



Full wwPDB EM Validation Report ⓘ

Mar 20, 2026 – 04:36 AM UTC

PDB ID : 7R72 / pdb_00007r72
EMDB ID : EMD-24290
Title : State E1 nucleolar 60S ribosome biogenesis intermediate - Spb4 local model
Authors : Cruz, V.E.; Sekulski, K.; Peddada, N.; Erzberger, J.P.
Deposited on : 2021-06-24
Resolution : 3.07 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

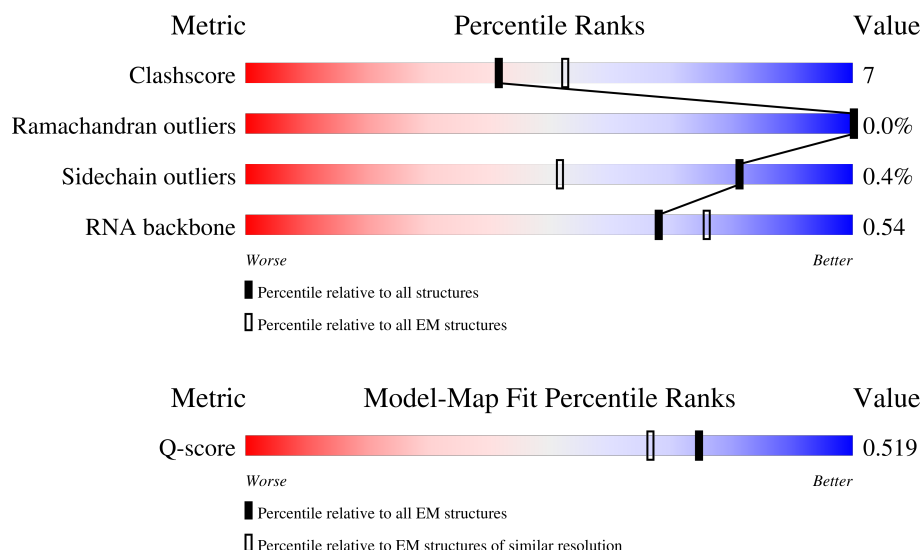
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 3.07 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.



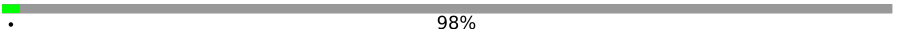
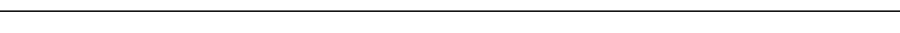
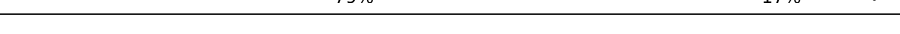
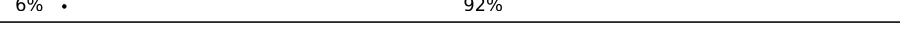
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	13977 (2.57 - 3.57)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	1	641	
2	2	72	
3	8	710	

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Mol	Chain	Length	Quality of chain
4	B	387	 98%
5	G	256	 7% 93%
6	I	663	 43% 8% 50%
7	P	184	 23% 72%
8	R	189	 6% 59% 12% 29%
9	U	121	 73% 11% 16%
10	X	142	 65% 31%
11	Z	136	 87% 12%
12	b	647	 6% 92%
13	c	105	 67% 26% 8%
14	d	113	 5% 40% 24% 36%
15	g	121	 79% 14% 7%
16	j	88	 31% 69%
17	k	78	 88% 10%
18	m	429	 79% 17%
19	n	104	 90% 9%
20	p	460	 8% 55% 18% 27%
21	t	322	 6% 92%
22	u	199	 21% 7% 72%
23	w	841	 5% 18% 5% 78%
24	x	606	 22% 71% 18% 11%

2 Entry composition

There are 25 unique types of molecules in this entry. The entry contains 39443 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 25S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	641	Total	C	N	O	P	0	0
			13716	6122	2470	4483	641		

- Molecule 2 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	59	Total	C	N	O	P	0	0
			1255	560	222	414	59		

- Molecule 3 is a protein called Nucleolar complex protein 2.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	8	58	Total	C	N	O	0	0
			480	290	103	87		

- Molecule 4 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	B	9	Total	C	N	O	S	0	0
			72	48	11	12	1		

- Molecule 5 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	G	19	Total	C	N	O	0	0
			175	115	34	26		

- Molecule 6 is a protein called Nucleolar complex-associated protein 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	I	334	Total	C	N	O	S	0	0
			2675	1691	467	507	10		

- Molecule 7 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	P	51	Total	C	N	O	0	0
			433	269	92	72		

- Molecule 8 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	R	134	Total	C	N	O	0	0
			1082	679	220	183		

- Molecule 9 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	U	102	Total	C	N	O	0	0
			808	524	132	152		

- Molecule 10 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	X	98	Total	C	N	O	S	0	0
			786	502	138	144	2		

- Molecule 11 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	Z	135	Total	C	N	O	0	0
			1092	710	202	180		

- Molecule 12 is a protein called Nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	b	53	Total	C	N	O	S	0	0
			431	267	86	74	4		

- Molecule 13 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	c	97	Total	C	N	O	S	0	0
			743	479	124	139	1		

- Molecule 14 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	d	72	Total	C	N	O	S	0	0
			593	384	115	93	1		

- Molecule 15 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	g	112	Total	C	N	O	S	0	0
			881	546	179	152	4		

- Molecule 16 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	j	27	Total	C	N	O	S	0	0
			212	127	45	36	4		

- Molecule 17 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	k	77	Total	C	N	O	S	0	0
			612	391	115	106			

- Molecule 18 is a protein called Ribosome biogenesis protein ERB1.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	m	412	Total	C	N	O	S	0	0
			3302	2123	583	586	10		

- Molecule 19 is a protein called Pescadillo homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	n	103	Total	C	N	O	S	0	0
			861	544	164	148	5		

- Molecule 20 is a protein called Ribosome biogenesis protein YTM1.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	p	337	Total	C	N	O	S	0	0
			2629	1634	470	518	7		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
p	454	ALA	GLY	conflict	UNP A6ZPA9

- Molecule 21 is a protein called Ribosome biogenesis protein RLP7.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	t	26	Total	C	N	O	0	0
			221	132	49	40		

- Molecule 22 is a protein called Ribosome biogenesis protein RLP24.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	u	56	Total	C	N	O	S	0	0
			481	303	98	79	1		

- Molecule 23 is a protein called 27S pre-rRNA (guanosine(2922)-2'-O)-methyltransferase.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	w	189	Total	C	N	O	S	0	0
			1562	957	287	309	9		

- Molecule 24 is a protein called ATP-dependent rRNA helicase SPB4.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	x	539	Total	C	N	O	S	0	0
			4340	2781	744	795	20		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
x	405	ALA	THR	conflict	UNP A7A237

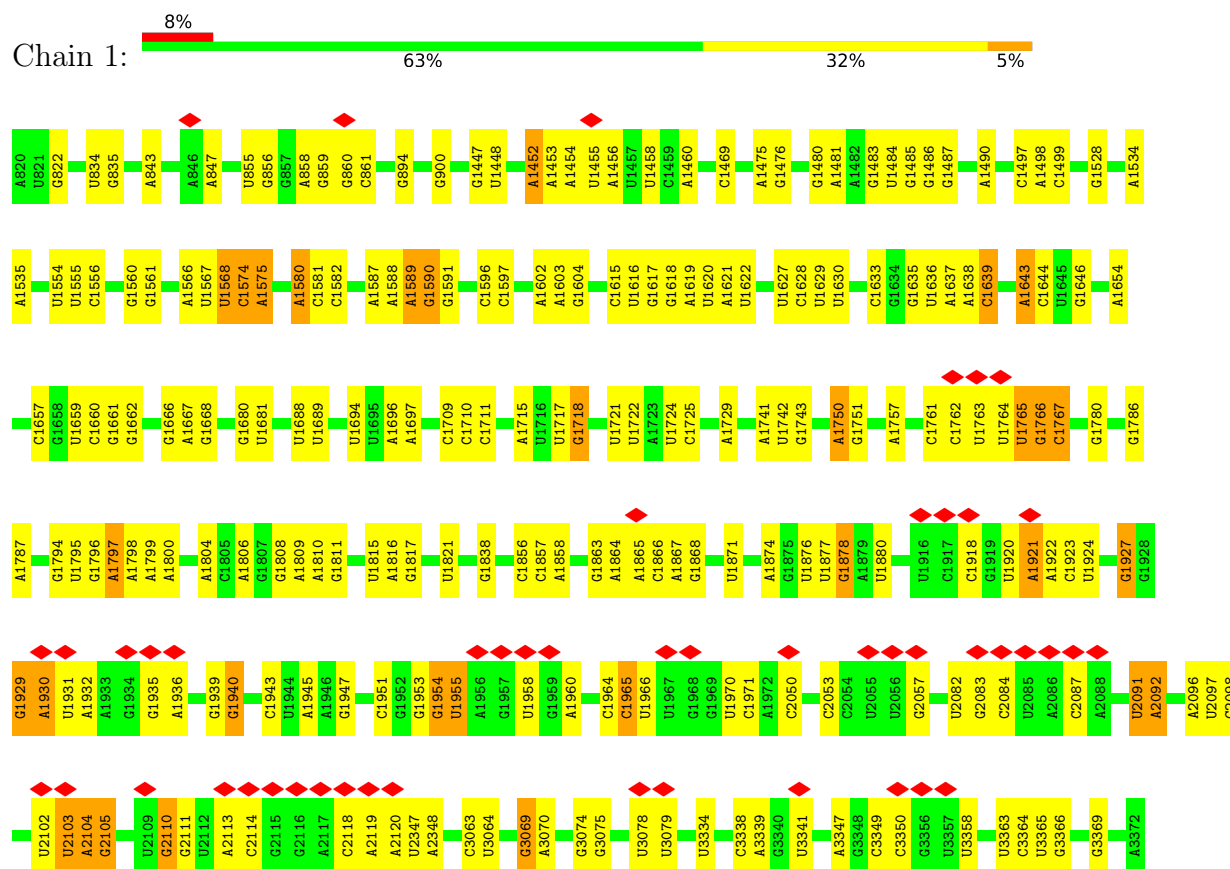
- Molecule 25 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
25	g	1	Total	Zn	0
			1	1	

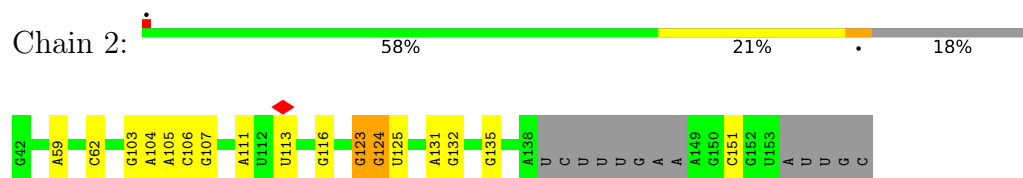
3 Residue-property plots

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

• Molecule 1: 25S rRNA



• Molecule 2: 5.8S rRNA

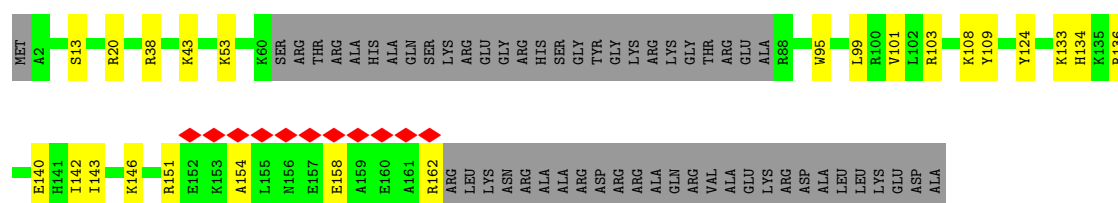


• Molecule 3: Nucleolar complex protein 2





- Molecule 8: 60S ribosomal protein L19-A



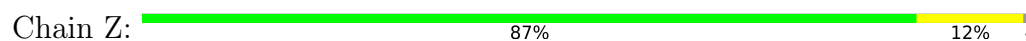
- Molecule 9: 60S ribosomal protein L22-A



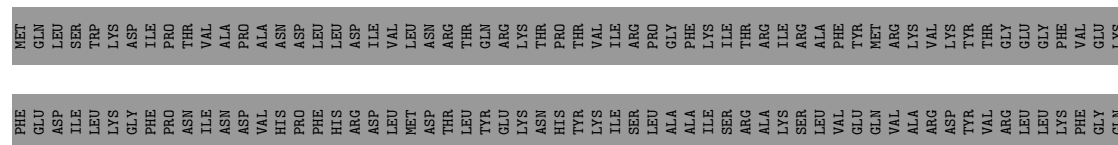
- Molecule 10: 60S ribosomal protein L25

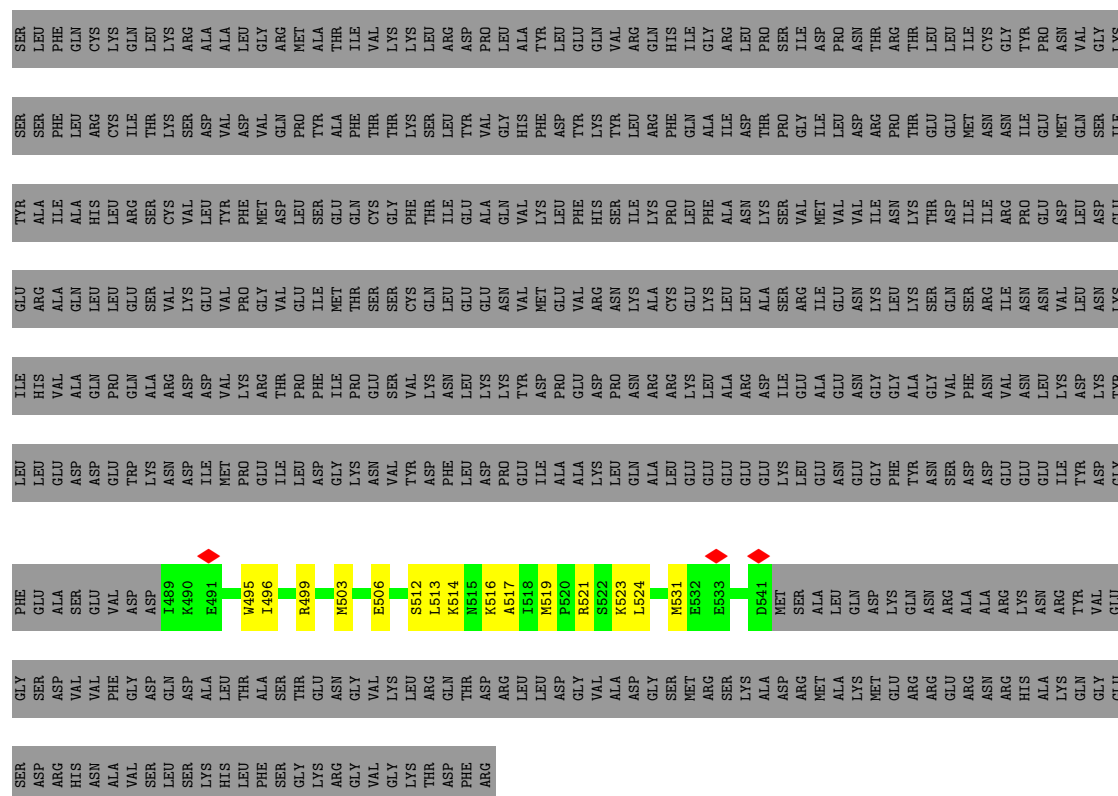


- Molecule 11: 60S ribosomal protein L27-A



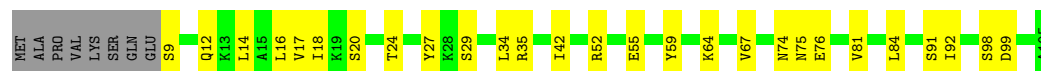
- Molecule 12: Nucleolar GTP-binding protein 1





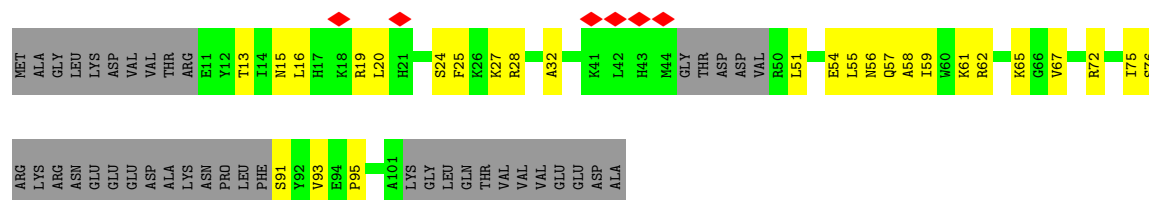
• Molecule 13: 60S ribosomal protein L30

Chain c: 67% 26% 8%



• Molecule 14: 60S ribosomal protein L31-A

Chain d: 5% 40% 24% 36%



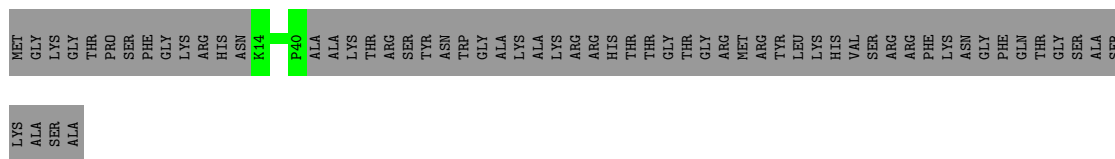
• Molecule 15: 60S ribosomal protein L34-A

Chain g: 79% 14% 7%



• Molecule 16: 60S ribosomal protein L37-A

Chain j:  31% 69%



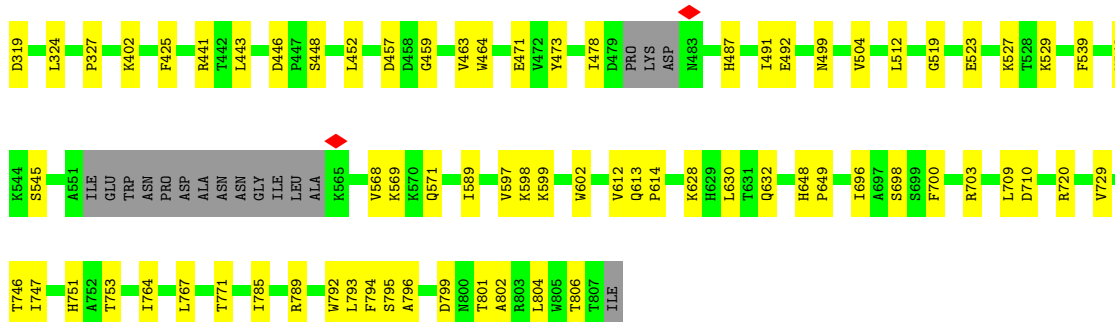
- Molecule 17: 60S ribosomal protein L38

Chain k:  88% 10%



- Molecule 18: Ribosome biogenesis protein ERB1

Chain m:  79% 17%



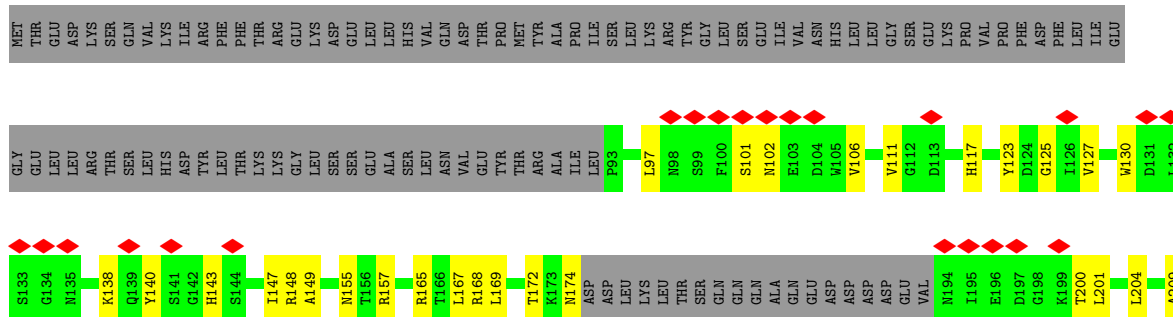
- Molecule 19: Pescadillo homolog

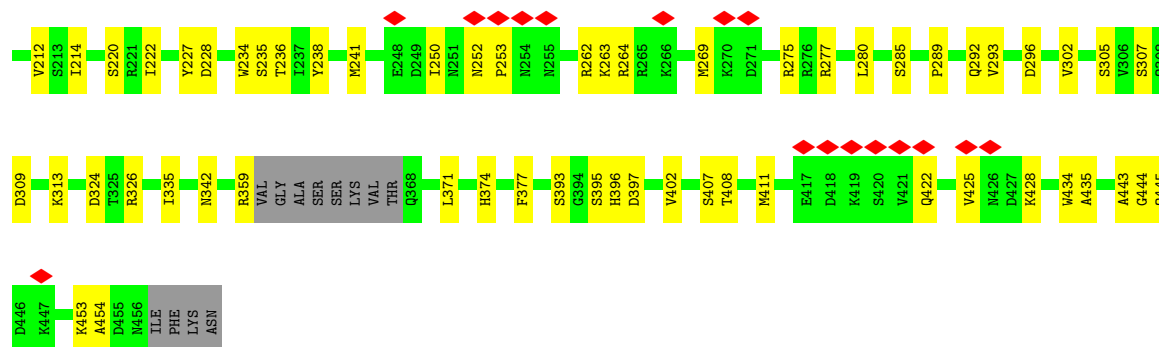
Chain n:  90% 9%



- Molecule 20: Ribosome biogenesis protein YTM1

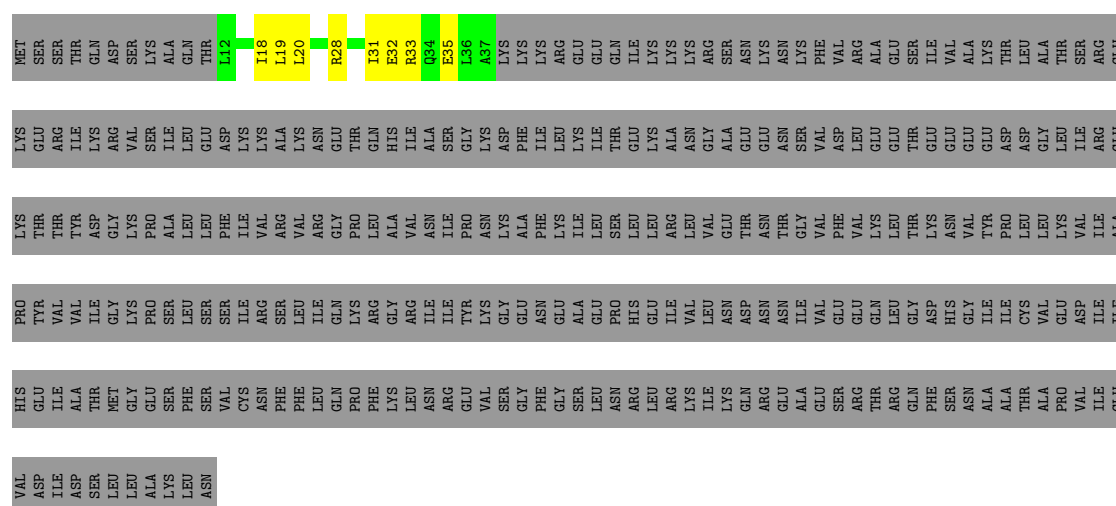
Chain p:  8% 55% 18% 27%





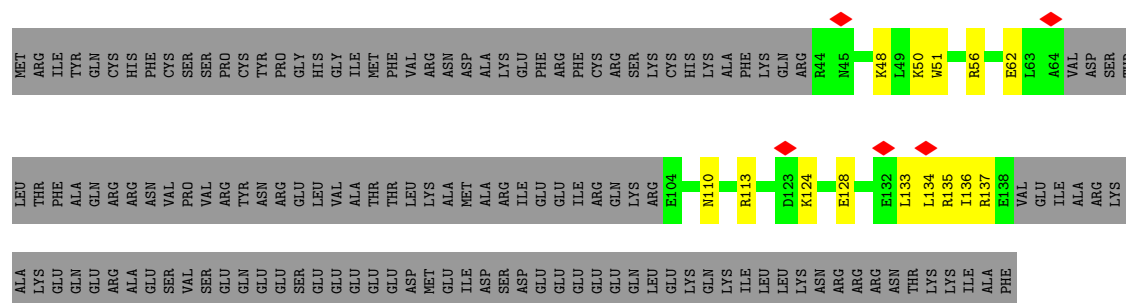
• Molecule 21: Ribosome biogenesis protein RLP7

Chain t: 6% 92%



• Molecule 22: Ribosome biogenesis protein RLP24

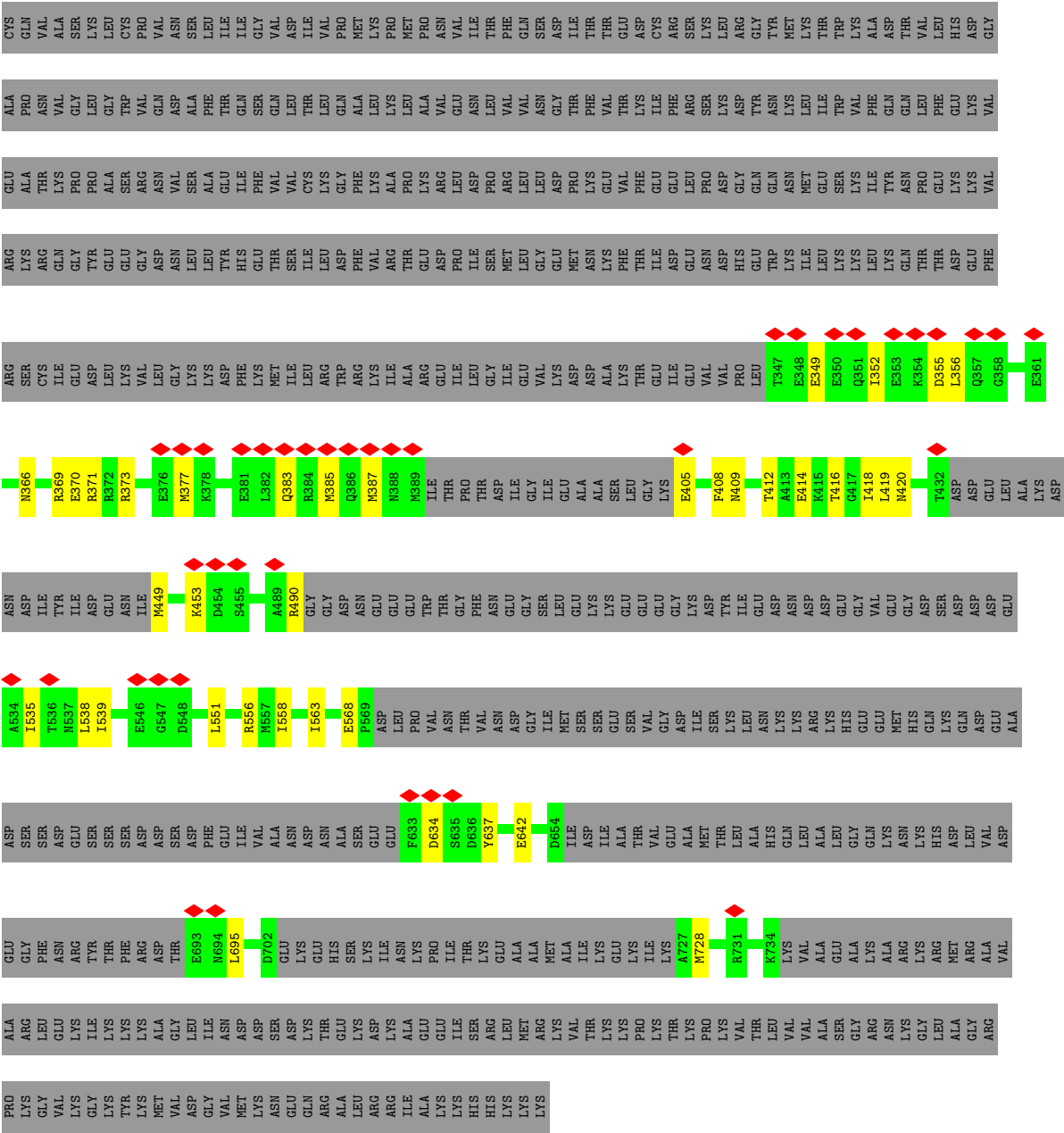
Chain u: 21% 72%



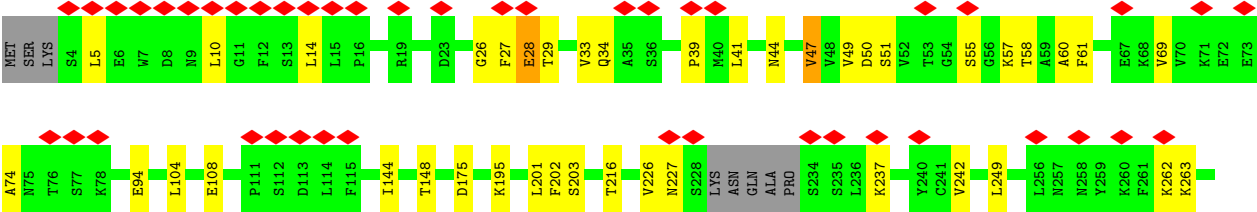
• Molecule 23: 27S pre-rRNA (guanosine(2922)-2'-O)-methyltransferase

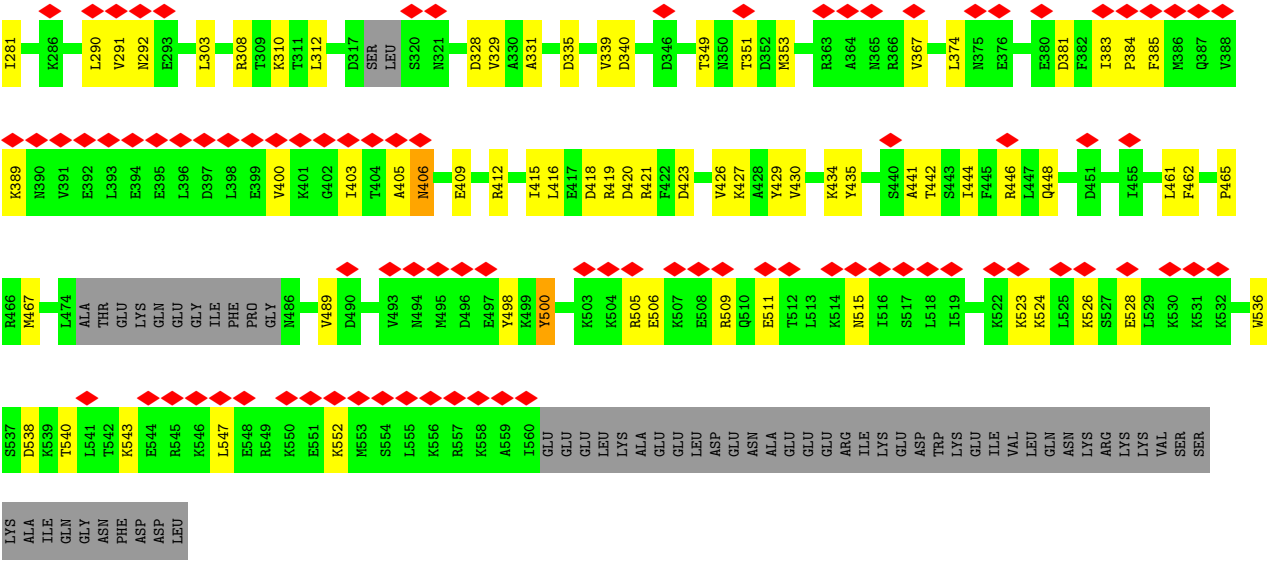
Chain w: 5% 18% 5% 78%





• Molecule 24: ATP-dependent rRNA helicase SPB4





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	211000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.2	Depositor
Minimum defocus (nm)	900	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	81000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.109	Depositor
Minimum map value	-0.056	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.012	Depositor
Map size ($\text{\AA}$)	453.6, 453.6, 453.6	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.08, 1.08, 1.08	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	1	0.14	0/15338	0.26	0/23887
2	2	0.14	0/1398	0.26	0/2169
3	8	0.10	0/482	0.22	0/630
4	B	0.14	0/72	0.27	0/93
5	G	0.14	0/179	0.29	0/239
6	I	0.13	0/2708	0.31	0/3643
7	P	0.18	0/439	0.55	1/579 (0.2%)
8	R	0.14	0/1095	0.25	0/1465
9	U	0.14	0/825	0.32	0/1120
10	X	0.15	0/794	0.29	0/1066
11	Z	0.14	0/1118	0.29	0/1497
12	b	0.11	0/436	0.30	0/575
13	c	0.12	0/751	0.25	0/1008
14	d	0.13	0/603	0.32	0/804
15	g	0.15	0/891	0.27	0/1191
16	j	0.12	0/216	0.25	0/286
17	k	0.15	0/618	0.30	0/826
18	m	0.16	0/3387	0.37	0/4594
19	n	0.15	0/872	0.31	0/1151
20	p	0.15	0/2675	0.37	0/3625
21	t	0.13	0/221	0.26	0/294
22	u	0.10	0/487	0.34	0/641
23	w	0.12	0/1573	0.29	0/2081
24	x	0.15	0/4419	0.31	0/5958
All	All	0.14	0/41597	0.30	1/59422 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	P	135	ARG	N-CA-C	5.14	117.92	110.42

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	1	13716	0	6905	147	0
2	2	1255	0	640	5	0
3	8	480	0	518	8	0
4	B	72	0	79	0	0
5	G	175	0	188	1	0
6	I	2675	0	2797	39	0
7	P	433	0	434	7	0
8	R	1082	0	1160	22	0
9	U	808	0	822	12	0
10	X	786	0	841	6	0
11	Z	1092	0	1155	14	0
12	b	431	0	460	17	0
13	c	743	0	797	19	0
14	d	593	0	640	20	0
15	g	881	0	945	15	0
16	j	212	0	210	0	0
17	k	612	0	682	5	0
18	m	3302	0	3354	46	0
19	n	861	0	920	5	0
20	p	2629	0	2614	54	0
21	t	221	0	233	9	0
22	u	481	0	511	13	0
23	w	1562	0	1554	42	0
24	x	4340	0	4468	83	0
25	g	1	0	0	0	0
All	All	39443	0	32927	484	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 7.

All (484) 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)
1:1:3350:C:H42	24:x:552:LYS:CE	1.70	1.04
1:1:3350:C:N4	24:x:552:LYS:HE3	1.74	1.02
18:m:519:GLY:HA3	20:p:165:ARG:HH22	1.27	0.99
1:1:3350:C:N4	24:x:552:LYS:CE	2.27	0.98
8:R:151:ARG:HH21	24:x:442:THR:HB	1.28	0.94
1:1:1924:U:OP1	8:R:136:ARG:NH2	2.01	0.92
18:m:443:LEU:HD23	18:m:796:ALA:HB2	1.61	0.82
7:P:128:ARG:NH1	7:P:130:TYR:CE1	2.53	0.77
8:R:158:GLU:CD	24:x:441:ALA:HA	2.10	0.76
1:1:3350:C:H42	24:x:552:LYS:HE2	1.51	0.75
24:x:263:LYS:HB2	24:x:339:VAL:HA	1.66	0.75
20:p:204:LEU:HD13	20:p:277:ARG:HB2	1.70	0.74
23:w:414:GLU:HG2	23:w:419:LEU:HD11	1.71	0.72
1:1:2082:U:H2'	1:1:2083:G:H8	1.54	0.72
1:1:1958:U:H3	1:1:2083:G:H1	1.35	0.72
24:x:57:LYS:HD3	24:x:202:PHE:HB3	1.71	0.72
1:1:1661:G:H2'	1:1:1662:G:C8	2.26	0.70
1:1:1654:A:OP2	6:I:371:LYS:NZ	2.24	0.70
23:w:352:ILE:HD11	24:x:446:ARG:CZ	2.21	0.70
13:c:17:VAL:HG11	13:c:92:ILE:HD12	1.73	0.70
15:g:54:ILE:HD11	15:g:78:GLY:HA2	1.74	0.69
24:x:418:ASP:HB3	24:x:421:ARG:HG3	1.75	0.69
1:1:1574:C:H2'	1:1:1575:A:H8	1.57	0.69
1:1:1715:A:P	24:x:195:LYS:HZ1	2.14	0.69
23:w:352:ILE:HD11	24:x:446:ARG:NH2	2.09	0.68
20:p:307:SER:OG	20:p:309:ASP:OD1	2.11	0.68
2:2:103:G:OP2	2:2:105:A:O2'	2.12	0.68
6:I:332:SER:OG	6:I:524:LEU:O	2.09	0.67
20:p:168:ARG:NH2	20:p:200:THR:OG1	2.26	0.67
20:p:395:SER:OG	20:p:397:ASP:OD1	2.12	0.67
6:I:335:ASN:HD22	6:I:527:PRO:HG3	1.60	0.66
13:c:9:SER:HB3	13:c:12:GLN:HG3	1.76	0.66
24:x:430:VAL:HG22	24:x:467:MET:HE2	1.75	0.66
1:1:3350:C:N4	24:x:552:LYS:CD	2.58	0.66
1:1:1924:U:H1'	1:1:2110:G:N2	2.11	0.66
13:c:64:LYS:HG2	23:w:535:ILE:HD13	1.78	0.65
1:1:1574:C:H2'	1:1:1575:A:C8	2.31	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:Z:10:VAL:O	11:Z:83:THR:OG1	2.15	0.65
20:p:204:LEU:HD12	20:p:234:TRP:CE3	2.30	0.65
18:m:599:LYS:HB2	18:m:612:VAL:HB	1.78	0.65
23:w:366:ASN:OD1	23:w:369:ARG:NH1	2.30	0.64
13:c:14:LEU:O	13:c:18:ILE:HG12	1.97	0.64
24:x:506:GLU:OE2	24:x:509:ARG:NH2	2.30	0.64
1:1:1639:C:OP2	15:g:74:ARG:NH1	2.29	0.64
13:c:20:SER:HB2	24:x:44:ASN:HB3	1.78	0.63
1:1:1554:U:H4'	1:1:1555:U:H5'	1.80	0.63
20:p:324:ASP:OD2	20:p:326:ARG:NH1	2.32	0.62
20:p:396:HIS:HD2	20:p:428:LYS:HD3	1.62	0.62
21:t:28:ARG:O	21:t:32:GLU:HG3	1.98	0.62
1:1:1475:A:H4'	14:d:57:GLN:HG3	1.81	0.62
1:1:3074:G:H2'	1:1:3075:G:H8	1.64	0.62
20:p:143:HIS:CD2	20:p:168:ARG:HD3	2.34	0.62
1:1:3350:C:N4	24:x:552:LYS:HD2	2.15	0.62
8:R:151:ARG:NH2	24:x:442:THR:HB	2.09	0.62
23:w:409:ASN:HB3	23:w:412:THR:HG22	1.82	0.62
1:1:3350:C:H41	24:x:552:LYS:HE3	1.60	0.61
1:1:3350:C:H42	24:x:552:LYS:HE3	1.43	0.61
18:m:543:LYS:HD2	18:m:630:LEU:HD13	1.83	0.61
1:1:1757:A:OP1	9:U:94:ARG:NH2	2.32	0.61
18:m:698:SER:HB3	18:m:729:VAL:HG13	1.81	0.61
19:n:33:ARG:NH1	19:n:63:TYR:OH	2.33	0.61
23:w:373:ARG:O	23:w:377:MET:HG3	2.01	0.61
18:m:463:VAL:HB	18:m:473:TYR:HB3	1.83	0.61
21:t:31:ILE:O	21:t:35:GLU:HG2	2.00	0.61
1:1:894:G:OP2	1:1:894:G:N2	2.16	0.60
15:g:83:ASN:O	15:g:87:GLU:HG3	2.01	0.60
23:w:551:LEU:O	23:w:556:ARG:NH1	2.34	0.60
1:1:1635:G:N2	1:1:1638:A:OP2	2.29	0.60
20:p:285:SER:OG	20:p:313:LYS:NZ	2.33	0.60
1:1:1580:A:N6	10:X:31:THR:OG1	2.35	0.60
18:m:446:ASP:OD2	18:m:448:SER:OG	2.17	0.60
3:8:22:GLN:O	3:8:26:GLU:HG2	2.02	0.60
9:U:49:ASN:O	9:U:49:ASN:ND2	2.28	0.60
11:Z:23:VAL:HG12	11:Z:45:GLY:HA3	1.84	0.59
18:m:751:HIS:NE2	18:m:753:THR:OG1	2.34	0.59
6:I:391:GLU:OE2	23:w:490:ARG:NH2	2.34	0.59
20:p:235:SER:HB2	20:p:280:LEU:HD11	1.84	0.59
23:w:352:ILE:HG13	24:x:446:ARG:NH1	2.18	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:151:C:O2	10:X:22:LYS:NZ	2.32	0.58
1:1:1786:G:H2'	1:1:1787:A:C8	2.37	0.58
15:g:98:GLN:HE22	23:w:412:THR:HG21	1.68	0.58
18:m:598:LYS:HD3	18:m:614:PRO:HG2	1.85	0.58
24:x:420:ASP:OD2	24:x:505:ARG:NH2	2.37	0.58
1:1:1947:G:OP2	1:1:1947:G:N2	2.26	0.57
3:8:55:GLN:HE22	6:I:350:THR:HG22	1.69	0.57
1:1:1596:C:H2'	1:1:1597:C:C6	2.38	0.57
7:P:128:ARG:NH1	7:P:130:TYR:CD1	2.72	0.57
22:u:110:ASN:O	22:u:113:ARG:NH1	2.37	0.57
3:8:12:GLN:HG2	3:8:16:LEU:HD22	1.86	0.57
11:Z:83:THR:HG22	15:g:93:PHE:CZ	2.39	0.57
1:1:1696:A:H2'	1:1:1697:A:C8	2.39	0.57
5:G:48:ARG:O	5:G:51:LYS:HG2	2.05	0.57
20:p:342:ASN:HD21	20:p:359:ARG:HD2	1.69	0.56
1:1:1591:G:OP1	15:g:37:LYS:NZ	2.38	0.56
20:p:127:VAL:HB	20:p:140:TYR:HB2	1.85	0.56
9:U:37:LEU:O	9:U:41:ILE:HG12	2.05	0.56
6:I:338:LEU:HD12	6:I:435:LYS:HD3	1.87	0.56
1:1:1497:C:O2'	1:1:1602:A:N3	2.33	0.56
1:1:1927:G:OP1	8:R:101:VAL:HG23	2.05	0.56
12:b:519:MET:HE2	12:b:524:LEU:HB3	1.88	0.56
18:m:806:THR:HG21	20:p:377:PHE:HZ	1.70	0.56
1:1:2103:U:O2	24:x:526:LYS:HD3	2.06	0.56
6:I:278:ARG:NH2	23:w:642:GLU:OE2	2.38	0.56
1:1:1729:A:O4'	13:c:52:ARG:NH1	2.38	0.55
23:w:414:GLU:OE2	23:w:538:LEU:N	2.30	0.55
1:1:1964:C:H3'	1:1:1965:C:H5''	1.88	0.55
8:R:13:SER:OG	8:R:38:ARG:NH2	2.39	0.55
20:p:167:LEU:HB2	20:p:204:LEU:HB2	1.88	0.55
20:p:292:GLN:HB3	20:p:335:ILE:HG22	1.88	0.55
24:x:51:SER:HG	24:x:55:SER:HG	1.54	0.55
1:1:1566:A:H5''	21:t:33:ARG:HH21	1.70	0.55
1:1:1615:C:H2'	1:1:1616:U:C6	2.41	0.55
6:I:284:ARG:HH22	23:w:634:ASP:HA	1.71	0.55
6:I:225:LYS:HB2	6:I:268:PHE:HE2	1.71	0.55
1:1:900:G:H1'	1:1:1589:A:N6	2.21	0.55
24:x:47:VAL:HG13	24:x:49:VAL:HG23	1.87	0.55
1:1:1722:U:OP2	8:R:103:ARG:NH1	2.40	0.55
1:1:1721:U:OP2	8:R:124:TYR:OH	2.24	0.55
1:1:3365:U:H2'	1:1:3366:G:C8	2.42	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:U:49:ASN:HD22	9:U:49:ASN:C	2.15	0.55
18:m:751:HIS:HB2	18:m:767:LEU:HD11	1.89	0.55
24:x:426:VAL:HA	24:x:461:LEU:HD11	1.89	0.54
12:b:512:SER:OG	12:b:513:LEU:N	2.40	0.54
9:U:92:TRP:CE3	12:b:531:MET:HG3	2.43	0.54
1:1:1954:G:O2'	1:1:1955:U:OP1	2.21	0.54
20:p:275:ARG:HD2	20:p:277:ARG:HH21	1.73	0.53
1:1:2104:A:H4'	1:1:2105:G:H4'	1.91	0.53
1:1:1920:U:H3'	1:1:1921:A:H8	1.73	0.53
13:c:42:ILE:HD11	13:c:67:VAL:HG22	1.91	0.53
24:x:409:GLU:OE1	24:x:412:ARG:NH2	2.40	0.53
15:g:95:ILE:HD13	23:w:405:GLU:HB2	1.90	0.53
23:w:420:ASN:ND2	23:w:535:ILE:O	2.42	0.53
24:x:10:LEU:HD11	24:x:39:PRO:HG3	1.90	0.53
6:I:377:ARG:HA	6:I:380:MET:HE2	1.91	0.53
14:d:76:SER:O	14:d:91:SER:HA	2.08	0.53
24:x:426:VAL:HG23	24:x:465:PRO:HG3	1.90	0.53
1:1:1750:A:OP1	17:k:44:LYS:NZ	2.33	0.52
13:c:75:ASN:OD1	13:c:76:GLU:N	2.42	0.52
20:p:212:VAL:HG11	20:p:227:TYR:CZ	2.44	0.52
14:d:16:LEU:HD13	14:d:67:VAL:HG11	1.91	0.52
24:x:303:LEU:HB2	24:x:308:ARG:HG3	1.90	0.52
1:1:1667:A:H2'	1:1:1668:G:H8	1.74	0.52
20:p:238:TYR:HA	20:p:241:MET:HE3	1.91	0.52
1:1:1799:A:H2'	1:1:1800:A:H8	1.75	0.52
1:1:1590:G:O2'	1:1:1797:A:N6	2.43	0.52
1:1:2082:U:H2'	1:1:2083:G:C8	2.41	0.52
11:Z:70:PRO:HG3	11:Z:115:LYS:HB2	1.92	0.52
18:m:492:GLU:HG2	18:m:602:TRP:HD1	1.75	0.52
24:x:249:LEU:HD11	24:x:281:ILE:HD11	1.92	0.52
17:k:32:ASN:HD21	17:k:36:LYS:HE3	1.75	0.52
1:1:1951:C:H5''	20:p:263:LYS:HD2	1.91	0.52
24:x:462:PHE:HB2	24:x:489:VAL:HG12	1.92	0.51
12:b:495:TRP:CH2	12:b:499:ARG:HD2	2.45	0.51
20:p:222:ILE:HB	20:p:234:TRP:HB2	1.92	0.51
1:1:1447:G:N7	7:P:25:SER:OG	2.44	0.51
11:Z:5:LEU:HD11	13:c:35:ARG:HD2	1.92	0.51
1:1:1568:U:OP2	21:t:33:ARG:NH2	2.44	0.51
1:1:3364:C:H2'	1:1:3365:U:C6	2.46	0.51
3:8:12:GLN:HA	3:8:16:LEU:HB2	1.93	0.51
18:m:799:ASP:OD2	18:m:801:THR:OG1	2.29	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:x:175:ASP:OD1	24:x:203:SER:OG	2.26	0.51
9:U:21:SER:OG	9:U:22:PRO:HD3	2.10	0.51
1:1:1688:U:H2'	1:1:1689:U:C6	2.45	0.51
13:c:16:LEU:HB3	13:c:98:SER:HB2	1.93	0.51
1:1:1498:A:H2'	1:1:1499:C:C6	2.46	0.51
23:w:370:GLU:HA	23:w:373:ARG:HG2	1.94	0.50
13:c:75:ASN:HB2	23:w:385:MET:HE3	1.94	0.50
20:p:111:VAL:HG21	20:p:435:ALA:HB2	1.92	0.50
20:p:204:LEU:HD11	20:p:241:MET:HE1	1.94	0.50
24:x:420:ASP:OD1	24:x:505:ARG:NH1	2.40	0.50
20:p:296:ASP:HB2	20:p:302:VAL:HB	1.94	0.50
20:p:434:TRP:CH2	20:p:454:ALA:HB1	2.47	0.50
9:U:91:ASP:OD1	12:b:521:ARG:NH2	2.38	0.50
14:d:55:LEU:HB2	14:d:95:PRO:HD3	1.94	0.50
24:x:381:ASP:HB3	24:x:444:ILE:HG12	1.93	0.50
1:1:1798:A:H2'	1:1:1799:A:C8	2.47	0.50
11:Z:56:LYS:HE3	21:t:28:ARG:HD2	1.94	0.50
24:x:5:LEU:O	24:x:29:THR:OG1	2.30	0.50
1:1:1681:U:OP2	12:b:521:ARG:NH1	2.45	0.50
1:1:1804:A:H5'	15:g:70:LYS:HD2	1.94	0.50
24:x:33:VAL:HG22	24:x:226:VAL:HG21	1.93	0.50
11:Z:52:LYS:O	11:Z:65:ARG:NH2	2.42	0.49
20:p:106:VAL:HB	20:p:443:ALA:HB1	1.93	0.49
23:w:535:ILE:HD12	23:w:538:LEU:HD21	1.93	0.49
1:1:3075:G:H5'	14:d:62:ARG:HG2	1.94	0.49
1:1:1643:A:H5''	1:1:1644:C:C4	2.47	0.49
1:1:1680:G:OP2	9:U:90:ARG:NH2	2.45	0.49
8:R:162:ARG:NH1	23:w:349:GLU:OE2	2.45	0.49
24:x:405:ALA:O	24:x:406:ASN:HB2	2.11	0.49
1:1:1717:U:H2'	1:1:1718:G:C8	2.47	0.49
6:I:179:LEU:HD21	6:I:251:LEU:HD12	1.94	0.49
24:x:34:GLN:HG2	24:x:60:ALA:HB2	1.95	0.49
12:b:496:ILE:HD11	22:u:134:LEU:HD21	1.94	0.49
14:d:20:LEU:HD11	14:d:32:ALA:HB2	1.94	0.49
17:k:26:LYS:HD2	17:k:78:LEU:HD13	1.94	0.49
12:b:496:ILE:HG23	22:u:133:LEU:HD23	1.94	0.49
20:p:293:VAL:HG23	20:p:305:SER:HB3	1.95	0.49
23:w:355:ASP:OD1	23:w:356:LEU:N	2.45	0.49
1:1:3338:C:H2'	1:1:3339:A:H8	1.77	0.49
1:1:1766:G:HO2'	1:1:1767:C:H6	1.61	0.49
1:1:1945:A:OP1	24:x:148:THR:OG1	2.31	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:3365:U:H2'	1:1:3366:G:H8	1.78	0.48
24:x:262:LYS:N	24:x:340:ASP:OD2	2.38	0.48
22:u:56:ARG:HE	22:u:62:GLU:HG2	1.78	0.48
24:x:94:GLU:HG2	24:x:312:LEU:HD22	1.95	0.48
1:1:1574:C:O2'	1:1:1575:A:O5'	2.28	0.48
1:1:1660:C:H2'	1:1:1661:G:H8	1.77	0.48
1:1:1666:G:H2'	1:1:1667:A:H8	1.79	0.48
20:p:250:ILE:HD12	20:p:262:ARG:HG3	1.95	0.48
1:1:2050:C:O2	1:1:2050:C:H2'	2.12	0.48
6:I:280:ILE:HD11	6:I:294:ILE:HB	1.95	0.48
22:u:135:ARG:O	22:u:135:ARG:NH1	2.46	0.48
18:m:459:GLY:HA2	18:m:478:ILE:HD12	1.96	0.48
20:p:227:TYR:HA	20:p:289:PRO:HB3	1.94	0.48
2:2:131:A:H2'	2:2:132:G:H8	1.78	0.48
17:k:11:PHE:CZ	17:k:43:PHE:HB3	2.49	0.48
18:m:785:ILE:HG22	18:m:794:PHE:HB2	1.95	0.48
24:x:58:THR:HA	24:x:61:PHE:CE2	2.48	0.48
1:1:1877:U:H4'	1:1:1878:G:C5	2.49	0.48
15:g:106:LYS:HA	15:g:109:THR:HG22	1.96	0.48
1:1:1480:G:O2'	1:1:1871:U:O4	2.26	0.48
24:x:69:VAL:HG21	24:x:144:ILE:HD11	1.95	0.48
1:1:1680:G:OP1	12:b:521:ARG:HG3	2.13	0.47
13:c:24:THR:OG1	13:c:91:SER:HB3	2.14	0.47
18:m:324:LEU:HD22	21:t:18:ILE:HD12	1.96	0.47
23:w:419:LEU:HD13	23:w:538:LEU:HD23	1.95	0.47
24:x:331:ALA:HB3	24:x:353:MET:HE2	1.96	0.47
24:x:524:LYS:O	24:x:528:GLU:HG2	2.14	0.47
24:x:543:LYS:HE2	24:x:547:LEU:HG	1.96	0.47
1:1:1643:A:H2'	1:1:1644:C:C2	2.50	0.47
1:1:1874:A:N7	8:R:20:ARG:NH1	2.62	0.47
9:U:35:LYS:HD2	9:U:38:ILE:HD11	1.96	0.47
18:m:478:ILE:HD11	18:m:487:HIS:HA	1.96	0.47
14:d:55:LEU:O	14:d:59:ILE:HG12	2.14	0.47
18:m:648:HIS:ND1	18:m:649:PRO:O	2.45	0.47
20:p:117:HIS:HA	20:p:130:TRP:O	2.14	0.47
1:1:1448:U:H5''	7:P:66:SER:HB3	1.95	0.47
1:1:1715:A:O5'	24:x:195:LYS:NZ	2.48	0.47
1:1:1717:U:H2'	1:1:1718:G:H8	1.78	0.47
20:p:125:GLY:HA2	20:p:147:ILE:HG12	1.97	0.47
20:p:422:GLN:HB2	20:p:425:VAL:HB	1.96	0.47
1:1:1856:C:H2'	1:1:1857:C:H6	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1940:G:N3	24:x:434:LYS:HB2	2.30	0.47
3:8:55:GLN:NE2	6:I:350:THR:HG22	2.28	0.47
23:w:637:TYR:OH	23:w:642:GLU:OE1	2.25	0.47
2:2:123:G:H2'	2:2:124:G:C8	2.50	0.47
1:1:1657:C:O2'	1:1:1796:G:O2'	2.27	0.47
1:1:3338:C:H2'	1:1:3339:A:C8	2.49	0.47
18:m:327:PRO:HD2	21:t:20:LEU:HD13	1.97	0.47
22:u:50:LYS:HB3	22:u:50:LYS:HE2	1.70	0.47
1:1:1616:U:H2'	1:1:1617:G:C8	2.49	0.47
6:I:441:ASN:N	23:w:728:MET:O	2.48	0.47
14:d:13:THR:OG1	14:d:72:ARG:NH1	2.36	0.46
1:1:1953:G:O4'	1:1:2092:A:N6	2.48	0.46
1:1:3364:C:H2'	1:1:3365:U:H6	1.81	0.46
24:x:419:ARG:NH1	24:x:498:TYR:HB3	2.31	0.46
1:1:1799:A:H2'	1:1:1800:A:C8	2.49	0.46
6:I:334:LEU:HD21	6:I:414:TYR:HE1	1.81	0.46
18:m:597:VAL:HA	18:m:613:GLN:HG3	1.97	0.46
1:1:1954:G:HO2'	1:1:1955:U:P	2.38	0.46
6:I:166:VAL:HG13	6:I:178:MET:HB2	1.97	0.46
12:b:495:TRP:HZ3	22:u:133:LEU:HG	1.80	0.46
20:p:209:ALA:HB3	20:p:228:ASP:HB3	1.98	0.46
20:p:252:ASN:HB3	20:p:253:PRO:HD3	1.97	0.46
8:R:133:LYS:HG3	8:R:134:HIS:ND1	2.30	0.46
14:d:65:LYS:HB3	14:d:65:LYS:HE2	1.69	0.46
22:u:124:LYS:O	22:u:128:GLU:HG3	2.15	0.46
24:x:69:VAL:HG13	24:x:74:ALA:HB3	1.97	0.46
6:I:178:MET:O	6:I:227:TYR:OH	2.30	0.46
18:m:527:LYS:HD3	20:p:264:ARG:HD3	1.97	0.46
20:p:374:HIS:NE2	20:p:393:SER:OG	2.42	0.46
23:w:539:ILE:H	23:w:539:ILE:HD12	1.81	0.46
1:1:1560:G:O2'	1:1:1561:G:O4'	2.19	0.46
18:m:545:SER:HB2	18:m:628:LYS:HD2	1.97	0.46
24:x:423:ASP:OD2	24:x:500:TYR:OH	2.22	0.46
1:1:1667:A:H2'	1:1:1668:G:C8	2.51	0.46
6:I:411:PHE:HE2	6:I:440:ALA:HB2	1.79	0.46
1:1:2347:U:H2'	1:1:2348:A:H8	1.81	0.46
6:I:179:LEU:HD12	23:w:563:ILE:HG13	1.98	0.46
13:c:27:TYR:OH	13:c:55:GLU:OE1	2.31	0.46
15:g:65:VAL:HG23	15:g:70:LYS:HE3	1.98	0.46
1:1:1620:U:H2'	1:1:1621:A:C8	2.51	0.45
1:1:1936:A:N3	1:1:1936:A:H2'	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:I:192:TYR:OH	6:I:217:GLU:OE2	2.30	0.45
8:R:134:HIS:NE2	8:R:136:ARG:HB2	2.32	0.45
24:x:351:THR:HG21	24:x:385:PHE:HE2	1.80	0.45
1:1:1929:G:OP2	8:R:108:LYS:NZ	2.47	0.45
6:I:292:ILE:HD11	6:I:524:LEU:HD12	1.98	0.45
6:I:347:ASP:O	6:I:350:THR:HG23	2.17	0.45
20:p:149:ALA:HB1	20:p:214:ILE:HG12	1.99	0.45
19:n:576:LYS:O	19:n:580:GLN:HG3	2.16	0.45
24:x:415:ILE:O	24:x:498:TYR:OH	2.35	0.45
6:I:157:ALA:O	6:I:161:ARG:HG2	2.16	0.45
6:I:292:ILE:HD12	6:I:525:ALA:HB2	1.98	0.45
18:m:402:LYS:HD2	21:t:19:LEU:HD22	1.97	0.45
20:p:123:TYR:OH	20:p:148:ARG:NH1	2.49	0.45
23:w:349:GLU:HA	23:w:352:ILE:HD13	1.98	0.45
1:1:1597:C:H5'	1:1:1696:A:H1'	1.99	0.45
20:p:165:ARG:HG2	20:p:209:ALA:N	2.32	0.45
1:1:1953:G:H22	1:1:2092:A:H2'	1.82	0.45
1:1:1680:G:H2'	1:1:1681:U:C6	2.52	0.45
1:1:2091:U:OP2	24:x:310:LYS:HE3	2.17	0.45
10:X:22:LYS:HE3	23:w:453:LYS:HG3	1.98	0.45
13:c:98:SER:OG	13:c:99:ASP:N	2.49	0.44
1:1:1618:G:H2'	1:1:1619:A:C8	2.53	0.44
1:1:1715:A:N7	13:c:84:LEU:HD12	2.33	0.44
1:1:1765:U:O2'	1:1:1766:G:O4'	2.35	0.44
18:m:443:LEU:HD13	18:m:452:LEU:HD11	1.98	0.44
20:p:402:VAL:HG23	20:p:411:MET:HG3	1.98	0.44
23:w:383:GLN:O	23:w:387:MET:HG2	2.18	0.44
1:1:1680:G:H2'	1:1:1681:U:H6	1.82	0.44
1:1:1810:A:H2'	1:1:1811:G:C8	2.53	0.44
1:1:2053:C:OP1	20:p:157:ARG:NH2	2.46	0.44
18:m:491:ILE:HG22	18:m:504:VAL:HG13	1.98	0.44
20:p:169:LEU:O	20:p:201:LEU:N	2.50	0.44
24:x:383:ILE:HB	24:x:384:PRO:HD3	2.00	0.44
1:1:1460:A:H5'	14:d:51:LEU:O	2.17	0.44
2:2:135:G:OP2	10:X:56:ARG:NH2	2.50	0.44
3:8:24:ARG:O	3:8:28:ILE:HG12	2.18	0.44
6:I:175:LYS:NZ	23:w:568:GLU:O	2.48	0.44
1:1:843:A:OP1	23:w:369:ARG:NH2	2.51	0.44
1:1:1621:A:H2'	1:1:1622:U:C6	2.53	0.44
3:8:36:ARG:HG3	3:8:37:ARG:H	1.82	0.44
1:1:1636:U:O2'	11:Z:79:HIS:ND1	2.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1947:G:H8	18:m:539:PHE:CE2	2.36	0.44
13:c:34:LEU:HD23	13:c:59:TYR:HB3	1.99	0.44
11:Z:27:LYS:HE3	11:Z:27:LYS:HB2	1.80	0.44
8:R:134:HIS:HE2	8:R:136:ARG:HB2	1.82	0.44
13:c:74:ASN:OD1	13:c:75:ASN:N	2.51	0.44
18:m:319:ASP:OD1	18:m:319:ASP:N	2.50	0.44
18:m:747:ILE:HG21	18:m:793:LEU:HD21	2.00	0.44
19:n:30:ALA:O	19:n:34:ARG:HG3	2.17	0.44
1:1:1639:C:H5'	15:g:52:GLN:HG2	1.99	0.43
23:w:366:ASN:HA	23:w:369:ARG:HG2	2.00	0.43
1:1:1659:U:H2'	1:1:1660:C:C6	2.52	0.43
1:1:1930:A:H3'	1:1:1931:U:C6	2.53	0.43
23:w:387:MET:HA	23:w:387:MET:HE2	2.00	0.43
24:x:10:LEU:HD23	24:x:14:LEU:HD11	2.00	0.43
24:x:335:ASP:OD1	24:x:335:ASP:N	2.49	0.43
18:m:746:THR:HG22	18:m:771:THR:HG22	2.00	0.43
24:x:50:ASP:HA	24:x:203:SER:O	2.18	0.43
24:x:242:VAL:HG22	24:x:374:LEU:HD12	2.00	0.43
1:1:1943:C:H5''	24:x:329:VAL:HB	1.99	0.43
9:U:20:SER:O	9:U:24:GLU:HG2	2.18	0.43
11:Z:17:ARG:HD3	15:g:73:SER:HB3	2.00	0.43
23:w:416:THR:HG23	23:w:418:ILE:H	1.82	0.43
1:1:1534:A:H2'	1:1:1535:A:C8	2.53	0.43
6:I:180:ALA:O	6:I:183:PRO:HD2	2.19	0.43
8:R:53:LYS:HB3	12:b:517:ALA:HB1	2.00	0.43
12:b:495:TRP:CZ3	22:u:137:ARG:HB2	2.54	0.43
18:m:441:ARG:HD2	18:m:457:ASP:OD1	2.18	0.43
18:m:499:ASN:OD1	18:m:529:LYS:HD3	2.18	0.43
18:m:519:GLY:O	18:m:523:GLU:HG3	2.18	0.43
20:p:269:MET:HE3	20:p:269:MET:HB2	1.88	0.43
1:1:2096:A:H2'	1:1:2097:U:C6	2.54	0.43
1:1:2097:U:H2'	1:1:2098:C:H6	1.82	0.43
23:w:695:LEU:HD23	23:w:695:LEU:HA	1.86	0.43
6:I:335:ASN:HA	6:I:338:LEU:HD23	2.01	0.43
18:m:448:SER:O	18:m:789:ARG:NH2	2.51	0.43
18:m:795:SER:O	18:m:802:ALA:HA	2.18	0.43
24:x:427:LYS:HE3	24:x:427:LYS:HB2	1.63	0.43
18:m:425:PHE:CD1	18:m:767:LEU:HD13	2.54	0.43
18:m:464:TRP:CZ3	18:m:471:GLU:HB2	2.54	0.43
18:m:568:VAL:HG23	18:m:632:GLN:HA	2.01	0.43
20:p:220:SER:OG	20:p:236:THR:HB	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:P:127:ARG:HG2	7:P:139:TYR:O	2.18	0.43
20:p:97:LEU:HD11	20:p:453:LYS:HA	2.01	0.43
20:p:143:HIS:NE2	20:p:168:ARG:HD3	2.34	0.43
1:1:1637:A:OP1	11:Z:73:LYS:NZ	2.52	0.43
1:1:1666:G:H2'	1:1:1667:A:C8	2.53	0.43
6:I:282:LYS:HD3	6:I:283:PRO:HD2	2.01	0.43
6:I:418:LEU:HD23	6:I:418:LEU:HA	1.92	0.43
14:d:24:SER:OG	14:d:27:LYS:NZ	2.52	0.43
15:g:98:GLN:HB2	23:w:408:PHE:HA	2.01	0.43
20:p:155:ASN:OD1	20:p:174:ASN:ND2	2.52	0.43
6:I:206:VAL:HG23	6:I:206:VAL:O	2.18	0.42
6:I:522:LEU:O	6:I:522:LEU:HD23	2.18	0.42
9:U:41:ILE:O	9:U:75:TYR:OH	2.22	0.42
18:m:703:ARG:HG3	18:m:720:ARG:HG2	2.00	0.42
24:x:94:GLU:OE1	24:x:94:GLU:N	2.46	0.42
1:1:834:U:H2'	1:1:835:G:O4'	2.19	0.42
6:I:434:THR:HG21	6:I:537:VAL:HG21	2.00	0.42
1:1:1566:A:OP1	21:t:33:ARG:NH2	2.53	0.42
1:1:1711:C:OP1	11:Z:78:ASN:ND2	2.52	0.42
1:1:1930:A:H3'	1:1:1931:U:H6	1.83	0.42
10:X:110:VAL:HG22	10:X:124:VAL:HG22	2.00	0.42
1:1:1709:C:H2'	1:1:1710:C:H6	1.85	0.42
1:1:1936:A:N1	24:x:523:LYS:HD2	2.35	0.42
22:u:110:ASN:O	22:u:113:ARG:HG2	2.19	0.42
18:m:569:LYS:HD2	18:m:571:GLN:OE1	2.20	0.42
1:1:1528:G:O2'	1:1:1588:A:N3	2.49	0.42
1:1:1953:G:N2	1:1:2092:A:C8	2.88	0.42
1:1:3069:G:C2	1:1:3070:A:C8	3.07	0.42
14:d:75:ILE:HG23	14:d:93:VAL:HG22	2.01	0.42
24:x:237:LYS:NZ	24:x:367:VAL:HG13	2.34	0.42
24:x:351:THR:HG21	24:x:385:PHE:CE2	2.55	0.42
1:1:1643:A:H5''	1:1:1644:C:C5	2.55	0.42
6:I:524:LEU:H	6:I:524:LEU:HD23	1.84	0.42
20:p:428:LYS:HB2	20:p:445:GLN:HB2	2.02	0.42
24:x:290:LEU:HD23	24:x:290:LEU:H	1.85	0.42
1:1:1476:G:OP2	12:b:516:LYS:HE3	2.20	0.42
8:R:142:ILE:HG22	8:R:146:LYS:HE3	2.02	0.42
14:d:58:ALA:HA	14:d:61:LYS:HE2	2.02	0.42
20:p:138:LYS:HD3	20:p:172:THR:HG21	2.01	0.42
22:u:48:LYS:HD2	22:u:48:LYS:HA	1.91	0.42
1:1:894:G:N1	3:8:39:ASN:OD1	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2097:U:H2'	1:1:2098:C:C6	2.54	0.42
7:P:135:ARG:HB2	7:P:135:ARG:CZ	2.50	0.42
13:c:18:ILE:HG13	13:c:81:VAL:HG13	2.01	0.42
20:p:407:SER:OG	20:p:408:THR:N	2.52	0.42
23:w:728:MET:O	23:w:728:MET:HG3	2.20	0.42
24:x:10:LEU:HD12	24:x:10:LEU:HA	1.85	0.42
24:x:104:LEU:O	24:x:108:GLU:HG2	2.20	0.42
1:1:855:U:H2'	1:1:856:G:O4'	2.20	0.41
1:1:1490:A:H61	1:1:1838:G:H1'	1.85	0.41
1:1:1646:G:H1'	1:1:1809:A:N6	2.35	0.41
1:1:1856:C:H2'	1:1:1857:C:C6	2.54	0.41
6:I:411:PHE:CE2	6:I:440:ALA:HB2	2.55	0.41
12:b:523:LYS:HD3	12:b:523:LYS:HA	1.82	0.41
18:m:519:GLY:HA3	20:p:165:ARG:NH2	2.12	0.41
24:x:201:LEU:HD21	24:x:216:THR:HG21	2.02	0.41
1:1:1929:G:N1	8:R:109:TYR:OH	2.40	0.41
14:d:15:ASN:H	14:d:19:ARG:NH2	2.18	0.41
14:d:25:PHE:HA	14:d:28:ARG:HG3	2.01	0.41
24:x:227:ASN:OD1	24:x:227:ASN:N	2.53	0.41
24:x:448:GLN:H	24:x:448:GLN:CD	2.29	0.41
12:b:503:MET:HA	12:b:506:GLU:HG2	2.02	0.41
20:p:101:SER:C	20:p:102:ASN:HD22	2.28	0.41
1:1:1452:A:H5'	1:1:1453:A:C8	2.56	0.41
1:1:3063:C:H2'	1:1:3064:U:H6	1.85	0.41
14:d:54:GLU:CD	14:d:54:GLU:H	2.29	0.41
24:x:27:PHE:C	24:x:29:THR:H	2.28	0.41
24:x:351:THR:OG1	24:x:389:LYS:NZ	2.52	0.41
1:1:1458:U:O2	14:d:56:ASN:ND2	2.51	0.41
11:Z:115:LYS:HE3	11:Z:119:GLU:OE2	2.21	0.41
14:d:15:ASN:H	14:d:19:ARG:HH21	1.68	0.41
15:g:51:LEU:HB3	15:g:54:ILE:HD12	2.01	0.41
20:p:428:LYS:O	20:p:444:GLY:HA3	2.21	0.41
1:1:1965:C:H2'	1:1:1966:U:O4'	2.20	0.41
14:d:25:PHE:CD2	14:d:65:LYS:HE3	2.56	0.41
24:x:511:GLU:OE2	24:x:515:ASN:ND2	2.53	0.41
15:g:74:ARG:HG2	15:g:75:ALA:N	2.35	0.41
18:m:512:LEU:HB2	18:m:589:ILE:HG22	2.01	0.41
18:m:792:TRP:HB3	18:m:804:LEU:HD11	2.02	0.41
1:1:1603:A:OP1	8:R:38:ARG:NH1	2.54	0.41
1:1:1742:U:H2'	1:1:1743:G:H8	1.86	0.41
7:P:126:ARG:HG3	7:P:140:GLU:HG2	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:Z:104:PRO:HG2	18:m:700:PHE:CG	2.56	0.41
17:k:63:LYS:HA	17:k:63:LYS:HD2	1.94	0.41
22:u:51:TRP:CD1	22:u:51:TRP:H	2.38	0.41
24:x:536:TRP:O	24:x:540:THR:HG23	2.21	0.41
1:l:1940:G:H1'	24:x:434:LYS:HD2	2.03	0.41
6:I:145:VAL:CG1	23:w:558:ILE:HD13	2.50	0.41
19:n:53:ASN:O	19:n:55:GLY:N	2.53	0.41
20:p:371:LEU:HD23	20:p:408:THR:HA	2.03	0.41
24:x:41:LEU:HD13	24:x:47:VAL:HB	2.03	0.40
24:x:328:ASP:HB3	24:x:353:MET:HE1	2.02	0.40
1:l:1659:U:H2'	1:l:1660:C:H6	1.85	0.40
1:l:1794:G:H2'	1:l:1794:G:N3	2.36	0.40
6:I:280:ILE:HD13	6:I:280:ILE:HA	1.92	0.40
8:R:43:LYS:HE3	8:R:43:LYS:HB2	1.75	0.40
24:x:412:ARG:O	24:x:416:LEU:HG	2.20	0.40
1:l:858:A:H2'	1:l:859:G:C8	2.57	0.40
1:l:2083:G:H2'	1:l:2084:C:C6	2.57	0.40
6:I:147:LYS:HE2	6:I:158:ALA:HB2	2.04	0.40
10:X:26:VAL:HG23	23:w:449:MET:N	2.37	0.40
24:x:429:TYR:HE2	24:x:465:PRO:HD2	1.87	0.40
1:l:847:A:OP1	23:w:371:ARG:NH1	2.54	0.40
6:I:214:ARG:O	6:I:218:GLN:HG2	2.22	0.40
6:I:239:SER:O	6:I:239:SER:OG	2.38	0.40
8:R:140:GLU:HA	8:R:143:ILE:HG12	2.04	0.40
12:b:513:LEU:HD11	14:d:61:LYS:O	2.21	0.40
13:c:24:THR:HB	13:c:29:SER:HB3	2.02	0.40
18:m:696:ILE:HD12	18:m:729:VAL:HB	2.02	0.40
18:m:709:LEU:O	18:m:710:ASP:HB2	2.22	0.40
22:u:133:LEU:HA	22:u:136:ILE:HG22	2.03	0.40
23:w:352:ILE:CG1	24:x:446:ARG:NH1	2.84	0.40
8:R:95:TRP:CZ2	8:R:99:LEU:HD22	2.57	0.40
8:R:154:ALA:O	8:R:158:GLU:HG3	2.21	0.40
9:U:35:LYS:HA	9:U:38:ILE:HG12	2.03	0.40
12:b:513:LEU:O	12:b:514:LYS:C	2.64	0.40
18:m:764:ILE:O	19:n:558:MET:HE2	2.22	0.40
23:w:352:ILE:HD12	23:w:352:ILE:H	1.86	0.40
24:x:26:GLY:C	24:x:28:GLU:H	2.29	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	8	56/710 (8%)	56 (100%)	0	0	100	100
4	B	7/387 (2%)	7 (100%)	0	0	100	100
5	G	17/256 (7%)	16 (94%)	1 (6%)	0	100	100
6	I	330/663 (50%)	318 (96%)	12 (4%)	0	100	100
7	P	41/184 (22%)	38 (93%)	3 (7%)	0	100	100
8	R	130/189 (69%)	129 (99%)	1 (1%)	0	100	100
9	U	100/121 (83%)	96 (96%)	4 (4%)	0	100	100
10	X	94/142 (66%)	93 (99%)	1 (1%)	0	100	100
11	Z	133/136 (98%)	129 (97%)	4 (3%)	0	100	100
12	b	51/647 (8%)	49 (96%)	2 (4%)	0	100	100
13	c	95/105 (90%)	94 (99%)	1 (1%)	0	100	100
14	d	66/113 (58%)	62 (94%)	4 (6%)	0	100	100
15	g	110/121 (91%)	109 (99%)	1 (1%)	0	100	100
16	j	25/88 (28%)	25 (100%)	0	0	100	100
17	k	75/78 (96%)	73 (97%)	2 (3%)	0	100	100
18	m	404/429 (94%)	385 (95%)	19 (5%)	0	100	100
19	n	99/104 (95%)	95 (96%)	4 (4%)	0	100	100
20	p	331/460 (72%)	308 (93%)	23 (7%)	0	100	100
21	t	24/322 (8%)	24 (100%)	0	0	100	100
22	u	52/199 (26%)	52 (100%)	0	0	100	100
23	w	175/841 (21%)	171 (98%)	4 (2%)	0	100	100
24	x	531/606 (88%)	508 (96%)	22 (4%)	1 (0%)	43	71
All	All	2946/6901 (43%)	2837 (96%)	108 (4%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
24	x	406	ASN

5.3.2 Protein sidechains ⓘ

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

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	8	52/647 (8%)	52 (100%)	0	100	100
4	B	8/323 (2%)	8 (100%)	0	100	100
5	G	19/208 (9%)	19 (100%)	0	100	100
6	I	306/602 (51%)	306 (100%)	0	100	100
7	P	46/146 (32%)	46 (100%)	0	100	100
8	R	112/154 (73%)	112 (100%)	0	100	100
9	U	89/107 (83%)	88 (99%)	1 (1%)	65	76
10	X	87/118 (74%)	87 (100%)	0	100	100
11	Z	115/116 (99%)	115 (100%)	0	100	100
12	b	46/573 (8%)	46 (100%)	0	100	100
13	c	81/88 (92%)	81 (100%)	0	100	100
14	d	62/97 (64%)	62 (100%)	0	100	100
15	g	95/103 (92%)	95 (100%)	0	100	100
16	j	25/71 (35%)	25 (100%)	0	100	100
17	k	68/69 (99%)	68 (100%)	0	100	100
18	m	367/381 (96%)	367 (100%)	0	100	100
19	n	92/93 (99%)	92 (100%)	0	100	100
20	p	300/413 (73%)	300 (100%)	0	100	100
21	t	24/287 (8%)	24 (100%)	0	100	100
22	u	49/180 (27%)	49 (100%)	0	100	100
23	w	171/745 (23%)	171 (100%)	0	100	100
24	x	489/548 (89%)	479 (98%)	10 (2%)	48	69
All	All	2703/6069 (44%)	2692 (100%)	11 (0%)	81	84

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
9	U	49	ASN
24	x	28	GLU
24	x	47	VAL
24	x	291	VAL
24	x	292	ASN
24	x	349	THR
24	x	400	VAL
24	x	403	ILE
24	x	435	TYR
24	x	500	TYR
24	x	538	ASP

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

Mol	Chain	Res	Type
3	8	55	GLN
6	I	226	ASN
10	X	85	GLN
12	b	500	GLN
14	d	15	ASN
17	k	57	ASN
18	m	494	ASN
18	m	576	ASN
18	m	582	GLN
19	n	48	ASN
19	n	563	GLN
20	p	137	GLN
20	p	255	ASN
20	p	292	GLN
20	p	342	ASN
20	p	396	HIS
23	w	379	GLN
23	w	645	GLN
24	x	98	GLN
24	x	356	HIS
24	x	375	ASN
24	x	486	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	629/641 (98%)	107 (17%)	2 (0%)
2	2	55/72 (76%)	10 (18%)	1 (1%)
All	All	684/713 (95%)	117 (17%)	3 (0%)

All (117) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	822	G
1	1	860	G
1	1	861	C
1	1	1452	A
1	1	1454	A
1	1	1455	U
1	1	1456	A
1	1	1469	C
1	1	1481	A
1	1	1483	G
1	1	1484	U
1	1	1485	G
1	1	1486	G
1	1	1487	G
1	1	1556	C
1	1	1567	U
1	1	1568	U
1	1	1575	A
1	1	1580	A
1	1	1581	C
1	1	1582	C
1	1	1587	A
1	1	1589	A
1	1	1590	G
1	1	1604	G
1	1	1627	U
1	1	1628	C
1	1	1629	U
1	1	1630	U
1	1	1633	C
1	1	1639	C
1	1	1643	A
1	1	1694	U
1	1	1718	G
1	1	1724	U
1	1	1725	C

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Mol	Chain	Res	Type
1	1	1741	A
1	1	1750	A
1	1	1751	G
1	1	1761	C
1	1	1762	C
1	1	1763	U
1	1	1764	U
1	1	1765	U
1	1	1766	G
1	1	1767	C
1	1	1780	G
1	1	1795	U
1	1	1797	A
1	1	1806	A
1	1	1808	G
1	1	1815	U
1	1	1816	A
1	1	1817	G
1	1	1821	U
1	1	1858	A
1	1	1863	G
1	1	1864	A
1	1	1865	A
1	1	1866	C
1	1	1867	A
1	1	1868	G
1	1	1876	U
1	1	1878	G
1	1	1880	U
1	1	1918	C
1	1	1921	A
1	1	1922	A
1	1	1923	C
1	1	1927	G
1	1	1929	G
1	1	1930	A
1	1	1932	A
1	1	1935	G
1	1	1939	G
1	1	1940	G
1	1	1954	G
1	1	1955	U

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Mol	Chain	Res	Type
1	1	1960	A
1	1	1965	C
1	1	1970	U
1	1	1971	C
1	1	2057	G
1	1	2087	C
1	1	2091	U
1	1	2092	A
1	1	2102	U
1	1	2103	U
1	1	2104	A
1	1	2105	G
1	1	2110	G
1	1	2111	G
1	1	2113	A
1	1	2114	C
1	1	2118	C
1	1	2119	A
1	1	2120	A
1	1	3069	G
1	1	3078	U
1	1	3079	U
1	1	3334	U
1	1	3341	U
1	1	3347	A
1	1	3349	C
1	1	3358	U
1	1	3363	U
1	1	3369	G
2	2	59	A
2	2	62	C
2	2	104	A
2	2	106	C
2	2	107	G
2	2	111	A
2	2	113	U
2	2	116	G
2	2	124	G
2	2	125	U

All (3) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	1574	C
1	1	1954	G
2	2	123	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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	1	12
2	2	2
19	n	1
18	m	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	1	905:U	O3'	1446:A	P	67.43
1	n	70:TYR	C	550:GLU	N	62.35
1	1	2356:A	O3'	3061:G	P	60.76
1	1	1884:A	O3'	1916:U	P	56.47
1	1	2120:A	O3'	2347:U	P	35.66
1	1	864:G	O3'	893:C	P	34.24
1	2	62:C	O3'	98:U	P	20.83
1	1	2058:G	O3'	2080:C	P	18.14
1	1	1541:G	O3'	1552:G	P	18.10
1	2	47:C	O3'	56:G	P	17.79
1	1	3081:C	O3'	3333:G	P	17.16
1	m	330:PRO	C	392:LEU	N	16.93
1	1	1972:A	O3'	2050:C	P	16.91
1	1	3350:C	O3'	3356:G	P	15.54
1	1	1568:U	O3'	1574:C	P	11.27
1	1	1838:G	O3'	1853:U	P	9.55

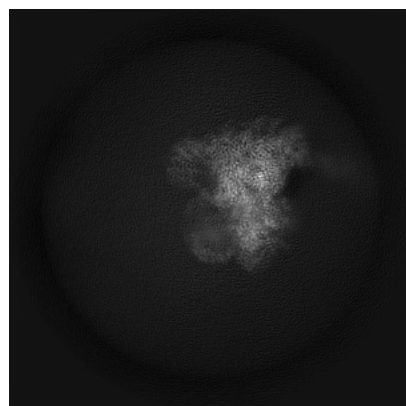
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-24290. These allow visual inspection of the internal detail of the map and identification of artifacts.

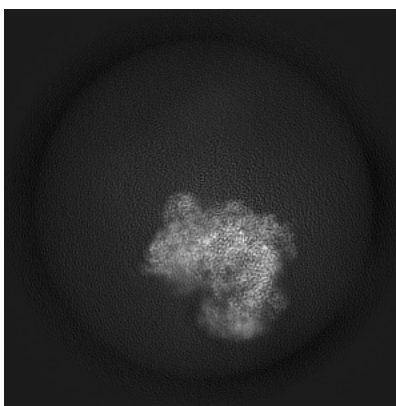
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

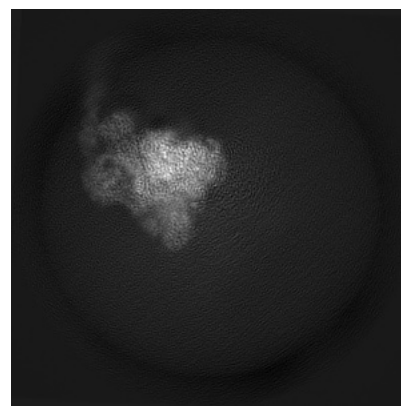
6.1.1 Primary map



X

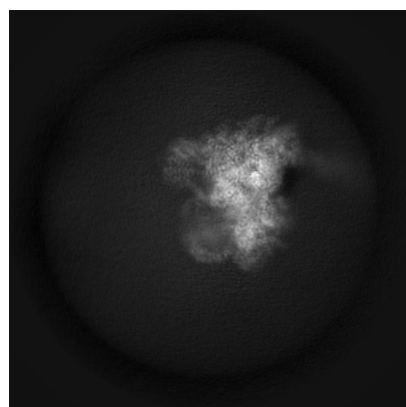


Y

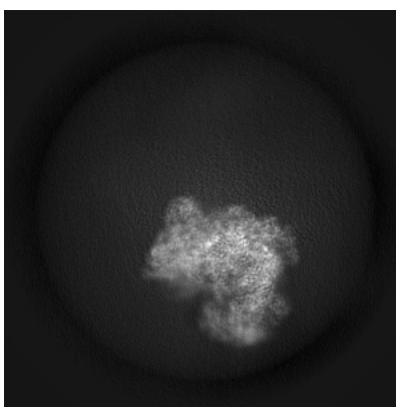


Z

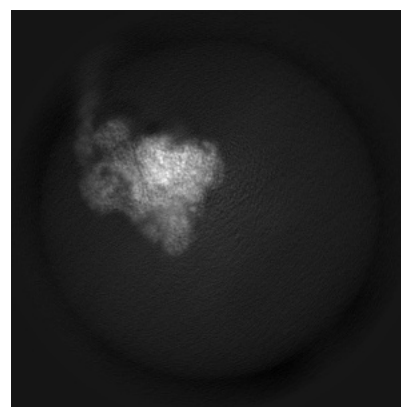
6.1.2 Raw map



X



Y

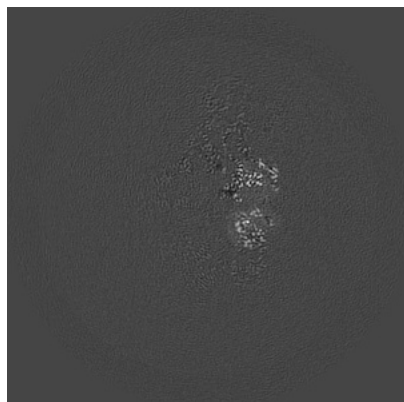


Z

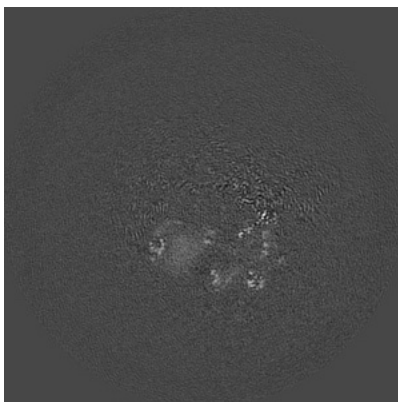
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

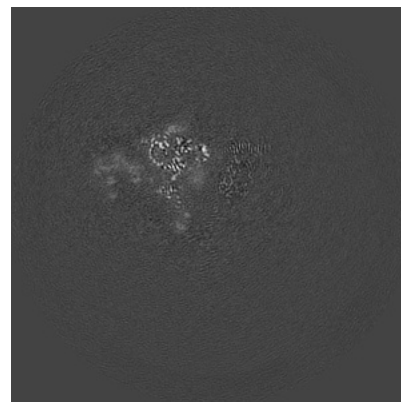
6.2.1 Primary map



X Index: 210

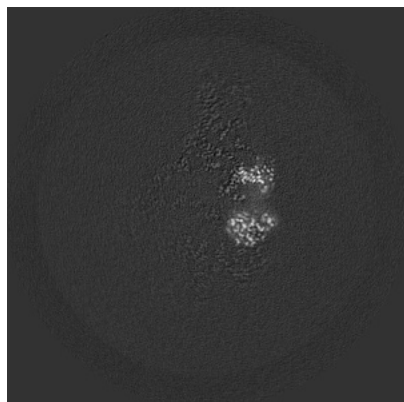


Y Index: 210

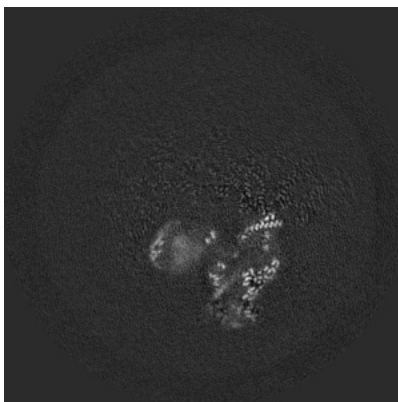


Z Index: 210

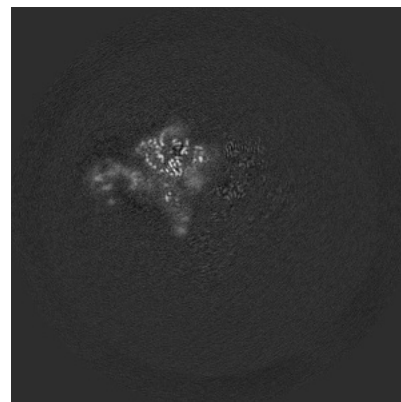
6.2.2 Raw map



X Index: 210



Y Index: 210

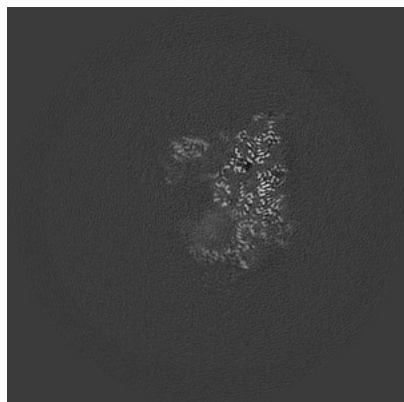


Z Index: 210

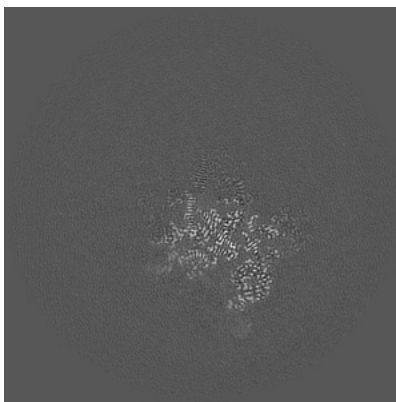
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

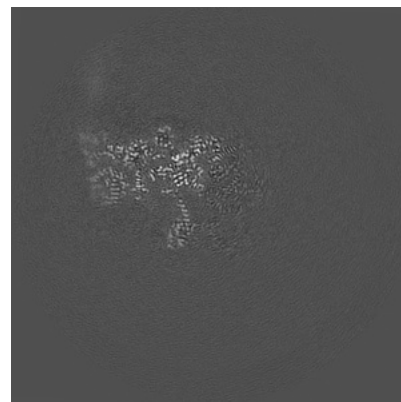
6.3.1 Primary map



X Index: 161

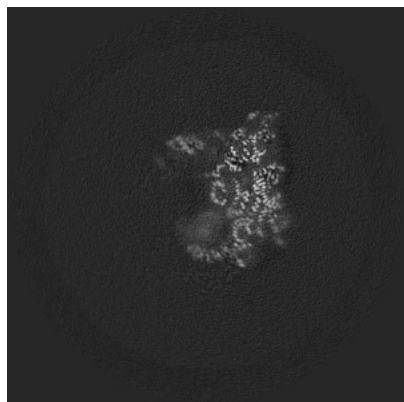


Y Index: 271

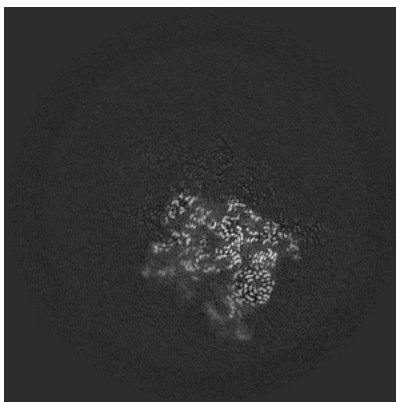


Z Index: 247

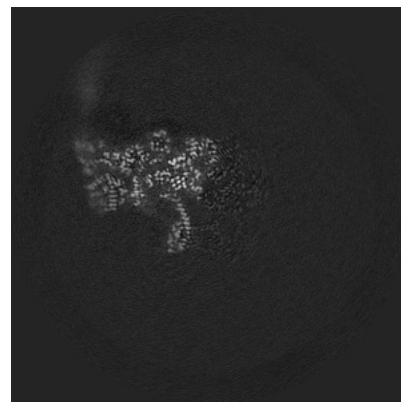
6.3.2 Raw map



X Index: 158



Y Index: 260

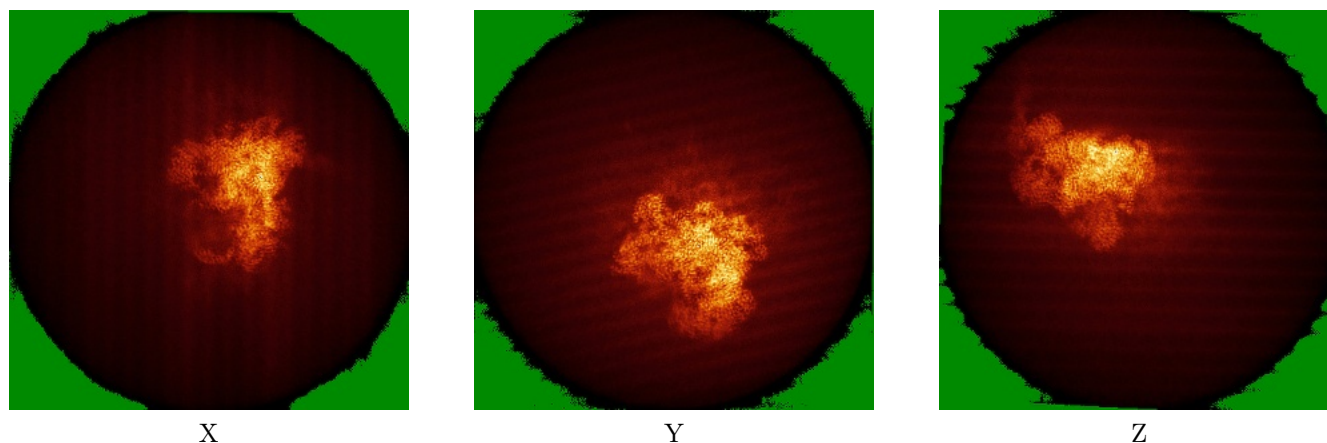


Z Index: 249

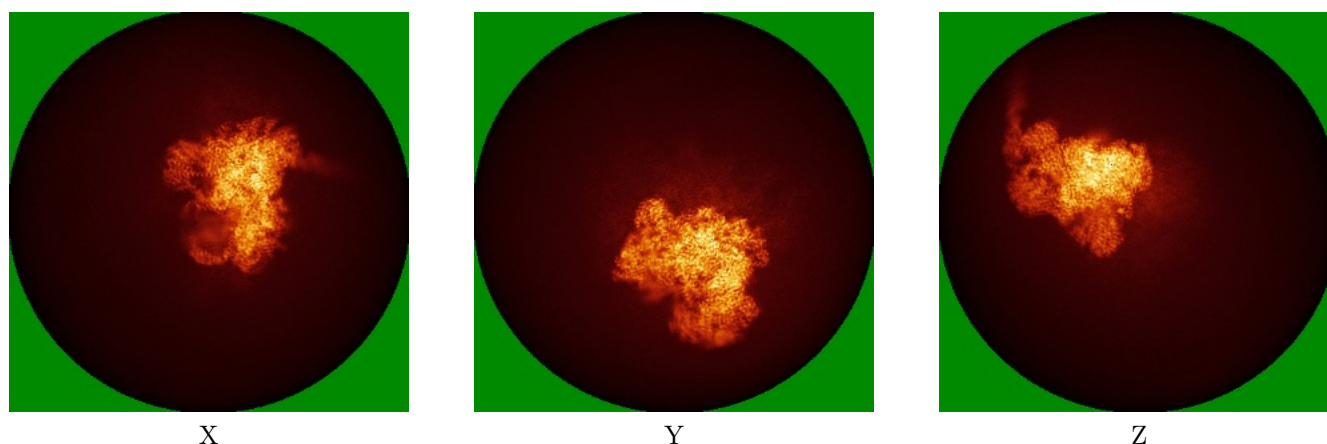
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw map



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

6.5 Orthogonal surface views [i](#)

This section was not generated.

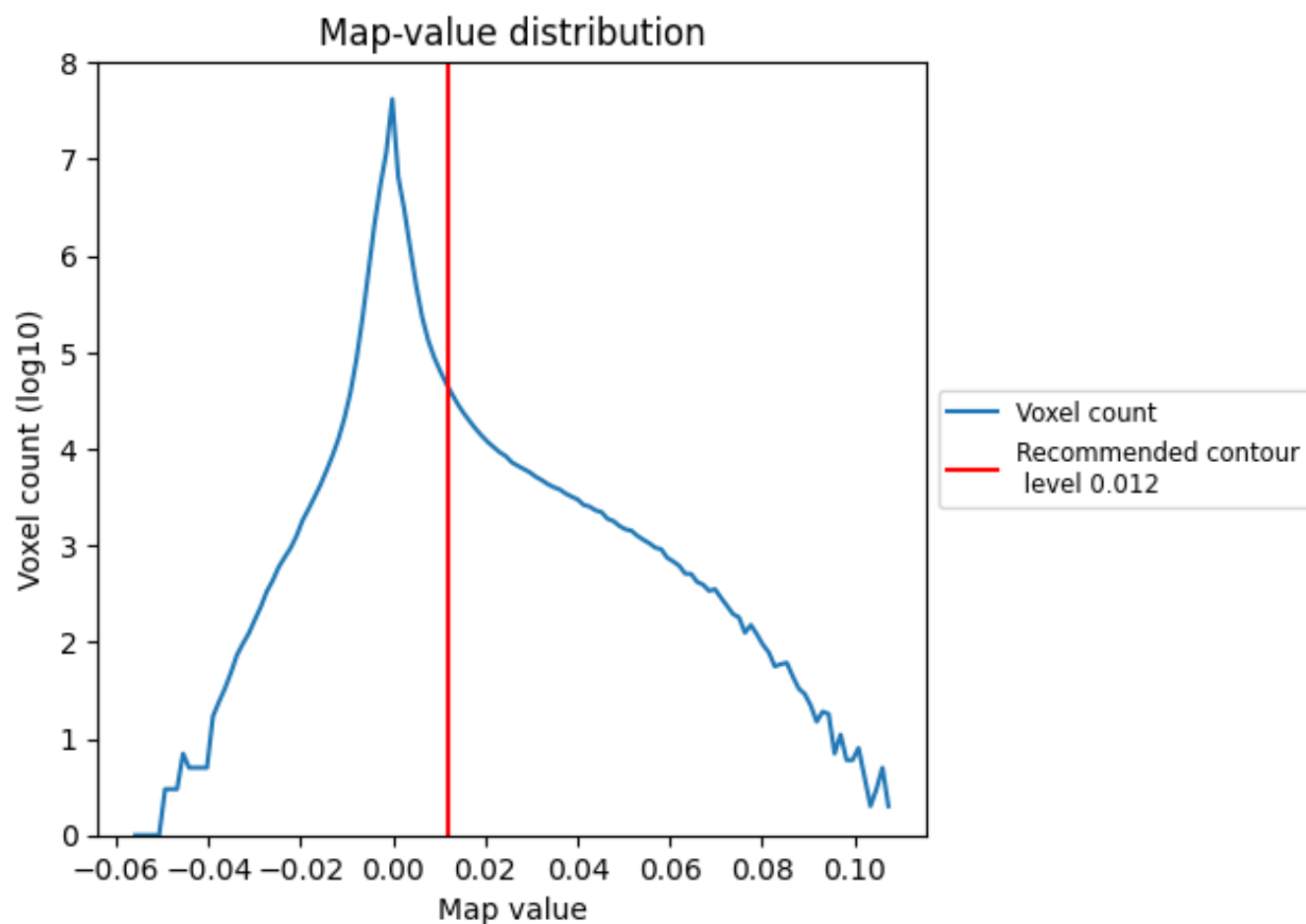
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

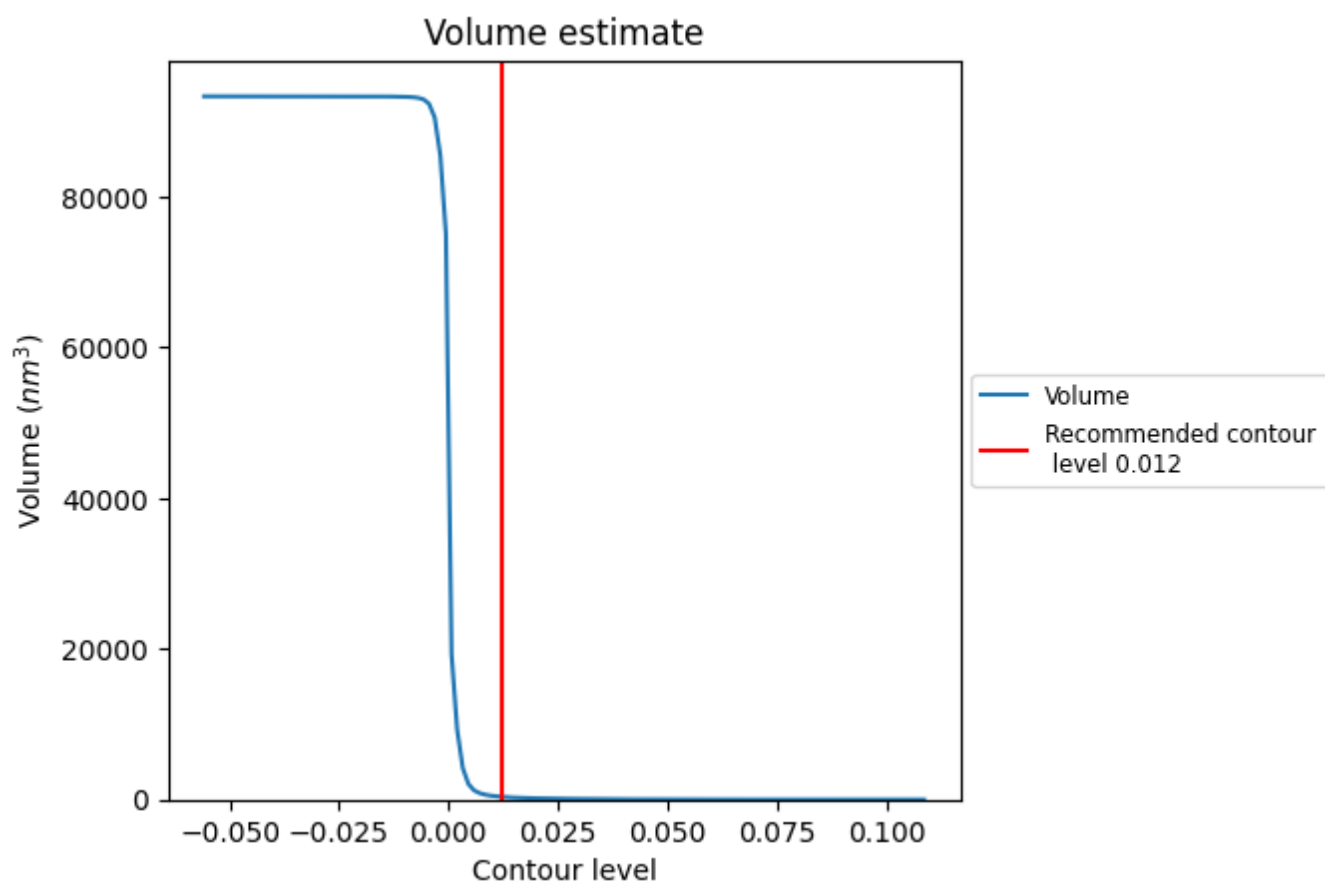
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

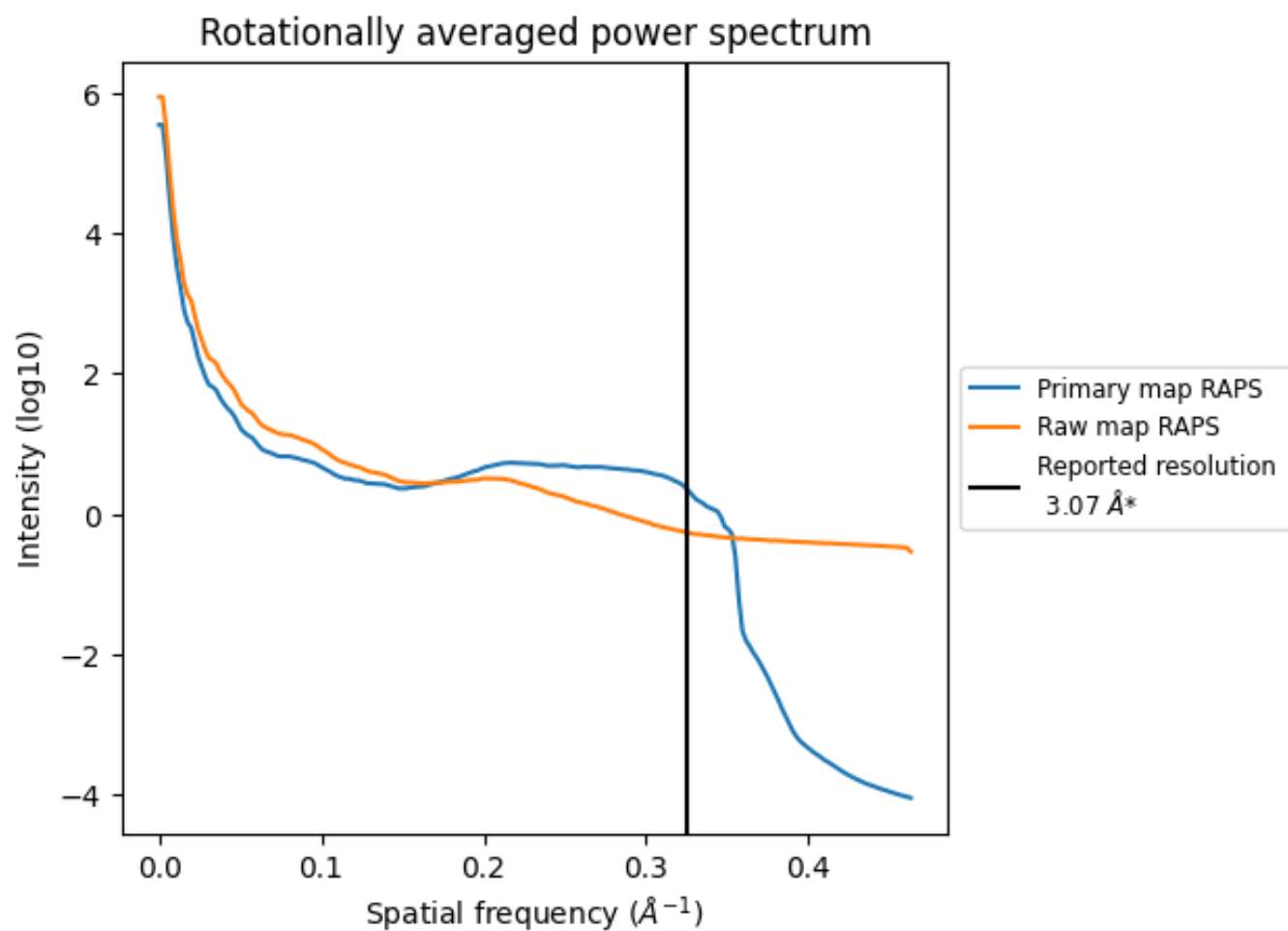
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 369 nm³; this corresponds to an approximate mass of 334 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

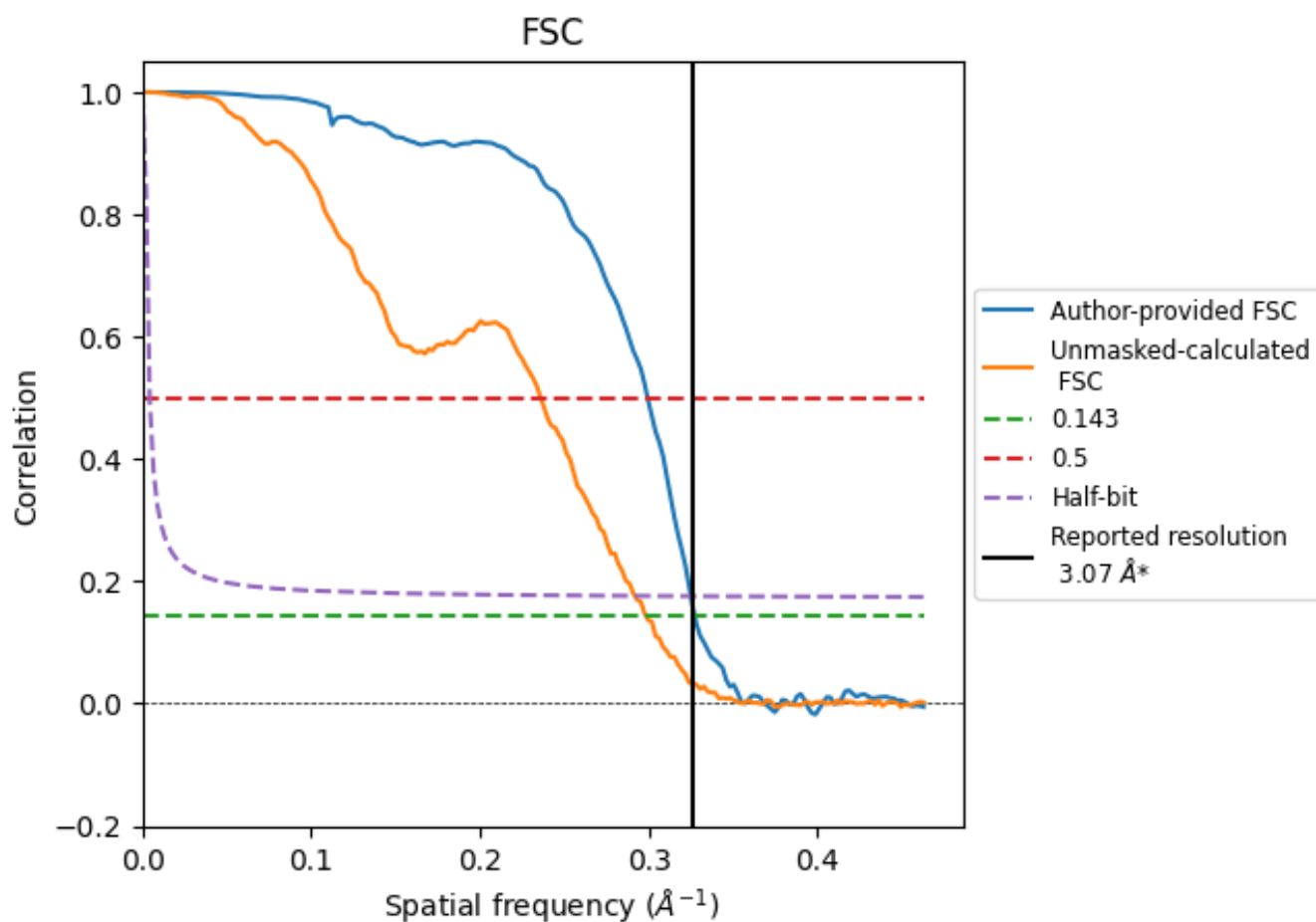


*Reported resolution corresponds to spatial frequency of 0.326 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of $0.326 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

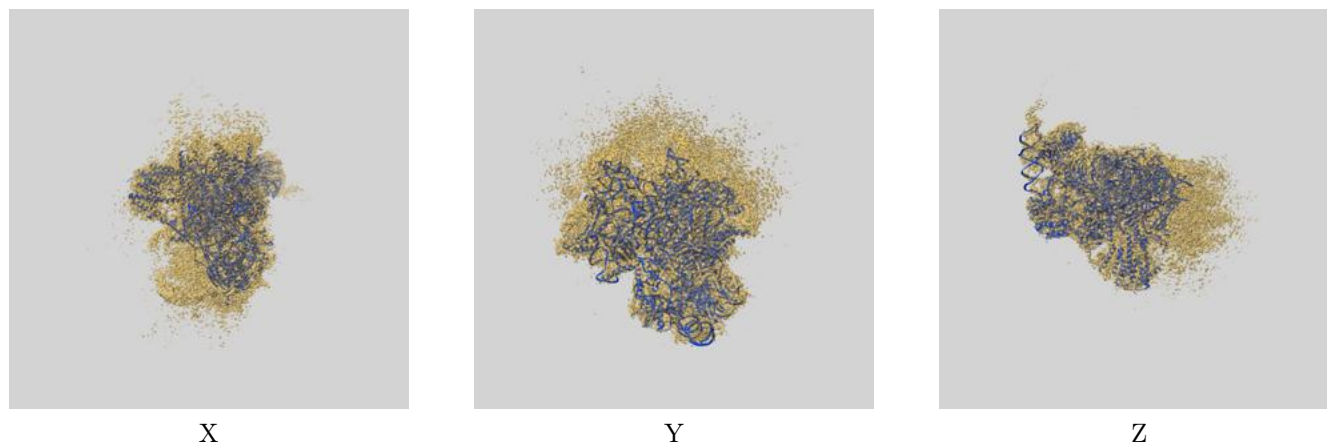
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.07	-	-
Author-provided FSC curve	3.06	3.34	3.08
Unmasked-calculated*	3.35	4.24	3.43

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

9 Map-model fit [i](#)

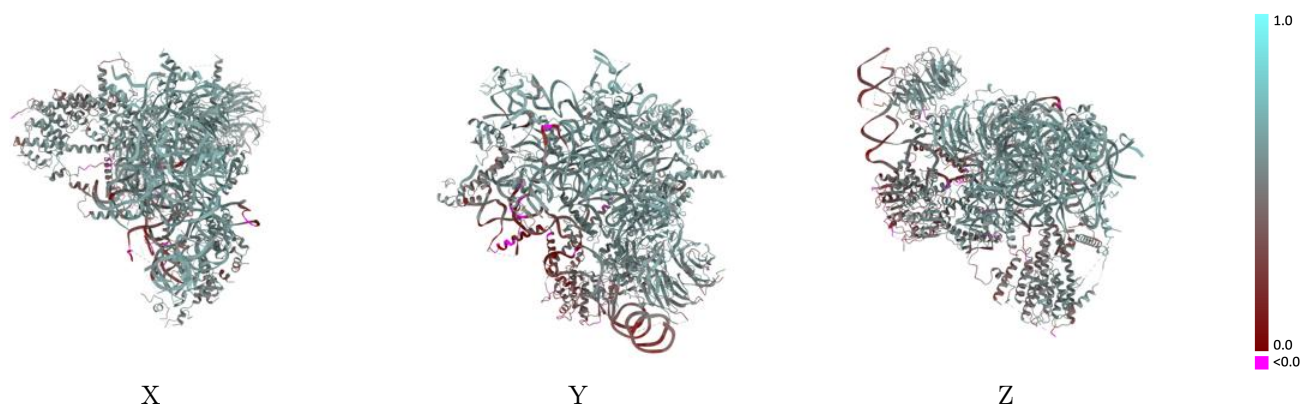
This section contains information regarding the fit between EMDB map EMD-24290 and PDB model 7R72. Per-residue inclusion information can be found in [section 3](#) on [page 8](#).

9.1 Map-model overlay [i](#)



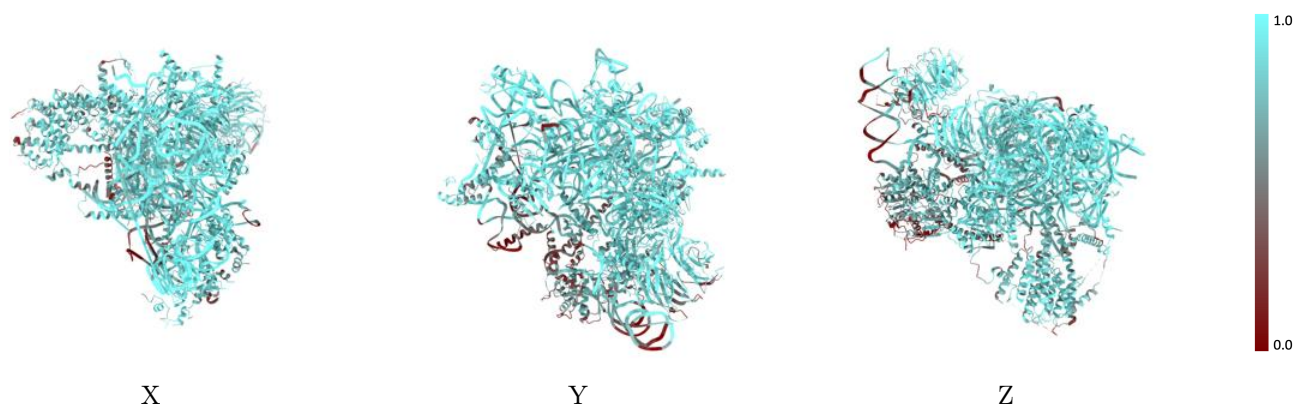
The images above show the 3D surface view of the map at the recommended contour level 0.012 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



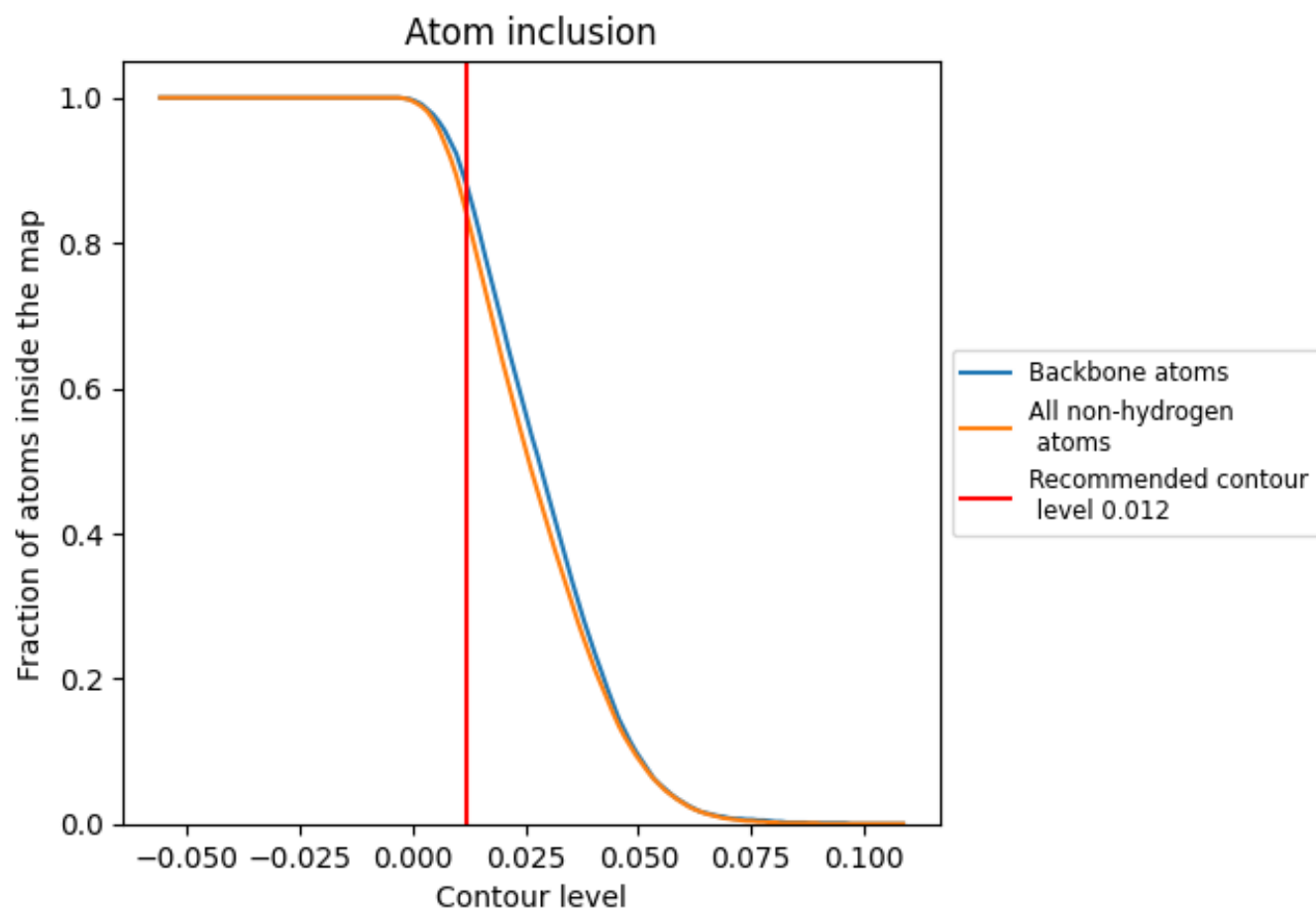
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.012).

9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 84% 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 (0.012) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8400	 0.5190
1	 0.8820	 0.5180
2	 0.9450	 0.5870
8	 0.8310	 0.5190
B	 0.8890	 0.4960
G	 0.9220	 0.5630
I	 0.7920	 0.4860
P	 0.8060	 0.5180
R	 0.8630	 0.5490
U	 0.8750	 0.5370
X	 0.9440	 0.5930
Z	 0.9460	 0.6070
b	 0.7740	 0.4770
c	 0.9370	 0.5790
d	 0.8460	 0.5550
g	 0.9540	 0.6010
j	 0.9120	 0.6040
k	 0.9010	 0.5760
m	 0.9490	 0.5980
n	 0.9470	 0.5950
p	 0.7910	 0.5200
t	 0.9090	 0.5980
u	 0.7830	 0.4630
w	 0.6350	 0.4580
x	 0.6010	 0.3860

