



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 10:35 AM UTC

PDB ID : 7QWQ / pdb_00007qwq
EMDB ID : EMD-14191
Title : Ternary complex of ribosome nascent chain with SRP and NAC
Authors : Jomaa, A.; Gamerdinger, M.; Hsieh, H.; Wallisch, A.; Chandrasekaran, V.;
Ulusoy, Z.; Scaiola, A.; Hegde, R.; Shan, S.; Ban, N.; Deuerling, E.
Deposited on : 2022-01-25
Resolution : 2.83 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

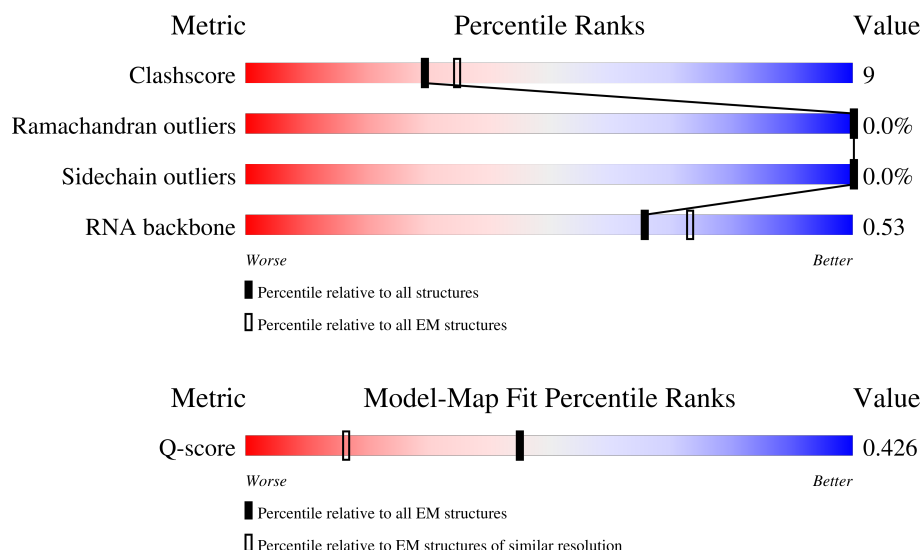
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.83 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	11847 (2.33 - 3.33)

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	167	100% 47% 46% 7%
2	q	144	73% 56% 17% 27%
3	s	112	48% 47% 50%

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Mol	Chain	Length	Quality of chain
4	u	162	
5	v	627	
6	x	504	
7	A	244	
8	b	223	
9	5	4754	
10	B	403	
11	c	115	
12	C	413	
13	d	125	
14	D	297	
15	e	157	
16	E	291	
17	f	110	
18	F	225	
19	g	129	
20	G	319	
21	h	123	
22	H	192	
23	i	102	
24	I	214	
25	j	97	
26	J	178	
27	k	69	
28	L	210	

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Mol	Chain	Length	Quality of chain
29	l	51	
30	M	218	
31	m	128	
32	N	204	
33	n	25	
34	O	500	
35	o	141	
36	P	153	
37	p	92	
38	Q	187	
39	r	137	
40	R	196	
41	S	175	
42	T	160	
43	U	102	
44	V	140	
45	W	157	
46	X	156	
47	7	120	
48	Y	145	
49	8	156	
50	Z	136	
51	a	148	
52	t	215	

2 Entry composition

There are 54 unique types of molecules in this entry. The entry contains 143809 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 SRP RNA 7SL.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	167	Total	C	N	O	P	0	0
			3583	1596	658	1162	167		

- Molecule 2 is a protein called Signal recognition particle 19 kDa protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	q	105	Total	C	N	O	S	0	0
			844	534	152	152	6		

- Molecule 3 is a protein called Nascent chain preprolactin.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	s	56	Total	C	N	O	0	0
			283	171	56	56		

- Molecule 4 is a protein called Isoform 2 of Transcription factor BTF3.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	u	32	Total	C	N	O	S	0	0
			252	156	53	42	1		

- Molecule 5 is a protein called Signal recognition particle subunit SRP68.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	v	197	Total	C	N	O	S	0	0
			1648	1034	309	297	8		

- Molecule 6 is a protein called Signal recognition particle 54 kDa protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	x	488	Total	C	N	O	S	0	0
			3778	2380	650	715	33		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
x	226	GLU	GLY	engineered mutation	UNP P61011

- Molecule 7 is a protein called L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	A	244	Total	C	N	O	S	0	0
			1868	1171	382	309	6		

- Molecule 8 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	b	75	Total	C	N	O	S	0	0
			609	378	130	98	3		

- Molecule 9 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	5	3493	Total	C	N	O	P	0	0
			74854	33335	13681	24346	3492		

- Molecule 10 is a protein called uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	B	394	Total	C	N	O	S	0	0
			3148	2007	591	537	13		

- Molecule 11 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	c	94	Total	C	N	O	S	0	0
			732	465	130	131	6		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
c	34	THR	SER	conflict	UNP G1TDL2

- Molecule 12 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	C	362	Total	C	N	O	S	0	0
			2883	1812	577	480	14		

- Molecule 13 is a protein called Ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	d	107	Total	C	N	O	S	0	0
			888	560	171	155	2		

- Molecule 14 is a protein called Ribosomal_L18_c domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	D	292	Total	C	N	O	S	0	0
			2386	1509	437	426	14		

- Molecule 15 is a protein called Ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	e	128	Total	C	N	O	S	0	0
			1053	667	216	165	5		

- Molecule 16 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	E	236	Total	C	N	O	S	0	0
			1898	1215	362	318	3		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	126	ARG	LYS	conflict	UNP G1SKF7
E	217	GLN	LYS	conflict	UNP G1SKF7

- Molecule 17 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	f	109	Total	C	N	O	S	0	0
			876	555	174	143	4		

- Molecule 18 is a protein called uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	F	225	Total	C	N	O	S	0	0
			1870	1202	358	301	9		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	175	ALA	THR	conflict	UNP G1SV32
F	185	GLY	ASN	conflict	UNP G1SV32
F	202	ARG	HIS	conflict	UNP G1SV32
F	233	GLU	GLY	conflict	UNP G1SV32

- Molecule 19 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	g	114	Total	C	N	O	S	0	0
			906	566	187	147	6		

- Molecule 20 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	G	241	Total	C	N	O	S	0	0
			1934	1233	371	326	4		

- Molecule 21 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	h	122	Total	C	N	O	S	0	0
			1013	640	204	168	1		

- Molecule 22 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	H	190	Total	C	N	O	S	0	0
			1516	954	284	272	6		

- Molecule 23 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	i	102	Total	C	N	O	S	0	0
			830	520	176	129	5		

- Molecule 24 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	I	204	Total	C	N	O	S	0	0
			1655	1051	319	272	13		

- Molecule 25 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	j	86	Total	C	N	O	S	0	0
			705	434	155	111	5		

- Molecule 26 is a protein called Ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	J	169	Total	C	N	O	S	0	0
			1353	855	252	240	6		

- Molecule 27 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	k	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

- Molecule 28 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	L	210	Total	C	N	O	S	0	0
			1703	1065	354	280	4		

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	47	ALA	-	insertion	UNP G1TPV0
L	48	PRO	-	insertion	UNP G1TPV0
L	49	ARG	-	insertion	UNP G1TPV0
L	50	PRO	-	insertion	UNP G1TPV0
L	51	ALA	-	insertion	UNP G1TPV0
L	52	SER	-	insertion	UNP G1TPV0
L	53	GLY	-	insertion	UNP G1TPV0
L	54	PRO	-	insertion	UNP G1TPV0
L	55	LEU	-	insertion	UNP G1TPV0

- Molecule 29 is a protein called Ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	l	50	Total	C	N	O	S	0	0
			444	281	98	64	1		

- Molecule 30 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	M	138	Total	C	N	O	S	0	0
			1137	727	221	182	7		

- Molecule 31 is a protein called Ubiquitin A-52 residue ribosomal protein fusion product 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	m	52	Total	C	N	O	S	0	0
			429	266	90	67	6		

- Molecule 32 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	N	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		

- Molecule 33 is a protein called 60s ribosomal protein l41.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	n	23	Total	C	N	O	S	0	0
			222	134	61	25	2		

- Molecule 34 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	O	199	Total	C	N	O	S	0	0
			1638	1056	321	256	5		

- Molecule 35 is a protein called eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	o	104	Total	C	N	O	S	0	0
			851	533	174	138	6		

- Molecule 36 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	P	153	Total	C	N	O	S	0	0
			1242	777	241	215	9		

- Molecule 37 is a protein called eL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	p	91	Total	C	N	O	S	0	0
			708	445	136	120	7		

- Molecule 38 is a protein called eL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Q	187	Total	C	N	O	S	0	0
			1506	941	311	249	5		

- Molecule 39 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	r	125	Total	C	N	O	S	0	0
			1001	621	206	168	6		

- Molecule 40 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	R	180	Total	C	N	O	S	0	0
			1508	933	328	238	9		

- Molecule 41 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	S	175	Total	C	N	O	S	0	0
			1454	925	284	235	10		

- Molecule 42 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	T	159	Total	C	N	O	S	0	0
			1298	823	252	217	6		

- Molecule 43 is a protein called Ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	U	102	Total	C	N	O	S	0	0
			833	533	146	152	2		

- Molecule 44 is a protein called Ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	V	131	Total	C	N	O	S	0	0
			979	618	184	172	5		

- Molecule 45 is a protein called Ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	W	63	Total	C	N	O	S	0	0
			528	337	103	85	3		

- Molecule 46 is a protein called Ribosomal_L23eN domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	X	119	Total	C	N	O	S	0	0
			976	624	183	168	1		

- Molecule 47 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	7	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		

- Molecule 48 is a protein called Ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	Y	134	Total	C	N	O	S	0	0
			1115	700	226	186	3		

- Molecule 49 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	8	156	Total	C	N	O	P	0	0
			3314	1480	585	1094	155		

- Molecule 50 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	Z	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 51 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	a	147	Total	C	N	O	S	0	0
			1162	734	239	185	4		

- Molecule 52 is a protein called Nascent polypeptide-associated complex subunit alpha.

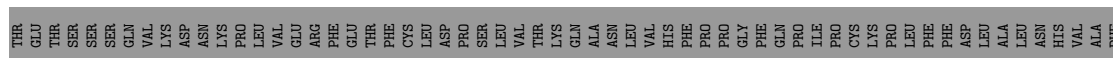
Mol	Chain	Residues	Atoms					AltConf	Trace
52	t	47	Total	C	N	O	S	0	0
			359	217	62	77	3		

- Molecule 53 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
53	5	96	Total	Mg	0
			96	96	
53	B	1	Total	Mg	0
			1	1	

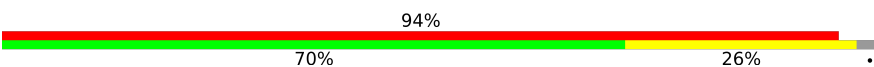
- Molecule 54 is ZINC ION (CCD ID: ZN) (formula: Zn).

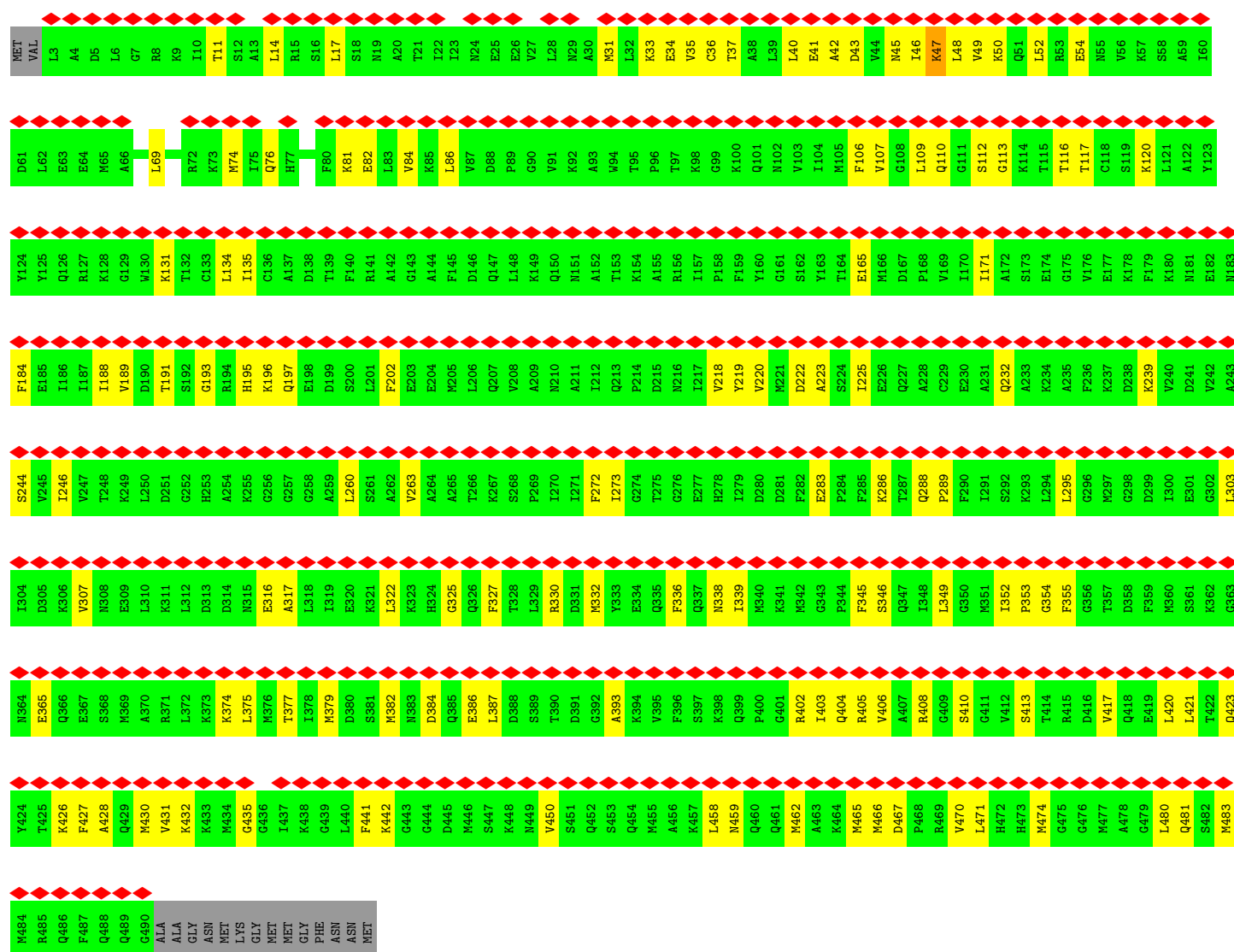
Mol	Chain	Residues	Atoms		AltConf
54	g	1	Total	Zn	0
			1	1	
54	j	1	Total	Zn	0
			1	1	
54	m	1	Total	Zn	0
			1	1	
54	o	1	Total	Zn	0
			1	1	
54	p	1	Total	Zn	0
			1	1	



PRO PRO
LEU LEU
GLU ASP
LYS LYS
LEU LEU
GLN GLN
LYS LYS
THR THR
SER SER
GLY GLY
LEU LEU
THR THR
GLY GLY
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ILE ILE
PHE PHE
GLY GLY
PHE PHE
ARG ARG
SER SER

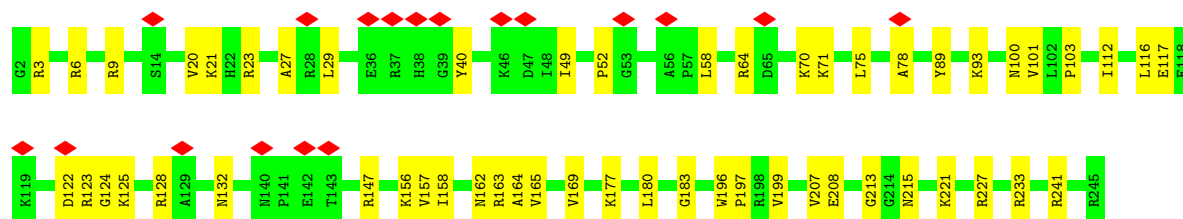
• Molecule 6: Signal recognition particle 54 kDa protein

Chain x: 

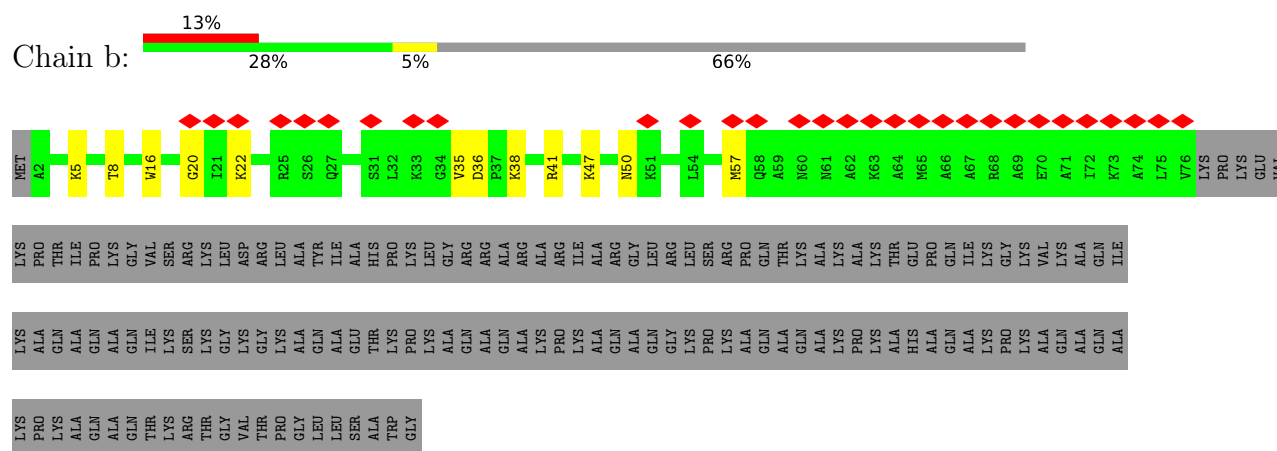


• Molecule 7: L8

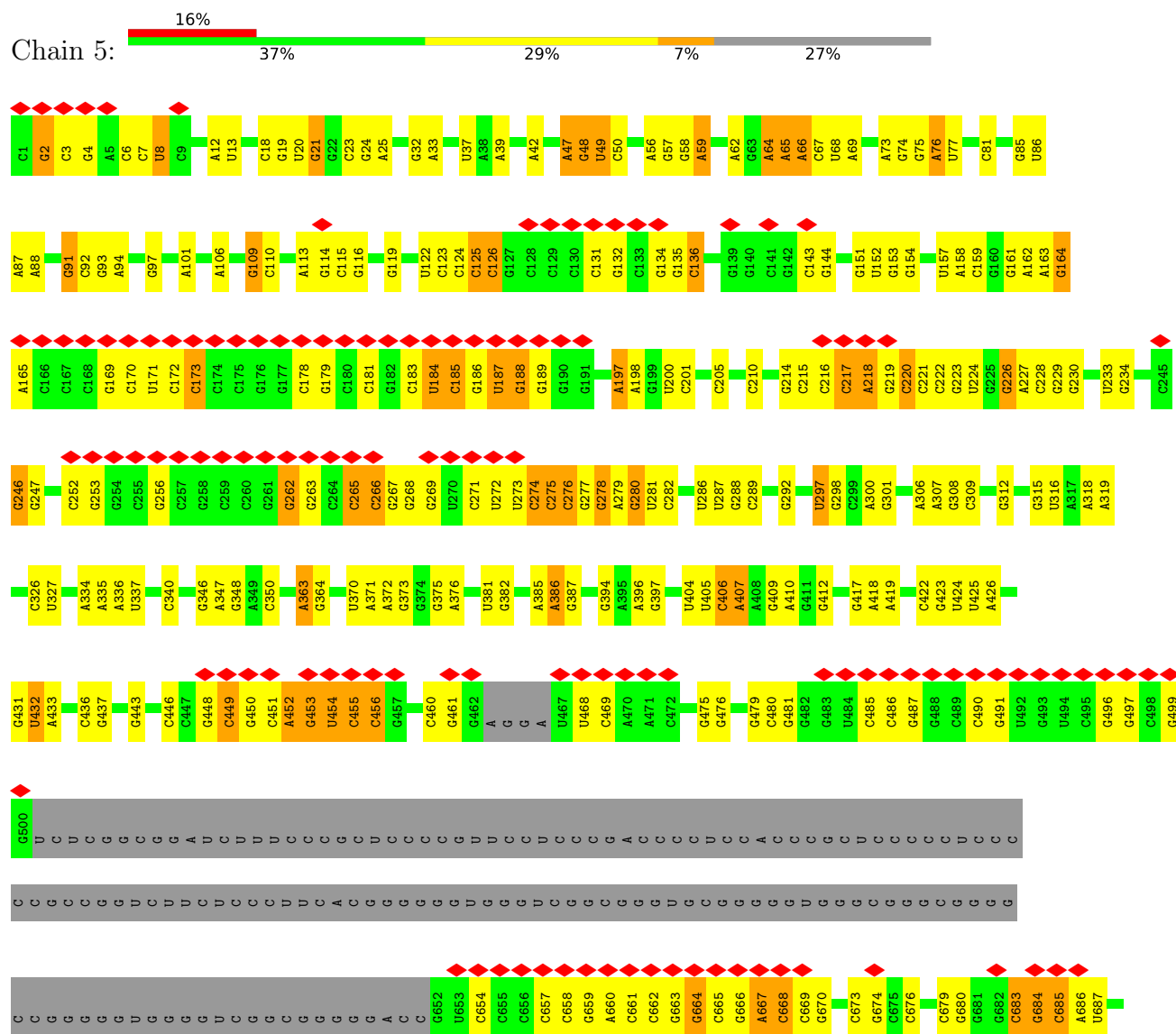
Chain A: 



- Molecule 8: 60S ribosomal protein L29



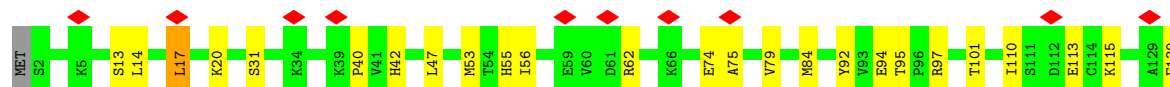
- Molecule 9: 28S rRNA

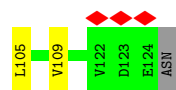




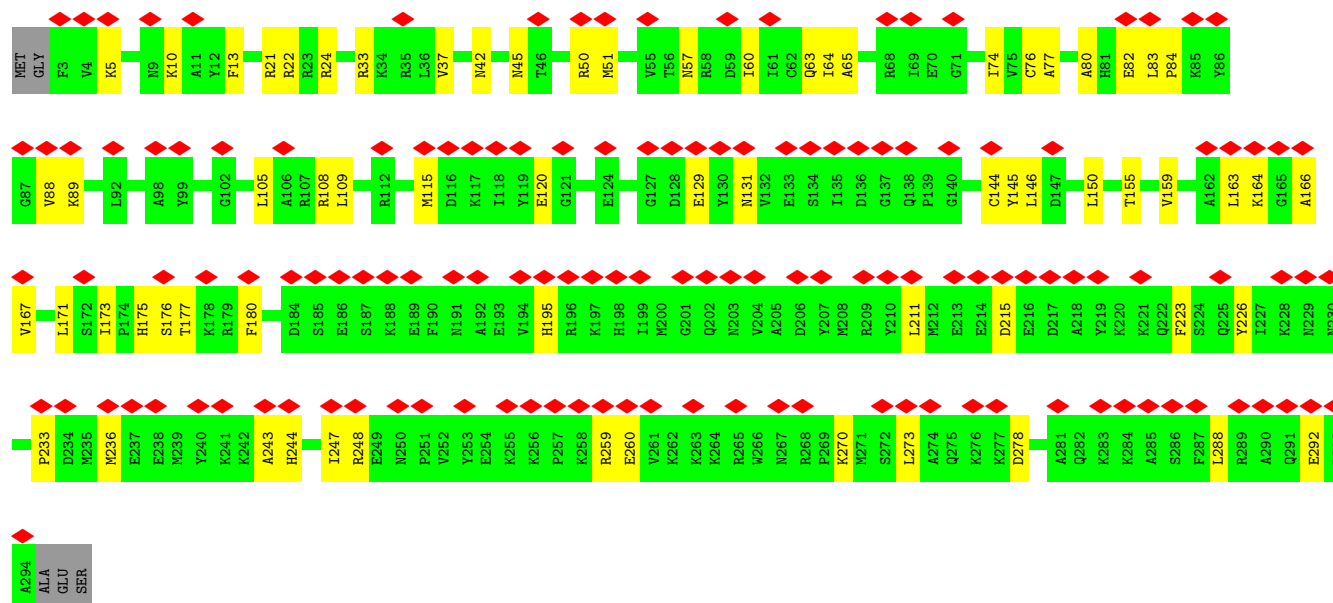
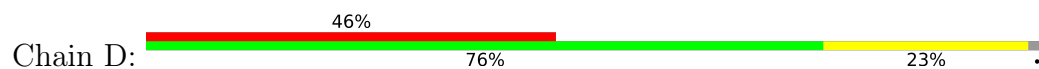
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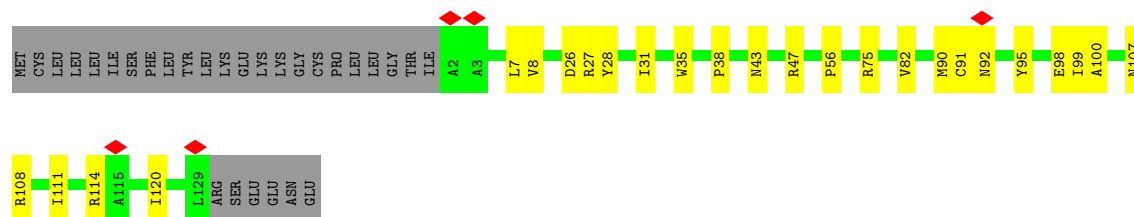




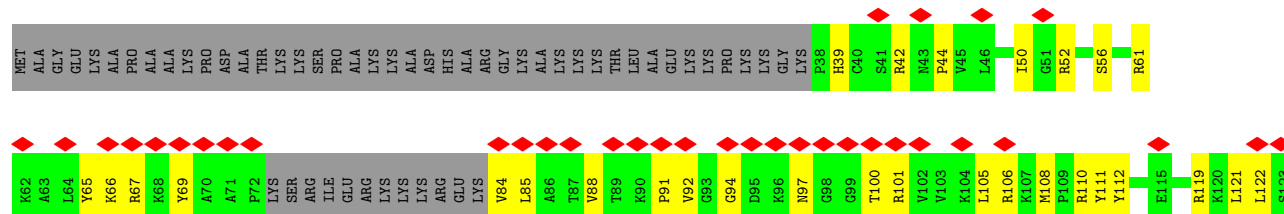
• Molecule 14: Ribosomal_L18_c domain-containing protein

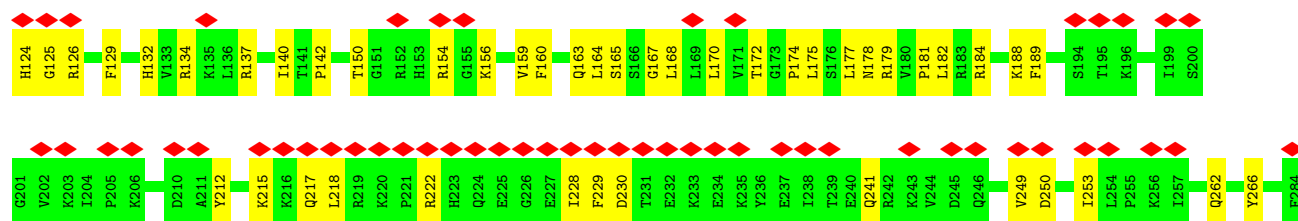


• Molecule 15: Ribosomal protein L32

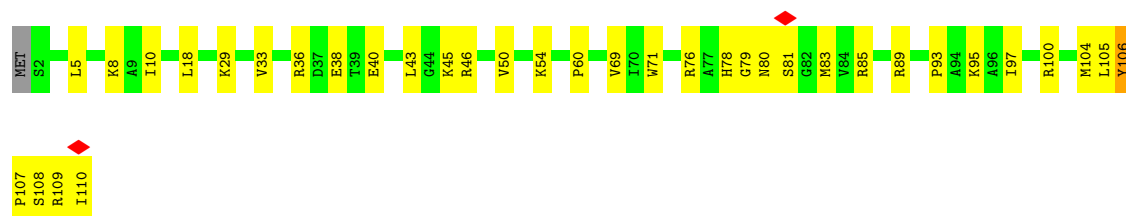


• Molecule 16: 60S ribosomal protein L6

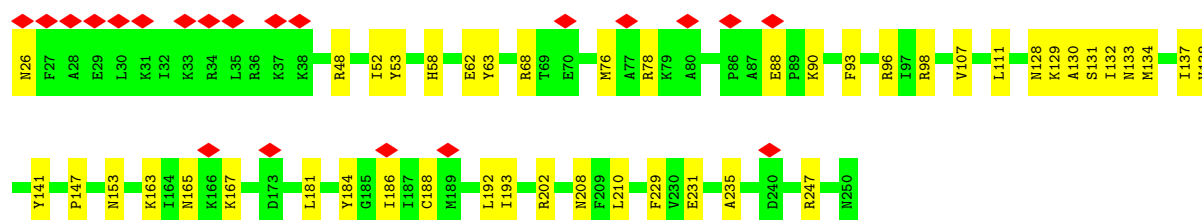
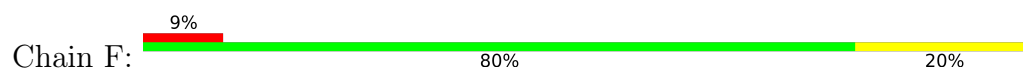




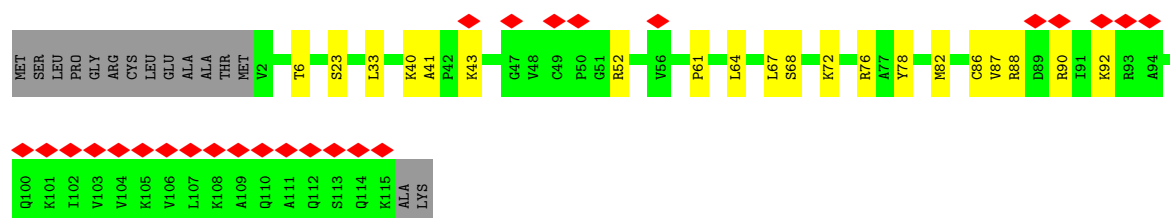
• Molecule 17: 60S ribosomal protein L35a



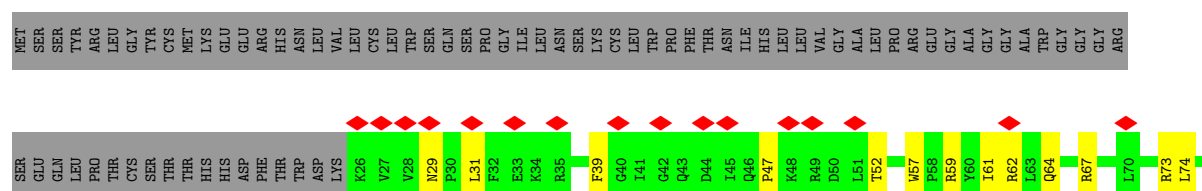
• Molecule 18: uL30

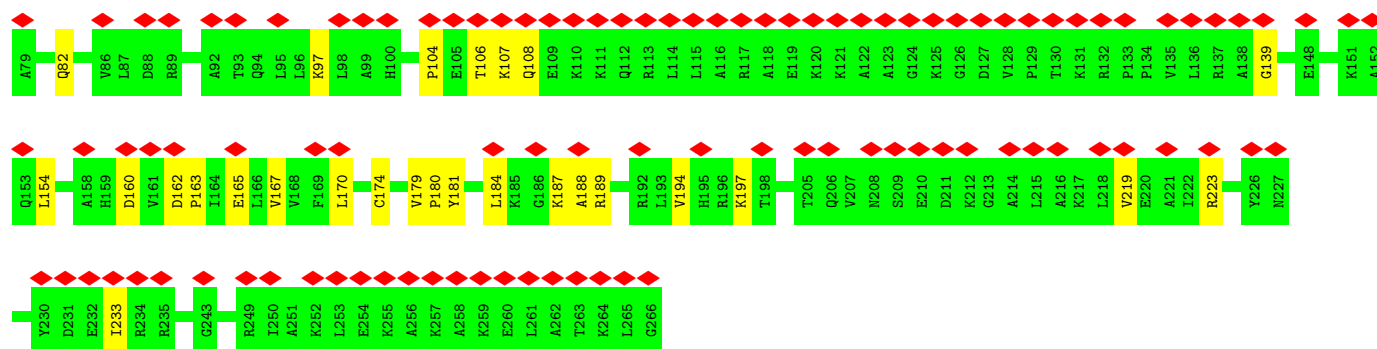


• Molecule 19: 60S ribosomal protein L34

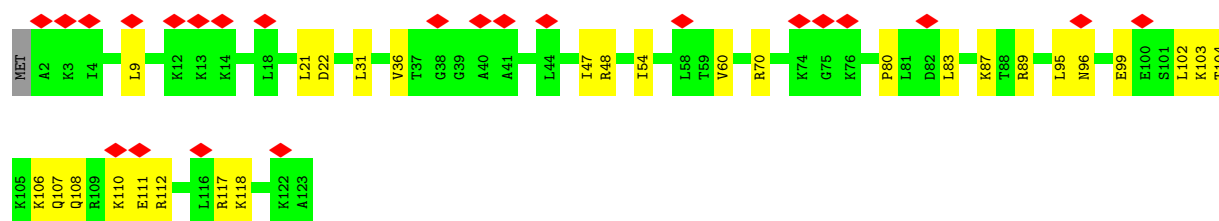
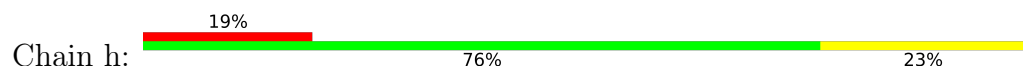


• Molecule 20: 60S ribosomal protein L7a

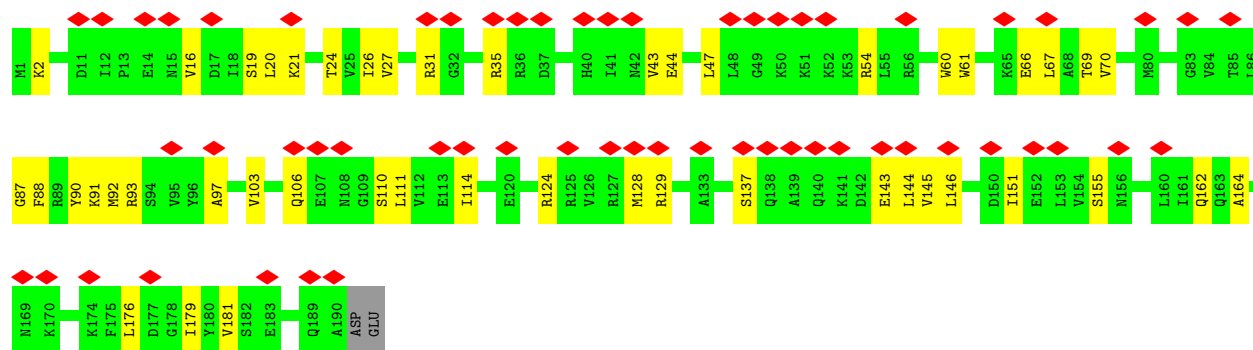
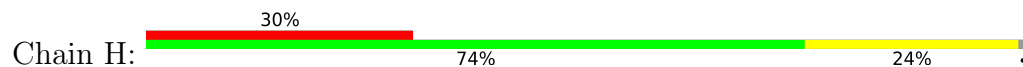




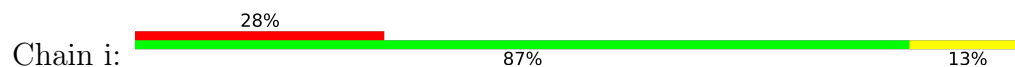
• Molecule 21: 60S ribosomal protein L35



• Molecule 22: 60S ribosomal protein L9

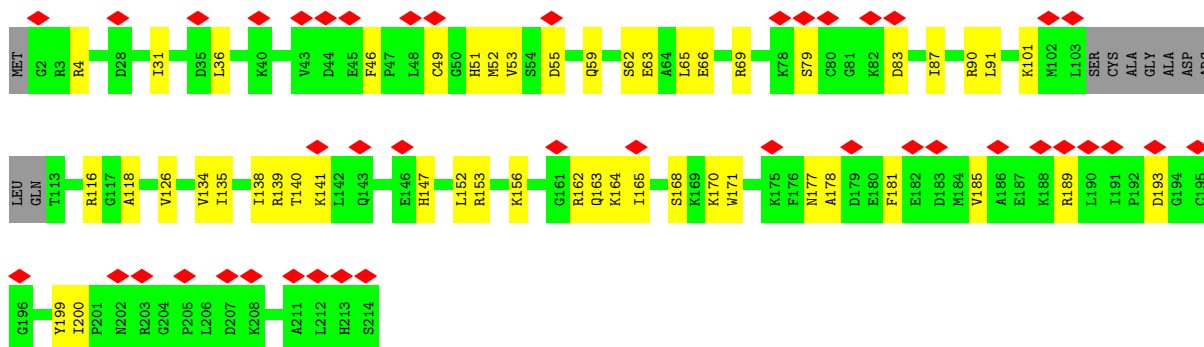


• Molecule 23: 60S ribosomal protein L36



• Molecule 24: 60S ribosomal protein L10

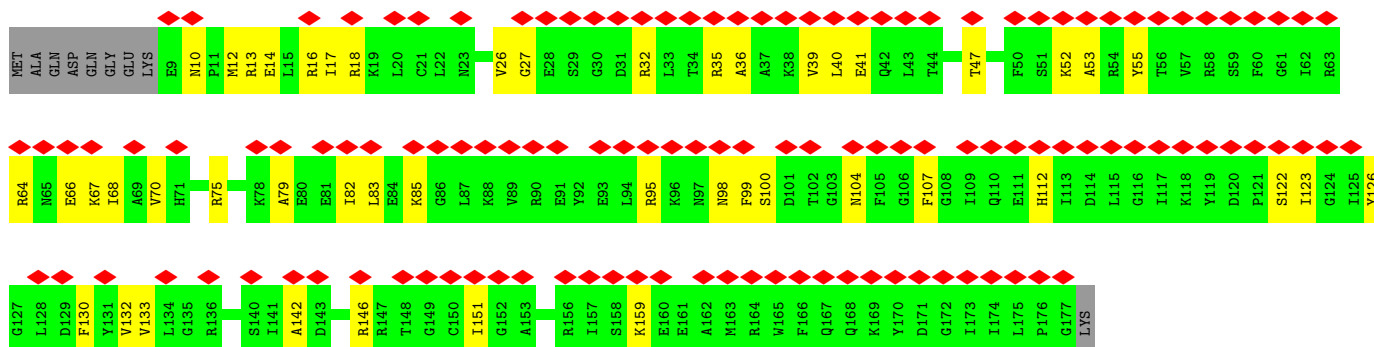




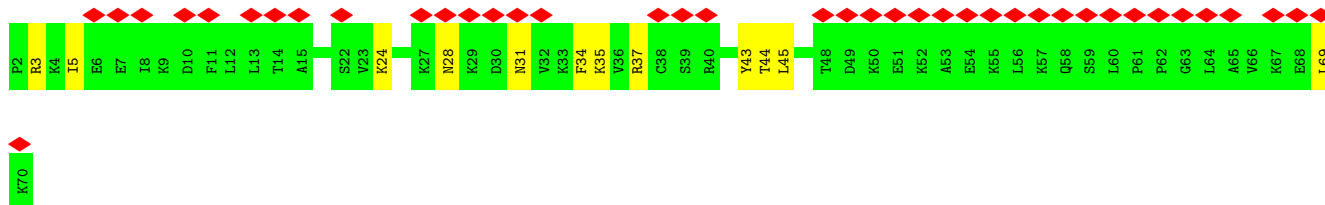
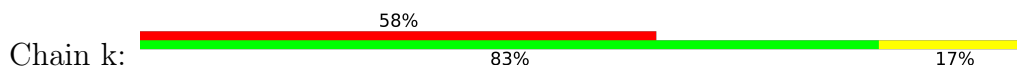
• Molecule 25: Ribosomal protein L37



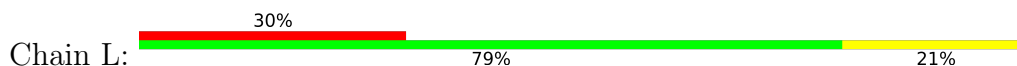
• Molecule 26: Ribosomal protein L11

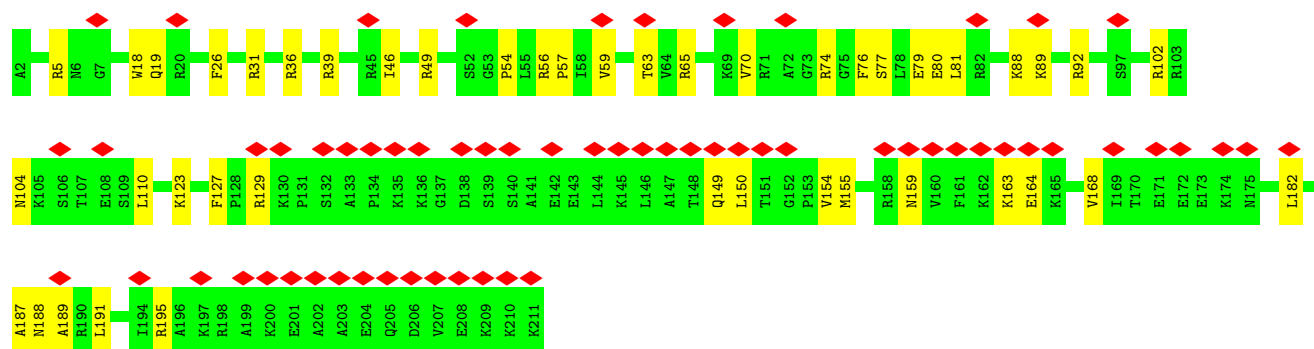


• Molecule 27: 60S ribosomal protein L38



• Molecule 28: 60S ribosomal protein L13

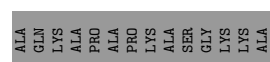
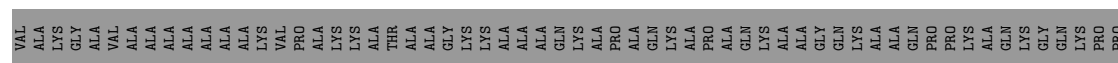
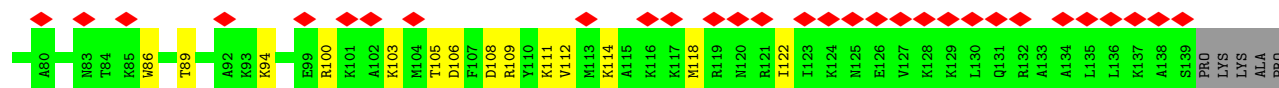




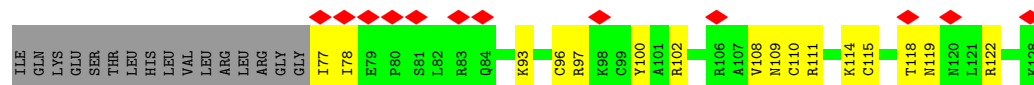
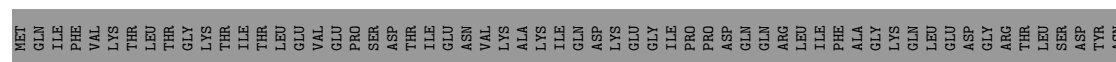
- Molecule 29: Ribosomal protein L39



- Molecule 30: 60S ribosomal protein L14



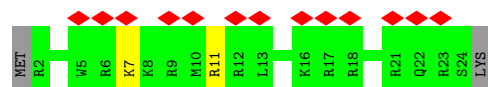
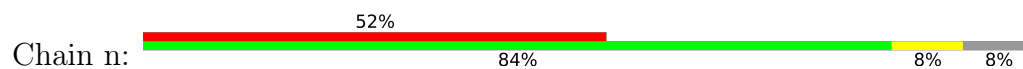
- Molecule 31: Ubiquitin A-52 residue ribosomal protein fusion product 1



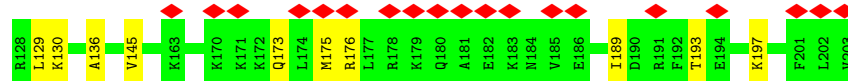
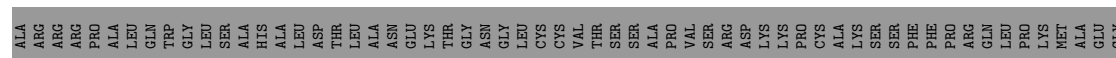
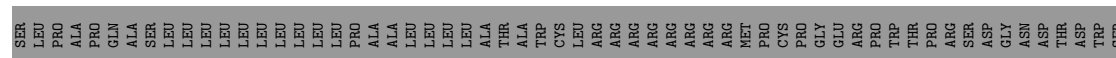
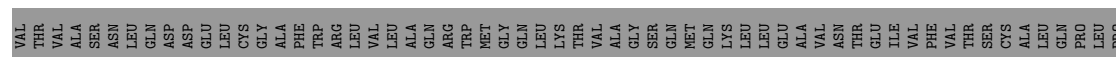
- Molecule 32: Ribosomal protein L15



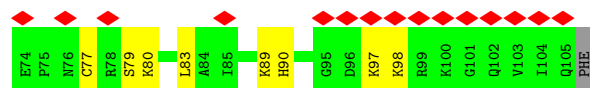
- Molecule 33: 60s ribosomal protein l41



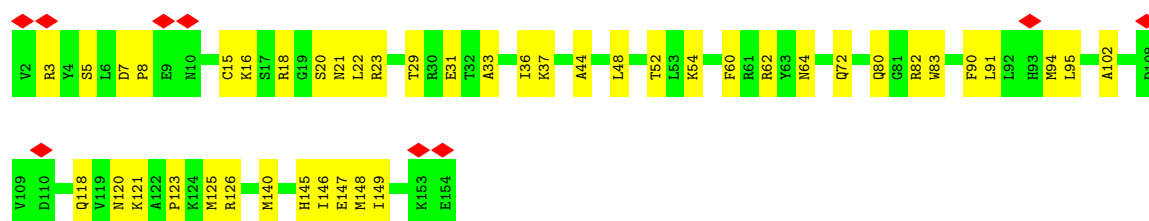
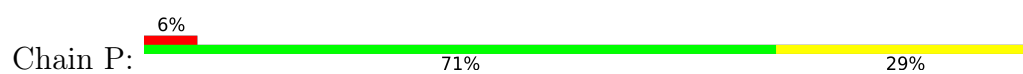
- Molecule 34: 60S ribosomal protein L13a



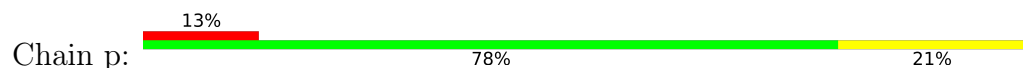
- Molecule 35: eL42



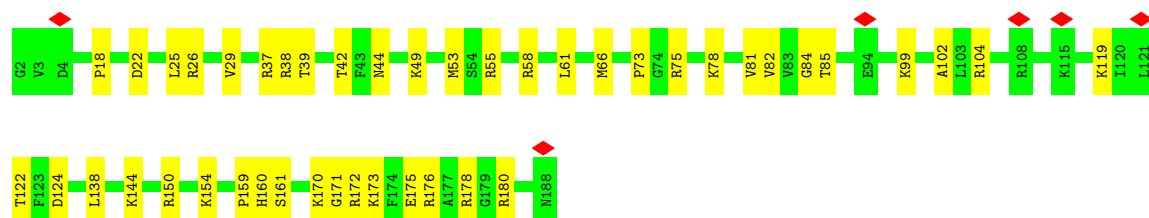
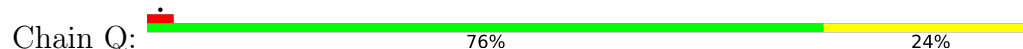
- Molecule 36: 60S ribosomal protein L17



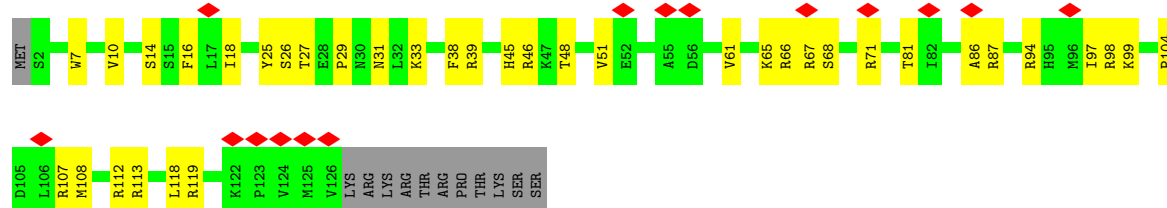
• Molecule 37: eL43



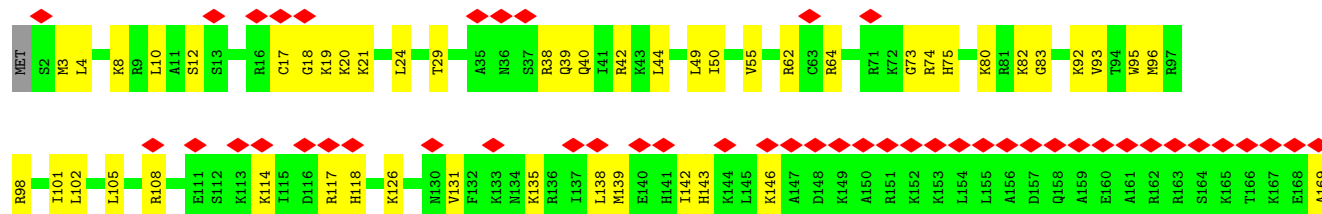
• Molecule 38: eL18

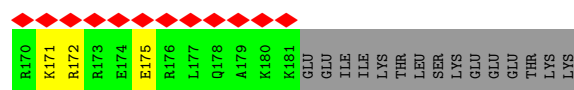


• Molecule 39: 60S ribosomal protein L28

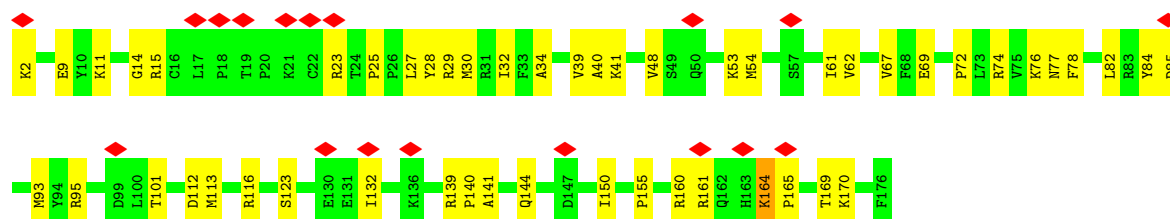


• Molecule 40: 60S ribosomal protein L19

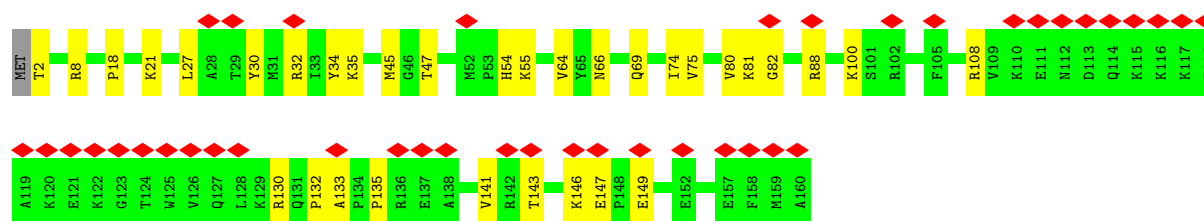
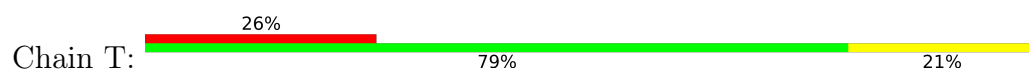




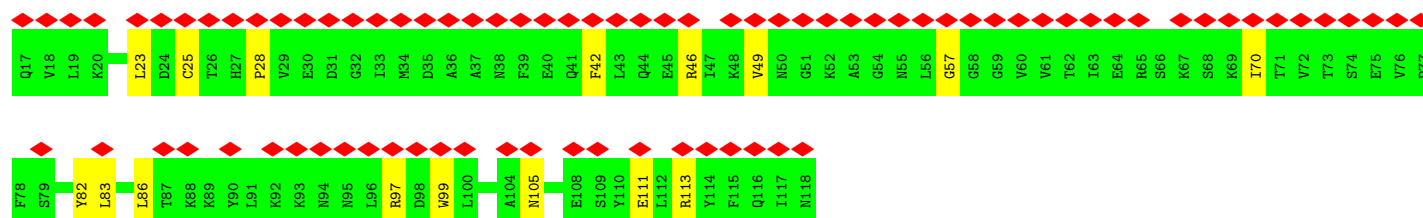
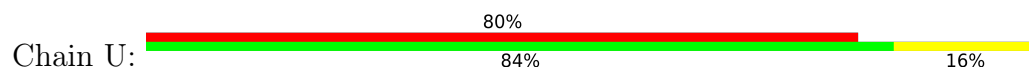
- Molecule 41: 60S ribosomal protein L18a



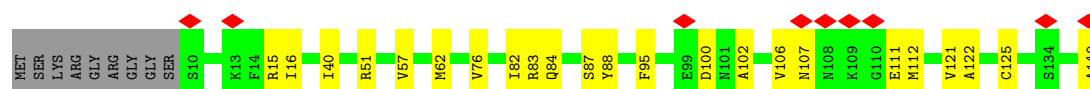
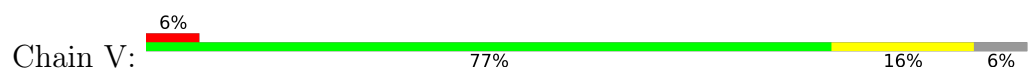
- Molecule 42: 60S ribosomal protein L21



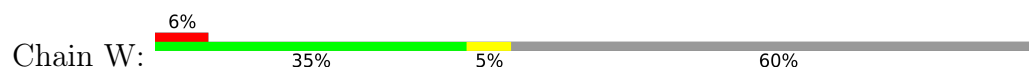
- Molecule 43: Ribosomal protein L22



- Molecule 44: Ribosomal protein L23



- Molecule 45: Ribosomal protein L24



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	51843	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.210	Depositor
Minimum map value	-0.094	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.010	Depositor
Recommended contour level	0.027	Depositor
Map size ($\text{\AA}$)	483.84003, 483.84003, 483.84003	wwPDB
Map dimensions	448, 448, 448	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.08, 1.08, 1.08	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	0.10	0/4009	0.23	0/6253
2	q	0.16	0/858	0.38	0/1156
4	u	0.06	0/252	0.19	0/331
5	v	0.11	0/1676	0.29	0/2244
6	x	0.24	0/3830	0.47	0/5131
7	A	0.13	0/1906	0.36	0/2556
8	b	0.13	0/619	0.31	0/818
9	5	0.09	0/83726	0.24	1/130593 (0.0%)
10	B	0.13	0/3216	0.34	0/4311
11	c	0.11	0/742	0.26	0/996
12	C	0.13	0/2937	0.33	0/3946
13	d	0.13	0/903	0.31	0/1216
14	D	0.15	0/2432	0.35	0/3257
15	e	0.11	0/1071	0.29	0/1429
16	E	0.16	0/1936	0.41	0/2600
17	f	0.12	0/895	0.38	0/1198
18	F	0.13	0/1905	0.31	0/2539
19	g	0.14	0/916	0.32	0/1220
20	G	0.14	0/1967	0.36	0/2647
21	h	0.12	0/1021	0.28	0/1348
22	H	0.14	0/1535	0.35	0/2063
23	i	0.12	0/841	0.35	0/1112
24	I	0.15	0/1693	0.35	0/2260
25	j	0.13	0/720	0.32	0/952
26	J	0.10	0/1376	0.31	0/1841
27	k	0.12	0/575	0.30	0/761
28	L	0.14	0/1734	0.35	0/2317
29	l	0.10	0/454	0.28	0/599
30	M	0.15	0/1158	0.34	0/1547
31	m	0.10	0/435	0.34	0/575
32	N	0.16	0/1746	0.36	0/2338
33	n	0.07	0/223	0.15	0/284

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
34	O	0.13	0/1671	0.31	0/2234
35	o	0.12	0/864	0.38	0/1140
36	P	0.12	0/1268	0.31	0/1700
37	p	0.10	0/718	0.28	0/953
38	Q	0.12	0/1530	0.33	0/2041
39	r	0.27	1/1017 (0.1%)	0.52	1/1364 (0.1%)
40	R	0.12	0/1524	0.35	0/2013
41	S	0.15	0/1493	0.36	1/2002 (0.0%)
42	T	0.15	0/1326	0.32	0/1770
43	U	0.10	0/847	0.29	0/1137
44	V	0.22	0/993	0.43	2/1332 (0.2%)
45	W	0.10	0/541	0.29	0/720
46	X	0.10	0/993	0.29	0/1334
47	7	0.08	0/2858	0.20	0/4455
48	Y	0.11	0/1132	0.28	0/1504
49	8	0.09	0/3701	0.21	0/5766
50	Z	0.13	0/1130	0.36	0/1507
51	a	0.08	0/1191	0.26	0/1590
52	t	0.93	0/358	1.14	0/480
All	All	0.12	1/154462 (0.0%)	0.29	5/227480 (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
10	B	0	1
17	f	0	1
41	S	0	1
All	All	0	3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
39	r	29	PRO	CG-CD	-5.67	1.31	1.50

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
39	r	29	PRO	N-CD-CG	-9.06	89.61	103.20
41	S	140	PRO	CA-N-CD	-7.01	102.18	112.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	V	84	GLN	CA-C-N	5.39	127.45	120.44
44	V	84	GLN	C-N-CA	5.39	127.45	120.44
9	5	5061	A	P-O3'-C3'	5.14	127.92	120.20

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
10	B	17	LEU	Peptide
41	S	164	LYS	Peptide
17	f	106	TYR	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	3583	0	1809	60	0
2	q	844	0	861	21	0
3	s	283	0	64	2	0
4	u	252	0	283	4	0
5	v	1648	0	1659	22	0
6	x	3778	0	3858	90	0
7	A	1868	0	1959	44	0
8	b	609	0	650	10	0
9	5	74854	0	37827	1175	0
10	B	3148	0	3267	71	0
11	c	732	0	766	16	0
12	C	2883	0	3053	73	0
13	d	888	0	930	8	0
14	D	2386	0	2419	55	0
15	e	1053	0	1147	19	0
16	E	1898	0	2035	64	0
17	f	876	0	912	32	0
18	F	1870	0	1994	36	0
19	g	906	0	999	17	0
20	G	1934	0	2085	31	0
21	h	1013	0	1147	24	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
22	H	1516	0	1597	35	0
23	i	830	0	916	11	0
24	I	1655	0	1704	36	0
25	j	705	0	737	14	0
26	J	1353	0	1386	32	0
27	k	569	0	637	9	0
28	L	1703	0	1820	45	0
29	l	444	0	483	9	0
30	M	1137	0	1211	36	0
31	m	429	0	465	12	0
32	N	1701	0	1749	50	0
33	n	222	0	264	1	0
34	O	1638	0	1777	35	0
35	o	851	0	920	10	0
36	P	1242	0	1274	36	0
37	p	708	0	757	16	0
38	Q	1506	0	1623	37	0
39	r	1001	0	1060	26	0
40	R	1508	0	1664	44	0
41	S	1454	0	1496	43	0
42	T	1298	0	1366	28	0
43	U	833	0	856	10	0
44	V	979	0	1039	16	0
45	W	528	0	541	6	0
46	X	976	0	1053	20	0
47	7	2558	0	1296	34	0
48	Y	1115	0	1205	24	0
49	8	3314	0	1683	51	0
50	Z	1107	0	1182	29	0
51	a	1162	0	1209	26	0
52	t	359	0	363	34	0
53	5	96	0	0	0	0
53	B	1	0	0	0	0
54	g	1	0	0	0	0
54	j	1	0	0	0	0
54	m	1	0	0	0	0
54	o	1	0	0	0	0
54	p	1	0	0	0	0
All	All	143809	0	105057	2247	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 9.

The worst 5 of 2247 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)
52:t:181:ILE:HG21	52:t:196:VAL:HG22	1.38	1.04
48:Y:74:TYR:HE2	48:Y:77:LYS:HE3	1.25	1.00
6:x:46:ILE:HG12	52:t:211:MET:HE2	1.44	1.00
9:5:2557:G:H1	9:5:2570:U:H3	1.11	0.97
9:5:2845:A:H61	9:5:3843:C:H42	0.98	0.97

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	
2	q	103/144 (72%)	101 (98%)	2 (2%)	0	100	100
4	u	30/162 (18%)	30 (100%)	0	0	100	100
5	v	195/627 (31%)	192 (98%)	3 (2%)	0	100	100
6	x	486/504 (96%)	464 (96%)	20 (4%)	2 (0%)	30	48
7	A	242/244 (99%)	225 (93%)	17 (7%)	0	100	100
8	b	73/223 (33%)	70 (96%)	3 (4%)	0	100	100
10	B	392/403 (97%)	380 (97%)	12 (3%)	0	100	100
11	c	92/115 (80%)	91 (99%)	1 (1%)	0	100	100
12	C	360/413 (87%)	348 (97%)	12 (3%)	0	100	100
13	d	105/125 (84%)	102 (97%)	3 (3%)	0	100	100
14	D	290/297 (98%)	278 (96%)	12 (4%)	0	100	100
15	e	126/157 (80%)	119 (94%)	7 (6%)	0	100	100
16	E	232/291 (80%)	204 (88%)	28 (12%)	0	100	100
17	f	107/110 (97%)	101 (94%)	6 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
18	F	223/225 (99%)	216 (97%)	7 (3%)	0	100	100
19	g	112/129 (87%)	112 (100%)	0	0	100	100
20	G	239/319 (75%)	222 (93%)	17 (7%)	0	100	100
21	h	120/123 (98%)	116 (97%)	4 (3%)	0	100	100
22	H	188/192 (98%)	179 (95%)	9 (5%)	0	100	100
23	i	100/102 (98%)	94 (94%)	6 (6%)	0	100	100
24	I	200/214 (94%)	193 (96%)	7 (4%)	0	100	100
25	j	84/97 (87%)	82 (98%)	2 (2%)	0	100	100
26	J	167/178 (94%)	155 (93%)	12 (7%)	0	100	100
27	k	67/69 (97%)	63 (94%)	4 (6%)	0	100	100
28	L	208/210 (99%)	192 (92%)	16 (8%)	0	100	100
29	l	48/51 (94%)	42 (88%)	6 (12%)	0	100	100
30	M	136/218 (62%)	129 (95%)	7 (5%)	0	100	100
31	m	50/128 (39%)	47 (94%)	3 (6%)	0	100	100
32	N	201/204 (98%)	193 (96%)	8 (4%)	0	100	100
33	n	21/25 (84%)	21 (100%)	0	0	100	100
34	O	197/500 (39%)	194 (98%)	3 (2%)	0	100	100
35	o	102/141 (72%)	95 (93%)	7 (7%)	0	100	100
36	P	151/153 (99%)	149 (99%)	2 (1%)	0	100	100
37	p	89/92 (97%)	84 (94%)	5 (6%)	0	100	100
38	Q	185/187 (99%)	179 (97%)	6 (3%)	0	100	100
39	r	123/137 (90%)	114 (93%)	9 (7%)	0	100	100
40	R	178/196 (91%)	174 (98%)	4 (2%)	0	100	100
41	S	173/175 (99%)	165 (95%)	8 (5%)	0	100	100
42	T	157/160 (98%)	146 (93%)	11 (7%)	0	100	100
43	U	100/102 (98%)	94 (94%)	6 (6%)	0	100	100
44	V	129/140 (92%)	125 (97%)	4 (3%)	0	100	100
45	W	61/157 (39%)	60 (98%)	1 (2%)	0	100	100
46	X	117/156 (75%)	113 (97%)	4 (3%)	0	100	100
48	Y	132/145 (91%)	130 (98%)	2 (2%)	0	100	100
50	Z	133/136 (98%)	123 (92%)	10 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
51	a	145/148 (98%)	137 (94%)	8 (6%)	0	100	100
52	t	45/215 (21%)	38 (84%)	6 (13%)	1 (2%)	5	11
All	All	7214/9239 (78%)	6881 (95%)	330 (5%)	3 (0%)	100	100

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	x	42	ALA
52	t	201	ASN
6	x	450	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	
2	q	92/121 (76%)	92 (100%)	0	100	100
4	u	26/136 (19%)	26 (100%)	0	100	100
5	v	173/529 (33%)	173 (100%)	0	100	100
6	x	410/421 (97%)	409 (100%)	1 (0%)	87	95
7	A	187/187 (100%)	187 (100%)	0	100	100
8	b	62/170 (36%)	62 (100%)	0	100	100
10	B	336/348 (97%)	336 (100%)	0	100	100
11	c	79/98 (81%)	79 (100%)	0	100	100
12	C	302/337 (90%)	302 (100%)	0	100	100
13	d	98/110 (89%)	98 (100%)	0	100	100
14	D	247/250 (99%)	247 (100%)	0	100	100
15	e	114/141 (81%)	114 (100%)	0	100	100
16	E	208/251 (83%)	208 (100%)	0	100	100
17	f	88/89 (99%)	88 (100%)	0	100	100
18	F	194/195 (100%)	194 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
19	g	98/109 (90%)	98 (100%)	0	100	100
20	G	206/273 (76%)	206 (100%)	0	100	100
21	h	109/110 (99%)	109 (100%)	0	100	100
22	H	169/171 (99%)	169 (100%)	0	100	100
23	i	86/86 (100%)	86 (100%)	0	100	100
24	I	174/181 (96%)	174 (100%)	0	100	100
25	j	73/80 (91%)	73 (100%)	0	100	100
26	J	142/149 (95%)	142 (100%)	0	100	100
27	k	64/64 (100%)	64 (100%)	0	100	100
28	L	176/176 (100%)	176 (100%)	0	100	100
29	l	47/48 (98%)	47 (100%)	0	100	100
30	M	117/160 (73%)	117 (100%)	0	100	100
31	m	48/116 (41%)	48 (100%)	0	100	100
32	N	171/172 (99%)	171 (100%)	0	100	100
33	n	22/24 (92%)	22 (100%)	0	100	100
34	O	171/433 (40%)	171 (100%)	0	100	100
35	o	92/121 (76%)	92 (100%)	0	100	100
36	P	134/134 (100%)	134 (100%)	0	100	100
37	p	74/75 (99%)	74 (100%)	0	100	100
38	Q	163/163 (100%)	163 (100%)	0	100	100
39	r	109/121 (90%)	109 (100%)	0	100	100
40	R	159/175 (91%)	159 (100%)	0	100	100
41	S	156/156 (100%)	156 (100%)	0	100	100
42	T	139/140 (99%)	139 (100%)	0	100	100
43	U	92/92 (100%)	92 (100%)	0	100	100
44	V	101/107 (94%)	101 (100%)	0	100	100
45	W	55/126 (44%)	55 (100%)	0	100	100
46	X	107/134 (80%)	107 (100%)	0	100	100
48	Y	124/135 (92%)	124 (100%)	0	100	100
50	Z	117/118 (99%)	117 (100%)	0	100	100
51	a	119/120 (99%)	119 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
52	t	41/183 (22%)	40 (98%)	1 (2%)	43 67
All	All	6271/7835 (80%)	6269 (100%)	2 (0%)	100 100

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	x	47	LYS
52	t	197	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 136 such sidechains are listed below:

Mol	Chain	Res	Type
40	R	86	ASN
42	T	54	HIS
48	Y	20	ASN
16	E	280	HIS
16	E	131	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	166/167 (99%)	35 (21%)	2 (1%)
47	7	119/120 (99%)	11 (9%)	0
49	8	155/156 (99%)	31 (20%)	1 (0%)
9	5	3478/4754 (73%)	693 (19%)	70 (2%)
All	All	3918/5197 (75%)	770 (19%)	73 (1%)

5 of 770 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	99	C
1	1	100	C
1	1	101	G
1	1	102	A
1	1	105	G

5 of 73 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
9	5	4528	G
9	5	5061	A
9	5	4699	U
9	5	4948	C
9	5	1238	A

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 102 ligands modelled in this entry, 102 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](#)

There are no chain breaks in this entry.

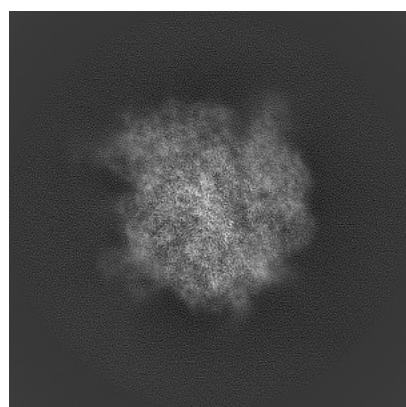
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-14191. These allow visual inspection of the internal detail of the map and identification of artifacts.

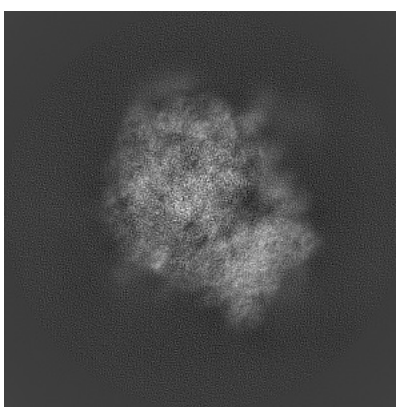
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

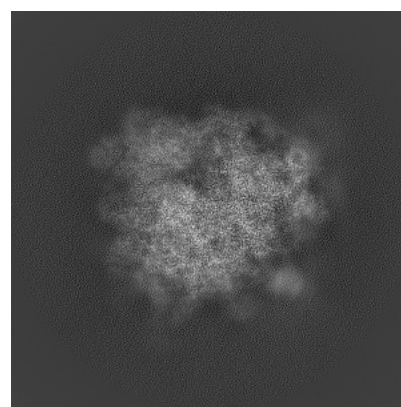
6.1.1 Primary map



X



Y

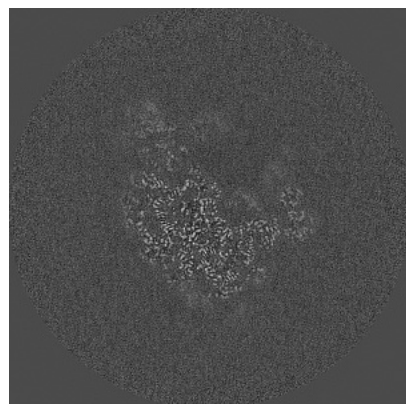


Z

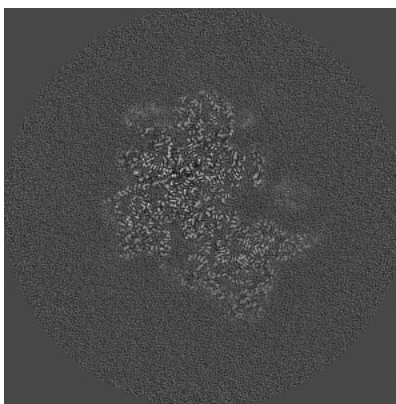
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

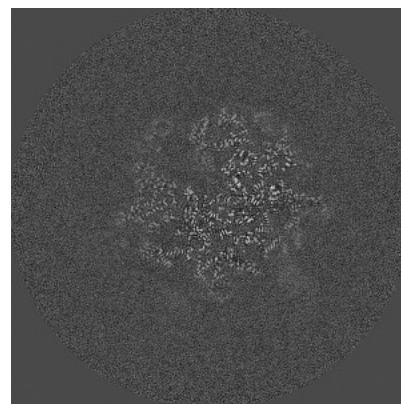
6.2.1 Primary map



X Index: 224



Y Index: 224

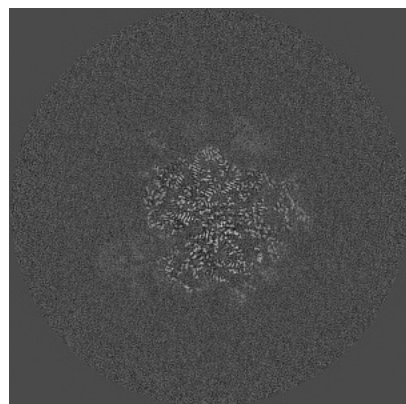


Z Index: 224

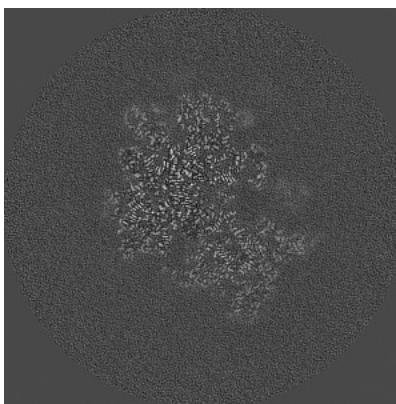
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

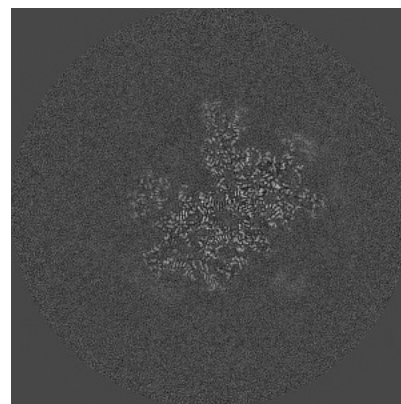
6.3.1 Primary map



X Index: 258



Y Index: 226

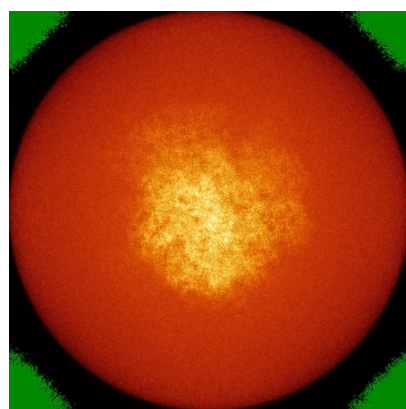


Z Index: 207

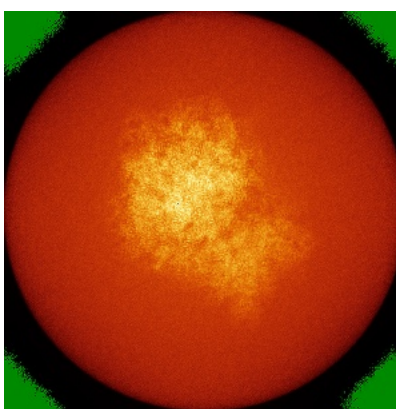
The images above show the largest variance slices of the map in three orthogonal directions.

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

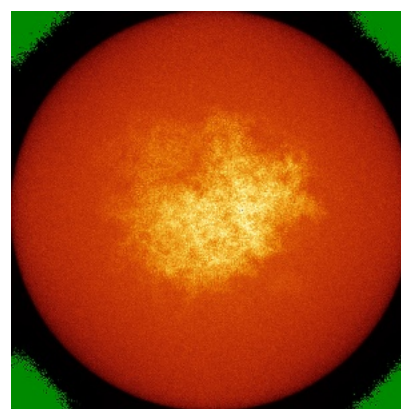
6.4.1 Primary map



X



Y

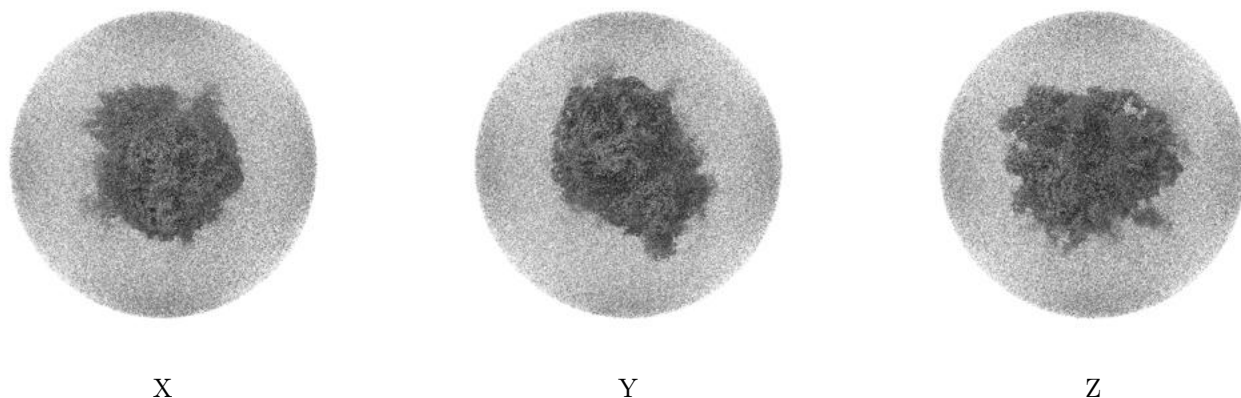


Z

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

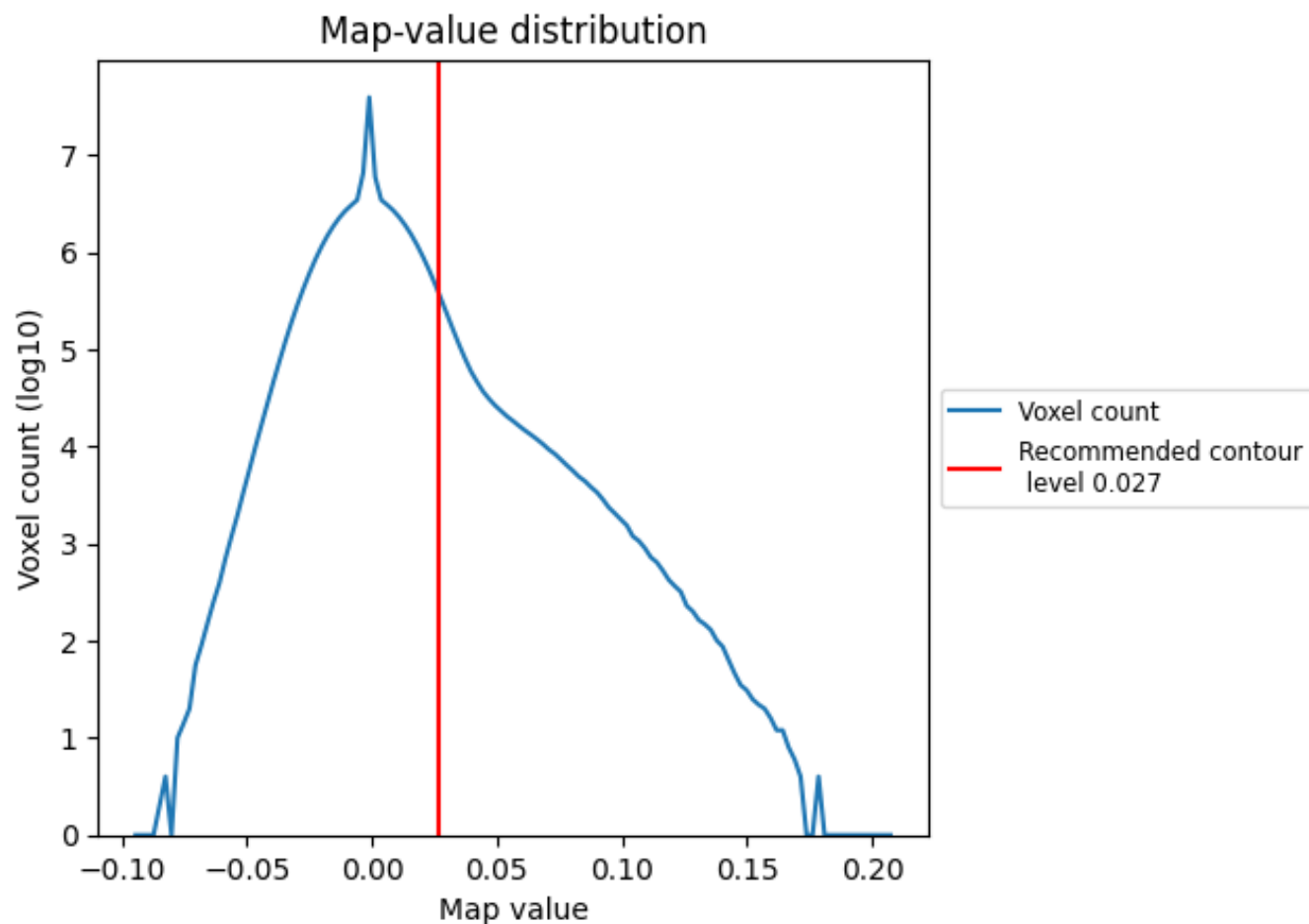
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

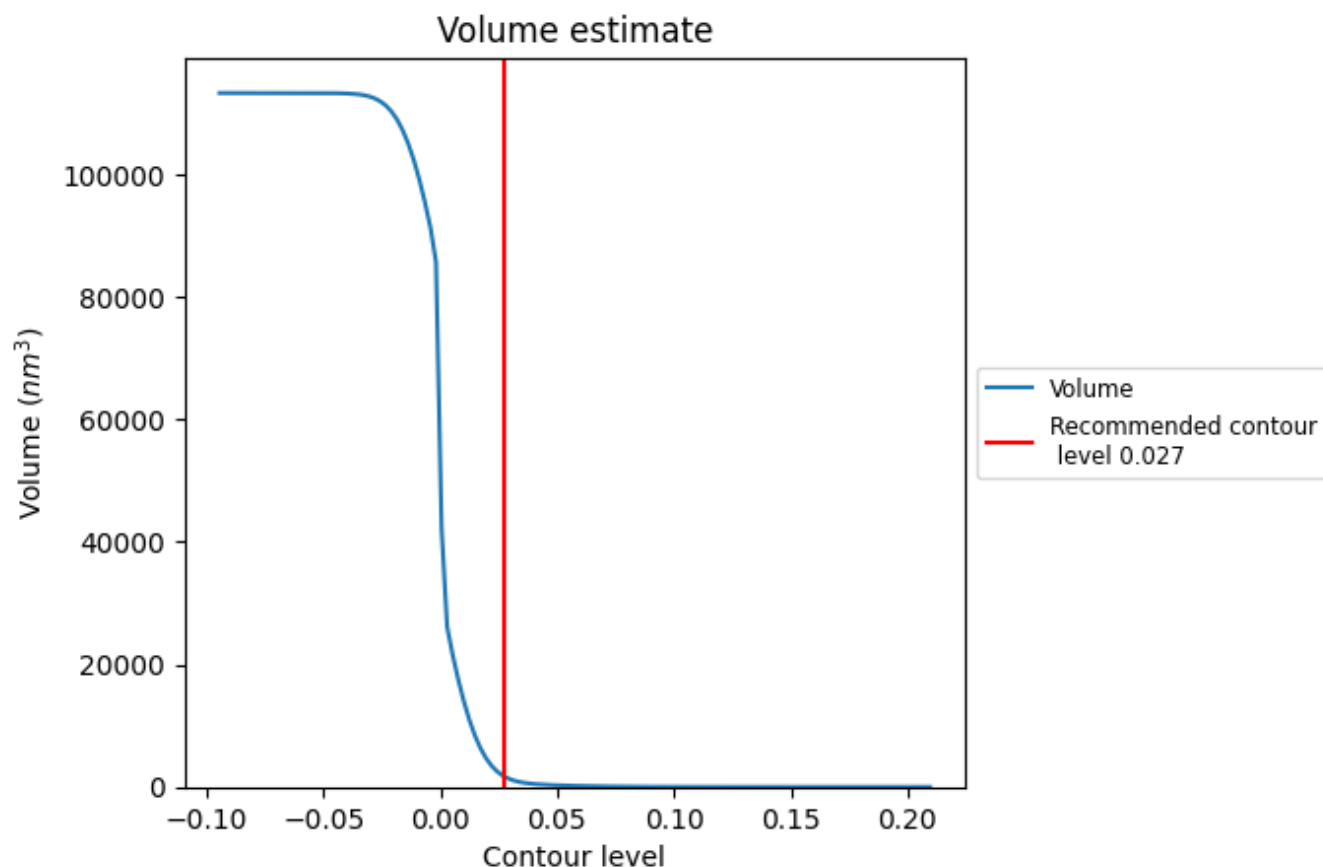
This section contains the results of statistical analysis of the map.

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.

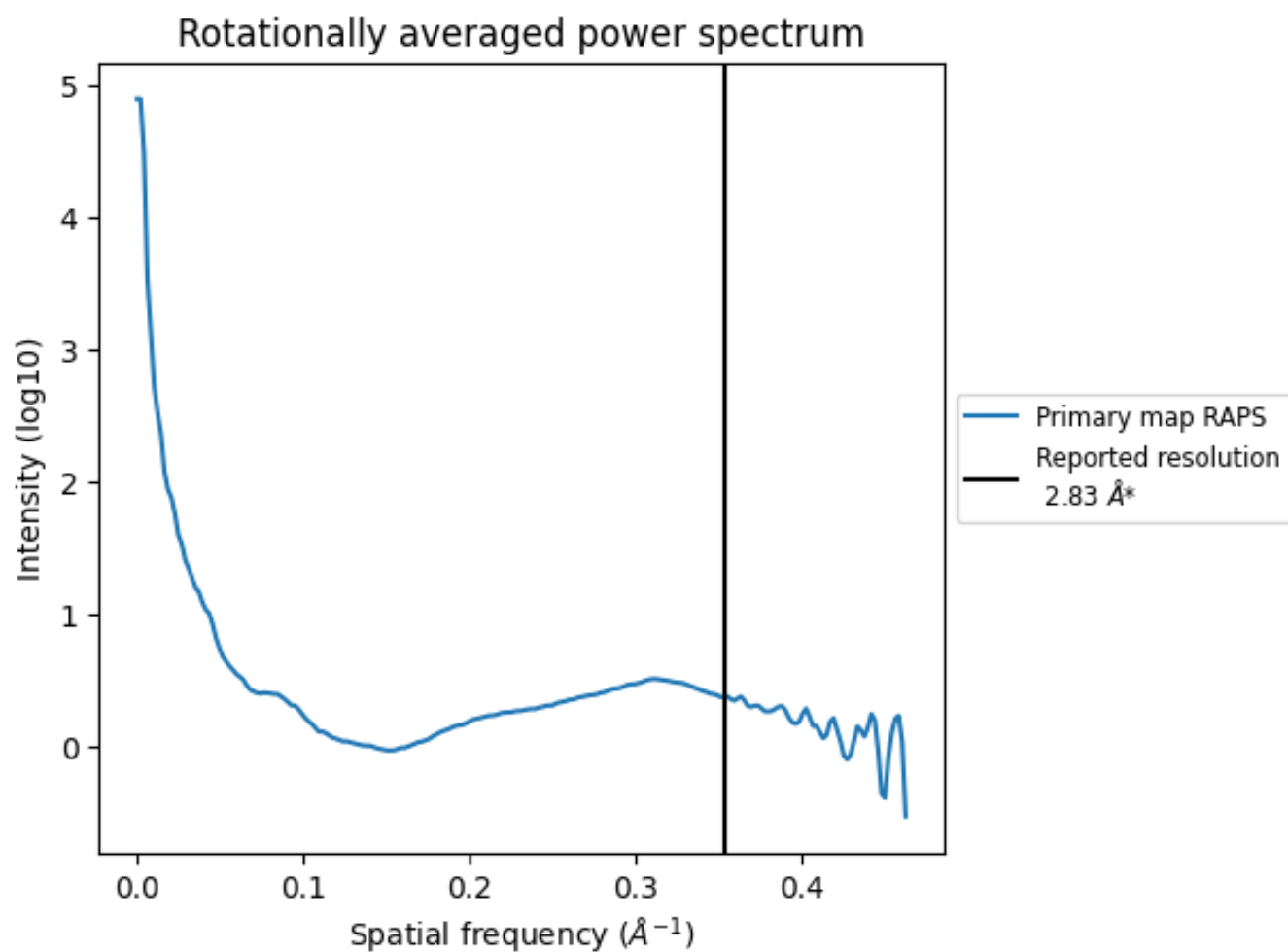
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1806 nm³; this corresponds to an approximate mass of 1632 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 0.353 Å⁻¹

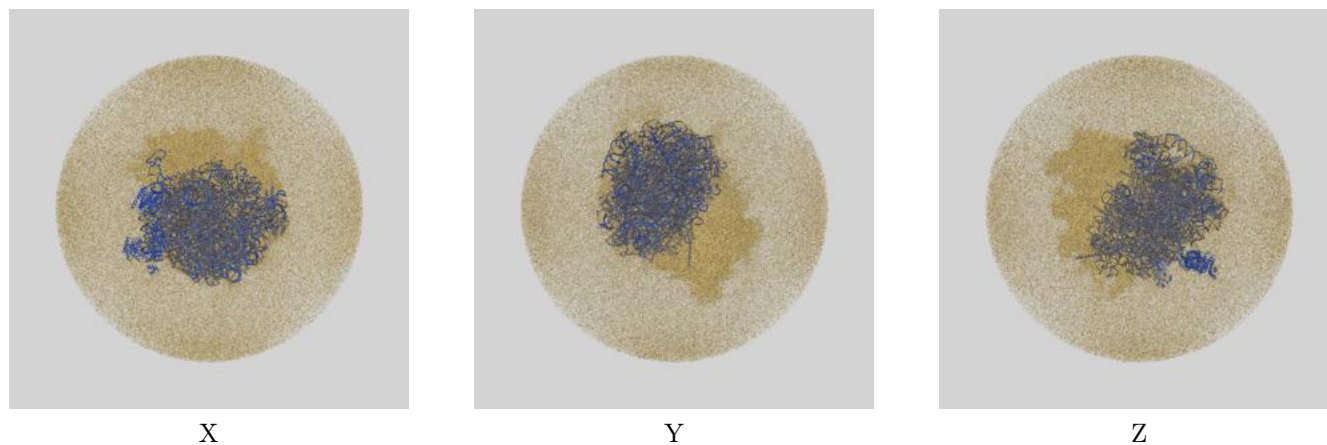
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

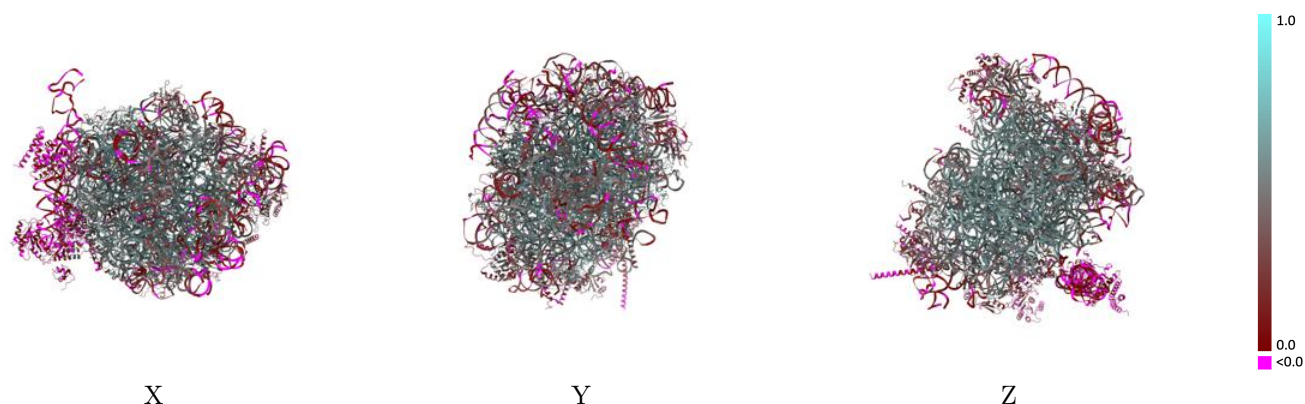
This section contains information regarding the fit between EMDB map EMD-14191 and PDB model 7QWQ. Per-residue inclusion information can be found in [section 3](#) on [page 14](#).

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.027 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](#)

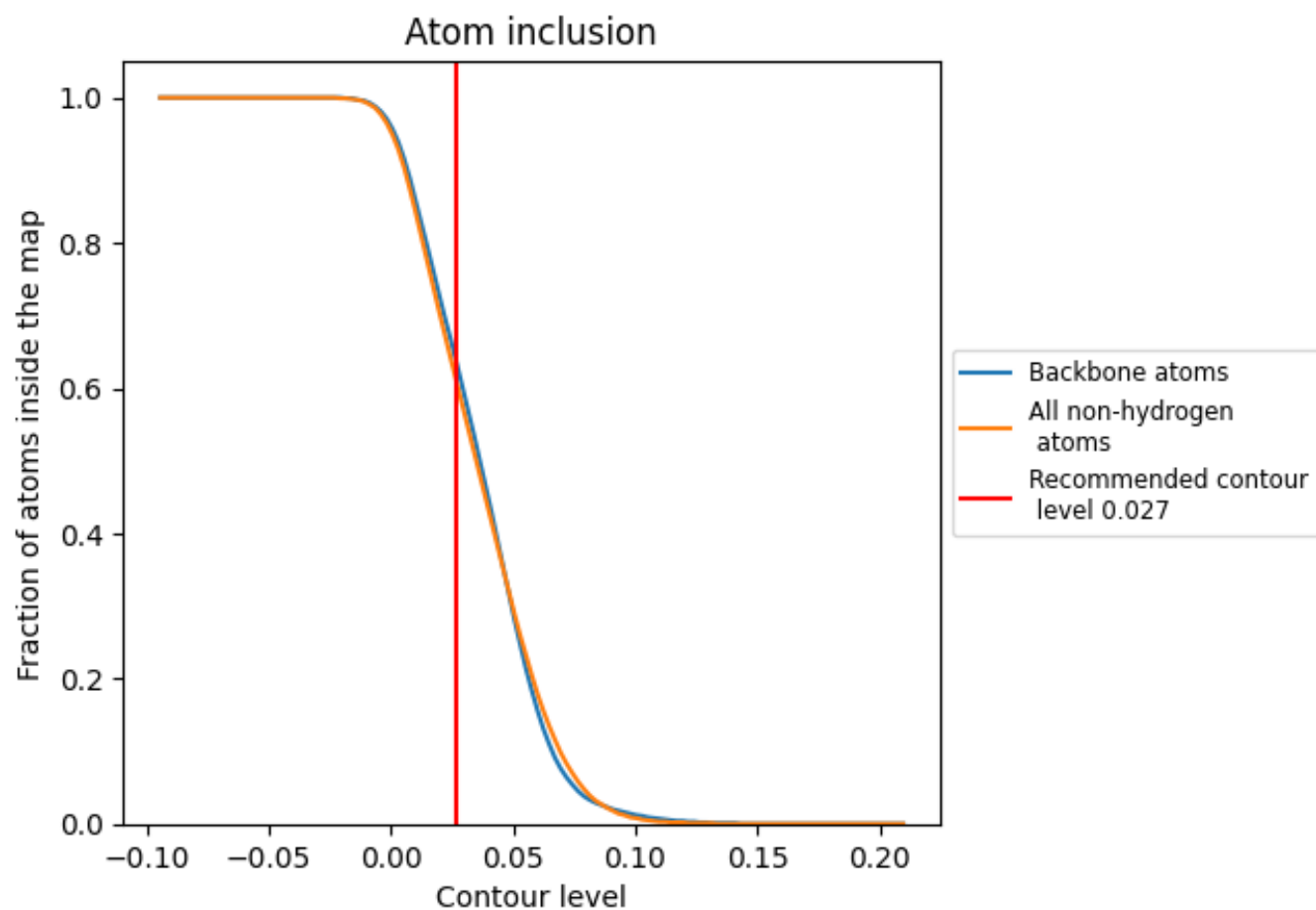


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 63% of all backbone atoms, 61% 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 (0.027) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6060	 0.4260
1	 0.0220	 0.0320
5	 0.6720	 0.4520
7	 0.6920	 0.4260
8	 0.7220	 0.4840
A	 0.7640	 0.5540
B	 0.7230	 0.5330
C	 0.7130	 0.5270
D	 0.4240	 0.3040
E	 0.4640	 0.3410
F	 0.7380	 0.5250
G	 0.4250	 0.3260
H	 0.5020	 0.3800
I	 0.6320	 0.4870
J	 0.3030	 0.2270
L	 0.5740	 0.4280
M	 0.5550	 0.3830
N	 0.7700	 0.5380
O	 0.7470	 0.5310
P	 0.7840	 0.5780
Q	 0.7570	 0.5580
R	 0.5450	 0.3790
S	 0.6970	 0.4990
T	 0.6160	 0.4770
U	 0.2170	 0.3430
V	 0.7220	 0.5260
W	 0.6400	 0.4820
X	 0.6120	 0.4690
Y	 0.6710	 0.5000
Z	 0.3710	 0.2430
a	 0.7590	 0.5320
b	 0.5160	 0.4270
c	 0.4010	 0.2660
d	 0.6300	 0.4740
e	 0.7950	 0.5870



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Chain	Atom inclusion	Q-score
f	 0.7990	 0.5640
g	 0.5920	 0.4240
h	 0.6030	 0.4630
i	 0.5250	 0.4080
j	 0.8220	 0.5760
k	 0.3390	 0.2670
l	 0.6830	 0.5250
m	 0.5960	 0.4340
n	 0.4180	 0.3770
o	 0.6250	 0.4870
p	 0.6650	 0.4980
q	 0.0120	 0.0720
r	 0.6800	 0.4950
s	 0.0500	 0.1370
t	 0.0390	 0.0670
u	 0.0450	 0.2840
v	 0.0080	 0.0480
x	 0.0560	 0.1430