



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 05:33 AM UTC

PDB ID : 4V7F / pdb_00004v7f
EMDB ID : EMD-2528
Title : Arx1 pre-60S particle.
Authors : Leidig, C.; Thoms, M.; Holdermann, I.; Bradatsch, B.; Berninghausen, O.;
Bange, G.; Sinning, I.; Hurt, E.; Beckmann, R.
Deposited on : 2013-12-10
Resolution : 8.70 Å(reported)
Based on initial model : 3U5D

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:

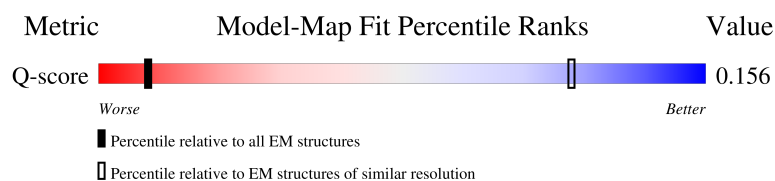
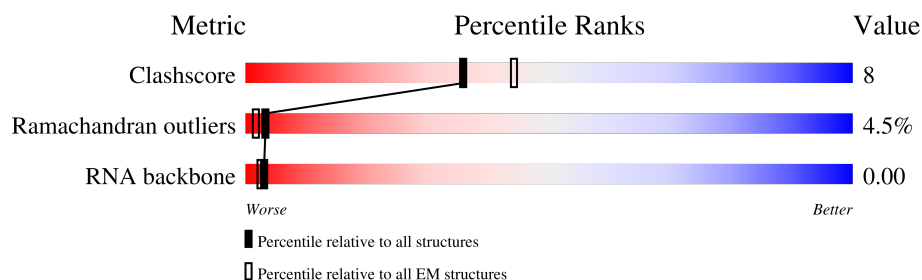
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 8.70 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	-
RNA backbone	8273	3508	-
Q-score	-	25397	282 (8.20 - 9.20)

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	3396	13% 91% 9%
2	2	158	98% .
3	3	121	91% 9%
4	A	217	98% 69% 29% .

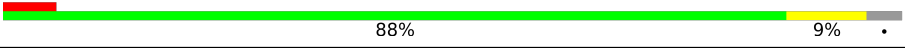
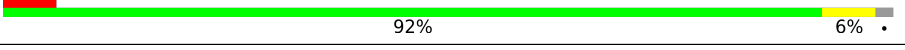
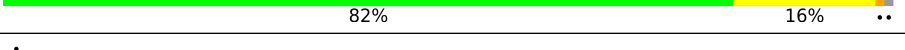
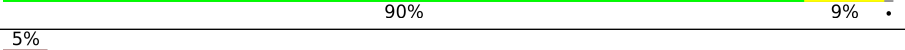
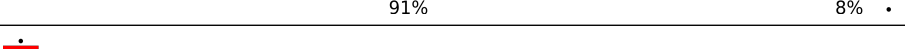
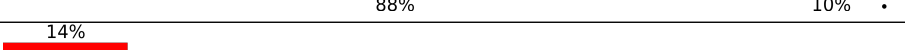
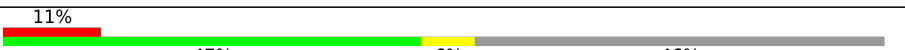
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Mol	Chain	Length	Quality of chain
5	B	254	
6	C	387	
7	D	362	
8	E	174	
9	F	191	
10	G	176	
11	H	256	
12	I	165	
13	J	199	
14	K	199	
15	L	137	
16	M	138	
17	N	149	
18	O	204	
19	P	297	
20	Q	186	
21	R	189	
22	S	172	
23	T	160	
24	U	184	
25	V	121	
26	W	142	
27	X	127	
28	Y	136	
29	Z	120	

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Mol	Chain	Length	Quality of chain
30	a	244	
31	b	105	
32	c	113	
33	d	130	
34	e	107	
35	f	121	
36	g	100	
37	h	88	
38	i	78	
39	j	51	
40	k	92	
41	l	593	
42	m	245	
43	n	236	
44	o	647	
45	p	199	
46	q	515	
47	r	322	
47	s	322	

2 Entry composition

There are 47 unique types of molecules in this entry. The entry contains 47221 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 ribosomal RNA.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	1	3394	Total	C	O	P	0	0
			20363	10182	6788	3393		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
2	2	158	Total	C	O	P	0	0
			948	474	316	158		

- Molecule 3 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	3	121	Total	C	O	P	0	0
			725	363	242	120		

- Molecule 4 is a protein called 60S ribosomal protein L1.

Mol	Chain	Residues	Atoms			AltConf	Trace
4	A	217	Total	C	N	0	0
			651	434	217		

- Molecule 5 is a protein called 60S ribosomal protein L2.

Mol	Chain	Residues	Atoms			AltConf	Trace
5	B	252	Total	C	N	0	0
			756	504	252		

- Molecule 6 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms			AltConf	Trace
6	C	386	Total	C	N	0	0
			1158	772	386		

- Molecule 7 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms			AltConf	Trace
7	D	361	Total	C	N	0	0
			1083	722	361		

- Molecule 8 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms			AltConf	Trace
8	E	169	Total	C	N	0	0
			507	338	169		

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

Mol	Chain	Residues	Atoms			AltConf	Trace
9	F	191	Total	C	N	0	0
			573	382	191		

- Molecule 10 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms			AltConf	Trace
10	G	175	Total	C	N	0	0
			525	350	175		

- Molecule 11 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms			AltConf	Trace
11	H	233	Total	C	N	0	0
			699	466	233		

- Molecule 12 is a protein called 60S ribosomal protein L12.

Mol	Chain	Residues	Atoms			AltConf	Trace
12	I	127	Total	C	N	0	0
			381	254	127		

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

Mol	Chain	Residues	Atoms			AltConf	Trace
13	J	197	Total	C	N	0	0
			591	394	197		

- Molecule 14 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms			AltConf	Trace
14	K	193	Total	C	N	0	0
			579	386	193		

- Molecule 15 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms			AltConf	Trace
15	L	136	Total	C	N	0	0
			408	272	136		

- Molecule 16 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms			AltConf	Trace
16	M	136	Total	C	N	0	0
			408	272	136		

- Molecule 17 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms			AltConf	Trace
17	N	148	Total	C	N	0	0
			444	296	148		

- Molecule 18 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues	Atoms			AltConf	Trace
18	O	203	Total	C	N	0	0
			609	406	203		

- Molecule 19 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms			AltConf	Trace
19	P	269	Total	C	N	0	0
			807	538	269		

- Molecule 20 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms			AltConf	Trace
20	Q	185	Total	C	N	0	0
			555	370	185		

- Molecule 21 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms			AltConf	Trace
21	R	188	Total	C	N	0	0
			564	376	188		

- Molecule 22 is a protein called 60S ribosomal protein L20.

Mol	Chain	Residues	Atoms			AltConf	Trace
22	S	172	Total	C	N	0	0
			516	344	172		

- Molecule 23 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms			AltConf	Trace
23	T	159	Total	C	N	0	0
			477	318	159		

- Molecule 24 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms			AltConf	Trace
24	U	183	Total	C	N	0	0
			549	366	183		

- Molecule 25 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms			AltConf	Trace
25	V	100	Total	C	N	0	0
			300	200	100		

- Molecule 26 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms			AltConf	Trace
26	W	121	Total	C	N	0	0
			363	242	121		

- Molecule 27 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms			AltConf	Trace
27	X	126	Total	C	N	0	0
			378	252	126		

- Molecule 28 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms			AltConf	Trace
28	Y	135	Total	C	N	0	0
			405	270	135		

- Molecule 29 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms			AltConf	Trace
29	Z	119	Total	C	N	0	0
			357	238	119		

- Molecule 30 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms			AltConf	Trace
30	a	222	Total	C	N	0	0
			666	444	222		

- Molecule 31 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms			AltConf	Trace
31	b	97	Total	C	N	0	0
			291	194	97		

- Molecule 32 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms			AltConf	Trace
32	c	109	Total	C	N	0	0
			327	218	109		

- Molecule 33 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms			AltConf	Trace
33	d	127	Total	C	N	0	0
			381	254	127		

- Molecule 34 is a protein called 60S ribosomal protein L33.

Mol	Chain	Residues	Atoms			AltConf	Trace
34	e	106	Total	C	N	0	0
			318	212	106		

- Molecule 35 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms			AltConf	Trace
35	f	112	Total	C	N	0	0
			336	224	112		

- Molecule 36 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms			AltConf	Trace
36	g	99	Total	C	N	0	0
			297	198	99		

- Molecule 37 is a protein called 60S ribosomal protein L37.

Mol	Chain	Residues	Atoms			AltConf	Trace
37	h	87	Total	C	N	0	0
			261	174	87		

- Molecule 38 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms			AltConf	Trace
38	i	77	Total	C	N	0	0
			231	154	77		

- Molecule 39 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms			AltConf	Trace
39	j	50	Total	C	N	0	0
			150	100	50		

- Molecule 40 is a protein called 60S ribosomal protein L43.

Mol	Chain	Residues	Atoms			AltConf	Trace
40	k	91	Total	C	N	0	0
			273	182	91		

- Molecule 41 is a protein called metalloprotease ARX1.

Mol	Chain	Residues	Atoms			AltConf	Trace
41	l	380	Total	C	N	0	0
			1140	760	380		

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

Mol	Chain	Residues	Atoms			AltConf	Trace
42	m	224	Total	C	N	0	0
			672	448	224		

- Molecule 43 is a protein called mRNA turnover protein 4.

Mol	Chain	Residues	Atoms			AltConf	Trace
43	n	236	Total	C	N	0	0
			708	472	236		

- Molecule 44 is a protein called Nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms			AltConf	Trace
44	o	347	Total	C	N	0	0
			1041	694	347		

- Molecule 45 is a protein called Ribosome biogenesis protein RLP24.

Mol	Chain	Residues	Atoms			AltConf	Trace
45	p	63	Total	C	N	0	0
			189	126	63		

- Molecule 46 is a protein called Ribosome assembly protein 4.

Mol	Chain	Residues	Atoms			AltConf	Trace
46	q	443	Total	C	N	0	0
			1329	886	443		

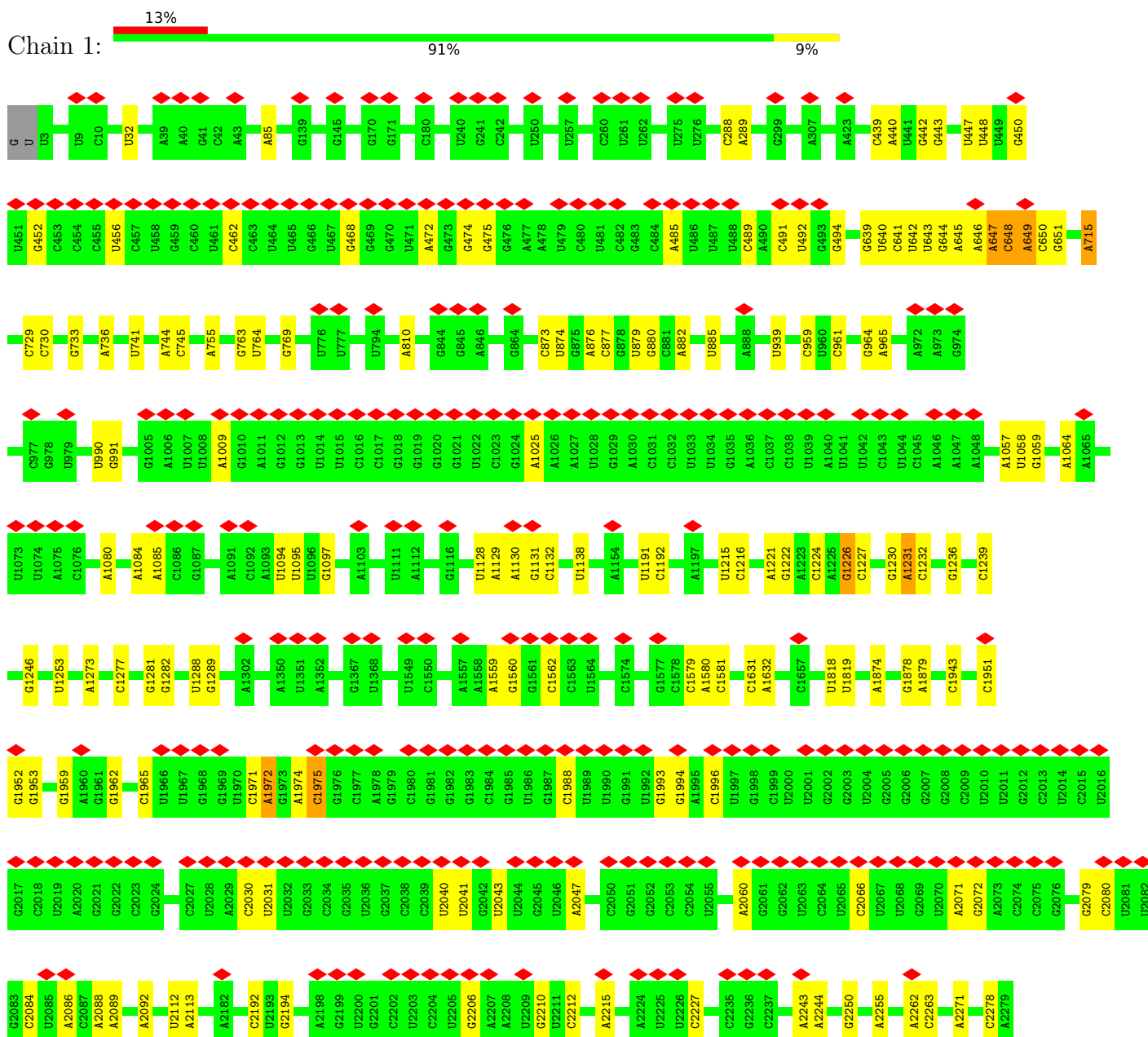
- Molecule 47 is a protein called Ribosome biogenesis protein RLP7.

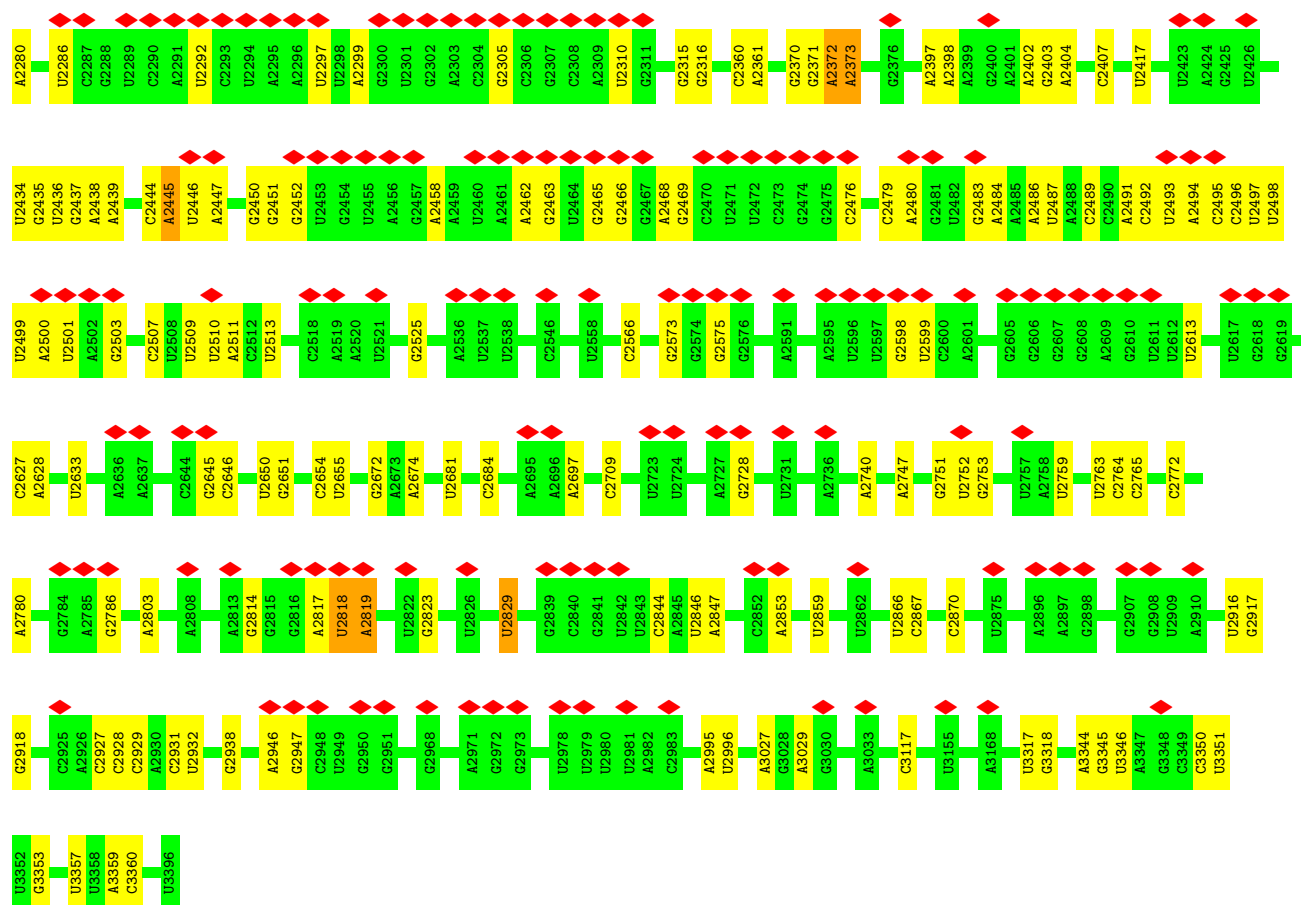
Mol	Chain	Residues	Atoms			AltConf	Trace
47	r	322	Total	C	N	0	0
			966	644	322		
47	s	322	Total	C	N	0	0
			966	644	322		

3 Residue-property plots

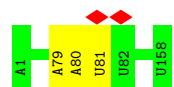
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

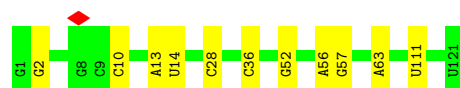




• Molecule 2: 5.8S ribosomal RNA



• Molecule 3: 5S ribosomal RNA

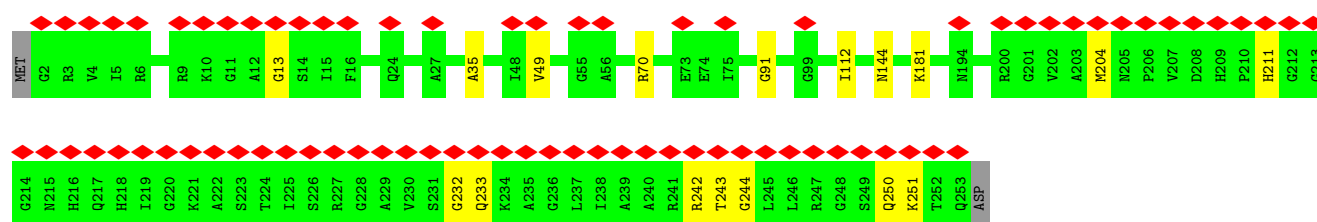
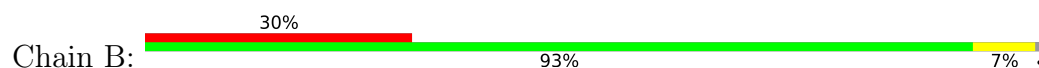


• Molecule 4: 60S ribosomal protein L1

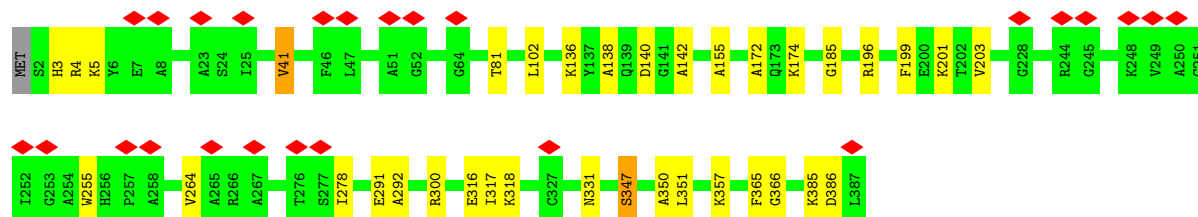
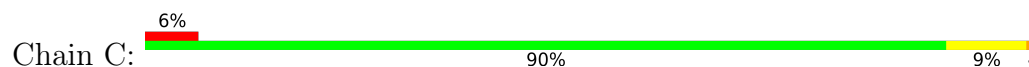




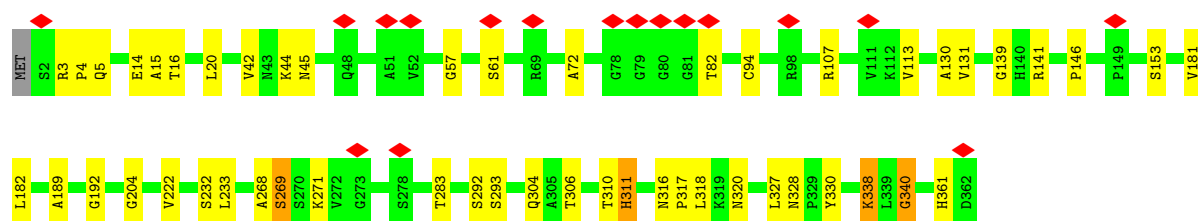
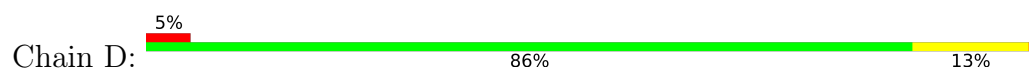
• Molecule 5: 60S ribosomal protein L2



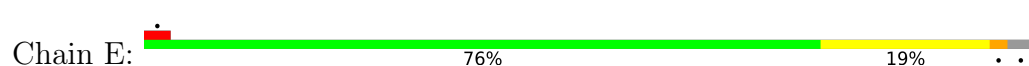
• Molecule 6: 60S ribosomal protein L3

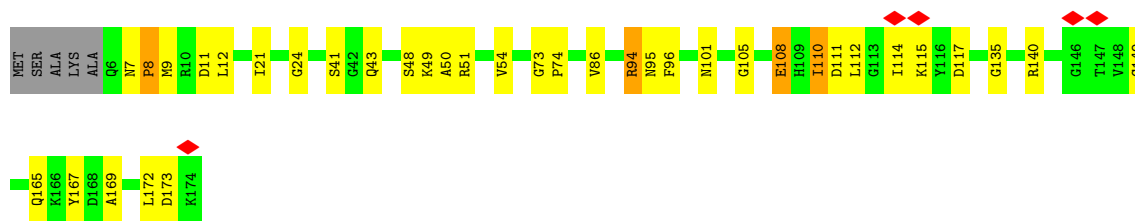


• Molecule 7: 60S ribosomal protein L4

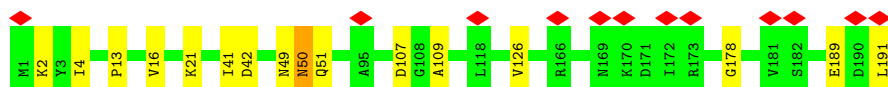
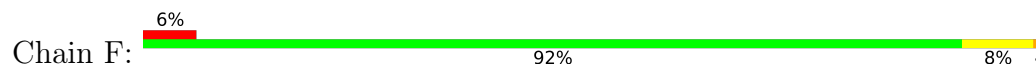


• Molecule 8: 60S ribosomal protein L11

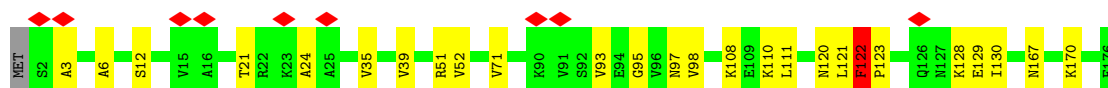
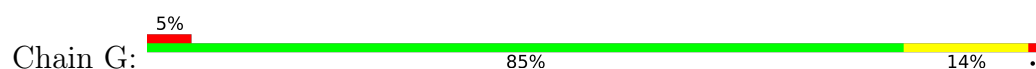




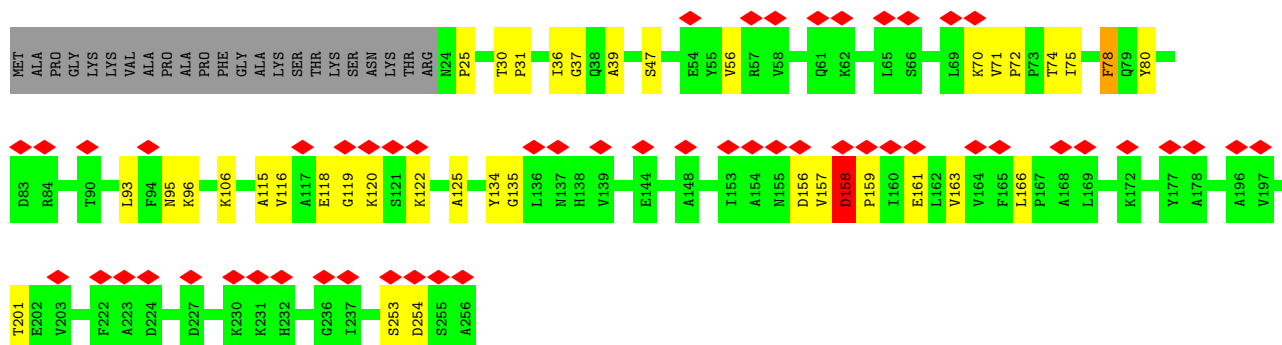
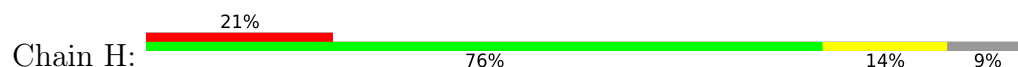
- Molecule 9: 60S ribosomal protein L9



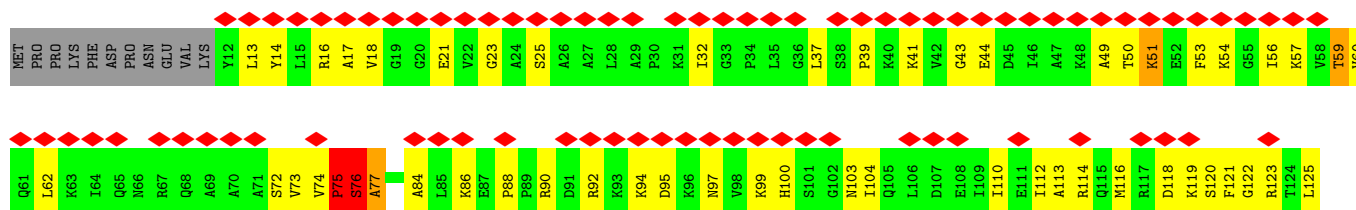
- Molecule 10: 60S ribosomal protein L6

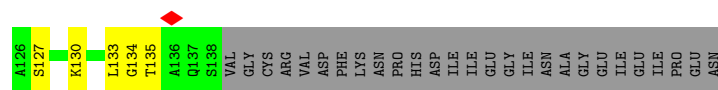


- Molecule 11: 60S ribosomal protein L8



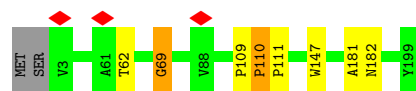
- Molecule 12: 60S ribosomal protein L12





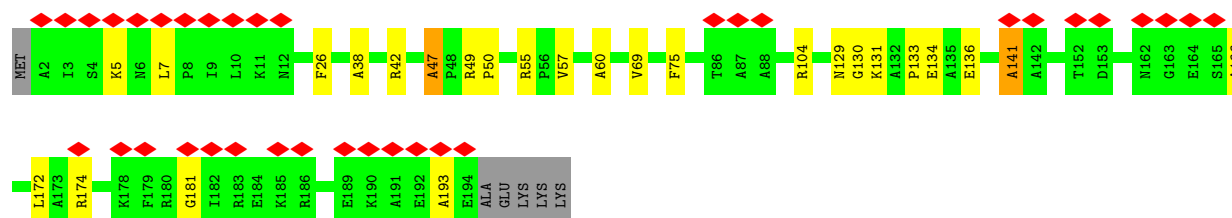
- Molecule 13: 60S ribosomal protein L16

Chain J: 95%



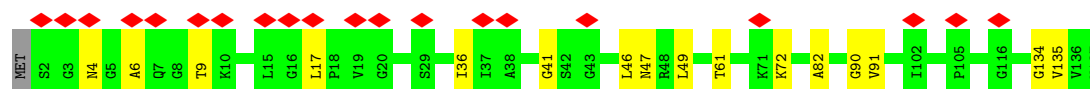
- Molecule 14: 60S ribosomal protein L13

Chain K: 84%



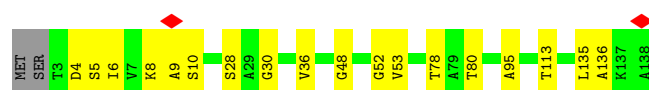
- Molecule 15: 60S ribosomal protein L23

Chain L: 88%



- Molecule 16: 60S ribosomal protein L14

Chain M: 86%

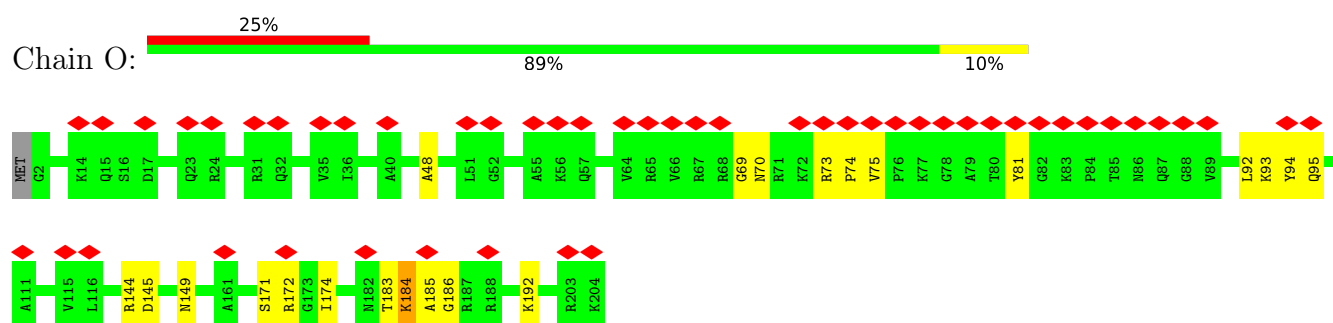


- Molecule 17: 60S ribosomal protein L28

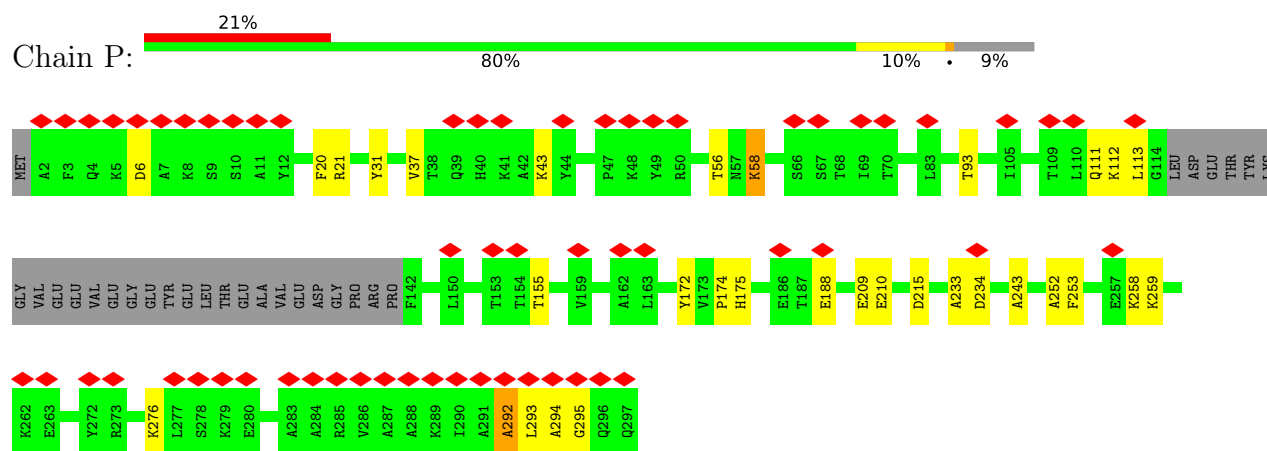
Chain N: 83%



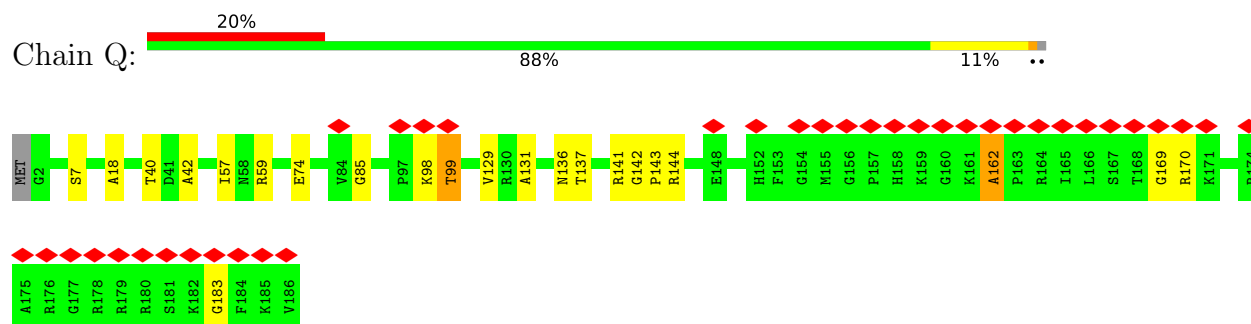
- Molecule 18: 60S ribosomal protein L15



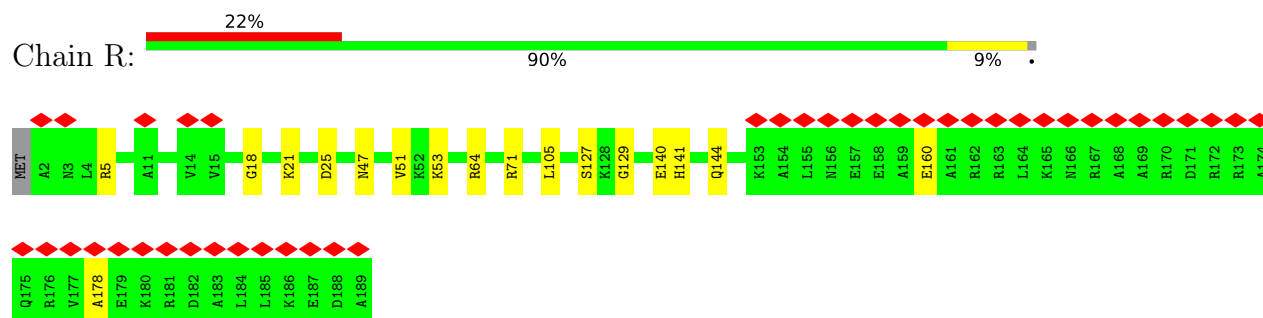
• Molecule 19: 60S ribosomal protein L5



• Molecule 20: 60S ribosomal protein L18

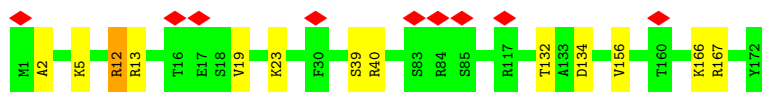


• Molecule 21: 60S ribosomal protein L19

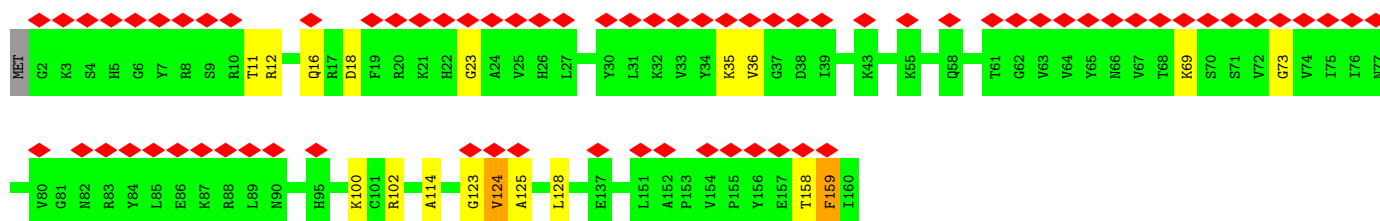
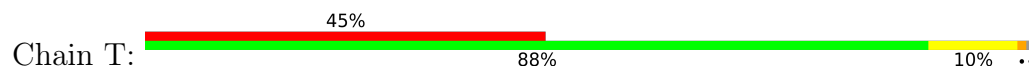


• Molecule 22: 60S ribosomal protein L20

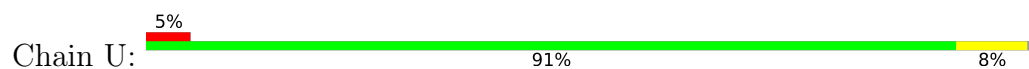




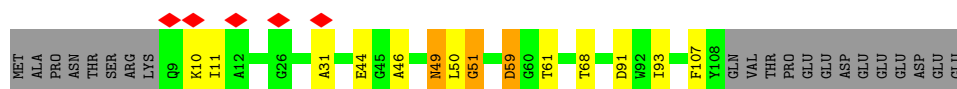
- Molecule 23: 60S ribosomal protein L21



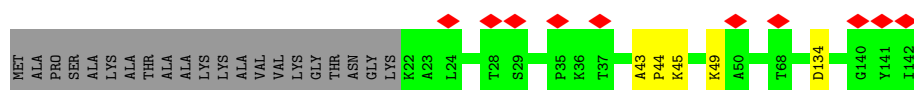
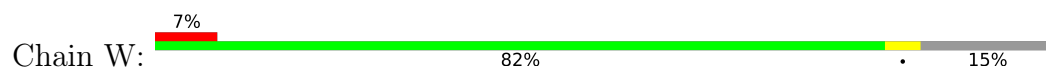
- Molecule 24: 60S ribosomal protein L17



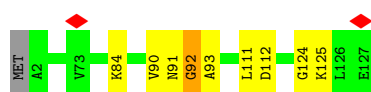
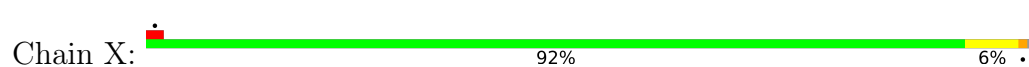
- Molecule 25: 60S ribosomal protein L22



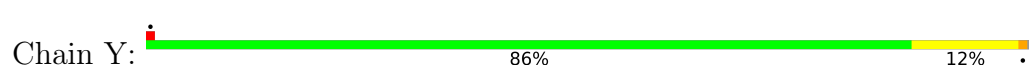
- Molecule 26: 60S ribosomal protein L25

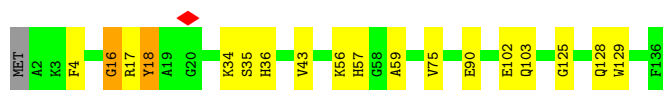


- Molecule 27: 60S ribosomal protein L26

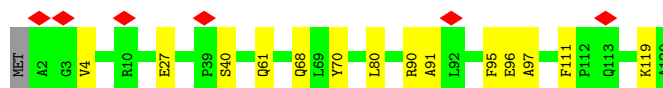
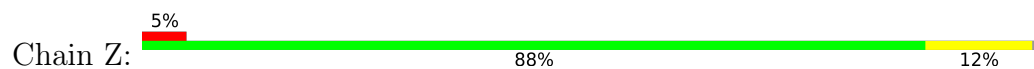


- Molecule 28: 60S ribosomal protein L27

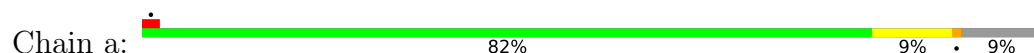




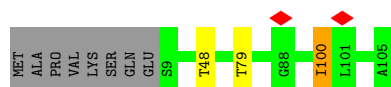
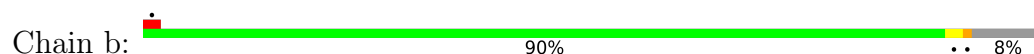
- Molecule 29: 60S ribosomal protein L35



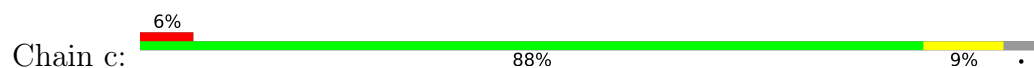
- Molecule 30: 60S ribosomal protein L7



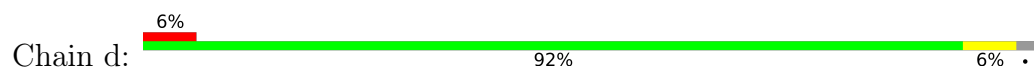
- Molecule 31: 60S ribosomal protein L30



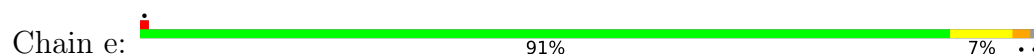
- Molecule 32: 60S ribosomal protein L31

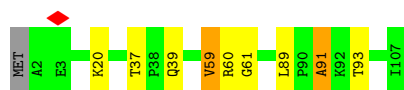


- Molecule 33: 60S ribosomal protein L32

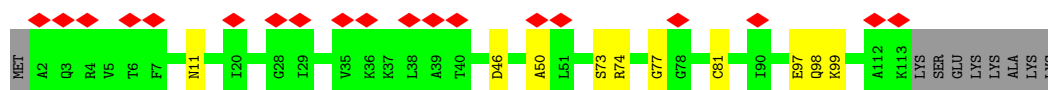
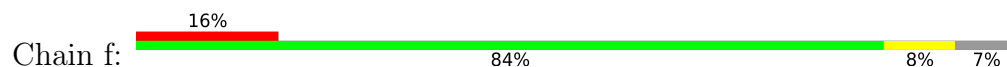


- Molecule 34: 60S ribosomal protein L33

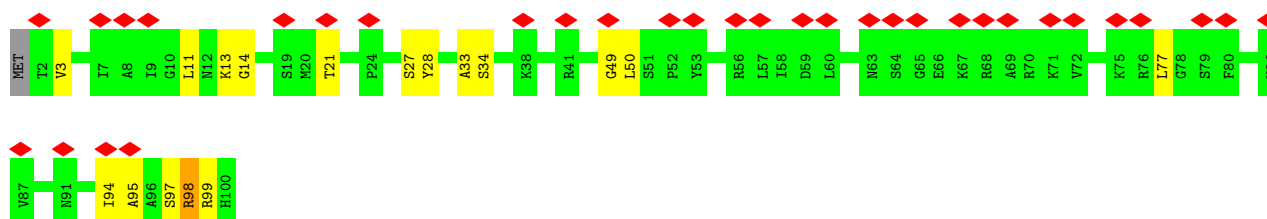
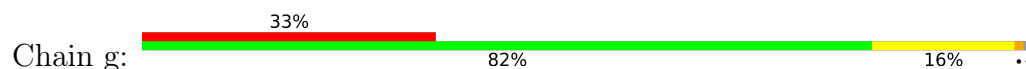




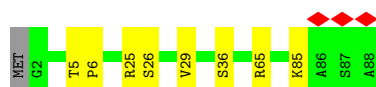
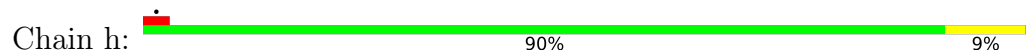
- Molecule 35: 60S ribosomal protein L34



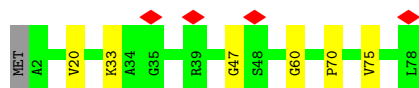
- Molecule 36: 60S ribosomal protein L36



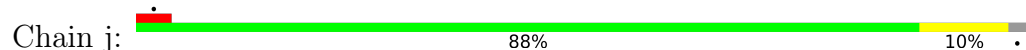
- Molecule 37: 60S ribosomal protein L37



- Molecule 38: 60S ribosomal protein L38

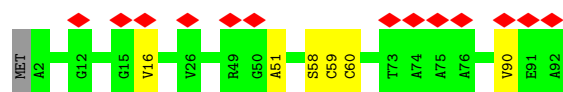


- Molecule 39: 60S ribosomal protein L39



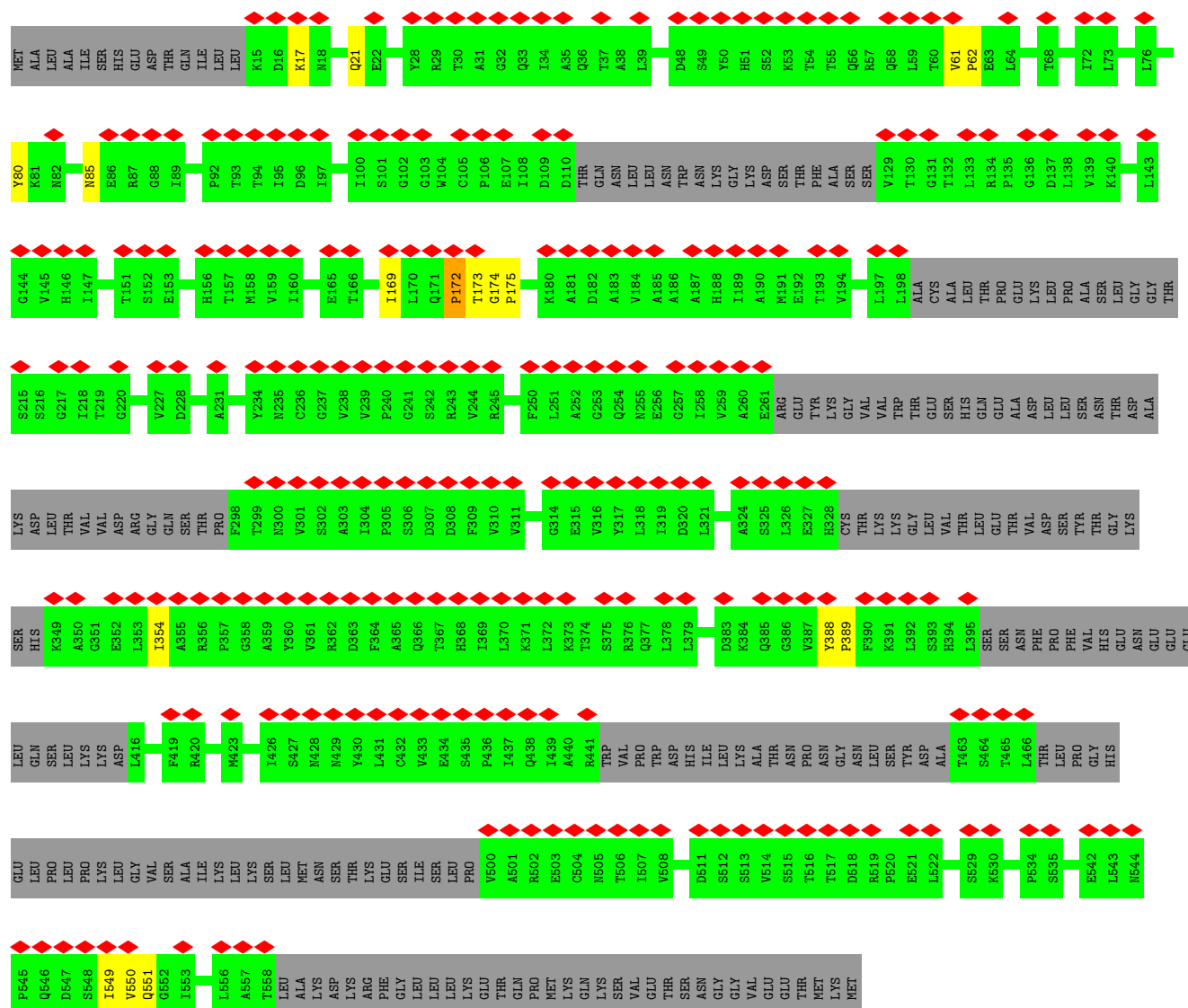
- Molecule 40: 60S ribosomal protein L43





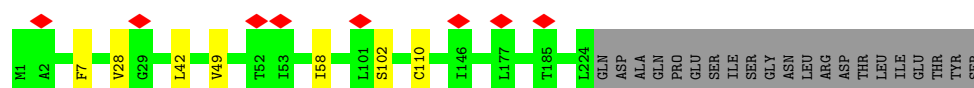
- Molecule 41: metalloprotease ARX1

Chain 1: 42% 61% 36%

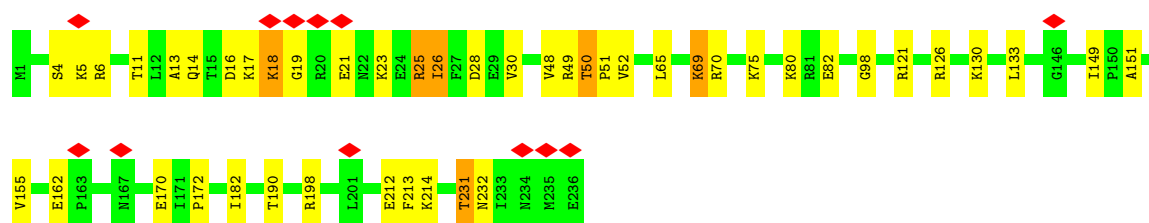
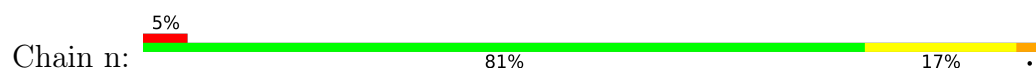


- Molecule 42: Eukaryotic translation initiation factor 6

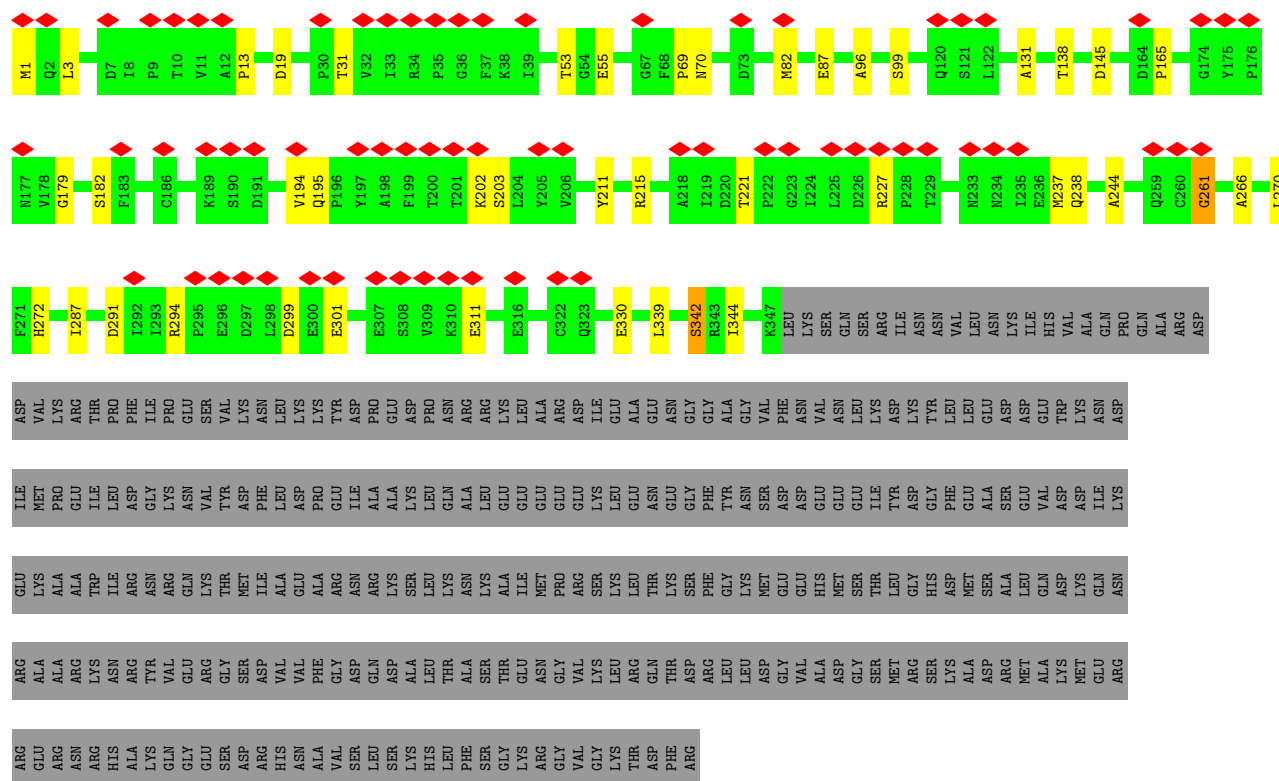
Chain m: 89% 9%



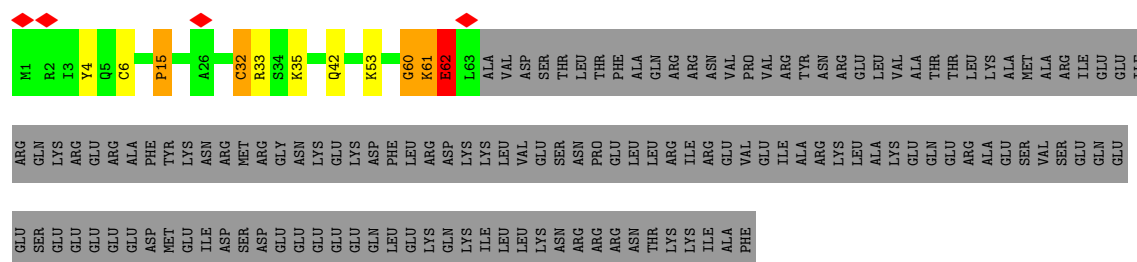
- Molecule 43: mRNA turnover protein 4



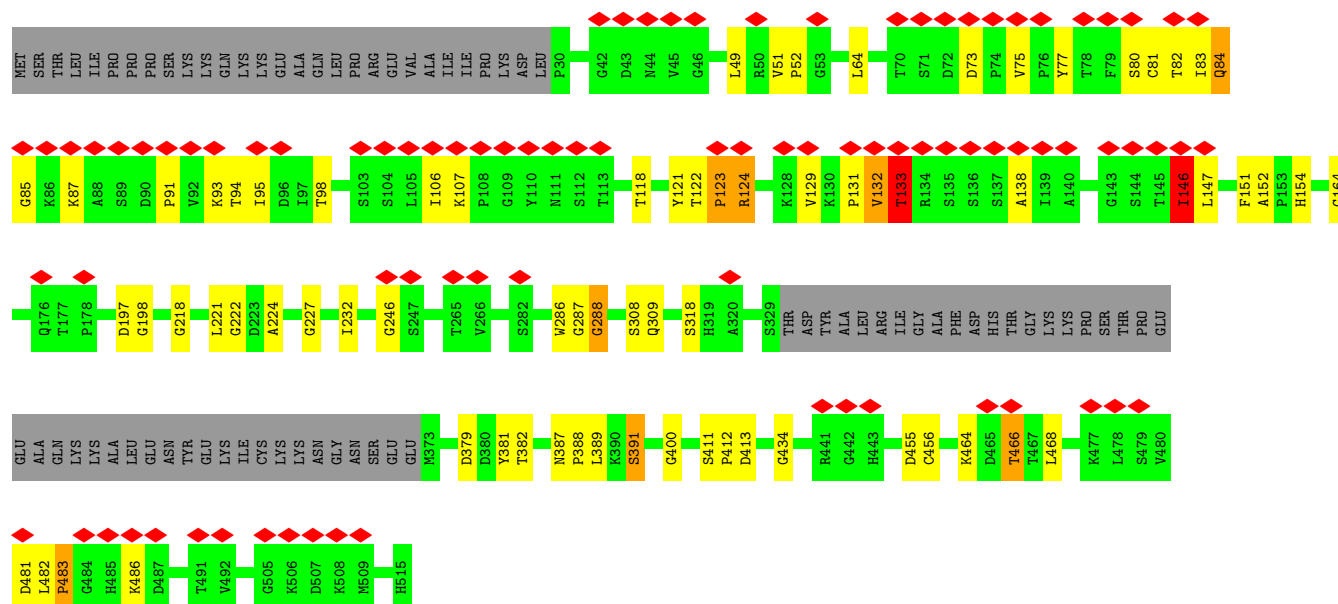
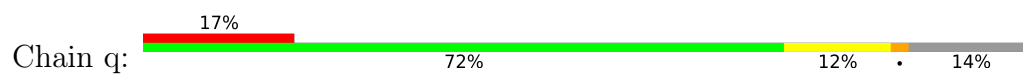
• Molecule 44: Nucleolar GTP-binding protein 1



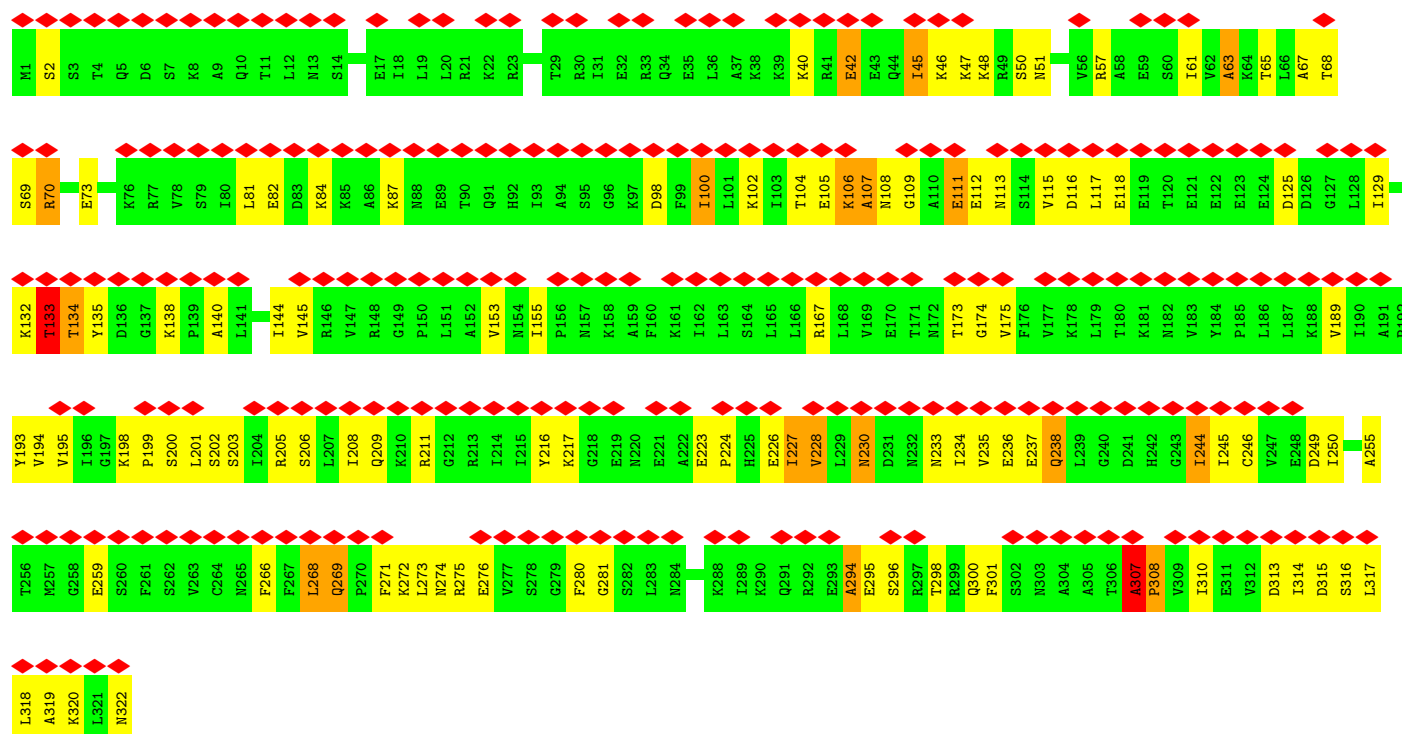
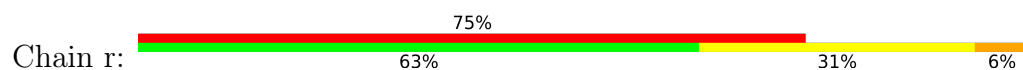
• Molecule 45: Ribosome biogenesis protein RLP24



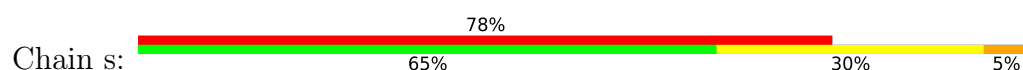
• Molecule 46: Ribosome assembly protein 4

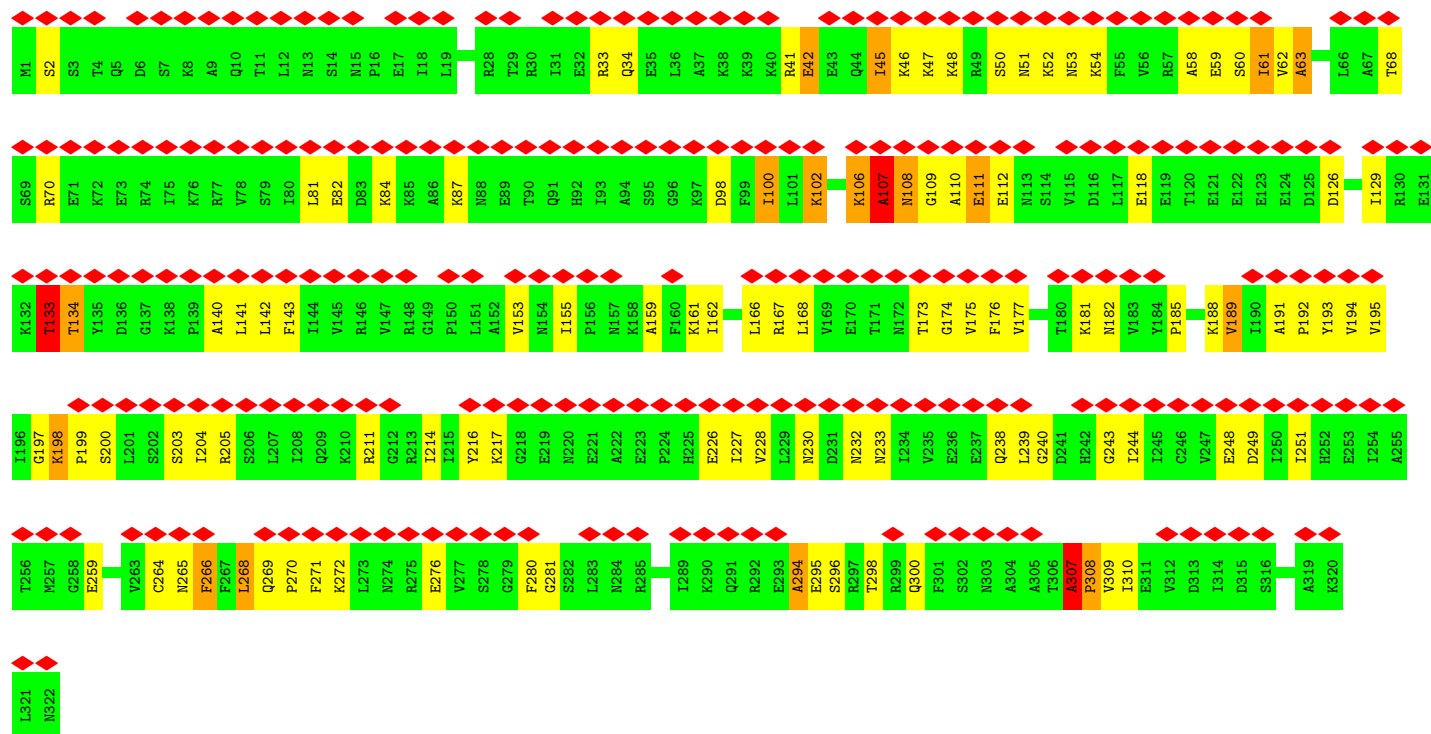


• Molecule 47: Ribosome biogenesis protein RLP7



• Molecule 47: Ribosome biogenesis protein RLP7





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	75887	Depositor
Resolution determination method	Not provided	
CTF correction method	Not provided	
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	TVIPS TEMCAM-F416 (4k x 4k)	Depositor
Maximum map value	2.010	Depositor
Minimum map value	-0.822	Depositor
Average map value	0.006	Depositor
Map value standard deviation	0.155	Depositor
Recommended contour level	0.45	Depositor
Map size ($\text{\AA}$)	439.047, 439.047, 439.047	wwPDB
Map dimensions	414, 414, 414	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.0605, 1.0605, 1.0605	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	1.08	31/20361 (0.2%)	1.80	334/20359 (1.6%)
2	2	0.86	0/947	0.93	0/946
3	3	1.29	1/724 (0.1%)	1.66	4/723 (0.6%)
4	A	2.36	22/650 (3.4%)	3.29	78/649 (12.0%)
5	B	0.98	0/755	1.89	11/754 (1.5%)
6	C	1.14	0/1157	1.98	21/1156 (1.8%)
7	D	1.16	2/1082 (0.2%)	2.10	31/1081 (2.9%)
8	E	0.94	0/506	1.87	6/505 (1.2%)
9	F	0.97	0/572	1.76	7/571 (1.2%)
10	G	1.21	1/524 (0.2%)	1.95	20/523 (3.8%)
11	H	0.85	0/698	1.83	17/697 (2.4%)
12	I	3.02	35/380 (9.2%)	3.54	60/379 (15.8%)
13	J	0.80	0/590	1.68	5/589 (0.8%)
14	K	1.11	1/578 (0.2%)	2.17	19/577 (3.3%)
15	L	1.02	0/407	1.92	11/406 (2.7%)
16	M	1.10	0/407	1.99	11/406 (2.7%)
17	N	1.28	3/443 (0.7%)	2.15	14/442 (3.2%)
18	O	1.14	0/608	1.98	11/607 (1.8%)
19	P	0.93	0/805	1.72	6/803 (0.7%)
20	Q	1.21	0/554	2.20	18/553 (3.3%)
21	R	0.97	1/563 (0.2%)	1.76	9/562 (1.6%)
22	S	1.25	1/515 (0.2%)	1.96	10/514 (1.9%)
23	T	1.10	0/476	1.83	7/475 (1.5%)
24	U	1.14	0/548	1.90	7/547 (1.3%)
25	V	0.77	0/299	1.63	4/298 (1.3%)
26	W	0.91	0/362	1.84	4/361 (1.1%)
27	X	1.04	0/377	1.86	5/376 (1.3%)
28	Y	0.76	0/404	1.75	6/403 (1.5%)
29	Z	1.00	0/356	1.85	6/355 (1.7%)
30	a	1.18	0/665	2.02	19/664 (2.9%)
31	b	0.71	0/290	1.67	4/289 (1.4%)
32	c	1.01	0/326	1.82	6/325 (1.8%)
33	d	1.17	0/380	1.89	5/379 (1.3%)
34	e	1.32	0/317	2.04	8/316 (2.5%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	f	0.96	0/335	1.83	6/334 (1.8%)
36	g	1.07	1/296 (0.3%)	1.89	4/295 (1.4%)
37	h	1.23	1/260 (0.4%)	2.19	6/259 (2.3%)
38	i	0.79	0/230	1.81	5/229 (2.2%)
39	j	1.00	0/149	1.95	4/148 (2.7%)
40	k	1.03	0/272	1.83	3/271 (1.1%)
41	l	0.84	3/1138 (0.3%)	1.28	8/1136 (0.7%)
42	m	0.42	0/671	1.48	5/670 (0.7%)
43	n	2.01	6/707 (0.8%)	2.70	49/706 (6.9%)
44	o	1.91	4/1040 (0.4%)	2.60	57/1039 (5.5%)
45	p	2.74	3/188 (1.6%)	2.93	10/187 (5.3%)
46	q	1.96	9/1327 (0.7%)	2.54	63/1325 (4.8%)
47	r	1.93	2/965 (0.2%)	2.43	46/964 (4.8%)
47	s	1.93	2/965 (0.2%)	2.43	46/964 (4.8%)
All	All	1.25	129/47169 (0.3%)	1.96	1096/47117 (2.3%)

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
6	C	0	1
7	D	0	1
8	E	0	1
9	F	0	1
10	G	0	1
11	H	0	3
12	I	0	5
13	J	0	1
23	T	0	1
30	a	0	1
32	c	0	1
43	n	0	2
45	p	0	1
46	q	0	7
47	r	0	1
47	s	0	1
All	All	0	31

The worst 5 of 129 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
45	p	61	LYS	C-N	23.23	1.66	1.33
1	1	648	C	O5'-C5'	20.94	2.05	1.42
1	1	2819	A	C5'-C4'	15.12	1.82	1.52
12	I	76	SER	N-CA	13.81	1.64	1.46
1	1	648	C	P-O5'	-13.35	1.33	1.60

The worst 5 of 1096 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	885	U	P-O3'-C3'	35.13	172.90	120.20
1	1	649	A	P-O5'-C5'	33.74	170.61	120.00
1	1	2819	A	O5'-C5'-C4'	33.06	160.39	110.80
1	1	648	C	P-O5'-C5'	-30.57	74.15	120.00
1	1	647	A	O3'-P-O5'	-24.75	66.87	104.00

There are no chirality outliers.

5 of 31 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	A	19	TYR	Peptide
4	A	210	MET	Peptide
6	C	172	ALA	Peptide
7	D	318	LEU	Peptide
8	E	8	PRO	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	20363	0	6792	187	0
2	2	948	0	317	2	0
3	3	725	0	244	8	0
4	A	651	0	230	0	0
5	B	756	0	310	3	0
6	C	1158	0	433	2	0
7	D	1083	0	399	4	0
8	E	507	0	193	26	0
9	F	573	0	215	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	G	525	0	179	2	0
11	H	699	0	242	5	0
12	I	381	0	140	7	0
13	J	591	0	214	1	0
14	K	579	0	199	3	0
15	L	408	0	162	13	0
16	M	408	0	145	0	0
17	N	444	0	176	11	0
18	O	609	0	221	11	0
19	P	807	0	293	14	0
20	Q	555	0	204	23	0
21	R	564	0	202	6	0
22	S	516	0	175	0	0
23	T	477	0	175	9	0
24	U	549	0	196	0	0
25	V	300	0	109	2	0
26	W	363	0	121	0	0
27	X	378	0	134	2	0
28	Y	405	0	142	3	0
29	Z	357	0	118	2	0
30	a	666	0	241	0	0
31	b	291	0	113	0	0
32	c	327	0	114	0	0
33	d	381	0	135	0	0
34	e	318	0	117	4	0
35	f	336	0	121	1	0
36	g	297	0	109	2	0
37	h	261	0	104	0	0
38	i	231	0	79	1	0
39	j	150	0	47	1	0
40	k	273	0	108	0	0
41	l	1140	0	412	6	0
42	m	672	0	257	2	0
43	n	708	0	251	30	0
44	o	1041	0	359	19	0
45	p	189	0	68	2	0
46	q	1329	0	491	13	0
47	r	966	0	321	209	0
47	s	966	0	316	212	0
All	All	47221	0	16443	498	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 8.

The worst 5 of 498 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)
1:1:3027:A:H5'	44:o:194:VAL:C	1.16	1.58
47:r:50:SER:H	47:s:61:ILE:C	1.11	1.57
1:1:2819:A:C5'	1:1:2819:A:C4'	1.82	1.51
1:1:3027:A:C5'	44:o:194:VAL:C	1.86	1.48
47:r:199:PRO:CA	47:s:177:VAL:CA	1.90	1.47

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	215/217 (99%)	194 (90%)	11 (5%)	10 (5%)	2	16
5	B	250/254 (98%)	230 (92%)	14 (6%)	6 (2%)	4	27
6	C	384/387 (99%)	333 (87%)	37 (10%)	14 (4%)	2	20
7	D	359/362 (99%)	304 (85%)	34 (10%)	21 (6%)	1	14
8	E	167/174 (96%)	120 (72%)	26 (16%)	21 (13%)	0	4
9	F	189/191 (99%)	166 (88%)	17 (9%)	6 (3%)	3	21
10	G	173/176 (98%)	147 (85%)	16 (9%)	10 (6%)	1	14
11	H	231/256 (90%)	186 (80%)	26 (11%)	19 (8%)	0	9
12	I	125/165 (76%)	107 (86%)	11 (9%)	7 (6%)	1	14
13	J	195/199 (98%)	180 (92%)	11 (6%)	4 (2%)	5	30
14	K	191/199 (96%)	161 (84%)	18 (9%)	12 (6%)	1	13
15	L	134/137 (98%)	124 (92%)	9 (7%)	1 (1%)	18	56
16	M	134/138 (97%)	117 (87%)	8 (6%)	9 (7%)	1	12
17	N	146/149 (98%)	120 (82%)	15 (10%)	11 (8%)	1	10

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
18	O	201/204 (98%)	184 (92%)	10 (5%)	7 (4%)	3	20
19	P	265/297 (89%)	220 (83%)	27 (10%)	18 (7%)	1	11
20	Q	183/186 (98%)	163 (89%)	16 (9%)	4 (2%)	5	29
21	R	186/189 (98%)	170 (91%)	12 (6%)	4 (2%)	5	29
22	S	170/172 (99%)	154 (91%)	12 (7%)	4 (2%)	4	27
23	T	157/160 (98%)	140 (89%)	10 (6%)	7 (4%)	2	17
24	U	181/184 (98%)	155 (86%)	17 (9%)	9 (5%)	1	16
25	V	98/121 (81%)	75 (76%)	14 (14%)	9 (9%)	0	8
26	W	119/142 (84%)	106 (89%)	11 (9%)	2 (2%)	7	36
27	X	124/127 (98%)	107 (86%)	15 (12%)	2 (2%)	7	38
28	Y	133/136 (98%)	114 (86%)	9 (7%)	10 (8%)	1	10
29	Z	117/120 (98%)	99 (85%)	10 (8%)	8 (7%)	1	11
30	a	220/244 (90%)	200 (91%)	11 (5%)	9 (4%)	2	18
31	b	95/105 (90%)	86 (90%)	8 (8%)	1 (1%)	11	46
32	c	107/113 (95%)	94 (88%)	8 (8%)	5 (5%)	2	16
33	d	125/130 (96%)	111 (89%)	10 (8%)	4 (3%)	3	21
34	e	104/107 (97%)	100 (96%)	2 (2%)	2 (2%)	6	32
35	f	110/121 (91%)	97 (88%)	9 (8%)	4 (4%)	2	20
36	g	97/100 (97%)	75 (77%)	11 (11%)	11 (11%)	0	5
37	h	85/88 (97%)	71 (84%)	11 (13%)	3 (4%)	3	20
38	i	75/78 (96%)	66 (88%)	8 (11%)	1 (1%)	9	42
39	j	48/51 (94%)	44 (92%)	4 (8%)	0	100	100
40	k	89/92 (97%)	77 (86%)	9 (10%)	3 (3%)	3	21
41	l	376/593 (63%)	354 (94%)	14 (4%)	8 (2%)	5	30
42	m	222/245 (91%)	208 (94%)	13 (6%)	1 (0%)	24	63
43	n	234/236 (99%)	219 (94%)	9 (4%)	6 (3%)	4	25
44	o	345/647 (53%)	330 (96%)	9 (3%)	6 (2%)	7	36
45	p	61/199 (31%)	53 (87%)	4 (7%)	4 (7%)	1	12
46	q	439/515 (85%)	377 (86%)	40 (9%)	22 (5%)	1	16
47	r	320/322 (99%)	266 (83%)	31 (10%)	23 (7%)	1	11
47	s	320/322 (99%)	266 (83%)	31 (10%)	23 (7%)	1	11

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	8299/9350 (89%)	7270 (88%)	658 (8%)	371 (4%)	3 17

5 of 371 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	A	21	ASN
4	A	74	VAL
4	A	135	PRO
4	A	151	VAL
5	B	144	ASN

5.3.2 Protein sidechains [i](#)

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

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	0/3396	-	-
2	2	0/158	-	-
3	3	0/121	-	-
All	All	0/3675	-	-

There are no RNA backbone outliers to report.

There are no RNA pucker outliers to report.

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](#)

There are no ligands in this entry.

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	1
45	p	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	1	439:C	O3'	440:A	P	1.76
1	p	61:LYS	C	62:GLU	N	1.66

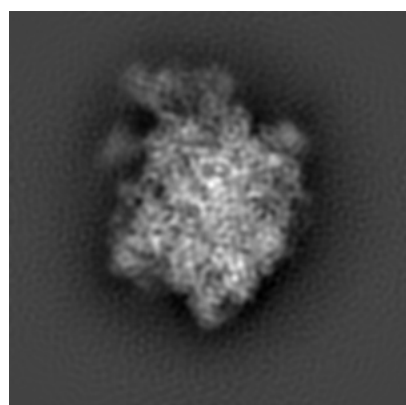
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-2528. These allow visual inspection of the internal detail of the map and identification of artifacts.

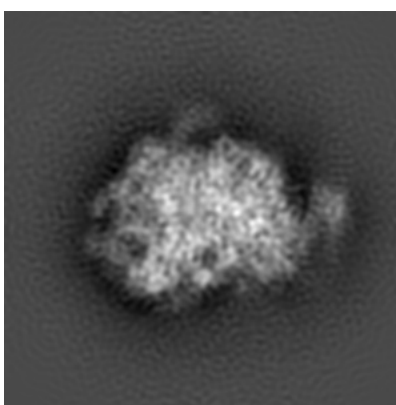
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

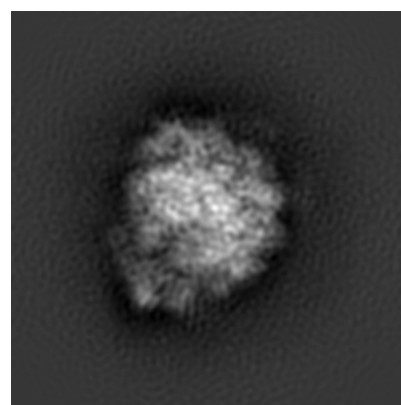
6.1.1 Primary map



X



Y

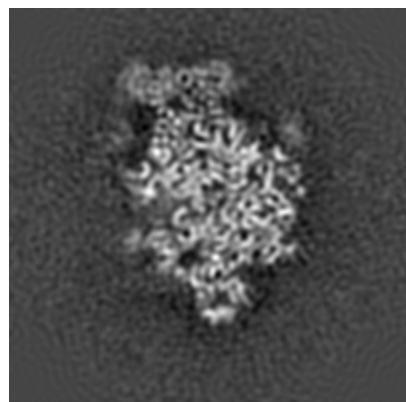


Z

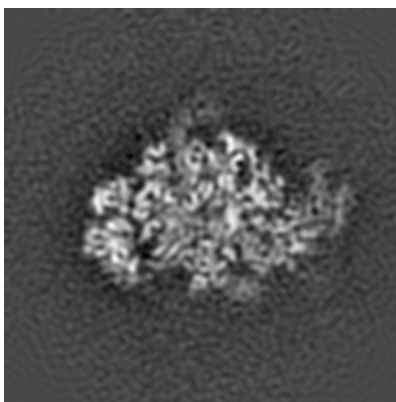
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

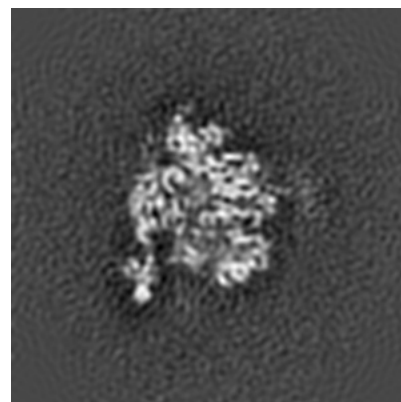
6.2.1 Primary map



X Index: 207



Y Index: 207

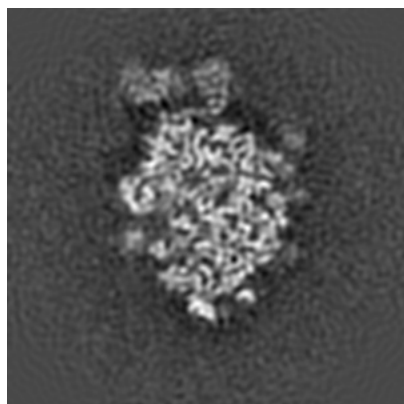


Z Index: 207

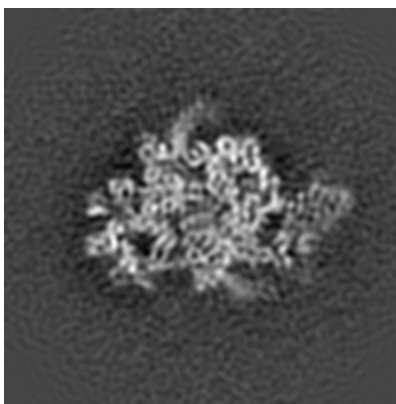
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

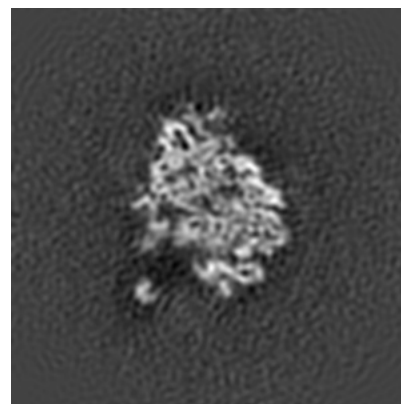
6.3.1 Primary map



X Index: 218



Y Index: 215

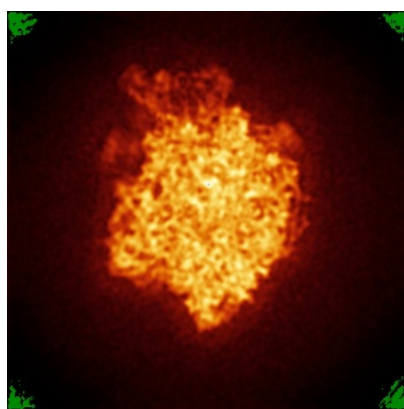


Z Index: 223

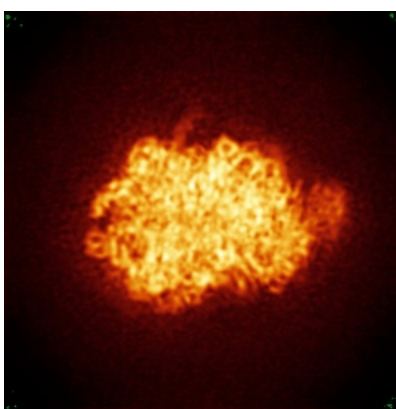
The images above show the largest variance slices of the map in three orthogonal directions.

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

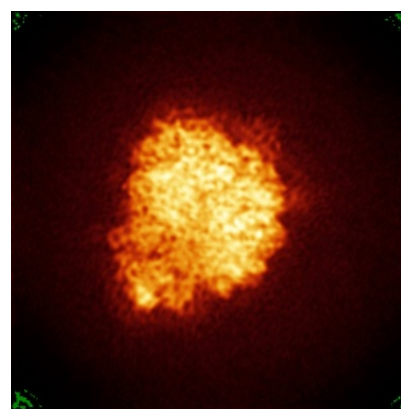
6.4.1 Primary map



X



Y

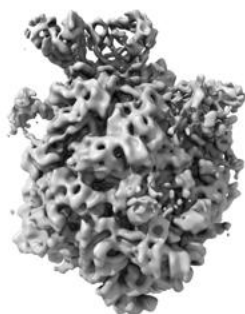


Z

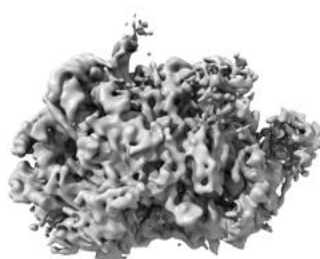
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

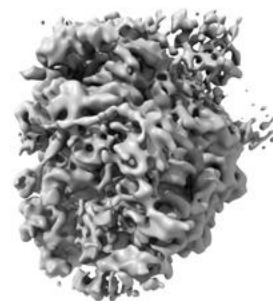
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.45. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

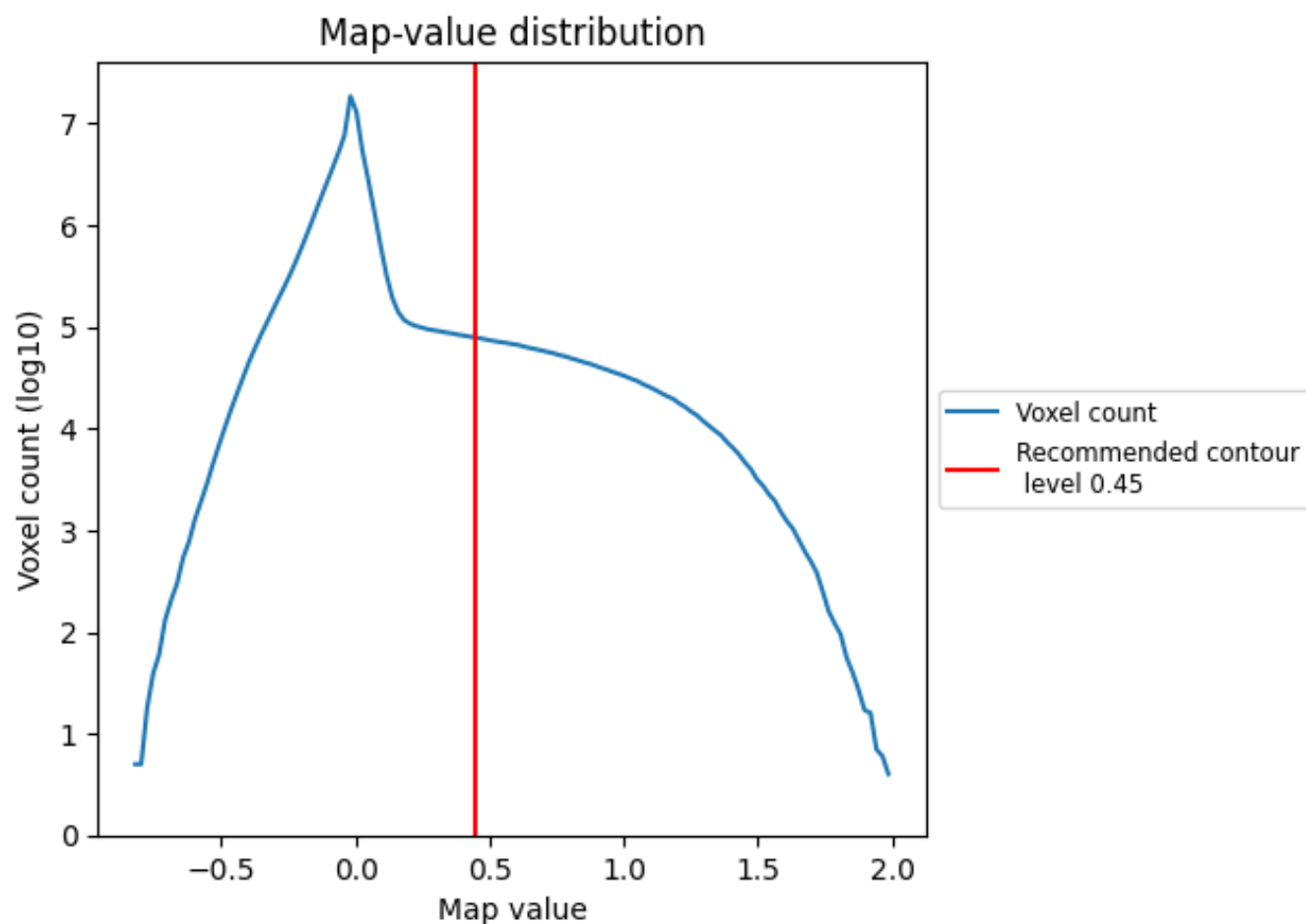
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

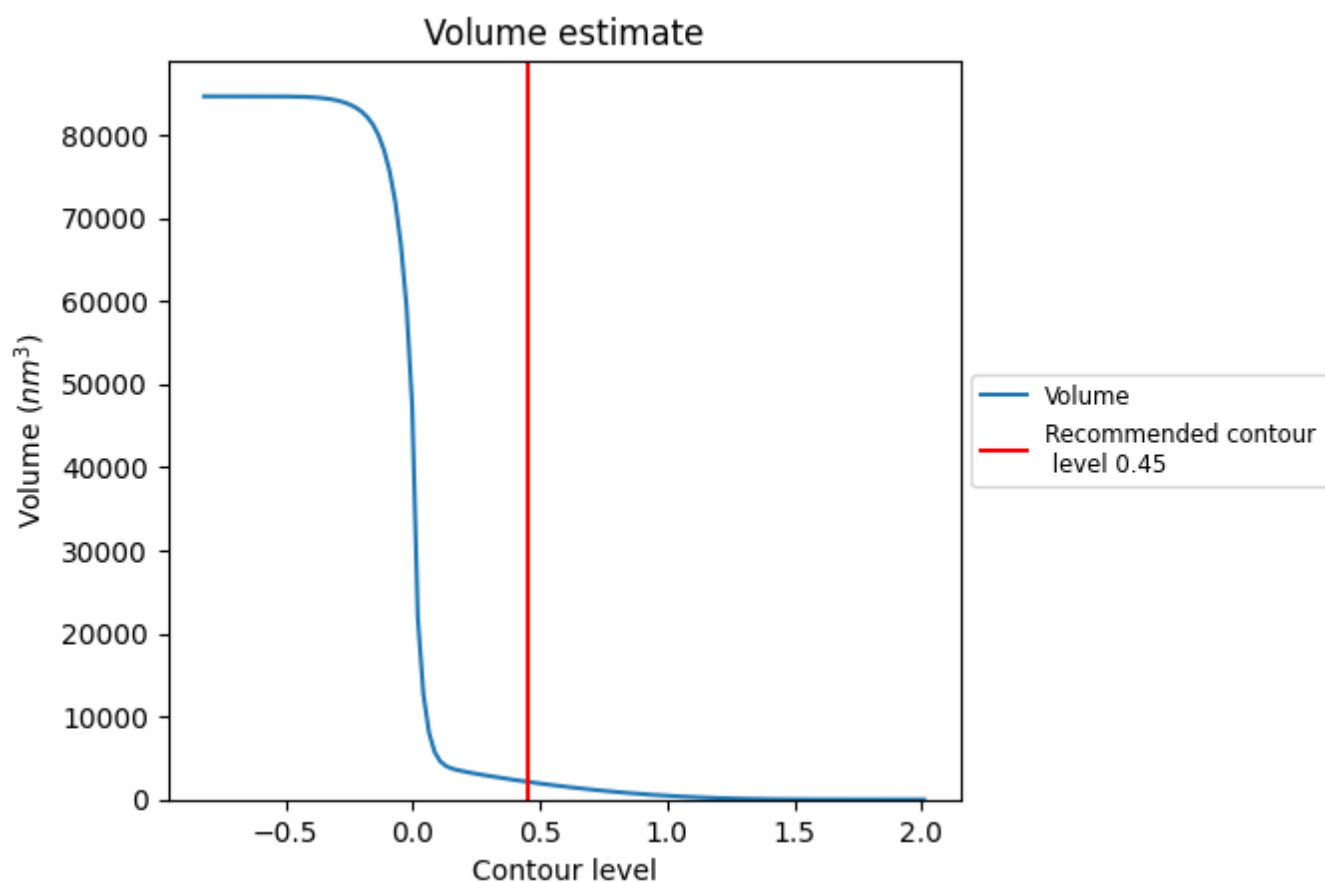
This section contains the results of statistical analysis of the map.

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.

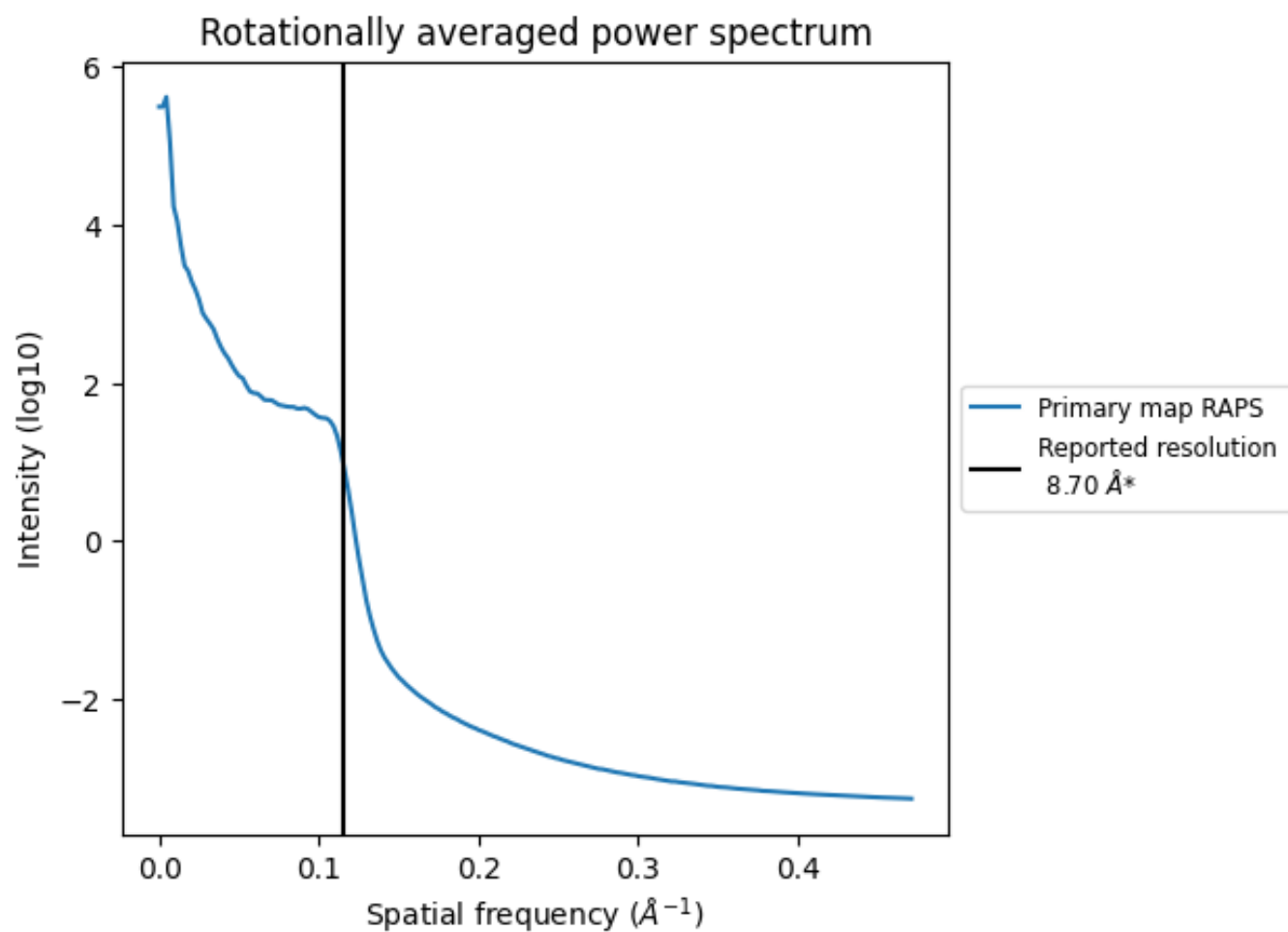
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2140 nm³; this corresponds to an approximate mass of 1933 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 0.115 $\text{\AA}^{-1}$

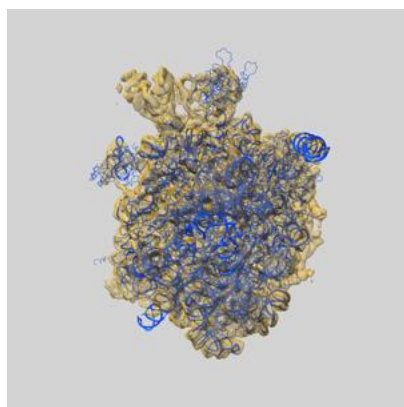
8 Fourier-Shell correlation

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

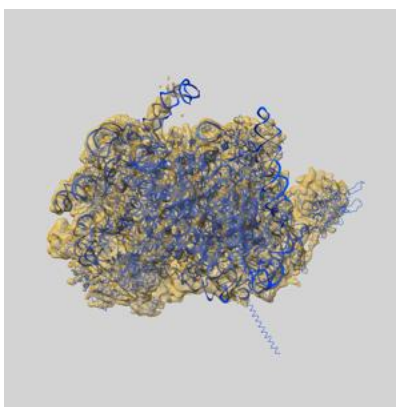
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-2528 and PDB model 4V7F. Per-residue inclusion information can be found in [section 3](#) on [page 12](#).

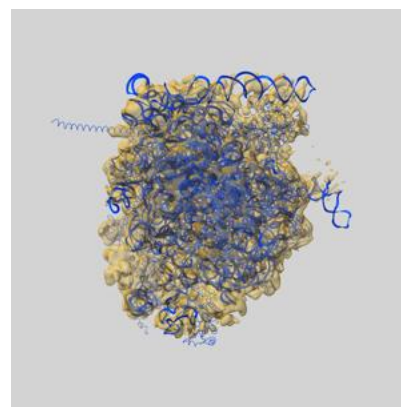
9.1 Map-model overlay [i](#)



X



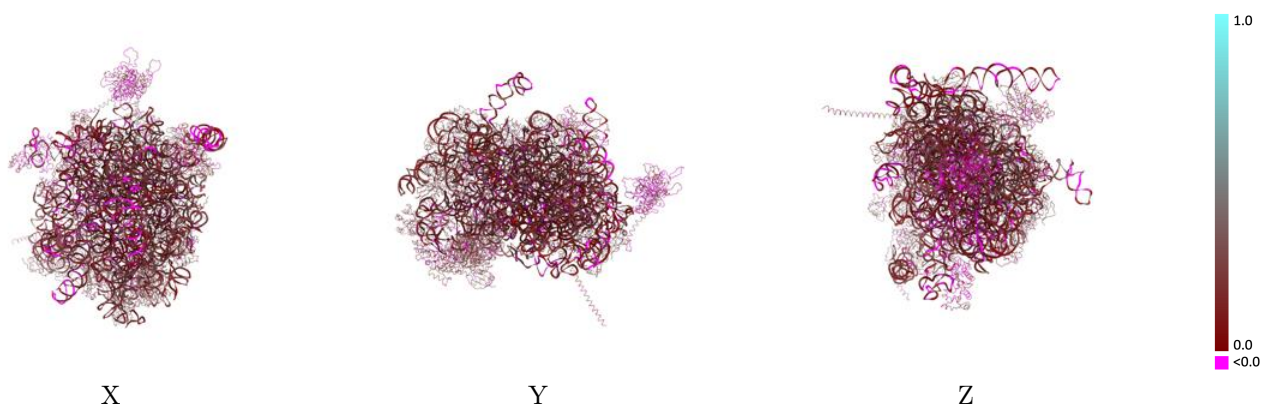
Y



Z

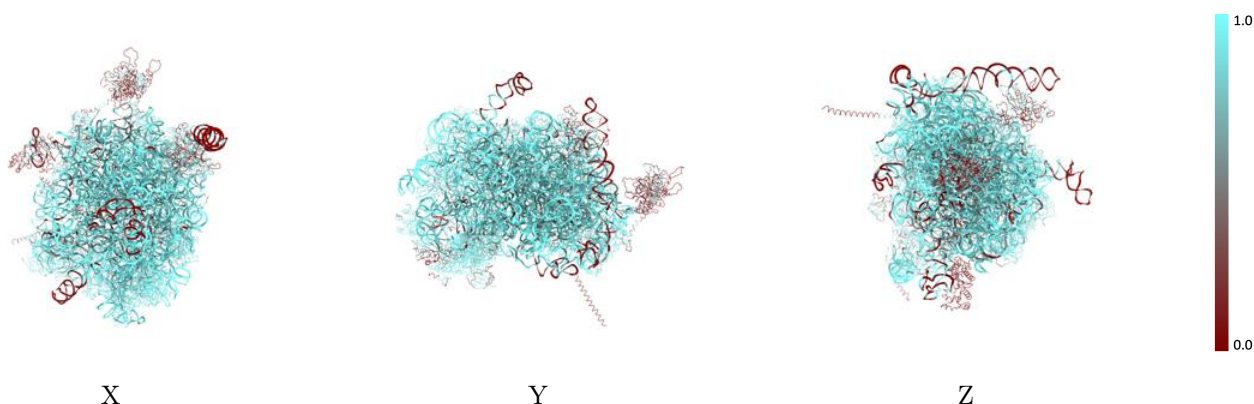
The images above show the 3D surface view of the map at the recommended contour level 0.45 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



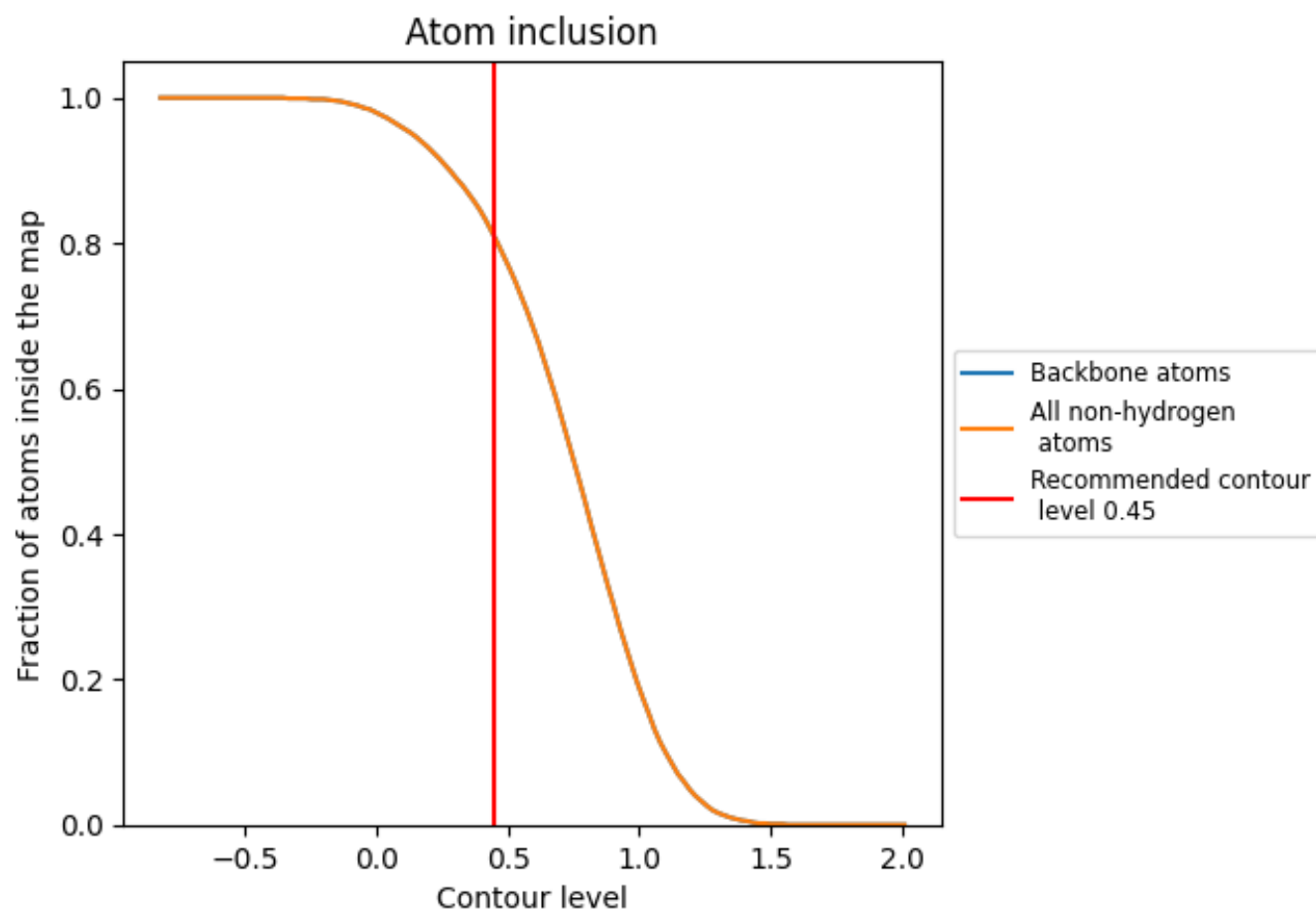
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.45).

9.4 Atom inclusion [i](#)



At the recommended contour level, 81% of all backbone atoms, 81% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.45) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8080	 0.1560
1	 0.8440	 0.1400
2	 0.9670	 0.1700
3	 0.9720	 0.1540
A	 0.0250	 0.0170
B	 0.6840	 0.1120
C	 0.9380	 0.1990
D	 0.9400	 0.2090
E	 0.9650	 0.1880
F	 0.9280	 0.2120
G	 0.9520	 0.2310
H	 0.7670	 0.1650
I	 0.3600	 0.0670
J	 0.9800	 0.2570
K	 0.8120	 0.1400
L	 0.8580	 0.1920
M	 0.9800	 0.2690
N	 0.5810	 0.0550
O	 0.7590	 0.1340
P	 0.7810	 0.1580
Q	 0.7870	 0.1820
R	 0.7730	 0.2020
S	 0.9420	 0.2150
T	 0.5410	 0.0560
U	 0.9490	 0.2170
V	 0.9400	 0.2290
W	 0.9010	 0.2300
X	 0.9820	 0.2090
Y	 0.9850	 0.2490
Z	 0.9610	 0.2350
a	 0.9760	 0.2420
b	 0.9830	 0.2430
c	 0.9360	 0.2360
d	 0.9260	 0.2230
e	 0.9840	 0.1910



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Chain	Atom inclusion	Q-score
f	 0.8270	 0.1640
g	 0.6700	 0.1370
h	 0.9430	 0.1650
i	 0.9570	 0.2660
j	 0.9670	 0.2530
k	 0.8500	 0.1810
l	 0.3630	 0.1410
m	 0.9630	 0.2360
n	 0.9450	 0.1950
o	 0.8010	 0.1900
p	 0.9420	 0.2080
q	 0.8130	 0.1440
r	 0.2470	 0.0310
s	 0.2280	 0.0010