



wwPDB EM Validation Summary Report ⓘ

Mar 23, 2026 – 05:32 PM UTC

PDB ID : 6C0F / pdb_00006c0f
EMDB ID : EMD-7324
Title : Yeast nucleolar pre-60S ribosomal subunit (state 2)
Authors : Sanghai, Z.A.; Miller, L.; Barandun, J.; Hunziker, M.; Chaker-Margot, M.;
Klinge, S.
Deposited on : 2017-12-29
Resolution : 3.70 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

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

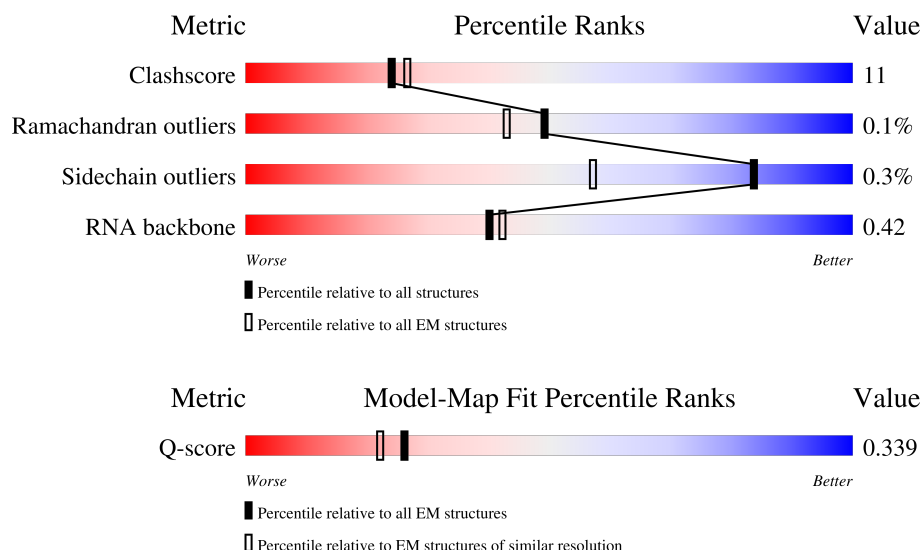
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.70 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.



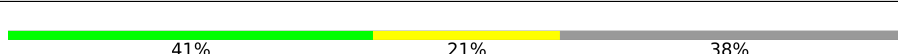
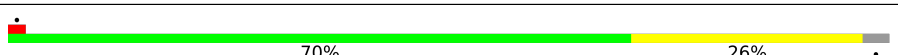
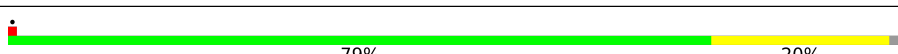
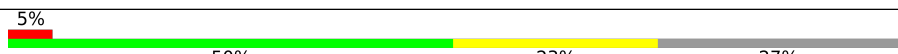
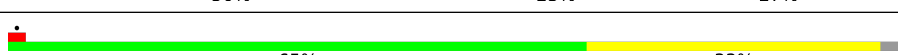
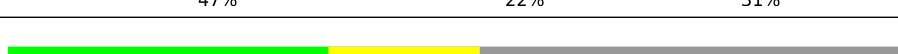
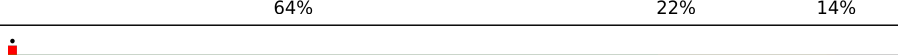
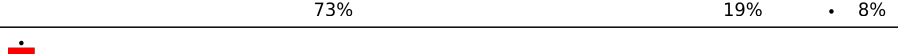
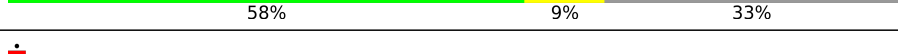
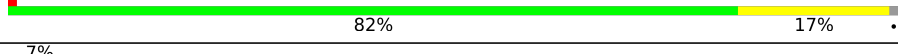
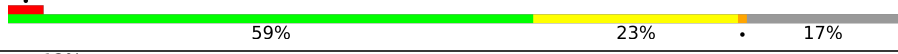
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	11569 (3.20 - 4.20)

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	3395	
2	2	158	
3	6	232	

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Mol	Chain	Length	Quality of chain
4	A	463	
5	B	387	
6	C	362	
7	D	306	
8	E	176	
9	F	244	
10	G	256	
11	I	295	
12	K	376	
13	L	199	
14	M	138	
15	N	204	
16	O	199	
17	P	184	
18	Q	186	
19	S	172	
20	V	137	
21	W	647	
22	Y	127	
23	7	231	
24	8	434	
25	b	291	
26	e	130	
27	f	107	
28	h	120	

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Mol	Chain	Length	Quality of chain
29	i	100	
30	j	88	
31	x	28	
32	m	74	
33	n	605	
34	o	220	
35	p	505	
36	q	285	
37	s	807	
38	t	322	
39	u	199	
40	v	453	
41	w	250	
42	y	245	
43	z	278	

2 Entry composition

There are 44 unique types of molecules in this entry. The entry contains 91742 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 *Saccharomyces cerevisiae* S288c 35S pre-ribosomal RNA miscRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	1357	Total	C	N	O	P	0	0
			29055	12970	5242	9486	1357		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	?	-	U	deletion	GB 259147931

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	158	Total	C	N	O	P	0	0
			3353	1500	586	1109	158		

- Molecule 3 is a RNA chain called ITS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	6	87	Total	C	N	O	P	0	0
			1838	823	309	619	87		

- Molecule 4 is a protein called Ribosome biogenesis protein NSA1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	A	394	Total	C	N	O	S	0	0
			3126	1997	525	593	11		

- Molecule 5 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	B	324	Total	C	N	O	S	0	0
			2577	1635	478	458	6		

- Molecule 6 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	C	314	Total	C	N	O	S	0	0
			2418	1531	454	430	3		

- Molecule 7 is a protein called Protein MAK16.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	D	190	Total	C	N	O	S	0	0
			1578	996	297	275	10		

- Molecule 8 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	E	170	Total	C	N	O	S	0	0
			1366	882	244	239	1		

- Molecule 9 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	F	242	Total	C	N	O	S	0	0
			1941	1249	352	339	1		

- Molecule 10 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	G	187	Total	C	N	O	S	0	0
			1453	934	253	264	2		

- Molecule 11 is a protein called Ribosome production factor 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	I	288	Total	C	N	O	S	0	0
			2429	1544	439	442	4		

- Molecule 12 is a protein called Proteasome-interacting protein CIC1.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	K	260	Total	C	N	O	S	0	0
			2099	1352	346	398	3		

- Molecule 13 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	L	106	Total	C	N	O		
			845	531	174	140	0	0

- Molecule 14 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	M	128	Total	C	N	O	S		
			997	641	190	164	2	0	0

- Molecule 15 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	N	176	Total	C	N	O	S		
			1509	946	319	243	1	0	0

- Molecule 16 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	O	184	Total	C	N	O	S		
			1451	936	268	246	1	0	0

- Molecule 17 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	P	124	Total	C	N	O		
			975	612	184	179	0	0

- Molecule 18 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Q	132	Total	C	N	O	S		
			1015	648	191	175	1	0	0

- Molecule 19 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	171	Total	C	N	O	S		
			1437	925	266	243	3	0	0

- Molecule 20 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	V	122	Total	C	N	O	S	0	0
			903	567	169	160	7		

- Molecule 21 is a protein called Nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	W	98	Total	C	N	O	S	0	0
			806	509	132	164	1		

- Molecule 22 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Y	126	Total	C	N	O	S	0	0
			993	625	192	176			

- Molecule 23 is a protein called Nucleolar protein 16.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	7	156	Total	C	N	O	S	0	0
			1295	813	250	228	4		

- Molecule 24 is a protein called Ribosomal RNA-processing protein 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	8	98	Total	C	N	O	S	0	0
			836	515	165	154	2		

- Molecule 25 is a protein called Ribosome biogenesis protein BRX1.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	b	242	Total	C	N	O	S	0	0
			1919	1221	344	350	4		

- Molecule 26 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	e	114	Total	C	N	O	S	0	0
			914	580	181	152	1		

- Molecule 27 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	f	106	Total	C	N	O	S	0	0
			850	540	165	144	1		

- Molecule 28 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	h	119	Total	C	N	O	S	0	0
			969	615	186	167	1		

- Molecule 29 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	i	84	Total	C	N	O	S	0	0
			665	413	136	114	2		

- Molecule 30 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	j	72	Total	C	N	O	S	0	0
			575	350	125	95	5		

- Molecule 31 is a protein called Brx1-associated peptide.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	x	28	Total	C	N	O	0	0
			140	84	28	28		

- Molecule 32 is a protein called rRNA-processing protein EBP2.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	m	74	Total	C	N	O	0	0
			370	222	74	74		

- Molecule 33 is a protein called Pescadillo homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	n	341	Total	C	N	O	S	0	0
			2794	1823	470	492	9		

- Molecule 34 is a protein called Ribosome biogenesis protein 15.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	o	133	Total	C	N	O	S	0	0
			1107	716	198	189	4		

- Molecule 35 is a protein called ATP-dependent RNA helicase HAS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	p	437	Total	C	N	O	S	0	0
			3486	2247	600	627	12		

- Molecule 36 is a protein called Protein MAK11.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	q	285	Total	C	N	O	S	0	0
			1409	839	285	285			

- Molecule 37 is a protein called Ribosome biogenesis protein ERB1.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	s	157	Total	C	N	O	S	0	0
			1069	672	203	191	3		

- Molecule 38 is a protein called Ribosome biogenesis protein RLP7.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	t	248	Total	C	N	O	S	0	0
			1965	1254	350	358	3		

- Molecule 39 is a protein called Ribosome biogenesis protein RLP24.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	u	129	Total	C	N	O	S	0	0
			1088	682	220	178	8		

- Molecule 40 is a protein called Ribosome biogenesis protein SSF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	v	225	Total	C	N	O	S	0	0
			1795	1142	320	324	9		

- Molecule 41 is a protein called Ribosomal RNA-processing protein 15.

Mol	Chain	Residues	Atoms				AltConf	Trace
41	w	70	Total	C	N	O	0	0
			562	357	96	109		

- Molecule 42 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	y	226	Total	C	N	O	S	0	0
			1709	1060	296	346	7		

- Molecule 43 is a protein called Ribosomal RNA-processing protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	z	243	Total	C	N	O	S	0	0
			2058	1334	353	366	5		

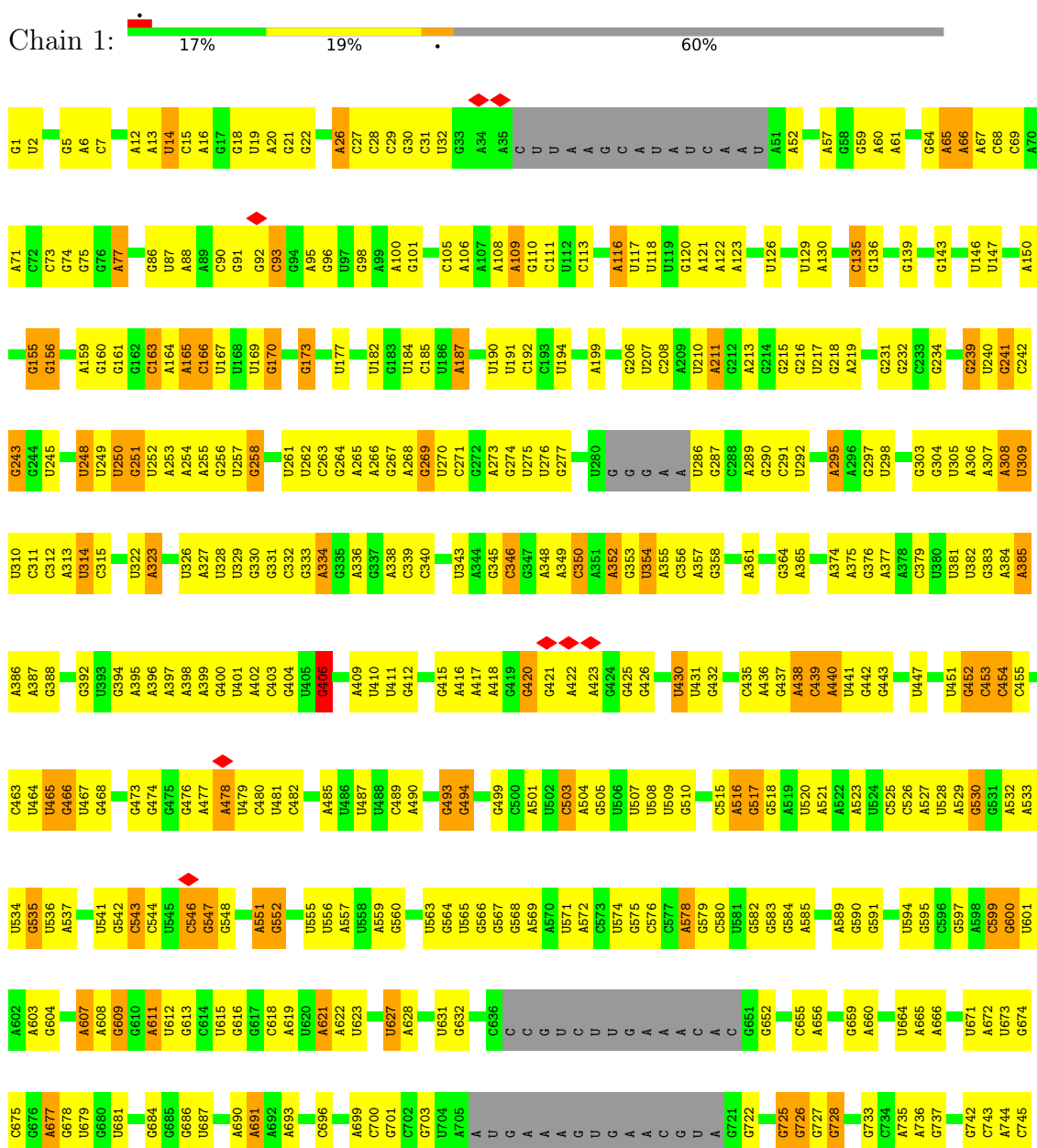
- Molecule 44 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
44	D	1	Total	Zn	0
			1	1	
44	j	1	Total	Zn	0
			1	1	
44	u	1	Total	Zn	0
			1	1	

3 Residue-property plots

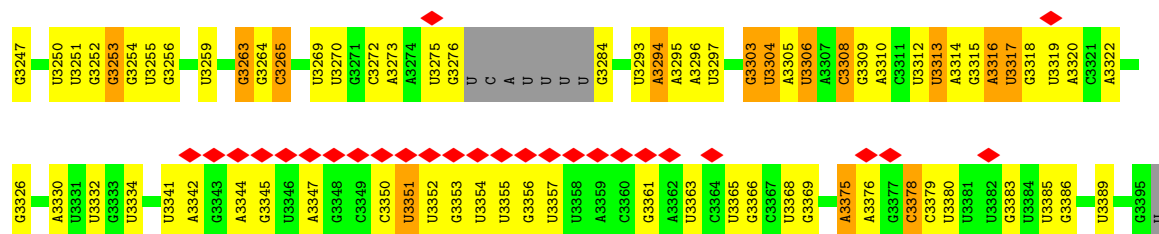
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: *Saccharomyces cerevisiae* S288c 35S pre-ribosomal RNA miscRNA

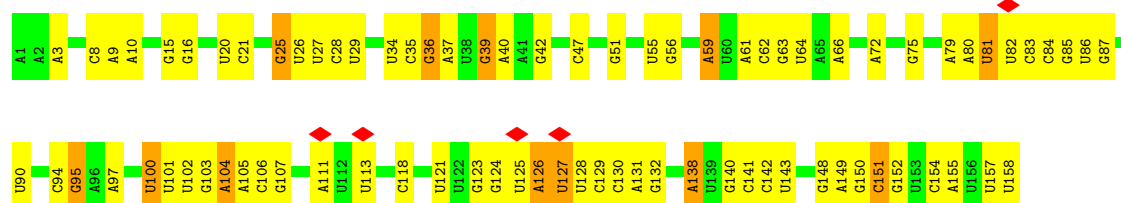




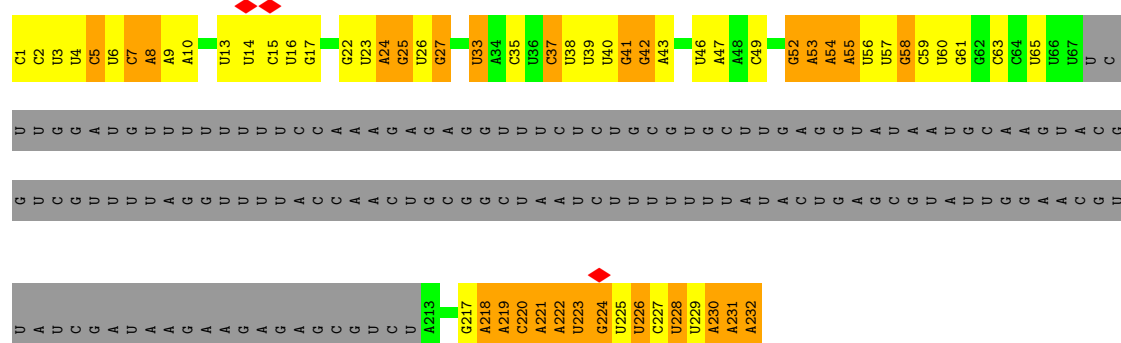




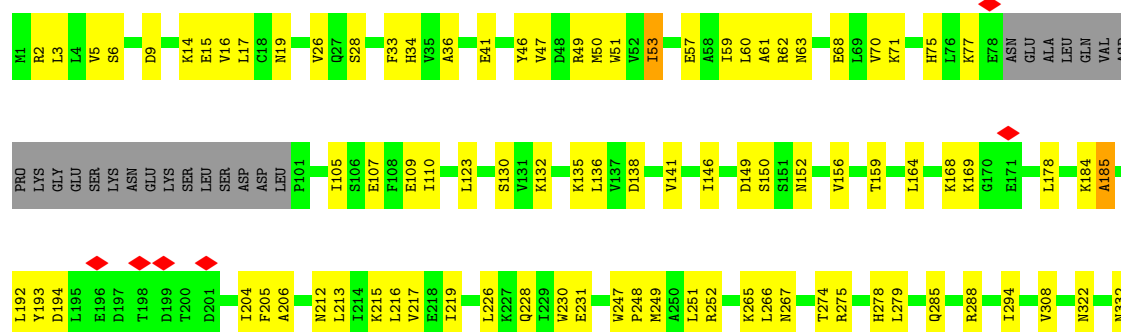
• Molecule 2: 5.8S rRNA



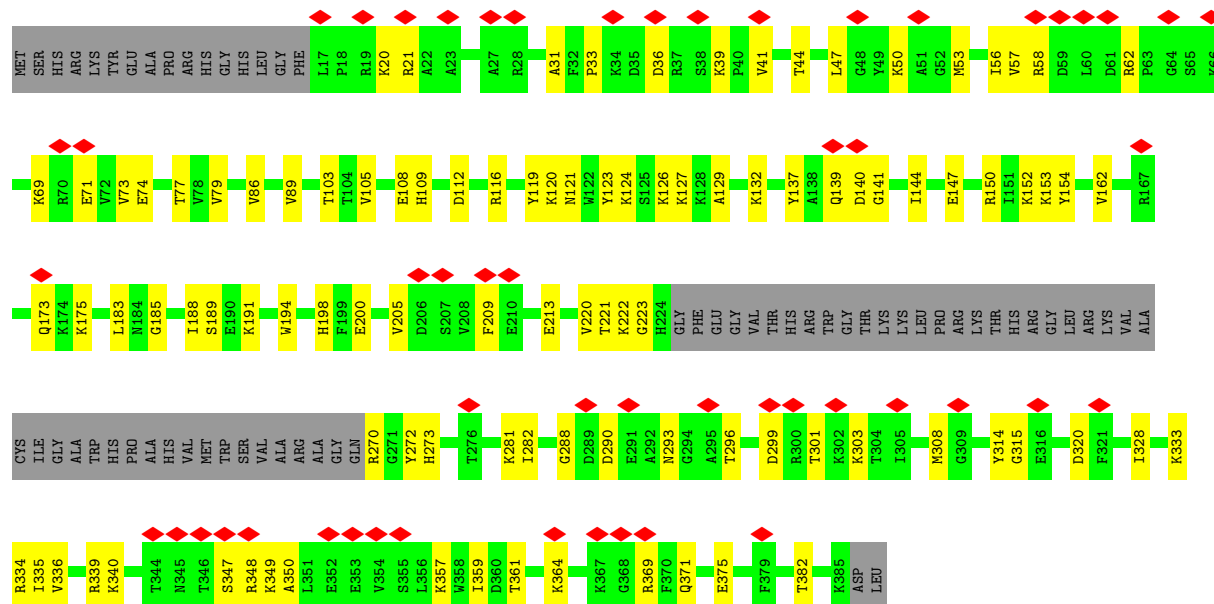
• Molecule 3: ITS2



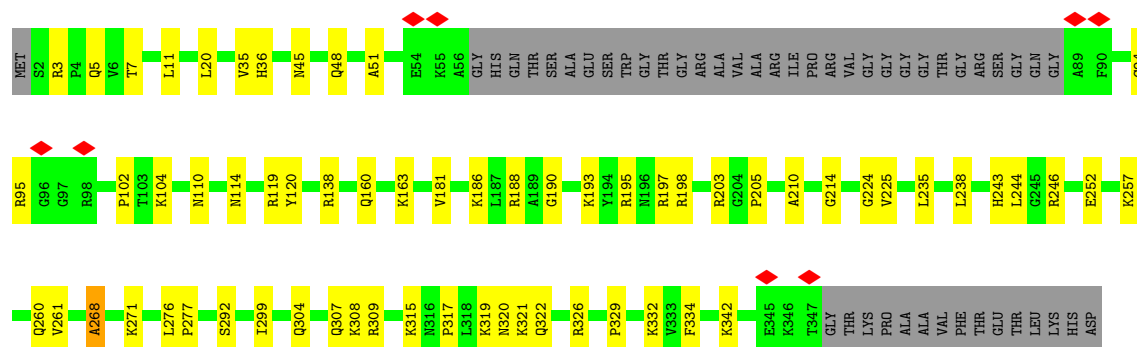
• Molecule 4: Ribosome biogenesis protein NSA1



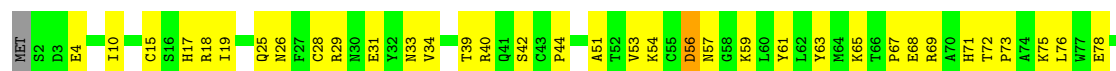
- Molecule 5: 60S ribosomal protein L3

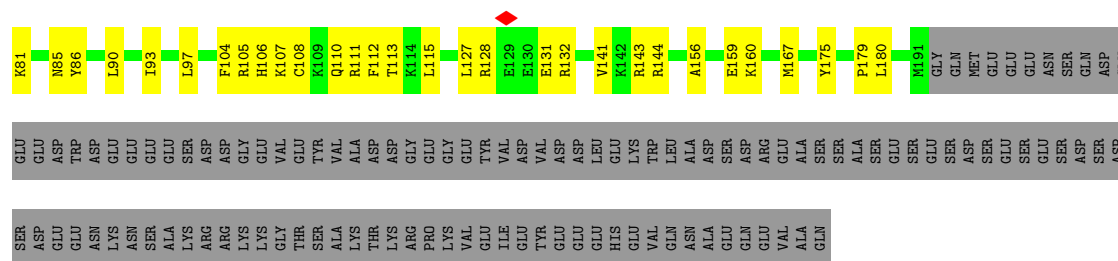


- Molecule 6: 60S ribosomal protein L4-A



- Molecule 7: Protein MAK16

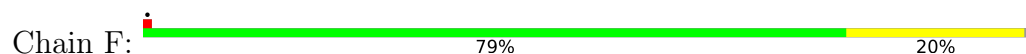




• Molecule 8: 60S ribosomal protein L6-A



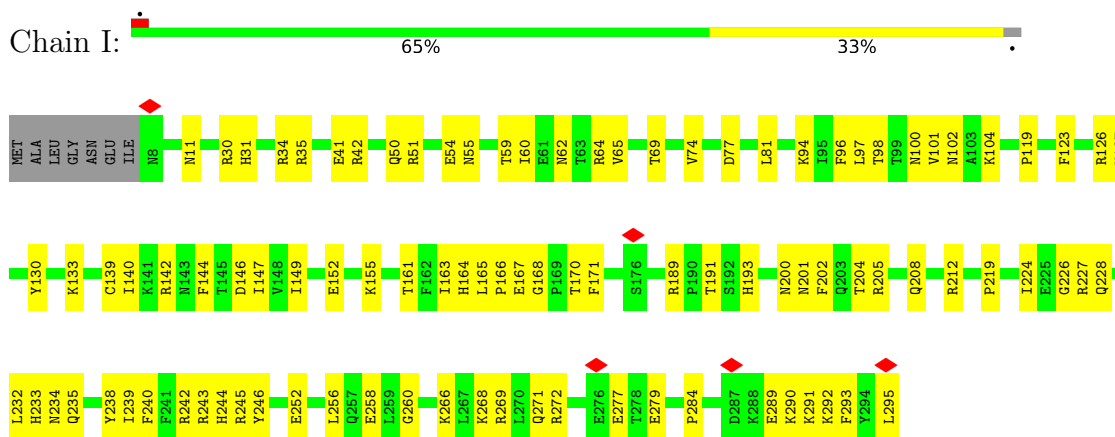
• Molecule 9: 60S ribosomal protein L7-A



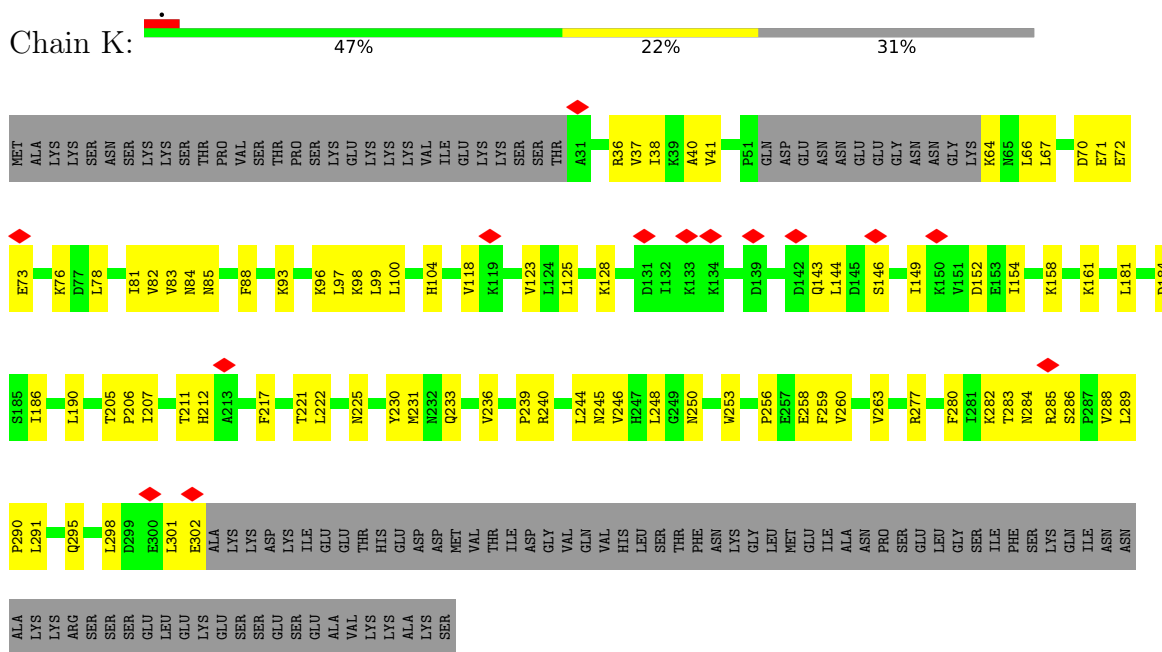
• Molecule 10: 60S ribosomal protein L8-A



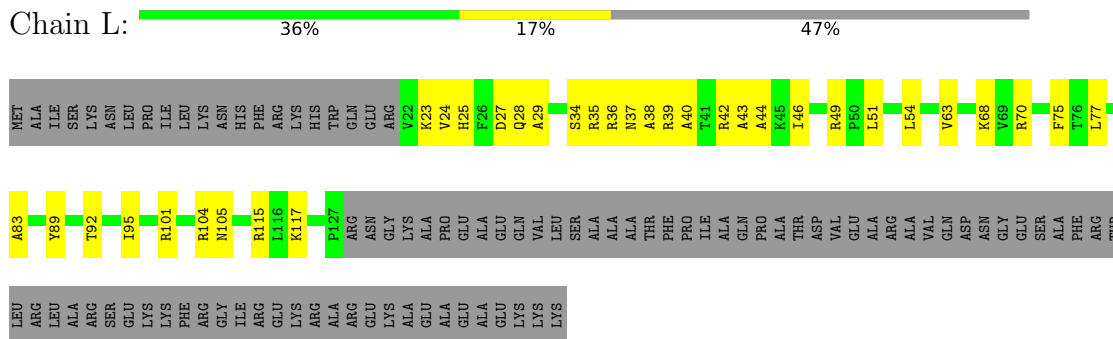
• Molecule 11: Ribosome production factor 1



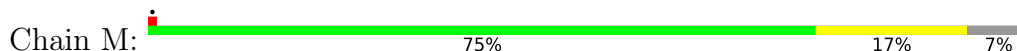
- Molecule 12: Proteasome-interacting protein C1C1

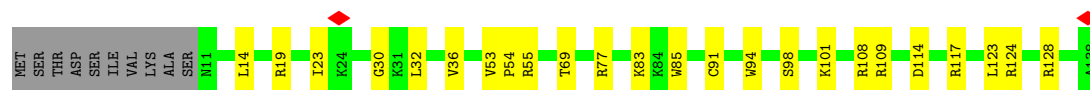


- Molecule 13: 60S ribosomal protein L13-A

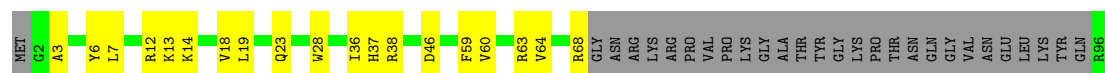


- Molecule 14: 60S ribosomal protein L14-A

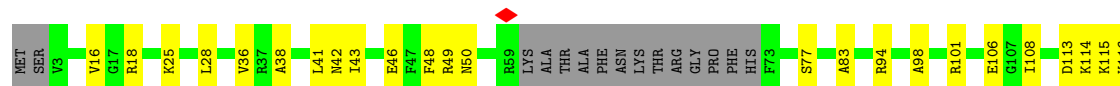




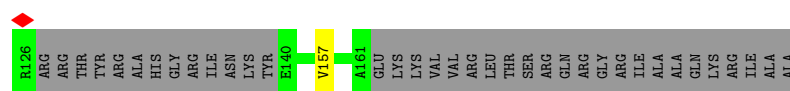
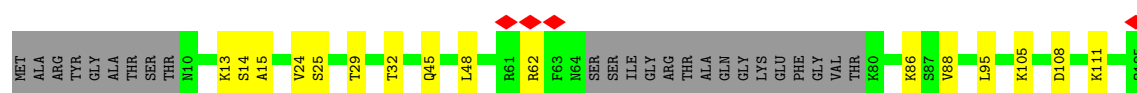
• Molecule 15: 60S ribosomal protein L15-A



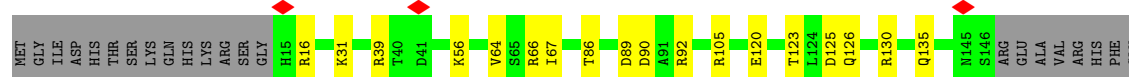
• Molecule 16: 60S ribosomal protein L16-A



• Molecule 17: 60S ribosomal protein L17-A

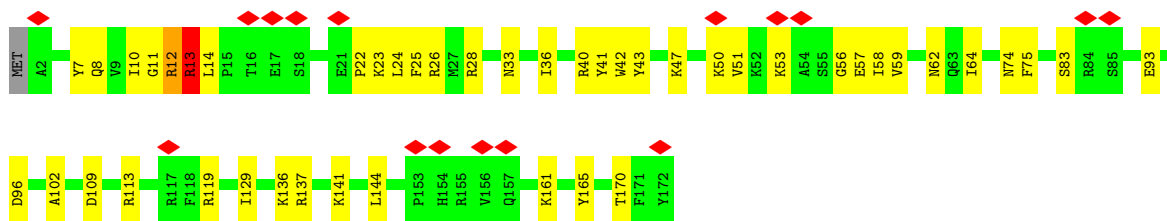


• Molecule 18: 60S ribosomal protein L18-A



• Molecule 19: 60S ribosomal protein L20-A

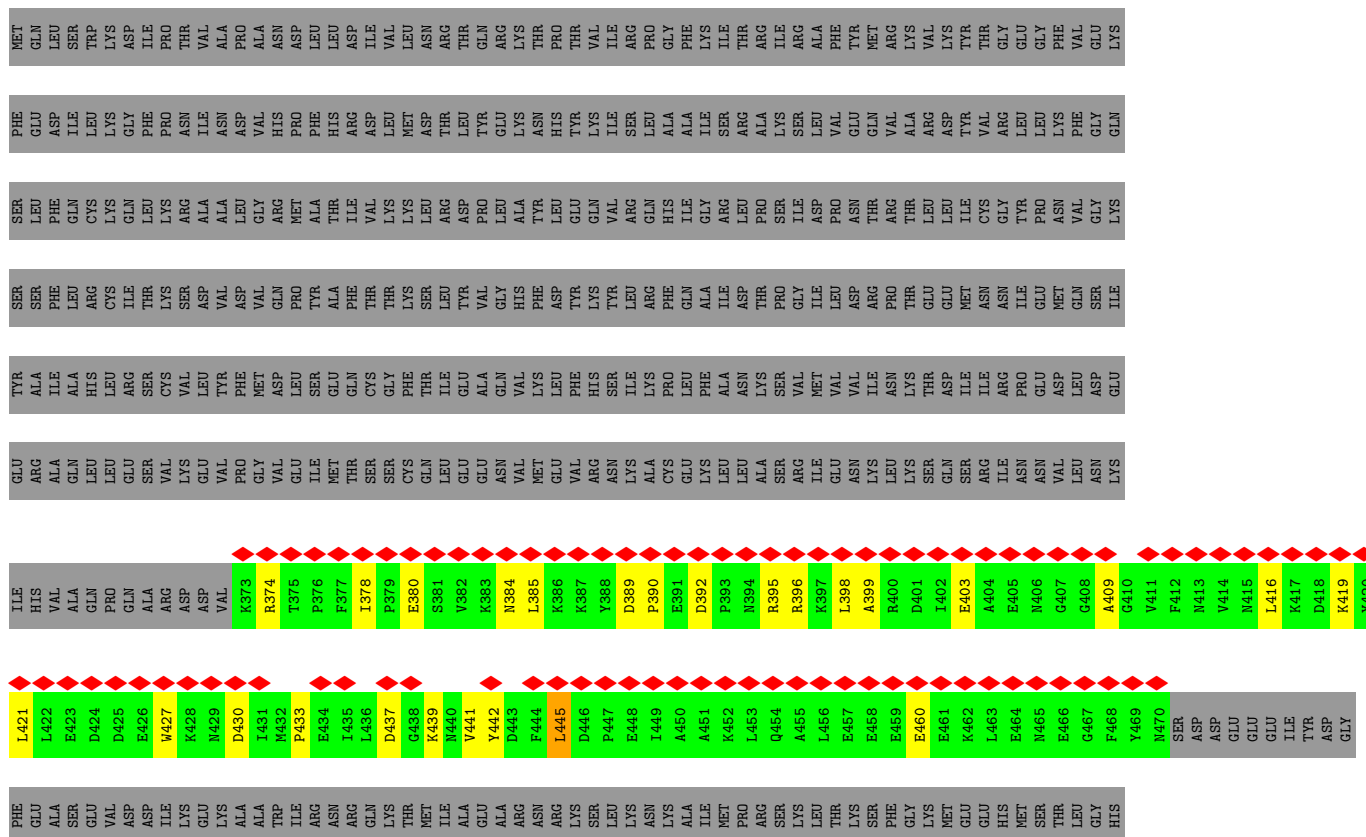




• Molecule 20: 60S ribosomal protein L23-A

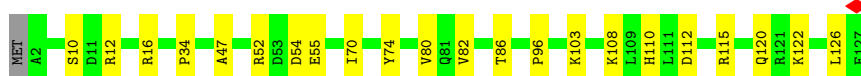


• Molecule 21: Nucleolar GTP-binding protein 1

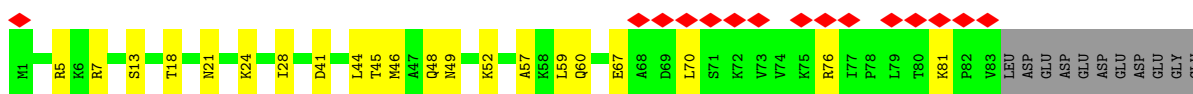


LYS	ALA	ASP	ARG	MET	ALA	LYS	MET	GLU	ARG	GLU	ASN	ARG	HIS	ALA	LYS	GLN	GLY	GLU	SER	ASP	ARG	HIS	ASN	ALA	VAL	SER	SER	LEU	SER	LYS	HIS	LEU	PHE	SER	GLY	LYS	ARG	GLY	VAL	GLY	LYS	THR	ASP	PHE	ARG
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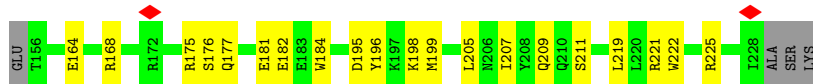
Chain Y: 82% 17%



Chain 7: 7% 50% 18% 25%



ASP	GLU	GLN	ASN	ASP	TYR	ASN	ALA	ALA	THR	VAL	GLU	LEU	ASP	GLU	ASN	GLU	ILE	PRO	GLU	GLY	GLY	ALA	ARG	ARG	ILE	GLN	ARG	ASP	LYS	ASN	GLY	ASP	VAL	VAL	ARG	VAL	VAL	TYR	LYS	GLY	LYS	LYS	LYS	ASN	PHE	ALA	ARG	ASP	THR	THR.
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Chain 8: 11% 19% 77%

MET	SER	ASN	LEU	GLU	GLU	ARG	ARG	ALA	ASN	SER	ALA	PHE	ASP	GLY	LEU	LEU	ALA	LEU	ILE	PRO	ALA	LYS	TYR	TYR	TYR	ASP	GLU	LYS	SER	GLN	GLN	TRP	LYS	LYS	LYS	LYS	THR	LYS	ASN	ASP	LYS	LEU	LEU	ASP	PRO	GLU	GLN
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ASP	ASP	GLU	THR	SER	SER	THR	LEU	GLU	VAL	MET	LYS	LYS	LYS	GLU	GLU	VAL	ASP	ASP	ALA	LYS	PRO	VAL	VAL	LEU	PRO	GLY	LYS	LYS	PHE	LYS	HIS	MET	LYS	MET	MET	GLN	LYS	GLN	LYS	GLU	GLU	ALA	ALA	THR	THR	SER	SER	ASP	ASP	LEU	ASN	ASP	PRO	PRO	MET	ILE	ILE
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PRO	ASP	GLU	GLU	GLU	GLU	GLU	GLU	GLU	ASP	ASP	ASP	ASP	ASP	ASP	GLU	GLU	GLY	ASN	LYS	LYS	LYS	LYS	THR	THR	GLU	GLU	PRO	PRO	ASP	ASP	ARG	SER	SER	VAL	GLU	LYS	LYS	LYS	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLN	LYS	LYS	LYS	ASN	LEU	LEU	ALA	ALA	LEU	ARG	SER	SER	...
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LEU	GLN	ALA	ALA	LYS	SER	ASP	MET	LYS	LYS	LYS	ARG	LYS	LYS	PRO	GLY	GLY	ARG	GLU	ALA	ALA	ILE	ILE	ALA	GLN	LYS	ARG	ARG	LYS	LYS	LYS	GLU	GLU	LEU	LEU	GLU	SER	SER	GLU	GLU	GLN	GLU	GLN	ASP	ASP	ILE	ALA	SER	ASP	SER	ASP	MET	GLU	ASP	ILE	ILE	ASP	SER
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Age Group	Percentage
18-24	35%
25-34	25%
35-44	15%
45-54	10%
55-64	8%
65-74	5%
75-84	3%
85+	2%

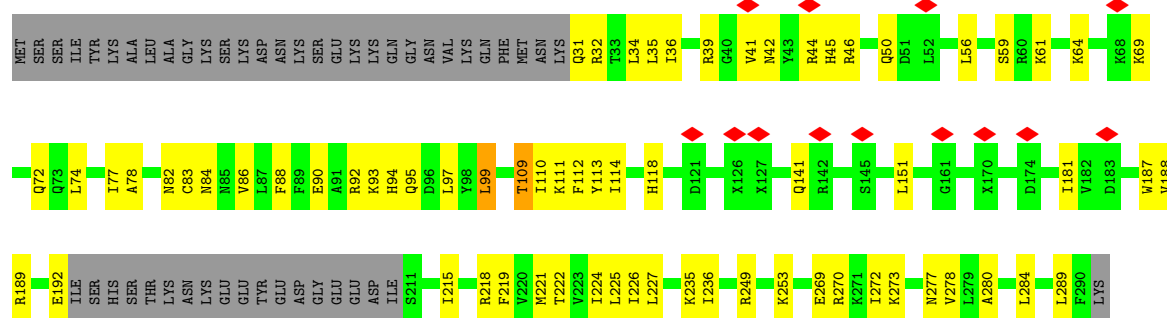
[illegible]

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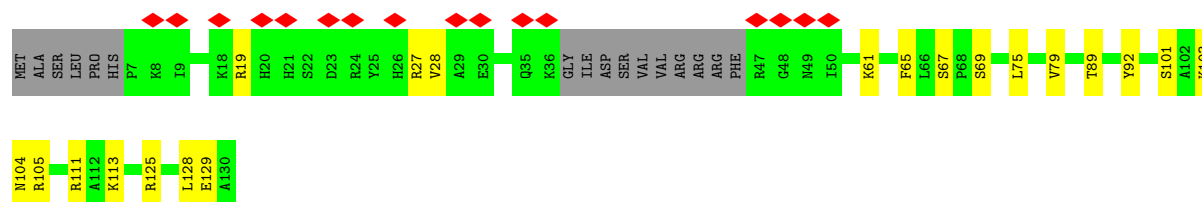
A horizontal timeline with red diamond markers. A green segment highlights the first 10 markers, while the remaining 10 markers are on a grey background.

E3	R3	Q3	K3	R3	R3	E3	N3	L3	R3	T3	R3	K3	D3	N3	LY	GL	LY	LY	LY	LY	GL	GL	GL	GL	ME	LY	AR	PR	SE	AL	VA	VA	LY	LY	TH	GL	LY	LY	LY	GL	GL
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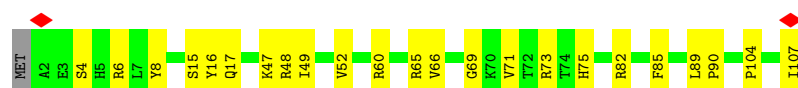
Chain b: 59% 23% 17%



Chain e:



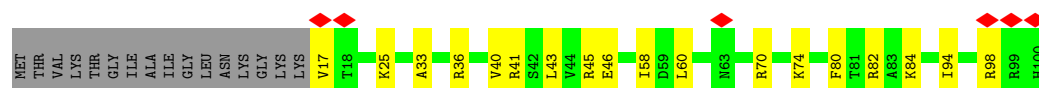
Chain f: 78% 21%



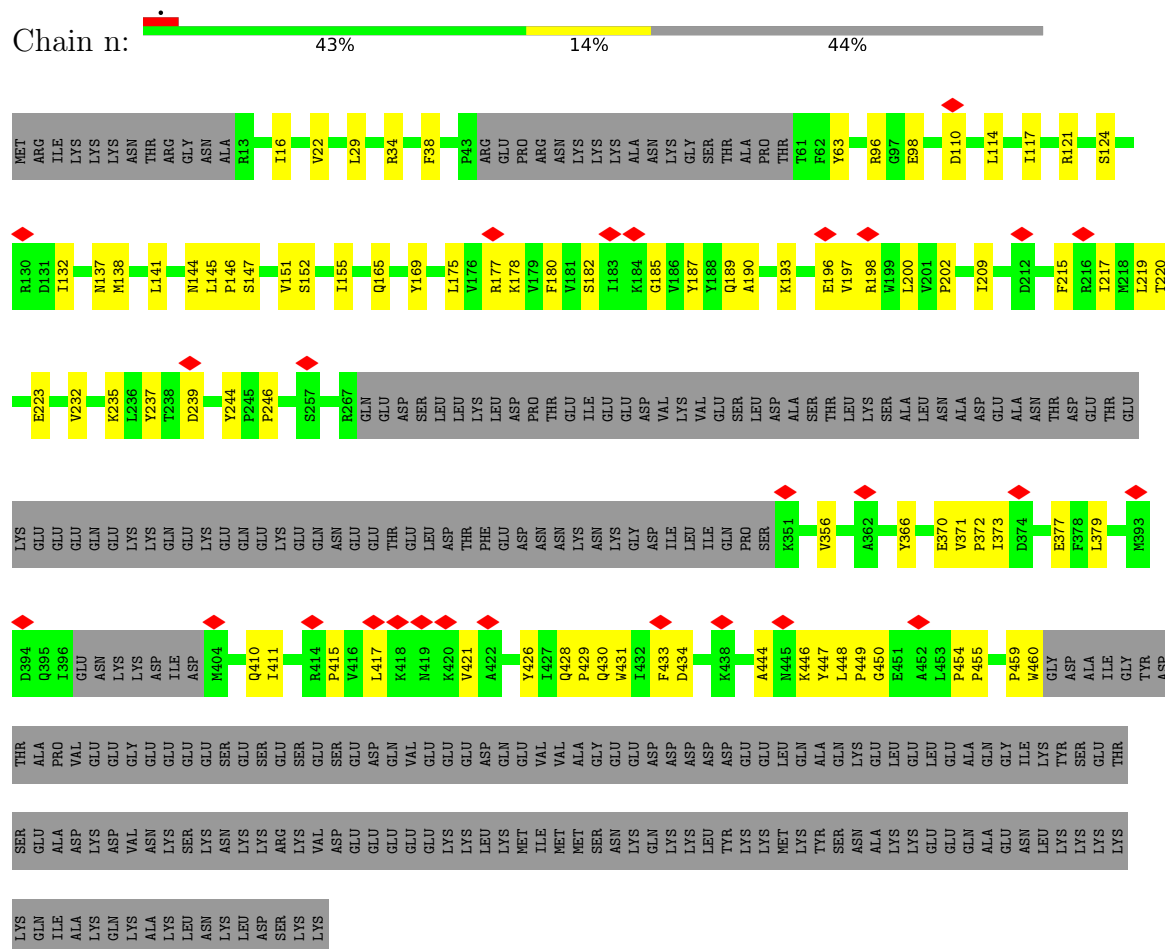
Chain h:



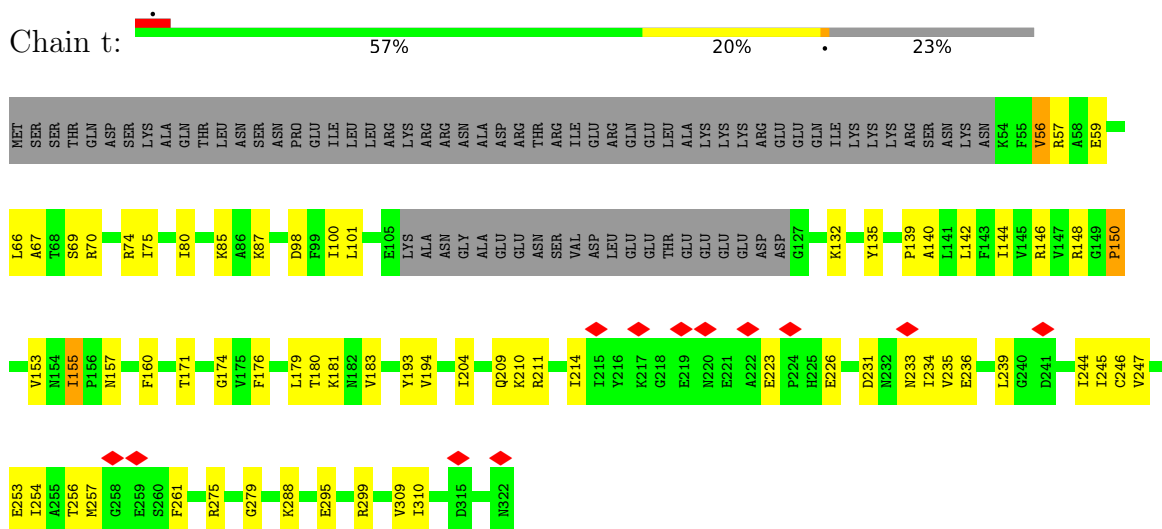
Chain i:



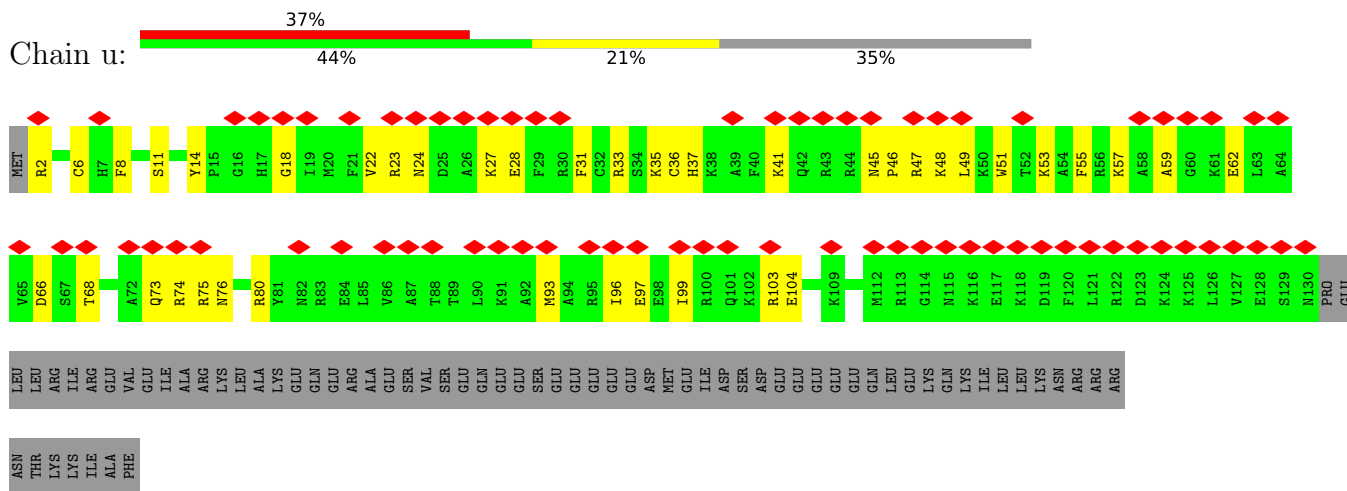
WORLDWIDE
PDB
PROTEIN DATA BANK



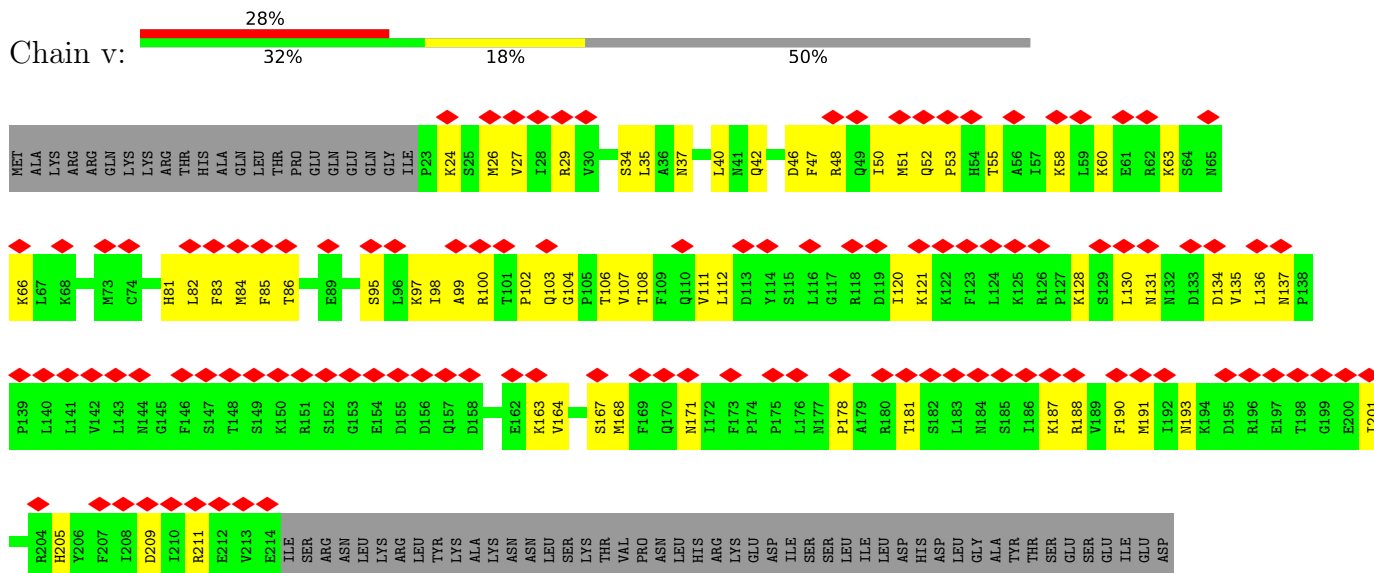


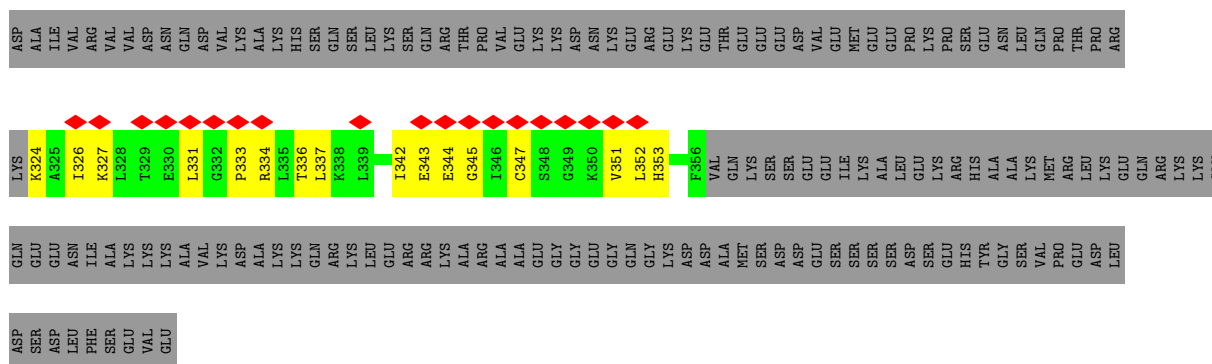


- Molecule 39: Ribosome biogenesis protein RLP24

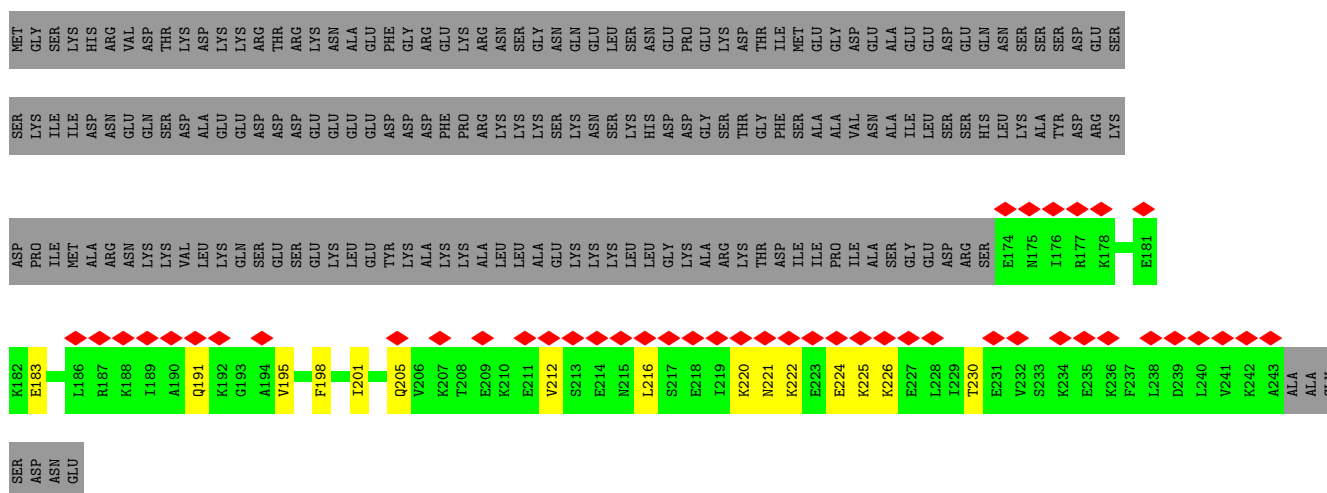


- Molecule 40: Ribosome biogenesis protein SSF1

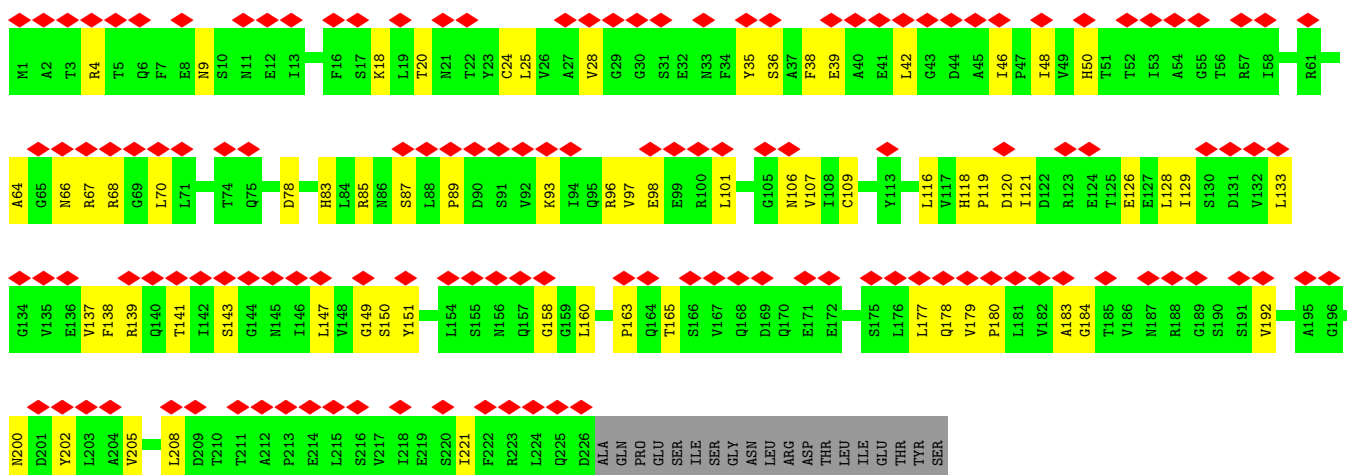




- Molecule 41: Ribosomal RNA-processing protein 15

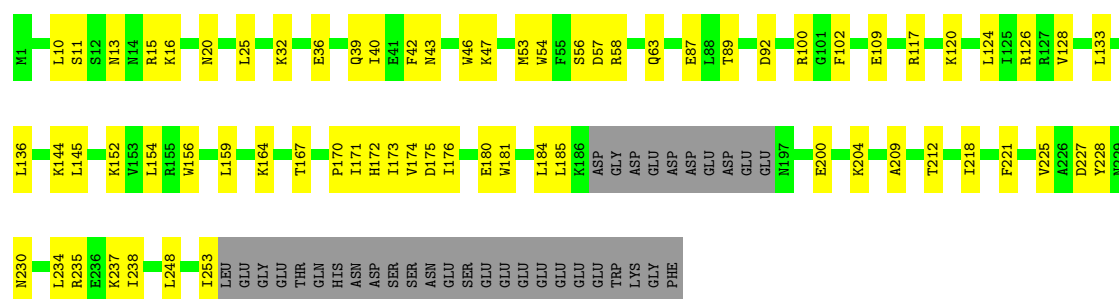


- Molecule 42: Eukaryotic translation initiation factor 6



- Molecule 43: Ribosomal RNA-processing protein 1

App Type	Percentage
Shopping app	63%
Social media app	25%
Productivity app	13%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	201114	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 ($e^-/\text{\AA}^2$)	1.56	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.173	Depositor
Minimum map value	-0.043	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.02	Depositor
Map size ($\text{\AA}$)	624.0, 624.0, 624.0	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.3, 1.3, 1.3	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	0.35	0/32512	0.44	3/50669 (0.0%)
2	2	0.35	0/3746	0.44	0/5832
3	6	0.33	0/2050	0.57	0/3186
4	A	0.35	0/3182	0.63	4/4288 (0.1%)
5	B	0.29	0/2628	0.65	2/3529 (0.1%)
6	C	0.38	0/2462	0.71	0/3333
7	D	0.40	0/1609	0.63	0/2157
8	E	0.32	0/1390	0.65	2/1866 (0.1%)
9	F	0.33	0/1979	0.68	2/2661 (0.1%)
10	G	0.37	0/1477	0.79	4/1994 (0.2%)
11	I	0.36	0/2476	0.66	0/3323
12	K	0.30	0/2133	0.69	2/2879 (0.1%)
13	L	0.38	0/858	0.75	0/1154
14	M	0.31	0/1012	0.59	0/1362
15	N	0.36	0/1540	0.63	0/2060
16	O	0.32	0/1476	0.64	0/1980
17	P	0.30	0/991	0.58	0/1334
18	Q	0.35	0/1030	0.63	0/1393
19	S	0.30	0/1473	0.67	2/1980 (0.1%)
20	V	0.20	0/917	0.50	0/1235
21	W	0.23	0/821	0.52	0/1106
22	Y	0.37	0/1004	0.66	0/1341
23	7	0.37	0/1312	0.72	2/1744 (0.1%)
24	8	0.21	0/840	0.46	0/1105
25	b	0.32	0/1868	0.69	0/2522
26	e	0.33	0/931	0.62	0/1243
27	f	0.37	0/868	0.63	0/1168
28	h	0.31	0/978	0.70	0/1301
29	i	0.30	0/672	0.66	0/894
30	j	0.29	0/587	0.63	0/778
33	n	0.30	0/2862	0.62	0/3870
34	o	0.31	0/1129	0.64	2/1502 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	p	0.31	0/3552	0.68	2/4789 (0.0%)
37	s	0.34	0/720	0.68	0/964
38	t	0.34	0/1991	0.74	0/2679
39	u	0.26	0/1109	0.59	0/1474
40	v	0.26	0/1825	0.69	0/2453
41	w	0.21	0/563	0.59	0/748
42	y	0.25	0/1730	0.60	0/2354
43	z	0.33	0/2104	0.63	0/2832
All	All	0.33	0/94407	0.57	27/135082 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
4	A	0	2
7	D	0	1
9	F	0	1
10	G	0	1
19	S	0	4
28	h	0	1
33	n	0	1
36	q	0	1
37	s	0	1
38	t	0	3
All	All	0	16

There are no bond length outliers.

The worst 5 of 27 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
19	S	13	ARG	CA-C-N	6.71	138.17	121.80
19	S	13	ARG	C-N-CA	6.71	138.17	121.80
10	G	119	GLY	CA-C-N	6.41	133.24	121.70
10	G	119	GLY	C-N-CA	6.41	133.24	121.70
10	G	145	ASN	CA-C-N	6.03	132.56	121.70

There are no chirality outliers.

5 of 16 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	A	185	ALA	Peptide
4	A	53	ILE	Peptide
7	D	56	ASP	Peptide
9	F	158	LYS	Peptide
10	G	76	ALA	Peptide

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	29055	0	14598	537	0
2	2	3353	0	1695	63	0
3	6	1838	0	927	52	0
4	A	3126	0	3178	92	0
5	B	2577	0	2655	76	0
6	C	2418	0	2541	58	0
7	D	1578	0	1619	57	0
8	E	1366	0	1466	36	0
9	F	1941	0	2037	41	0
10	G	1453	0	1536	50	0
11	I	2429	0	2472	90	0
12	K	2099	0	2180	62	0
13	L	845	0	898	30	0
14	M	997	0	1090	24	0
15	N	1509	0	1561	40	0
16	O	1451	0	1554	35	0
17	P	975	0	988	14	0
18	Q	1015	0	1096	16	0
19	S	1437	0	1475	32	0
20	V	903	0	946	29	0
21	W	806	0	777	24	0
22	Y	993	0	1081	18	0
23	7	1295	0	1383	34	0
24	8	836	0	897	13	0
25	b	1919	0	1858	51	0
26	e	914	0	977	18	0
27	f	850	0	880	20	0
28	h	969	0	1078	28	0
29	i	665	0	721	18	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
30	j	575	0	579	17	0
31	x	140	0	34	1	0
32	m	370	0	76	3	0
33	n	2794	0	2845	64	0
34	o	1107	0	1159	36	0
35	p	3486	0	3618	77	0
36	q	1409	0	308	9	0
37	s	1069	0	820	27	0
38	t	1965	0	2077	53	0
39	u	1088	0	1118	35	0
40	v	1795	0	1877	63	0
41	w	562	0	614	16	0
42	y	1709	0	1701	52	0
43	z	2058	0	2096	51	0
44	D	1	0	0	0	0
44	j	1	0	0	0	0
44	u	1	0	0	0	0
All	All	91742	0	75086	1716	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 11.

The worst 5 of 1716 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)
38:t:139:PRO:HA	38:t:179:LEU:O	1.61	0.99
1:1:182:U:H3	1:1:234:G:H1	1.07	0.97
1:1:160:G:H1	1:1:261:U:H3	1.09	0.97
1:1:509:U:H3	1:1:582:G:H1	1.10	0.95
4:A:57:GLU:OE2	4:A:169:LYS:NZ	1.99	0.95

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	A	390/463 (84%)	368 (94%)	22 (6%)	0	100	100
5	B	320/387 (83%)	302 (94%)	18 (6%)	0	100	100
6	C	310/362 (86%)	285 (92%)	23 (7%)	2 (1%)	21	52
7	D	188/306 (61%)	177 (94%)	11 (6%)	0	100	100
8	E	168/176 (96%)	158 (94%)	10 (6%)	0	100	100
9	F	240/244 (98%)	225 (94%)	15 (6%)	0	100	100
10	G	185/256 (72%)	170 (92%)	14 (8%)	1 (0%)	24	56
11	I	286/295 (97%)	272 (95%)	14 (5%)	0	100	100
12	K	256/376 (68%)	243 (95%)	13 (5%)	0	100	100
13	L	104/199 (52%)	96 (92%)	7 (7%)	1 (1%)	12	43
14	M	126/138 (91%)	123 (98%)	3 (2%)	0	100	100
15	N	172/204 (84%)	162 (94%)	10 (6%)	0	100	100
16	O	180/199 (90%)	173 (96%)	7 (4%)	0	100	100
17	P	118/184 (64%)	113 (96%)	5 (4%)	0	100	100
18	Q	130/186 (70%)	128 (98%)	2 (2%)	0	100	100
19	S	169/172 (98%)	154 (91%)	15 (9%)	0	100	100
20	V	120/137 (88%)	115 (96%)	5 (4%)	0	100	100
21	W	96/647 (15%)	94 (98%)	2 (2%)	0	100	100
22	Y	124/127 (98%)	118 (95%)	6 (5%)	0	100	100
23	7	152/231 (66%)	137 (90%)	15 (10%)	0	100	100
24	8	96/434 (22%)	96 (100%)	0	0	100	100
25	b	220/291 (76%)	207 (94%)	13 (6%)	0	100	100
26	e	110/130 (85%)	106 (96%)	4 (4%)	0	100	100
27	f	104/107 (97%)	99 (95%)	5 (5%)	0	100	100
28	h	117/120 (98%)	111 (95%)	6 (5%)	0	100	100
29	i	82/100 (82%)	78 (95%)	4 (5%)	0	100	100
30	j	70/88 (80%)	66 (94%)	4 (6%)	0	100	100
33	n	333/605 (55%)	322 (97%)	11 (3%)	0	100	100
34	o	131/220 (60%)	123 (94%)	8 (6%)	0	100	100
35	p	433/505 (86%)	422 (98%)	11 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
37	s	82/807 (10%)	77 (94%)	5 (6%)	0	100	100
38	t	244/322 (76%)	220 (90%)	23 (9%)	1 (0%)	30	60
39	u	127/199 (64%)	127 (100%)	0	0	100	100
40	v	221/453 (49%)	207 (94%)	14 (6%)	0	100	100
41	w	68/250 (27%)	64 (94%)	4 (6%)	0	100	100
42	y	224/245 (91%)	214 (96%)	10 (4%)	0	100	100
43	z	239/278 (86%)	228 (95%)	11 (5%)	0	100	100
All	All	6735/10443 (64%)	6380 (95%)	350 (5%)	5 (0%)	49	78

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	C	268	ALA
6	C	292	SER
13	L	63	VAL
10	G	127	PRO
38	t	56	VAL

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	
4	A	352/410 (86%)	352 (100%)	0	100	100
5	B	272/323 (84%)	272 (100%)	0	100	100
6	C	257/289 (89%)	256 (100%)	1 (0%)	84	81
7	D	171/274 (62%)	171 (100%)	0	100	100
8	E	149/153 (97%)	149 (100%)	0	100	100
9	F	204/205 (100%)	204 (100%)	0	100	100
10	G	152/208 (73%)	152 (100%)	0	100	100
11	I	271/276 (98%)	271 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
12	K	241/346 (70%)	240 (100%)	1 (0%)	84	81
13	L	85/159 (54%)	85 (100%)	0	100	100
14	M	100/109 (92%)	100 (100%)	0	100	100
15	N	153/176 (87%)	153 (100%)	0	100	100
16	O	150/162 (93%)	149 (99%)	1 (1%)	76	77
17	P	100/146 (68%)	99 (99%)	1 (1%)	68	74
18	Q	108/151 (72%)	108 (100%)	0	100	100
19	S	155/156 (99%)	155 (100%)	0	100	100
20	V	94/105 (90%)	94 (100%)	0	100	100
21	W	87/573 (15%)	86 (99%)	1 (1%)	65	73
22	Y	109/110 (99%)	108 (99%)	1 (1%)	70	75
23	7	141/205 (69%)	141 (100%)	0	100	100
24	8	90/388 (23%)	90 (100%)	0	100	100
25	b	203/247 (82%)	201 (99%)	2 (1%)	68	74
26	e	97/111 (87%)	97 (100%)	0	100	100
27	f	90/91 (99%)	90 (100%)	0	100	100
28	h	104/105 (99%)	104 (100%)	0	100	100
29	i	70/82 (85%)	67 (96%)	3 (4%)	26	50
30	j	60/71 (84%)	59 (98%)	1 (2%)	53	67
33	n	309/548 (56%)	308 (100%)	1 (0%)	86	83
34	o	118/199 (59%)	118 (100%)	0	100	100
35	p	381/440 (87%)	379 (100%)	2 (0%)	81	80
37	s	77/653 (12%)	77 (100%)	0	100	100
38	t	219/287 (76%)	217 (99%)	2 (1%)	70	75
39	u	114/180 (63%)	114 (100%)	0	100	100
40	v	208/413 (50%)	208 (100%)	0	100	100
41	w	63/219 (29%)	63 (100%)	0	100	100
42	y	194/211 (92%)	194 (100%)	0	100	100
43	z	225/257 (88%)	225 (100%)	0	100	100
All	All	5973/9038 (66%)	5956 (100%)	17 (0%)	84	83

5 of 17 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
35	p	405	LEU
38	t	155	ILE
25	b	109	THR
29	i	43	LEU
29	i	58	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 125 such sidechains are listed below:

Mol	Chain	Res	Type
20	V	132	ASN
40	v	42	GLN
25	b	158	HIS
40	v	38	HIS
42	y	168	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	1343/3395 (39%)	352 (26%)	28 (2%)
2	2	157/158 (99%)	35 (22%)	3 (1%)
3	6	85/232 (36%)	44 (51%)	5 (5%)
All	All	1585/3785 (41%)	431 (27%)	36 (2%)

5 of 431 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	2	U
1	1	7	C
1	1	12	A
1	1	13	A
1	1	14	U

5 of 36 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	2	36	G
3	6	225	U
2	2	123	G
3	6	25	G
1	1	1329	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 3 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
36	q	5

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	q	398:UNK	C	400:UNK	N	14.84
1	q	136:UNK	C	137:UNK	N	9.43
1	q	114:UNK	C	115:UNK	N	7.34
1	q	257:UNK	C	259:UNK	N	6.77
1	q	242:UNK	C	247:UNK	N	4.06

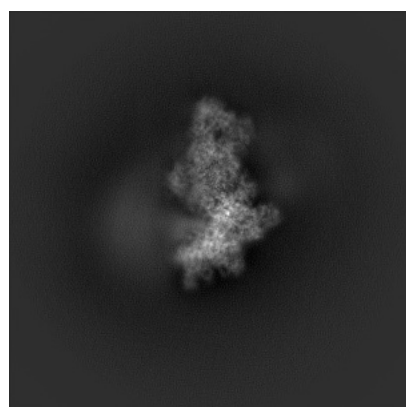
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-7324. These allow visual inspection of the internal detail of the map and identification of artifacts.

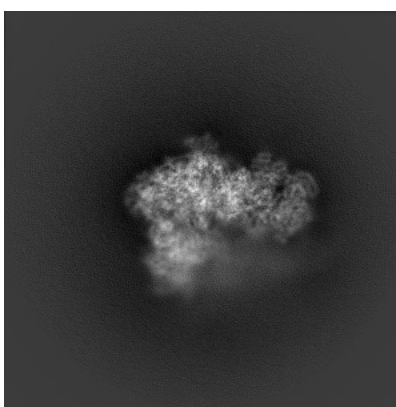
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

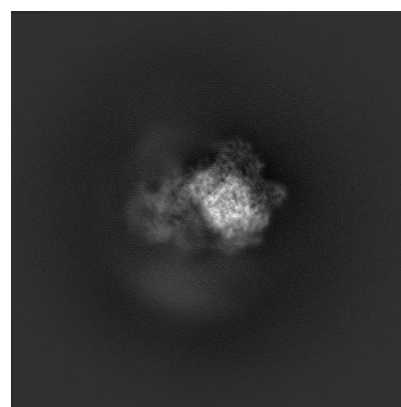
6.1.1 Primary map



X



Y

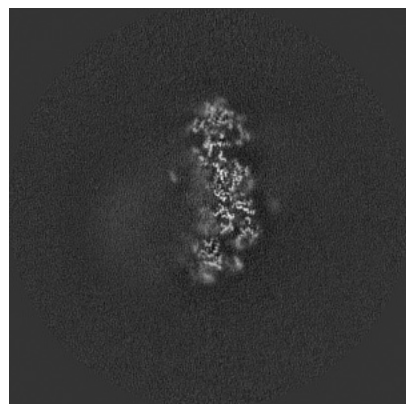


Z

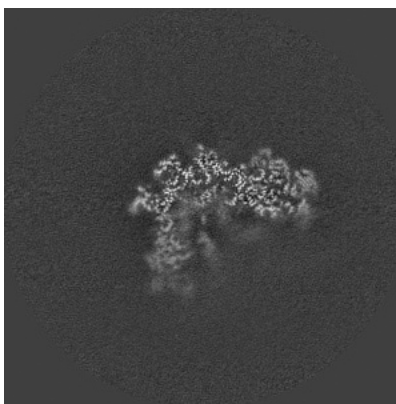
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

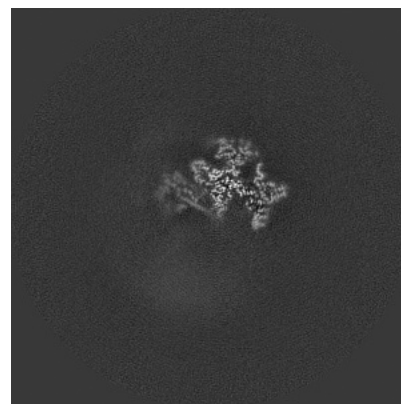
6.2.1 Primary map



X Index: 240



Y Index: 240

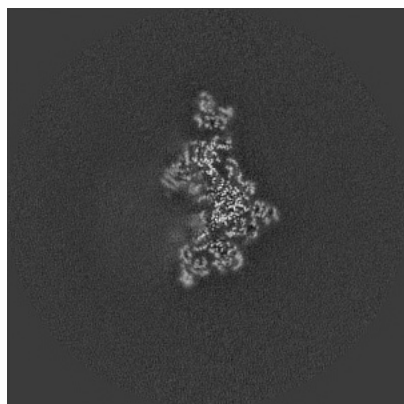


Z Index: 240

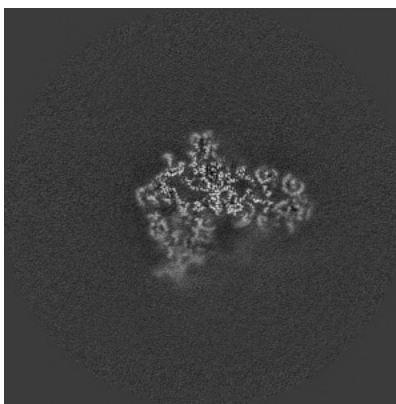
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

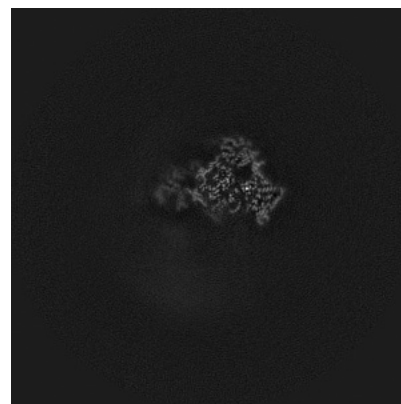
6.3.1 Primary map



X Index: 264



Y Index: 257

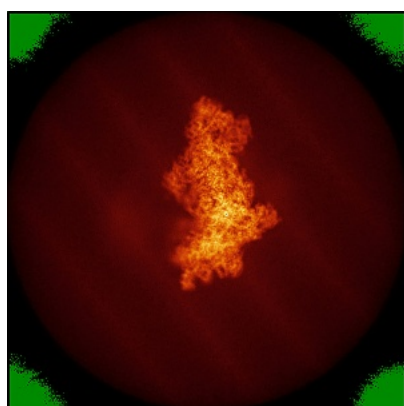


Z Index: 235

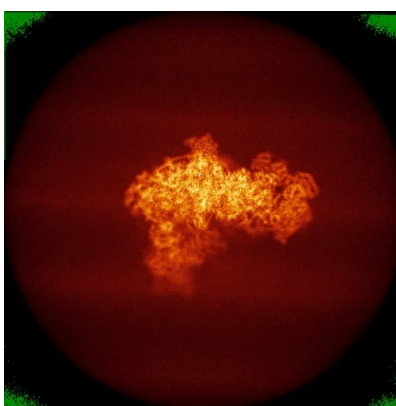
The images above show the largest variance slices of the map in three orthogonal directions.

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

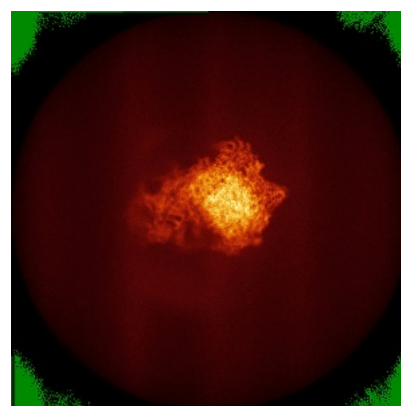
6.4.1 Primary map



X



Y

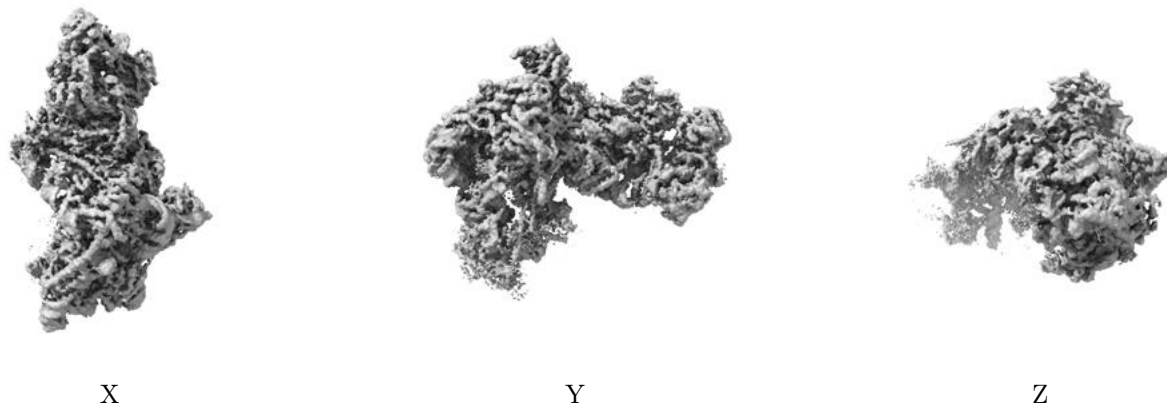


Z

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

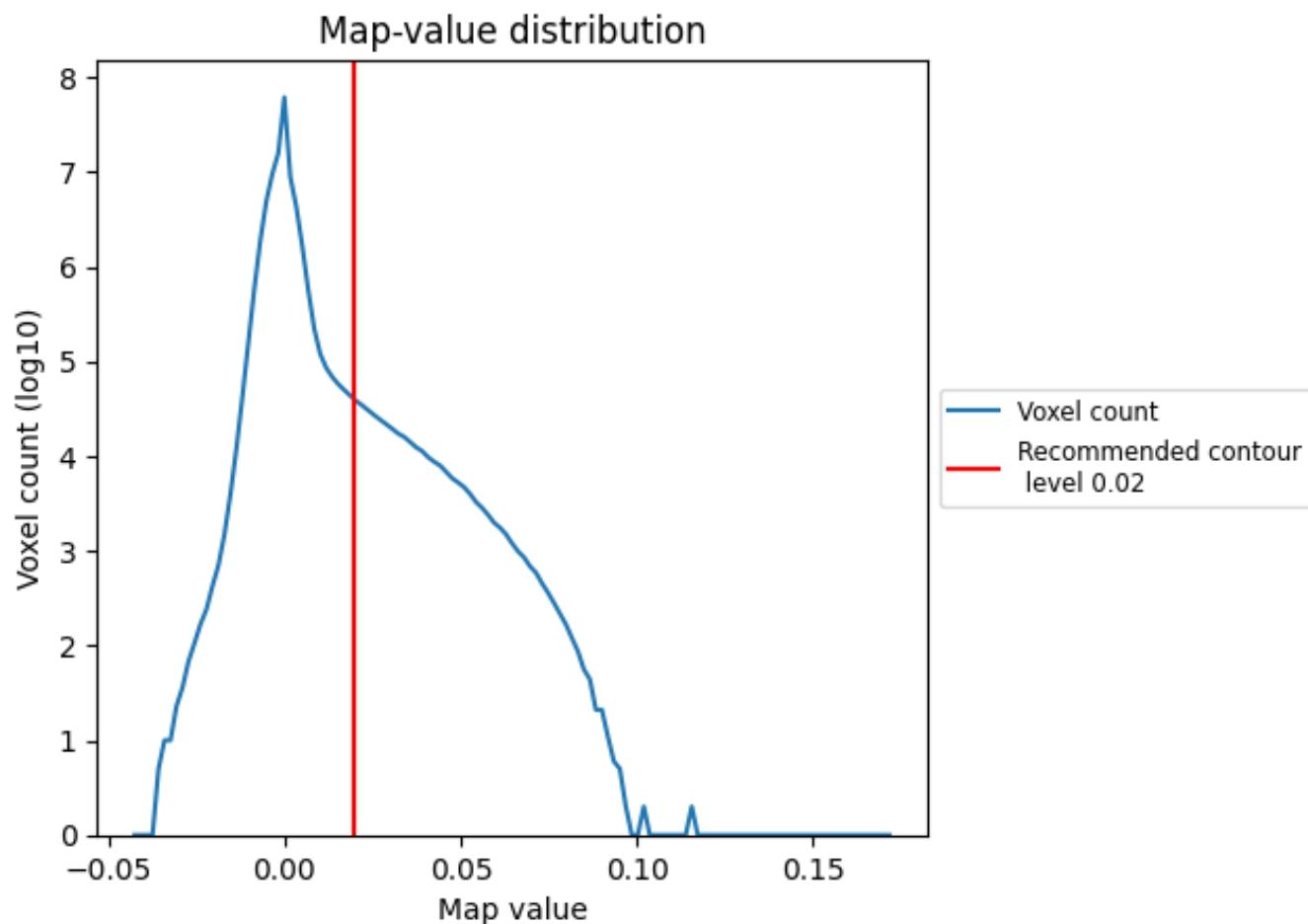
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

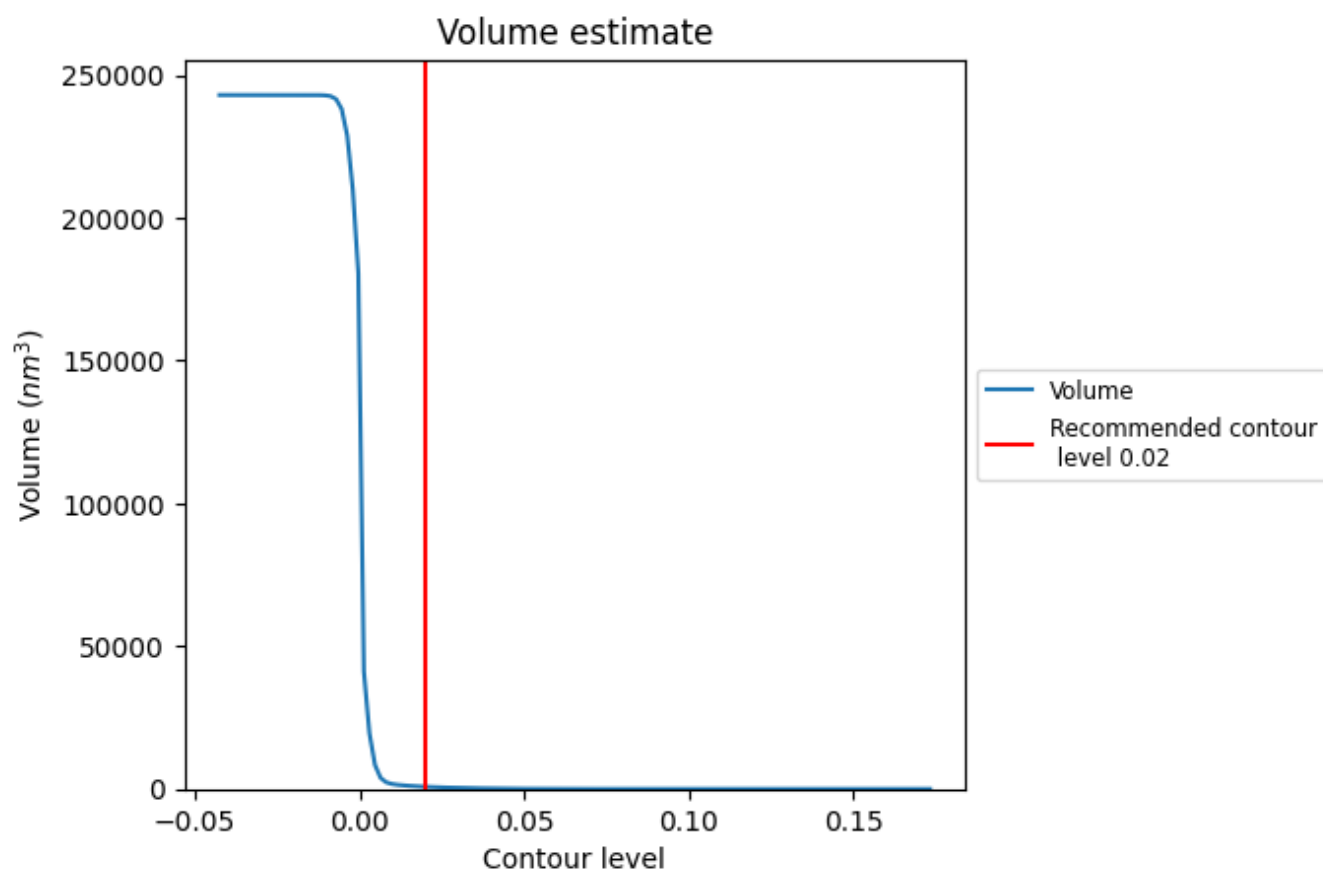
This section contains the results of statistical analysis of the map.

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.

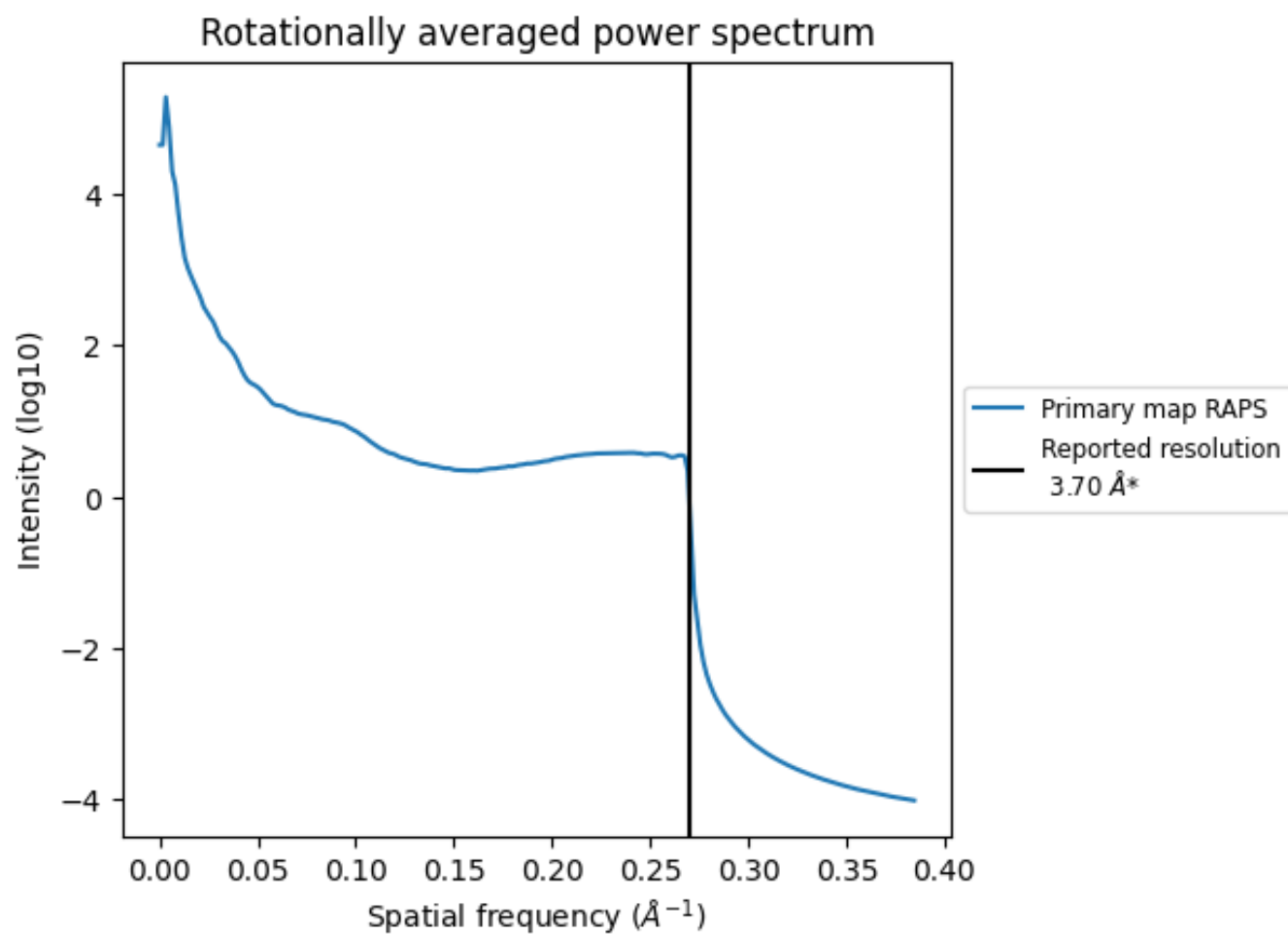
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 766 nm^3 ; this corresponds to an approximate mass of 692 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 0.270 Å⁻¹

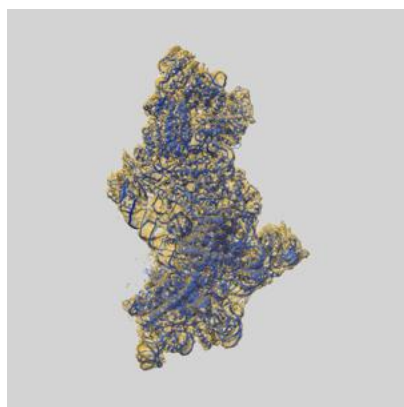
8 Fourier-Shell correlation

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

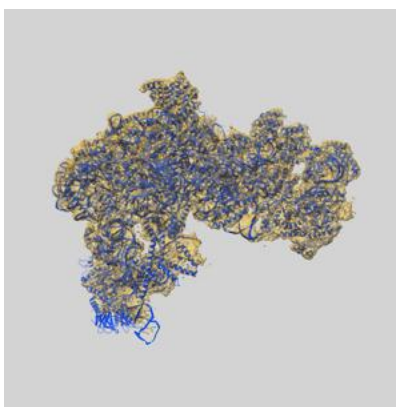
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-7324 and PDB model 6C0F. Per-residue inclusion information can be found in section [3](#) on page [12](#).

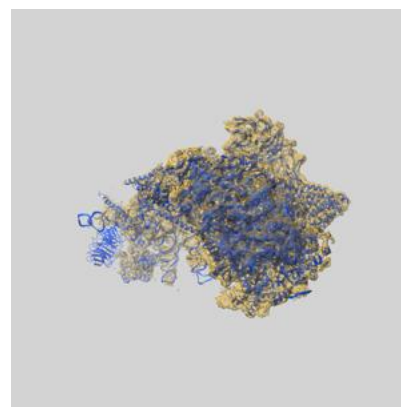
9.1 Map-model overlay [i](#)



X



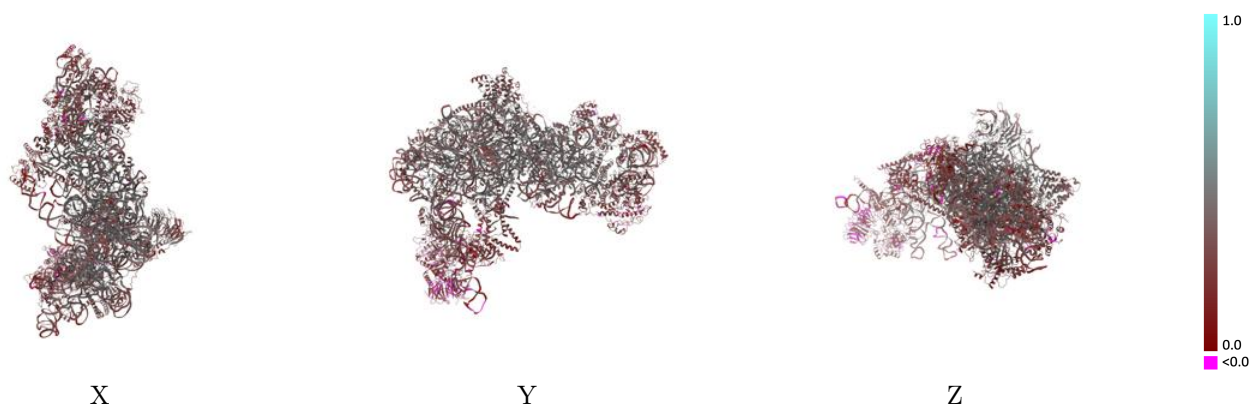
Y



Z

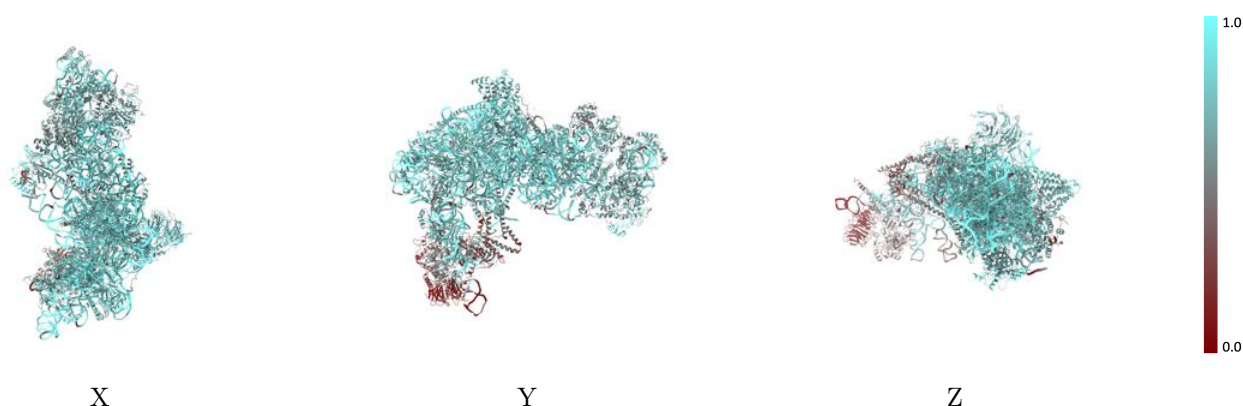
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



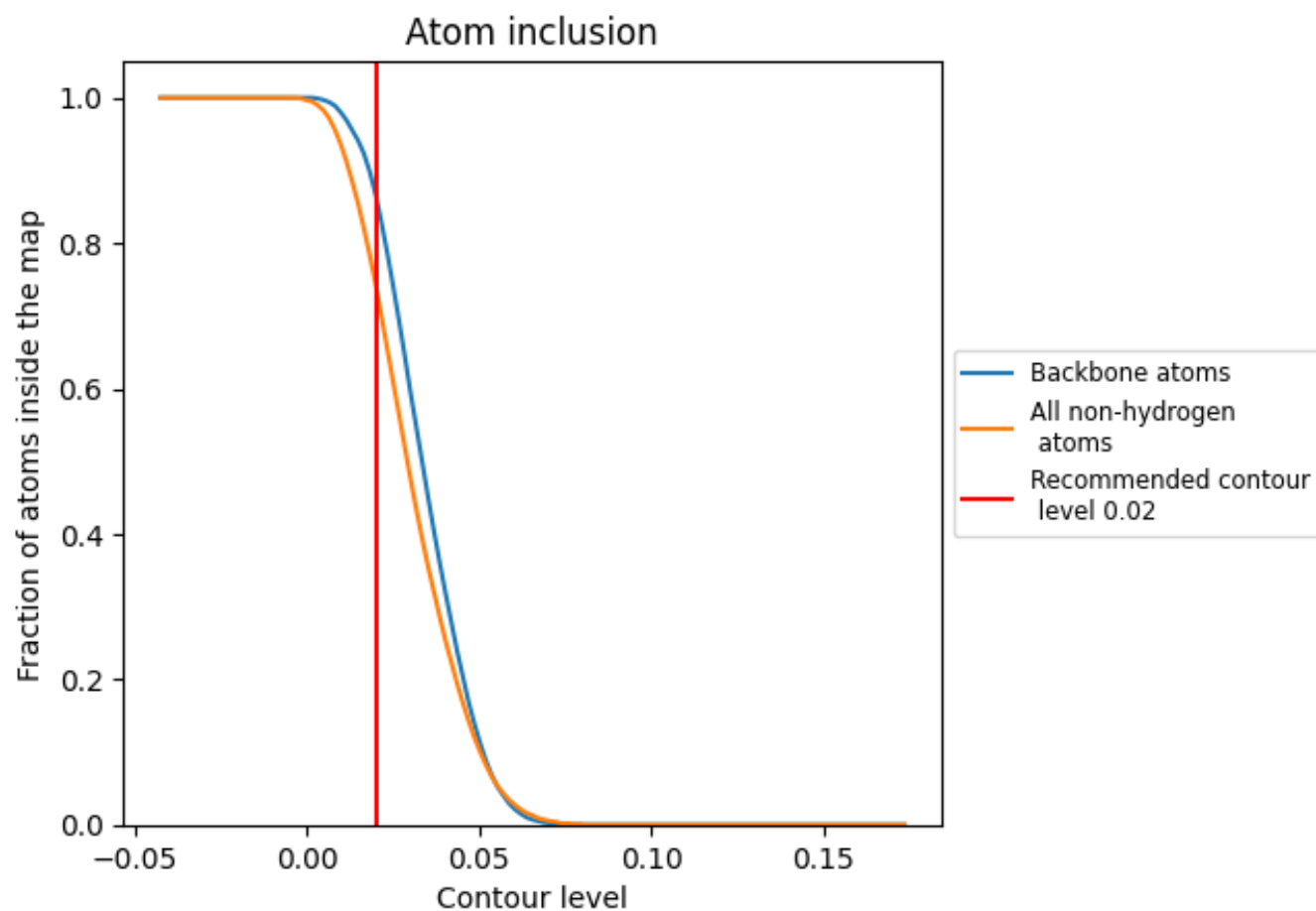
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.02).

9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 74% 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 (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7410	 0.3390
1	 0.8830	 0.3610
2	 0.8970	 0.3760
6	 0.9050	 0.3320
7	 0.6840	 0.3700
8	 0.3980	 0.2320
A	 0.7580	 0.3680
B	 0.6190	 0.3050
C	 0.8040	 0.4470
D	 0.8070	 0.4120
E	 0.7670	 0.3790
F	 0.7610	 0.3610
G	 0.7080	 0.3880
I	 0.7410	 0.3890
K	 0.6770	 0.2960
L	 0.8330	 0.4340
M	 0.7690	 0.3460
N	 0.7530	 0.4110
O	 0.7670	 0.3700
P	 0.7000	 0.4030
Q	 0.7990	 0.4310
S	 0.6840	 0.2910
V	 0.3040	 0.2010
W	 0.1450	 0.1650
Y	 0.7890	 0.4300
b	 0.6940	 0.3020
e	 0.6760	 0.4540
f	 0.8110	 0.4470
h	 0.7010	 0.3560
i	 0.7040	 0.3450
j	 0.7590	 0.4070
m	 0.8540	 0.2610
n	 0.6680	 0.2740
o	 0.6850	 0.2810
p	 0.6210	 0.3030



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Chain	Atom inclusion	Q-score
q	 0.0020	 0.0870
s	 0.7210	 0.3360
t	 0.6750	 0.2990
u	 0.3820	 0.1730
v	 0.3600	 0.2200
w	 0.2850	 0.1910
x	 0.8790	 0.3140
y	 0.3610	 0.1580
z	 0.7750	 0.3490