



wwPDB EM Validation Summary Report ⓘ

Mar 23, 2026 – 08:27 PM UTC

PDB ID : 8ESR / pdb_00008esr
EMDB ID : EMD-24422
Title : Ytm1 associated nascent 60S ribosome (-fkbp39) State 2
Authors : Zhou, X.; Bilokapic, S.; Deshmukh, A.A.; Halic, M.
Deposited on : 2022-10-14
Resolution : 3.20 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

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

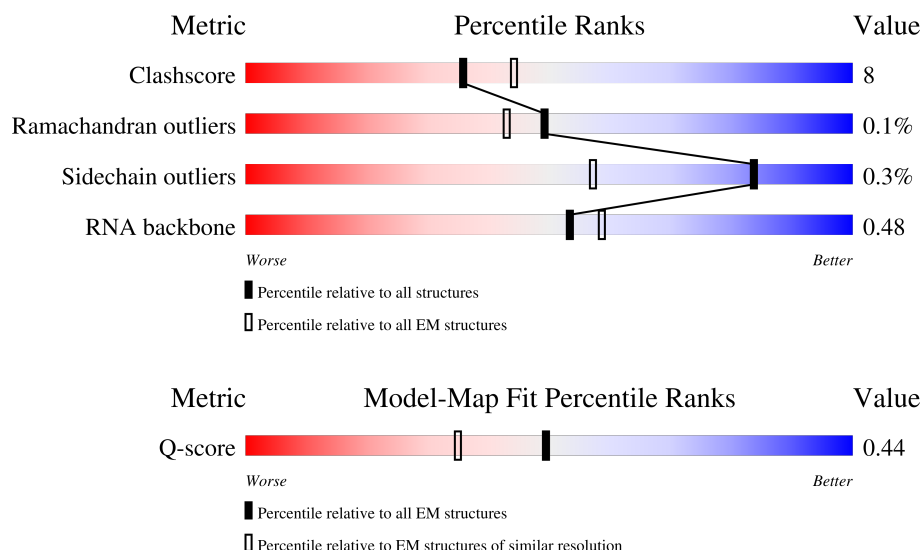
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.20 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)	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	15020 (2.70 - 3.70)

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	3497	
2	2	165	
3	6	300	

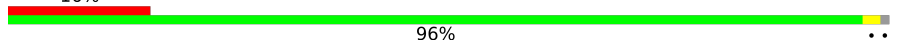
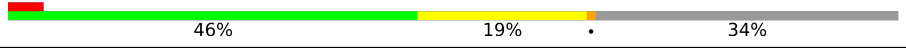
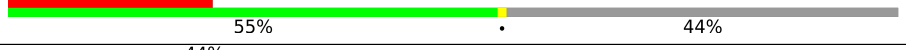
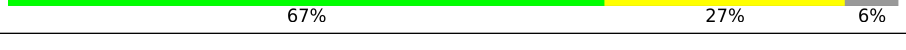
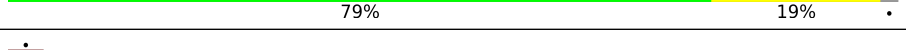
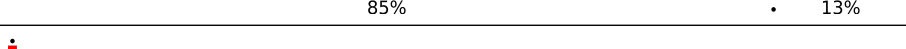
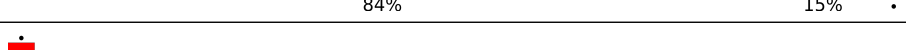
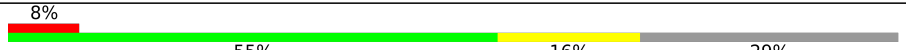
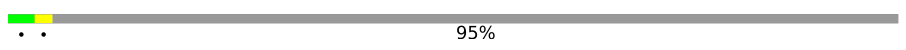
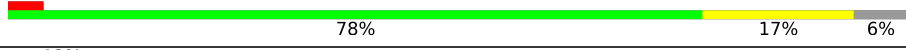
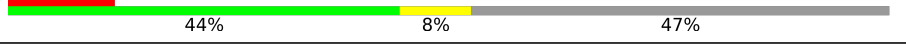
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Mol	Chain	Length	Quality of chain
4	7	707	
5	8	51	
6	A	295	
7	B	388	
8	C	363	
9	D	578	
10	E	195	
11	F	250	
12	G	259	
13	H	190	
14	I	747	
15	J	333	
16	K	373	
17	L	208	
18	M	134	
19	N	201	
20	O	197	
21	P	187	
22	Q	187	
23	R	193	
24	S	176	
25	U	117	
26	V	139	
27	W	241	
28	X	141	

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Mol	Chain	Length	Quality of chain
29	Y	126	
30	Z	136	
31	a	148	
32	b	642	
33	c	117	
34	d	113	
35	e	127	
36	f	108	
37	g	112	
38	h	122	
39	i	99	
40	j	91	
41	k	74	
42	l	180	
43	m	740	
44	n	607	
45	o	276	
46	p	440	
47	q	608	
48	r	260	
49	s	470	
50	t	249	
51	u	192	
52	v	209	
53	w	802	

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Mol	Chain	Length	Quality of chain
54	y	244	11% 90% 9%
55	z	117	16% 16% 13% 70%
56	T	160	5% 9% 89%

2 Entry composition

There are 57 unique types of molecules in this entry. The entry contains 116762 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called RNA (2142-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	2143	Total	C	N	O	P	0	0
			45883	20493	8324	14923	2143		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	1741	C	U	conflict	GB 157310483

- Molecule 2 is a RNA chain called RNA (150-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	150	Total	C	N	O	P	0	0
			3189	1427	564	1048	150		

- Molecule 3 is a RNA chain called RNA (79-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
3	6	79	Total	C	N	O	P	0	0
			1674	751	288	556	79		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
6	137	C	U	conflict	GB 157310483
6	146	G	U	conflict	GB 157310483

- Molecule 4 is a protein called Noc2.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	7	110	Total	C	N	O	0	0
			548	328	110	110		

- Molecule 5 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	8	22	Total	C	N	O	0	0
			187	119	40	28		

- Molecule 6 is a protein called Ribosome biogenesis protein brx1.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	A	204	Total	C	N	O	S	0	0
			1652	1057	295	293	7		

- Molecule 7 is a protein called 60S ribosomal protein L3-A.

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

- Molecule 8 is a protein called 60S ribosomal protein L4-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	C	359	Total	C	N	O	S	0	0
			2795	1765	536	491	3		

- Molecule 9 is a protein called ATP-dependent RNA helicase has1.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	D	418	Total	C	N	O	S	0	0
			3320	2140	570	599	11		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
10	E	156	Total	C	N	O	S	0	0
			1213	777	226	207	3		

- Molecule 11 is a protein called 60S ribosomal protein L7-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	F	214	Total	C	N	O	S	0	0
			1745	1124	320	298	3		

- Molecule 12 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	G	206	Total	C	N	O	S	0	0
			1607	1030	294	280	3		

- Molecule 13 is a protein called 60S ribosomal protein L9-A.

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

- Molecule 14 is a protein called Nucleolar complex-associated protein 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	I	409	Total	C	N	O		0	0
			2032	1214	409	409			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
I	607	LYS	LEU	conflict	UNP O94288

- Molecule 15 is a protein called Probable rRNA-processing protein ebp2.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	J	115	Total	C	N	O		0	0
			574	344	115	115			

- Molecule 16 is a protein called Putative ribosome biogenesis protein C8F11.04.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	K	250	Total	C	N	O	S	0	0
			1964	1256	336	366	6		

- Molecule 17 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	L	116	Total	C	N	O	S	0	0
			942	592	198	151	1		

- Molecule 18 is a protein called 60S ribosomal protein L14.

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

- Molecule 19 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	N	165	Total	C	N	O	S	0	0
			1392	872	289	228	3		

- Molecule 20 is a protein called 60S ribosomal protein L16-B.

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

- Molecule 21 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	P	149	Total	C	N	O	S	0	0
			1168	742	216	207	3		

- Molecule 22 is a protein called 60S ribosomal protein L18-A.

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

- Molecule 23 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	R	112	Total	C	N	O	S	0	0
			729	445	148	133	3		

- Molecule 24 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	S	167	Total	C	N	O	S	0	0
			1401	905	262	229	5		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
25	U	98	Total	C	N	O	0	0
			484	288	98	98		

- Molecule 26 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	V	132	Total	C	N	O	S	0	0
			991	625	182	176	8		

- Molecule 27 is a protein called Ribosome assembly factor mrt4.

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

- Molecule 28 is a protein called 60S ribosomal protein L25-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	X	132	Total	C	N	O	S	0	0
			1044	664	194	185	1		

- Molecule 29 is a protein called 60S ribosomal protein L26.

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

- Molecule 30 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	Z	134	Total	C	N	O	0	0
			662	393	134	135		

- Molecule 31 is a protein called 60S ribosomal protein L28-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	a	97	Total	C	N	O	0	0
			762	483	145	134		

- Molecule 32 is a protein called Probable nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	b	359	Total	C	N	O	0	0
			1780	1062	359	359		

- Molecule 33 is a protein called 60S ribosomal protein L30-2.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	c	94	Total	C	N	O	0	0
			462	274	94	94		

- Molecule 34 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	d	96	Total	C	N	O	S	0	0
			801	507	158	133	3		

- Molecule 35 is a protein called 60S ribosomal protein L32-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	e	119	Total	C	N	O	S	0	0
			953	597	193	158	5		

- Molecule 36 is a protein called 60S ribosomal protein L33-B.

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

- Molecule 37 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
37	g	97	Total	C	N	O	0	0
			478	284	97	97		

- Molecule 38 is a protein called 60S ribosomal protein L35.

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

- Molecule 39 is a protein called 60S ribosomal protein L36-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	i	85	Total	C	N	O	S	0	0
			696	431	148	116	1		

- Molecule 40 is a protein called 60S ribosomal protein L37-B.

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

- Molecule 41 is a protein called 60S ribosomal protein L38-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	k	70	Total	C	N	O	S	0	0
			564	357	104	102	1		

- Molecule 42 is a protein called 60S ribosome subunit biogenesis protein nip7.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	l	174	Total	C	N	O		0	0
			860	512	174	174			

- Molecule 43 is a protein called Ribosome biogenesis protein erb1.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	m	572	Total	C	N	O	S	0	0
			4526	2883	790	842	11		

- Molecule 44 is a protein called Pescadillo homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	n	432	Total	C	N	O	S	0	0
			3517	2262	606	637	12		

- Molecule 45 is a protein called Uncharacterized RNA-binding protein C1827.05c.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	o	137	Total	C	N	O	S	0	0
			1138	732	213	187	6		

- Molecule 46 is a protein called Ribosome biogenesis protein ytm1.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	p	275	Total	C	N	O	0	0
			1357	807	275	275		

- Molecule 47 is a protein called 25S rRNA (cytosine-C(5))-methyltransferase nop2.

Mol	Chain	Residues	Atoms				AltConf	Trace
47	q	260	Total	C	N	O	0	0
			1282	762	260	260		

- Molecule 48 is a protein called Ribosome biogenesis protein nsa2.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	r	165	Total	C	N	O	S	0	0
			1081	653	223	204	1		

- Molecule 49 is a protein called GTPase grn1.

Mol	Chain	Residues	Atoms				AltConf	Trace
49	s	23	Total	C	N	O	0	0
			193	117	44	32		

- Molecule 50 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	t	235	Total	C	N	O	S	0	0
			1948	1242	367	334	5		

- Molecule 51 is a protein called Ribosome biogenesis protein rlp24.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	u	101	Total	C	N	O	S	0	0
			714	448	143	116	7		

- Molecule 52 is a protein called Nucleolar protein 16.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	v	161	Total	C	N	O	S	0	0
			1299	818	243	235	3		

- Molecule 53 is a protein called AdoMet-dependent rRNA methyltransferase spb1.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	w	180	Total	C	N	O	S	0	0
			1462	910	276	270	6		

- Molecule 54 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	y	223	Total	C	N	O		0	0
			1097	651	223	223			

- Molecule 55 is a protein called UPF0642 protein C32H8.05.

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

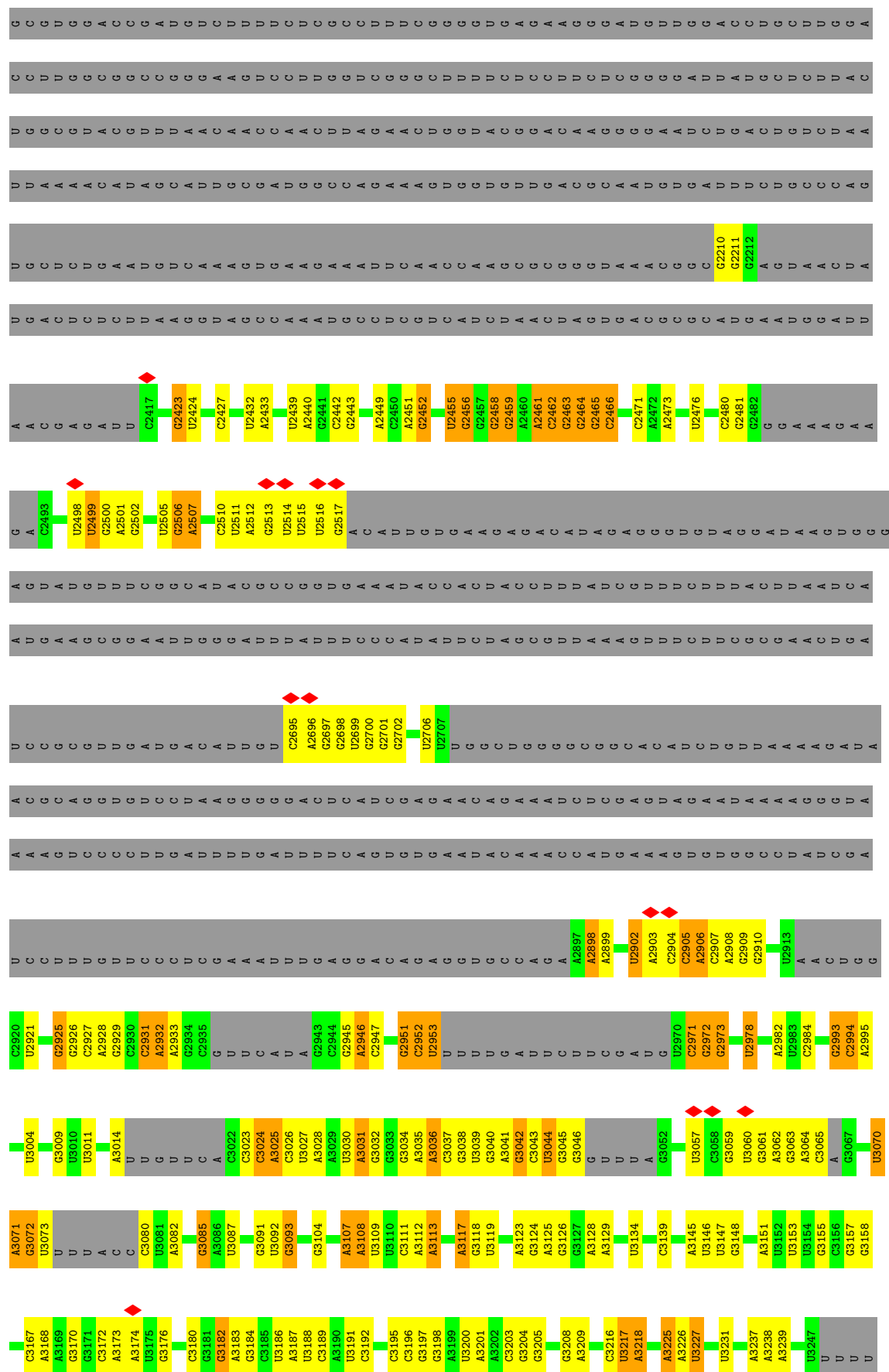
- Molecule 56 is a protein called 60S ribosomal protein L21-A.

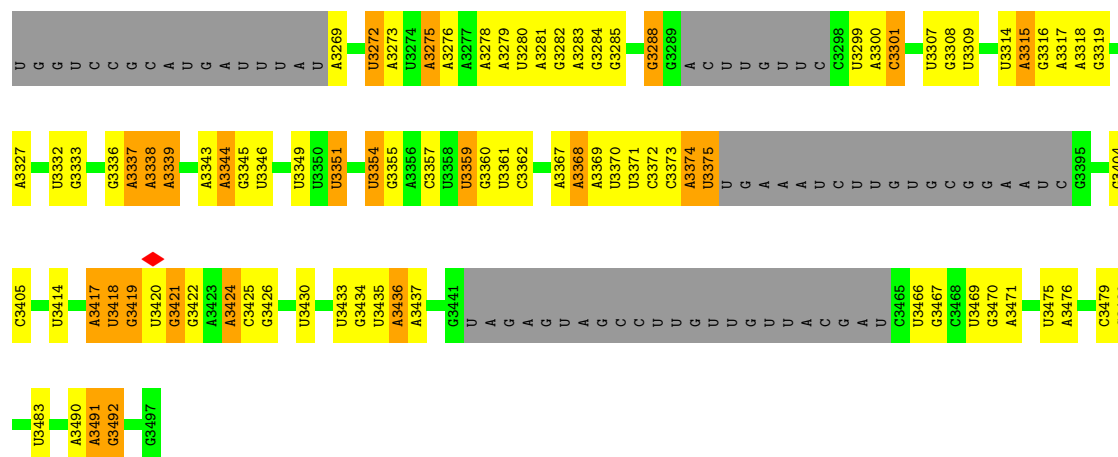
Mol	Chain	Residues	Atoms					AltConf	Trace
56	T	18	Total	C	N	O		0	0
			138	87	24	27			

- Molecule 57 is ZINC ION (CCD ID: ZN) (formula: Zn).

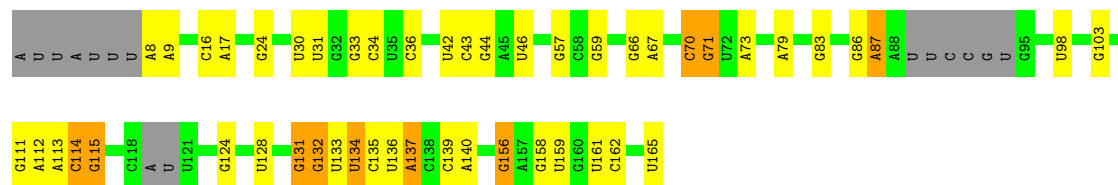
Mol	Chain	Residues	Atoms		AltConf
57	j	1	Total	Zn	0
			1	1	



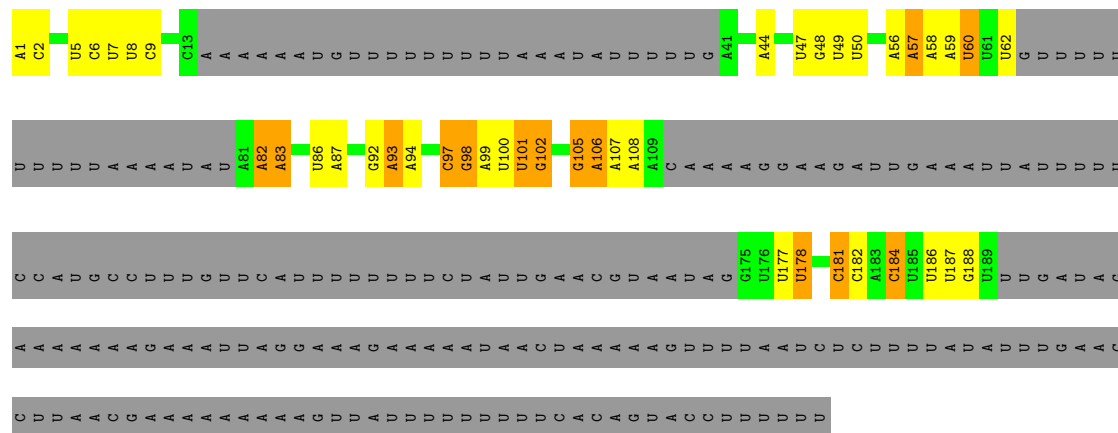




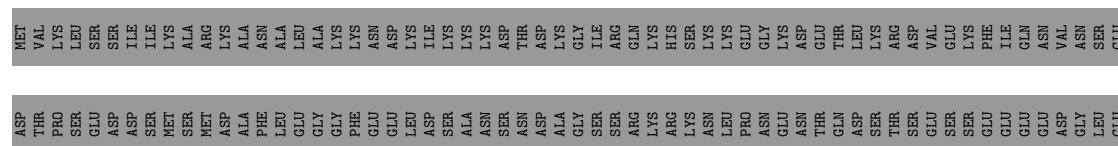
• Molecule 2: RNA (150-MER)



• Molecule 3: RNA (79-MER)



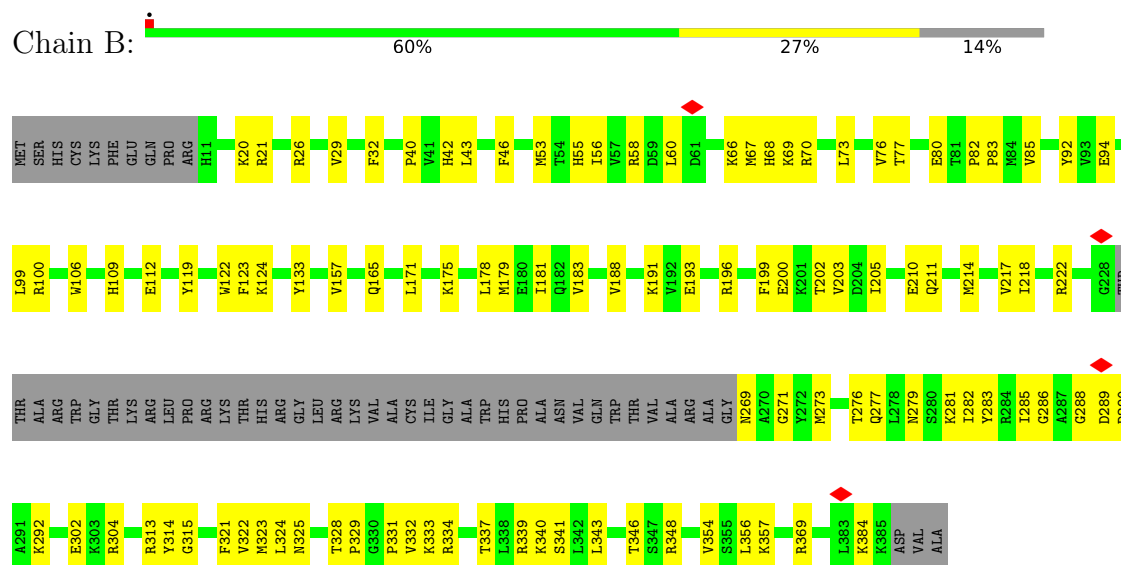
• Molecule 4: Noc2



ARG TYR VAL ASN ARG GLN GLU SER LYS LEU GLU ARG GLN VAL ASN ASP PHE ALA

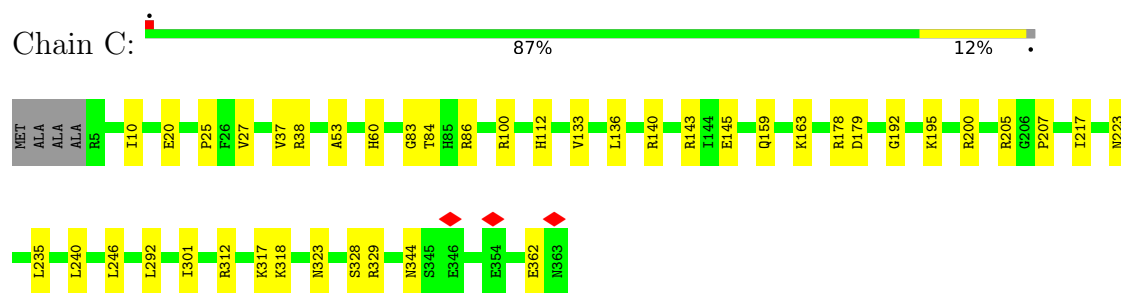
• Molecule 7: 60S ribosomal protein L3-A

Chain B:



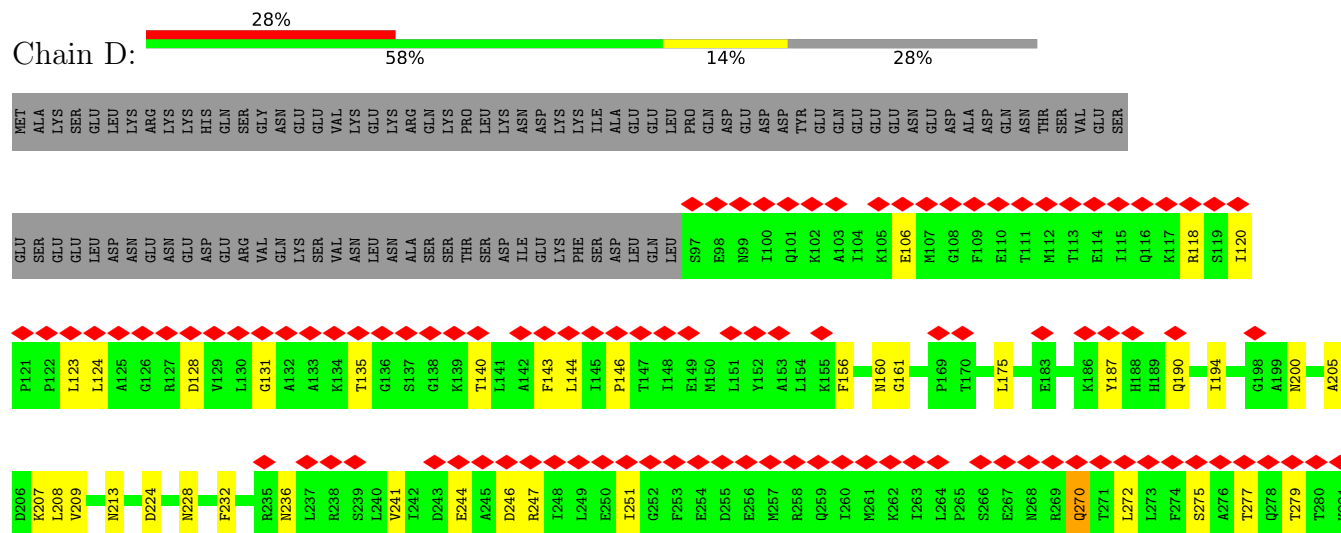
• Molecule 8: 60S ribosomal protein L4-B

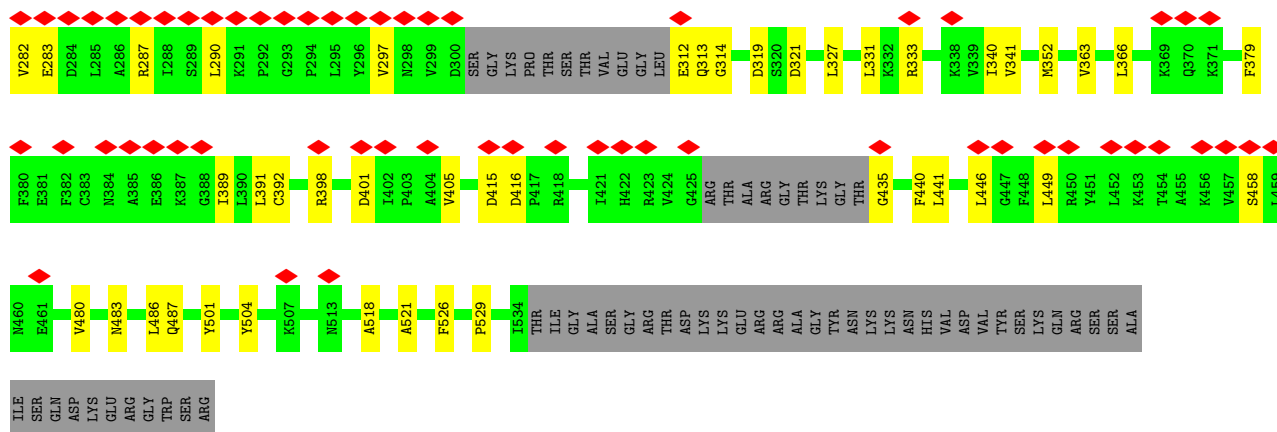
Chain C:



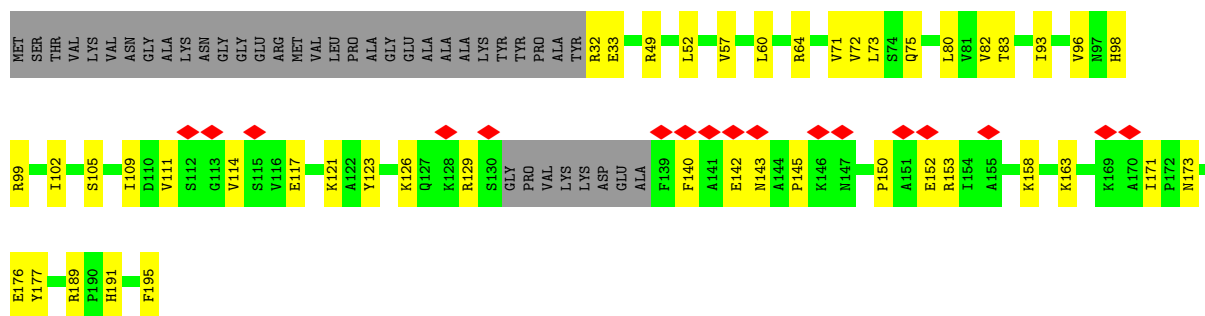
• Molecule 9: ATP-dependent RNA helicase has1

Chain D:

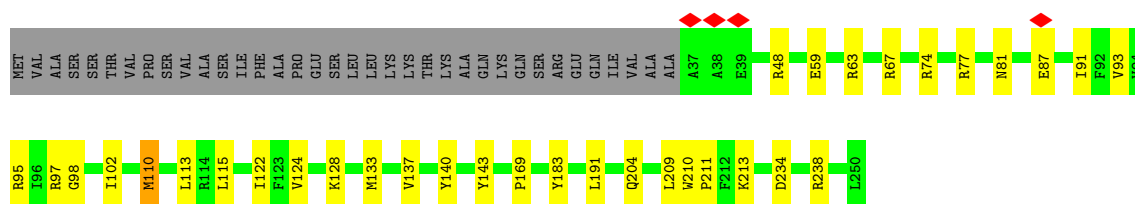




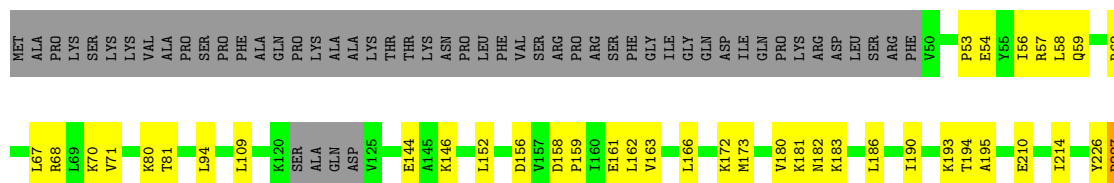
• Molecule 10: 60S ribosomal protein L6

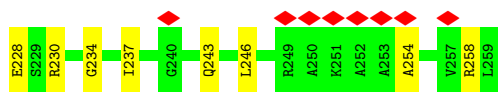


• Molecule 11: 60S ribosomal protein L7-B

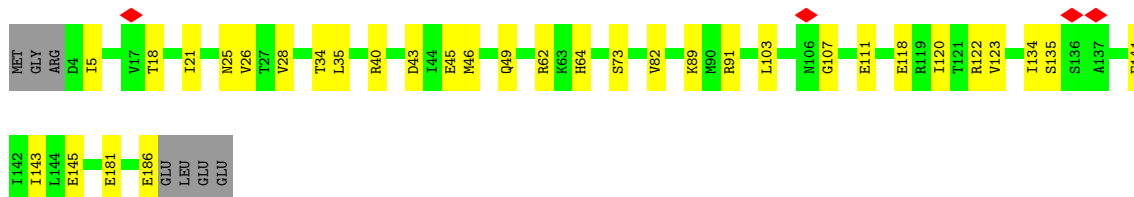
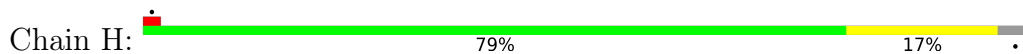


• Molecule 12: 60S ribosomal protein L8

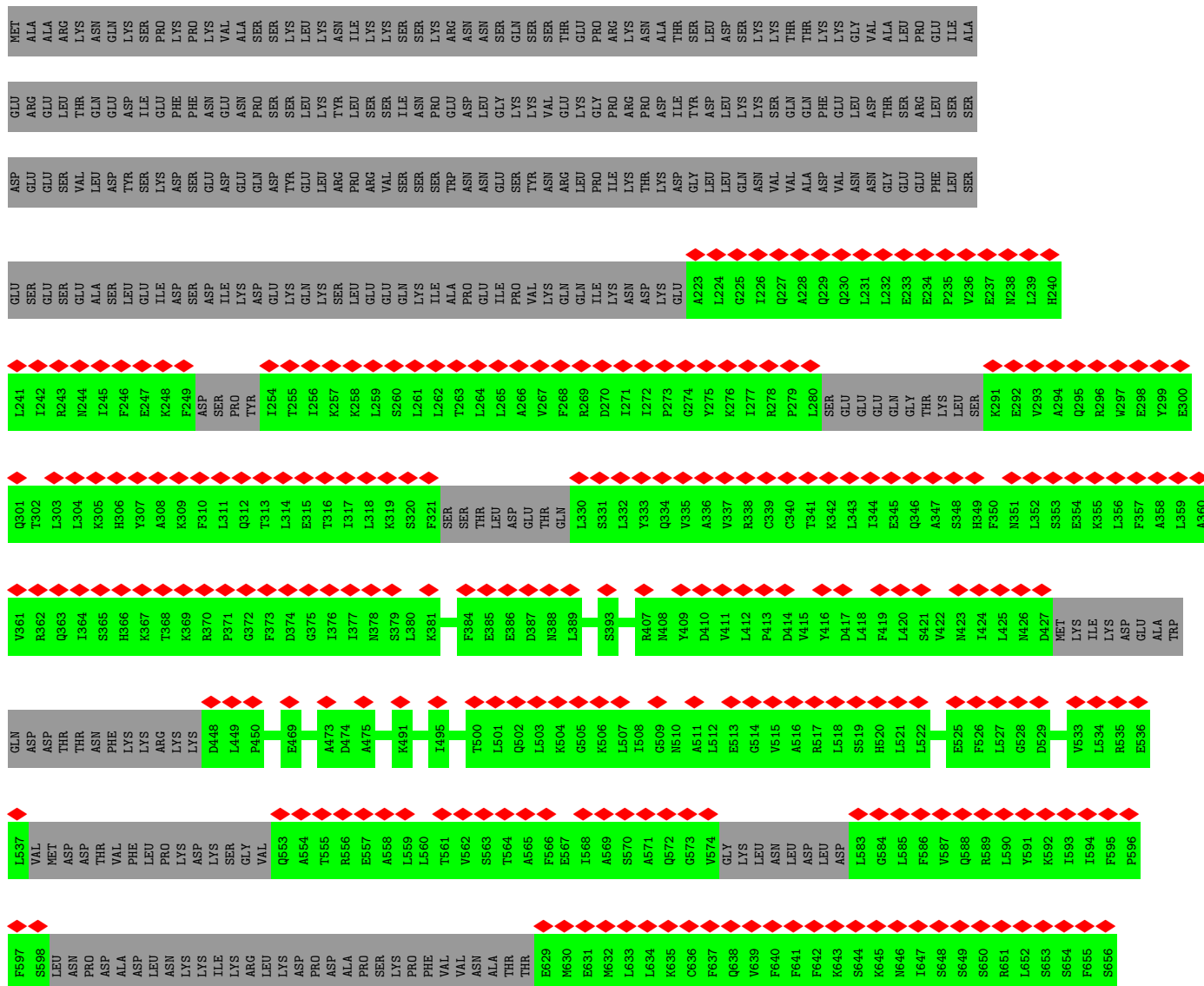
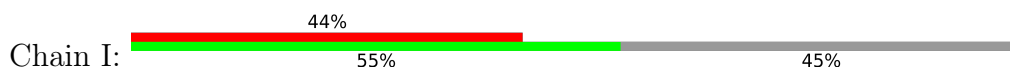


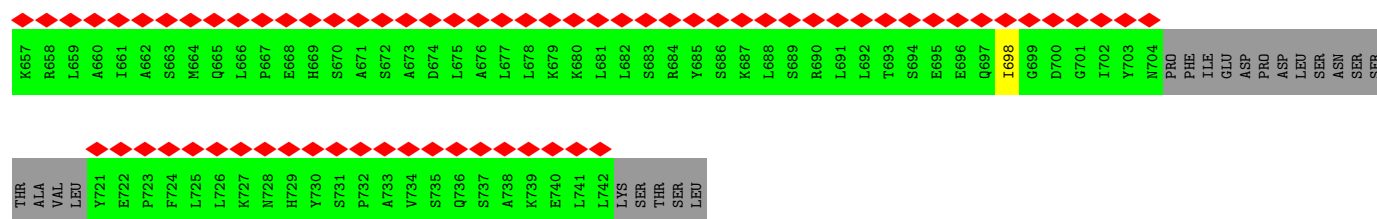


• Molecule 13: 60S ribosomal protein L9-A

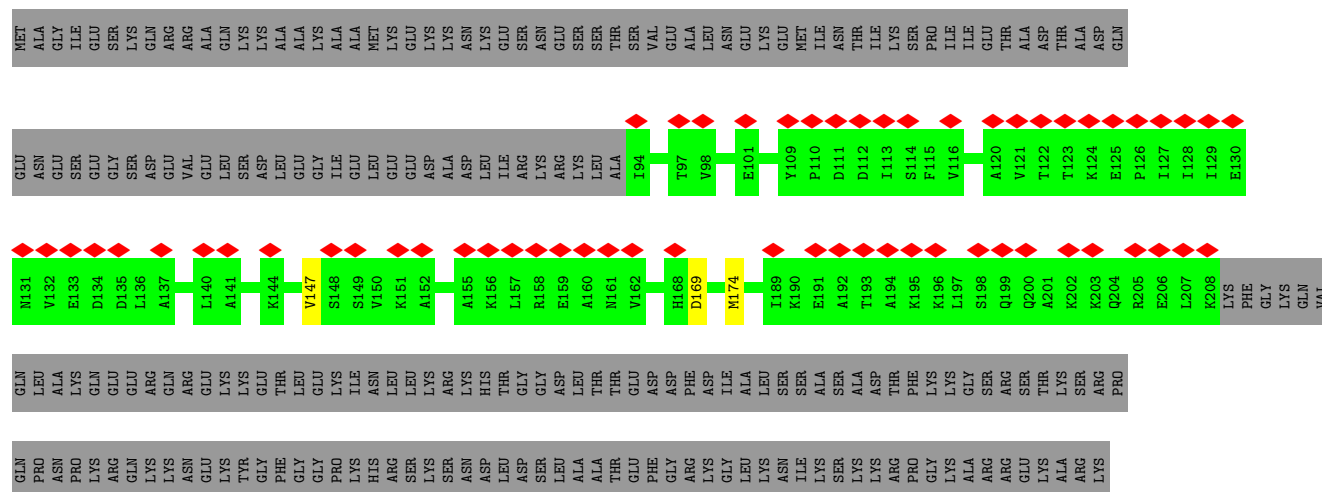


• Molecule 14: Nucleolar complex-associated protein 3

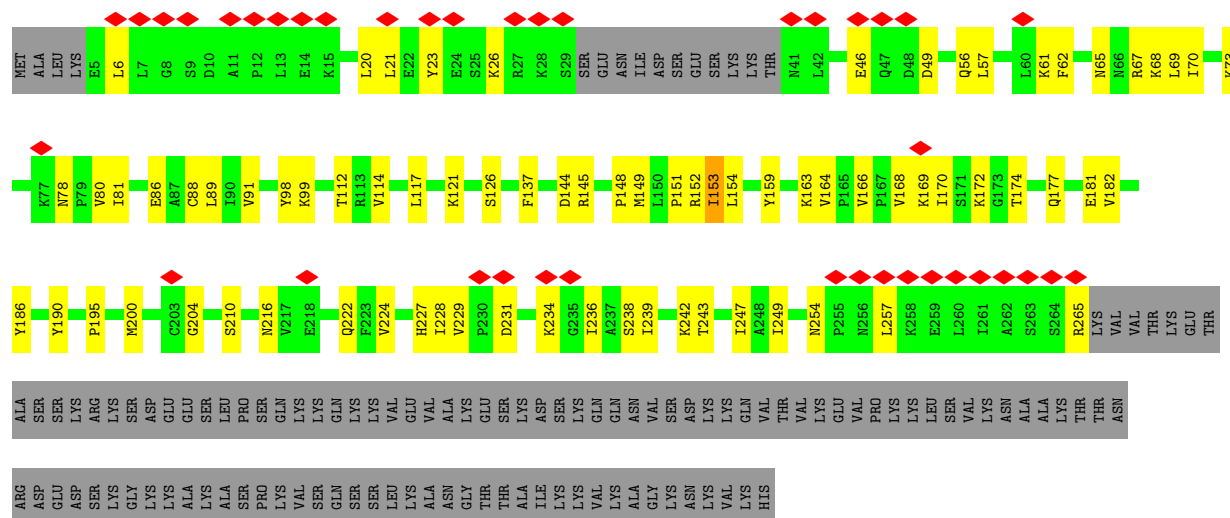




• Molecule 15: Probable rRNA-processing protein ebp2

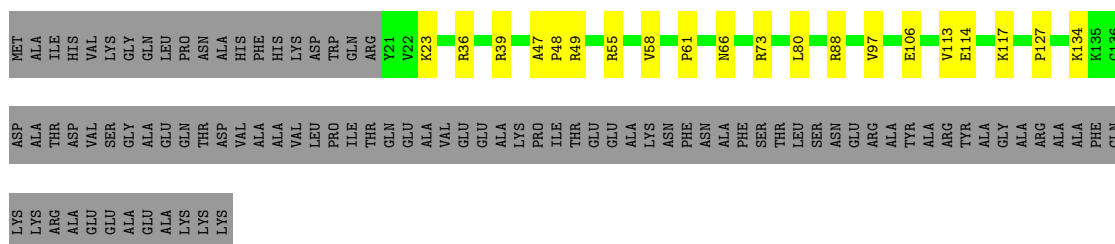


• Molecule 16: Putative ribosome biogenesis protein C8F11.04

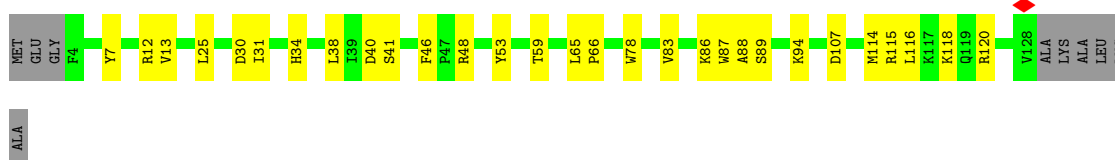


• Molecule 17: 60S ribosomal protein L13

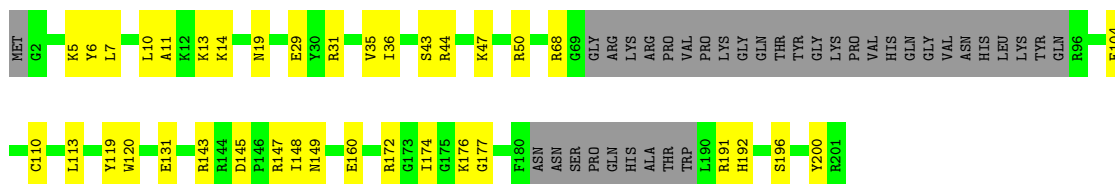




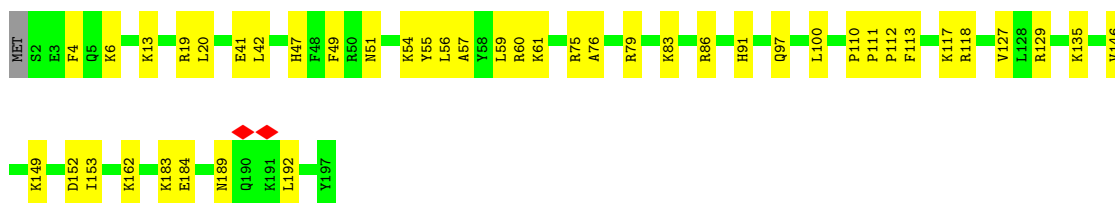
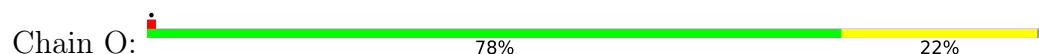
• Molecule 18: 60S ribosomal protein L14



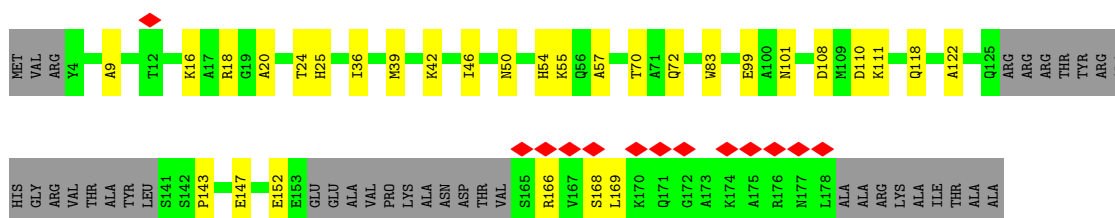
• Molecule 19: 60S ribosomal protein L15-A



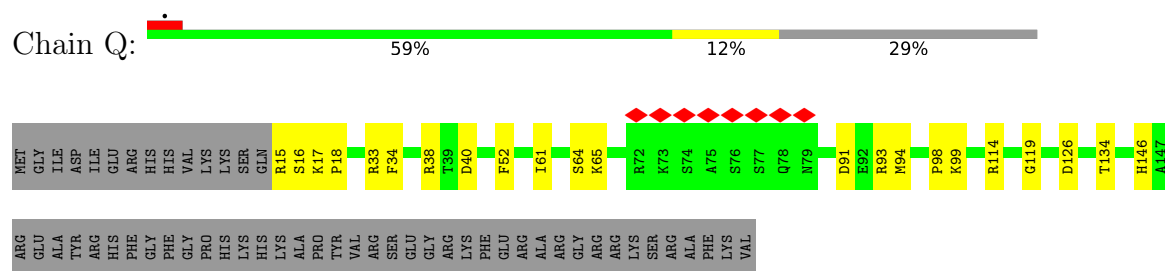
• Molecule 20: 60S ribosomal protein L16-B



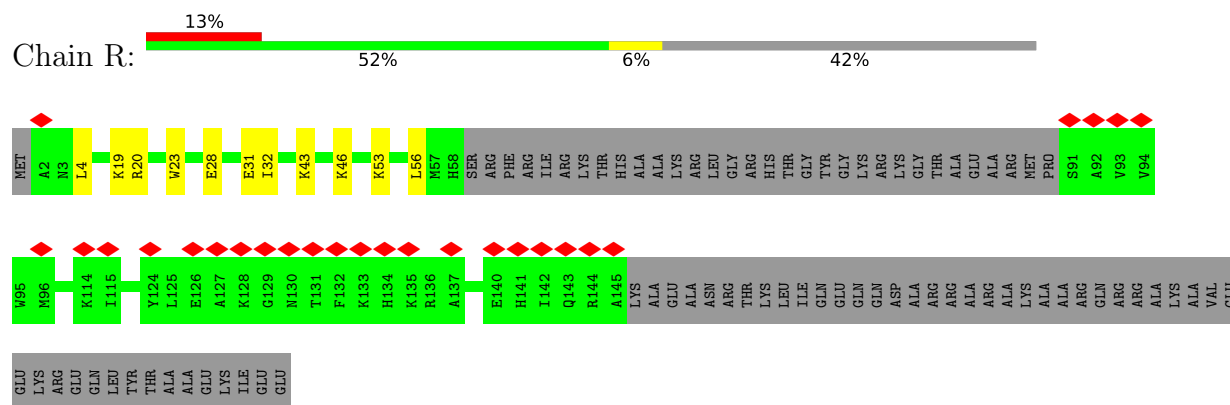
• Molecule 21: 60S ribosomal protein L17-A



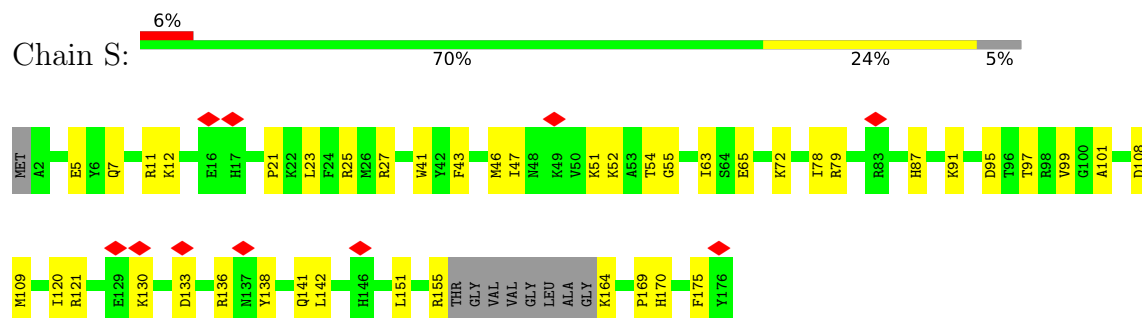
- Molecule 22: 60S ribosomal protein L18-A



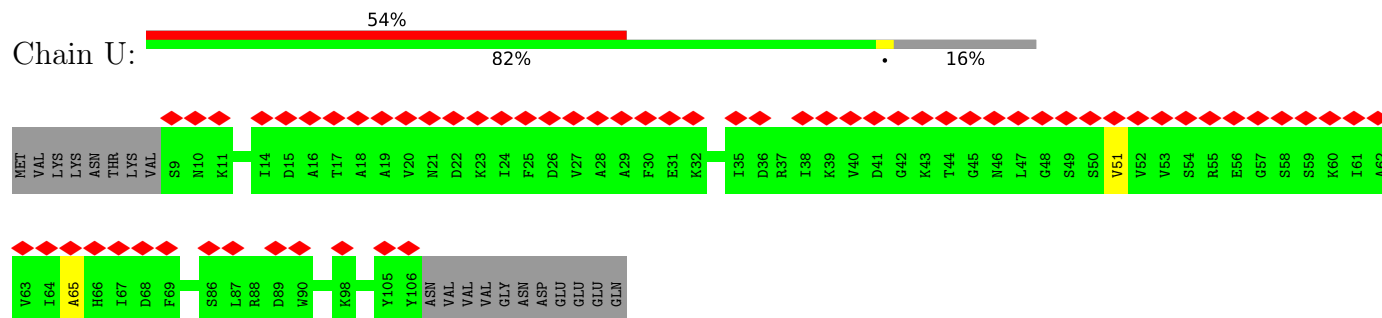
- Molecule 23: 60S ribosomal protein L19-A



- Molecule 24: 60S ribosomal protein L20-A

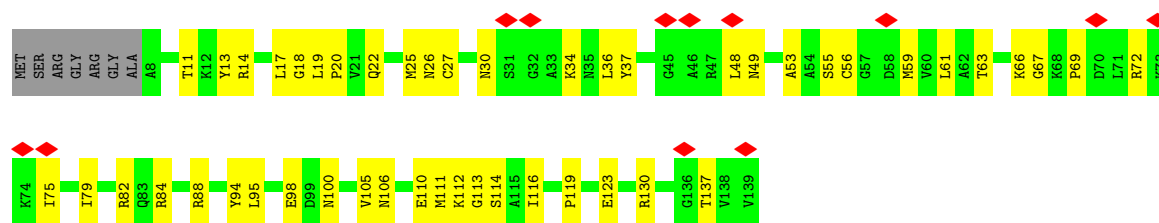


- Molecule 25: 60S ribosomal protein L22

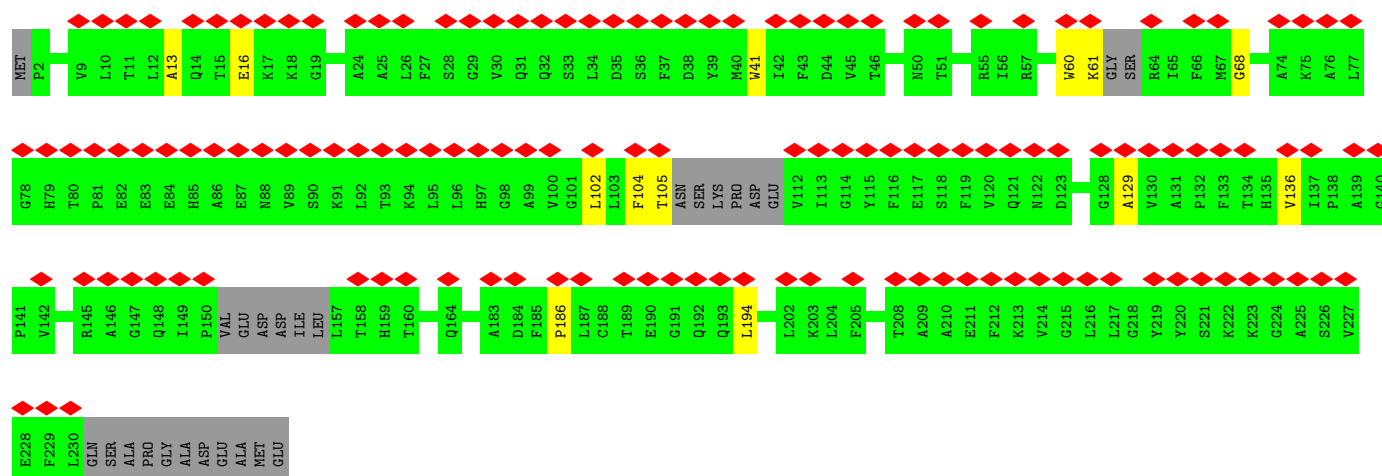
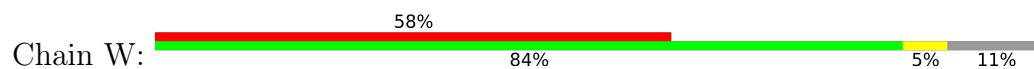


- Molecule 26: 60S ribosomal protein L23-A

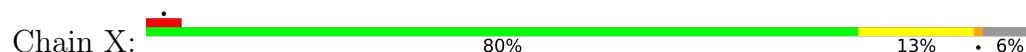




- Molecule 27: Ribosome assembly factor mrt4



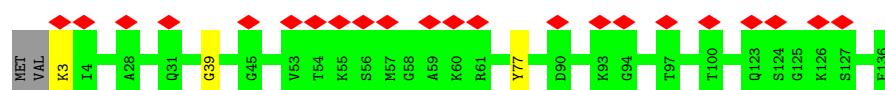
- Molecule 28: 60S ribosomal protein L25-A



- Molecule 29: 60S ribosomal protein L26



- Molecule 30: 60S ribosomal protein L27-A



- Molecule 31: 60S ribosomal protein L28-A

Frequency	Percentage
Daily	46%
Weekly	19%
Monthly	34%



Government	Percentage
Current government	23%
Opposition	55%
Current government	44%



Category	Percentage
Very bad	44%
Bad	79%
Good	20%
Very good	0%

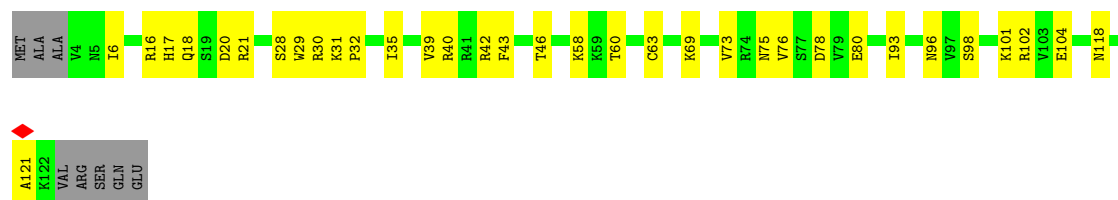


Chain d:  65% 19% 15%



- Molecule 35: 60S ribosomal protein L32-A

Chain e:  67% 27% 6%



- Molecule 36: 60S ribosomal protein L33-B

Chain f:  79% 19% 2%



- Molecule 37: 60S ribosomal protein L34-A

Chain g:  85% 13% 2%



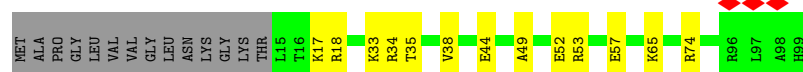
- Molecule 38: 60S ribosomal protein L35

Chain h:  84% 15% 1%



- Molecule 39: 60S ribosomal protein L36-B

Chain i:  73% 13% 14%



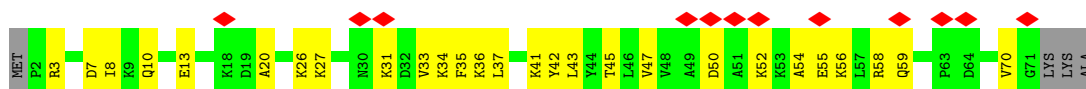
- Molecule 40: 60S ribosomal protein L37-B

Chain j: 

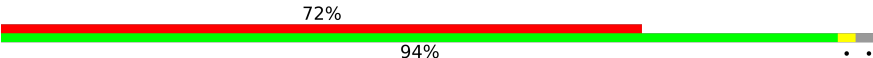


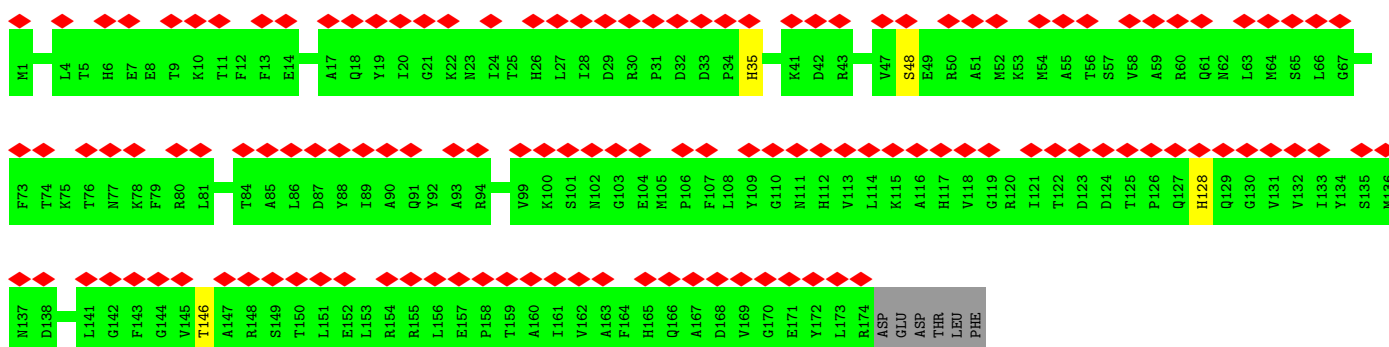
- Molecule 41: 60S ribosomal protein L38-1

Chain k: 



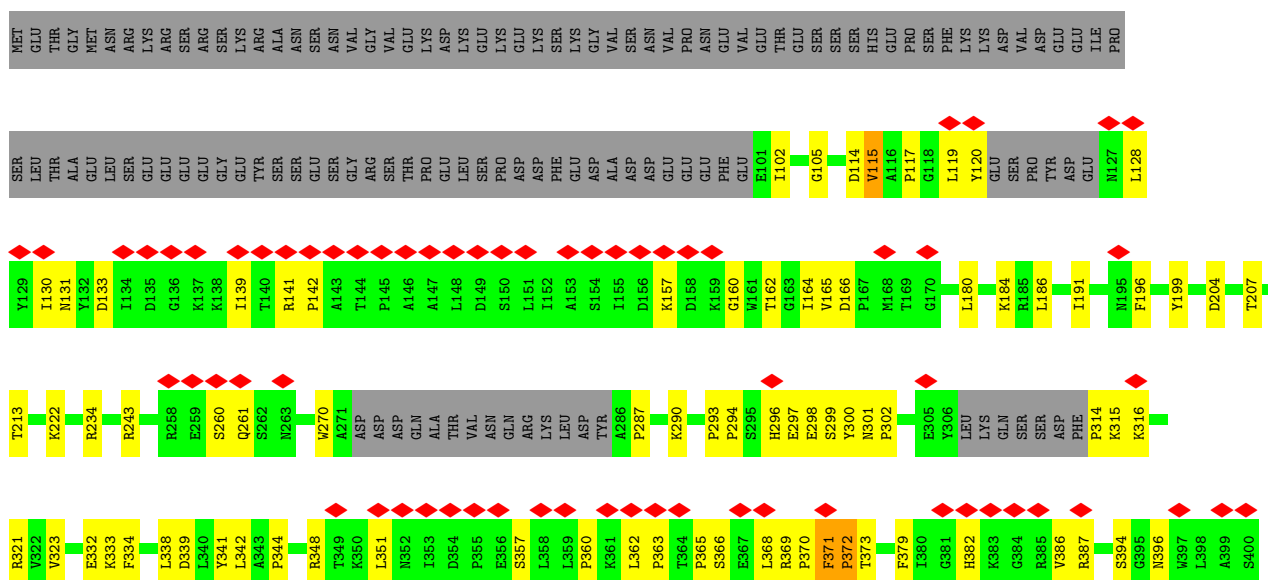
- Molecule 42: 60S ribosome subunit biogenesis protein nip7

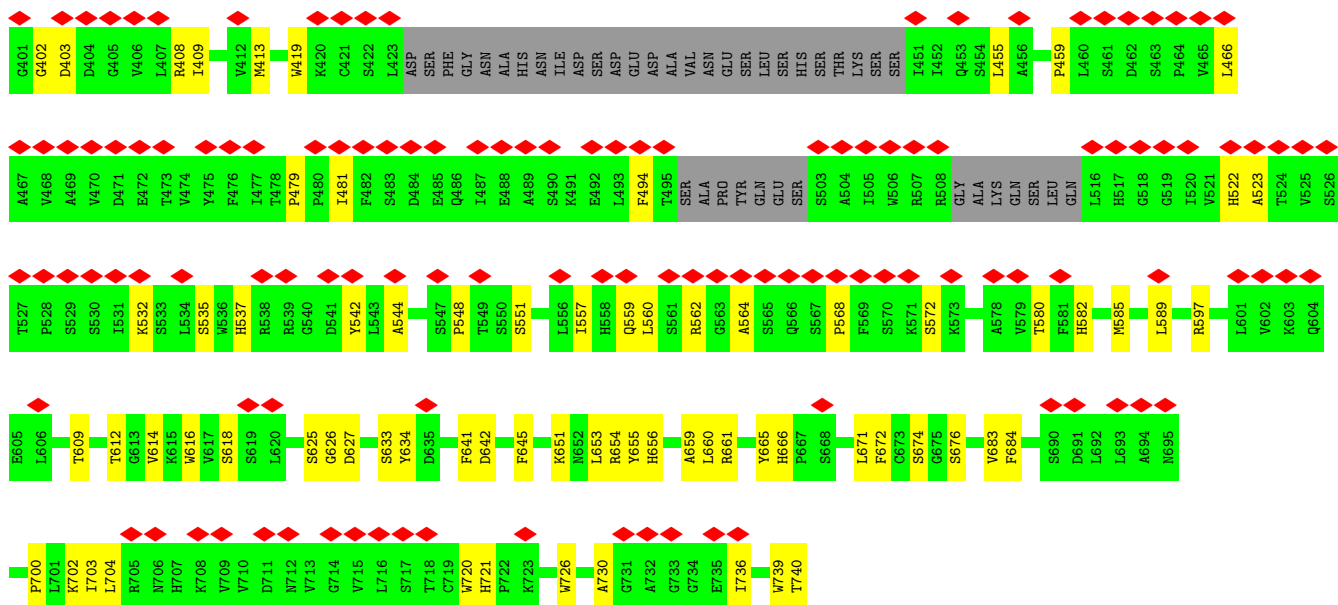
Chain l: 



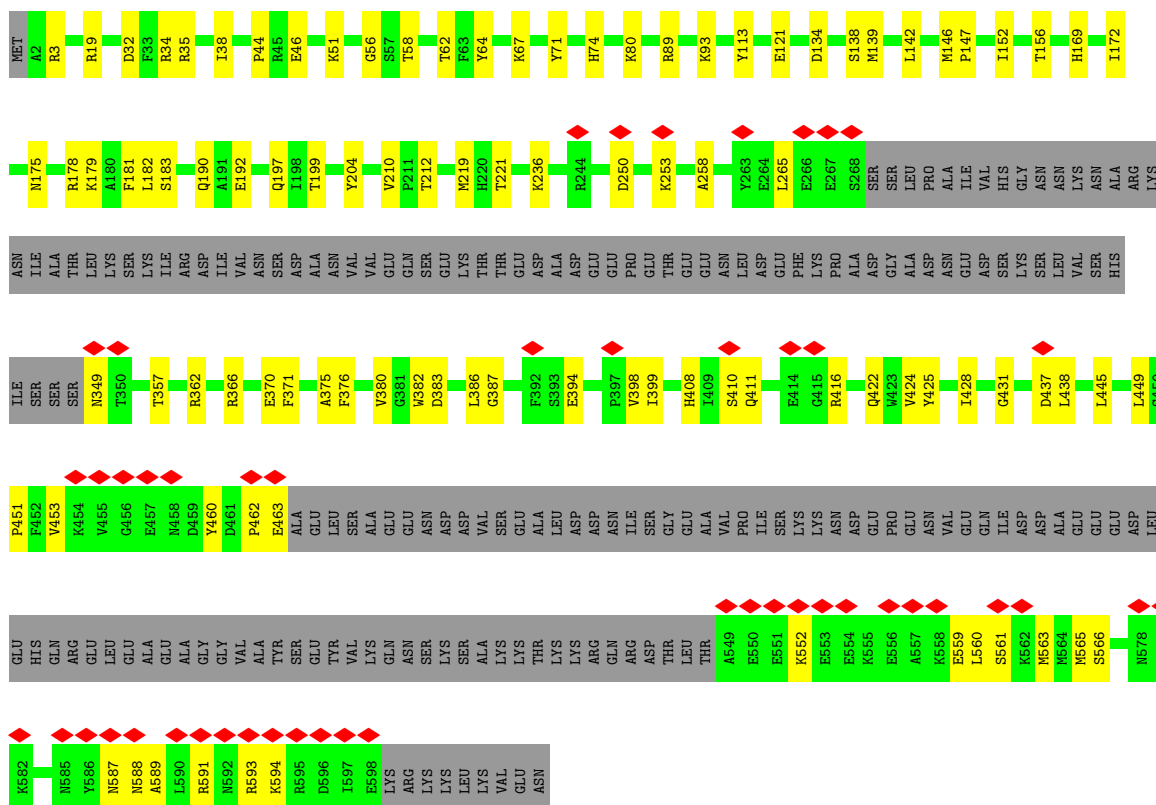
- Molecule 43: Ribosome biogenesis protein erbl

Chain m: 

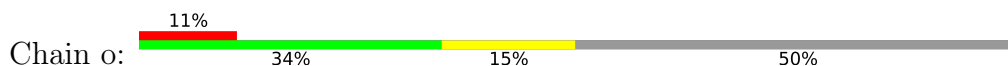


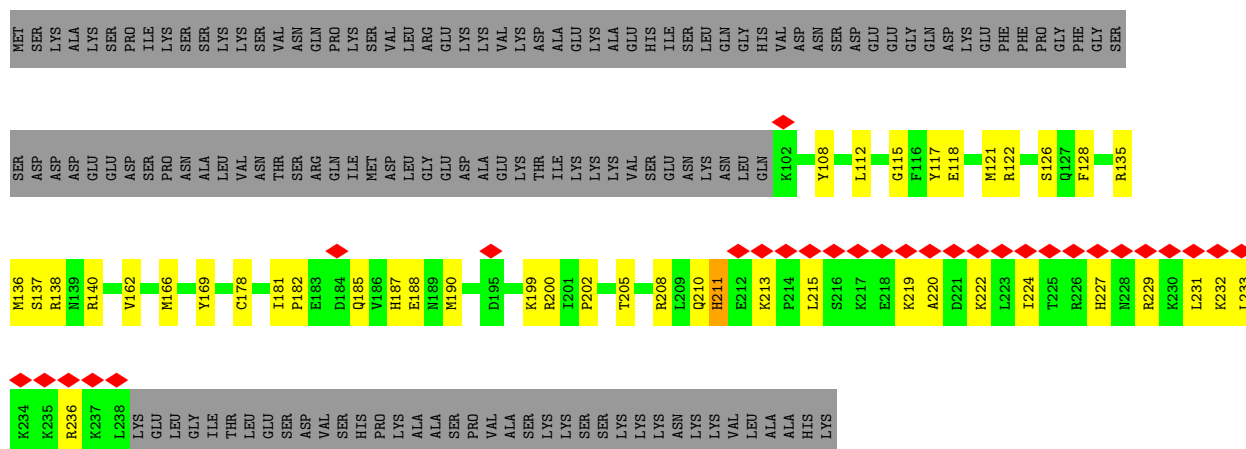


• Molecule 44: Pescadillo homolog

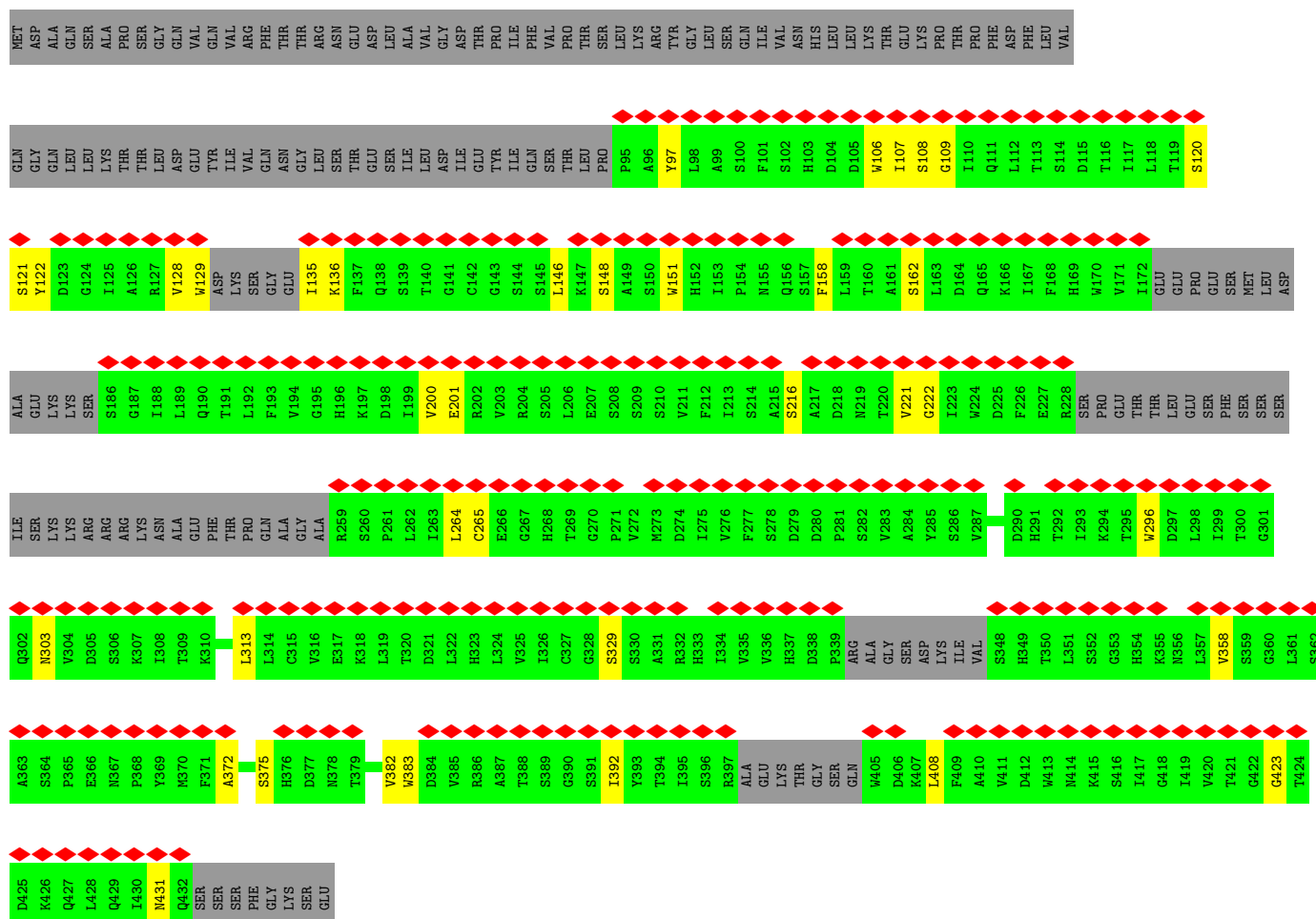


• Molecule 45: Uncharacterized RNA-binding protein C1827.05c

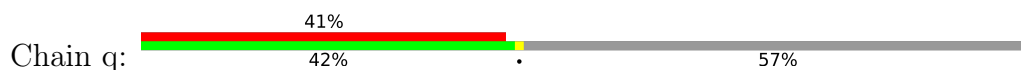




• Molecule 46: Ribosome biogenesis protein ytm1



• Molecule 47: 25S rRNA (cytosine-C(5))-methyltransferase nop2



- Molecule 52: Nucleolar protein 16

Frequency	Percentage
Daily	61%
Weekly	16%
Monthly	23%



- Molecule 53: AdoMet-dependent rRNA methyltransferase *spb1*

Device Type	Percentage
Smartphones	7%
Tablets	18%
Smart TVs	5%
Other devices	78%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	109000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.568	Depositor
Minimum map value	-0.215	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.009	Depositor
Recommended contour level	0.05	Depositor
Map size ($\text{\AA}$)	542.72, 542.72, 542.72	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.06, 1.06, 1.06	Depositor

5 Model quality

5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	1	0.10	0/51332	0.22	0/79942
2	2	0.11	0/3563	0.22	0/5543
3	6	0.09	0/1868	0.25	0/2898
4	7	0.05	0/544	0.16	0/754
5	8	0.10	0/191	0.24	0/254
6	A	0.11	0/1686	0.31	0/2272
7	B	0.10	0/2715	0.27	0/3647
8	C	0.11	0/2848	0.27	0/3842
9	D	0.10	0/3381	0.27	0/4559
10	E	0.12	0/1235	0.32	0/1663
11	F	0.12	0/1781	0.27	0/2389
12	G	0.13	0/1629	0.31	0/2192
13	H	0.13	0/1470	0.33	0/1982
14	I	0.07	0/2023	0.21	0/2810
15	J	0.05	0/573	0.18	0/800
16	K	0.13	0/1999	0.33	0/2702
17	L	0.13	0/960	0.29	0/1288
18	M	0.08	0/1024	0.24	0/1375
19	N	0.12	0/1420	0.26	0/1897
20	O	0.11	0/1588	0.26	0/2128
21	P	0.11	0/1188	0.30	0/1590
22	Q	0.11	0/1043	0.28	0/1401
23	R	0.11	0/732	0.28	0/992
24	S	0.10	0/1437	0.30	0/1929
25	U	0.07	0/483	0.21	0/671
26	V	0.14	0/1007	0.39	0/1357
27	W	0.08	0/1053	0.28	0/1457
28	X	0.12	0/1060	0.28	0/1422
29	Y	0.12	0/1008	0.29	0/1341
30	Z	0.06	0/661	0.17	0/917
31	a	0.12	0/775	0.37	1/1047 (0.1%)
32	b	0.07	0/1776	0.23	0/2471

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	c	0.08	0/461	0.20	0/639
34	d	0.14	0/815	0.34	0/1094
35	e	0.12	0/967	0.29	0/1289
36	f	0.10	0/859	0.25	0/1152
37	g	0.06	0/477	0.20	0/662
38	h	0.10	0/1008	0.26	0/1340
39	i	0.09	0/703	0.24	0/931
40	j	0.10	0/575	0.27	0/761
41	k	0.13	0/570	0.36	0/762
42	l	0.08	0/859	0.26	0/1195
43	m	0.12	0/4644	0.32	1/6313 (0.0%)
44	n	0.10	0/3598	0.25	0/4845
45	o	0.14	0/1163	0.40	0/1552
46	p	0.06	0/1351	0.20	0/1871
47	q	0.08	0/1280	0.19	0/1778
48	r	0.17	0/1086	0.40	0/1457
49	s	0.14	0/192	0.36	0/248
50	t	0.10	0/1979	0.27	0/2645
51	u	0.21	0/729	0.45	0/981
52	v	0.12	0/1319	0.28	0/1769
53	w	0.11	0/1478	0.29	0/1967
54	y	0.06	0/1096	0.22	0/1522
55	z	0.12	0/297	0.28	0/388
56	T	0.19	0/142	0.50	0/196
All	All	0.10	0/123701	0.26	2/178889 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
31	a	67	PRO	N-CA-CB	6.69	110.36	103.00
43	m	372	PRO	N-CA-C	-5.46	101.22	112.47

There are no chirality outliers.

There are no planarity outliers.

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	45883	0	23099	506	0
2	2	3189	0	1613	30	0
3	6	1674	0	844	24	0
4	7	548	0	228	0	0
5	8	187	0	202	5	0
6	A	1652	0	1688	41	0
7	B	2662	0	2742	75	0
8	C	2795	0	2918	34	0
9	D	3320	0	3431	54	0
10	E	1213	0	1295	33	0
11	F	1745	0	1818	23	0
12	G	1607	0	1736	34	0
13	H	1451	0	1511	25	0
14	I	2032	0	893	0	0
15	J	574	0	263	3	0
16	K	1964	0	2042	61	0
17	L	942	0	1012	20	0
18	M	1007	0	1072	21	0
19	N	1392	0	1431	32	0
20	O	1557	0	1652	34	0
21	P	1168	0	1198	25	0
22	Q	1032	0	1129	15	0
23	R	729	0	616	11	0
24	S	1401	0	1455	33	0
25	U	484	0	222	1	0
26	V	991	0	1039	37	0
27	W	1057	0	487	8	0
28	X	1044	0	1112	12	0
29	Y	998	0	1090	30	0
30	Z	662	0	305	2	0
31	a	762	0	796	25	0
32	b	1780	0	797	5	0
33	c	462	0	220	2	0
34	d	801	0	846	19	0
35	e	953	0	1018	24	0
36	f	839	0	866	16	0
37	g	478	0	216	1	0
38	h	999	0	1092	15	0
39	i	696	0	763	10	0
40	j	563	0	578	14	0
41	k	564	0	611	22	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
42	l	860	0	389	2	0
43	m	4526	0	4492	122	0
44	n	3517	0	3544	79	0
45	o	1138	0	1196	42	0
46	p	1357	0	596	19	0
47	q	1282	0	590	2	0
48	r	1081	0	837	31	0
49	s	193	0	226	10	0
50	t	1948	0	2066	30	0
51	u	714	0	616	16	0
52	v	1299	0	1347	29	0
53	w	1462	0	1537	29	0
54	y	1097	0	510	2	0
55	z	292	0	317	13	0
56	T	138	0	127	4	0
57	j	1	0	0	0	0
All	All	116762	0	86336	1477	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 1477 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)
43:m:370:PRO:HB2	43:m:671:LEU:HD11	1.47	0.96
53:w:696:PRO:HD2	53:w:699:LYS:HB2	1.53	0.89
2:2:132:G:H1	2:2:137:A:H61	1.22	0.87
1:1:643:C:H2'	1:1:644:A:C8	2.12	0.85
20:O:51:ASN:HA	20:O:54:LYS:HD2	1.61	0.83

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	7	102/707 (14%)	101 (99%)	1 (1%)	0	100	100
5	8	20/51 (39%)	20 (100%)	0	0	100	100
6	A	200/295 (68%)	194 (97%)	6 (3%)	0	100	100
7	B	331/388 (85%)	318 (96%)	13 (4%)	0	100	100
8	C	357/363 (98%)	342 (96%)	15 (4%)	0	100	100
9	D	412/578 (71%)	401 (97%)	11 (3%)	0	100	100
10	E	152/195 (78%)	142 (93%)	10 (7%)	0	100	100
11	F	212/250 (85%)	205 (97%)	7 (3%)	0	100	100
12	G	202/259 (78%)	196 (97%)	4 (2%)	2 (1%)	12	45
13	H	181/190 (95%)	173 (96%)	8 (4%)	0	100	100
14	I	391/747 (52%)	382 (98%)	8 (2%)	1 (0%)	36	68
15	J	113/333 (34%)	112 (99%)	1 (1%)	0	100	100
16	K	246/373 (66%)	232 (94%)	13 (5%)	1 (0%)	30	62
17	L	114/208 (55%)	112 (98%)	2 (2%)	0	100	100
18	M	123/134 (92%)	117 (95%)	6 (5%)	0	100	100
19	N	159/201 (79%)	158 (99%)	1 (1%)	0	100	100
20	O	194/197 (98%)	188 (97%)	6 (3%)	0	100	100
21	P	143/187 (76%)	139 (97%)	4 (3%)	0	100	100
22	Q	131/187 (70%)	127 (97%)	4 (3%)	0	100	100
23	R	108/193 (56%)	107 (99%)	1 (1%)	0	100	100
24	S	163/176 (93%)	154 (94%)	9 (6%)	0	100	100
25	U	96/117 (82%)	93 (97%)	3 (3%)	0	100	100
26	V	130/139 (94%)	126 (97%)	4 (3%)	0	100	100
27	W	207/241 (86%)	196 (95%)	11 (5%)	0	100	100
28	X	128/141 (91%)	124 (97%)	4 (3%)	0	100	100
29	Y	123/126 (98%)	117 (95%)	6 (5%)	0	100	100
30	Z	132/136 (97%)	130 (98%)	2 (2%)	0	100	100
31	a	93/148 (63%)	92 (99%)	1 (1%)	0	100	100
32	b	351/642 (55%)	346 (99%)	5 (1%)	0	100	100
33	c	92/117 (79%)	92 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
34	d	92/113 (81%)	91 (99%)	1 (1%)	0	100	100
35	e	117/127 (92%)	114 (97%)	3 (3%)	0	100	100
36	f	104/108 (96%)	99 (95%)	5 (5%)	0	100	100
37	g	95/112 (85%)	92 (97%)	3 (3%)	0	100	100
38	h	119/122 (98%)	118 (99%)	1 (1%)	0	100	100
39	i	83/99 (84%)	83 (100%)	0	0	100	100
40	j	69/91 (76%)	68 (99%)	1 (1%)	0	100	100
41	k	68/74 (92%)	66 (97%)	2 (3%)	0	100	100
42	l	172/180 (96%)	170 (99%)	2 (1%)	0	100	100
43	m	558/740 (75%)	529 (95%)	28 (5%)	1 (0%)	43	73
44	n	426/607 (70%)	415 (97%)	11 (3%)	0	100	100
45	o	135/276 (49%)	129 (96%)	6 (4%)	0	100	100
46	p	263/440 (60%)	257 (98%)	6 (2%)	0	100	100
47	q	256/608 (42%)	252 (98%)	4 (2%)	0	100	100
48	r	157/260 (60%)	157 (100%)	0	0	100	100
49	s	21/470 (4%)	18 (86%)	3 (14%)	0	100	100
50	t	233/249 (94%)	221 (95%)	12 (5%)	0	100	100
51	u	97/192 (50%)	94 (97%)	3 (3%)	0	100	100
52	v	157/209 (75%)	151 (96%)	5 (3%)	1 (1%)	21	56
53	w	174/802 (22%)	170 (98%)	4 (2%)	0	100	100
54	y	221/244 (91%)	218 (99%)	3 (1%)	0	100	100
55	z	33/117 (28%)	31 (94%)	1 (3%)	1 (3%)	3	23
56	T	16/160 (10%)	16 (100%)	0	0	100	100
All	All	9072/14419 (63%)	8795 (97%)	270 (3%)	7 (0%)	49	79

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
52	v	130	ILE
12	G	227	ASP
16	K	153	ILE
12	G	182	ASN
55	z	104	ARG

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	
5	8	19/47 (40%)	19 (100%)	0	100	100
6	A	184/266 (69%)	182 (99%)	2 (1%)	65	79
7	B	284/326 (87%)	284 (100%)	0	100	100
8	C	296/297 (100%)	296 (100%)	0	100	100
9	D	362/505 (72%)	361 (100%)	1 (0%)	86	88
10	E	128/155 (83%)	128 (100%)	0	100	100
11	F	180/210 (86%)	178 (99%)	2 (1%)	65	79
12	G	167/212 (79%)	167 (100%)	0	100	100
13	H	164/170 (96%)	164 (100%)	0	100	100
16	K	223/333 (67%)	223 (100%)	0	100	100
17	L	97/167 (58%)	97 (100%)	0	100	100
18	M	108/113 (96%)	108 (100%)	0	100	100
19	N	145/176 (82%)	145 (100%)	0	100	100
20	O	161/162 (99%)	161 (100%)	0	100	100
21	P	121/149 (81%)	121 (100%)	0	100	100
22	Q	114/159 (72%)	114 (100%)	0	100	100
23	R	51/162 (32%)	51 (100%)	0	100	100
24	S	149/154 (97%)	149 (100%)	0	100	100
26	V	103/107 (96%)	103 (100%)	0	100	100
28	X	114/122 (93%)	112 (98%)	2 (2%)	51	74
29	Y	110/111 (99%)	110 (100%)	0	100	100
31	a	81/122 (66%)	80 (99%)	1 (1%)	63	79
34	d	88/102 (86%)	88 (100%)	0	100	100
35	e	101/107 (94%)	101 (100%)	0	100	100
36	f	89/91 (98%)	89 (100%)	0	100	100
38	h	106/107 (99%)	106 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
39	i	74/84 (88%)	74 (100%)	0	100	100
40	j	58/71 (82%)	58 (100%)	0	100	100
41	k	63/66 (96%)	63 (100%)	0	100	100
43	m	504/659 (76%)	500 (99%)	4 (1%)	73	82
44	n	378/532 (71%)	377 (100%)	1 (0%)	86	88
45	o	123/246 (50%)	122 (99%)	1 (1%)	73	82
48	r	63/224 (28%)	61 (97%)	2 (3%)	34	65
49	s	21/409 (5%)	21 (100%)	0	100	100
50	t	211/223 (95%)	211 (100%)	0	100	100
51	u	55/168 (33%)	55 (100%)	0	100	100
52	v	138/181 (76%)	138 (100%)	0	100	100
53	w	158/697 (23%)	158 (100%)	0	100	100
55	z	31/107 (29%)	31 (100%)	0	100	100
56	T	16/139 (12%)	16 (100%)	0	100	100
All	All	5638/8438 (67%)	5622 (100%)	16 (0%)	84	88

5 of 16 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
48	r	37	LEU
45	o	211	HIS
43	m	114	ASP
44	n	139	MET
31	a	134	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 41 such sidechains are listed below:

Mol	Chain	Res	Type
29	Y	54	GLN
44	n	411	GLN
34	d	11	GLN
44	n	190	GLN
48	r	60	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	2101/3497 (60%)	497 (23%)	21 (0%)
2	2	147/165 (89%)	24 (16%)	1 (0%)
3	6	75/300 (25%)	32 (42%)	0
All	All	2323/3962 (58%)	553 (23%)	22 (0%)

5 of 553 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	6	A
1	1	26	A
1	1	34	A
1	1	36	C
1	1	49	A

5 of 22 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	2951	G
1	1	3041	A
1	1	3024	C
1	1	3070	U
1	1	996	G

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 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	1	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	1	3315:A	O3'	3316:G	P	3.15

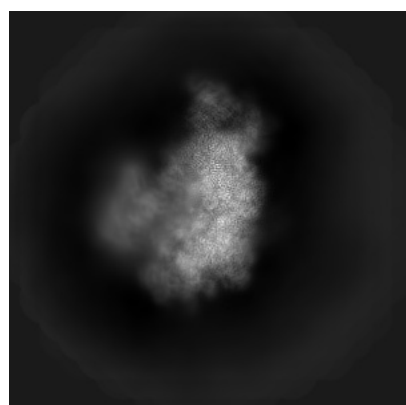
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-24422. These allow visual inspection of the internal detail of the map and identification of artifacts.

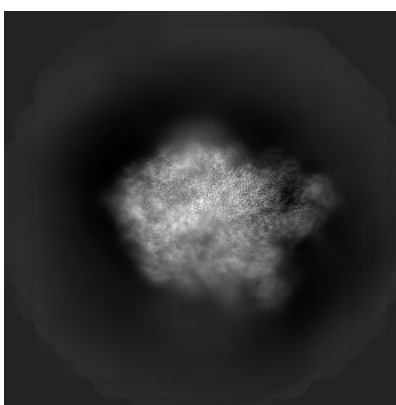
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

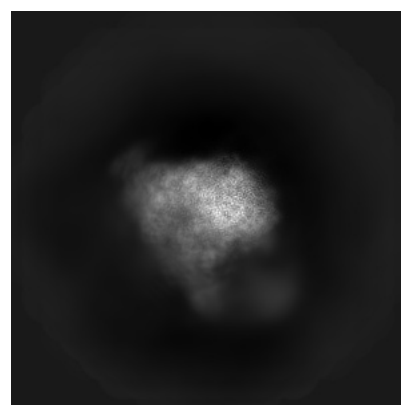
6.1.1 Primary map



X



Y

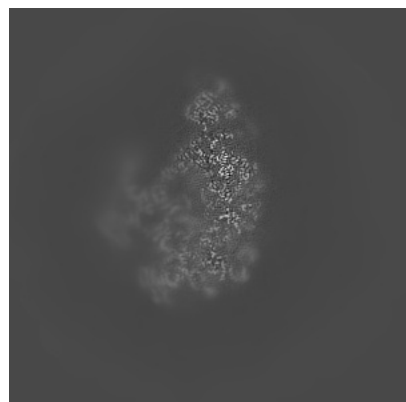


Z

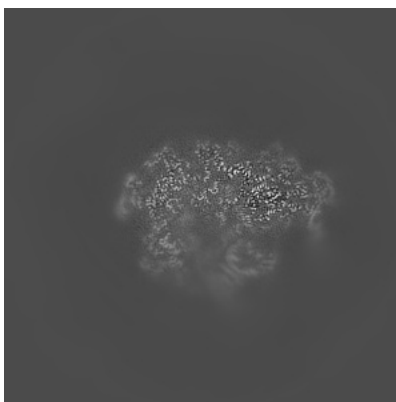
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

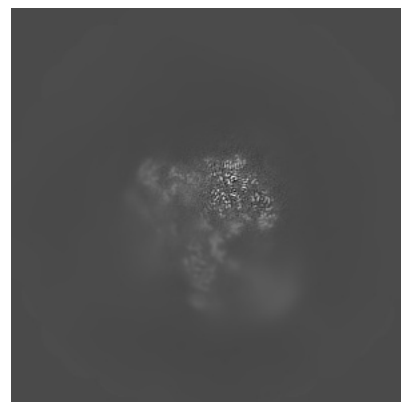
6.2.1 Primary map



X Index: 256



Y Index: 256

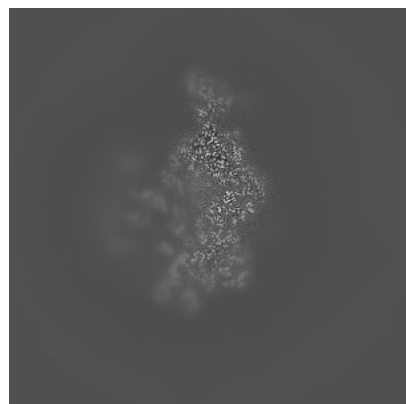


Z Index: 256

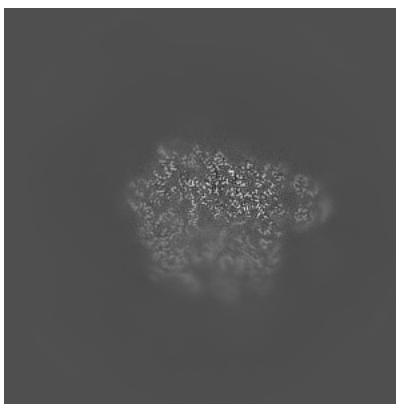
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

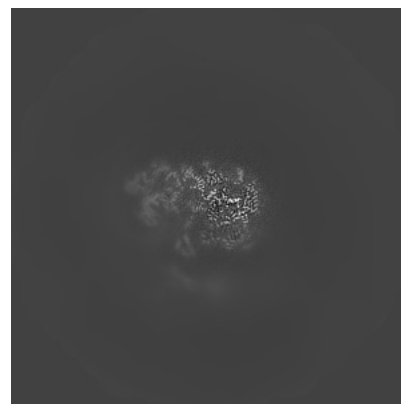
6.3.1 Primary map



X Index: 271



Y Index: 273

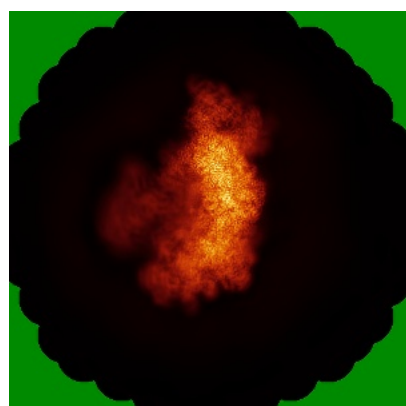


Z Index: 314

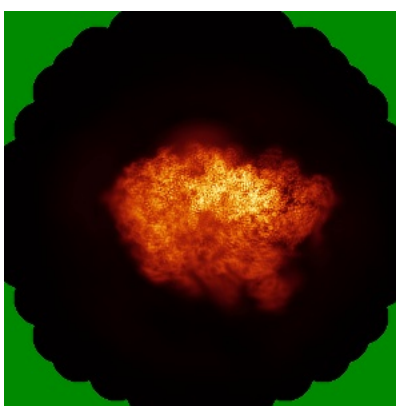
The images above show the largest variance slices of the map in three orthogonal directions.

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

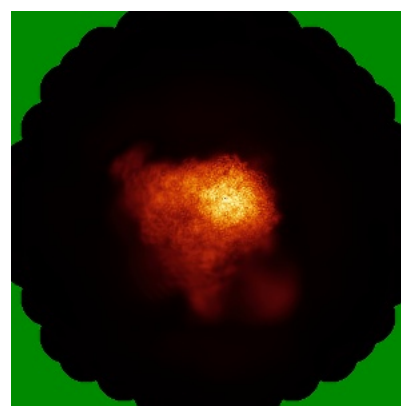
6.4.1 Primary map



X



Y

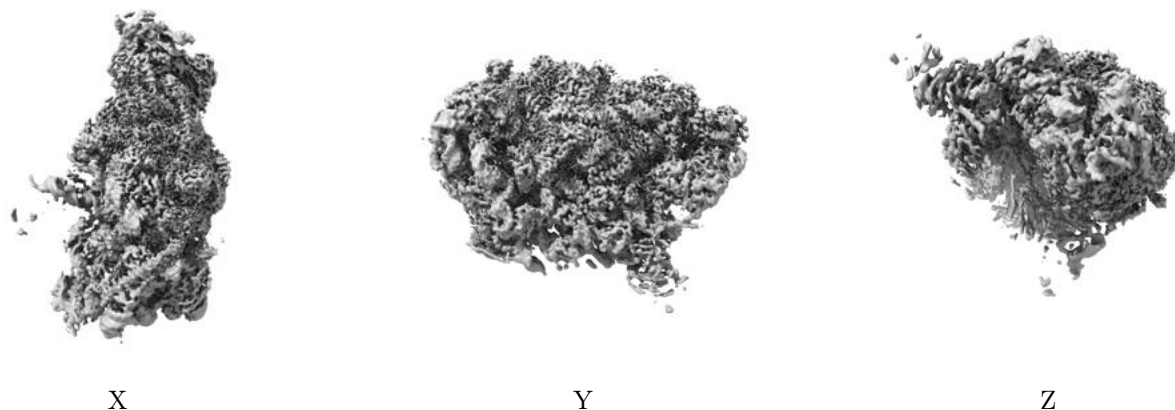


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



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

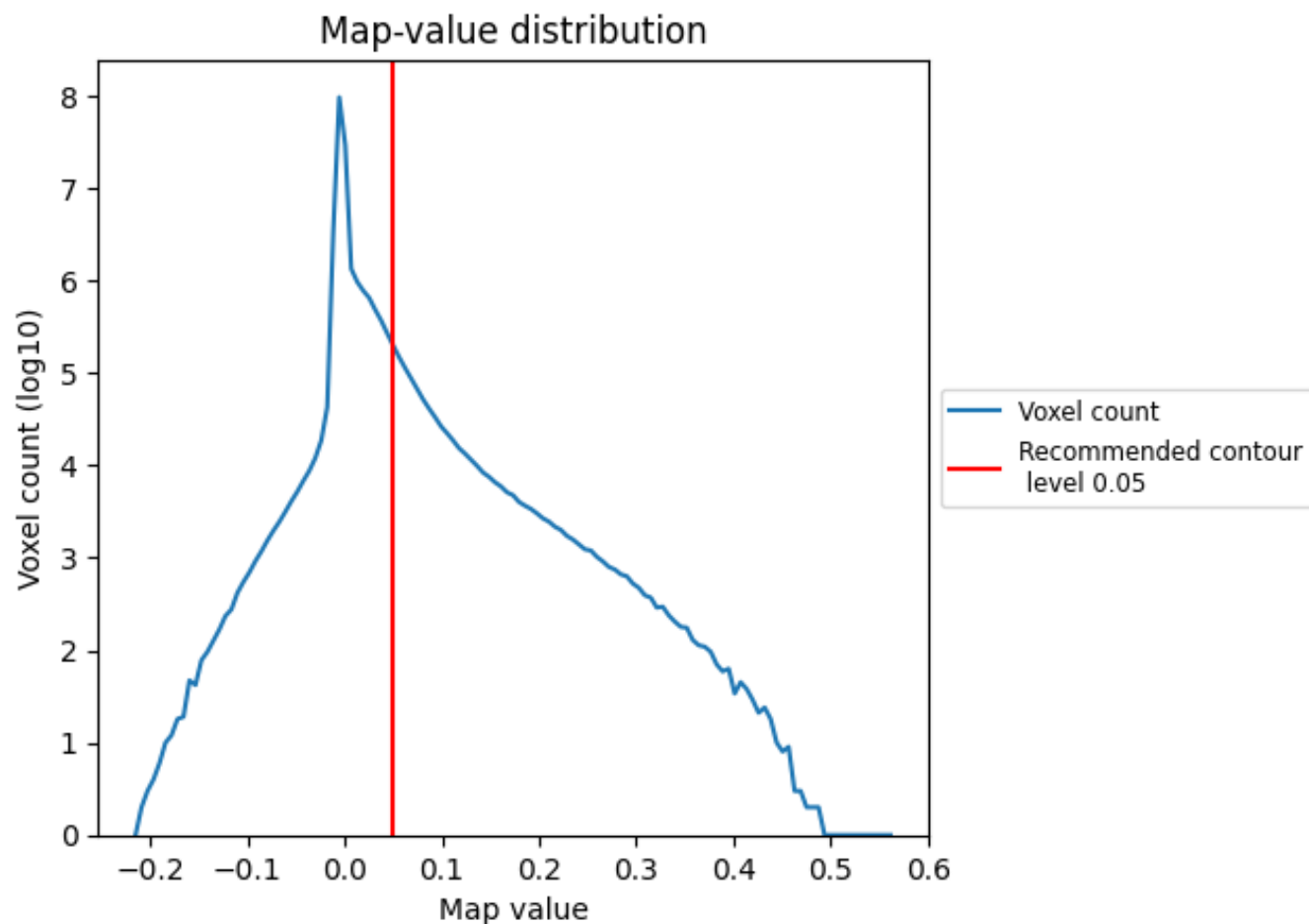
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

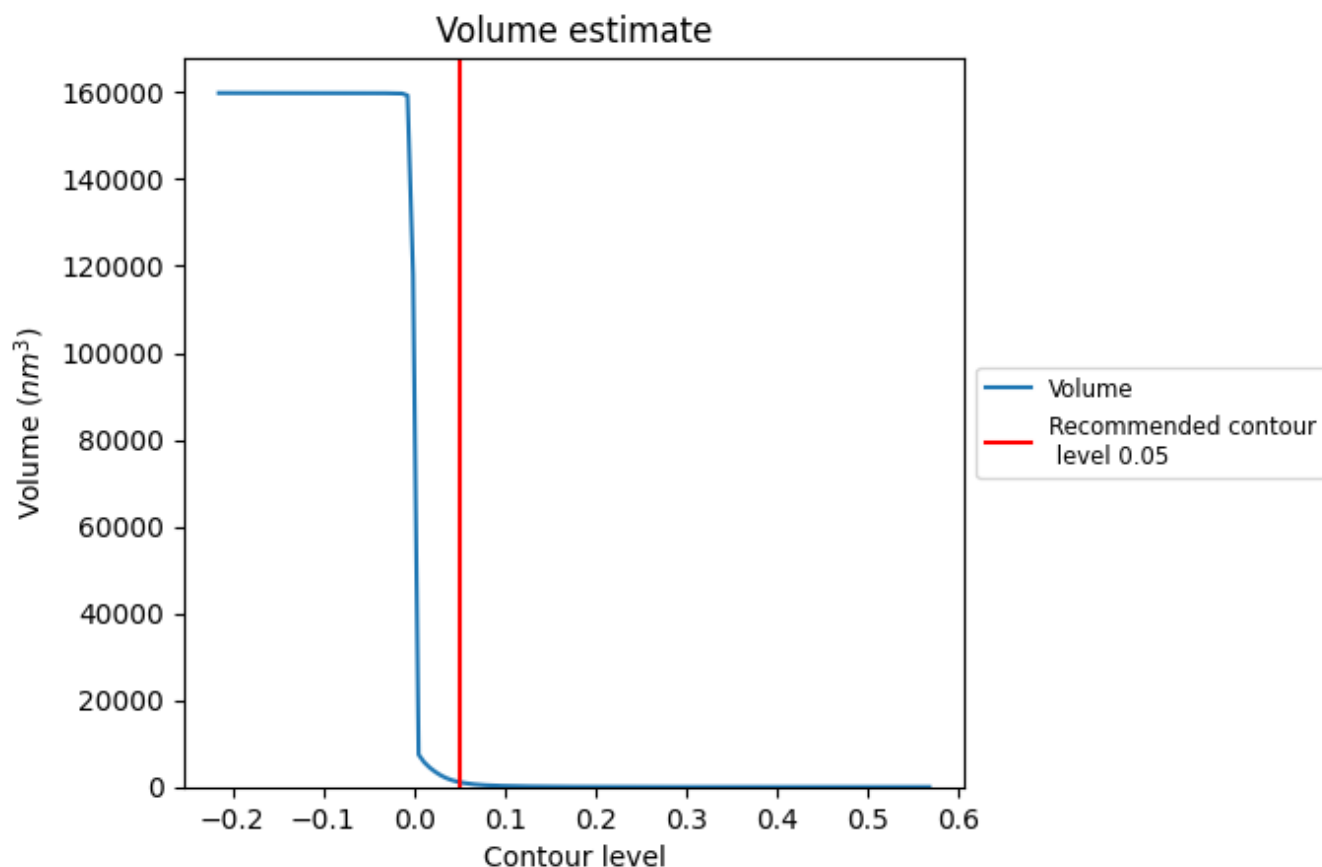
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

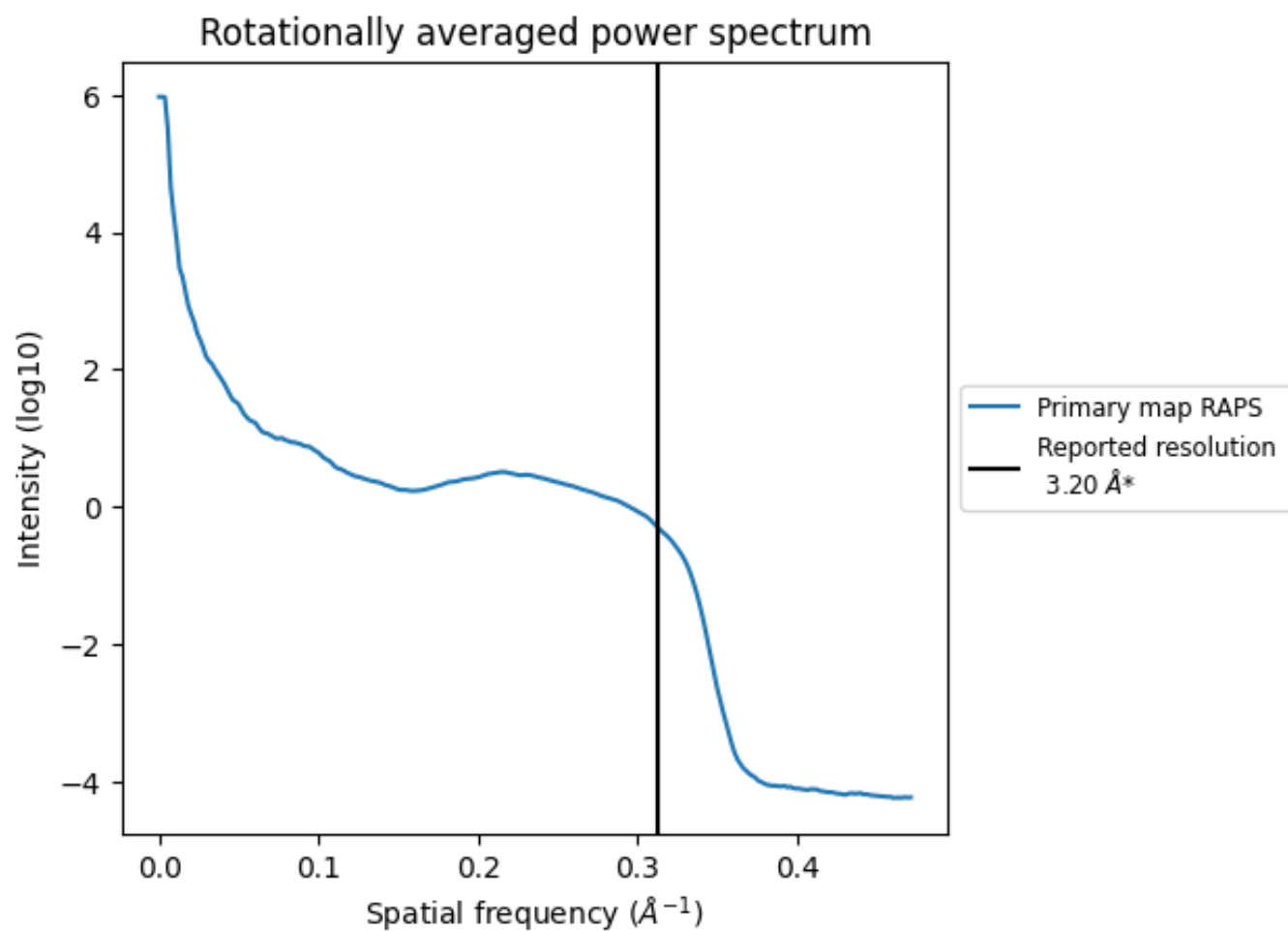
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1113 nm^3 ; this corresponds to an approximate mass of 1006 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

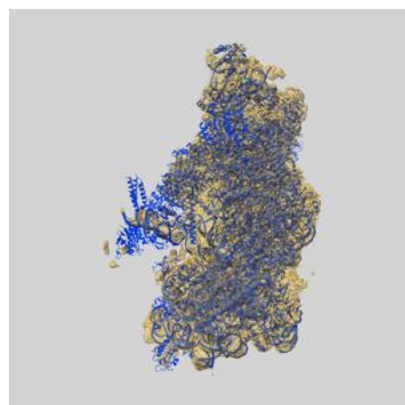
8 Fourier-Shell correlation

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

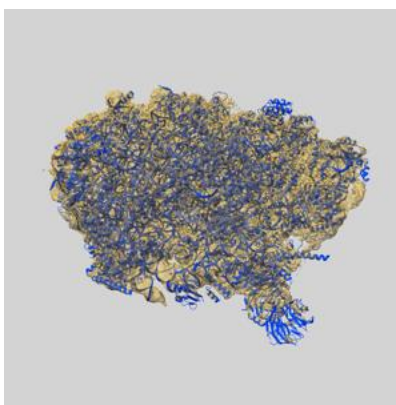
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-24422 and PDB model 8ESR. Per-residue inclusion information can be found in section [3](#) on page [15](#).

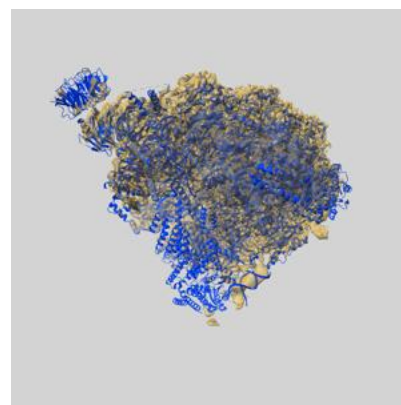
9.1 Map-model overlay [i](#)



X



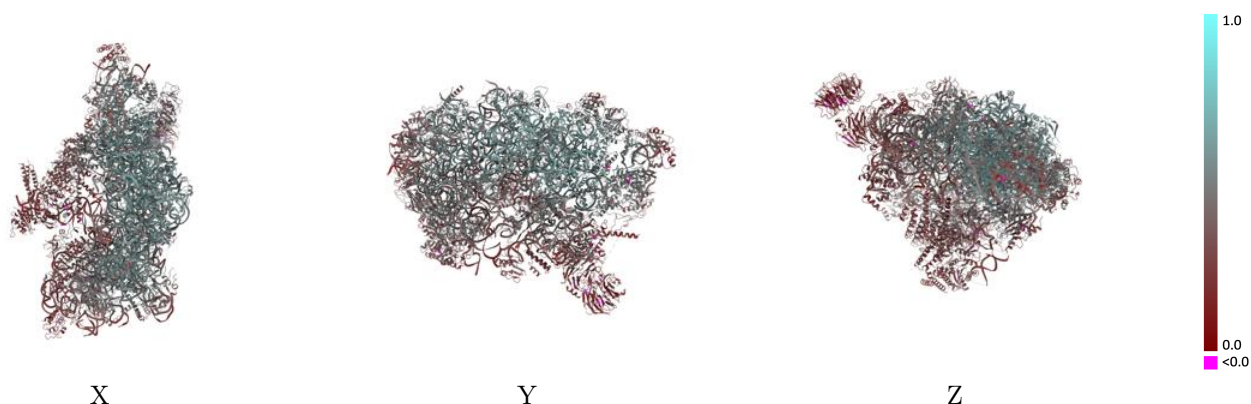
Y



Z

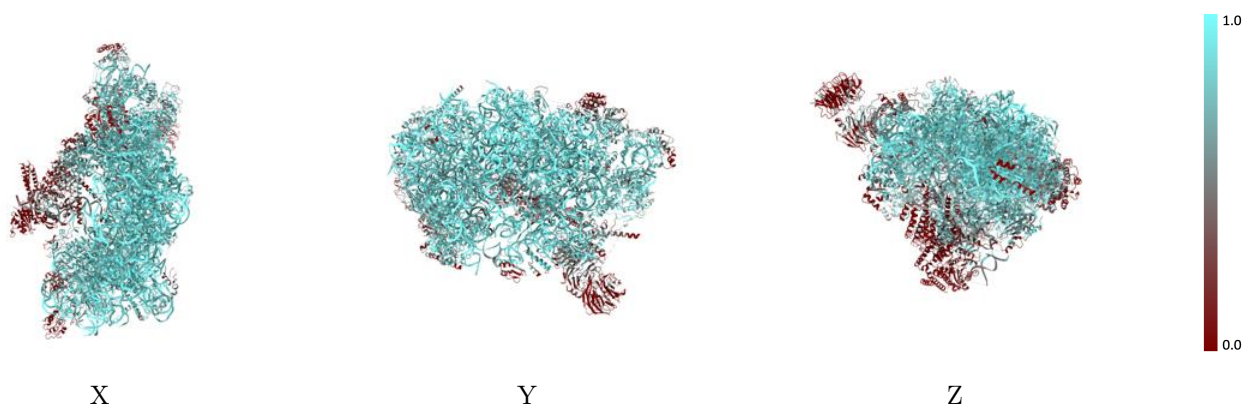
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



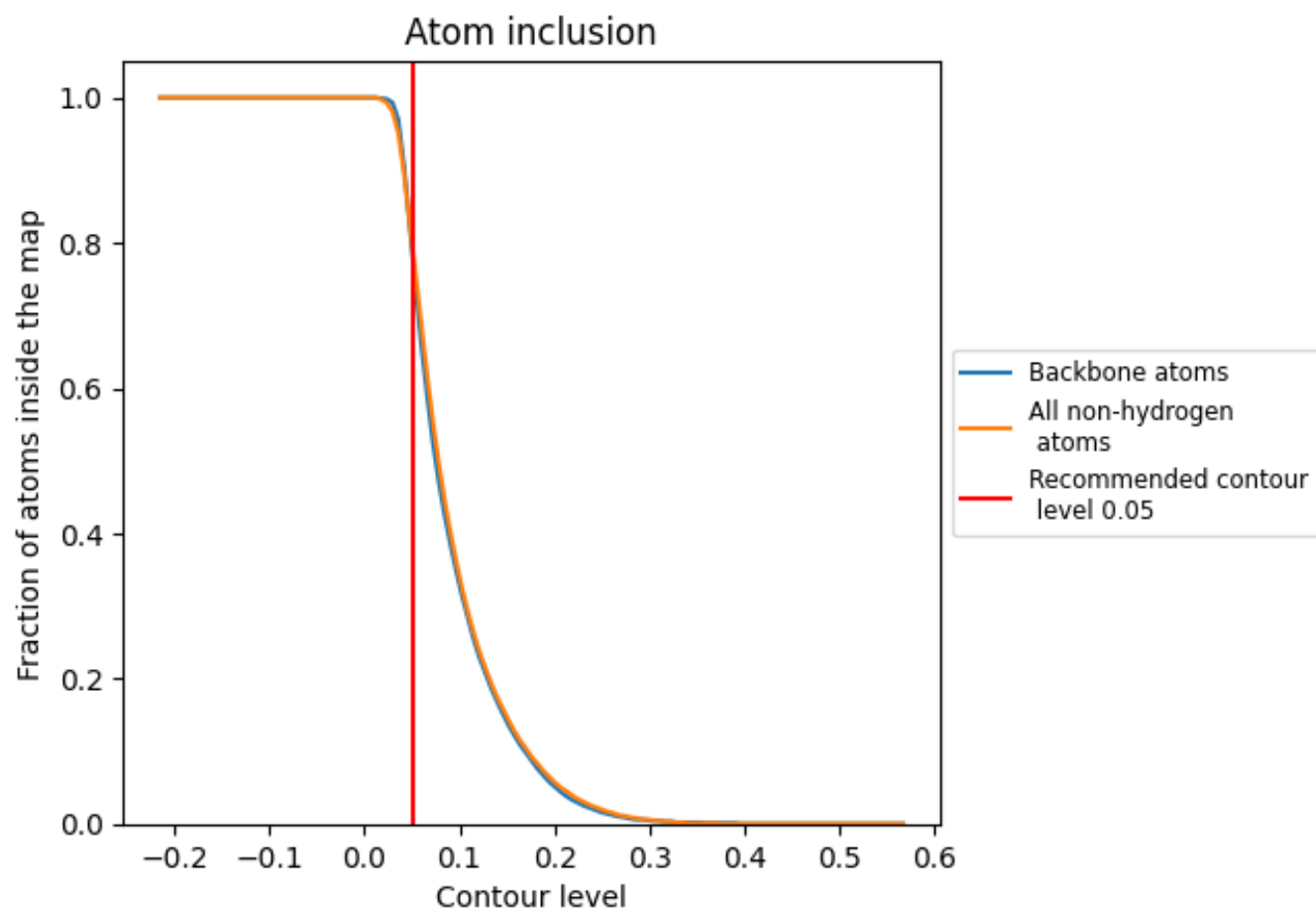
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.05).

9.4 Atom inclusion ⓘ



At the recommended contour level, 79% of all backbone atoms, 80% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8000	 0.4400
1	 0.9350	 0.4440
2	 0.9790	 0.5630
6	 0.8860	 0.4240
7	 0.0000	 0.2620
8	 0.7330	 0.4100
A	 0.6940	 0.3800
B	 0.8780	 0.4640
C	 0.9420	 0.5670
D	 0.4980	 0.4460
E	 0.7720	 0.4590
F	 0.8940	 0.5070
G	 0.8960	 0.5620
H	 0.8000	 0.4020
I	 0.1920	 0.3030
J	 0.4620	 0.3280
K	 0.6690	 0.4160
L	 0.9740	 0.5950
M	 0.8690	 0.4500
N	 0.9900	 0.6090
O	 0.9050	 0.4940
P	 0.8410	 0.5050
Q	 0.8850	 0.5220
R	 0.7290	 0.3660
S	 0.8120	 0.4390
T	 0.4490	 0.3560
U	 0.3220	 0.2920
V	 0.6940	 0.3970
W	 0.3380	 0.2720
X	 0.8910	 0.5290
Y	 0.9250	 0.5570
Z	 0.7460	 0.3650
a	 0.8010	 0.5060
b	 0.5360	 0.3310
c	 0.4330	 0.2760



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Chain	Atom inclusion	Q-score
d	 0.8040	 0.4260
e	 0.9350	 0.5520
f	 0.9620	 0.5560
g	 0.8870	 0.4270
h	 0.9150	 0.5640
i	 0.9160	 0.5410
j	 0.9850	 0.5950
k	 0.6580	 0.3750
l	 0.2780	 0.2860
m	 0.5500	 0.3440
n	 0.7590	 0.4360
o	 0.6790	 0.4390
p	 0.0880	 0.2130
q	 0.0470	 0.2600
r	 0.6300	 0.3590
s	 0.7270	 0.3880
t	 0.8070	 0.4680
u	 0.7000	 0.3320
v	 0.8520	 0.5330
w	 0.5590	 0.3930
y	 0.7910	 0.3600
z	 0.3930	 0.2780