



## wwPDB EM Validation Summary Report ⓘ

May 4, 2025 – 02:49 PM EDT

PDB ID : 8ETJ / pdb\_00008etj  
EMDB ID : EMD-24396  
Title : Fkbp39 associated 60S nascent ribosome State 2  
Authors : Zhou, X.; Bilokapic, S.; Deshmukh, A.A.; Halic, M.  
Deposited on : 2022-10-17  
Resolution : 3.20 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.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

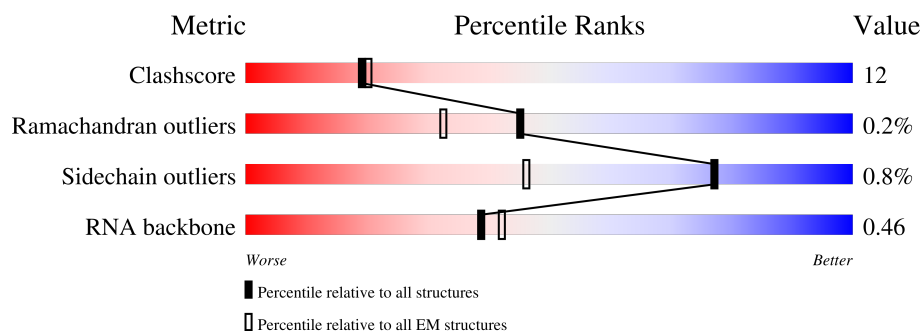
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.20 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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion  $< 40\%$ ). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	1	3497	
2	2	165	
3	3	302	
4	B	388	
5	C	363	
6	E	195	
7	F	250	

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Mol	Chain	Length	Quality of chain
8	G	259	
9	H	190	
10	L	208	
11	M	134	
12	N	201	
13	O	197	
14	P	187	
15	Q	187	
16	R	193	
17	S	176	
18	V	139	
19	W	241	
20	Y	126	
21	a	148	
22	b	642	
23	d	113	
24	e	127	
25	f	108	
26	h	122	
27	i	99	
28	j	91	
29	r	260	
30	s	470	
31	u	192	
32	w	802	

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Mol	Chain	Length	Quality of chain
33	y	244	<div><div><div></div><div></div><div></div></div><div>5%59%33%8%</div></div>
34	z	117	<div><div><div></div><div></div><div></div></div><div>16%14%70%</div></div>
35	T	160	<div><div><div></div><div></div><div></div></div><div>5%6%90%</div></div>

## 2 Entry composition

There are 36 unique types of molecules in this entry. The entry contains 79857 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 RNA (1758-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	1817	Total	C	N	O	P	0	0
			38913	17383	7069	12644	1817		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	2930	U	C	conflict	GB 157310483
1	2948	A	G	conflict	GB 157310483
1	3196	U	C	conflict	GB 157310483

- Molecule 2 is a RNA chain called RNA (144-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	144	Total	C	N	O	P	0	0
			3069	1373	551	1001	144		

- Molecule 3 is a protein called Protein mak16.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	123	Total	C	N	O	S	0	0
			1042	657	199	180	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	B	335	Total	C	N	O	S	0	0
			2662	1687	492	474	9		

- Molecule 5 is a protein called 60S ribosomal protein L4-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	C	325	Total	C	N	O	S	0	0
			2553	1620	483	447	3		

- Molecule 6 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	E	165	Total	C	N	O	S	0	0
			1283	822	237	221	3		

- Molecule 7 is a protein called 60S ribosomal protein L7-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	F	217	Total	C	N	O	S	0	0
			1750	1128	322	297	3		

- Molecule 8 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	G	168	Total	C	N	O	S	2	0
			1307	837	229	239	2		

- Molecule 9 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	H	183	Total	C	N	O	S	0	0
			1451	914	266	265	6		

- Molecule 10 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	L	180	Total	C	N	O	S	0	0
			1427	891	284	251	1		

- Molecule 11 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	M	125	Total	C	N	O	S	0	0
			1007	644	191	168	4		

- Molecule 12 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	N	166	Total	C	N	O	S	0	0
			1406	883	291	229	3		

- Molecule 13 is a protein called 60S ribosomal protein L16-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	O	196	Total	C	N	O	S	0	0
			1557	999	297	257	4		

- Molecule 14 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	P	156	Total	C	N	O	S	0	0
			1220	774	227	216	3		

- Molecule 15 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	Q	133	Total	C	N	O	S	0	0
			1032	650	199	182	1		

- Molecule 16 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	R	56	Total	C	N	O	0	0
			278	166	56	56		

- Molecule 17 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	S	168	Total	C	N	O	S	0	0
			1408	909	263	231	5		

- Molecule 18 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	V	137	Total	C	N	O	S	0	0
			1026	644	193	181	8		

- Molecule 19 is a protein called Ribosome assembly factor mrt4.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	W	215	Total	C	N	O	0	0
			1057	627	215	215		

- Molecule 20 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	Y	125	Total	C	N	O	S	0	0
			998	622	201	173	2		

- Molecule 21 is a protein called 60S ribosomal protein L28-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	a	94	Total	C	N	O		0	0
			747	474	142	131			

- Molecule 22 is a protein called Probable nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	b	415	Total	C	N	O	S	0	0
			2837	1765	535	534	3		

- Molecule 23 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	d	97	Total	C	N	O	S	0	0
			810	512	159	136	3		

- Molecule 24 is a protein called 60S ribosomal protein L32-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	e	118	Total	C	N	O	S	0	0
			944	591	191	157	5		

- Molecule 25 is a protein called 60S ribosomal protein L33-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	f	106	Total	C	N	O	S	0	0
			839	534	162	140	3		

- Molecule 26 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	h	121	Total	C	N	O		0	0
			999	629	194	176			

- Molecule 27 is a protein called 60S ribosomal protein L36-B.



Mol	Chain	Residues	Atoms					AltConf	Trace
27	i	94	Total	C	N	O	S	0	0
			748	466	155	126	1		

- Molecule 28 is a protein called 60S ribosomal protein L37-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	j	71	Total	C	N	O	S	0	0
			563	346	121	90	6		

- Molecule 29 is a protein called Ribosome biogenesis protein nsa2.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	r	166	Total	C	N	O	S	0	0
			1086	656	224	205	1		

- Molecule 30 is a protein called GTPase grn1.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	s	30	Total	C	N	O	0	0
			257	155	61	41		

- Molecule 31 is a protein called Ribosome biogenesis protein rlp24.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	u	114	Total	C	N	O	S	0	0
			944	598	190	147	9		

- Molecule 32 is a protein called AdoMet-dependent rRNA methyltransferase spb1.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	w	104	Total	C	N	O	1	0
			521	311	105	105		

- Molecule 33 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	y	225	Total	C	N	O	S	0	0
			1697	1058	293	341	5		

- Molecule 34 is a protein called UPF0642 protein C32H8.05.

Mol	Chain	Residues	Atoms				AltConf	Trace
34	z	35	Total	C	N	O	0	0
			292	183	63	46		

- Molecule 35 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
35	T	16	Total	C	N	O	0	0
			126	79	22	25		

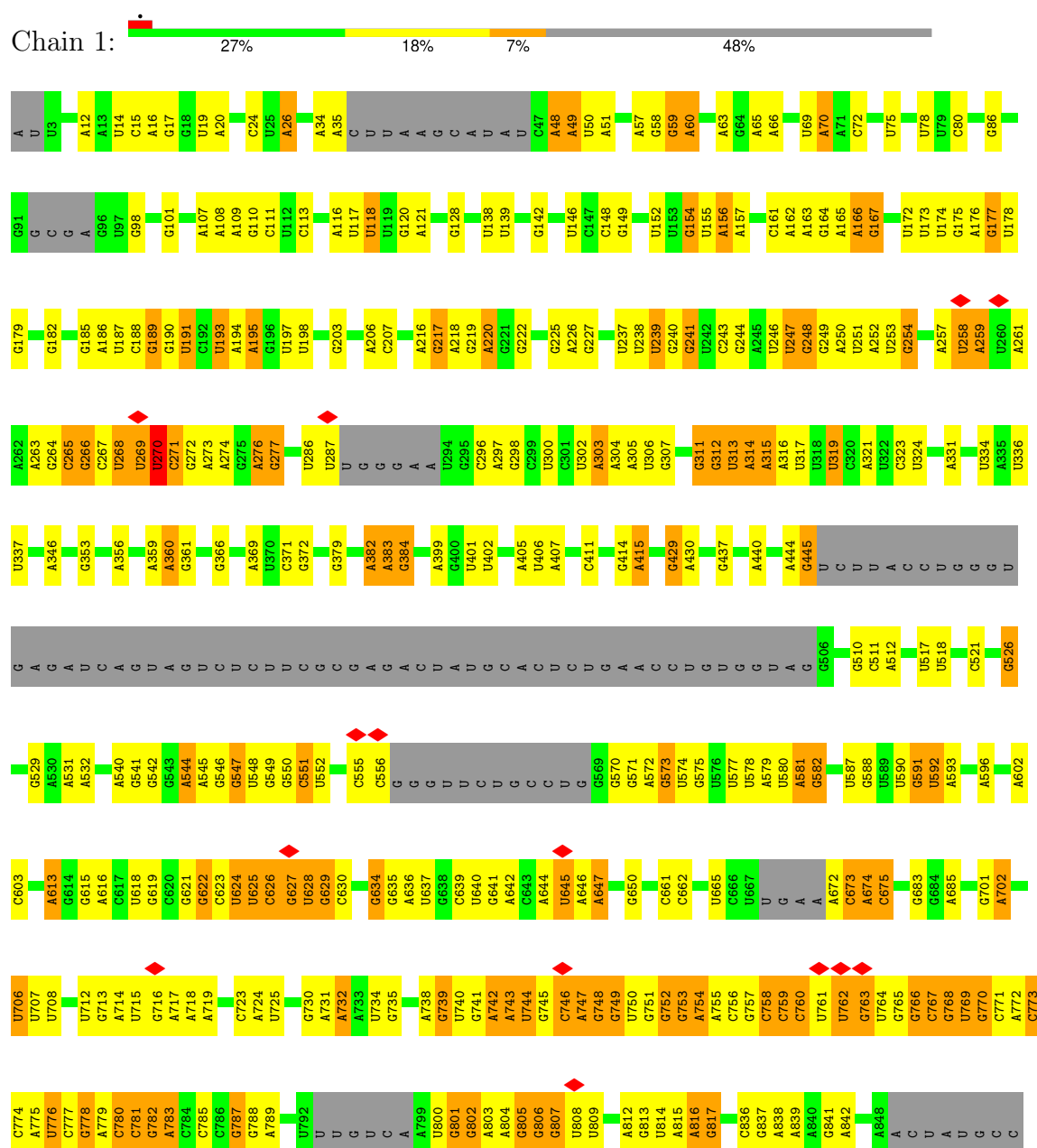
- Molecule 36 is ZINC ION (CCD ID: ZN) (formula: Zn).

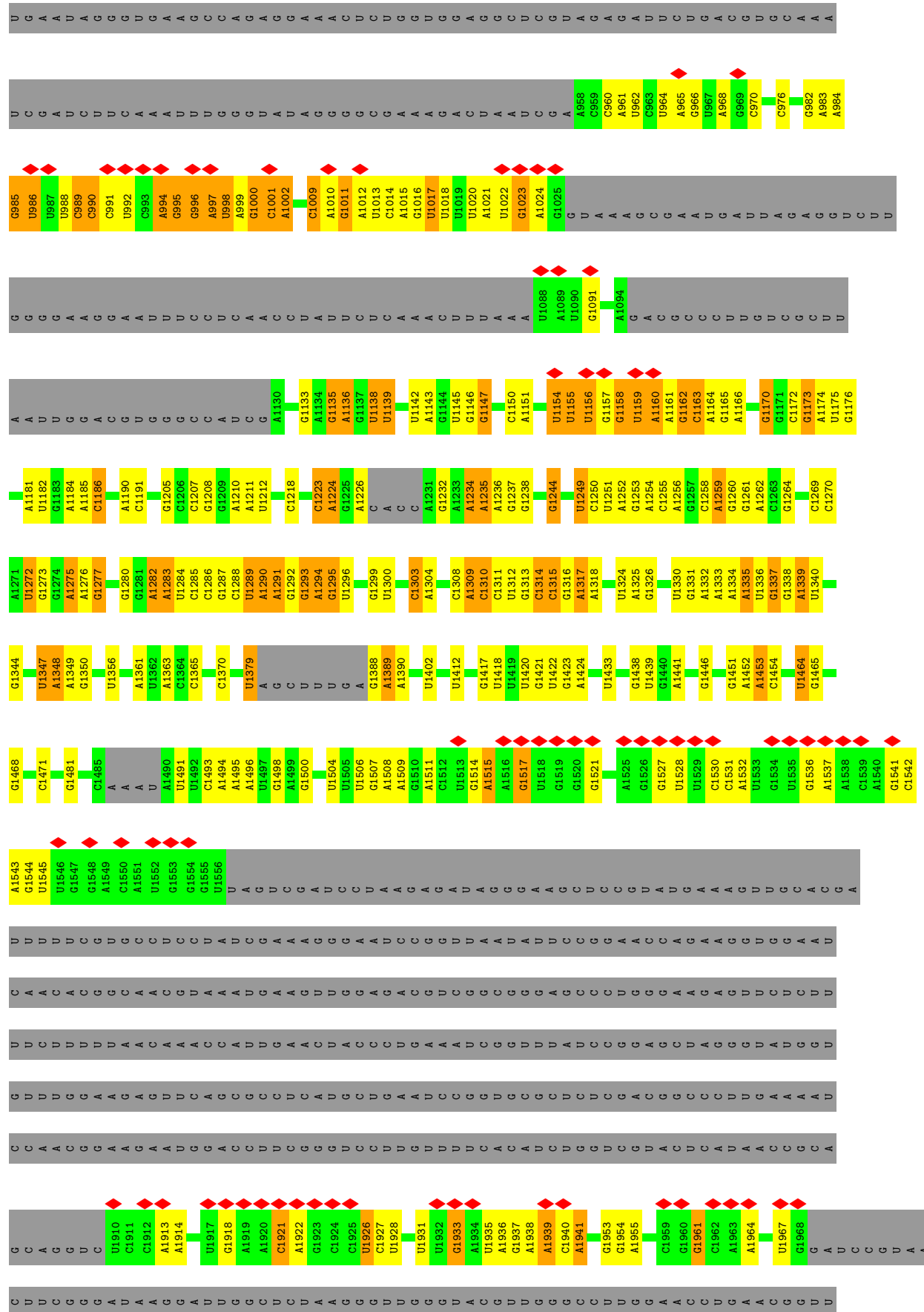
Mol	Chain	Residues	Atoms		AltConf
36	j	1	Total	Zn	0
			1	1	

### 3 Residue-property plots

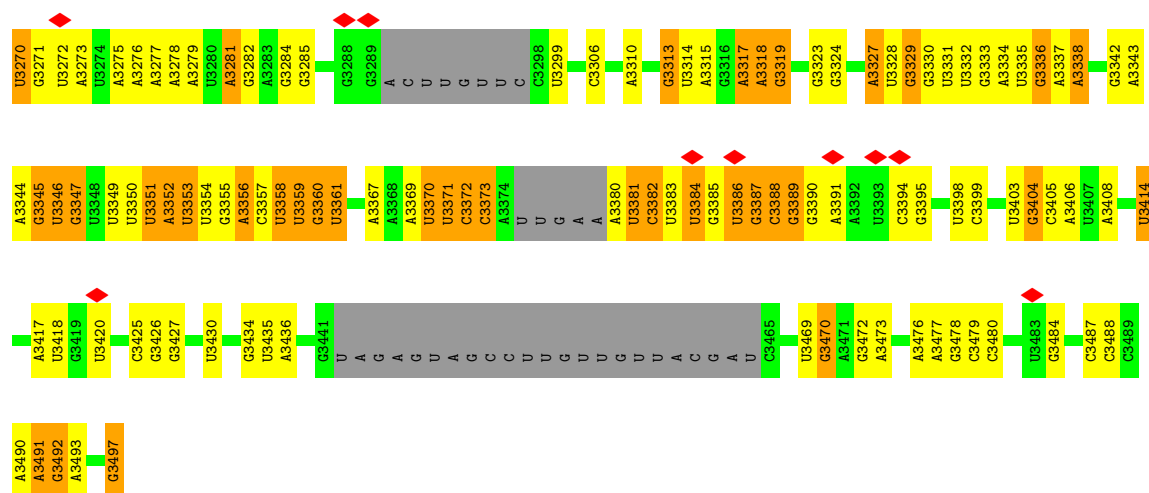
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: RNA (1758-MER)





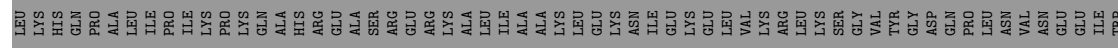
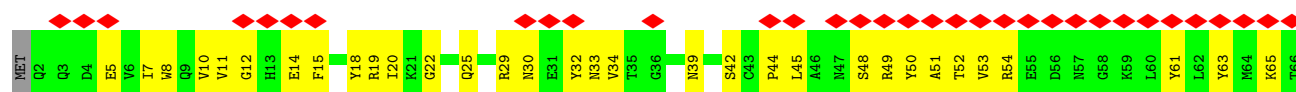




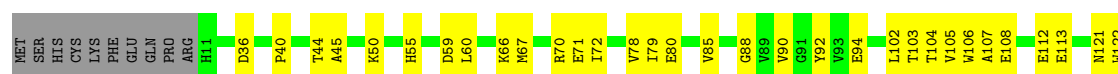
• Molecule 2: RNA (144-MER)

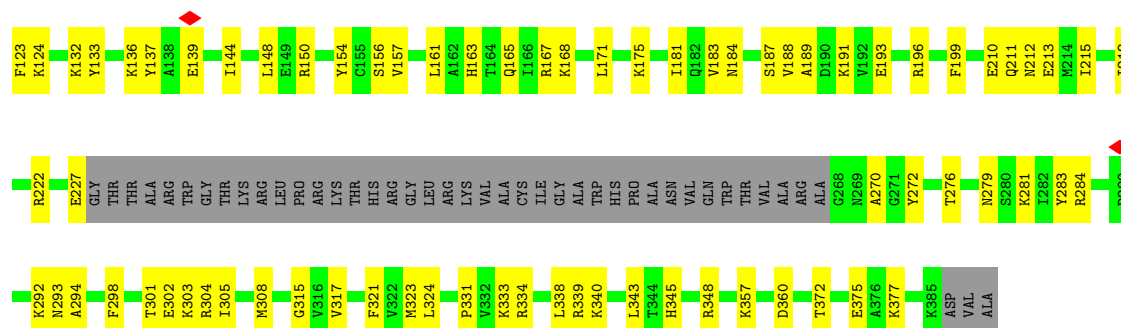


• Molecule 3: Protein mak16

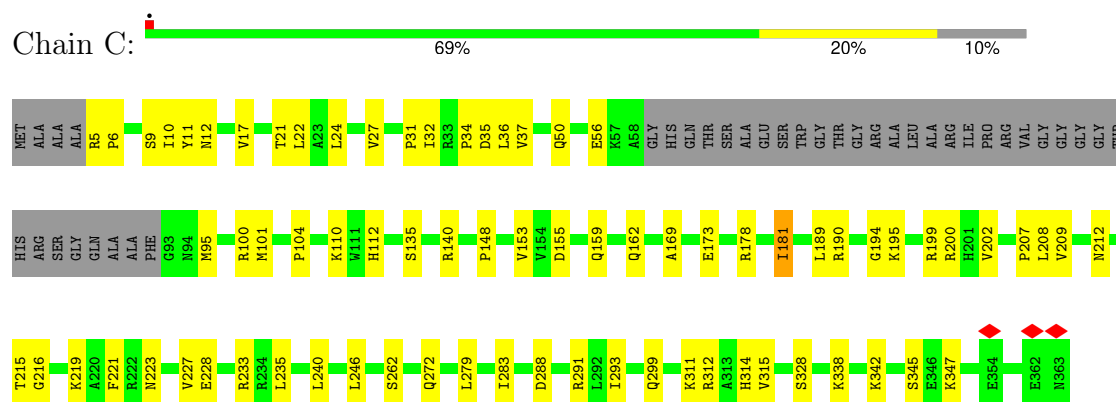


• Molecule 4: 60S ribosomal protein L3-A

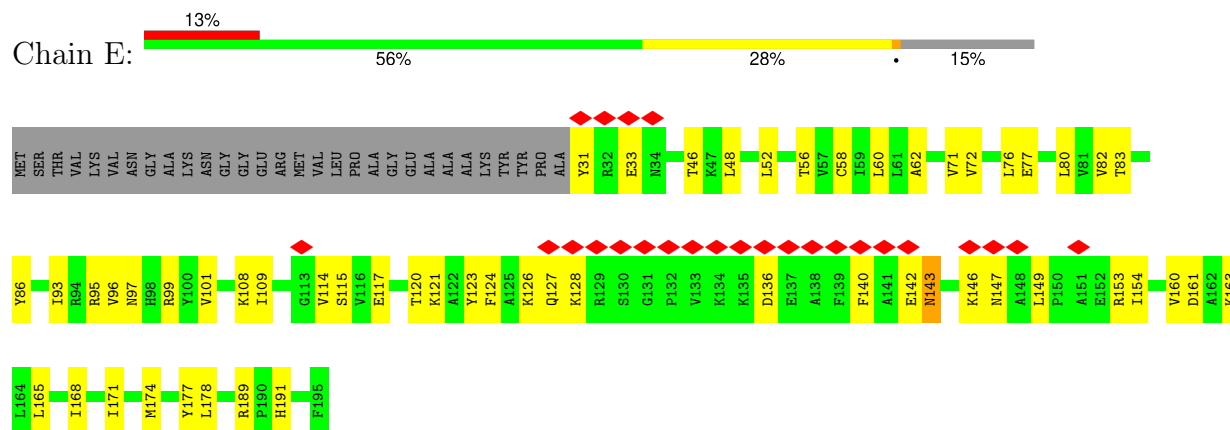




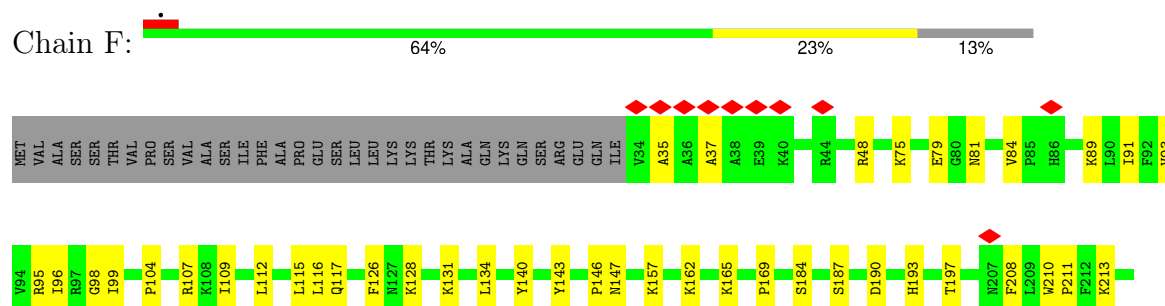
• Molecule 5: 60S ribosomal protein L4-B



• Molecule 6: 60S ribosomal protein L6

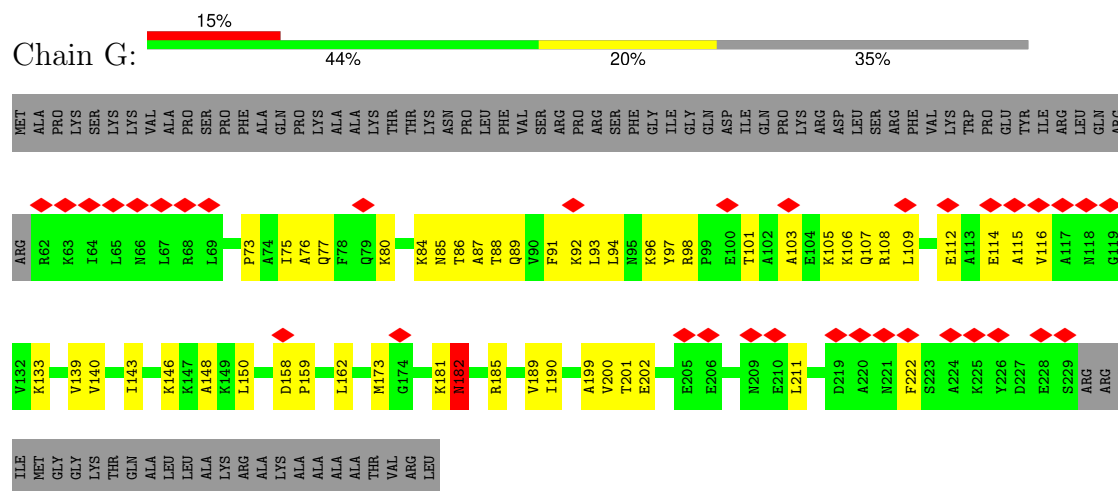


• Molecule 7: 60S ribosomal protein L7-B

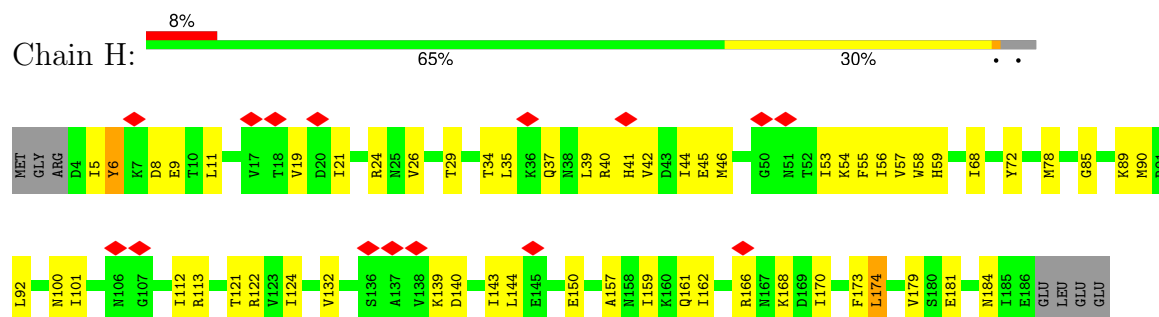




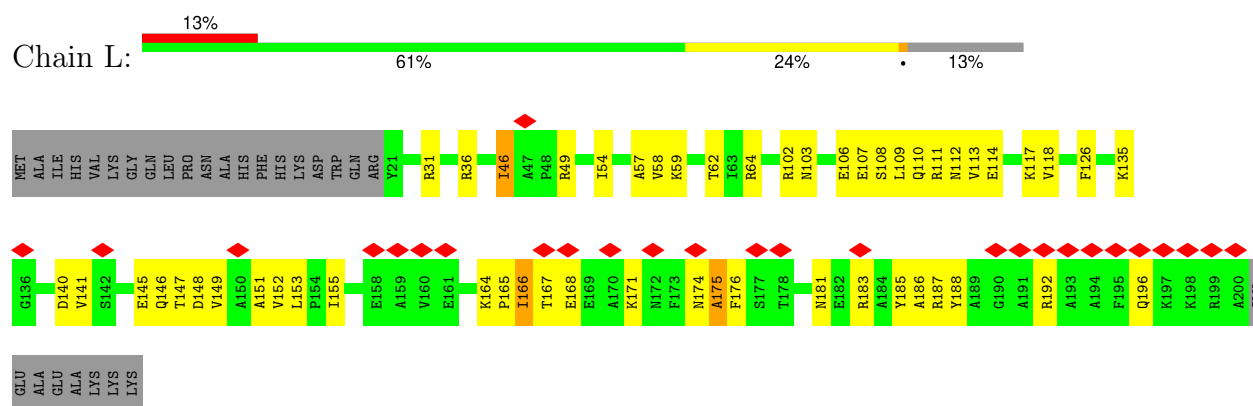
• Molecule 8: 60S ribosomal protein L8



• Molecule 9: 60S ribosomal protein L9-A



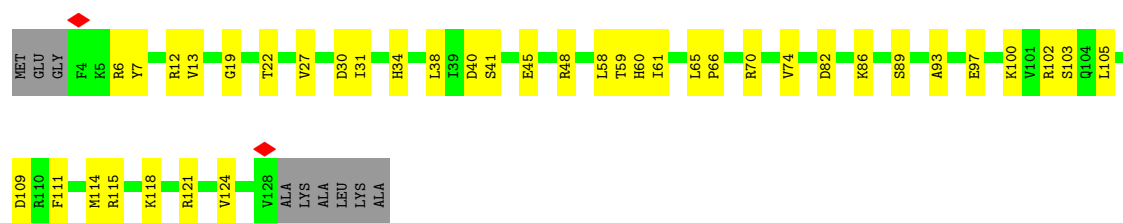
• Molecule 10: 60S ribosomal protein L13



• Molecule 11: 60S ribosomal protein L14

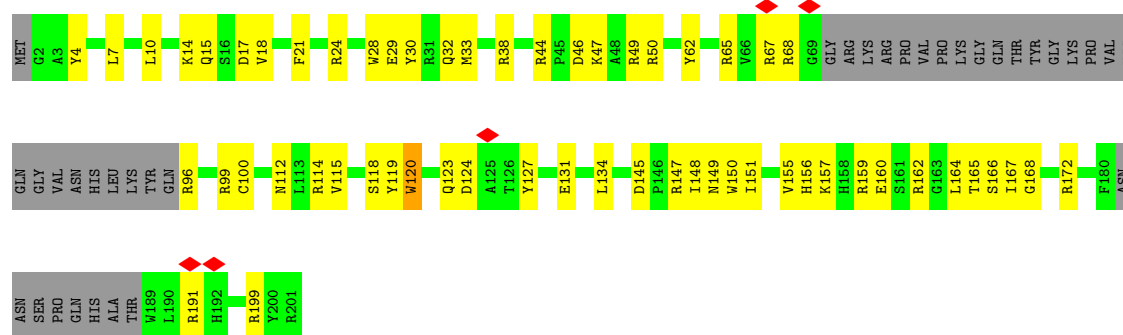






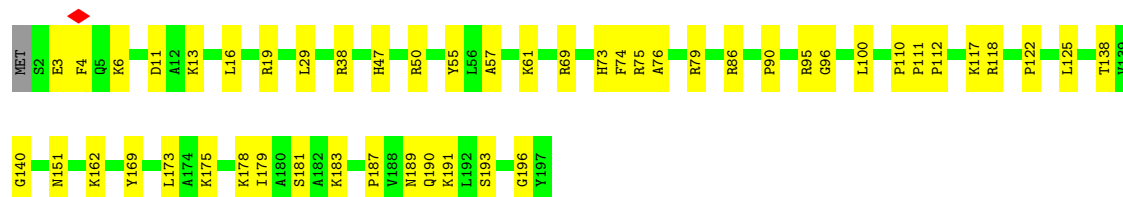
• Molecule 12: 60S ribosomal protein L15-A

Chain N: 54% 28% 17%



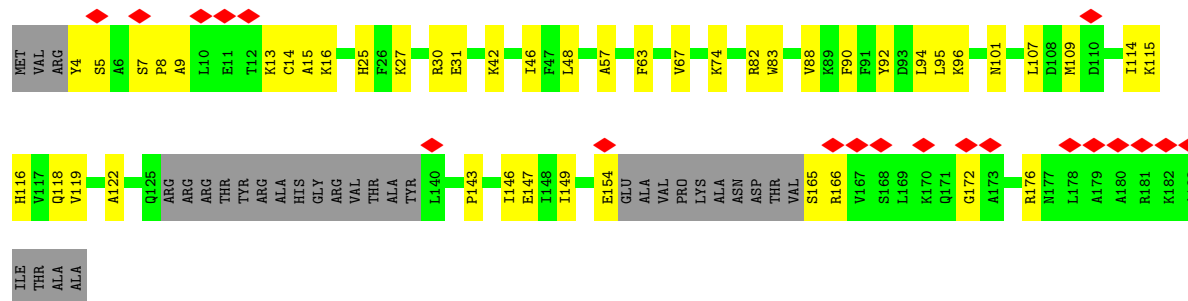
• Molecule 13: 60S ribosomal protein L16-B

Chain O: 75% 25%



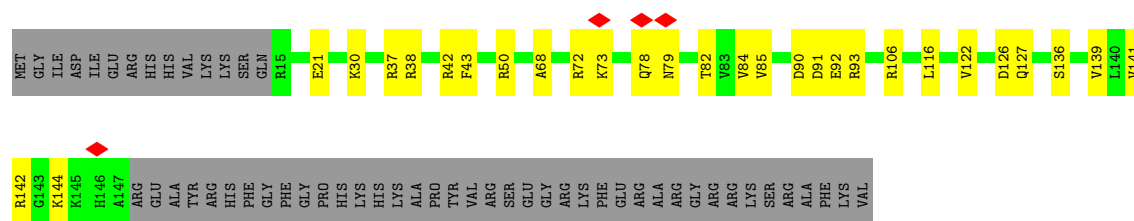
• Molecule 14: 60S ribosomal protein L17-A

Chain P: 11% 59% 25% 17%

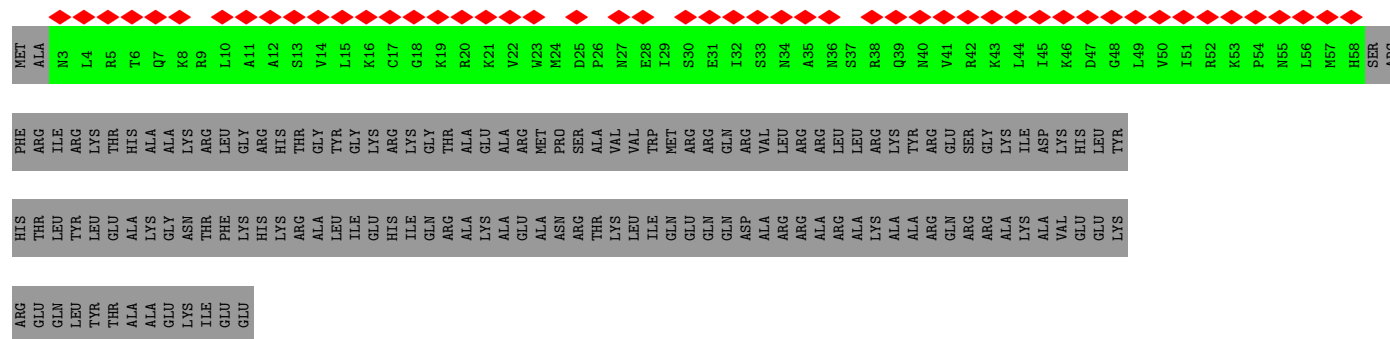


• Molecule 15: 60S ribosomal protein L18-A

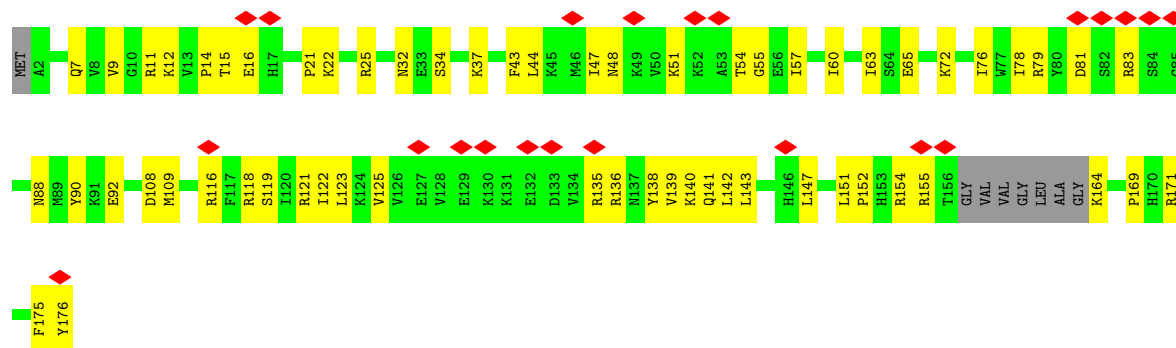
Chain Q: 56% 16% 29%



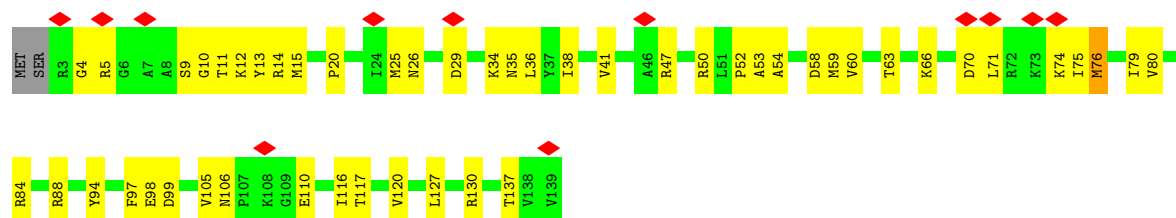
• Molecule 16: 60S ribosomal protein L19-A



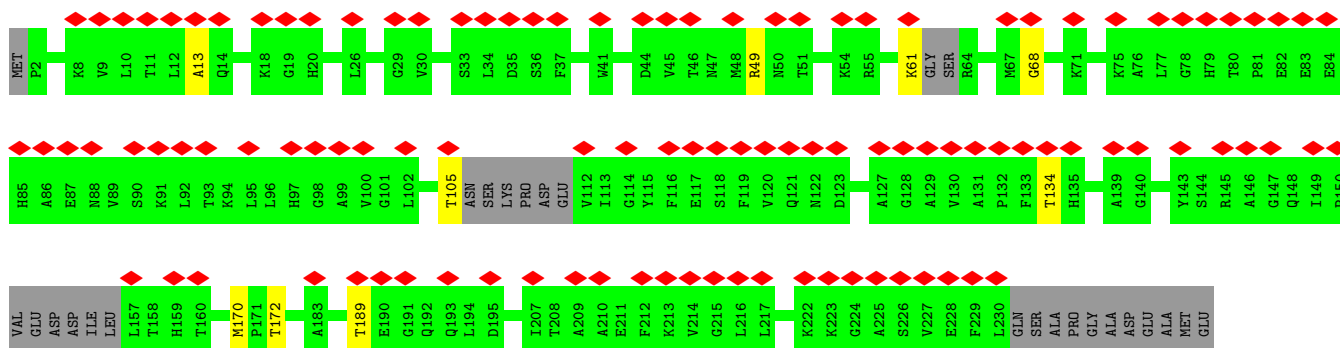
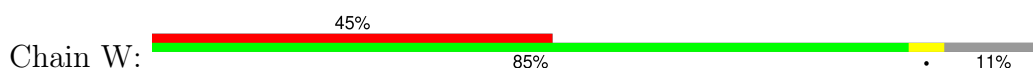
• Molecule 17: 60S ribosomal protein L20-A



• Molecule 18: 60S ribosomal protein L23-A



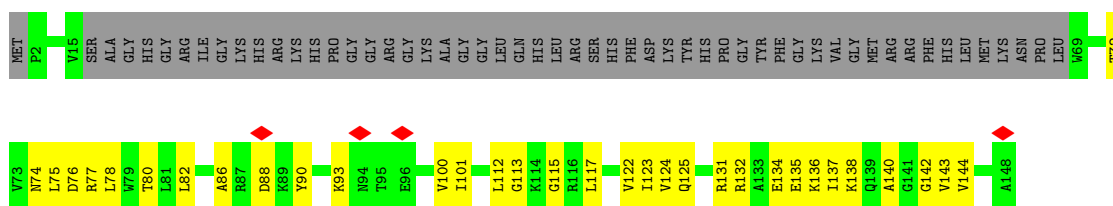
• Molecule 19: Ribosome assembly factor mrt4



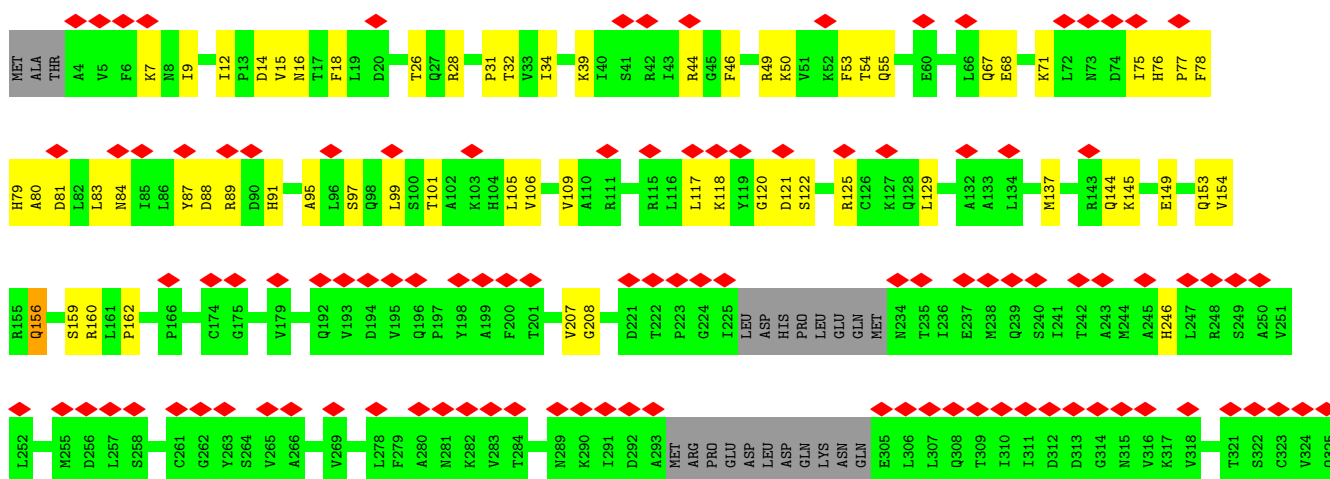
- Molecule 20: 60S ribosomal protein L26

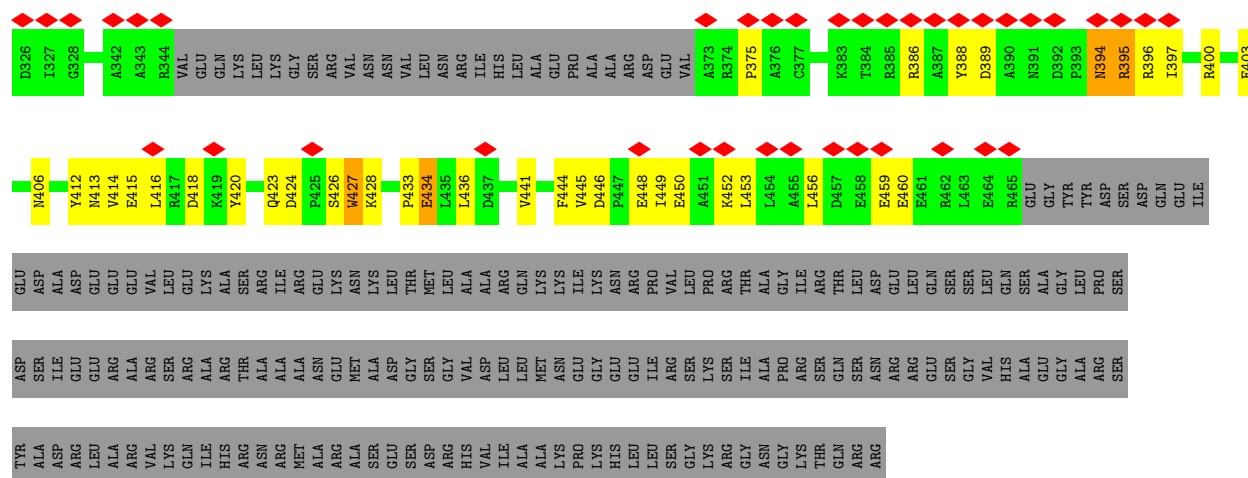


- Molecule 21: 60S ribosomal protein L28-A

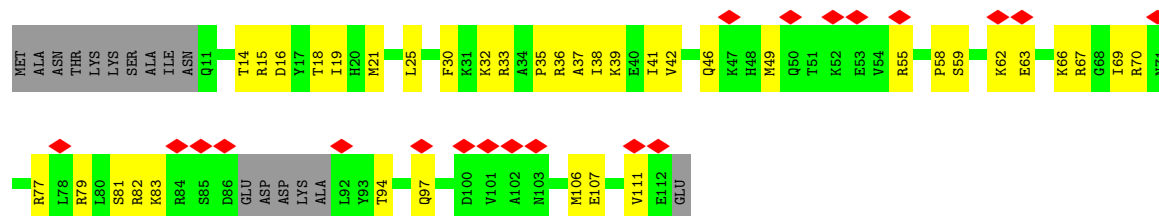


- Molecule 22: Probable nucleolar GTP-binding protein 1

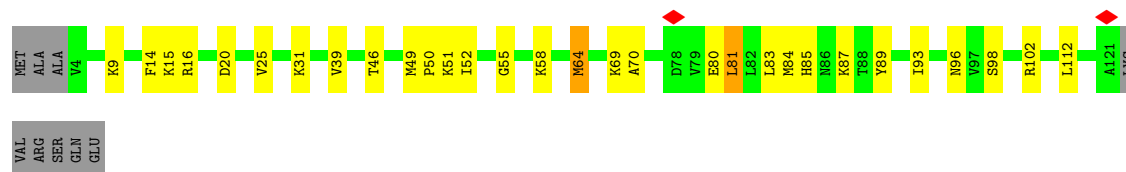




- Molecule 23: 60S ribosomal protein L31



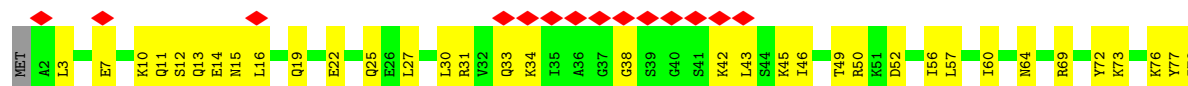
- Molecule 24: 60S ribosomal protein L32-A



- Molecule 25: 60S ribosomal protein L33-B



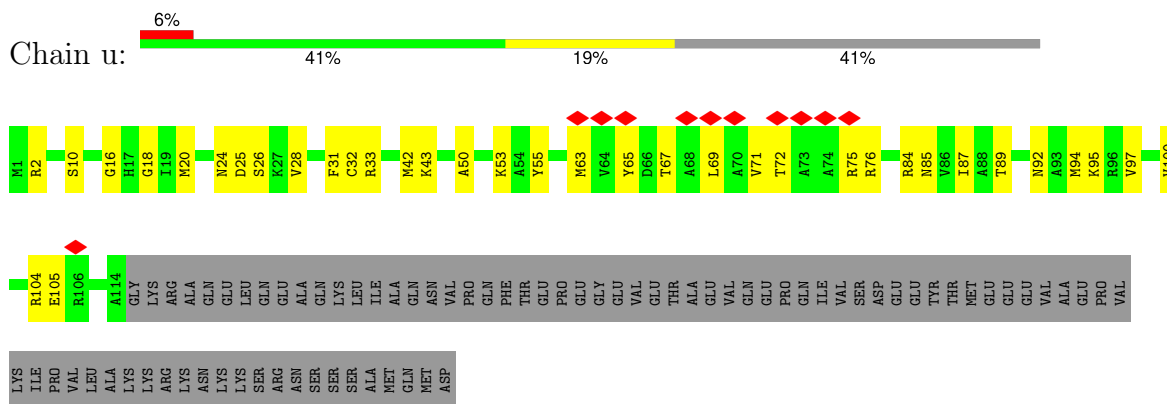
- Molecule 26: 60S ribosomal protein L35



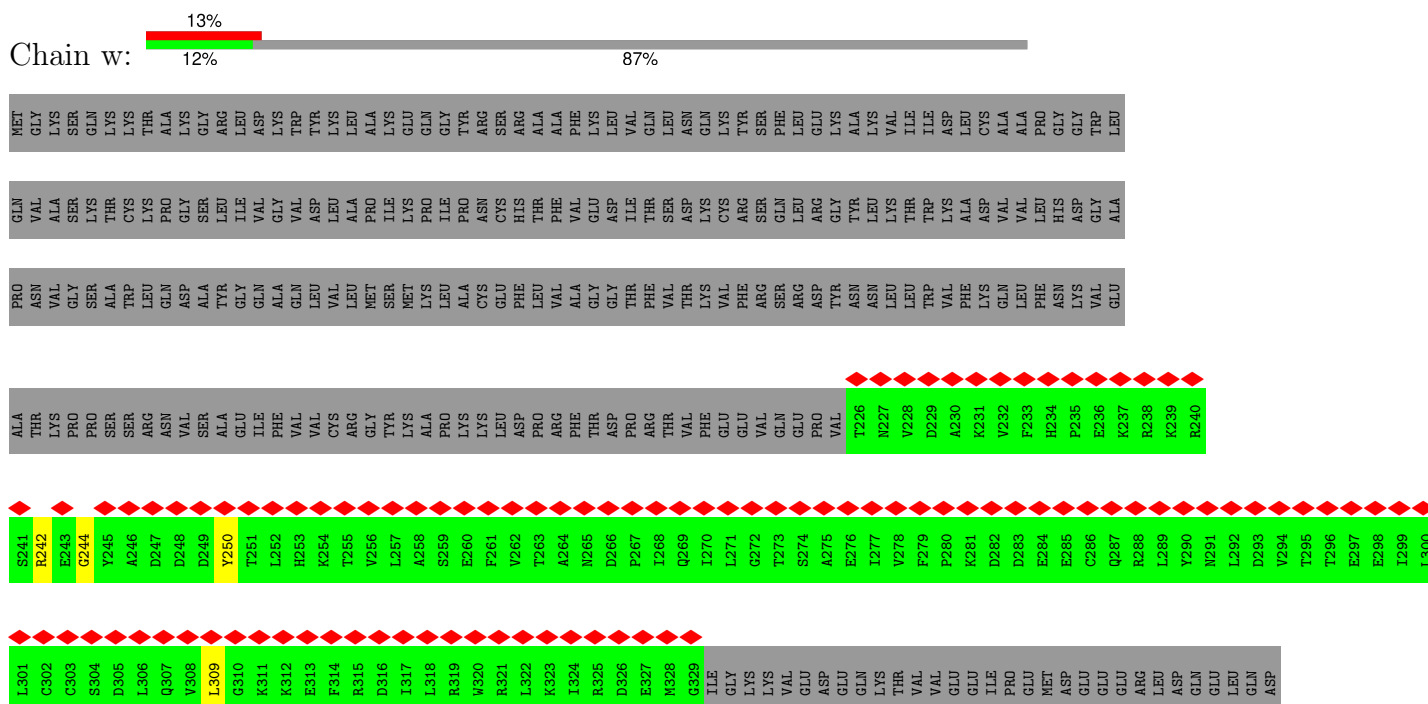


Ile	Gln	Ala	Ser	Val	Leu
Asn	Phe	Gly	Ser	Leu	Glu
Asp	Leu	Met	Thr	Ala	Gly
Trp	Ser	Thr	Ile	Ser	Ala
His	Arg	Thr	Ser	Ser	Pro
Ala	Val	Ser	Asn	Ala	Leu
Gly	Pro	Leu	Leu	Glu	Leu
Arg	Gly	Arg	Leu	Glu	Val
Ile	Gln	Glu	Lys	Lys	Asp
Glu	Leu	Val	Ser	Arg	Ser
Trp	Glu	Lys	Leu	Glu	Ser
Thr	Arg	Leu	Lys	Ile	Ser
Ala	Met	Asp	Ser	Phe	Tyr
Pro	Phe	Asn	Tyr	Val	Glu
Glu	Gln	Lys	Ser	Ile	Ala
Gly	Arg	Leu	Ala	Asn	Ser
Val	Tyr	Arg	Lys	Lys	Val
Ile	Glu	Leu	Lys	Ile	Lys
Asn	Leu	Val	Lys	Asp	Ala
Glu	Pro	Asp	Leu	Leu	Asp
Lys	Pro	Ser	Lys	Val	Thr
Asn	Leu	Pro	Ser	Pro	Ser
Ser	Leu	Asn	Ser	Ser	Arg
Ser	Asn	Ile	Leu	Glu	Lys
Glu	Thr	Val	Thr	Val	Ala
Val	Ser	Phe	Val	Leu	Tyr
Gln	Asp	Pro	Gly	Asn	Asp
Thr	Ile	Ser	Val	Lys	Lys
Thr	Asp	Ser	Ile	Trp	Glu
Thr	Asp	Asp	Gly	Val	Phe
Gln	Thr	Asp	Gly	Val	Lys
Ile	Ala	Ser	Tyr	Thr	Lys
Val	Thr	Lys	Pro	Tyr	Lys
Thr	Asp	Asp	Asn	Leu	Val
Glu	Phe	Asp	Val	Arg	Val
Trp	Leu	Leu	Gly	Asn	Glu
Ala	Val	Tyr	Lys	Phe	Ala
Lys	Asn	Arg	Ser	Phe	Ala
Glu	Ile	Leu	Ser	Phe	Ser
Phe	Ala	Val	Pro	Pro	Asp
		Val	Val	Thr	Val
		Met	Ile	Ile	Ile
		Leu	Asn	Pro	Leu
		Asn	Ala	Met	Tyr
		Ala	Ala	Arg	Val
		Val	Val	Ser	Leu
		Ser	Asn	Ala	Asp
		Ser	Arg	Ser	Ala
		Thr	Ser	Gly	Arg
		Lys	Ala	Ser	Asp
		Val	Asn	Gly	Pro
		Asp	Gly	Val	Glu
		Asp	Arg	Ser	Ser
		Thr	Ser	Leu	Thr
		Val	Ala	Lys	Arg
		Ala	Pro	Lys	Ser
		Val	Cys	His	Lys
		Thr	Pro	Gln	Val
		Ser	Ala	Ser	Ala
		Tyr	Gly	Ala	Val
		Thr	Gly	Glu	Ser
		Ile	Asn	Ser	Ala
		Thr	Val	Gln	Thr

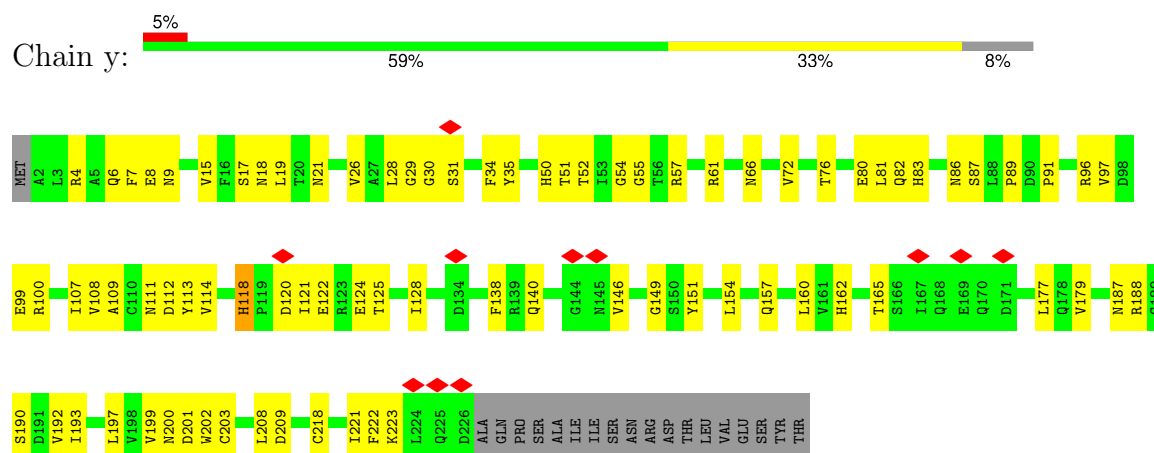
- Molecule 31: Ribosome biogenesis protein rlp24



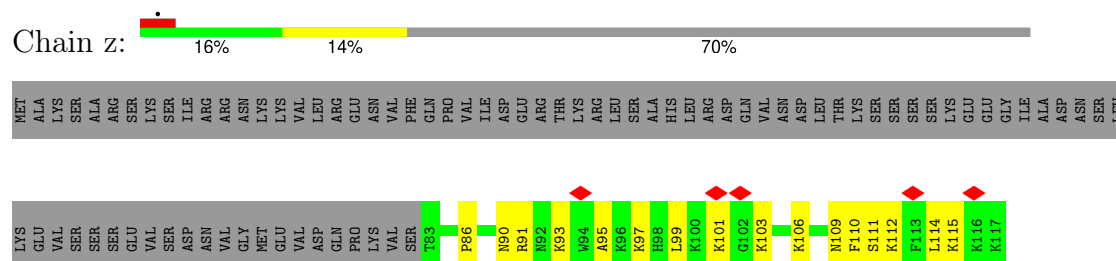
- Molecule 32: AdoMet-dependent rRNA methyltransferase *spb1*



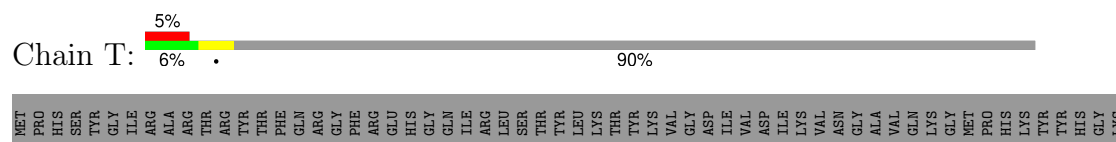
- Molecule 33: Eukaryotic translation initiation factor 6



- Molecule 34: UPF0642 protein C32H8.05



- Molecule 35: 60S ribosomal protein L21-A



ALA	GLN	GLY	LYS	THR	VAL	GLN	LEU	ARG	ARG	GLN	PRO	PRO	ALA	LYS	H138	H139	F140	V141	S142	T143	E144	N145	N146	E147	H152	P153	VAL	ALA	TYR	ASP	THR	THR	ILE
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	------	------	------	------	------	------	------	------	------	------	------	------	-----	-----	-----	-----	-----	-----	-----



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	22000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	60	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.402	Depositor
Minimum map value	-0.172	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.05	Depositor
Map size (Å)	542.72, 542.72, 542.72	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	Depositor

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

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

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	0.17	0/43553	0.26	1/67858 (0.0%)
2	2	0.15	0/3430	0.20	0/5335
3	3	0.18	0/1064	0.49	0/1431
4	B	0.20	0/2715	0.35	0/3647
5	C	0.22	0/2599	0.36	0/3505
6	E	0.20	0/1308	0.46	0/1763
7	F	0.21	0/1786	0.39	0/2399
8	G	0.18	0/1324	0.47	0/1790
9	H	0.18	0/1470	0.43	1/1982 (0.1%)
10	L	0.20	0/1452	0.45	0/1955
11	M	0.15	0/1024	0.36	0/1375
12	N	0.21	0/1436	0.42	0/1920
13	O	0.20	0/1588	0.36	0/2128
14	P	0.16	0/1240	0.37	0/1659
15	Q	0.16	0/1043	0.32	0/1401
16	R	0.05	0/277	0.18	0/385
17	S	0.17	0/1444	0.37	0/1939
18	V	0.18	0/1042	0.40	0/1402
19	W	0.08	0/1053	0.27	0/1457
20	Y	0.20	0/1008	0.42	0/1341
21	a	0.20	0/760	0.49	0/1026
22	b	0.21	0/2868	0.50	1/3902 (0.0%)
23	d	0.18	0/824	0.43	0/1106
24	e	0.21	0/958	0.35	0/1278
25	f	0.23	0/859	0.37	0/1152
26	h	0.20	0/1008	0.48	0/1340
27	i	0.18	0/755	0.54	0/1003
28	j	0.15	0/575	0.35	0/761
29	r	0.14	0/1091	0.36	0/1464
30	s	0.13	0/256	0.36	0/329
31	u	0.17	0/966	0.41	0/1292
32	w	0.06	0/520	0.23	0/724

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
33	y	0.16	0/1720	0.39	0/2345
34	z	0.22	0/297	0.56	0/388
35	T	0.22	0/130	0.53	0/179
All	All	0.18	0/85443	0.33	3/124961 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	b	12	ILE	N-CA-C	7.75	115.30	108.63
9	H	6	TYR	N-CA-C	6.05	120.33	107.70
1	1	270	U	C4'-C3'-O3'	5.01	116.92	109.40

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	38913	0	19569	685	0
2	2	3069	0	1553	39	0
3	3	1042	0	1046	49	0
4	B	2662	0	2742	78	0
5	C	2553	0	2687	58	0
6	E	1283	0	1365	43	0
7	F	1750	0	1818	46	0
8	G	1307	0	1385	34	0
9	H	1451	0	1511	49	0
10	L	1427	0	1482	48	0
11	M	1007	0	1072	34	0
12	N	1406	0	1441	50	0
13	O	1557	0	1652	43	0
14	P	1220	0	1256	42	0
15	Q	1032	0	1129	25	0
16	R	278	0	120	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
17	S	1408	0	1462	54	0
18	V	1026	0	1076	50	0
19	W	1057	0	487	6	0
20	Y	998	0	1090	29	0
21	a	747	0	790	38	0
22	b	2837	0	2413	92	0
23	d	810	0	852	39	0
24	e	944	0	1005	25	0
25	f	839	0	866	26	0
26	h	999	0	1092	44	0
27	i	748	0	827	36	0
28	j	563	0	578	17	0
29	r	1086	0	842	39	0
30	s	257	0	304	5	0
31	u	944	0	983	34	0
32	w	521	0	224	4	0
33	y	1697	0	1679	64	0
34	z	292	0	317	16	0
35	T	126	0	113	11	0
36	j	1	0	0	0	0
All	All	79857	0	58828	1656	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 12.

The worst 5 of 1656 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)
21:a:75:LEU:HA	21:a:78:LEU:HD23	1.48	0.95
22:b:456:LEU:HD13	31:u:69:LEU:HA	1.49	0.95
1:l:157:A:H5''	26:h:104:LEU:HD21	1.49	0.93
10:L:166:ILE:HG13	10:L:167:THR:H	1.34	0.93
1:l:3269:A:H4'	1:l:3270:U:H5'	1.49	0.92

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	3	121/302 (40%)	115 (95%)	6 (5%)	0	100	100
4	B	331/388 (85%)	320 (97%)	11 (3%)	0	100	100
5	C	321/363 (88%)	308 (96%)	13 (4%)	0	100	100
6	E	163/195 (84%)	144 (88%)	17 (10%)	2 (1%)	11	43
7	F	215/250 (86%)	202 (94%)	13 (6%)	0	100	100
8	G	168/259 (65%)	151 (90%)	14 (8%)	3 (2%)	7	35
9	H	181/190 (95%)	168 (93%)	13 (7%)	0	100	100
10	L	178/208 (86%)	161 (90%)	15 (8%)	2 (1%)	12	44
11	M	123/134 (92%)	115 (94%)	7 (6%)	1 (1%)	16	51
12	N	160/201 (80%)	156 (98%)	4 (2%)	0	100	100
13	O	194/197 (98%)	190 (98%)	4 (2%)	0	100	100
14	P	150/187 (80%)	144 (96%)	6 (4%)	0	100	100
15	Q	131/187 (70%)	127 (97%)	4 (3%)	0	100	100
16	R	54/193 (28%)	53 (98%)	1 (2%)	0	100	100
17	S	164/176 (93%)	153 (93%)	11 (7%)	0	100	100
18	V	135/139 (97%)	130 (96%)	5 (4%)	0	100	100
19	W	207/241 (86%)	195 (94%)	12 (6%)	0	100	100
20	Y	123/126 (98%)	115 (94%)	8 (6%)	0	100	100
21	a	90/148 (61%)	86 (96%)	4 (4%)	0	100	100
22	b	407/642 (63%)	388 (95%)	17 (4%)	2 (0%)	25	60
23	d	93/113 (82%)	90 (97%)	3 (3%)	0	100	100
24	e	116/127 (91%)	115 (99%)	1 (1%)	0	100	100
25	f	104/108 (96%)	95 (91%)	9 (9%)	0	100	100
26	h	119/122 (98%)	117 (98%)	2 (2%)	0	100	100
27	i	92/99 (93%)	87 (95%)	5 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	j	69/91 (76%)	64 (93%)	5 (7%)	0	100	100
29	r	158/260 (61%)	157 (99%)	1 (1%)	0	100	100
30	s	28/470 (6%)	27 (96%)	1 (4%)	0	100	100
31	u	112/192 (58%)	106 (95%)	6 (5%)	0	100	100
32	w	103/802 (13%)	100 (97%)	3 (3%)	0	100	100
33	y	223/244 (91%)	209 (94%)	14 (6%)	0	100	100
34	z	33/117 (28%)	30 (91%)	3 (9%)	0	100	100
35	T	14/160 (9%)	12 (86%)	2 (14%)	0	100	100
All	All	4880/7631 (64%)	4630 (95%)	240 (5%)	10 (0%)	45	75

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
10	L	175	ALA
6	E	143	ASN
22	b	427	TRP
6	E	136	ASP
8	G	222	PHE

### 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	3	111/271 (41%)	110 (99%)	1 (1%)	75	89
4	B	284/326 (87%)	284 (100%)	0	100	100
5	C	275/297 (93%)	274 (100%)	1 (0%)	89	94
6	E	135/155 (87%)	134 (99%)	1 (1%)	81	92
7	F	178/210 (85%)	178 (100%)	0	100	100
8	G	139/212 (66%)	135 (97%)	4 (3%)	37	67
9	H	164/170 (96%)	163 (99%)	1 (1%)	84	92
10	L	144/167 (86%)	143 (99%)	1 (1%)	81	92

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	M	108/113 (96%)	107 (99%)	1 (1%)	75	89
12	N	146/176 (83%)	145 (99%)	1 (1%)	81	92
13	O	161/162 (99%)	161 (100%)	0	100	100
14	P	125/149 (84%)	125 (100%)	0	100	100
15	Q	114/159 (72%)	114 (100%)	0	100	100
17	S	150/154 (97%)	149 (99%)	1 (1%)	81	92
18	V	105/107 (98%)	104 (99%)	1 (1%)	73	87
20	Y	110/111 (99%)	108 (98%)	2 (2%)	54	77
21	a	81/122 (66%)	81 (100%)	0	100	100
22	b	214/556 (38%)	208 (97%)	6 (3%)	38	68
23	d	89/102 (87%)	89 (100%)	0	100	100
24	e	100/107 (94%)	97 (97%)	3 (3%)	36	66
25	f	89/91 (98%)	88 (99%)	1 (1%)	70	86
26	h	106/107 (99%)	102 (96%)	4 (4%)	28	60
27	i	80/84 (95%)	79 (99%)	1 (1%)	65	83
28	j	58/71 (82%)	58 (100%)	0	100	100
29	r	63/224 (28%)	63 (100%)	0	100	100
30	s	28/409 (7%)	28 (100%)	0	100	100
31	u	99/168 (59%)	99 (100%)	0	100	100
33	y	189/206 (92%)	188 (100%)	1 (0%)	86	93
34	z	31/107 (29%)	31 (100%)	0	100	100
35	T	15/139 (11%)	15 (100%)	0	100	100
All	All	3691/5432 (68%)	3660 (99%)	31 (1%)	77	90

5 of 31 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
20	Y	96	VAL
26	h	94	LEU
22	b	394	ASN
27	i	5	LEU
25	f	99	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 38 such sidechains are listed below:

Mol	Chain	Res	Type
25	f	43	GLN
33	y	82	GLN
25	f	89	ASN
27	i	93	GLN
35	T	139	HIS

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	1793/3497 (51%)	474 (26%)	28 (1%)
2	2	140/165 (84%)	26 (18%)	1 (0%)
All	All	1933/3662 (52%)	500 (25%)	29 (1%)

5 of 500 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	12	A
1	1	14	U
1	1	26	A
1	1	48	A
1	1	49	A

5 of 29 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	1272	U
1	1	3387	G
1	1	1338	G
1	1	3268	U
1	1	1333	A

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

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

## 5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.



## 5.6 Ligand geometry

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

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

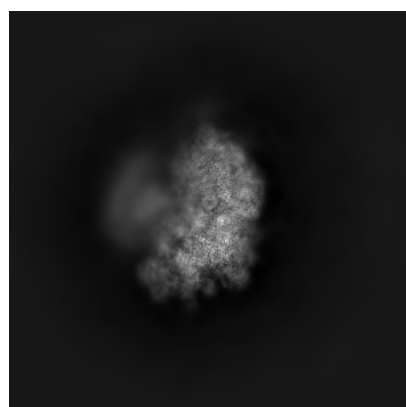
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-24396. These allow visual inspection of the internal detail of the map and identification of artifacts.

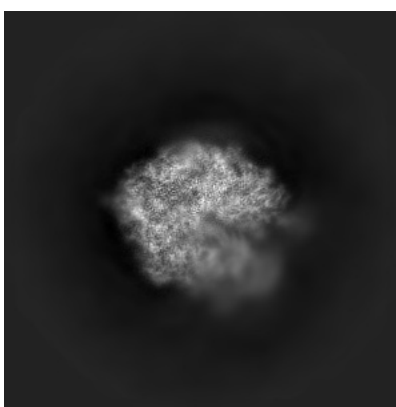
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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

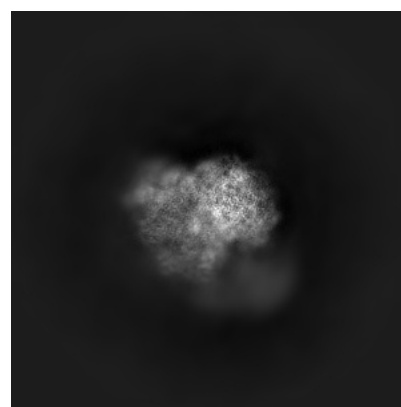
#### 6.1.1 Primary map



X



Y

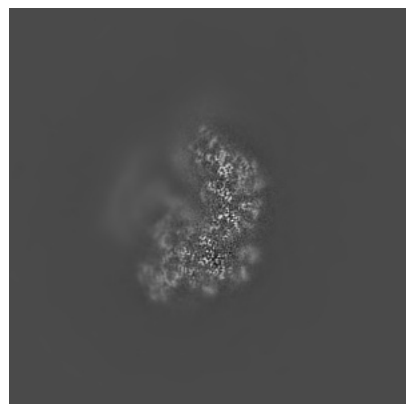


Z

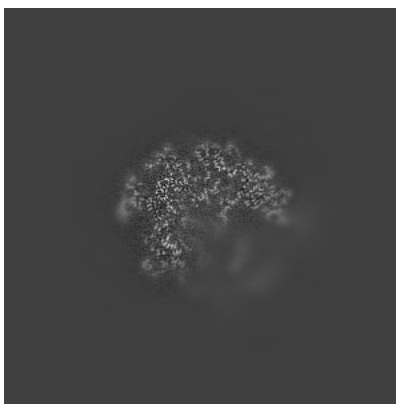
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

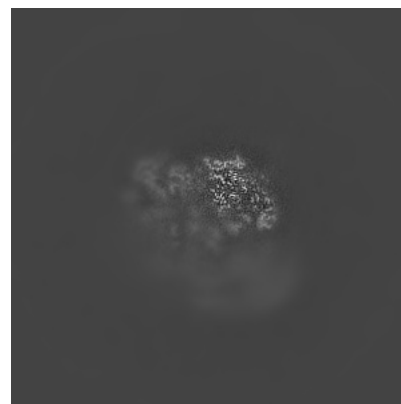
#### 6.2.1 Primary map



X Index: 256



Y Index: 256

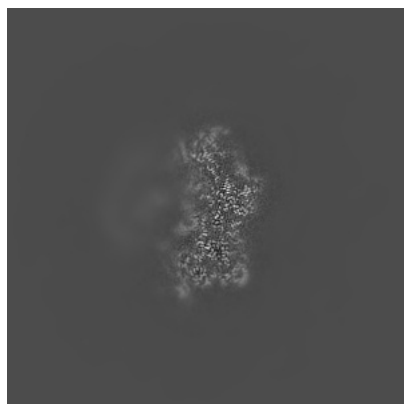


Z Index: 256

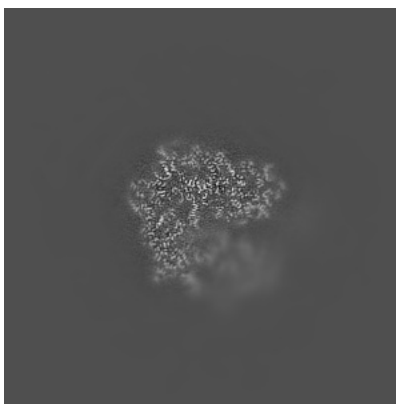
The images above show central slices of the map in three orthogonal directions.

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

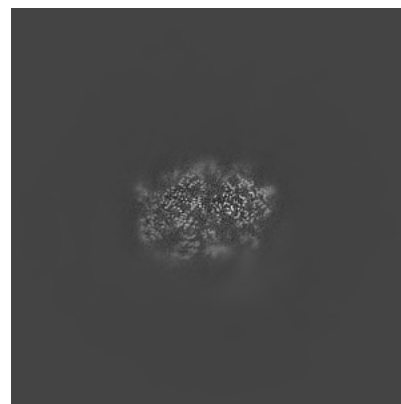
### 6.3.1 Primary map



X Index: 282



Y Index: 272

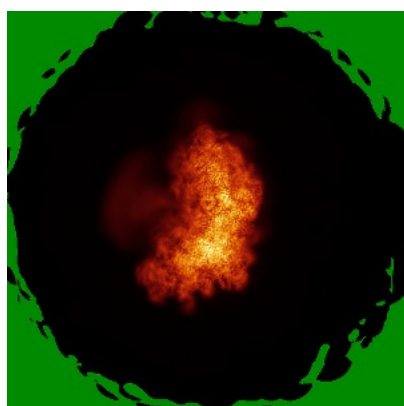


Z Index: 204

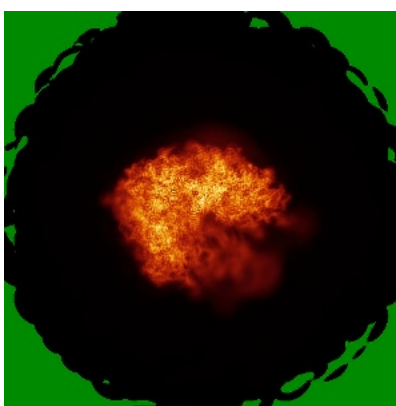
The images above show the largest variance slices of the map in three orthogonal directions.

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

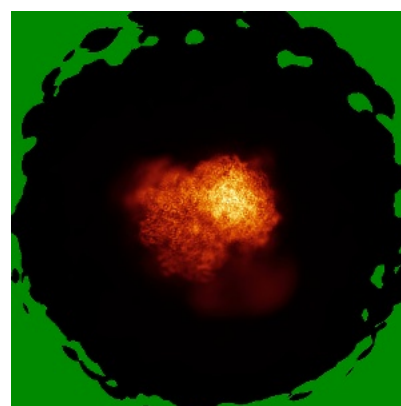
### 6.4.1 Primary map



X



Y

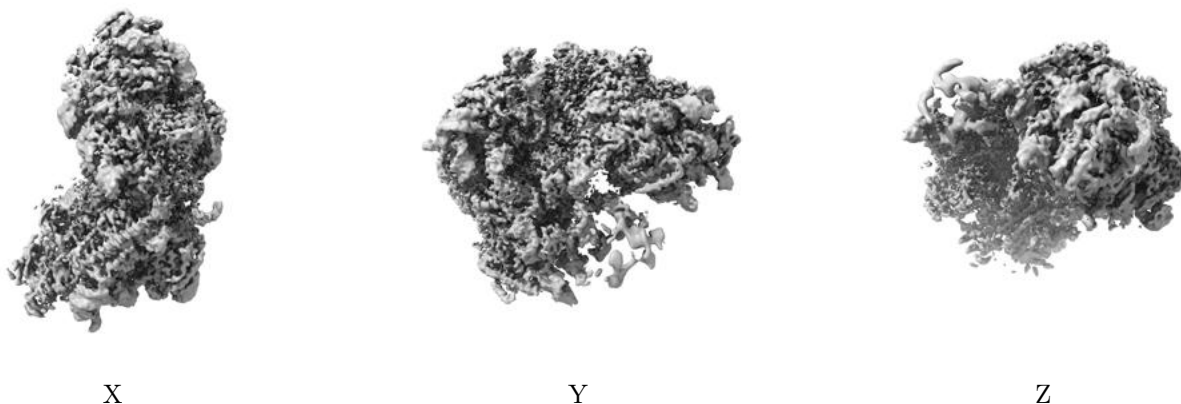


Z

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



The images above show the 3D surface view of the map at the recommended contour level 0.05. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

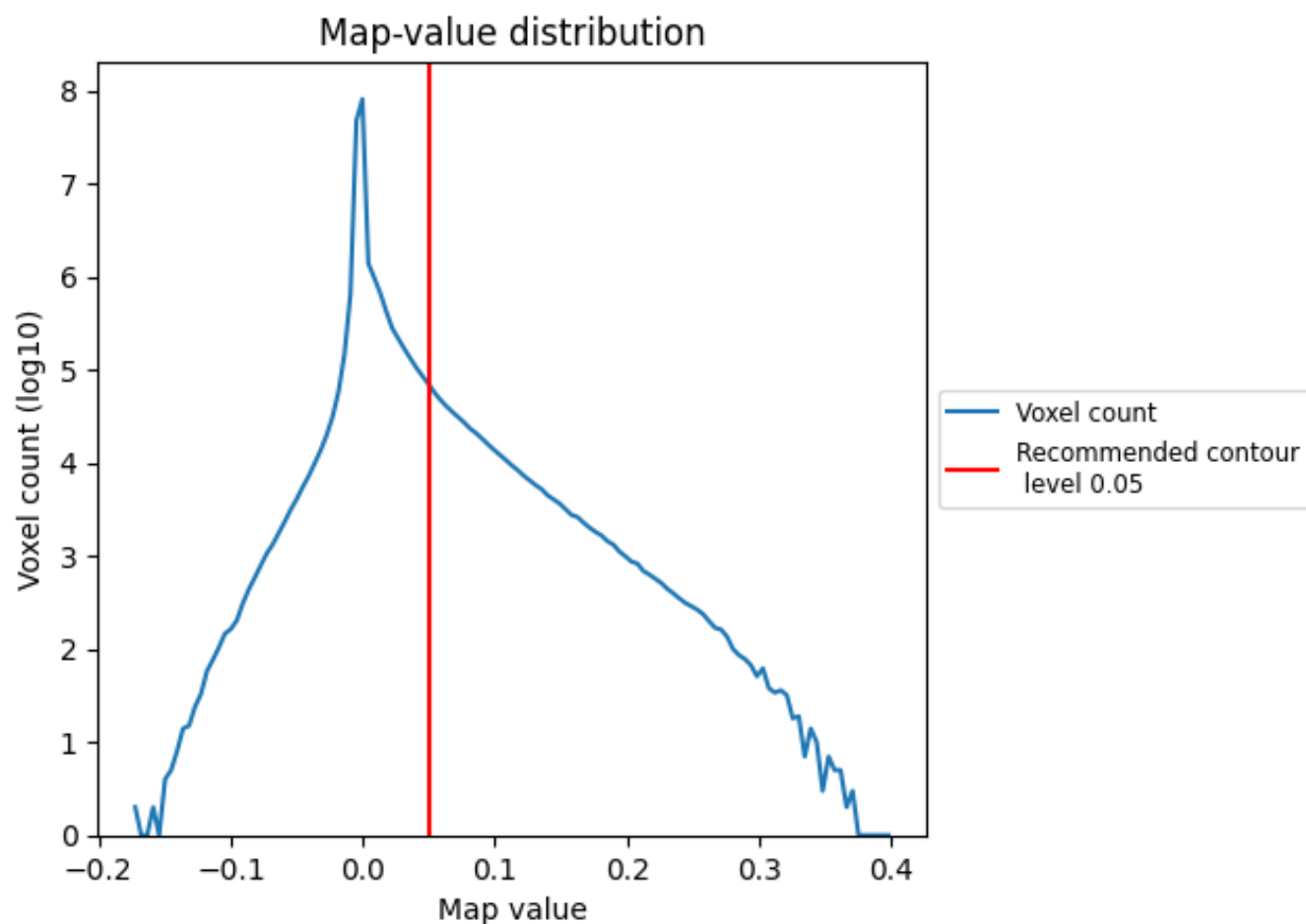
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

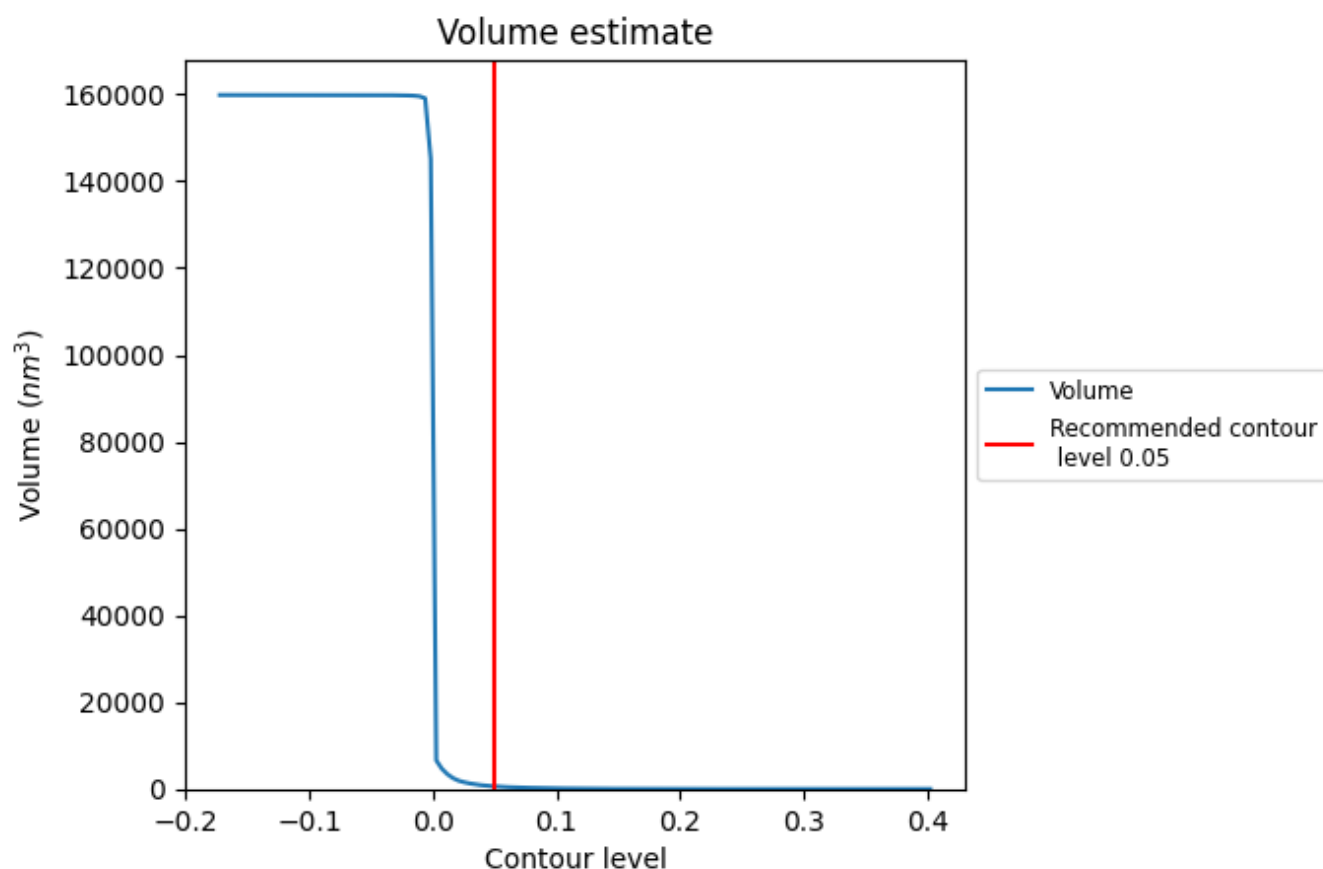
This section contains the results of statistical analysis of the map.

### 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.

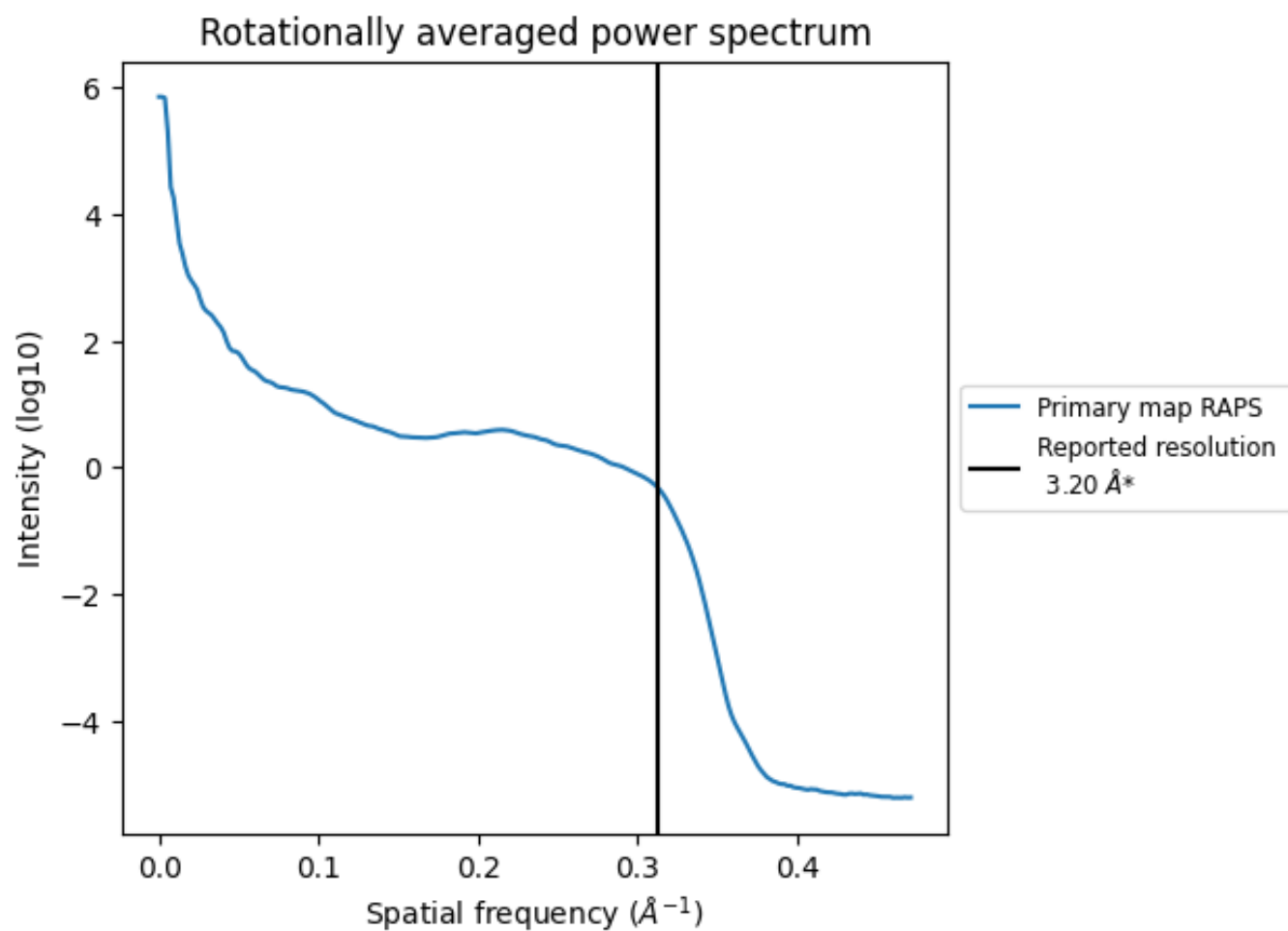
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 598  $\text{nm}^3$ ; this corresponds to an approximate mass of 540 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 0.312 Å<sup>-1</sup>

## 8 Fourier-Shell correlation

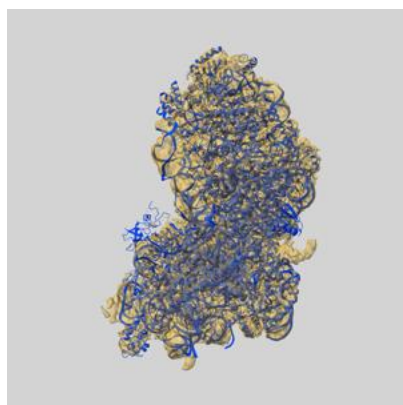
This section was not generated. No FSC curve or half-maps provided.



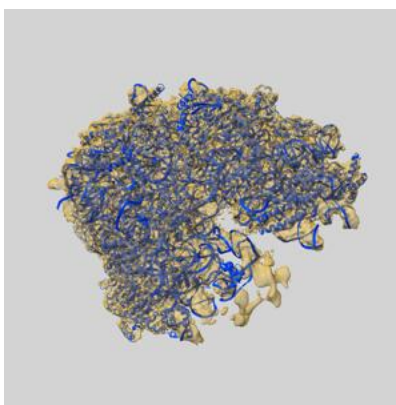
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-24396 and PDB model 8ETJ. Per-residue inclusion information can be found in section [3](#) on page [11](#).

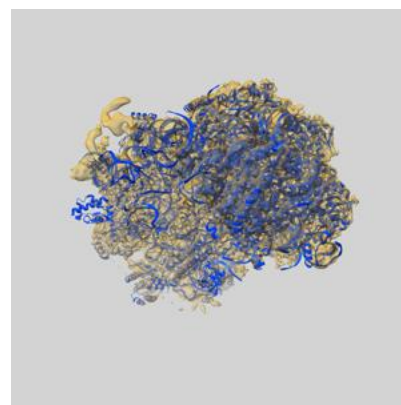
### 9.1 Map-model overlay [i](#)



X



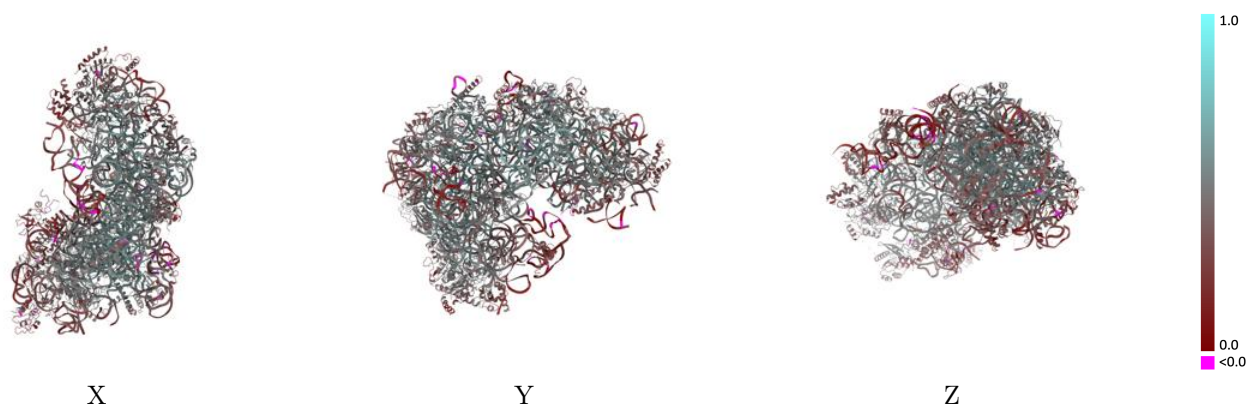
Y



Z

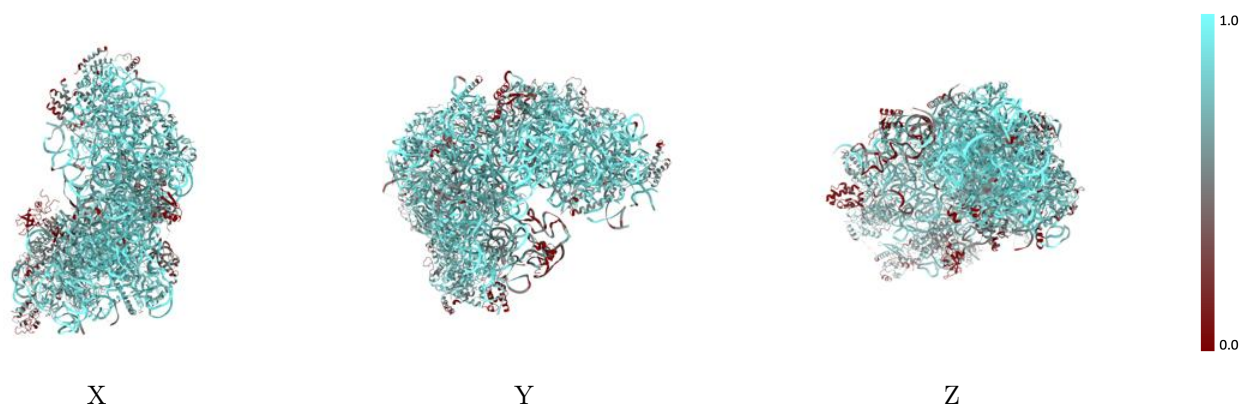
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



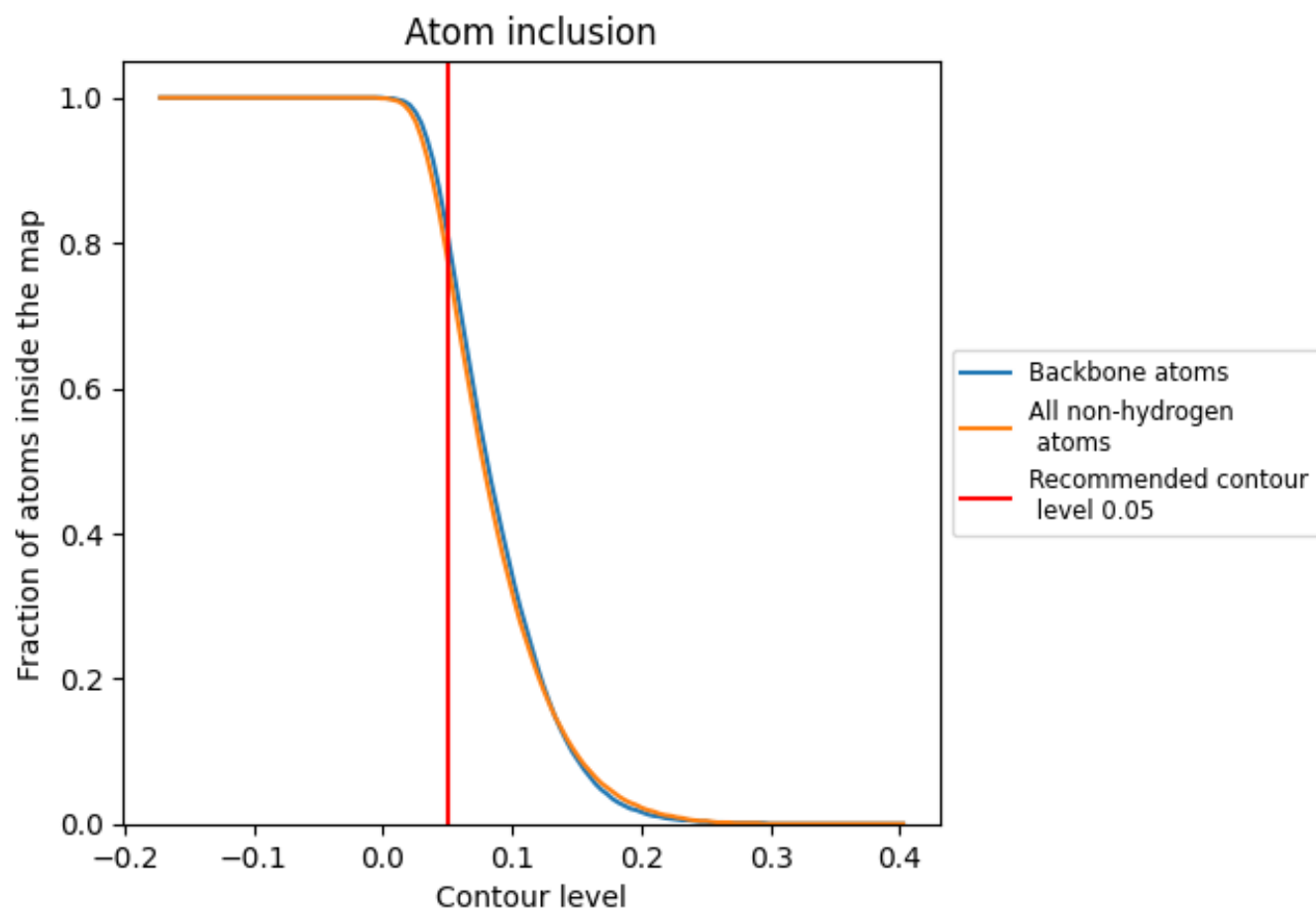
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.05).









































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 81% of all backbone atoms, 78% 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 (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7770	 0.4360
1	 0.8500	 0.4230
2	 0.8650	 0.4220
3	 0.2760	 0.3470
B	 0.8550	 0.5270
C	 0.8410	 0.5250
E	 0.7000	 0.4480
F	 0.8130	 0.4970
G	 0.5790	 0.3520
H	 0.6950	 0.4620
L	 0.7150	 0.4550
M	 0.8110	 0.4750
N	 0.8080	 0.5040
O	 0.8710	 0.5360
P	 0.7090	 0.4850
Q	 0.7850	 0.4940
R	 0.1330	 0.2820
S	 0.7030	 0.4540
T	 0.4360	 0.3540
V	 0.6890	 0.4740
W	 0.4590	 0.3390
Y	 0.8260	 0.5090
a	 0.7550	 0.4620
b	 0.5210	 0.3430
d	 0.6070	 0.4240
e	 0.8670	 0.5460
f	 0.9080	 0.5570
h	 0.6720	 0.4160
i	 0.5930	 0.3440
j	 0.8500	 0.5350
r	 0.3830	 0.3640
s	 0.3830	 0.3580
u	 0.7330	 0.4260
w	 0.0600	 0.3310
y	 0.7050	 0.4300
z	 0.6210	 0.4330

