



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 08:22 PM UTC

PDB ID : 7QWR / pdb_00007qwr
EMDB ID : EMD-14192
Title : Structure of the ribosome-nascent chain containing an ER signal sequence in complex with 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 : 2.90 Å (reported)
Based on initial model : 7OBR

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

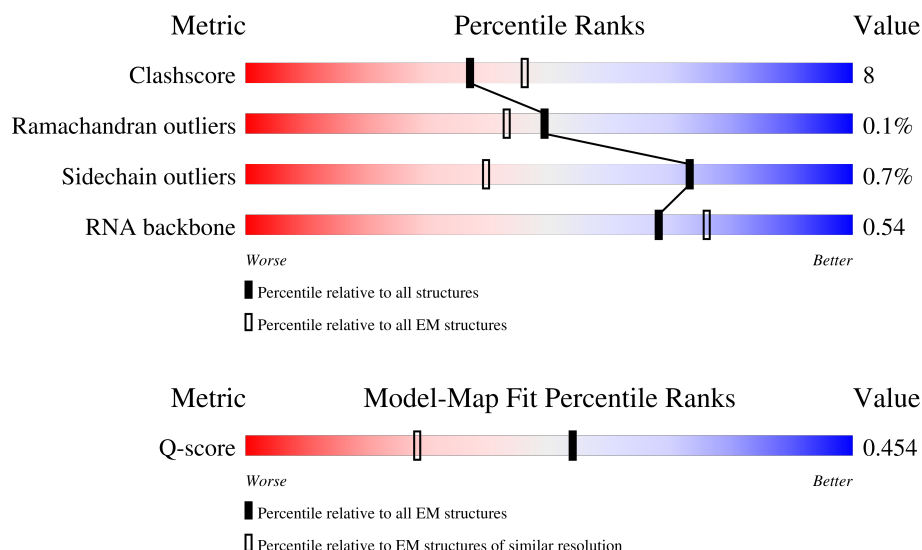
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.90 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	13054 (2.40 - 3.40)

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	s	24	100% 100%
2	t	215	31% 23% 8% 69%
3	u	162	58% 53% 13% 33%

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Mol	Chain	Length	Quality of chain
4	A	245	
5	b	223	
6	B	403	
7	c	115	
8	C	413	
9	d	125	
10	D	297	
11	e	157	
12	E	291	
13	f	110	
14	F	225	
15	g	129	
16	G	319	
17	h	123	
18	H	192	
19	i	102	
20	I	214	
21	j	97	
22	J	178	
23	k	69	
24	L	211	
25	l	51	
26	M	218	
27	m	128	
28	N	204	

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Mol	Chain	Length	Quality of chain
29	n	25	
30	O	500	
31	o	141	
32	P	153	
33	p	92	
34	Q	187	
35	r	137	
36	R	196	
37	S	175	
38	T	160	
39	U	105	
40	V	140	
41	W	157	
42	5	4754	
43	X	156	
44	7	120	
45	Y	145	
46	8	156	
47	Z	136	
48	a	148	

2 Entry composition

There are 50 unique types of molecules in this entry. The entry contains 134576 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 protein called Nascent chain pre-prolactin.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	s	24	Total	C	N	O	0	0
			120	72	24	24		

- Molecule 2 is a protein called Nascent polypeptide-associated complex subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	t	67	Total	C	N	O	S	0	0
			531	335	97	98	1		

- Molecule 3 is a protein called Isoform 2 of Transcription factor BTF3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	u	108	Total	C	N	O	S	0	0
			837	523	155	156	3		

- Molecule 4 is a protein called 60S ribosomal protein L8.

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

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	46	LYS	-	insertion	UNP A0A5F9D5B2
A	47	ASP	-	insertion	UNP A0A5F9D5B2
A	48	ILE	-	insertion	UNP A0A5F9D5B2
A	49	ILE	-	insertion	UNP A0A5F9D5B2
A	50	HIS	-	insertion	UNP A0A5F9D5B2
A	51	ASP	-	insertion	UNP A0A5F9D5B2
A	52	PRO	-	insertion	UNP A0A5F9D5B2
A	53	GLY	-	insertion	UNP A0A5F9D5B2
A	54	ARG	-	insertion	UNP A0A5F9D5B2

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Chain	Residue	Modelled	Actual	Comment	Reference
A	55	GLY	-	insertion	UNP A0A5F9D5B2
A	56	ALA	-	insertion	UNP A0A5F9D5B2
A	57	PRO	-	insertion	UNP A0A5F9D5B2
A	58	LEU	-	insertion	UNP A0A5F9D5B2
A	59	ALA	-	insertion	UNP A0A5F9D5B2
A	60	LYS	-	insertion	UNP A0A5F9D5B2
A	61	VAL	-	insertion	UNP A0A5F9D5B2
A	62	VAL	-	insertion	UNP A0A5F9D5B2
A	63	PHE	-	insertion	UNP A0A5F9D5B2
A	64	ARG	-	insertion	UNP A0A5F9D5B2
A	65	ASP	-	insertion	UNP A0A5F9D5B2
A	66	PRO	-	insertion	UNP A0A5F9D5B2
A	67	TYR	-	insertion	UNP A0A5F9D5B2
A	68	ARG	-	insertion	UNP A0A5F9D5B2
A	69	PHE	-	insertion	UNP A0A5F9D5B2

- Molecule 5 is a protein called 60S ribosomal protein L29.

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

- Molecule 6 is a protein called Ribosomal protein L3.

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

- Molecule 7 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	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 8 is a protein called 60S ribosomal protein L4.

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

- Molecule 9 is a protein called Ribosomal protein L31.

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

- Molecule 10 is a protein called Ribosomal_L18_c domain-containing protein.

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

- Molecule 11 is a protein called Ribosomal protein L32.

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

- Molecule 12 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	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 13 is a protein called 60S ribosomal protein L35a.

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

- Molecule 14 is a protein called uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	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 15 is a protein called 60S ribosomal protein L34.

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

- Molecule 16 is a protein called 60S ribosomal protein L7a.

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

- Molecule 17 is a protein called 60S ribosomal protein L35.

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

- Molecule 18 is a protein called 60S ribosomal protein L9.

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

- Molecule 19 is a protein called 60S ribosomal protein L36.

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

- Molecule 20 is a protein called 60S ribosomal protein L10.

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

- Molecule 21 is a protein called Ribosomal protein L37.

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

- Molecule 22 is a protein called Ribosomal protein L11.

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

- Molecule 23 is a protein called 60S ribosomal protein L38.

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

- Molecule 24 is a protein called L13.

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

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	52	SER	ALA	conflict	UNP G1TKB3
L	55	LEU	ILE	conflict	UNP G1TKB3
L	74	ARG	HIS	conflict	UNP G1TKB3
L	190	ARG	HIS	conflict	UNP G1TKB3

- Molecule 25 is a protein called Ribosomal protein L39.

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

- Molecule 26 is a protein called 60S ribosomal protein L14.

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

- Molecule 27 is a protein called 60S ribosomal protein L40.

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

- Molecule 28 is a protein called Ribosomal protein L15.

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

- Molecule 29 is a protein called 60s ribosomal protein l41.

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

- Molecule 30 is a protein called 60S ribosomal protein L13a.

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

- Molecule 31 is a protein called eL42.

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

- Molecule 32 is a protein called 60S ribosomal protein L17.

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

- Molecule 33 is a protein called eL43.

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

- Molecule 34 is a protein called eL18.

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

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Q	6	ARG	LEU	conflict	UNP G1TX70
Q	14	ARG	TRP	conflict	UNP G1TX70
Q	23	ILE	MET	conflict	UNP G1TX70
Q	24	TYR	CYS	conflict	UNP G1TX70
Q	38	ARG	HIS	conflict	UNP G1TX70
Q	57	ASN	LYS	conflict	UNP G1TX70
Q	66	MET	VAL	conflict	UNP G1TX70
Q	74	GLY	ASP	conflict	UNP G1TX70
Q	75	ARG	PRO	conflict	UNP G1TX70
Q	77	GLY	ASN	conflict	UNP G1TX70
Q	106	SER	THR	conflict	UNP G1TX70
Q	110	ARG	HIS	conflict	UNP G1TX70
Q	117	GLY	GLU	conflict	UNP G1TX70
Q	124	ASP	HIS	conflict	UNP G1TX70
Q	134	CYS	ARG	conflict	UNP G1TX70
Q	150	ARG	GLN	conflict	UNP G1TX70
Q	172	ARG	GLY	conflict	UNP G1TX70
Q	184	ARG	TRP	conflict	UNP G1TX70

- Molecule 35 is a protein called 60S ribosomal protein L28.

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

- Molecule 36 is a protein called 60S ribosomal protein L19.

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

- Molecule 37 is a protein called 60S ribosomal protein L18a.

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

- Molecule 38 is a protein called 60S ribosomal protein L21.

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

- Molecule 39 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	U	105	Total	C	N	O	S	0	0
			859	547	150	160	2		

- Molecule 40 is a protein called Ribosomal protein L23.

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

- Molecule 41 is a protein called Ribosomal protein L24.

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

- Molecule 42 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	5	3493	Total	C	N	O	P	0	0
			74854	33335	13681	24346	3492		

- Molecule 43 is a protein called Ribosomal_L23eN domain-containing protein.

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

- Molecule 44 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	7	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		

- Molecule 45 is a protein called Ribosomal protein L26.

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

- Molecule 46 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	8	156	Total	C	N	O	P	0	0
			3314	1480	585	1094	155		

- Molecule 47 is a protein called 60S ribosomal protein L27.

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

- Molecule 48 is a protein called 60S ribosomal protein L27a.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
a	1	MET	-	initiating methionine	UNP G1SNY0

- Molecule 49 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
49	g	1	Total	Zn	0
			1	1	
49	j	1	Total	Zn	0
			1	1	
49	m	1	Total	Zn	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
49	o	1	Total 1	Zn 1	0
49	p	1	Total 1	Zn 1	0

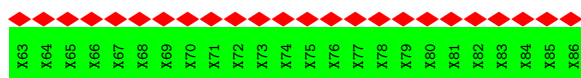
- Molecule 50 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
50	Q	1	Total 1	Mg 1	0
50	5	96	Total 96	Mg 96	0

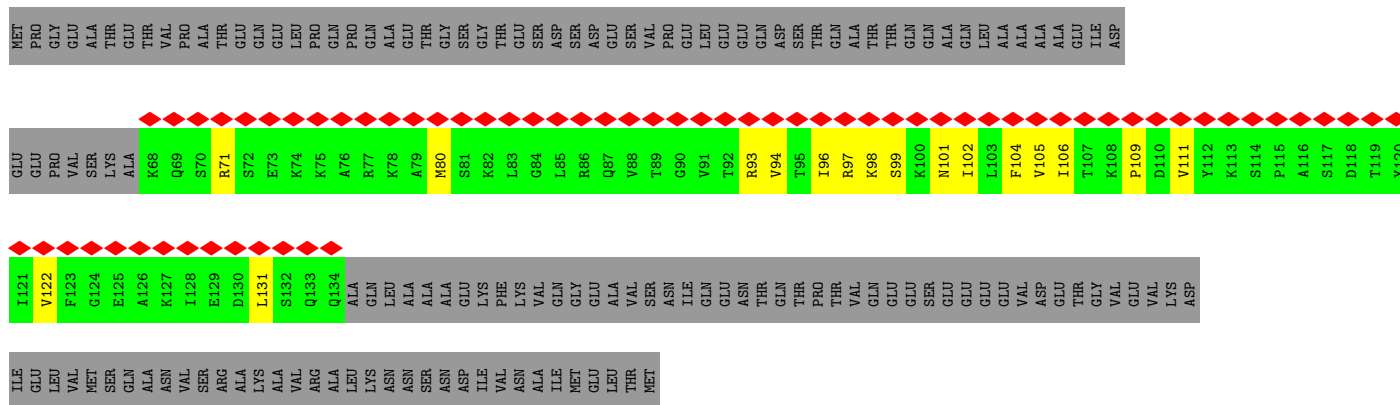
3 Residue-property plots

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.

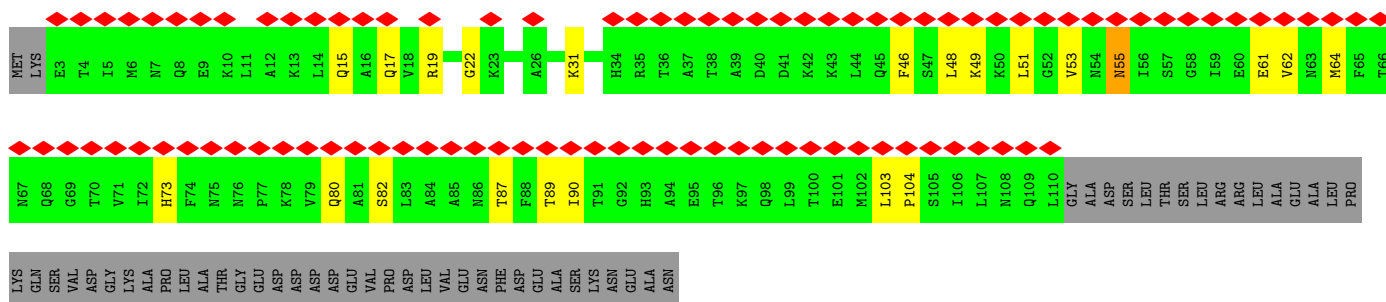
- Molecule 1: Nascent chain pre-prolactin



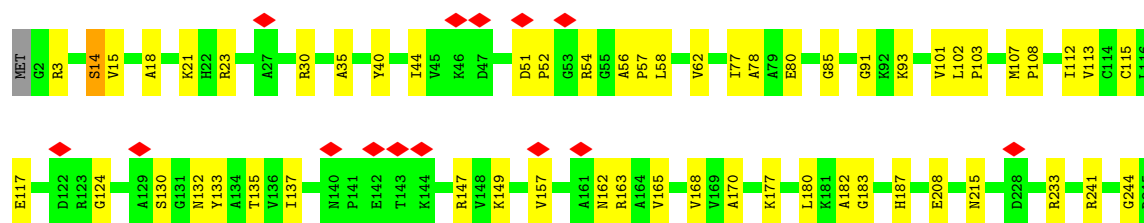
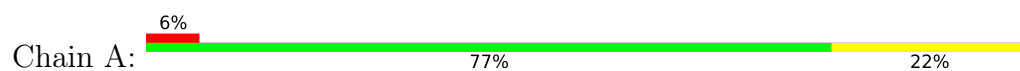
- Molecule 2: Nascent polypeptide-associated complex subunit alpha



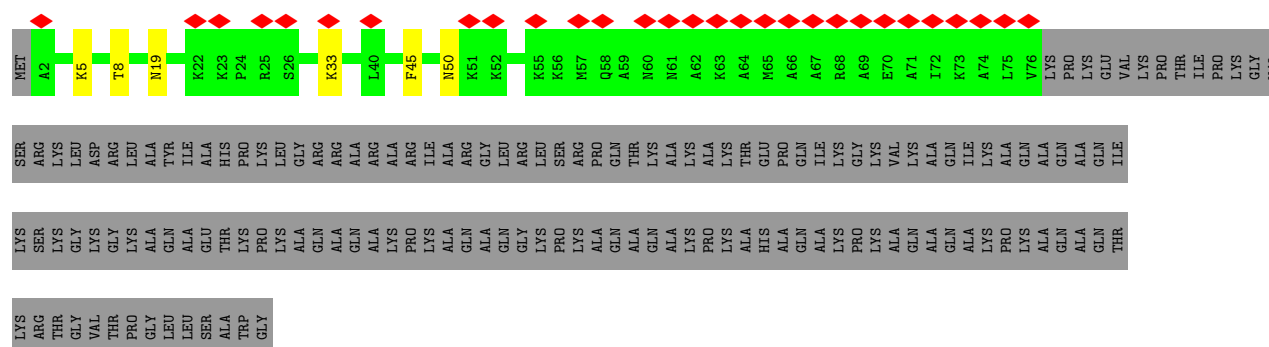
- Molecule 3: Isoform 2 of Transcription factor BTF3



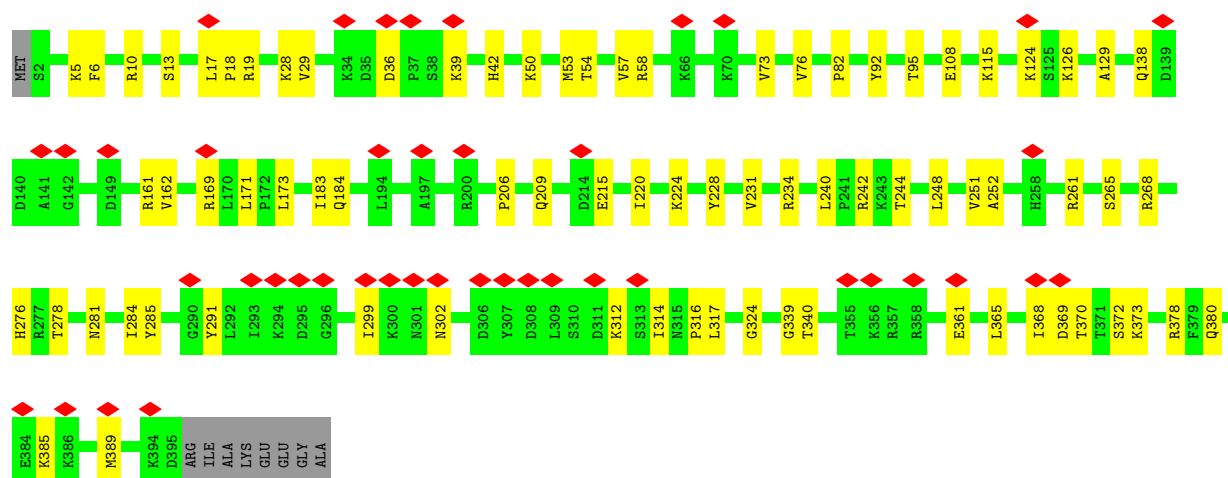
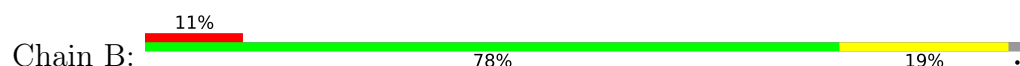
- Molecule 4: 60S ribosomal protein L8



- Molecule 5: 60S ribosomal protein L29



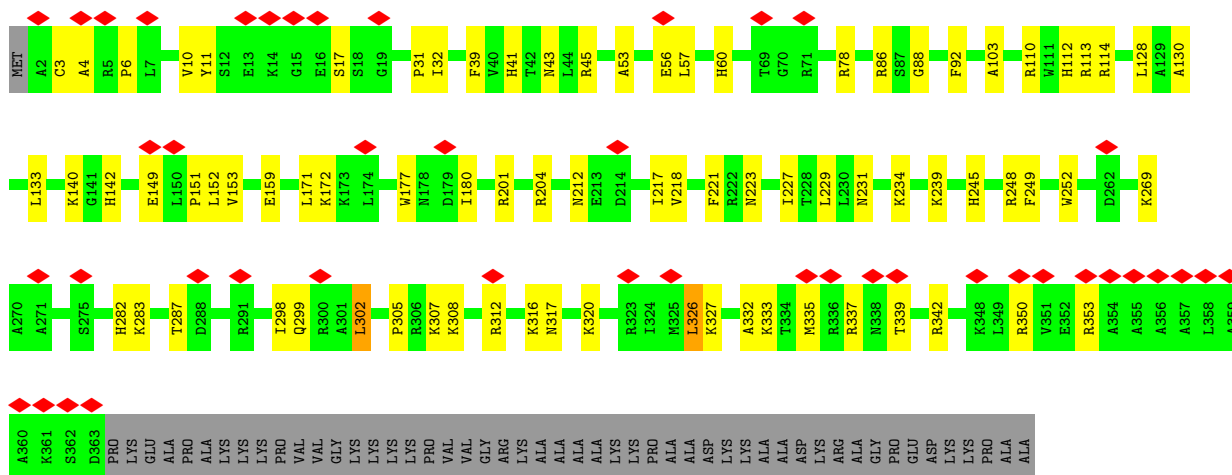
- Molecule 6: Ribosomal protein L3



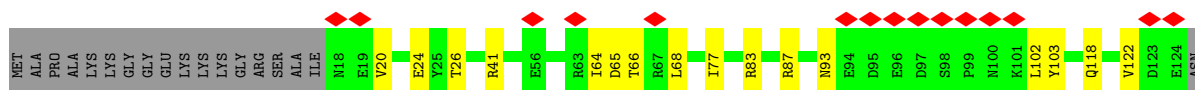
- Molecule 7: 60S ribosomal protein L30



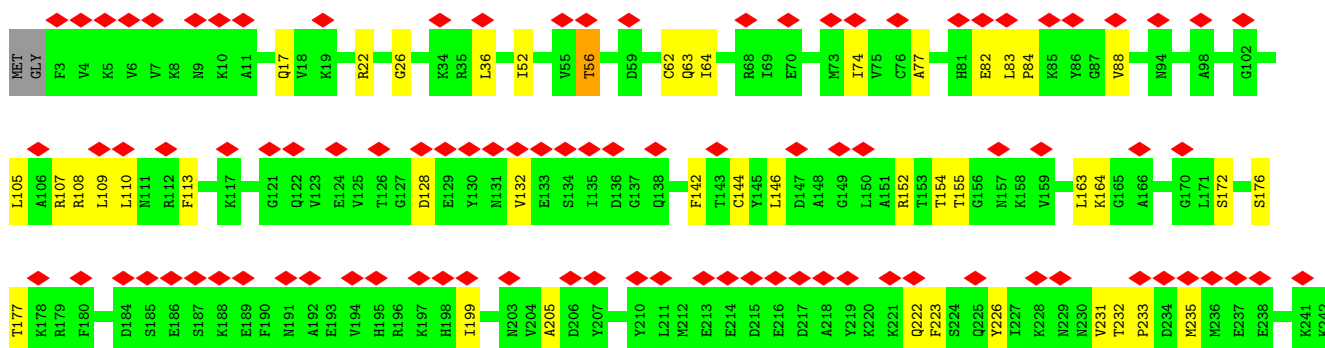
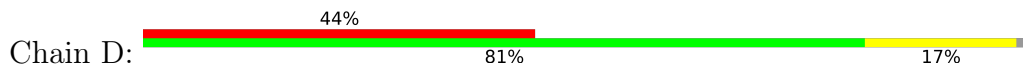
- Molecule 8: 60S ribosomal protein L4

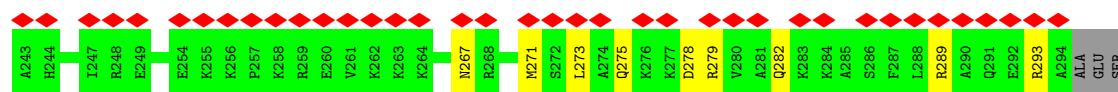


- Molecule 9: Ribosomal protein L31



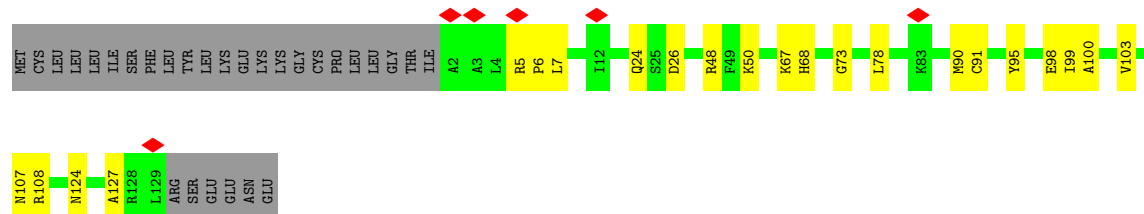
- Molecule 10: Ribosomal L18 c domain-containing protein





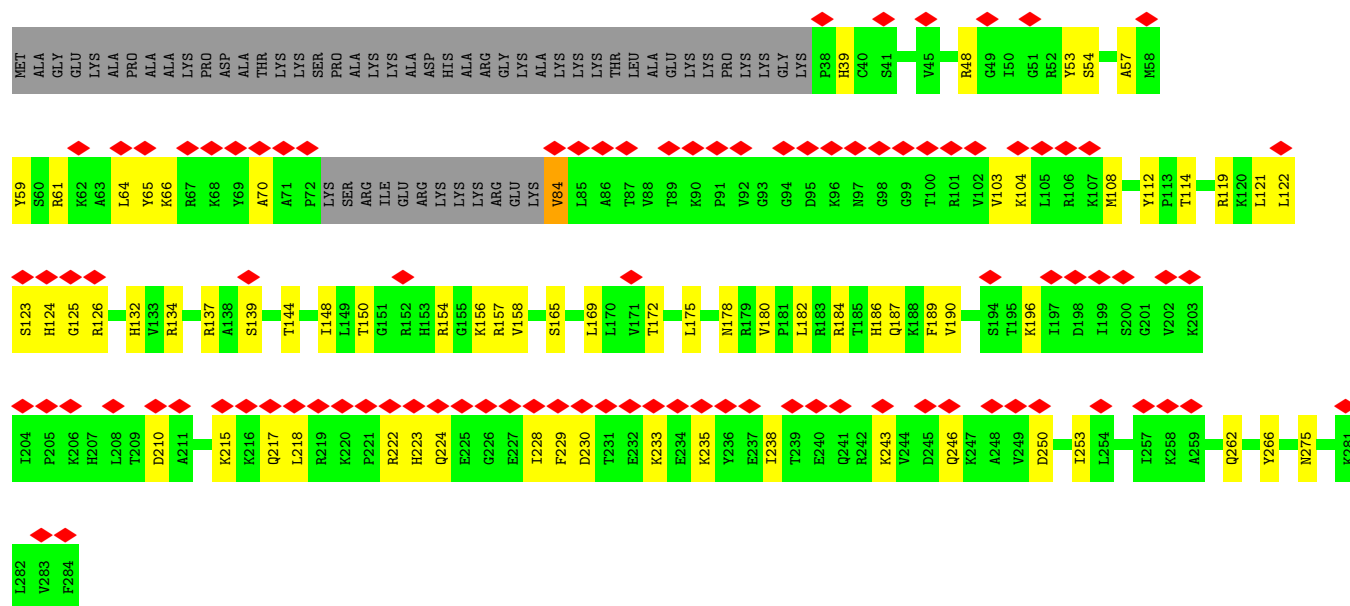
• Molecule 11: Ribosomal protein L32

Chain e: 68% 14% 18%



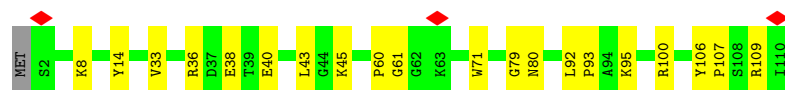
• Molecule 12: 60S ribosomal protein L6

Chain E: 33% 58% 23% 19%



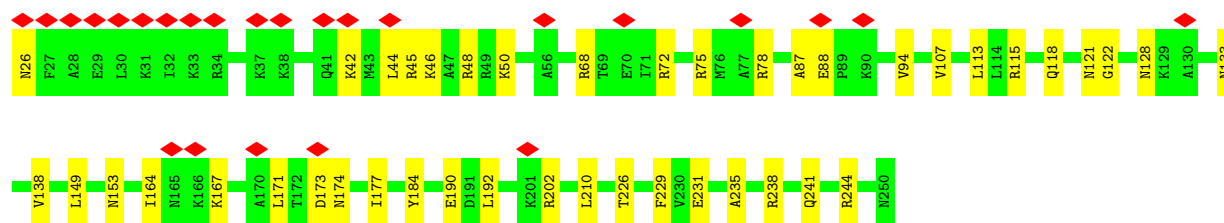
• Molecule 13: 60S ribosomal protein L35a

Chain f: 81% 18%

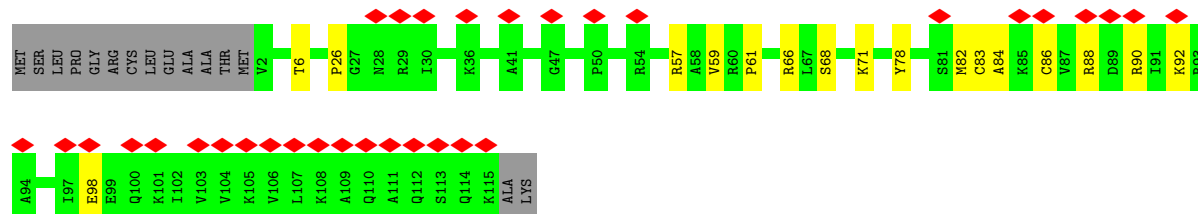
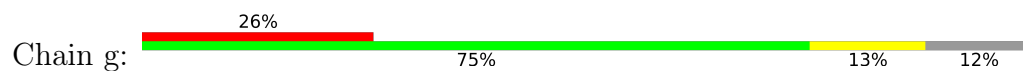


• Molecule 14: uL30

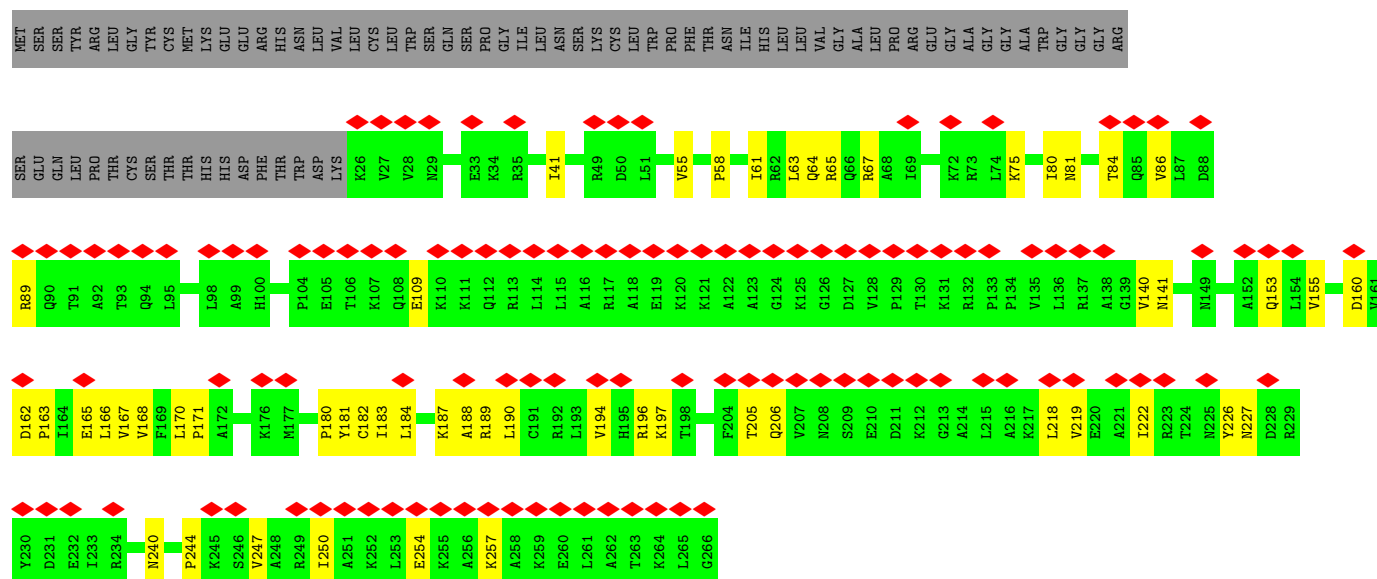
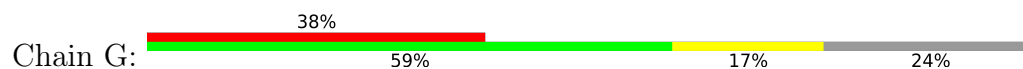
Chain F: 11% 81% 19%



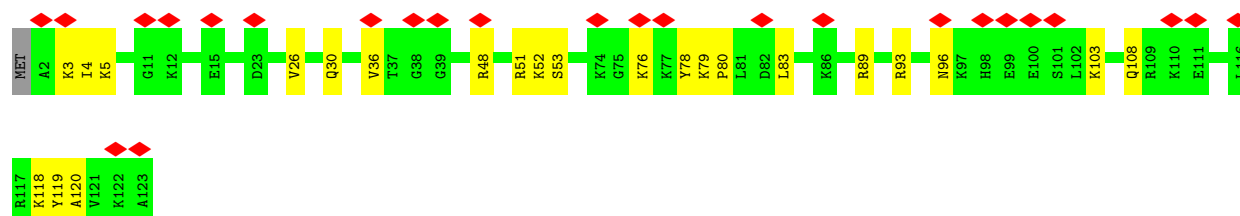
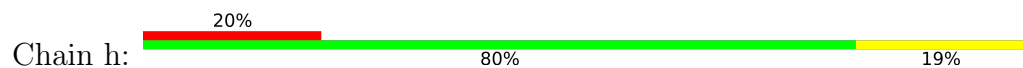
• Molecule 15: 60S ribosomal protein L34



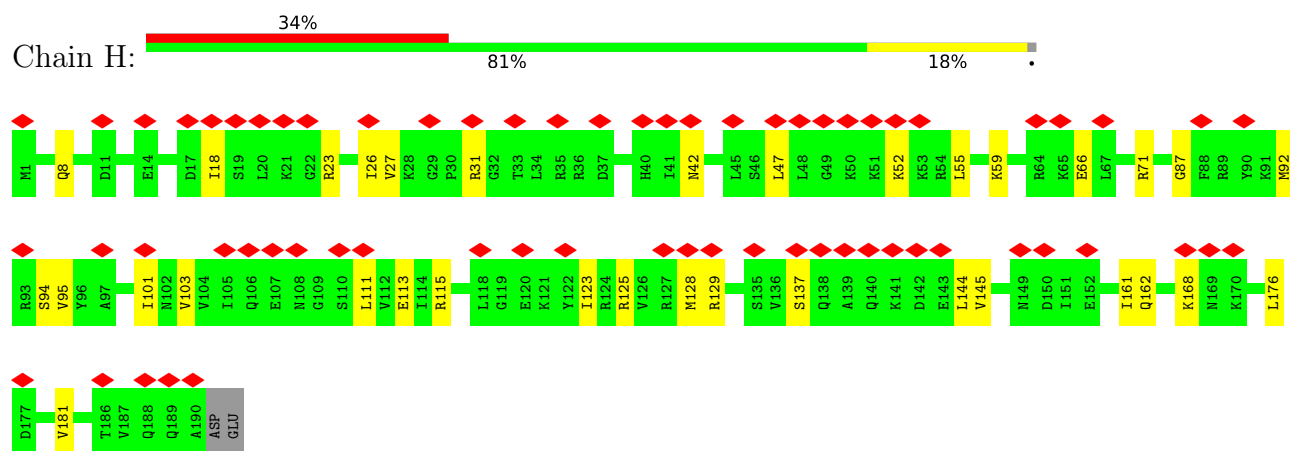
• Molecule 16: 60S ribosomal protein L7a



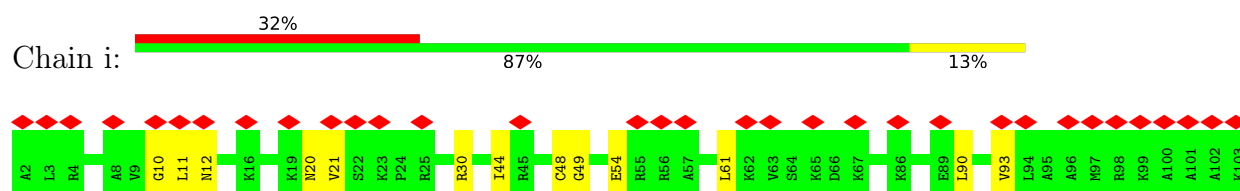
• Molecule 17: 60S ribosomal protein L35



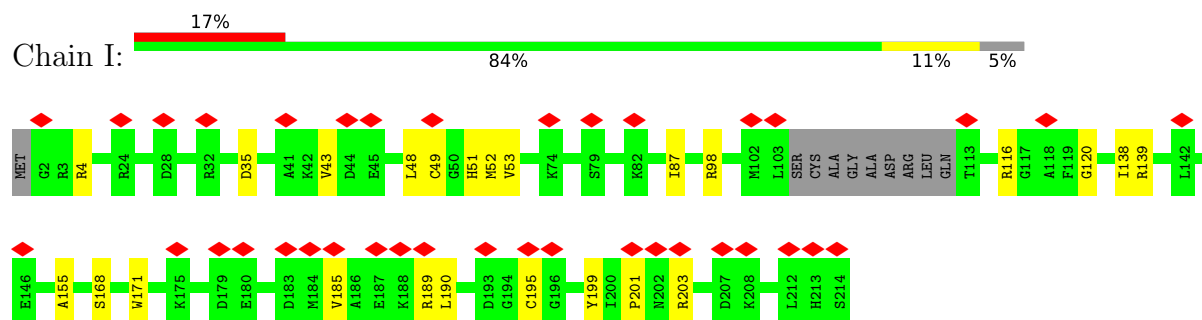
- Molecule 18: 60S ribosomal protein L9



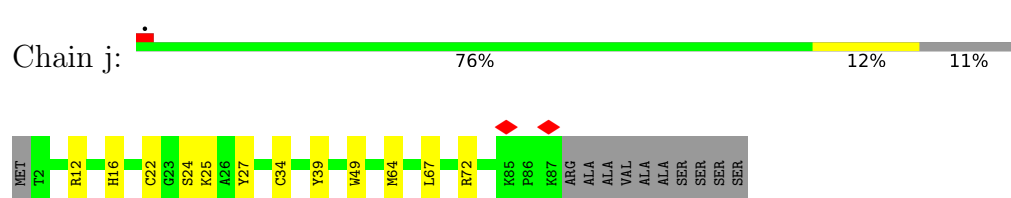
- Molecule 19: 60S ribosomal protein L36



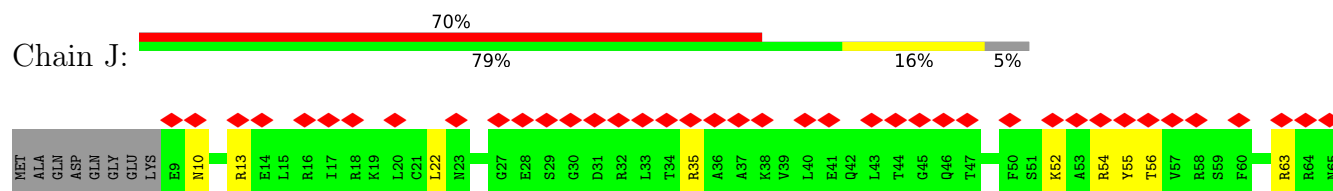
- Molecule 20: 60S ribosomal protein L10

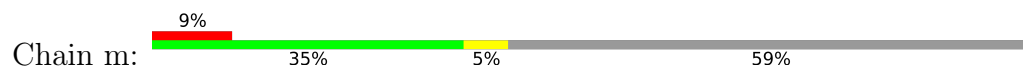


- Molecule 21: Ribosomal protein L37

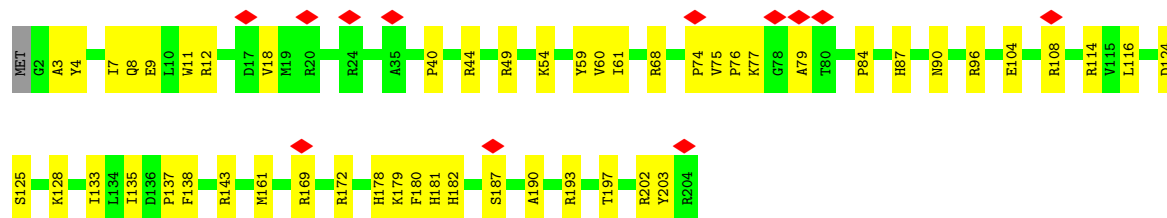
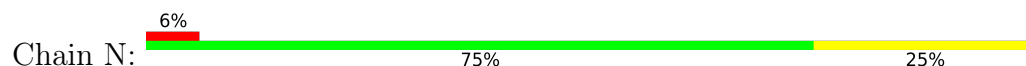


- Molecule 22: Ribosomal protein L11

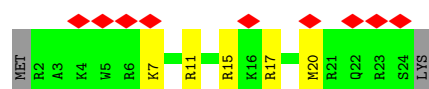




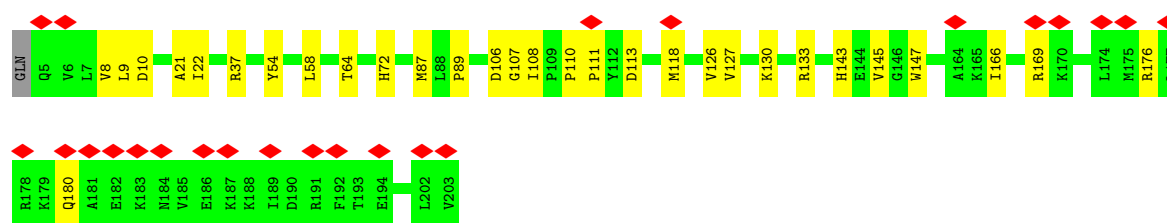
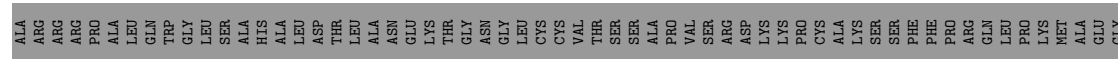
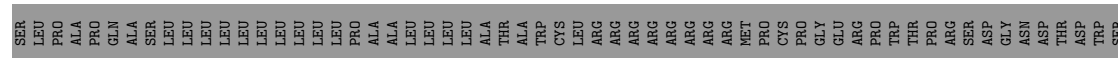
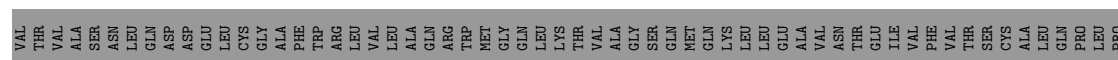
- Molecule 28: Ribosomal protein L15



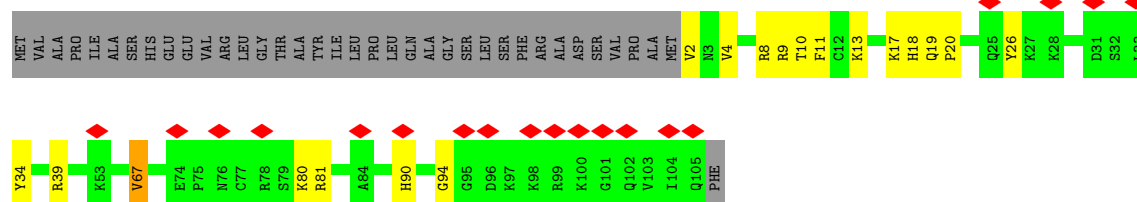
- Molecule 29: 60s ribosomal protein l41



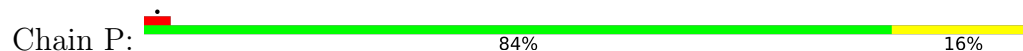
- Molecule 30: 60S ribosomal protein L13a



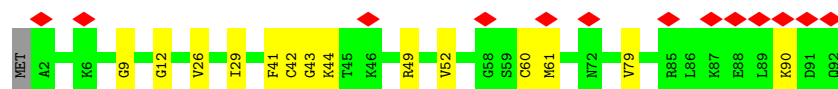
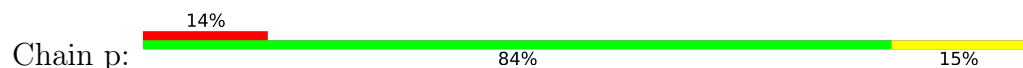
- Molecule 31: eL42



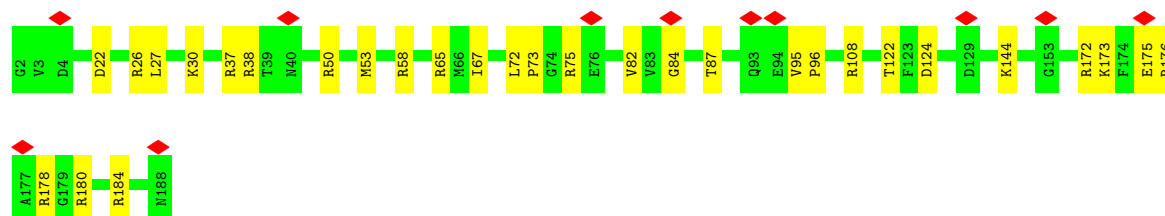
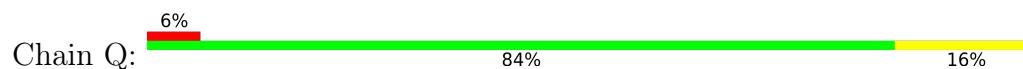
- Molecule 32: 60S ribosomal protein L17



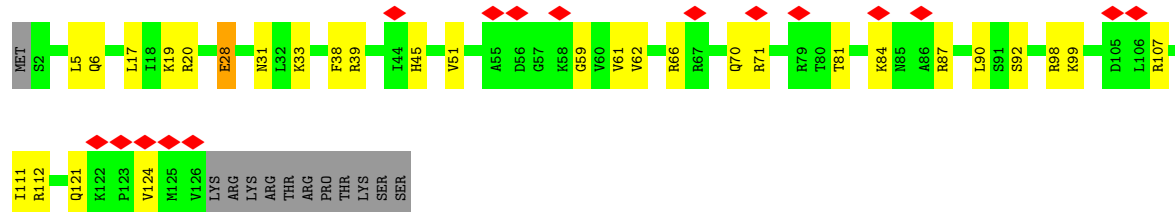
- Molecule 33: eL43



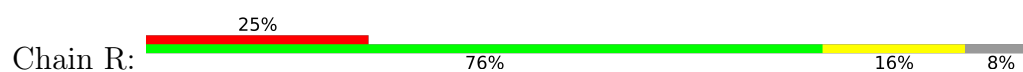
- Molecule 34: eL18

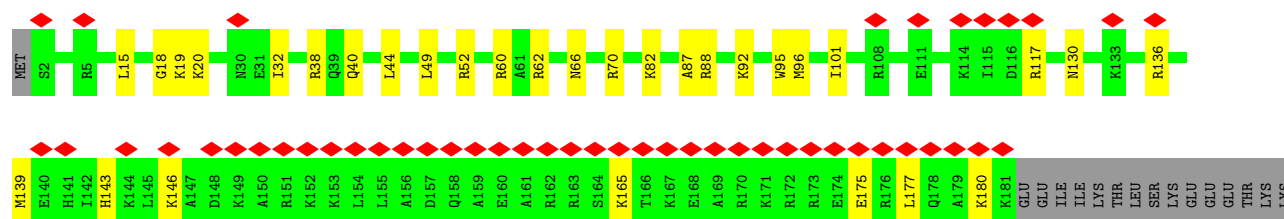


- Molecule 35: 60S ribosomal protein L28

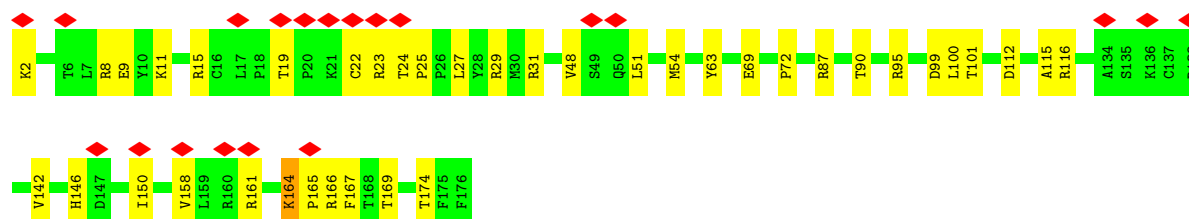
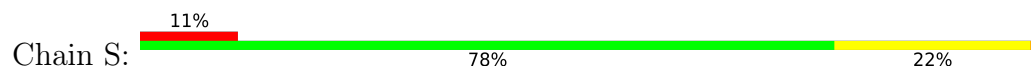


- Molecule 36: 60S ribosomal protein L19

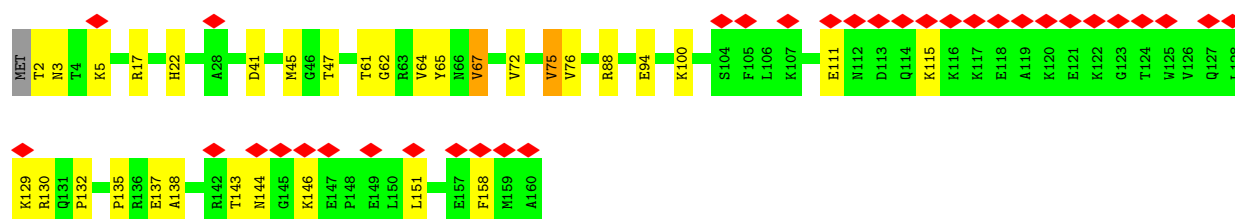
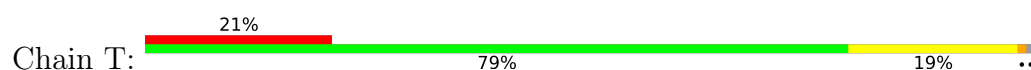




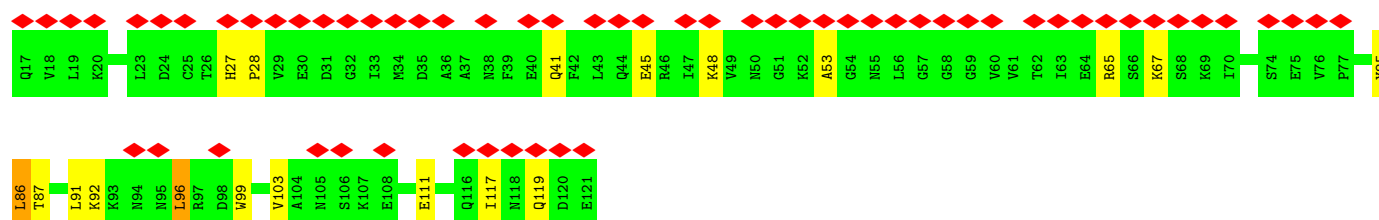
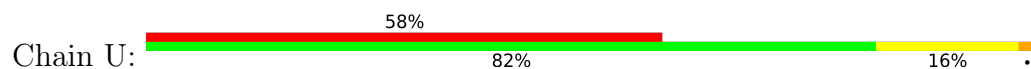
• Molecule 37: 60S ribosomal protein L18a



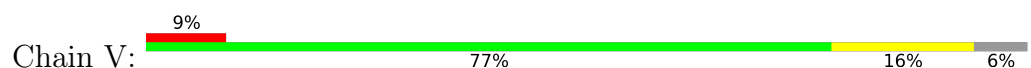
• Molecule 38: 60S ribosomal protein L21

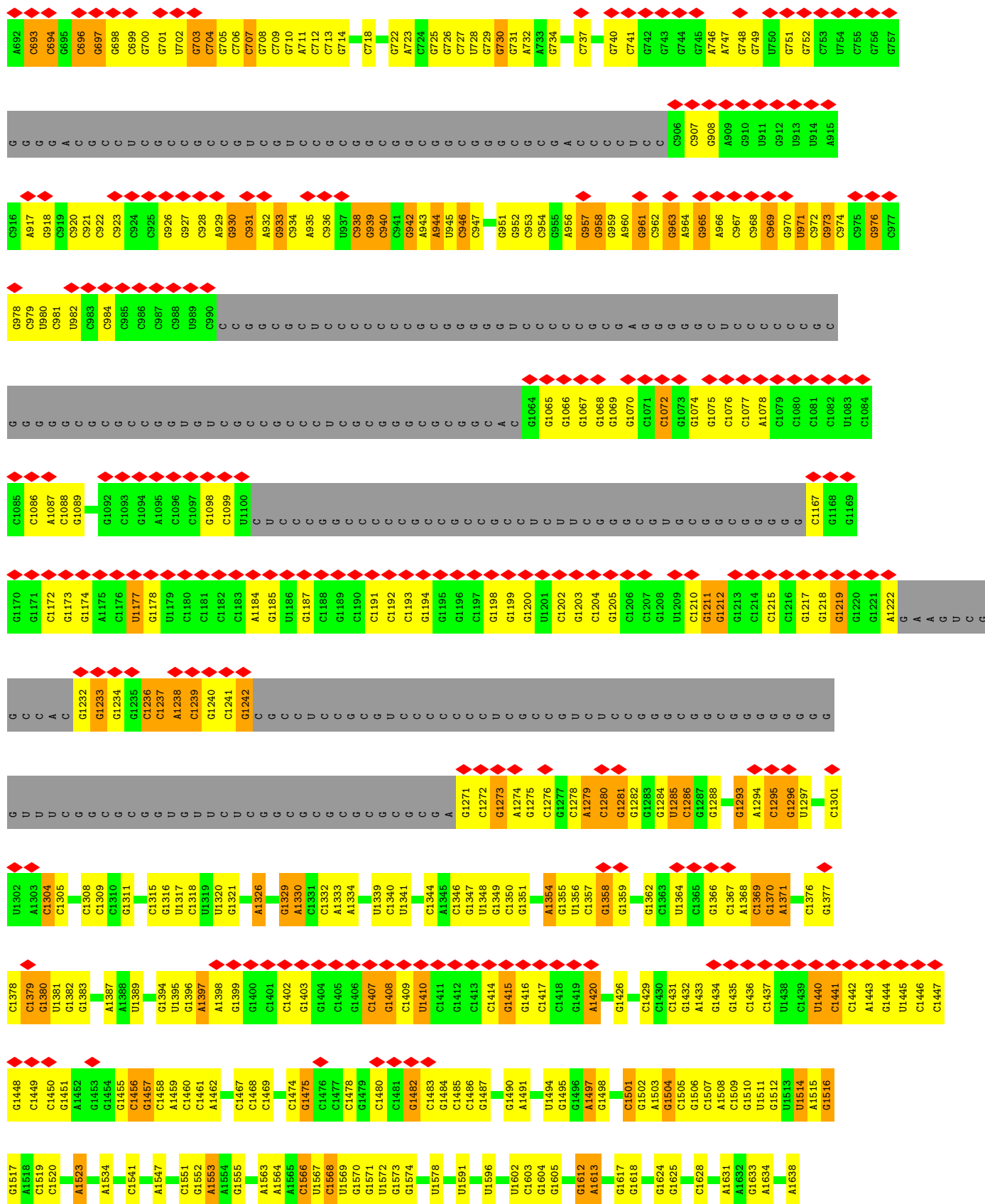


• Molecule 39: 60S ribosomal protein L22



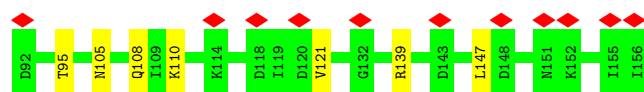
• Molecule 40: Ribosomal protein L23



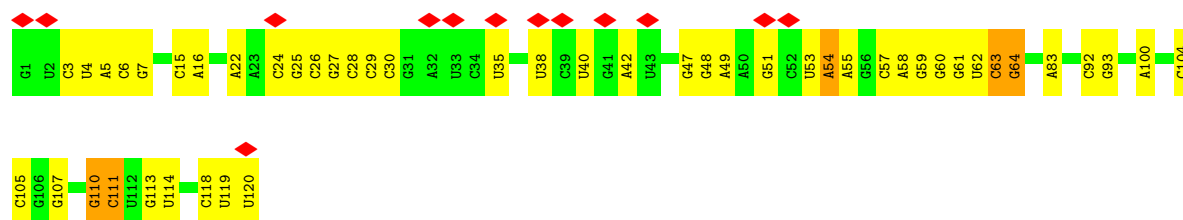




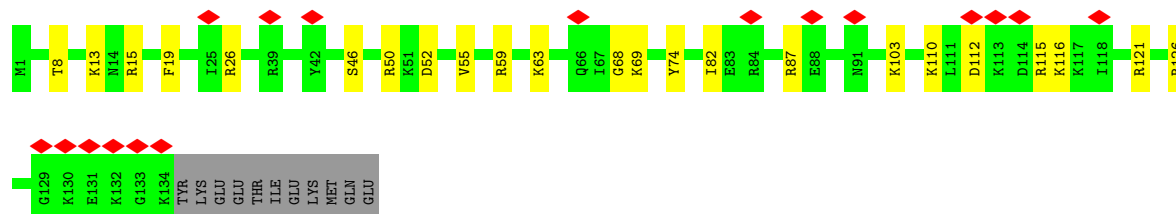
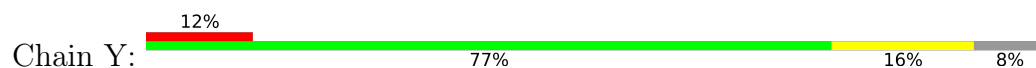




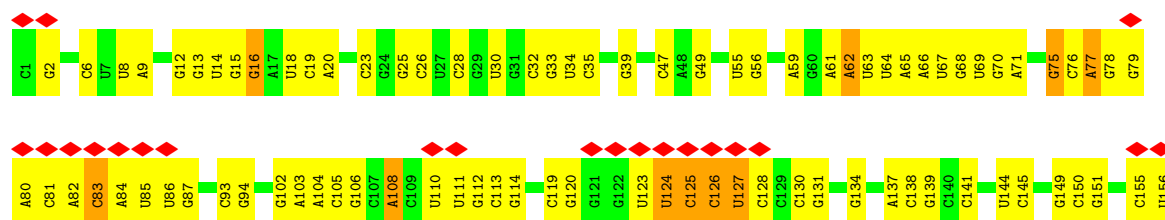
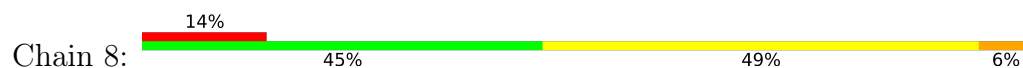
- Molecule 44: 5S ribosomal RNA



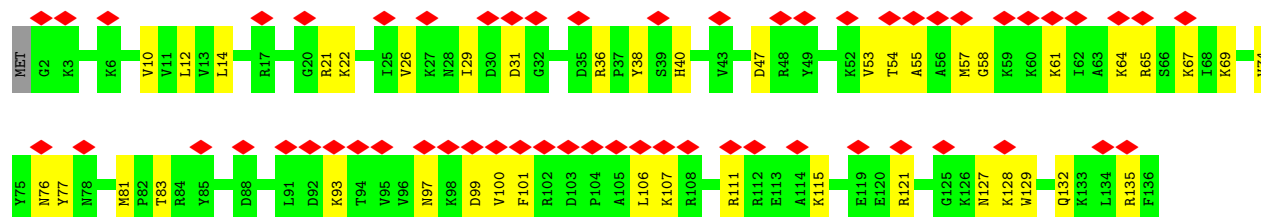
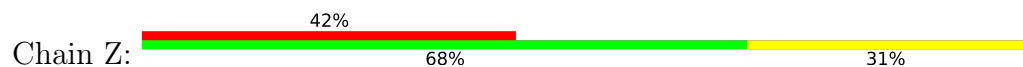
- Molecule 45: Ribosomal protein L26



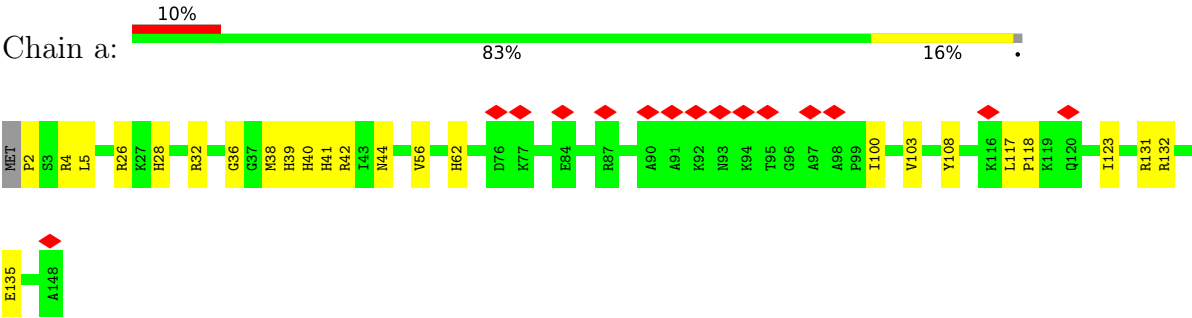
- Molecule 46: 5.8S ribosomal RNA



- Molecule 47: 60S ribosomal protein L27



- Molecule 48: 60S ribosomal protein L27a



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	44040	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	0.181	Depositor
Minimum map value	-0.088	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.010	Depositor
Recommended contour level	0.028	Depositor
Map size (Å)	483.84003, 483.84003, 483.84003	wwPDB
Map dimensions	448, 448, 448	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	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: MG, ZN

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
2	t	0.09	0/536	0.26	0/715
3	u	0.15	0/845	0.35	0/1134
4	A	0.10	0/1906	0.28	0/2556
5	b	0.09	0/619	0.24	0/818
6	B	0.11	0/3216	0.28	0/4311
7	c	0.08	0/742	0.21	0/996
8	C	0.09	0/2937	0.25	0/3946
9	d	0.10	0/903	0.25	0/1216
10	D	0.10	0/2432	0.30	0/3257
11	e	0.09	0/1071	0.25	0/1429
12	E	0.13	0/1936	0.36	0/2600
13	f	0.10	0/895	0.31	0/1198
14	F	0.09	0/1905	0.26	0/2539
15	g	0.09	0/916	0.25	0/1220
16	G	0.12	0/1967	0.32	1/2647 (0.0%)
17	h	0.09	0/1021	0.23	0/1348
18	H	0.11	0/1535	0.32	0/2063
19	i	0.09	0/841	0.23	0/1112
20	I	0.10	0/1693	0.24	0/2260
21	j	0.10	0/720	0.30	0/952
22	J	0.10	0/1376	0.25	0/1841
23	k	0.21	0/575	0.46	0/761
24	L	0.10	0/1734	0.28	0/2317
25	l	0.09	0/454	0.25	0/599
26	M	0.10	0/1158	0.25	0/1547
27	m	0.11	0/435	0.28	0/575
28	N	0.10	0/1746	0.26	0/2338
29	n	0.08	0/223	0.17	0/284
30	O	0.09	0/1671	0.25	0/2234
31	o	0.12	0/864	0.33	0/1140
32	P	0.09	0/1268	0.27	0/1700
33	p	0.10	0/718	0.24	0/953

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
34	Q	0.10	0/1530	0.26	0/2041
35	r	0.11	0/1017	0.34	0/1364
36	R	0.11	0/1524	0.27	0/2013
37	S	0.11	0/1493	0.28	0/2002
38	T	0.09	0/1326	0.25	0/1770
39	U	0.11	0/873	0.33	0/1172
40	V	0.11	0/993	0.29	0/1332
41	W	0.08	0/541	0.24	0/720
42	5	0.09	0/83726	0.23	1/130593 (0.0%)
43	X	0.08	0/993	0.24	0/1334
44	7	0.07	0/2858	0.18	0/4455
45	Y	0.08	0/1132	0.23	0/1504
46	8	0.08	0/3701	0.20	0/5766
47	Z	0.10	0/1130	0.28	0/1507
48	a	0.08	0/1191	0.25	0/1590
All	All	0.09	0/144886	0.25	2/213769 (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
13	f	0	1
37	S	0	1
All	All	0	2

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	G	168	VAL	N-CA-C	-6.33	107.69	113.71
42	5	5061	A	P-O3'-C3'	5.22	128.02	120.20

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
37	S	164	LYS	Peptide
13	f	106	TYR	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	s	120	0	31	0	0
2	t	531	0	573	12	0
3	u	837	0	880	17	0
4	A	1868	0	1959	45	0
5	b	609	0	650	6	0
6	B	3148	0	3267	54	0
7	c	732	0	766	11	0
8	C	2883	0	3053	59	0
9	d	888	0	930	9	0
10	D	2386	0	2419	41	0
11	e	1053	0	1147	20	0
12	E	1898	0	2035	56	0
13	f	876	0	912	12	0
14	F	1870	0	1994	32	0
15	g	906	0	998	15	0
16	G	1934	0	2085	35	0
17	h	1013	0	1147	16	0
18	H	1516	0	1597	24	0
19	i	830	0	916	8	0
20	I	1655	0	1704	17	0
21	j	705	0	737	10	0
22	J	1353	0	1386	17	0
23	k	569	0	637	5	0
24	L	1703	0	1820	21	0
25	l	444	0	483	3	0
26	M	1137	0	1211	14	0
27	m	429	0	465	8	0
28	N	1701	0	1749	41	0
29	n	222	0	264	3	0
30	O	1638	0	1777	20	0
31	o	851	0	920	12	0
32	P	1242	0	1274	19	0
33	p	708	0	756	12	0
34	Q	1506	0	1623	28	0
35	r	1001	0	1060	24	0
36	R	1508	0	1664	28	0
37	S	1454	0	1496	30	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	T	1298	0	1366	24	0
39	U	859	0	874	13	0
40	V	979	0	1039	14	0
41	W	528	0	541	5	0
42	5	74854	0	37827	1096	0
43	X	976	0	1053	9	0
44	7	2558	0	1296	39	0
45	Y	1115	0	1205	19	0
46	8	3314	0	1683	52	0
47	Z	1107	0	1182	32	0
48	a	1162	0	1209	19	0
49	g	1	0	0	0	0
49	j	1	0	0	0	0
49	m	1	0	0	0	0
49	o	1	0	0	0	0
49	p	1	0	0	0	0
50	5	96	0	0	0	0
50	Q	1	0	0	0	0
All	All	134576	0	97660	1729	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 1729 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)
42:5:1444:G:N2	42:5:2100:A:H62	1.59	1.01
42:5:1444:G:H21	42:5:2100:A:H62	1.09	1.00
42:5:1444:G:H21	42:5:2100:A:N6	1.62	0.97
42:5:2845:A:H61	42:5:3843:C:H42	1.03	0.95
42:5:2845:A:H61	42:5:3843:C:N4	1.71	0.88

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	t	65/215 (30%)	62 (95%)	3 (5%)	0	100	100
3	u	106/162 (65%)	101 (95%)	5 (5%)	0	100	100
4	A	242/245 (99%)	220 (91%)	20 (8%)	2 (1%)	16	44
5	b	73/223 (33%)	70 (96%)	3 (4%)	0	100	100
6	B	392/403 (97%)	377 (96%)	15 (4%)	0	100	100
7	c	92/115 (80%)	90 (98%)	2 (2%)	0	100	100
8	C	360/413 (87%)	344 (96%)	16 (4%)	0	100	100
9	d	105/125 (84%)	99 (94%)	6 (6%)	0	100	100
10	D	290/297 (98%)	275 (95%)	15 (5%)	0	100	100
11	e	126/157 (80%)	122 (97%)	4 (3%)	0	100	100
12	E	232/291 (80%)	201 (87%)	31 (13%)	0	100	100
13	f	107/110 (97%)	100 (94%)	7 (6%)	0	100	100
14	F	223/225 (99%)	217 (97%)	6 (3%)	0	100	100
15	g	112/129 (87%)	110 (98%)	2 (2%)	0	100	100
16	G	239/319 (75%)	220 (92%)	19 (8%)	0	100	100
17	h	120/123 (98%)	117 (98%)	3 (2%)	0	100	100
18	H	188/192 (98%)	176 (94%)	12 (6%)	0	100	100
19	i	100/102 (98%)	91 (91%)	8 (8%)	1 (1%)	12	39
20	I	200/214 (94%)	192 (96%)	8 (4%)	0	100	100
21	j	84/97 (87%)	82 (98%)	2 (2%)	0	100	100
22	J	167/178 (94%)	161 (96%)	6 (4%)	0	100	100
23	k	67/69 (97%)	61 (91%)	6 (9%)	0	100	100
24	L	208/211 (99%)	195 (94%)	12 (6%)	1 (0%)	24	54
25	l	48/51 (94%)	44 (92%)	4 (8%)	0	100	100
26	M	136/218 (62%)	127 (93%)	9 (7%)	0	100	100
27	m	50/128 (39%)	48 (96%)	2 (4%)	0	100	100
28	N	201/204 (98%)	190 (94%)	11 (6%)	0	100	100
29	n	21/25 (84%)	21 (100%)	0	0	100	100
30	O	197/500 (39%)	194 (98%)	3 (2%)	0	100	100
31	o	102/141 (72%)	93 (91%)	9 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
32	P	74/153 (48%)	71 (96%)	3 (4%)	0	100	100
33	p	89/92 (97%)	87 (98%)	2 (2%)	0	100	100
34	Q	185/187 (99%)	178 (96%)	7 (4%)	0	100	100
35	r	123/137 (90%)	112 (91%)	11 (9%)	0	100	100
36	R	178/196 (91%)	174 (98%)	4 (2%)	0	100	100
37	S	173/175 (99%)	164 (95%)	9 (5%)	0	100	100
38	T	157/160 (98%)	149 (95%)	7 (4%)	1 (1%)	21	51
39	U	103/105 (98%)	98 (95%)	5 (5%)	0	100	100
40	V	129/140 (92%)	124 (96%)	5 (4%)	0	100	100
41	W	61/157 (39%)	61 (100%)	0	0	100	100
43	X	117/156 (75%)	113 (97%)	4 (3%)	0	100	100
45	Y	132/145 (91%)	128 (97%)	4 (3%)	0	100	100
47	Z	133/136 (98%)	120 (90%)	13 (10%)	0	100	100
48	a	145/148 (98%)	134 (92%)	11 (8%)	0	100	100
All	All	6452/7969 (81%)	6113 (95%)	334 (5%)	5 (0%)	49	77

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	A	14	SER
4	A	180	LEU
19	i	11	LEU
24	L	63	THR
38	T	137	GLU

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	t	60/183 (33%)	59 (98%)	1 (2%)	53	82

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	u	92/136 (68%)	90 (98%)	2 (2%)	45	77
4	A	187/188 (100%)	185 (99%)	2 (1%)	65	88
5	b	62/170 (36%)	62 (100%)	0	100	100
6	B	336/348 (97%)	335 (100%)	1 (0%)	86	96
7	c	79/98 (81%)	79 (100%)	0	100	100
8	C	302/337 (90%)	300 (99%)	2 (1%)	76	92
9	d	98/110 (89%)	95 (97%)	3 (3%)	35	69
10	D	247/250 (99%)	245 (99%)	2 (1%)	73	90
11	e	114/141 (81%)	114 (100%)	0	100	100
12	E	208/251 (83%)	207 (100%)	1 (0%)	81	93
13	f	88/89 (99%)	88 (100%)	0	100	100
14	F	194/195 (100%)	194 (100%)	0	100	100
15	g	98/109 (90%)	98 (100%)	0	100	100
16	G	206/273 (76%)	204 (99%)	2 (1%)	68	89
17	h	109/110 (99%)	107 (98%)	2 (2%)	51	80
18	H	169/171 (99%)	168 (99%)	1 (1%)	78	93
19	i	86/86 (100%)	84 (98%)	2 (2%)	44	76
20	I	174/181 (96%)	174 (100%)	0	100	100
21	j	73/80 (91%)	73 (100%)	0	100	100
22	J	142/149 (95%)	142 (100%)	0	100	100
23	k	64/64 (100%)	63 (98%)	1 (2%)	55	83
24	L	176/177 (99%)	175 (99%)	1 (1%)	78	93
25	l	47/48 (98%)	47 (100%)	0	100	100
26	M	117/160 (73%)	117 (100%)	0	100	100
27	m	48/116 (41%)	48 (100%)	0	100	100
28	N	171/172 (99%)	171 (100%)	0	100	100
29	n	22/24 (92%)	22 (100%)	0	100	100
30	O	171/433 (40%)	169 (99%)	2 (1%)	63	86
31	o	92/121 (76%)	91 (99%)	1 (1%)	65	88
32	P	134/134 (100%)	134 (100%)	0	100	100
33	p	74/75 (99%)	73 (99%)	1 (1%)	59	85

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
34	Q	163/163 (100%)	162 (99%)	1 (1%)	78	93
35	r	109/121 (90%)	107 (98%)	2 (2%)	51	80
36	R	159/175 (91%)	158 (99%)	1 (1%)	78	93
37	S	156/156 (100%)	153 (98%)	3 (2%)	50	79
38	T	139/140 (99%)	135 (97%)	4 (3%)	37	71
39	U	95/95 (100%)	92 (97%)	3 (3%)	34	68
40	V	101/107 (94%)	101 (100%)	0	100	100
41	W	55/126 (44%)	55 (100%)	0	100	100
43	X	107/134 (80%)	107 (100%)	0	100	100
45	Y	124/135 (92%)	124 (100%)	0	100	100
47	Z	117/118 (99%)	117 (100%)	0	100	100
48	a	119/120 (99%)	119 (100%)	0	100	100
All	All	5684/6769 (84%)	5643 (99%)	41 (1%)	73	92

5 of 41 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
35	r	28	GLU
38	T	67	VAL
35	r	124	VAL
37	S	90	THR
38	T	143	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 121 such sidechains are listed below:

Mol	Chain	Res	Type
20	I	73	ASN
40	V	31	ASN
26	M	20	HIS
39	U	50	ASN
48	a	28	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
42	5	3478/4754 (73%)	688 (19%)	71 (2%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
44	7	119/120 (99%)	12 (10%)	0
46	8	155/156 (99%)	33 (21%)	1 (0%)
All	All	3752/5030 (74%)	733 (19%)	72 (1%)

5 of 733 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
42	5	2	G
42	5	8	U
42	5	12	A
42	5	13	U
42	5	21	G

5 of 72 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
42	5	4656	A
46	8	124	U
42	5	4719	G
42	5	4965	U
42	5	1236	C

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.

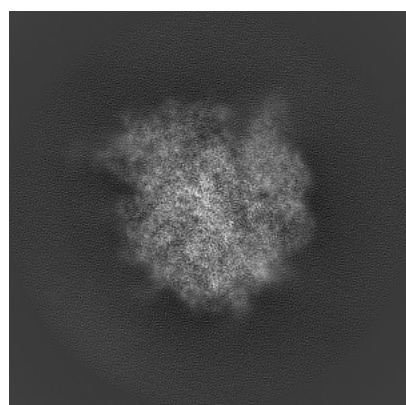
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-14192. These allow visual inspection of the internal detail of the map and identification of artifacts.

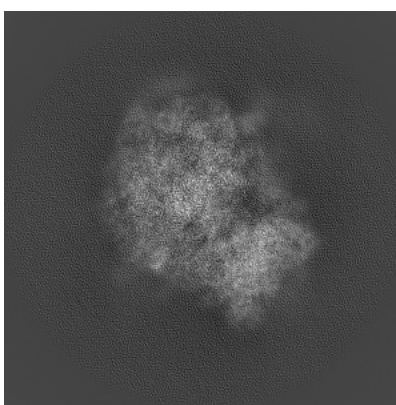
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

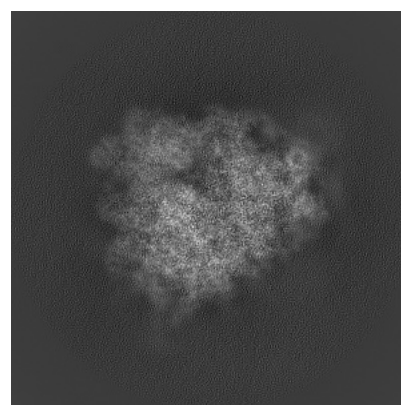
6.1.1 Primary map



X



Y

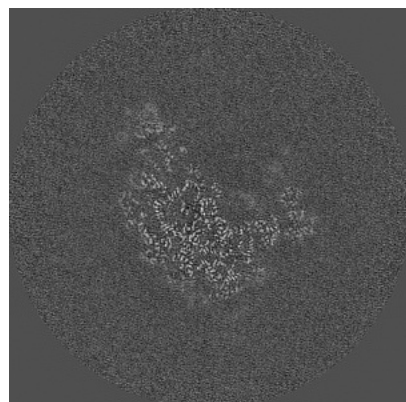


Z

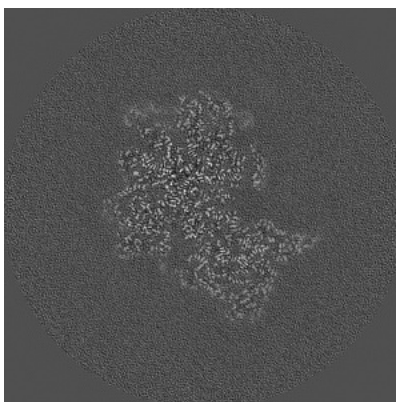
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

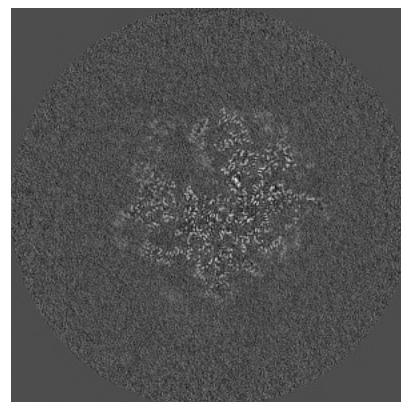
6.2.1 Primary map



X Index: 224



Y Index: 224

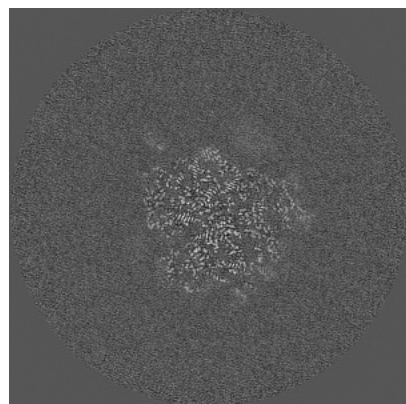


Z Index: 224

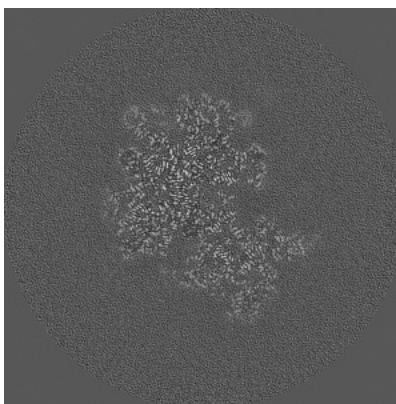
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

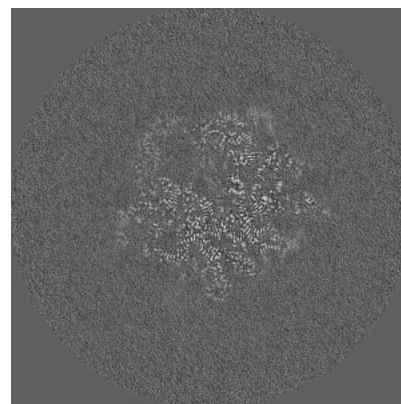
6.3.1 Primary map



X Index: 258



Y Index: 226

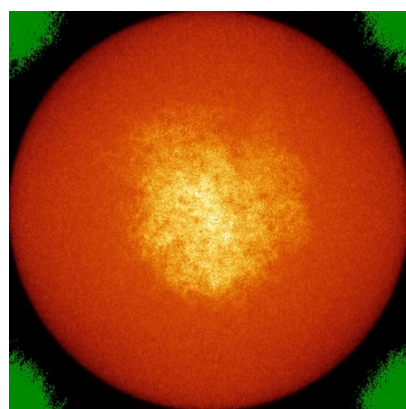


Z Index: 228

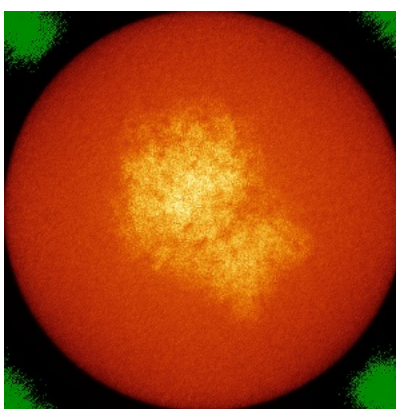
The images above show the largest variance slices of the map in three orthogonal directions.

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

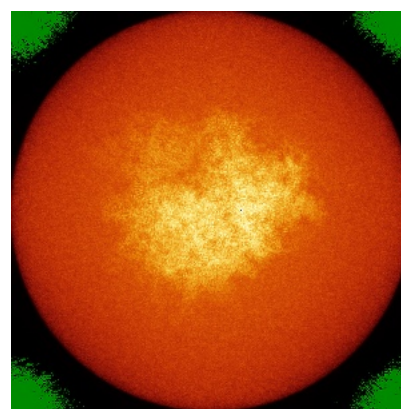
6.4.1 Primary map



X



Y

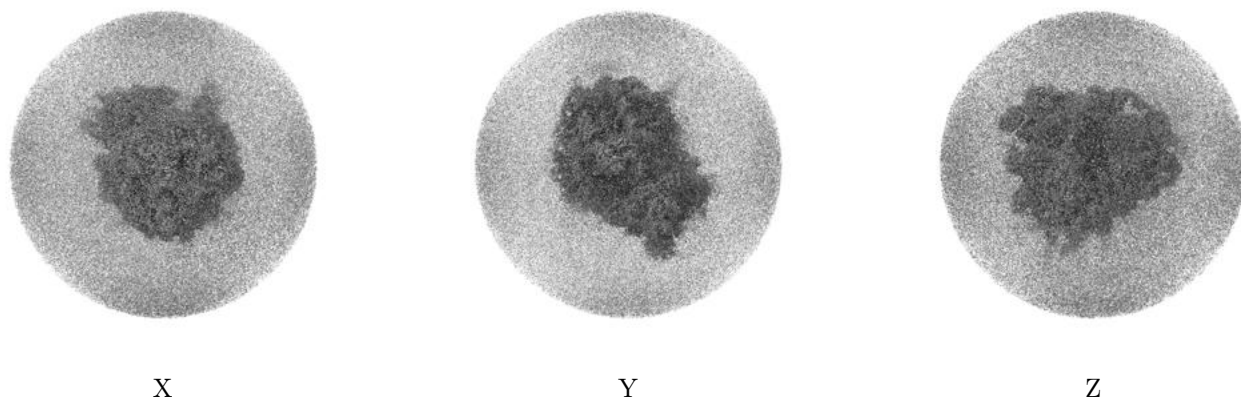


Z

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

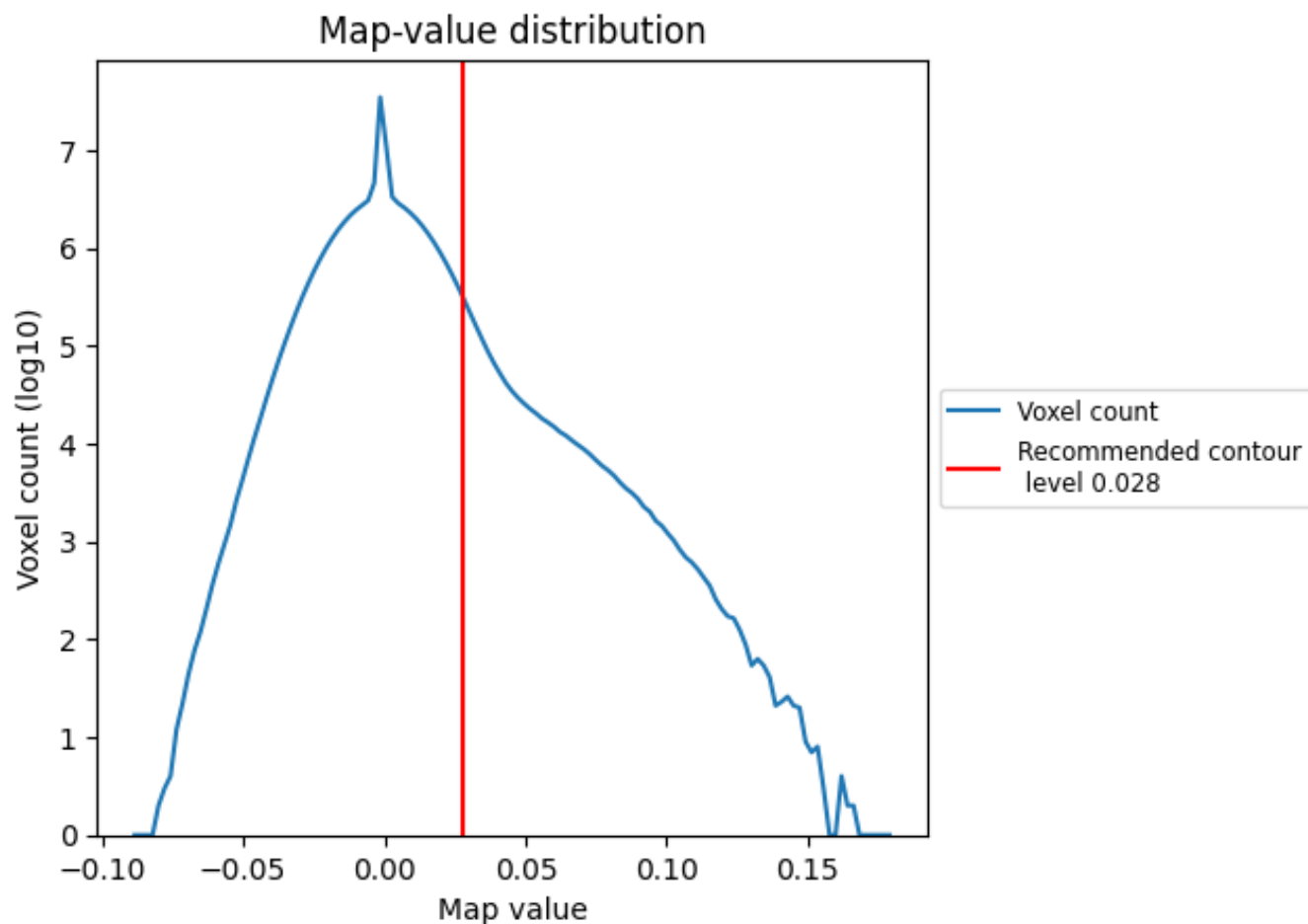
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

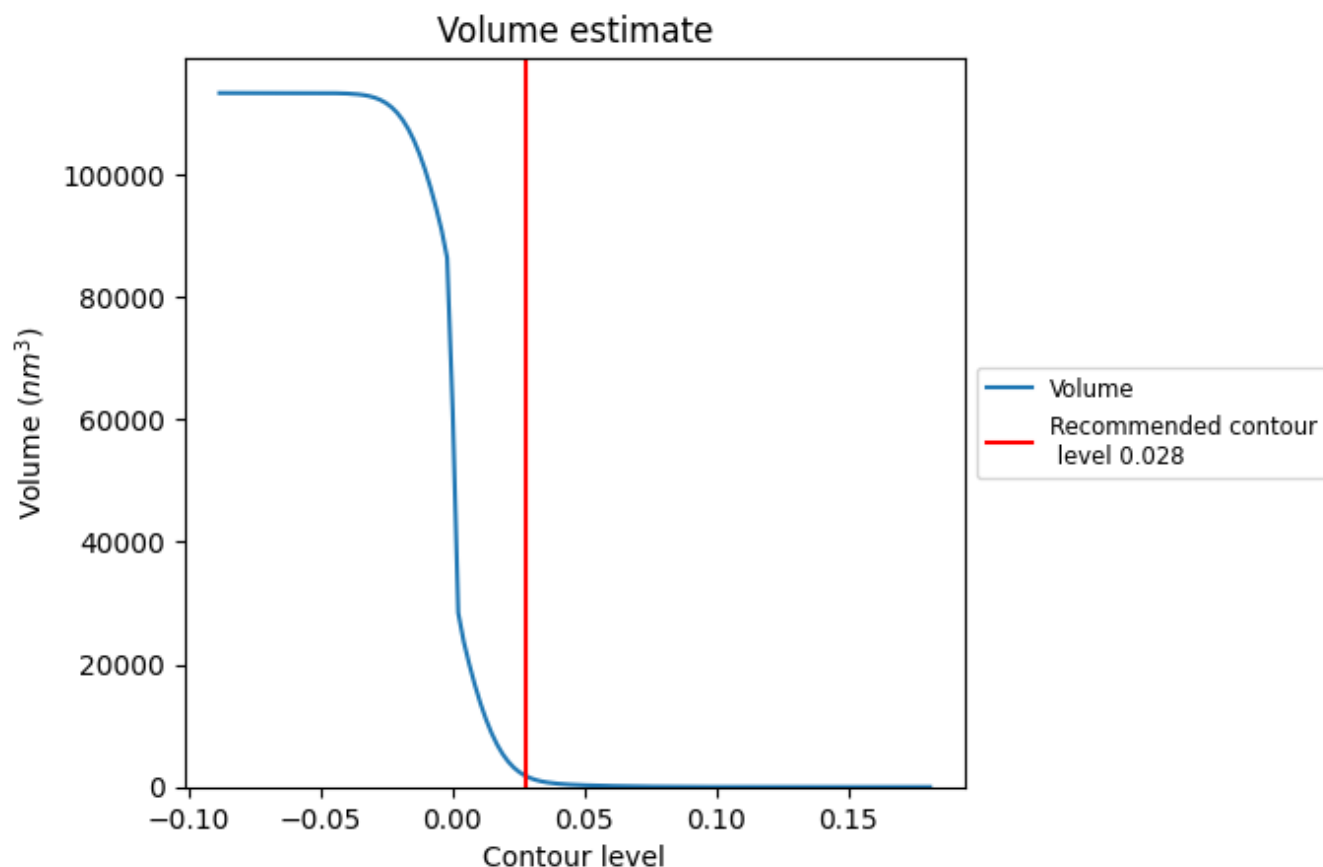
This section contains the results of statistical analysis of the map.

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.

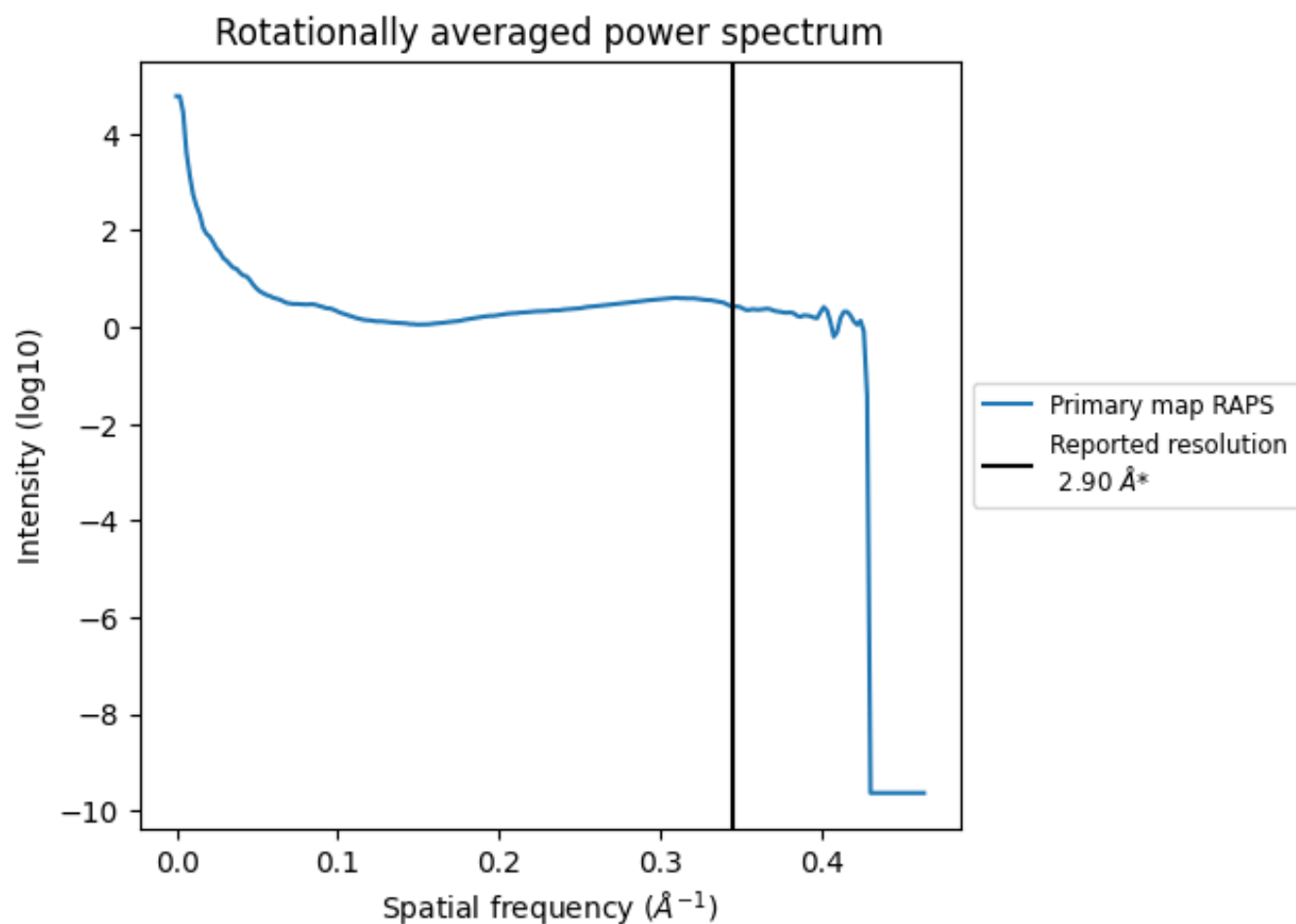
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1739 nm^3 ; this corresponds to an approximate mass of 1571 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 0.345 Å⁻¹

8 Fourier-Shell correlation

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

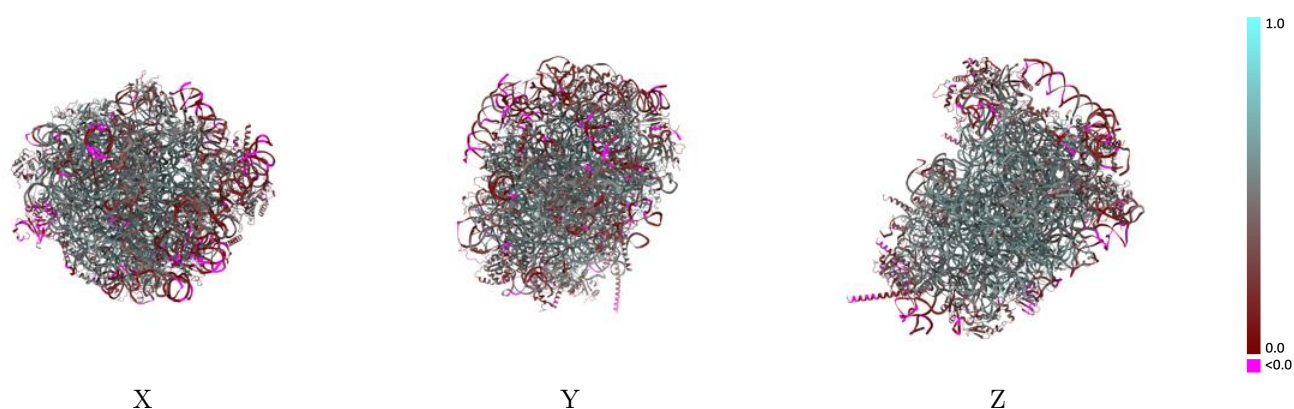
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-14192 and PDB model 7QWR. Per-residue inclusion information can be found in section 3 on page 15.

9.1 Map-model overlay [i](#)

This section was not generated.

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

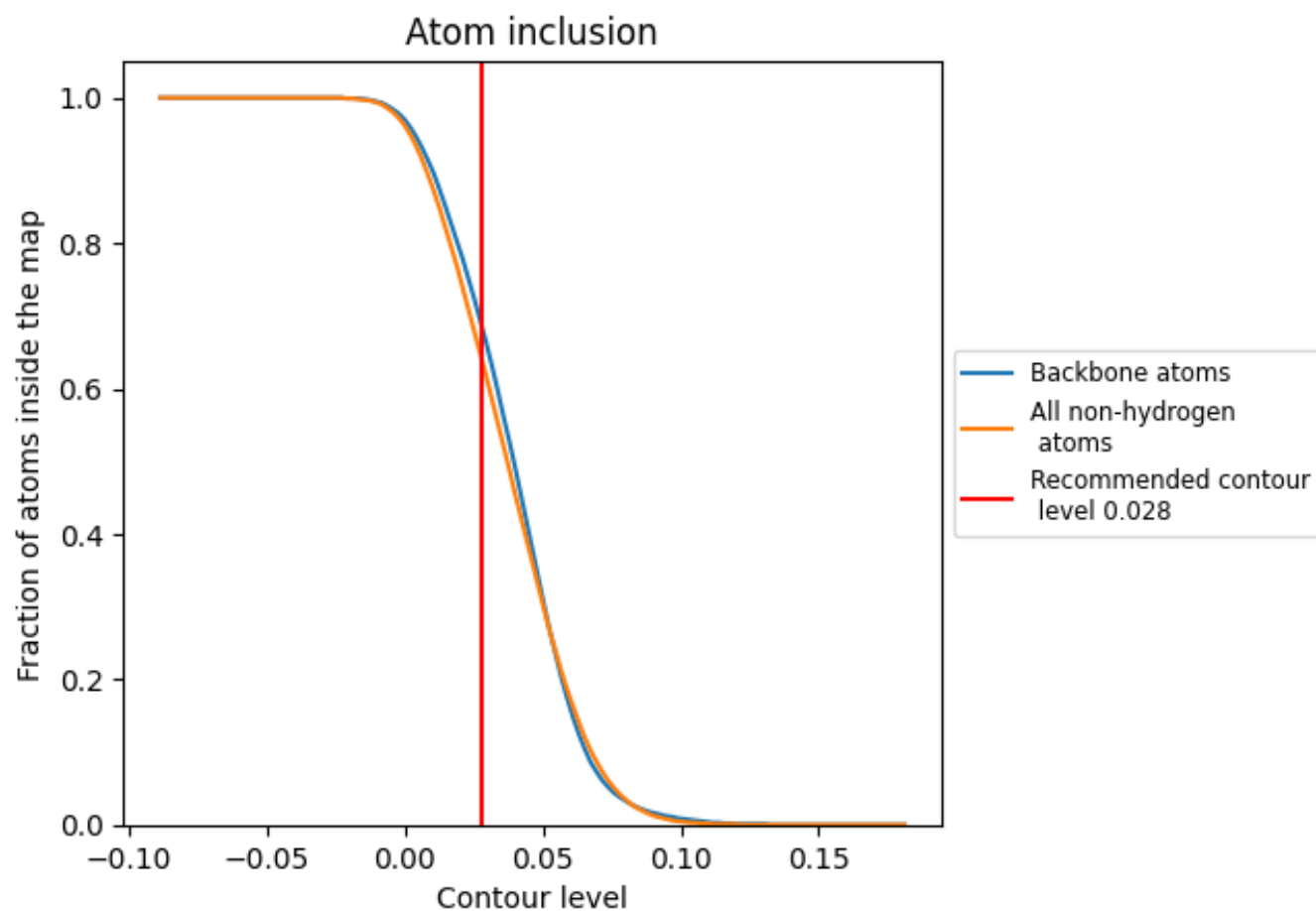


The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 68% of all backbone atoms, 64% 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 (0.028) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6390	 0.4540
5	 0.6640	 0.4480
7	 0.7060	 0.4490
8	 0.7110	 0.4850
A	 0.7390	 0.5580
B	 0.7020	 0.5300
C	 0.6930	 0.5190
D	 0.4420	 0.3270
E	 0.4700	 0.3630
F	 0.7030	 0.5180
G	 0.4070	 0.3530
H	 0.5030	 0.4000
I	 0.6300	 0.4890
J	 0.3130	 0.2550
L	 0.5550	 0.4390
M	 0.5520	 0.4110
N	 0.7460	 0.5440
O	 0.7040	 0.5290
P	 0.7500	 0.5610
Q	 0.7490	 0.5570
R	 0.5770	 0.4270
S	 0.6850	 0.5200
T	 0.6270	 0.4840
U	 0.3710	 0.4050
V	 0.6820	 0.5320
W	 0.6210	 0.4980
X	 0.6330	 0.5130
Y	 0.6550	 0.4990
Z	 0.4400	 0.3300
a	 0.7450	 0.5420
b	 0.5260	 0.4290
c	 0.4740	 0.3630
d	 0.6650	 0.5340
e	 0.7480	 0.5690
f	 0.7790	 0.5750



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Chain	Atom inclusion	Q-score
g	 0.5710	 0.4410
h	 0.5890	 0.4830
i	 0.5110	 0.4210
j	 0.7830	 0.5680
k	 0.3140	 0.2810
l	 0.6640	 0.5190
m	 0.5910	 0.4550
n	 0.4380	 0.3940
o	 0.6190	 0.4930
p	 0.6410	 0.4920
r	 0.6840	 0.4990
s	 0.0250	 0.2410
t	 0.0060	 0.0620
u	 0.1060	 0.1580