	961	U
1	3	962	C
1	3	964	U
1	3	965	U
1	3	966	A
1	3	969	C
1	3	970	A
2	4	12	C
2	4	124	U
2	4	141	A
2	4	143	G
2	4	144	G
2	4	330	G
2	4	331	G
2	4	336	G
2	4	337	U
2	4	338	U
2	4	346	U
2	4	348	U

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Mol	Chain	Res	Type
2	4	357	G
2	4	368	G
2	4	369	G
2	4	391	A
2	4	393	A
2	4	540	A
2	4	558	A
2	4	559	U
2	4	560	G
2	4	565	U
2	4	566	A
2	4	568	U
2	4	569	U
2	4	577	G
2	4	581	A
2	4	582	U
2	4	583	U
2	4	584	U
2	4	604	A
2	4	605	C
2	4	606	A
2	4	608	C
2	4	609	U

All (2) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	4	329	G
2	4	330	G

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

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

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

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.

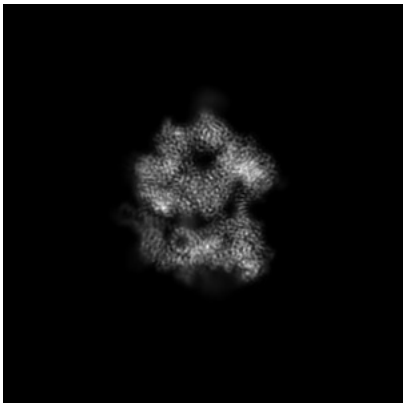
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-50964. These allow visual inspection of the internal detail of the map and identification of artifacts.

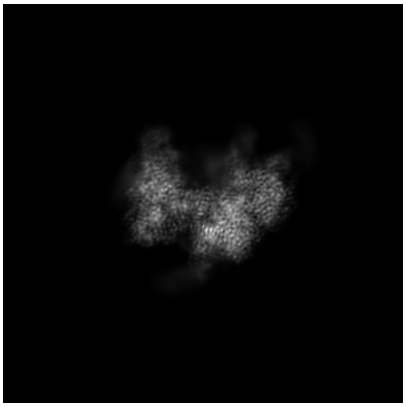
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

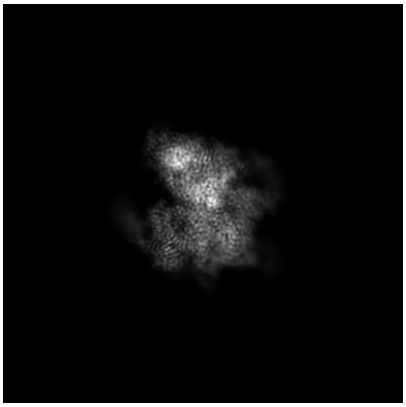
6.1.1 Primary map



X



Y



Z

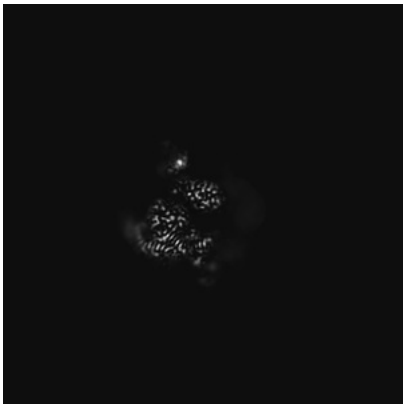
The images above show the map projected in three orthogonal directions.

6.2 Central slices

6.2.1 Primary map

X Index: 160

Y Index: 160



Z Index: 160

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: 165

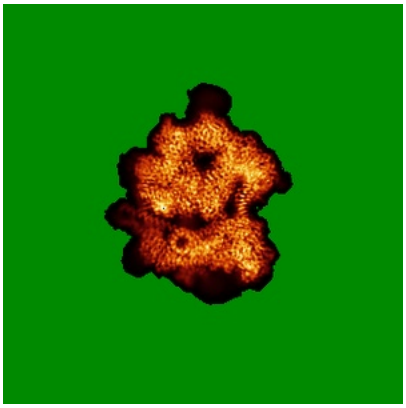
Y Index: 195

Z Index: 185

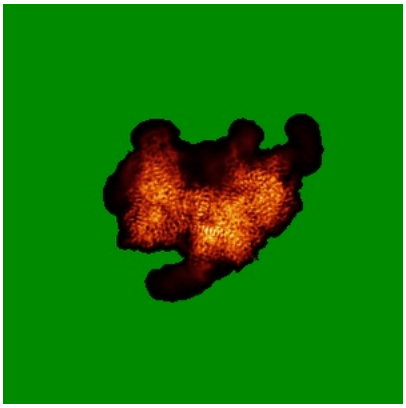
The images above show the largest variance slices of the map in three orthogonal directions.

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

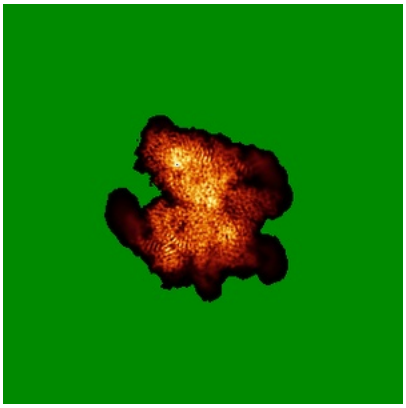
6.4.1 Primary map



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 0.6. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

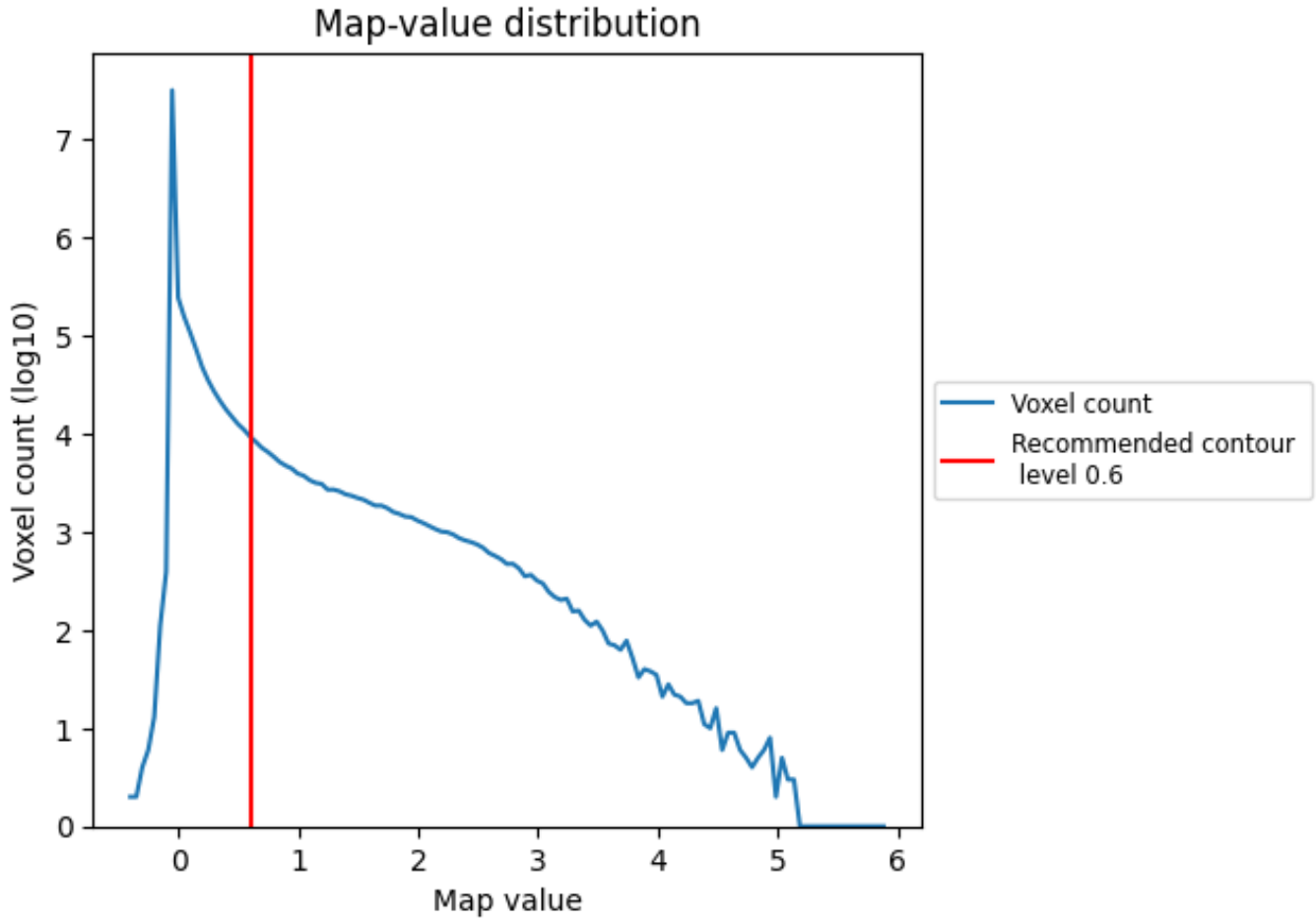
6.6 Mask visualisation (i)

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

7 Map analysis

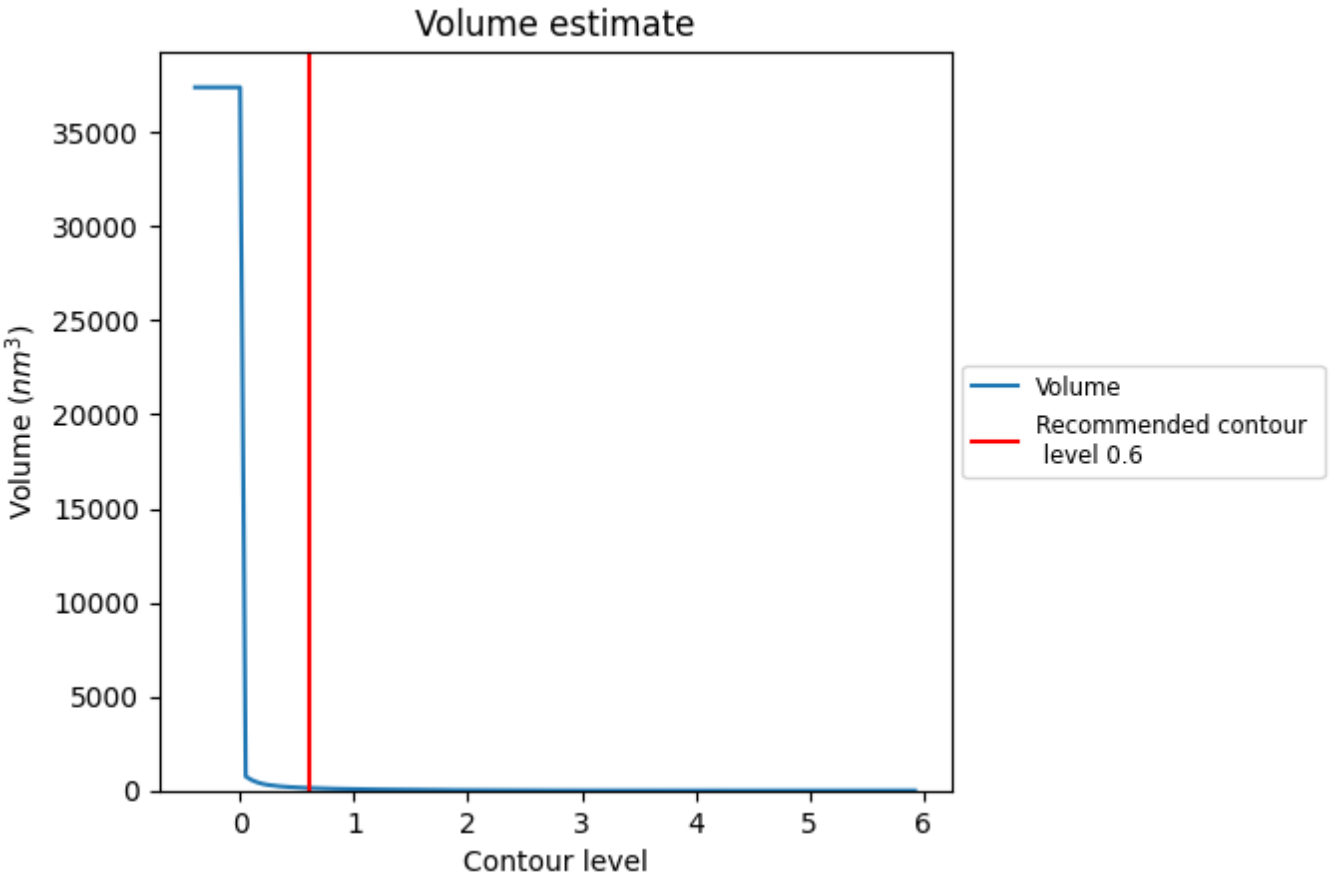
This section contains the results of statistical analysis of the map.

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.

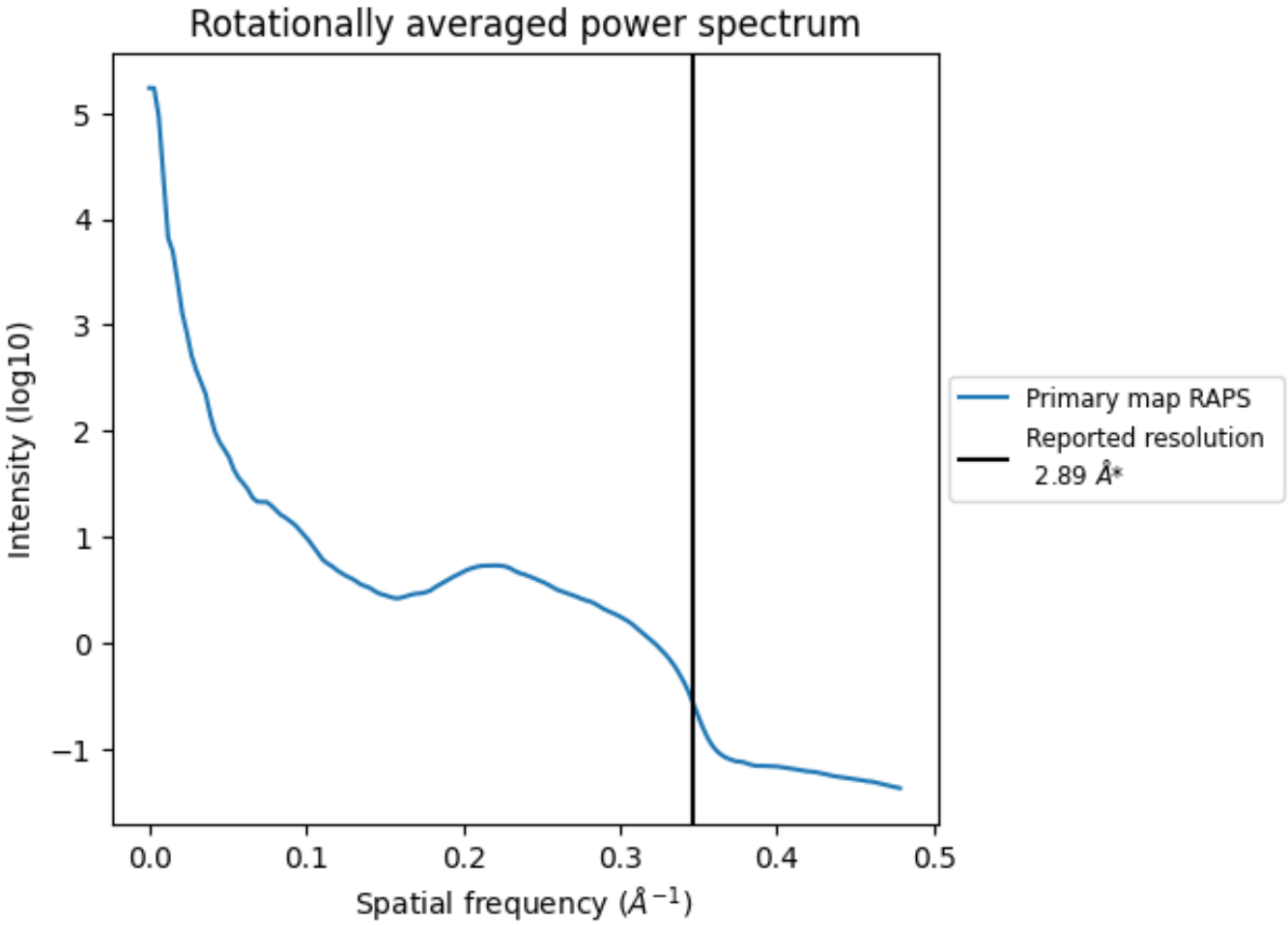
7.2 Volume estimate



The volume at the recommended contour level is 135 nm^3; this corresponds to an approximate mass of 122 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 0.346 Å^{-1}

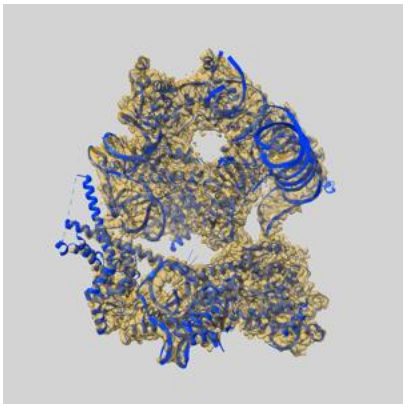
8 Fourier-Shell correlation (i)

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

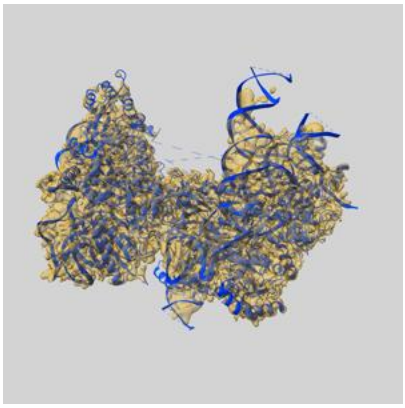
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-50964 and PDB model 9G25. Per-residue inclusion information can be found in section 3 on page 6.

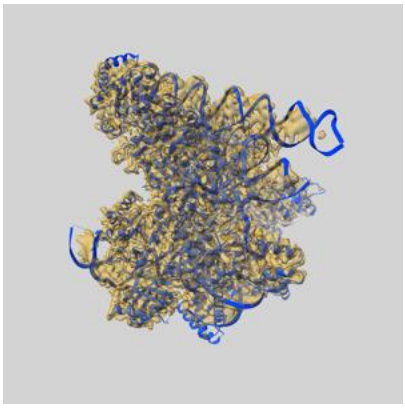
9.1 Map-model overlay



X



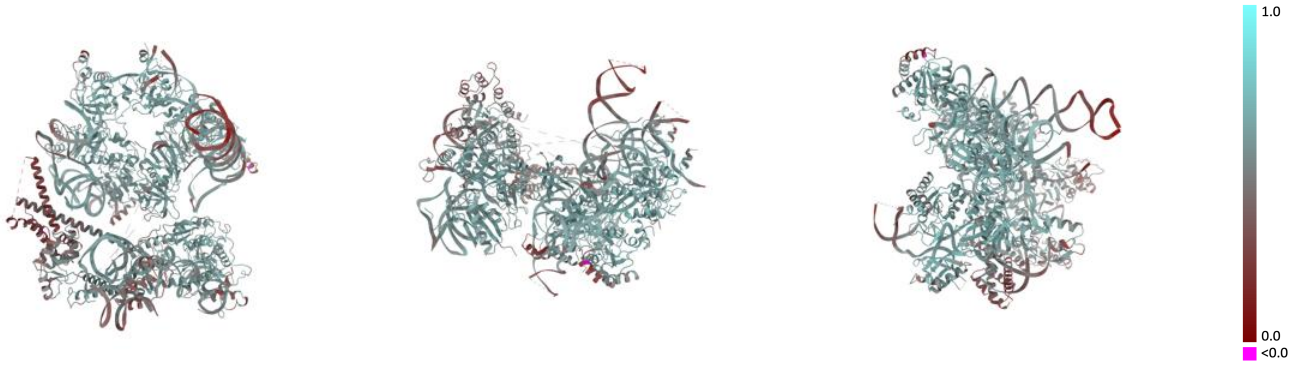
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.6 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.

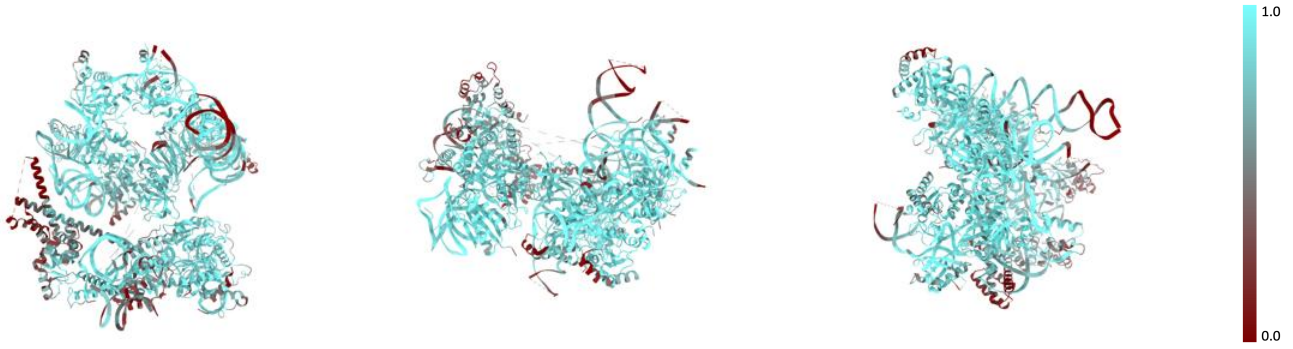
9.2 Q-score mapped to coordinate model (i)



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.

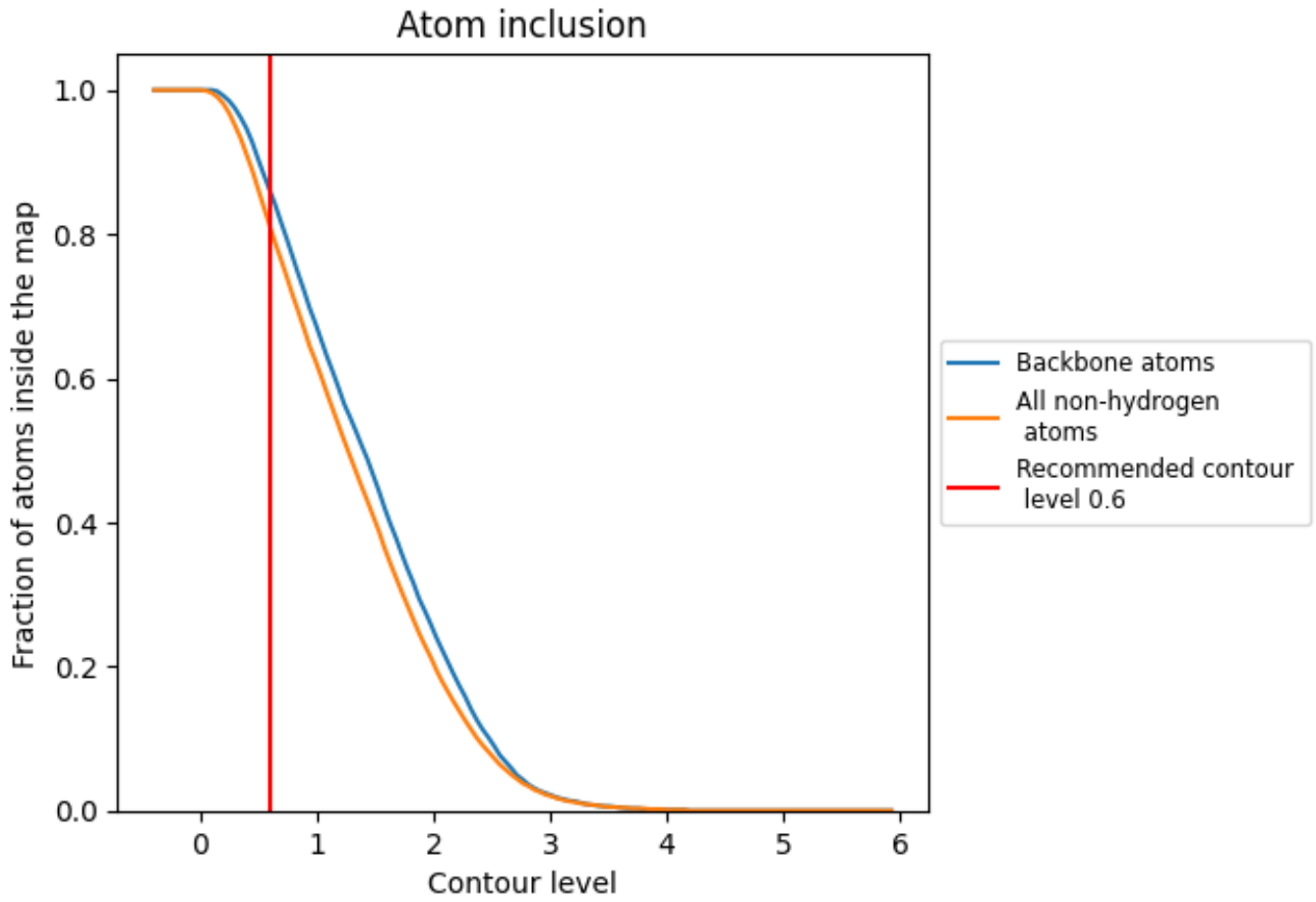
9.3 Atom inclusion mapped to coordinate model (i)



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 (0.6).

9.4 Atom inclusion (i)



At the recommended contour level, 86% of all backbone atoms, 81% 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 (0.6) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8080	0.5540
3	0.7660	0.5120
4	0.8480	0.5490
A	0.9330	0.6310
B	0.9100	0.6240
C	0.8840	0.5850
D	0.8060	0.5600
E	0.8820	0.6050
F	0.9050	0.6310
G	0.8350	0.5820
H	0.8610	0.5850
I	0.4830	0.4150
J	0.7560	0.5180
K	0.6130	0.4810
L	0.9000	0.5920