



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 06:10 AM UTC

PDB ID : 8ESQ / pdb_00008esq
EMDB ID : EMD-24411
Title : Ytm1 associated nascent 60S ribosome State 2
Authors : Zhou, X.; Bilokapic, S.; Deshmukh, A.A.; Halic, M.
Deposited on : 2022-10-14
Resolution : 2.80 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

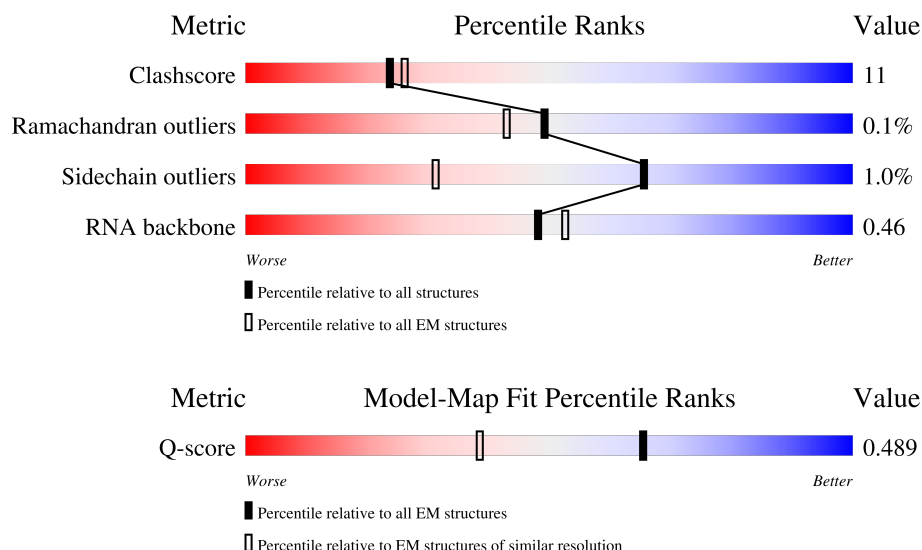
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.80 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.



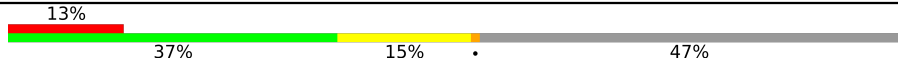
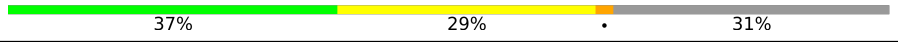
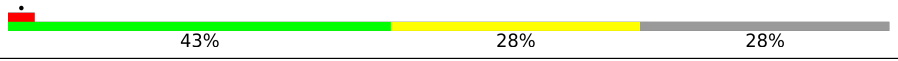
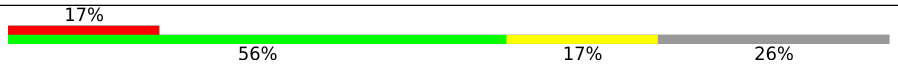
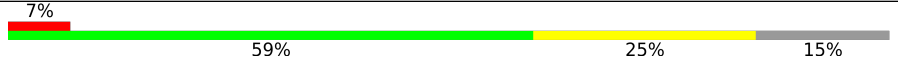
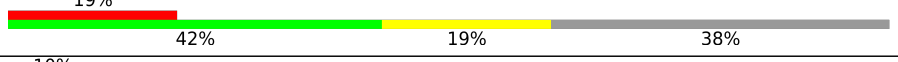
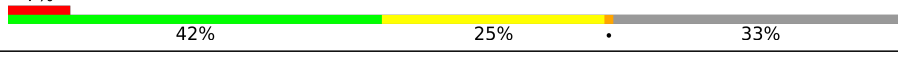
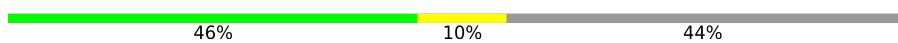
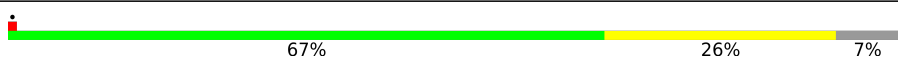
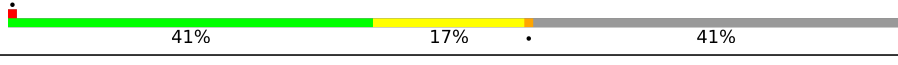
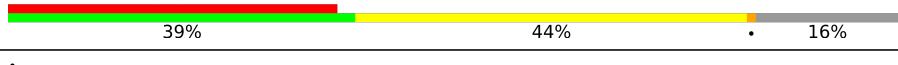
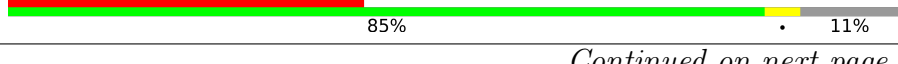
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	11806 (2.30 - 3.30)

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	7	707	
2	1	3497	
3	2	165	

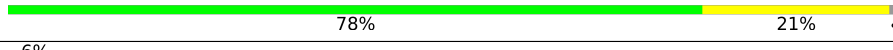
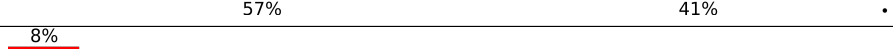
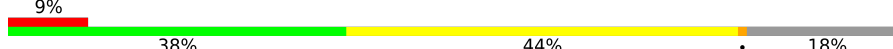
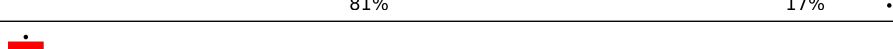
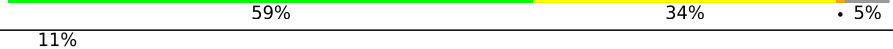
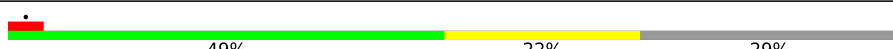
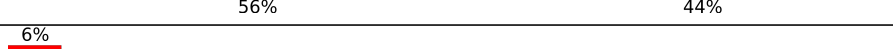
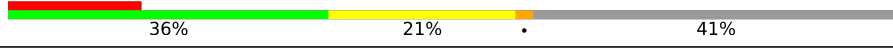
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Mol	Chain	Length	Quality of chain
4	3	302	
5	6	300	
6	8	51	
7	A	295	
8	B	388	
9	C	363	
10	D	578	
11	E	195	
12	F	250	
13	G	259	
14	H	190	
15	I	747	
16	J	333	
17	K	373	
18	L	208	
19	M	134	
20	N	201	
21	O	197	
22	P	187	
23	Q	187	
24	R	193	
25	S	176	
26	U	117	
27	V	139	
28	W	241	

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Mol	Chain	Length	Quality of chain
29	X	141	
30	Y	126	
31	Z	136	
32	a	148	
33	b	642	
34	c	117	
35	d	113	
36	e	127	
37	f	108	
38	g	112	
39	h	122	
40	i	99	
41	j	91	
42	k	74	
43	l	180	
44	m	740	
45	n	607	
46	o	276	
47	p	440	
48	q	608	
49	r	260	
50	s	470	
51	t	249	
52	u	192	
53	v	209	

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Mol	Chain	Length	Quality of chain
54	w	802	36% 44% 19% 37%
55	x	306	5% 11% 85%
56	y	244	5% 57% 34% 8%
57	z	117	10% 17% 70%
58	T	160	8% 12% 8% 79%

2 Entry composition

There are 59 unique types of molecules in this entry. The entry contains 130409 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 Noc2.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	7	245	Total	C	N	O	0	0
			1218	728	245	245		

- Molecule 2 is a RNA chain called RNA (2231-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	2230	Total	C	N	O	P	0	0
			47746	21325	8659	15532	2230		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	1746	C	U	conflict	GB 157310483

- Molecule 3 is a RNA chain called RNA (150-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	150	Total	C	N	O	P	0	0
			3189	1427	564	1048	150		

- Molecule 4 is a protein called Protein mak16.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	160	Total	C	N	O	S	0	0
			1336	845	257	228	6		

- Molecule 5 is a RNA chain called RNA (81-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
5	6	81	Total	C	N	O	P	0	0
			1717	770	296	570	81		

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 6 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	8	35	Total	C	N	O	0	0
			291	182	64	45		

- Molecule 7 is a protein called Ribosome biogenesis protein brx1.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	A	211	Total	C	N	O	S	0	0
			1686	1079	301	299	7		

- Molecule 8 is a protein called 60S ribosomal protein L3-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	B	339	Total	C	N	O	S	0	0
			2687	1701	499	478	9		

- Molecule 9 is a protein called 60S ribosomal protein L4-B.

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

- Molecule 10 is a protein called ATP-dependent RNA helicase has1.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	D	427	Total	C	N	O	S	0	0
			3396	2190	581	614	11		

- Molecule 11 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	E	165	Total	C	N	O	S	0	0
			1283	822	237	221	3		

- Molecule 12 is a protein called 60S ribosomal protein L7-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	F	237	Total	C	N	O	S	0	0
			1925	1238	353	331	3		

- Molecule 13 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	G	206	Total	C	N	O	S	1	0
			1615	1034	295	283	3		

- Molecule 14 is a protein called 60S ribosomal protein L9-A.

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

- Molecule 15 is a protein called Nucleolar complex-associated protein 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	I	460	Total	C	N	O	S	1	0
			3725	2412	620	682	11		

There is a discrepancy between the modelled and reference sequences:

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

- Molecule 16 is a protein called Probable rRNA-processing protein ebp2.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	J	118	Total	C	N	O	S	0	0
			959	607	166	184	2		

- Molecule 17 is a protein called Putative ribosome biogenesis protein C8F11.04.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	K	251	Total	C	N	O	S	0	0
			1973	1262	338	367	6		

- Molecule 18 is a protein called 60S ribosomal protein L13.

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

- Molecule 19 is a protein called 60S ribosomal protein L14.

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

- Molecule 20 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	N	166	Total	C	N	O	S	0	0
			1406	883	291	229	3		

- Molecule 21 is a protein called 60S ribosomal protein L16-B.

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

- Molecule 22 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	P	159	Total	C	N	O	S	0	0
			1248	794	233	218	3		

- Molecule 23 is a protein called 60S ribosomal protein L18-A.

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

- Molecule 24 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	R	114	Total	C	N	O	S	0	0
			949	596	195	153	5		

- Molecule 25 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	S	168	Total	C	N	O	S	0	0
			1408	909	263	231	5		

- Molecule 26 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	U	98	Total	C	N	O		0	0
			791	513	137	141			

- Molecule 27 is a protein called 60S ribosomal protein L23-A.

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

- Molecule 28 is a protein called Ribosome assembly factor mrt4.

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

- Molecule 29 is a protein called 60S ribosomal protein L25-A.

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

- Molecule 30 is a protein called 60S ribosomal protein L26.

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

- Molecule 31 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Z	134	Total	C	N	O	S	0	0
			1072	693	199	178	2		

- Molecule 32 is a protein called 60S ribosomal protein L28-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	a	80	Total	C	N	O	0	0
			634	404	116	114		

- Molecule 33 is a protein called Probable nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	b	403	Total	C	N	O	0	0
			1999	1193	403	403		

- Molecule 34 is a protein called 60S ribosomal protein L30-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	c	96	Total	C	N	O	S	0	0
			720	457	125	134	4		

- Molecule 35 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	d	97	Total	C	N	O	S	0	0
			810	512	159	136	3		

- Molecule 36 is a protein called 60S ribosomal protein L32-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	e	121	Total	C	N	O	S	0	0
			971	608	198	160	5		

- Molecule 37 is a protein called 60S ribosomal protein L33-B.

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

- Molecule 38 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	g	106	Total	C	N	O	S	0	0
			861	540	177	142	2		

- Molecule 39 is a protein called 60S ribosomal protein L35.

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

- Molecule 40 is a protein called 60S ribosomal protein L36-B.

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

- Molecule 41 is a protein called 60S ribosomal protein L37-B.

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

- Molecule 42 is a protein called 60S ribosomal protein L38-1.

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

- Molecule 43 is a protein called 60S ribosome subunit biogenesis protein nip7.

Mol	Chain	Residues	Atoms				AltConf	Trace
43	l	174	Total	C	N	O	S	
			1418	906	254	250	8	0

- Molecule 44 is a protein called Ribosome biogenesis protein erb1.

Mol	Chain	Residues	Atoms				AltConf	Trace
44	m	572	Total	C	N	O	S	
			4536	2891	790	843	12	0

- Molecule 45 is a protein called Pescadillo homolog.

Mol	Chain	Residues	Atoms				AltConf	Trace
45	n	433	Total	C	N	O	S	
			3526	2268	608	638	12	0

- Molecule 46 is a protein called Uncharacterized RNA-binding protein C1827.05c.

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

- Molecule 47 is a protein called Ribosome biogenesis protein ytm1.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	p	290	Total	C	N	O		0	0
			1431	851	290	290			

- Molecule 48 is a protein called 25S rRNA (cytosine-C(5))-methyltransferase nop2.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	q	341	Total	C	N	O		0	0
			1684	1002	341	341			

- Molecule 49 is a protein called Ribosome biogenesis protein nsa2.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	r	166	Total	C	N	O	S	0	0
			1357	850	259	243	5		

- Molecule 50 is a protein called GTPase grn1.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	s	32	Total	C	N	O		0	0
			269	163	63	43			

- Molecule 51 is a protein called 60S ribosomal protein L7-A.

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

- Molecule 52 is a protein called Ribosome biogenesis protein rlp24.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	u	114	Total	C	N	O	S	0	0
			944	598	190	147	9		

- Molecule 53 is a protein called Nucleolar protein 16.

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

- Molecule 54 is a protein called AdoMet-dependent rRNA methyltransferase spb1.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	w	504	Total	C	N	O	S	1	0
			4067	2573	723	753	18		

- Molecule 55 is a protein called Brix domain-containing protein C4F8.04.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	x	45	Total	C	N	O	S	0	0
			383	236	80	66	1		

- Molecule 56 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	y	225	Total	C	N	O	S	0	0
			1697	1058	293	341	5		

- Molecule 57 is a protein called UPF0642 protein C32H8.05.

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

- Molecule 58 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	T	34	Total	C	N	O	S	0	0
			269	168	50	50	1		

- Molecule 59 is ZINC ION (CCD ID: ZN) (formula: Zn).

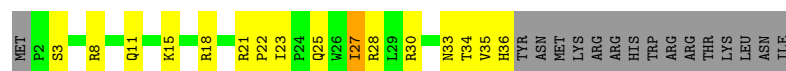
Mol	Chain	Residues	Atoms		AltConf
59	j	1	Total	Zn	0
			1	1	

- Molecule 2: RNA (2231-MER)

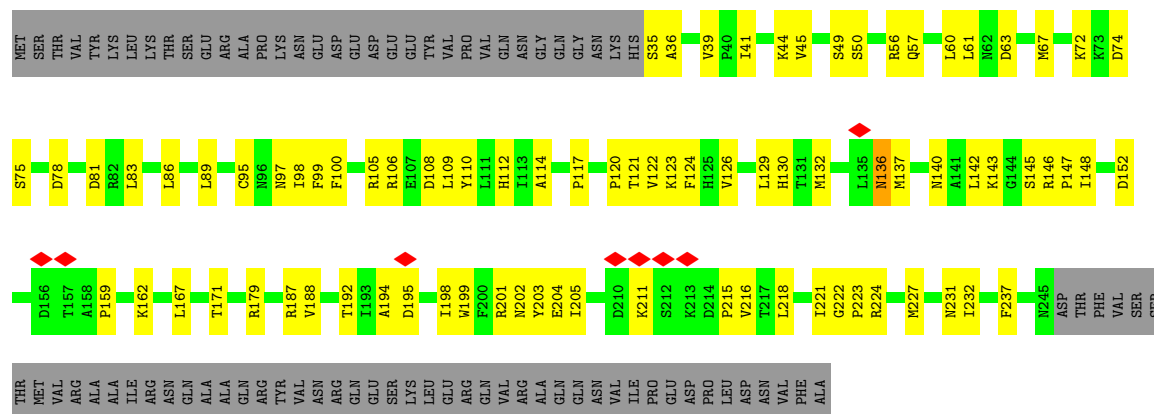
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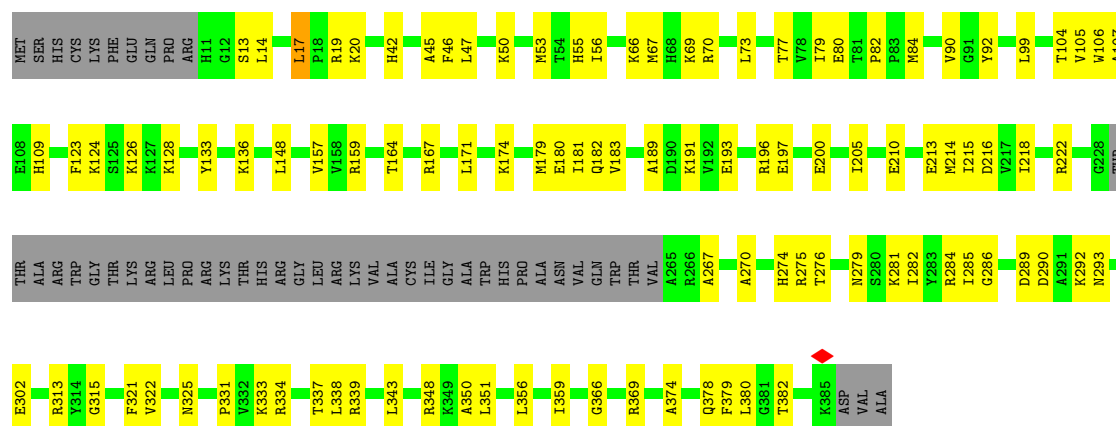




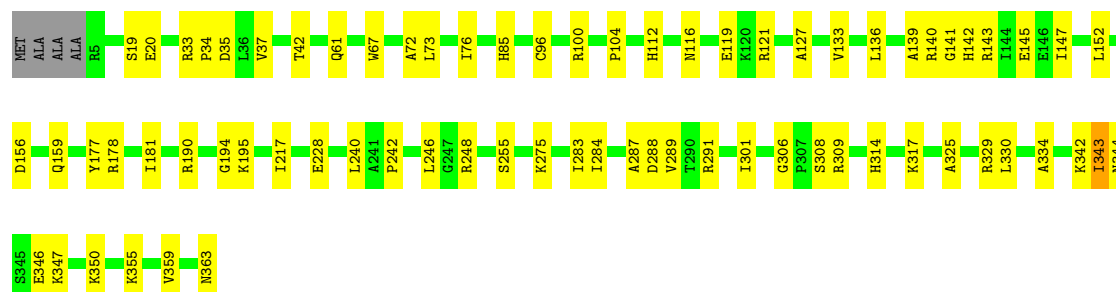
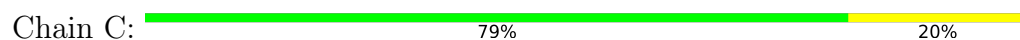
• Molecule 7: Ribosome biogenesis protein brx1

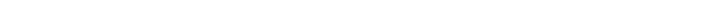


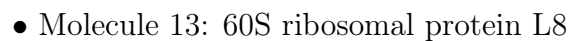
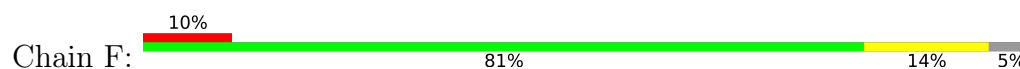
• Molecule 8: 60S ribosomal protein L3-A



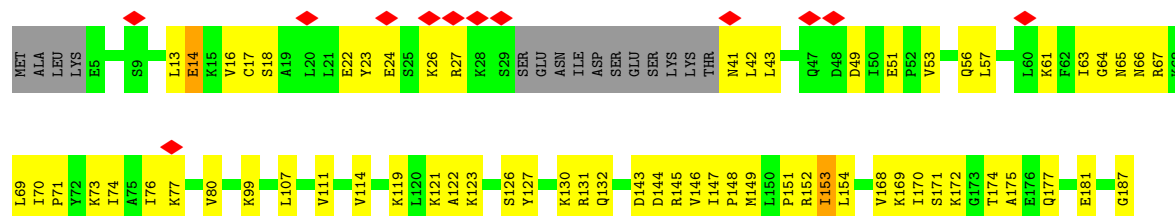
• Molecule 9: 60S ribosomal protein L4-B

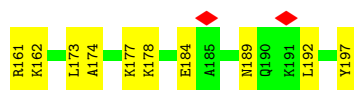


- Chain D: 

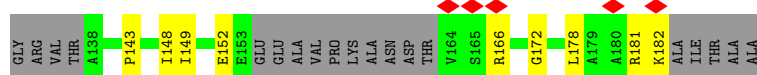
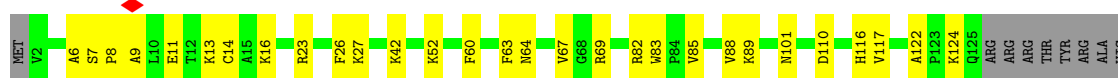




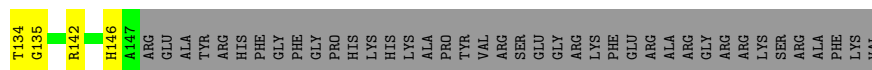




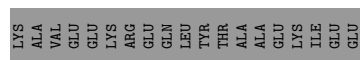
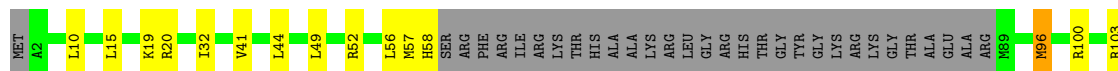
- Molecule 22: 60S ribosomal protein L17-A



- Molecule 23: 60S ribosomal protein L18-A



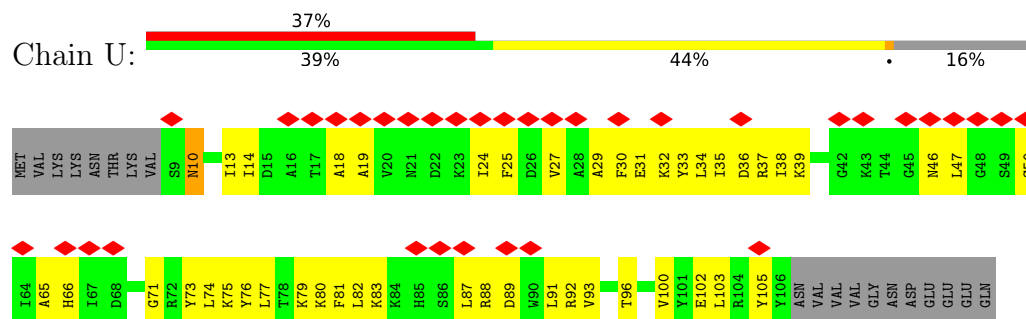
- Molecule 24: 60S ribosomal protein L19-A



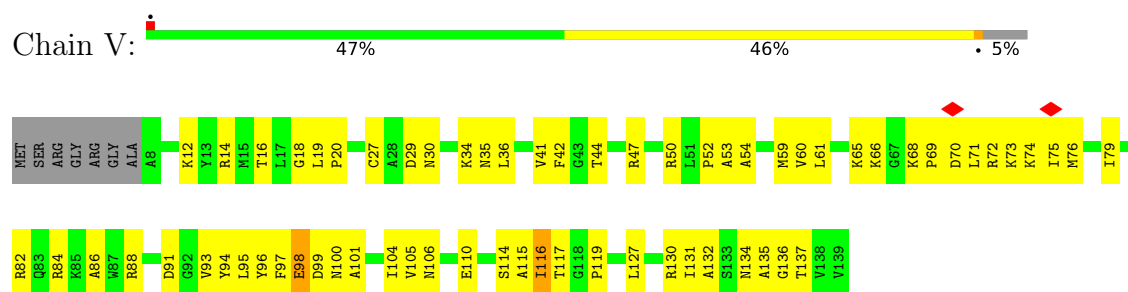
- Molecule 25: 60S ribosomal protein L20-A



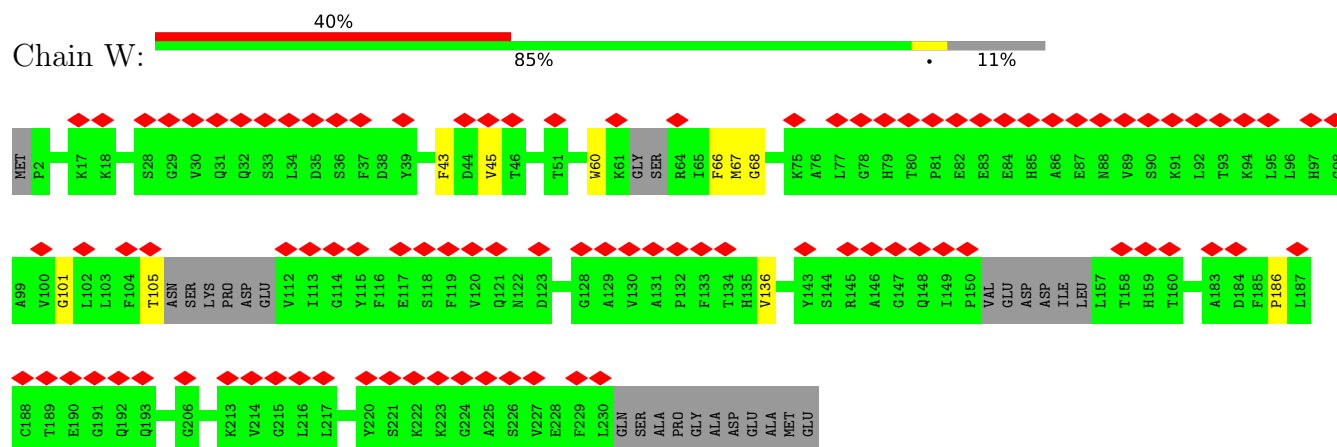
- Molecule 26: 60S ribosomal protein L22



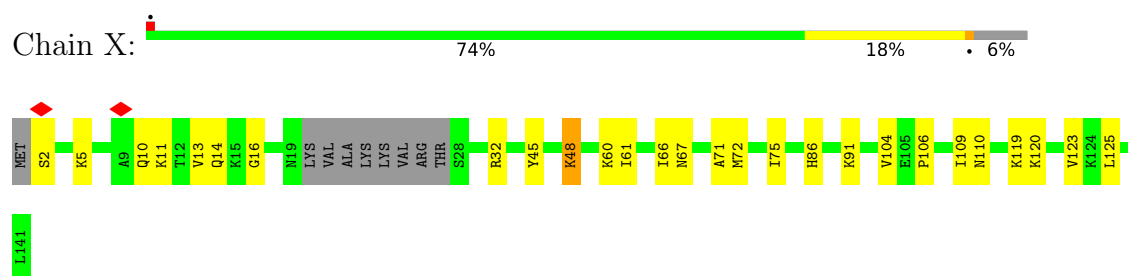
- Molecule 27: 60S ribosomal protein L23-A



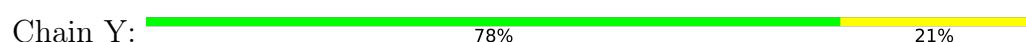
- Molecule 28: Ribosome assembly factor mrt4



- Molecule 29: 60S ribosomal protein L25-A



- Molecule 30: 60S ribosomal protein L26

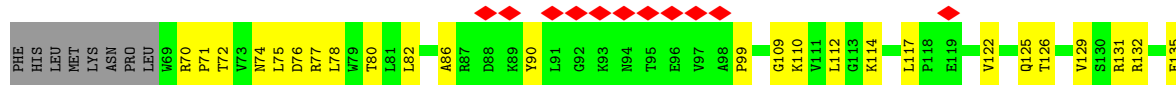
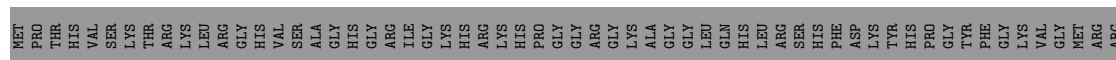
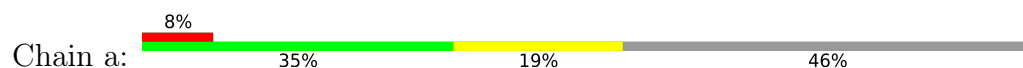




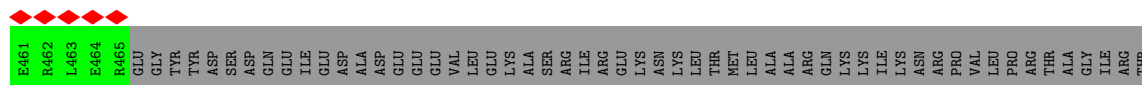
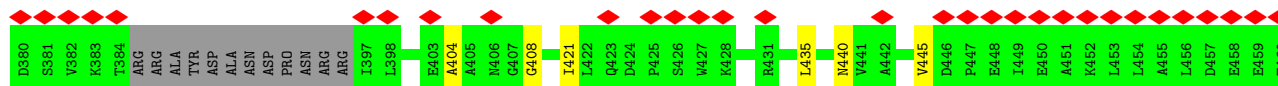
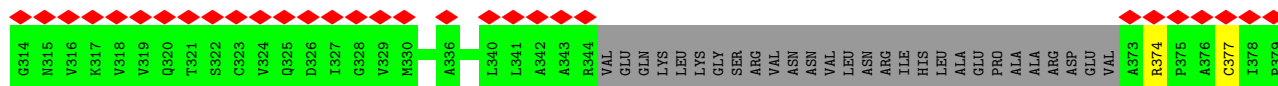
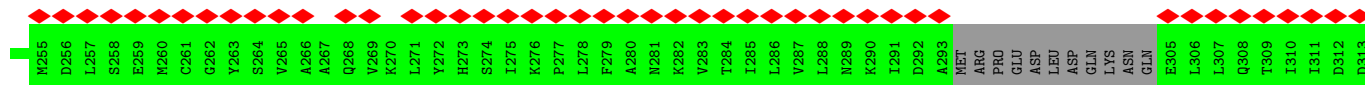
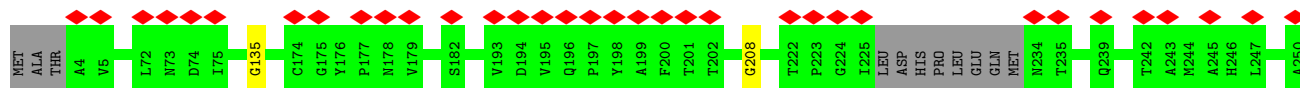
- Molecule 31: 60S ribosomal protein L27-A



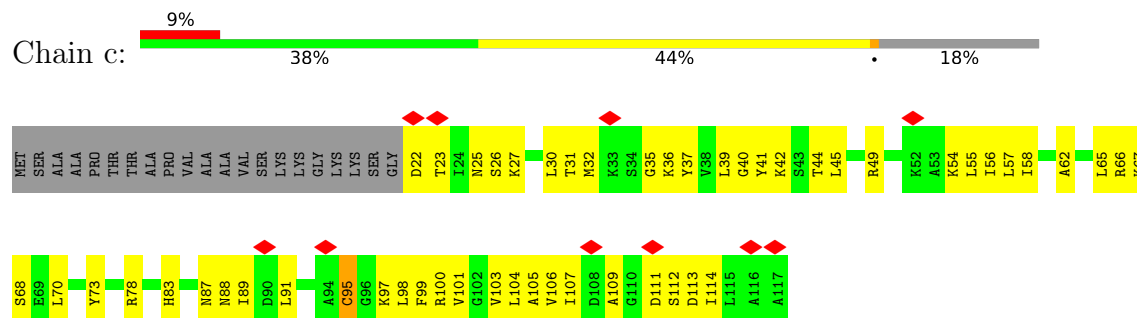
- Molecule 32: 60S ribosomal protein L28-A



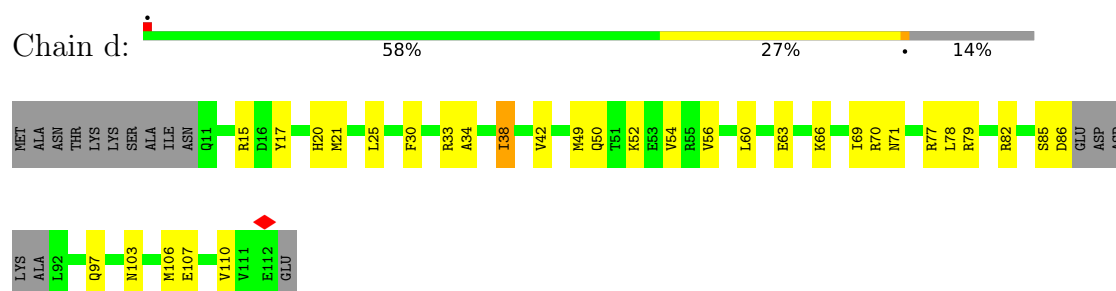
- Molecule 33: Probable nucleolar GTP-binding protein 1



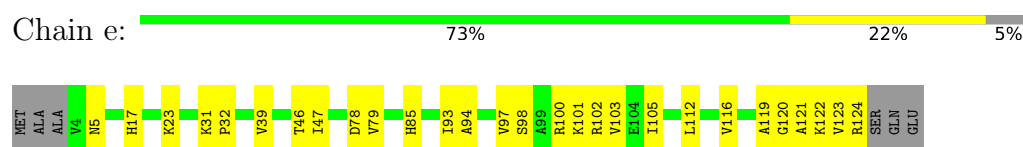
- Molecule 34: 60S ribosomal protein L30-2



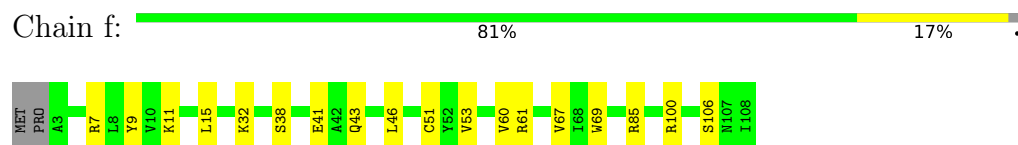
- Molecule 35: 60S ribosomal protein L31



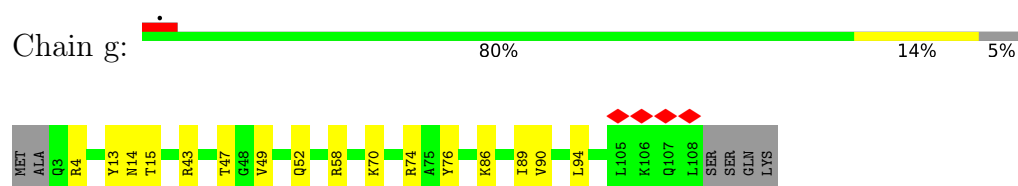
- Molecule 36: 60S ribosomal protein L32-A



- Molecule 37: 60S ribosomal protein L33-B



- Molecule 38: 60S ribosomal protein L34-A



- Molecule 39: 60S ribosomal protein L35

Chain h: 



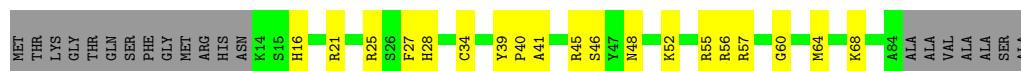
- Molecule 40: 60S ribosomal protein L36-B

Chain i: 



- Molecule 41: 60S ribosomal protein L37-B

Chain j: 



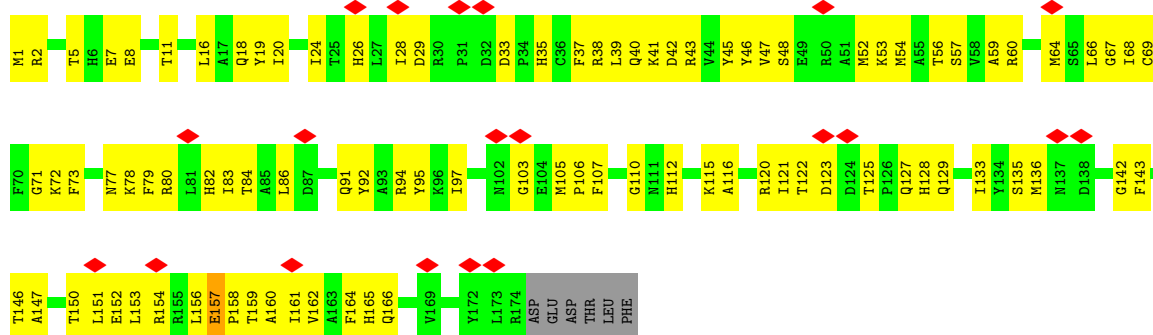
- Molecule 42: 60S ribosomal protein L38-1

Chain k: 



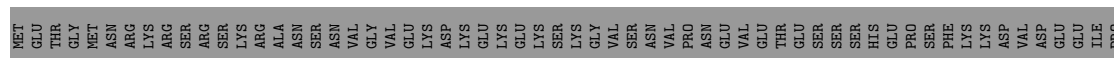
- Molecule 43: 60S ribosome subunit biogenesis protein nip7

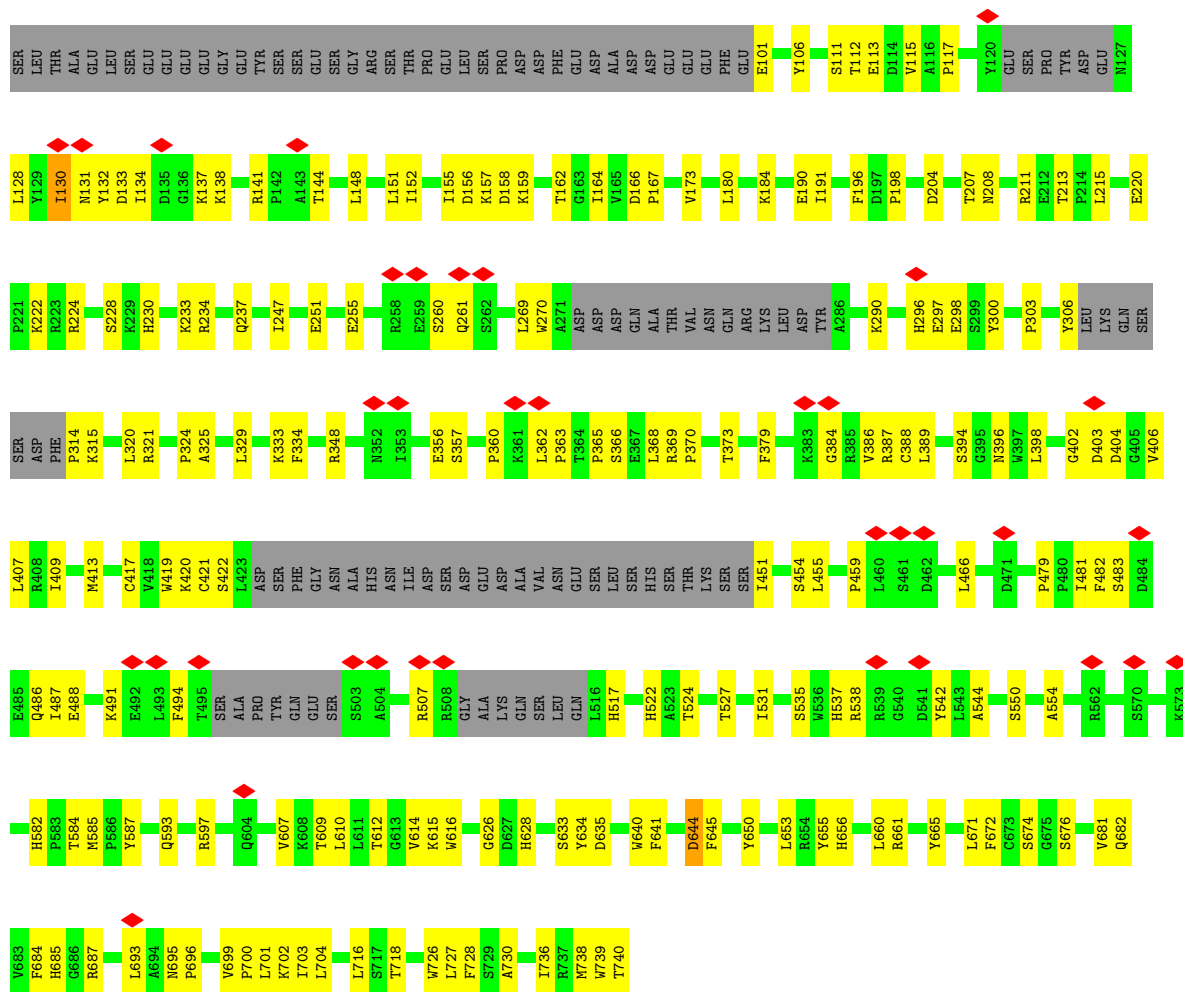
Chain l: 



- Molecule 44: Ribosome biogenesis protein erbl

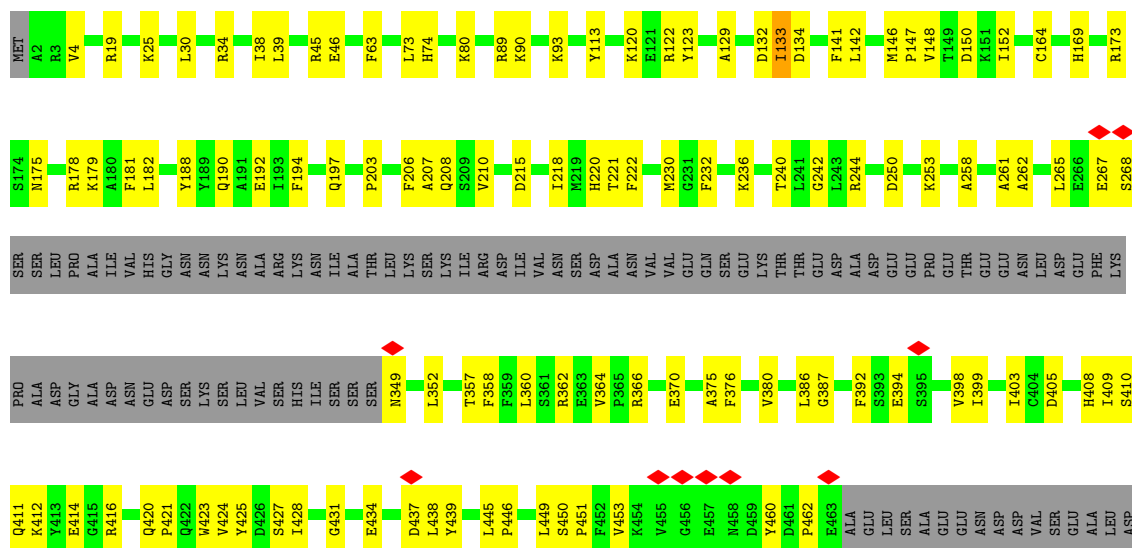
Chain m: 

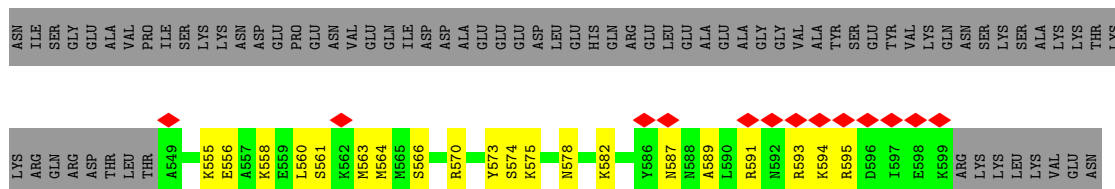




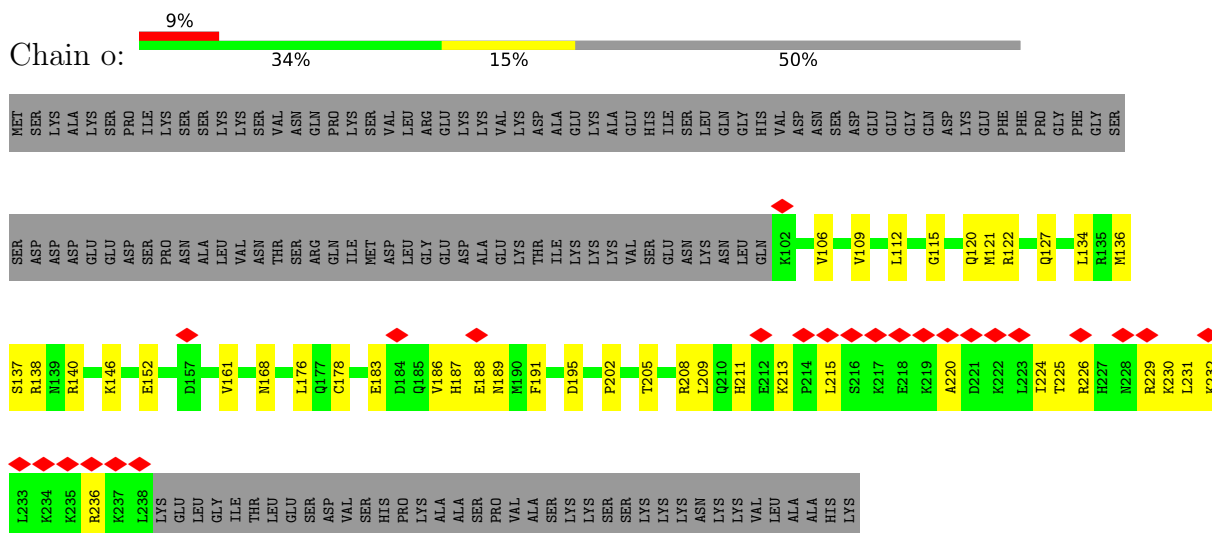
• Molecule 45: Pescadillo homolog

Chain n: 49% 22% 29%

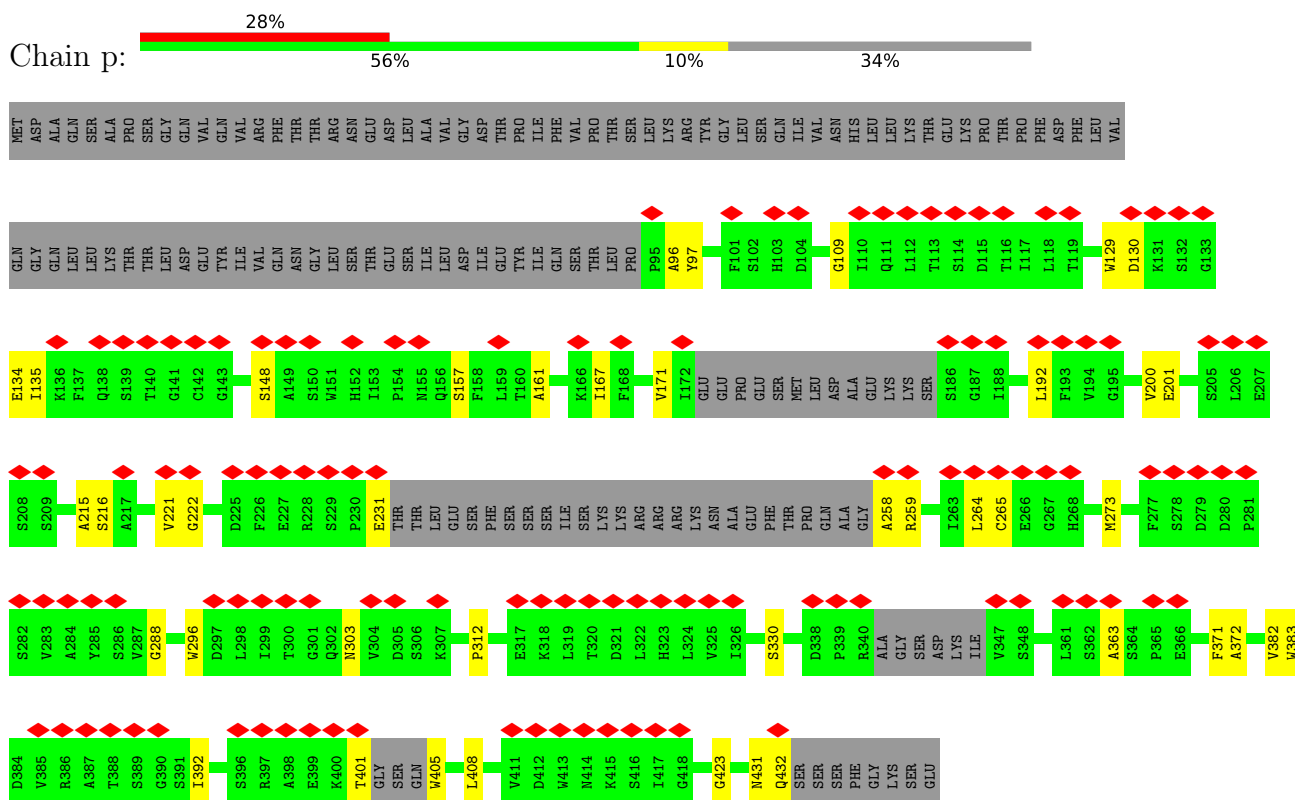




• Molecule 46: Uncharacterized RNA-binding protein C1827.05c

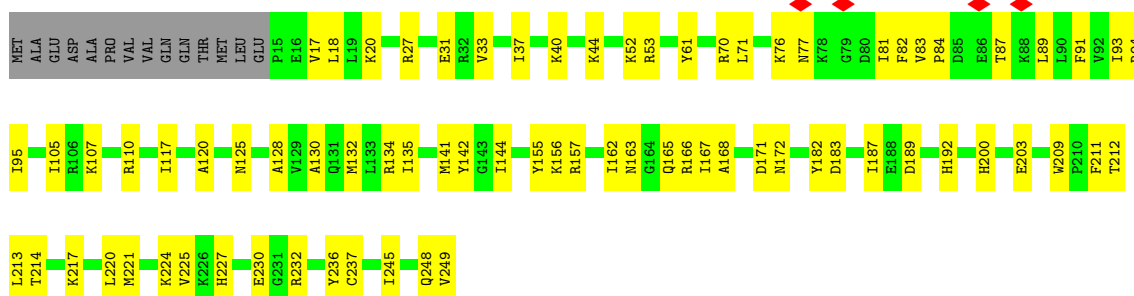


• Molecule 47: Ribosome biogenesis protein ytm1

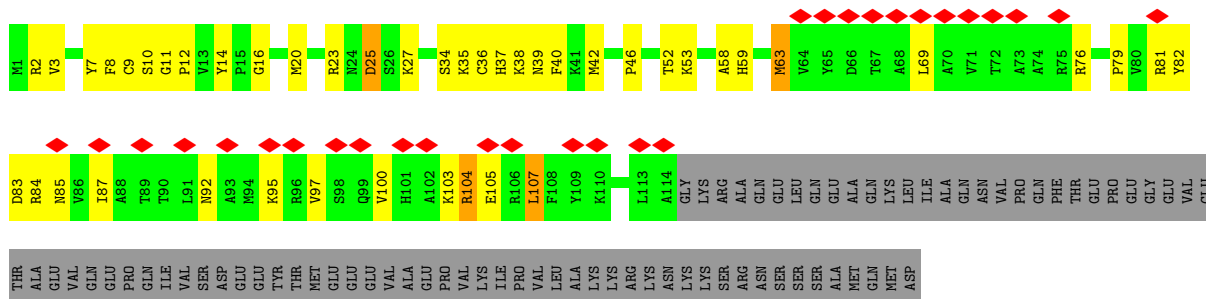
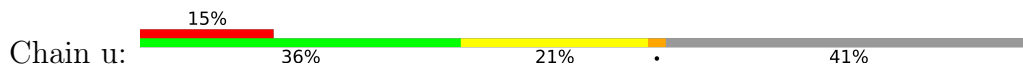


• Molecule 48: 25S rRNA (cytosine-C(5))-methyltransferase nop2

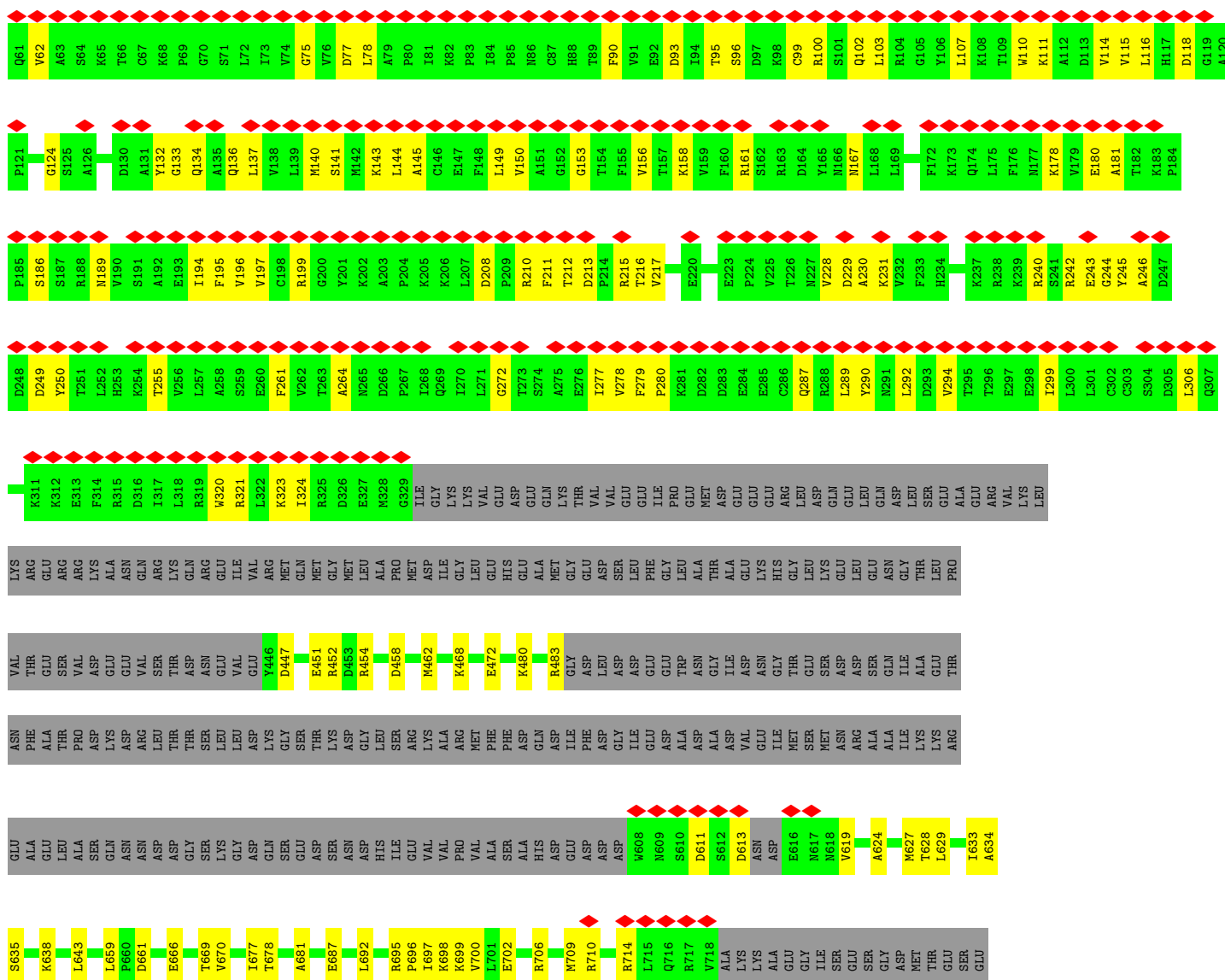
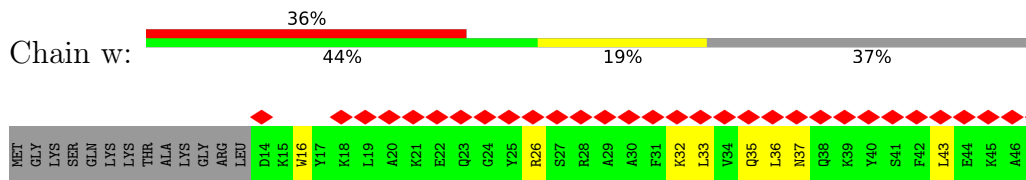
- Molecule 51: 60S ribosomal protein L7-A



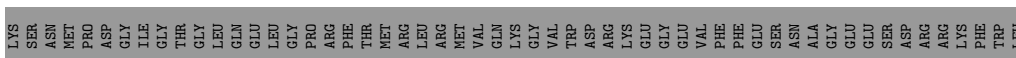
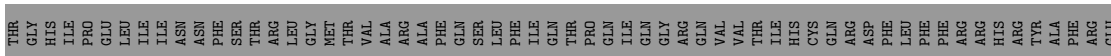
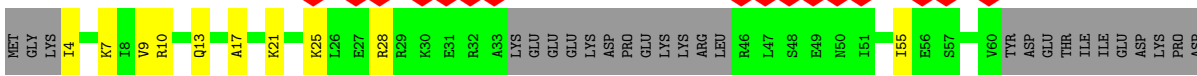
- Molecule 52: Ribosome biogenesis protein rlp24



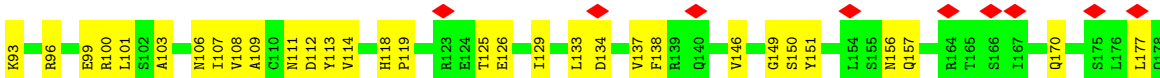
- Molecule 53: Nucleolar protein 16



- Molecule 55: Brix domain-containing protein C4F8.04



- Molecule 56: Eukaryotic translation initiation factor 6



- Molecule 57: UPF0642 protein C32H8.05



- Molecule 58: 60S ribosomal protein L21-A



[illegible]

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	172500	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	0.806	Depositor
Minimum map value	-0.343	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.011	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	7	0.05	0/1213	0.17	0/1686
2	1	0.16	0/53422	0.26	0/83211
3	2	0.22	0/3563	0.27	0/5543
4	3	0.15	0/1363	0.37	0/1832
5	6	0.12	0/1916	0.26	0/2973
6	8	0.19	0/298	0.52	0/399
7	A	0.14	0/1722	0.36	0/2325
8	B	0.14	0/2740	0.34	0/3680
9	C	0.18	0/2848	0.34	0/3842
10	D	0.13	0/3458	0.28	0/4662
11	E	0.17	0/1308	0.40	0/1763
12	F	0.15	0/1963	0.30	0/2632
13	G	0.21	0/1637	0.34	0/2203
14	H	0.15	0/1470	0.38	0/1982
15	I	0.11	0/3782	0.30	0/5087
16	J	0.17	0/972	0.40	0/1304
17	K	0.16	0/2008	0.40	0/2713
18	L	0.20	0/960	0.36	0/1288
19	M	0.15	0/1024	0.36	0/1375
20	N	0.22	0/1436	0.32	0/1920
21	O	0.15	0/1588	0.30	0/2128
22	P	0.13	0/1269	0.28	0/1699
23	Q	0.16	0/1043	0.32	0/1401
24	R	0.19	0/963	0.50	0/1284
25	S	0.14	0/1444	0.33	0/1939
26	U	0.17	0/805	0.48	0/1080
27	V	0.16	0/1007	0.42	0/1357
28	W	0.09	0/1053	0.33	0/1457
29	X	0.18	0/1060	0.35	0/1422
30	Y	0.17	0/1008	0.36	0/1341
31	Z	0.14	0/1095	0.34	0/1467
32	a	0.13	0/645	0.27	0/874

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	b	0.07	0/1994	0.23	0/2774
34	c	0.19	0/729	0.50	0/980
35	d	0.14	0/824	0.33	0/1106
36	e	0.16	0/985	0.29	0/1313
37	f	0.16	0/859	0.26	0/1152
38	g	0.13	0/873	0.33	0/1170
39	h	0.19	0/1008	0.32	0/1340
40	i	0.17	0/703	0.27	0/931
41	j	0.19	0/575	0.32	0/761
42	k	0.17	0/570	0.43	0/762
43	l	0.22	0/1452	0.58	0/1961
44	m	0.17	1/4655 (0.0%)	0.34	0/6327
45	n	0.17	0/3607	0.35	0/4856
46	o	0.17	0/1163	0.35	0/1552
47	p	0.07	0/1426	0.22	0/1977
48	q	0.07	0/1682	0.20	0/2339
49	r	0.13	0/1373	0.38	0/1827
50	s	0.10	0/268	0.29	0/346
51	t	0.15	0/1979	0.32	0/2645
52	u	0.14	0/966	0.35	0/1292
53	v	0.18	0/1319	0.33	0/1769
54	w	0.12	0/4139	0.30	0/5567
55	x	0.08	0/384	0.25	0/505
56	y	0.14	0/1720	0.34	0/2345
57	z	0.21	0/297	0.40	0/388
58	T	0.16	0/276	0.36	0/375
All	All	0.16	1/137909 (0.0%)	0.31	0/198229

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
44	m	156	ASP	CA-CB	5.40	1.62	1.53

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	7	1218	0	528	1	0
2	1	47746	0	24028	588	0
3	2	3189	0	1613	39	0
4	3	1336	0	1375	37	0
5	6	1717	0	866	20	0
6	8	291	0	309	28	0
7	A	1686	0	1704	78	0
8	B	2687	0	2768	83	0
9	C	2795	0	2918	60	0
10	D	3396	0	3509	67	0
11	E	1283	0	1365	36	0
12	F	1925	0	2014	22	0
13	G	1615	0	1739	29	0
14	H	1451	0	1511	44	0
15	I	3725	0	3886	102	0
16	J	959	0	977	58	0
17	K	1973	0	2055	86	0
18	L	942	0	1012	17	0
19	M	1007	0	1072	26	0
20	N	1406	0	1441	27	0
21	O	1557	0	1652	37	0
22	P	1248	0	1290	28	0
23	Q	1032	0	1129	22	0
24	R	949	0	1017	28	0
25	S	1408	0	1462	45	0
26	U	791	0	825	56	0
27	V	991	0	1039	65	0
28	W	1057	0	487	8	0
29	X	1044	0	1112	22	0
30	Y	998	0	1090	16	0
31	Z	1072	0	1145	50	0
32	a	634	0	666	22	0
33	b	1999	0	894	10	0
34	c	720	0	758	53	0
35	d	810	0	852	24	0
36	e	971	0	1040	23	0
37	f	839	0	866	15	0
38	g	861	0	930	16	0
39	h	999	0	1092	18	0
40	i	696	0	763	10	0
41	j	563	0	578	16	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
42	k	564	0	611	32	0
43	l	1418	0	1423	95	0
44	m	4536	0	4506	163	0
45	n	3526	0	3557	120	0
46	o	1138	0	1196	41	0
47	p	1431	0	633	21	0
48	q	1684	0	765	2	0
49	r	1357	0	1429	63	0
50	s	269	0	318	17	0
51	t	1948	0	2066	53	0
52	u	944	0	983	42	0
53	v	1299	0	1347	30	0
54	w	4067	0	4147	133	0
55	x	383	0	417	13	0
56	y	1697	0	1679	65	0
57	z	292	0	317	22	0
58	T	269	0	258	14	0
59	j	1	0	0	0	0
All	All	130409	0	103029	2446	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 11.

The worst 5 of 2446 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)
26:U:91:LEU:HD21	26:U:103:LEU:HB2	1.40	1.03
55:x:7:LYS:HA	55:x:10:ARG:HE	1.32	0.94
8:B:331:PRO:HD2	8:B:334:ARG:HE	1.31	0.93
2:1:873:A:H4'	24:R:126:GLU:HA	1.53	0.89
2:1:3336:G:H1	2:1:3351:U:H3	1.21	0.88

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	
1	7	235/707 (33%)	234 (100%)	1 (0%)	0	100	100
4	3	158/302 (52%)	150 (95%)	8 (5%)	0	100	100
6	8	33/51 (65%)	31 (94%)	2 (6%)	0	100	100
7	A	209/295 (71%)	197 (94%)	12 (6%)	0	100	100
8	B	335/388 (86%)	323 (96%)	12 (4%)	0	100	100
9	C	357/363 (98%)	334 (94%)	23 (6%)	0	100	100
10	D	421/578 (73%)	412 (98%)	9 (2%)	0	100	100
11	E	163/195 (84%)	150 (92%)	13 (8%)	0	100	100
12	F	235/250 (94%)	227 (97%)	8 (3%)	0	100	100
13	G	203/259 (78%)	193 (95%)	8 (4%)	2 (1%)	12	38
14	H	181/190 (95%)	172 (95%)	8 (4%)	1 (1%)	21	51
15	I	447/747 (60%)	422 (94%)	23 (5%)	2 (0%)	30	60
16	J	116/333 (35%)	111 (96%)	5 (4%)	0	100	100
17	K	247/373 (66%)	227 (92%)	18 (7%)	2 (1%)	16	44
18	L	114/208 (55%)	110 (96%)	4 (4%)	0	100	100
19	M	123/134 (92%)	117 (95%)	6 (5%)	0	100	100
20	N	160/201 (80%)	158 (99%)	2 (1%)	0	100	100
21	O	194/197 (98%)	190 (98%)	4 (2%)	0	100	100
22	P	153/187 (82%)	147 (96%)	6 (4%)	0	100	100
23	Q	131/187 (70%)	127 (97%)	4 (3%)	0	100	100
24	R	110/193 (57%)	109 (99%)	1 (1%)	0	100	100
25	S	164/176 (93%)	156 (95%)	8 (5%)	0	100	100
26	U	96/117 (82%)	89 (93%)	7 (7%)	0	100	100
27	V	130/139 (94%)	126 (97%)	4 (3%)	0	100	100
28	W	207/241 (86%)	194 (94%)	13 (6%)	0	100	100
29	X	128/141 (91%)	125 (98%)	3 (2%)	0	100	100
30	Y	123/126 (98%)	119 (97%)	4 (3%)	0	100	100
31	Z	132/136 (97%)	128 (97%)	4 (3%)	0	100	100
32	a	78/148 (53%)	77 (99%)	1 (1%)	0	100	100
33	b	393/642 (61%)	382 (97%)	11 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
34	c	94/117 (80%)	93 (99%)	1 (1%)	0	100	100
35	d	93/113 (82%)	91 (98%)	2 (2%)	0	100	100
36	e	119/127 (94%)	117 (98%)	2 (2%)	0	100	100
37	f	104/108 (96%)	96 (92%)	8 (8%)	0	100	100
38	g	104/112 (93%)	101 (97%)	3 (3%)	0	100	100
39	h	119/122 (98%)	117 (98%)	2 (2%)	0	100	100
40	i	83/99 (84%)	83 (100%)	0	0	100	100
41	j	69/91 (76%)	67 (97%)	2 (3%)	0	100	100
42	k	68/74 (92%)	67 (98%)	1 (2%)	0	100	100
43	l	172/180 (96%)	163 (95%)	9 (5%)	0	100	100
44	m	558/740 (75%)	527 (94%)	30 (5%)	1 (0%)	43	72
45	n	427/607 (70%)	404 (95%)	23 (5%)	0	100	100
46	o	135/276 (49%)	130 (96%)	5 (4%)	0	100	100
47	p	280/440 (64%)	271 (97%)	9 (3%)	0	100	100
48	q	337/608 (55%)	332 (98%)	5 (2%)	0	100	100
49	r	158/260 (61%)	158 (100%)	0	0	100	100
50	s	30/470 (6%)	29 (97%)	1 (3%)	0	100	100
51	t	233/249 (94%)	220 (94%)	13 (6%)	0	100	100
52	u	112/192 (58%)	105 (94%)	7 (6%)	0	100	100
53	v	157/209 (75%)	150 (96%)	6 (4%)	1 (1%)	21	51
54	w	495/802 (62%)	476 (96%)	19 (4%)	0	100	100
55	x	41/306 (13%)	41 (100%)	0	0	100	100
56	y	223/244 (91%)	215 (96%)	8 (4%)	0	100	100
57	z	33/117 (28%)	31 (94%)	2 (6%)	0	100	100
58	T	30/160 (19%)	30 (100%)	0	0	100	100
All	All	10050/15027 (67%)	9651 (96%)	390 (4%)	9 (0%)	49	77

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
15	I	698	ILE
17	K	153	ILE
13	G	227[A]	ASP

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Mol	Chain	Res	Type
13	G	227[B]	ASP
15	I	624	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	3	141/271 (52%)	133 (94%)	8 (6%)	18	49
6	8	31/47 (66%)	29 (94%)	2 (6%)	15	43
7	A	184/266 (69%)	183 (100%)	1 (0%)	81	93
8	B	285/326 (87%)	284 (100%)	1 (0%)	84	94
9	C	296/297 (100%)	294 (99%)	2 (1%)	76	91
10	D	371/505 (74%)	370 (100%)	1 (0%)	86	95
11	E	135/155 (87%)	132 (98%)	3 (2%)	45	78
12	F	199/210 (95%)	198 (100%)	1 (0%)	81	93
13	G	168/212 (79%)	166 (99%)	2 (1%)	63	87
14	H	164/170 (96%)	161 (98%)	3 (2%)	51	82
15	I	418/685 (61%)	417 (100%)	1 (0%)	87	96
16	J	104/288 (36%)	101 (97%)	3 (3%)	37	73
17	K	224/333 (67%)	222 (99%)	2 (1%)	70	89
18	L	97/167 (58%)	96 (99%)	1 (1%)	68	88
19	M	108/113 (96%)	107 (99%)	1 (1%)	70	89
20	N	146/176 (83%)	146 (100%)	0	100	100
21	O	161/162 (99%)	161 (100%)	0	100	100
22	P	128/149 (86%)	128 (100%)	0	100	100
23	Q	114/159 (72%)	114 (100%)	0	100	100
24	R	102/162 (63%)	101 (99%)	1 (1%)	68	88
25	S	150/154 (97%)	147 (98%)	3 (2%)	48	80
26	U	85/103 (82%)	84 (99%)	1 (1%)	63	87

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
27	V	103/107 (96%)	101 (98%)	2 (2%)	50	81
29	X	114/122 (93%)	113 (99%)	1 (1%)	70	89
30	Y	110/111 (99%)	108 (98%)	2 (2%)	51	82
31	Z	113/115 (98%)	112 (99%)	1 (1%)	70	89
32	a	68/122 (56%)	67 (98%)	1 (2%)	57	84
34	c	77/91 (85%)	76 (99%)	1 (1%)	61	86
35	d	89/102 (87%)	87 (98%)	2 (2%)	45	78
36	e	103/107 (96%)	102 (99%)	1 (1%)	68	88
37	f	89/91 (98%)	89 (100%)	0	100	100
38	g	92/97 (95%)	92 (100%)	0	100	100
39	h	106/107 (99%)	105 (99%)	1 (1%)	70	89
40	i	74/84 (88%)	74 (100%)	0	100	100
41	j	58/71 (82%)	58 (100%)	0	100	100
42	k	63/66 (96%)	61 (97%)	2 (3%)	34	70
43	l	152/158 (96%)	149 (98%)	3 (2%)	48	80
44	m	506/659 (77%)	501 (99%)	5 (1%)	68	88
45	n	379/532 (71%)	376 (99%)	3 (1%)	73	90
46	o	123/246 (50%)	122 (99%)	1 (1%)	73	90
49	r	146/224 (65%)	144 (99%)	2 (1%)	59	85
50	s	29/409 (7%)	29 (100%)	0	100	100
51	t	211/223 (95%)	211 (100%)	0	100	100
52	u	99/168 (59%)	95 (96%)	4 (4%)	28	63
53	v	138/181 (76%)	138 (100%)	0	100	100
54	w	444/697 (64%)	442 (100%)	2 (0%)	81	93
55	x	42/273 (15%)	42 (100%)	0	100	100
56	y	189/206 (92%)	187 (99%)	2 (1%)	65	87
57	z	31/107 (29%)	28 (90%)	3 (10%)	8	25
58	T	31/139 (22%)	29 (94%)	2 (6%)	15	43
All	All	7590/10725 (71%)	7512 (99%)	78 (1%)	65	88

5 of 78 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
44	m	190	GLU
56	y	50	HIS
45	n	133	ILE
52	u	25	ASP
57	z	108	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 69 such sidechains are listed below:

Mol	Chain	Res	Type
49	r	182	ASN
51	t	200	HIS
56	y	157	GLN
19	M	125	ASN
17	K	256	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	1	2191/3497 (62%)	555 (25%)	21 (0%)
3	2	147/165 (89%)	27 (18%)	1 (0%)
5	6	77/300 (25%)	31 (40%)	0
All	All	2415/3962 (60%)	613 (25%)	22 (0%)

5 of 613 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	1	14	U
2	1	34	A
2	1	36	C
2	1	49	A
2	1	57	A

5 of 22 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	1	1916	G
2	1	3081	U
2	1	3070	U
2	1	3217	U
2	1	1159	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 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](#)

There are no chain breaks in this entry.

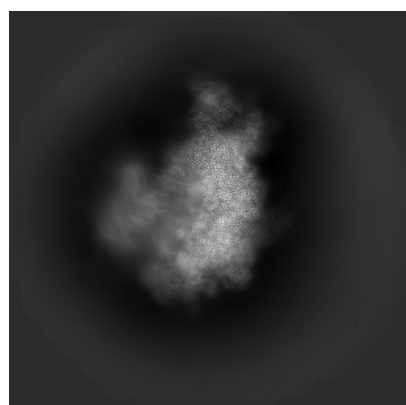
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-24411. These allow visual inspection of the internal detail of the map and identification of artifacts.

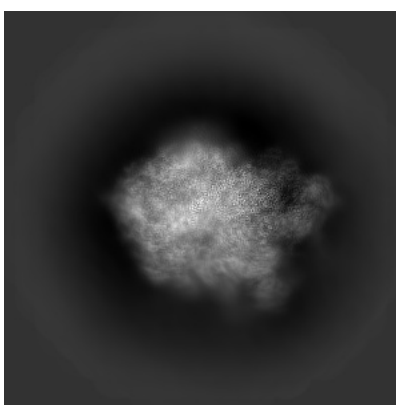
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

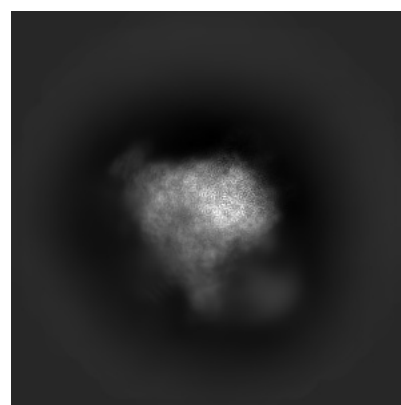
6.1.1 Primary map



X



Y

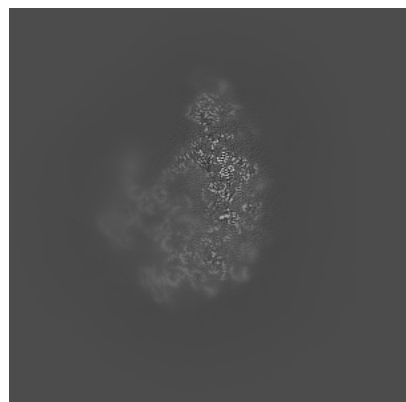


Z

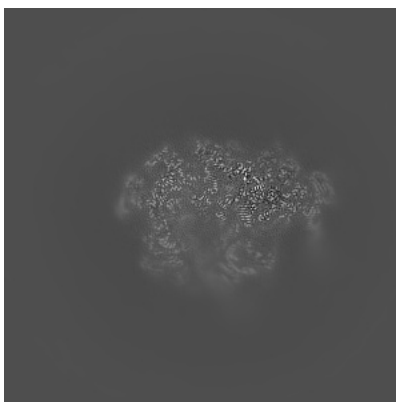
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

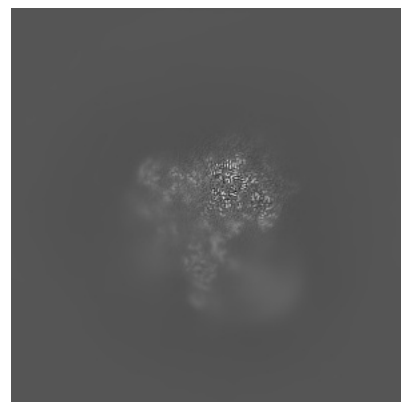
6.2.1 Primary map



X Index: 256



Y Index: 256

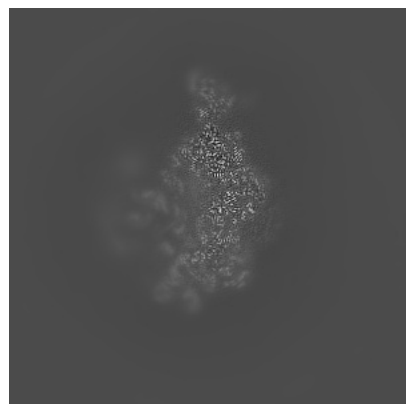


Z Index: 256

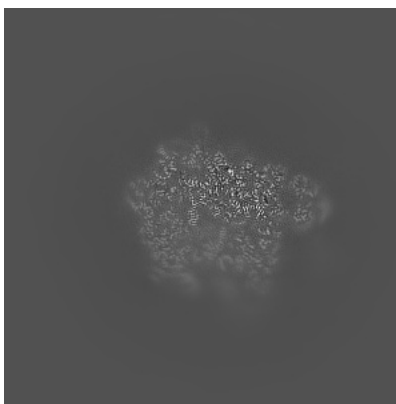
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

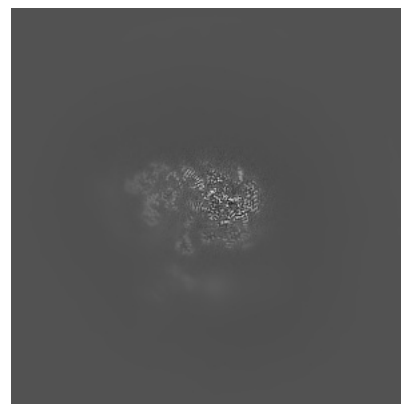
6.3.1 Primary map



X Index: 271



Y Index: 274

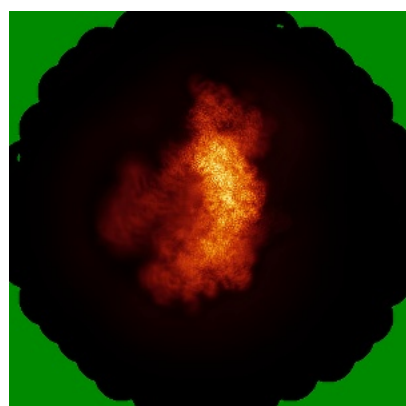


Z Index: 314

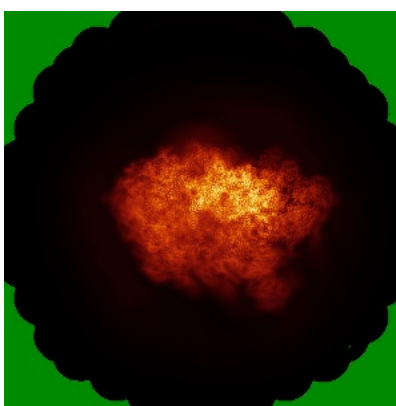
The images above show the largest variance slices of the map in three orthogonal directions.

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

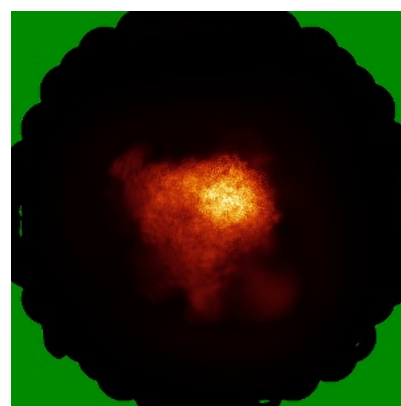
6.4.1 Primary map



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

This section was not generated.

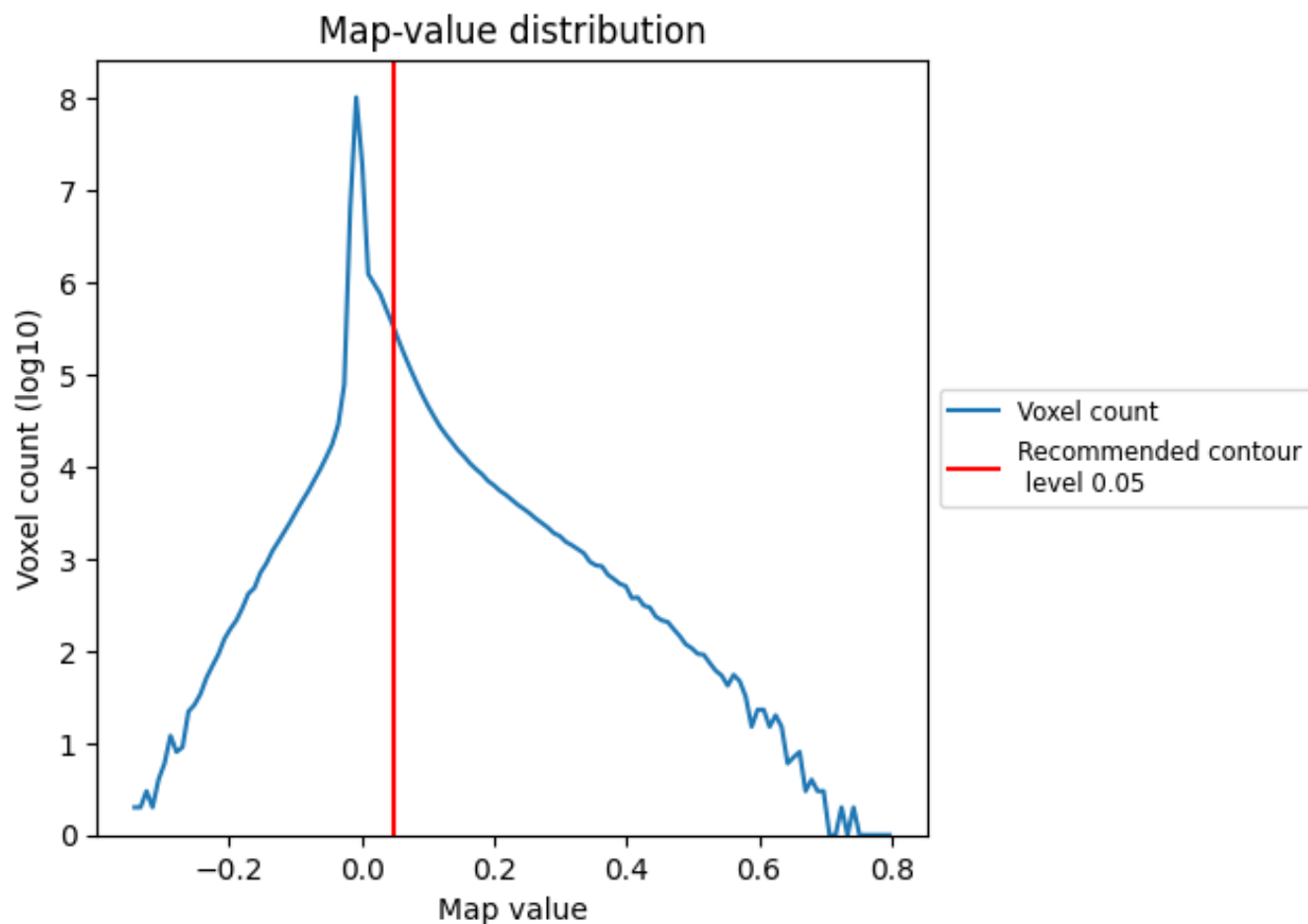
6.6 Mask visualisation

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

7 Map analysis [i](#)

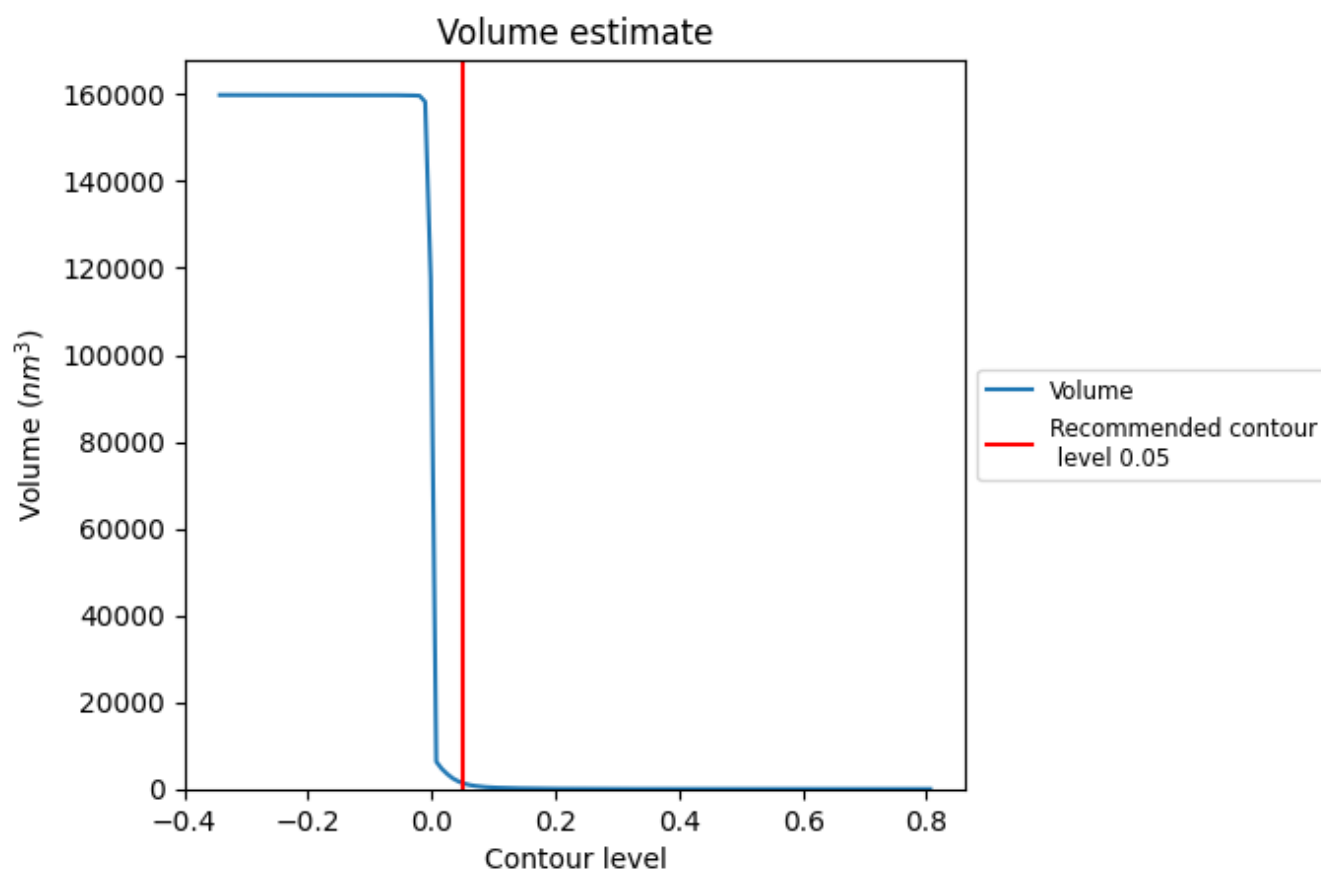
This section contains the results of statistical analysis of the map.

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.

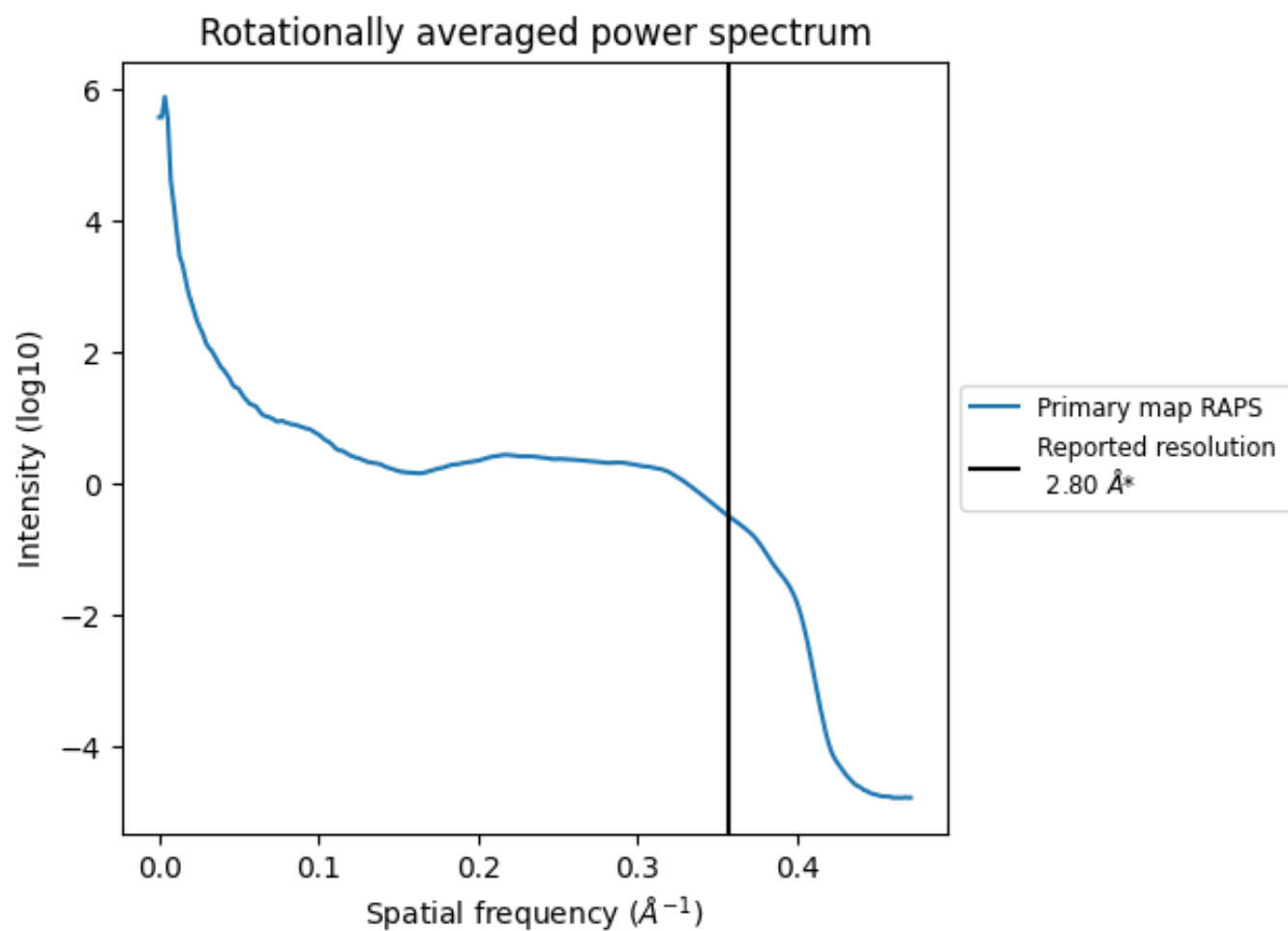
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1366 nm^3 ; this corresponds to an approximate mass of 1234 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 0.357 Å⁻¹

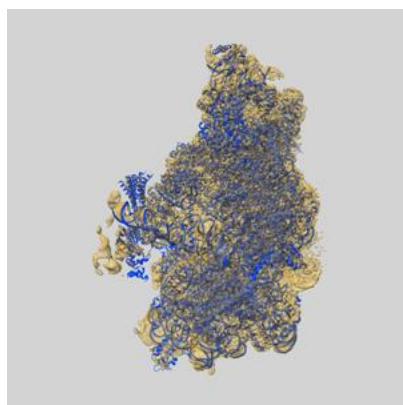
8 Fourier-Shell correlation

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

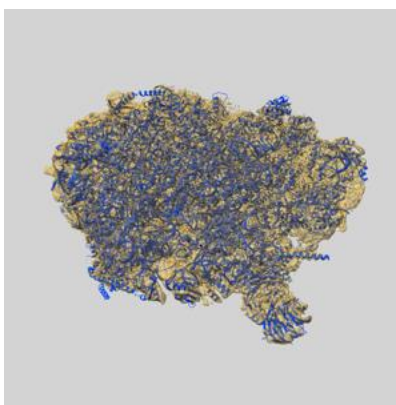
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-24411 and PDB model 8ESQ. Per-residue inclusion information can be found in section [3](#) on page [15](#).

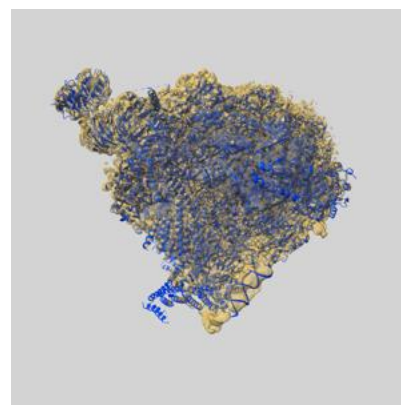
9.1 Map-model overlay [i](#)



X



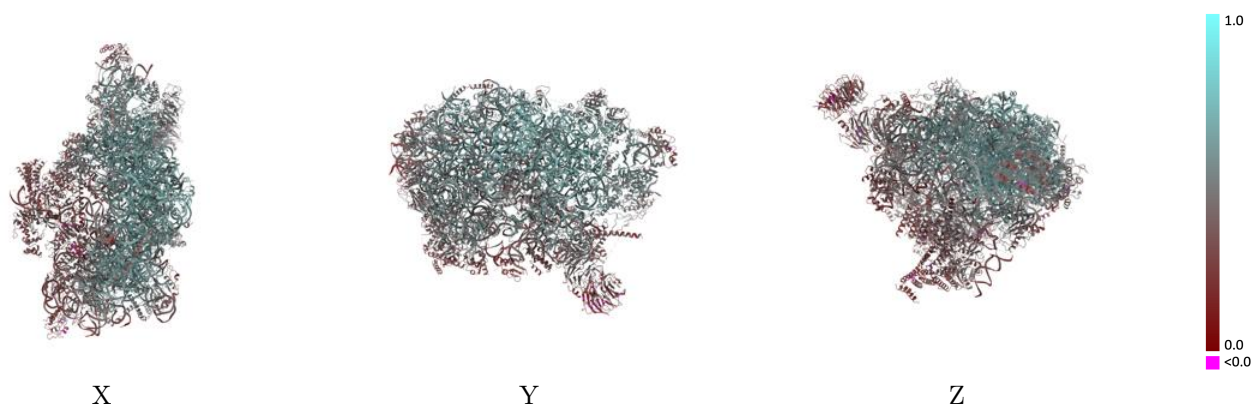
Y



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](#)

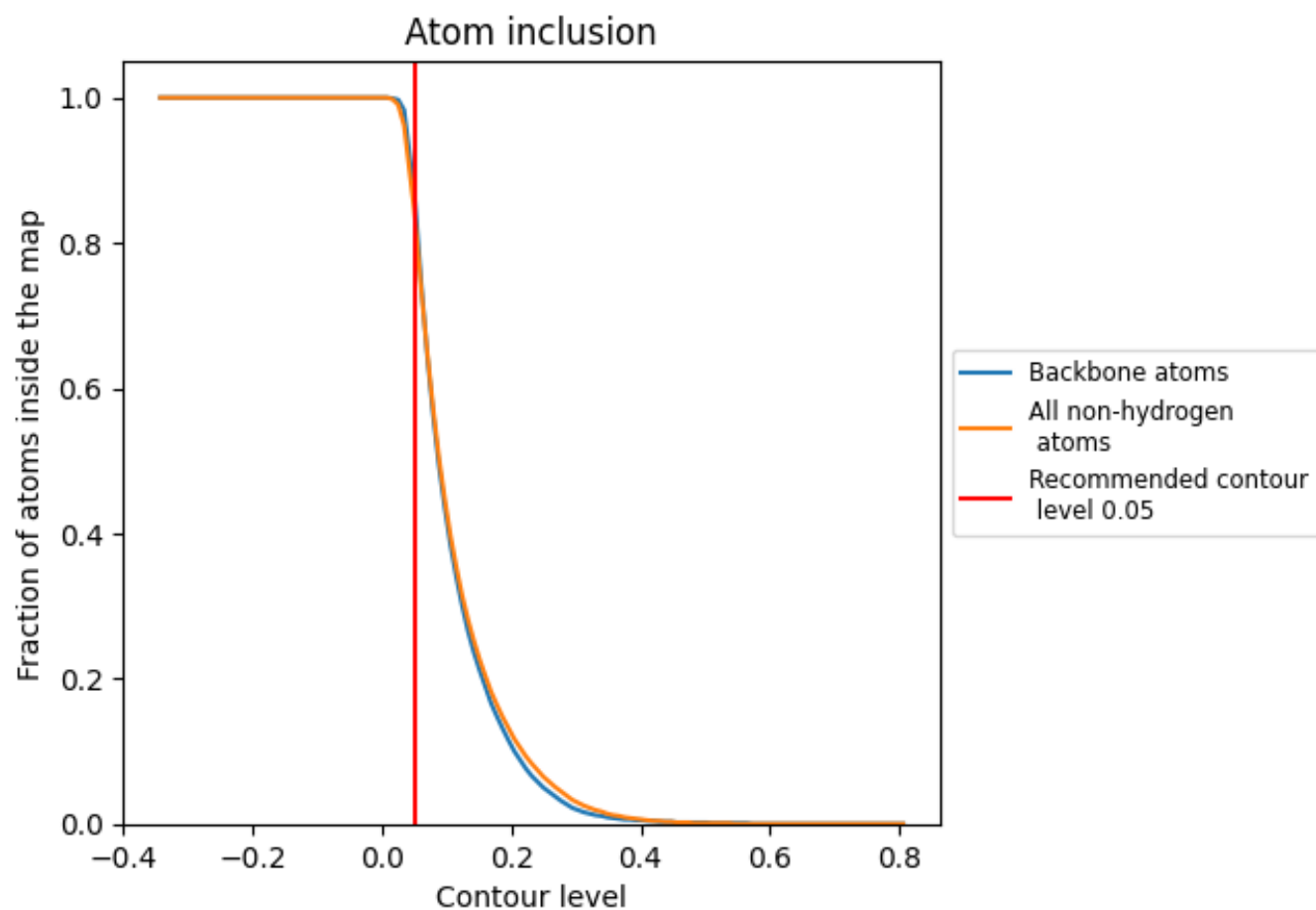


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 87% of all backbone atoms, 84% 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	 0.8450	 0.4890
1	 0.9670	 0.5130
2	 0.9890	 0.6270
3	 0.6620	 0.5250
6	 0.9450	 0.5020
7	 0.2230	 0.2600
8	 0.8680	 0.4260
A	 0.8410	 0.4450
B	 0.9270	 0.5150
C	 0.9720	 0.6220
D	 0.6480	 0.5090
E	 0.8220	 0.4660
F	 0.8430	 0.5430
G	 0.9500	 0.6220
H	 0.8770	 0.4450
I	 0.5250	 0.3430
J	 0.5650	 0.3300
K	 0.7440	 0.4620
L	 0.9790	 0.6500
M	 0.9590	 0.4900
N	 0.9960	 0.6690
O	 0.9560	 0.5490
P	 0.9130	 0.5590
Q	 0.9420	 0.5830
R	 0.8460	 0.4080
S	 0.8860	 0.4800
T	 0.5360	 0.2880
U	 0.4860	 0.2730
V	 0.8560	 0.4610
W	 0.4890	 0.3040
X	 0.9490	 0.5960
Y	 0.9620	 0.6190
Z	 0.8060	 0.4220
a	 0.7200	 0.5210
b	 0.5980	 0.3670



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Chain	Atom inclusion	Q-score
c	 0.7190	 0.3420
d	 0.9100	 0.5160
e	 0.9670	 0.6030
f	 0.9870	 0.6030
g	 0.9060	 0.5000
h	 0.9660	 0.6270
i	 0.9560	 0.6130
j	 0.9960	 0.6580
k	 0.7930	 0.4590
l	 0.6390	 0.3410
m	 0.7770	 0.4360
n	 0.8550	 0.5060
o	 0.7530	 0.5000
p	 0.5330	 0.2850
q	 0.4790	 0.3460
r	 0.7240	 0.3690
s	 0.6470	 0.3240
t	 0.8780	 0.5260
u	 0.6920	 0.3860
v	 0.9140	 0.5820
w	 0.3880	 0.3550
x	 0.5320	 0.4510
y	 0.7380	 0.3610
z	 0.6210	 0.3470